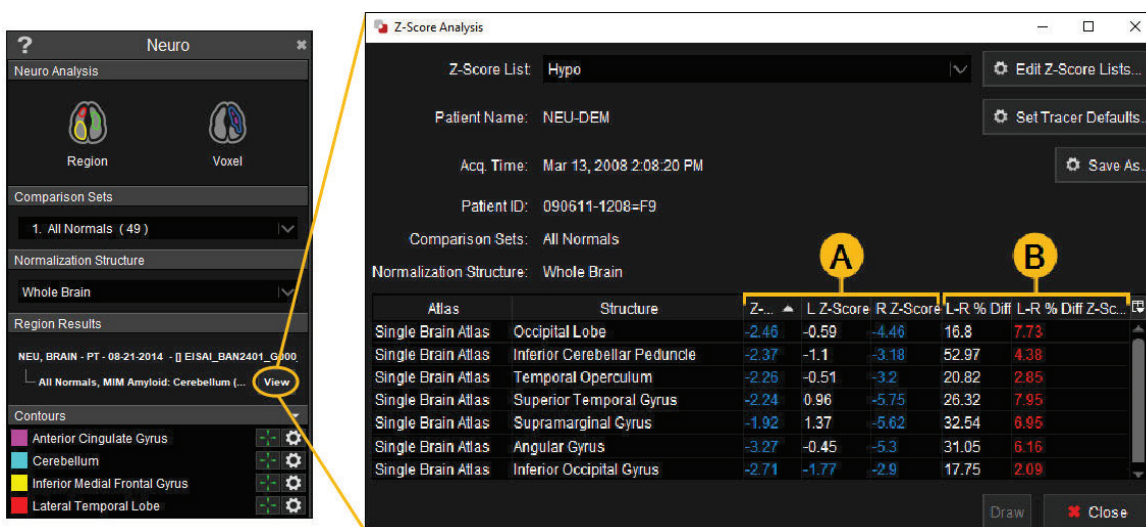


- **Cerebellum PET Normalization** displays the PET brain in the top row. The following rows contain a splash display of the z-score results fused to the PET brain and SSPs, normalized to the cerebellum.

For additional information on MIMneuro displays, see [View Color Scales and Stereotactic Surface Projections](#).

Review Z-Scores

The Z-Score Analysis window opens by default. You can also open it by clicking the **View** button in the Region Results section of the Neuro sidebar.



Z-Score Analysis

Z-Score List: **Hypo** [Edit Z-Score Lists...]

Patient Name: **NEU-DEM** [Set Tracer Defaults...]

Acq. Time: **Mar 13, 2008 2:08:20 PM** [Save As...]

Patient ID: **090611-1208=F9**

Comparison Sets: **All Normals**

Normalization Structure: **Whole Brain**

Atlas	Structure	Z-Score	L Z-Score	R Z-Score	L-R % Diff	L-R % Diff Z-Score
Single Brain Atlas	Occipital Lobe	-2.46	-0.59	-4.46	16.8	7.73
Single Brain Atlas	Inferior Cerebellar Peduncle	-2.37	-1.1	-3.18	52.97	4.38
Single Brain Atlas	Temporal Operculum	-2.26	-0.51	-3.2	20.82	2.85
Single Brain Atlas	Superior Temporal Gyrus	-2.24	0.96	-5.75	26.32	7.95
Single Brain Atlas	Supramarginal Gyrus	-1.92	1.37	-5.62	32.54	6.95
Single Brain Atlas	Angular Gyrus	-3.27	-0.45	-5.3	31.05	6.16
Single Brain Atlas	Inferior Occipital Gyrus	-2.71	-1.77	-2.9	17.75	2.09

[Draw] [Close]

- View the z-score for each structure. The z-score is the number of standard deviations the structure is away from the mean of the normal database for that structure (e.g., 43 normals for FDG).
 - *Areas of reduced uptake* are statistically significant when they are -1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in **blue**.
 - *Areas of increased uptake* are statistically significant when they are +1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in **red**.
- View the left/right percent difference z-score. The left/right percent difference is calculated first and then compared to the normal database to obtain the z-score value. It can show possible abnormalities on either the left or right hemisphere.
 - Negative z-scores indicate that there is less activity in the left hemisphere (a negative percent difference). These values display in **blue**.
 - Positive z-scores indicate that there is less activity in the right hemisphere (a positive percent difference). These values display in **red**.



Related: Refer to [Review Results in the Z-Score Analysis Window](#) for more information about the Z-Score Analysis window.

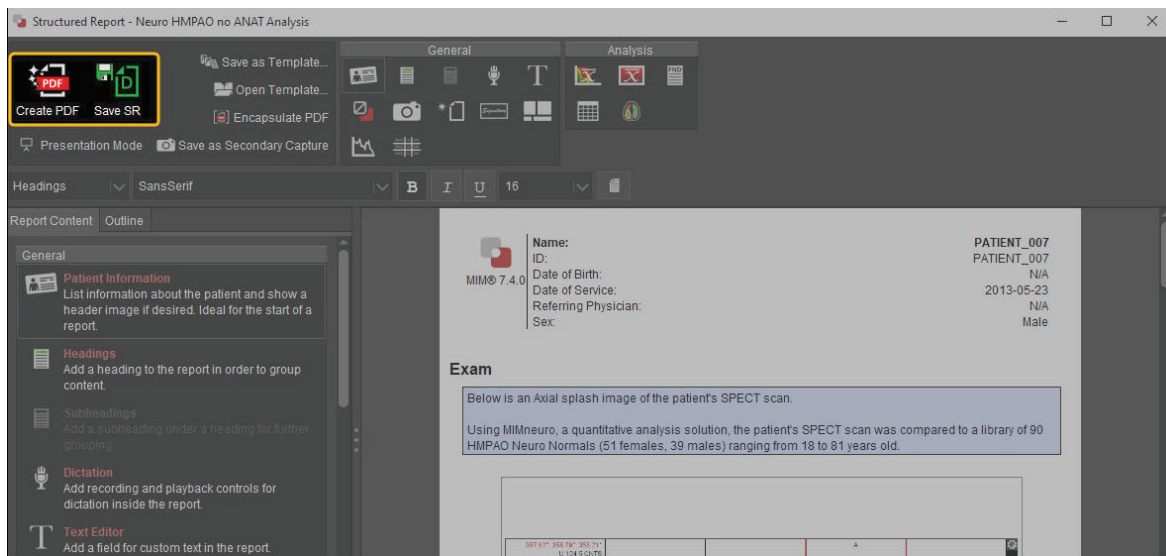
Review the Structured Report

A structured report opens by default. It includes:

- An axial splash image of the patient's scan
- The results from the region-based analysis (z-score table)
- The results from the voxel-based analysis (SSPs)

Save the report using in the buttons in the upper-left corner:

- Click **Create PDF** to download the structured report as a PDF, such as to share with other clinicians.
- Click **Save SR** to save the structured report as a DICOM object in MIM that you can access from your patient list.




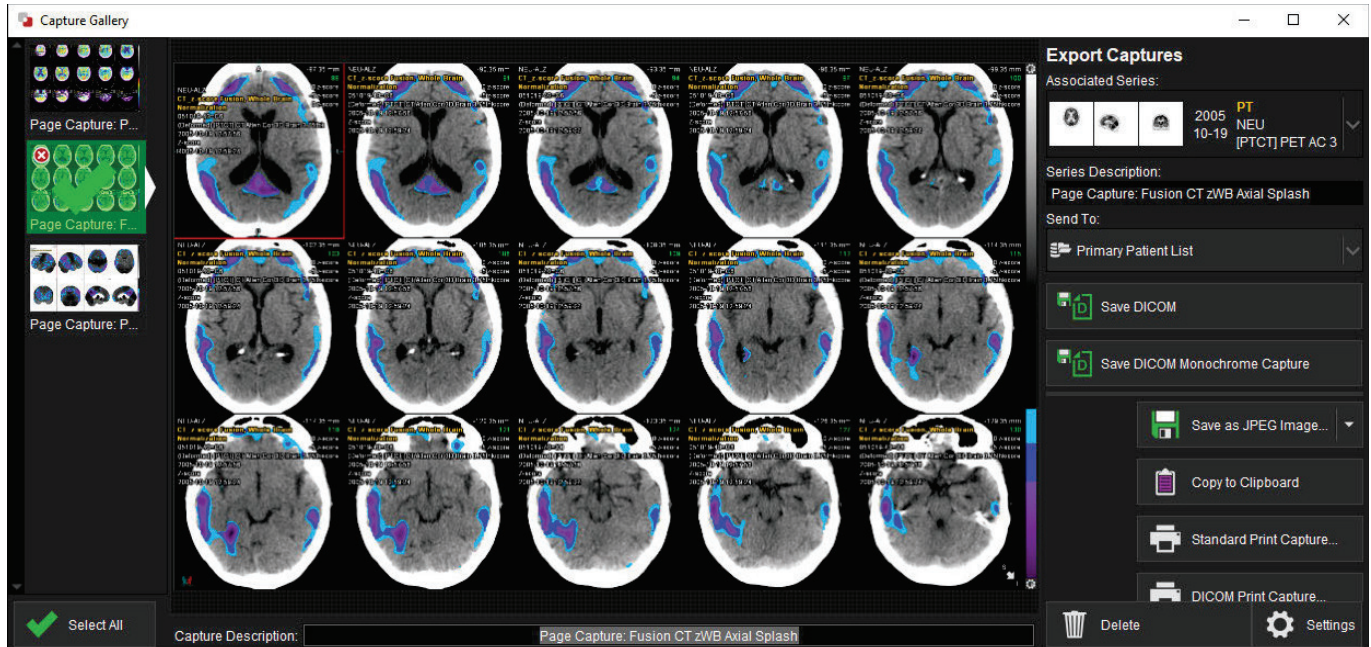
Related: Refer to [Create and Modify Structured Reports](#) for more information about working with structured reports.

Save Results

Save your work so you can return to it later or share it with others.

Save Your Captures

Open the Capture Gallery  in the upper-right corner of MIM to save screen captures. You can send the screen captures to other physicians or store them in your PACS system for later review.




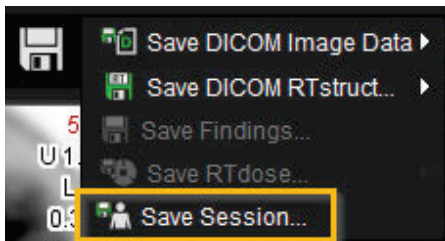
Refer to [Create and Save Secondary Captures](#) for more information about creating and saving captures.



Tip: You can also save Z-score windows as secondary captures. In the Z-Score Analysis window, click **Save As...** and select **Secondary Capture**. A capture of the z-score results is added to the Capture Gallery.

Save Your Session

Click the save  button in the MIM top toolbar and select **Save Session...** When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.



MIM Workflows[™] : Neuro HMPAO — Analysis

MIMTD-830 • 05 Dec 2023

Overview

Use the **Neuro HMPAO - Analysis** workflow for HMPAO studies, such as subtraction cases. This workflow performs both voxel-based analysis and region-based analysis.



Related: Refer to [MIM Workflows[™]: Neuro HMPAO — SPECT Reconstruction](#) if you have a raw SPECT image that first needs to be reconstructed.

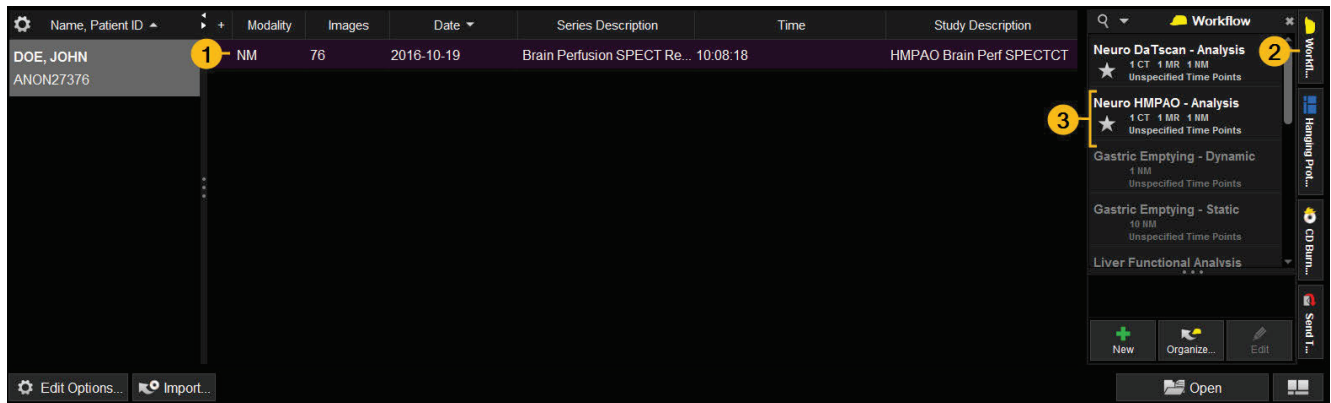
Contents


- [Run the Workflow](#)
- [Analyze the Results](#)
 - [Review Brain SPECT Displays](#)
 - [Review Z-Scores](#)
 - [Review the Structured Report](#)
- [Save Results](#)
 - [Save Your Captures](#)
 - [Save Your Session](#)

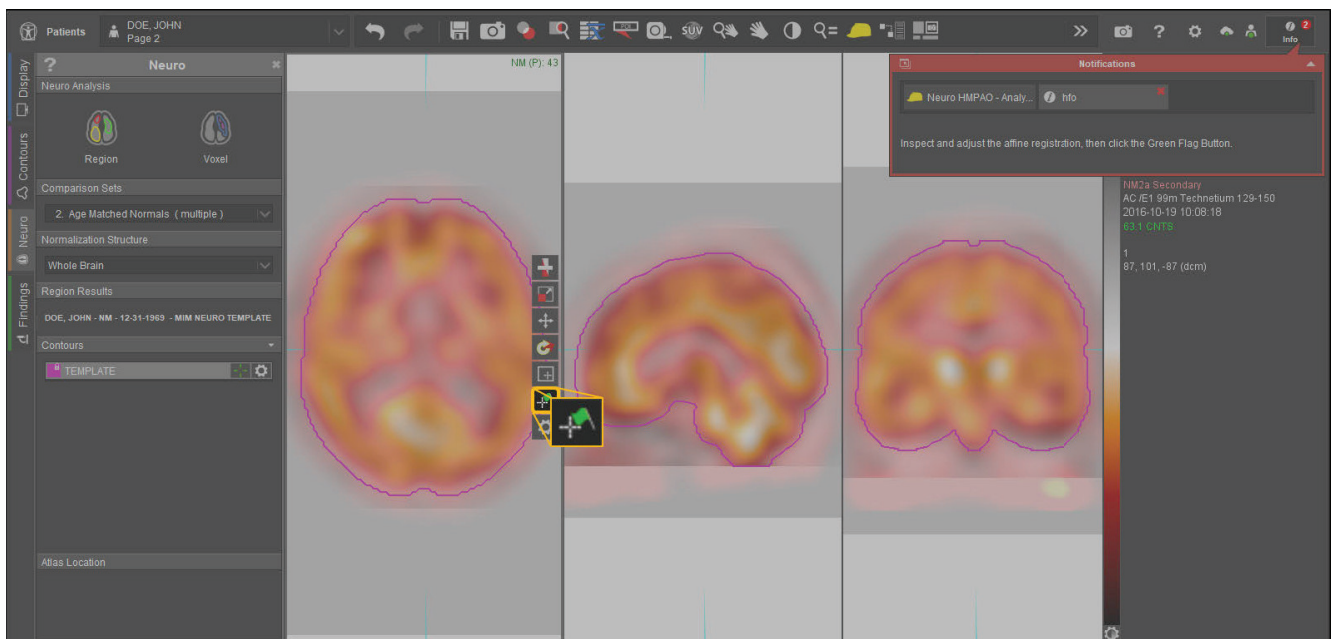
Run the Workflow

1. From the patient list, select the desired SPECT series. A CT or MR is optional for this workflow. You may select a CT or an MR series if you have one.
2. Select the **Workflow** tab in the patient list to expand it.

- Double-click the **Neuro HMPAO — Analysis** workflow from the list to launch it.



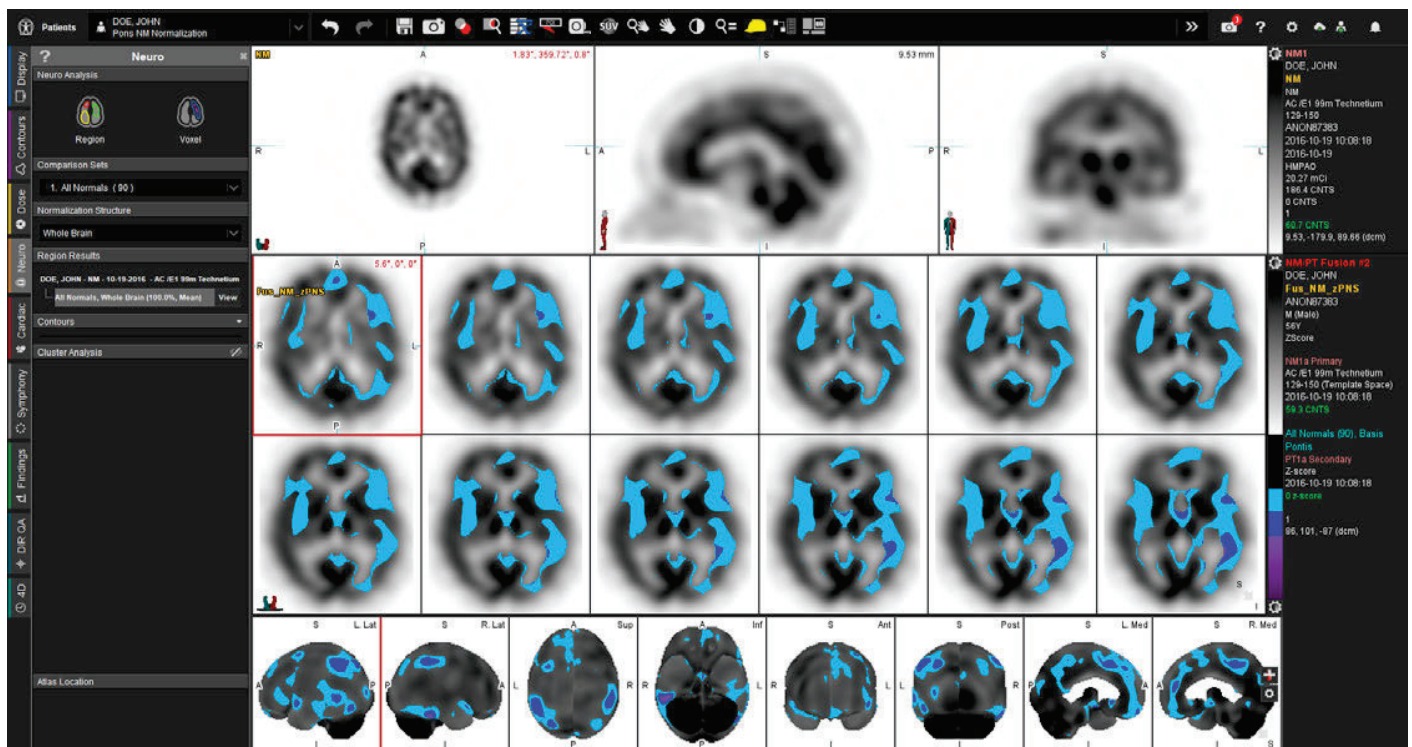
- The workflow performs an affine registration between your SPECT series (secondary series) and the template space (primary series). Check the registration to make sure the majority of the SPECT series fits within the pink Template contour. When you are ready, click the green flag button  to continue.



Tip: Affine registrations rarely require adjustment. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See [Adjust Affine Registration](#) for more information.

- ## Analyze the Results

Review Brain SPECT Displays



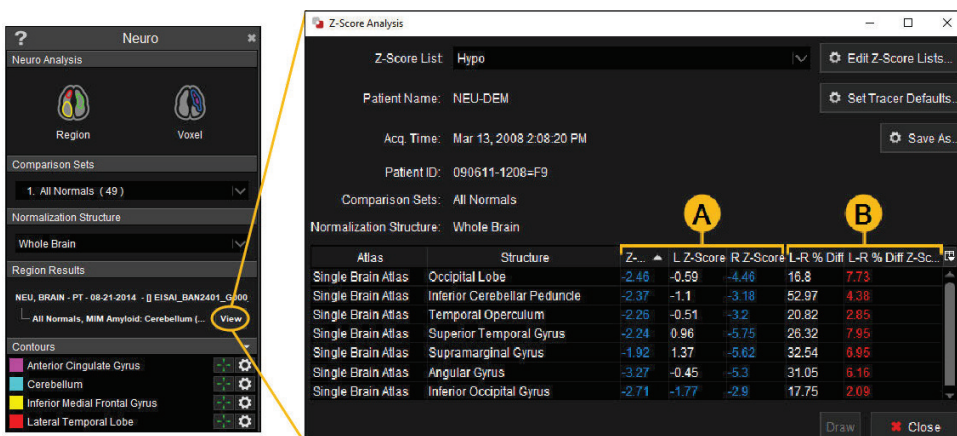
This workflow produces several pages for visualization and analysis. Use the left and right arrow keys to cycle through the pages.

- **Page 1** displays all loaded series and fusions. It is generally not used for analysis.
- **Compare WB - PNS - CBL**
 - Row 1 displays the SPECT brain.
 - Row 2 displays the z-score results fused to the stereotactic surface projections (SSPs) of the SPECT brain normalized to the whole brain.
 - Row 3 displays the z-score results fused to the SSPs of the SPECT brain normalized to the pons.
 - Row 4 displays the z-score results fused to the SSPs of the SPECT brain normalized to the cerebellum.
- **Whole Brain NM Normalization** displays the SPECT brain in the top row. The following rows contain a splash display of the z-score results fused to the SPECT brain and SSPs, normalized to the whole brain.
- **Pons NM Normalization** displays the SPECT brain in the top row. The following rows contain a splash display of the z-score results fused to the SPECT brain and SSPs, normalized to the pons.
- **Cerebellum NM Normalization** displays the SPECT brain in the top row. The following rows contain a splash display of the z-score results fused to the SPECT brain and SSPs, normalized to the cerebellum.

For additional information on MIMneuro displays, see [View Color Scales and Stereotactic Surface Projections](#).

Review Z-Scores

The Z-Score Analysis window opens by default. You can also open it by clicking the **View** button in the Region Results section of the Neuro sidebar.



Z-Score Analysis

Z-Score List: Hypo

Patient Name: NEU-DEM

Acq. Time: Mar 13, 2008 2:08:20 PM

Patient ID: 090611-1208=F9

Comparison Sets: All Normals

Normalization Structure: Whole Brain

Atlas	Structure	Z...	L Z-Score	R Z-Score	L-R % Diff	L-R % Diff Z-Score
Single Brain Atlas	Occipital Lobe	-2.46	-0.59	-4.46	16.8	7.73
Single Brain Atlas	Inferior Cerebellar Peduncle	-2.37	-1.1	-3.18	52.97	4.38
Single Brain Atlas	Temporal Operculum	-2.26	-0.51	-3.2	20.82	2.85
Single Brain Atlas	Superior Temporal Gyrus	-2.24	0.96	-5.75	26.32	7.95
Single Brain Atlas	Supramarginal Gyrus	-1.92	1.37	-5.62	32.54	8.95
Single Brain Atlas	Angular Gyrus	-3.27	-0.45	-5.3	31.05	6.16
Single Brain Atlas	Inferior Occipital Gyrus	-2.71	-1.77	-2.9	17.75	2.09

- A. View the z-score for each structure. The z-score is the number of standard deviations the structure is away from the mean of the normal database for that structure (e.g., 90 normals for HMPAO).

- *Areas of reduced uptake* are statistically significant when they are -1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in **blue**.
- *Areas of increased uptake* are statistically significant when they are +1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in **red**.

B. View the left/right percent difference z-score. The left/right percent difference is calculated first and then compared to the normal database to obtain the z-score value. It can show possible abnormalities on either the left or right hemisphere.

- Negative z-scores indicate that there is less activity in the left hemisphere (a negative percent difference). These values display in **blue**.
- Positive z-scores indicate that there is less activity in the right hemisphere (a positive percent difference). These values display in **red**.



Related: Refer to [Review Results in the Z-Score Analysis Window](#) for more information about the Z-Score Analysis window.

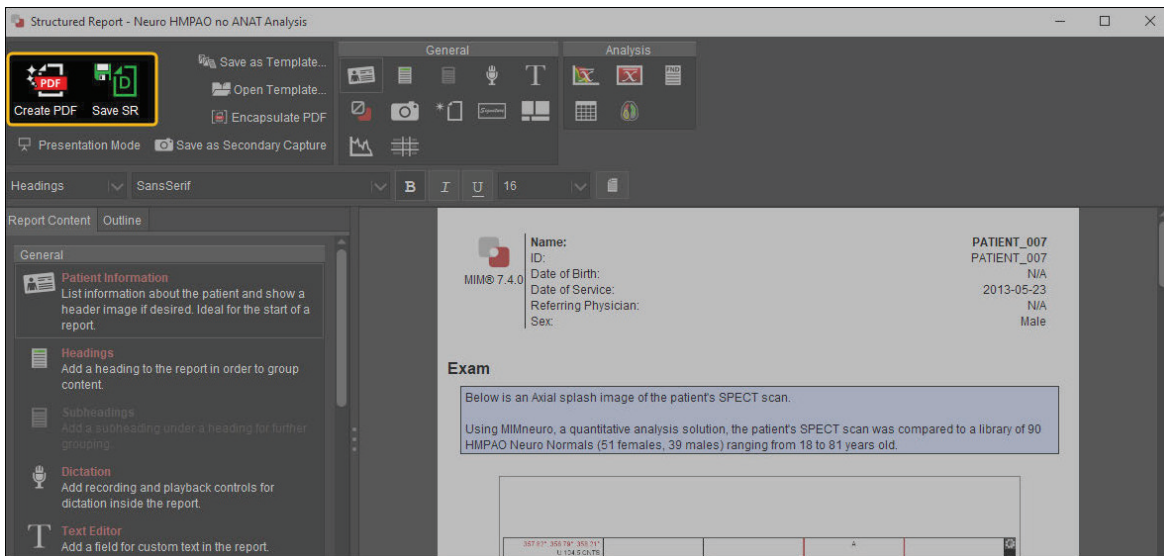
Review the Structured Report

A structured report opens by default. It includes:

- An axial splash image of the patient's SPECT scan
- The results from the region-based analysis (z-score table)
- The results from the voxel-based analysis (SSPs)

Save the report using in the buttons in the upper-left corner:

- Click **Create PDF** to download the structured report as a PDF, such as to share with other clinicians.
- Click **Save SR** to save the structured report as a DICOM object in MIM that you can access from your patient list.




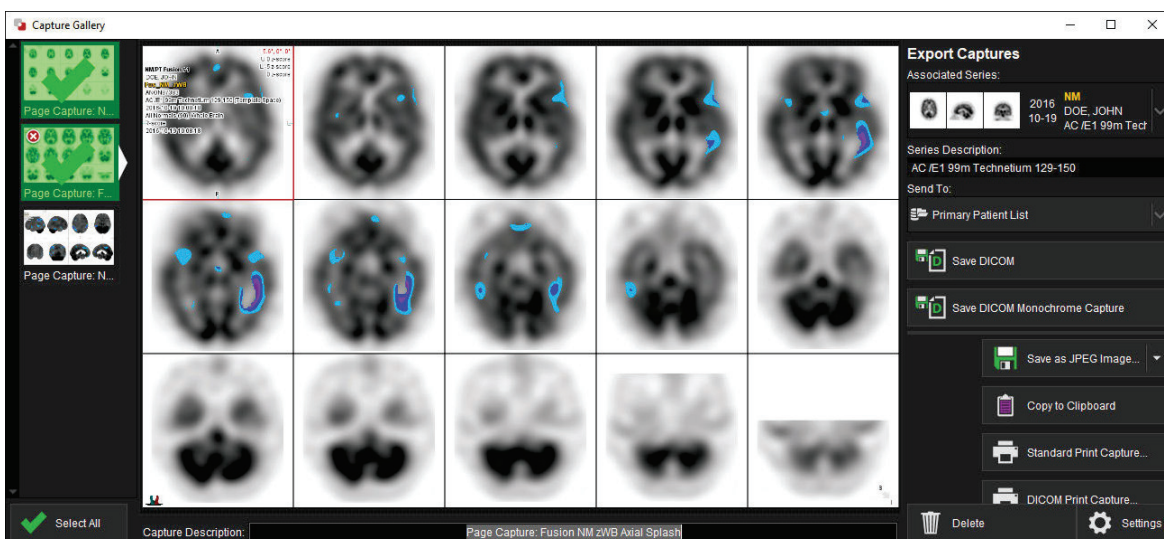
Related: Refer to [Create and Modify Structured Reports](#) for more information about working with structured reports.

Save Results

Save your work so you can return to it later or share it with others.

Save Your Captures

Open the Capture Gallery  in the upper-right corner of MIM to save screen captures. You can send the screen captures to other physicians or store them in your PACS system for later review.




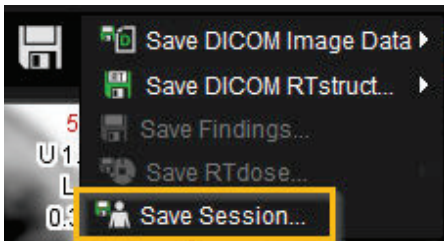
Refer to [Create and Save Secondary Captures](#) for more information about creating and saving captures.



Tip: You can also save Z-score windows as secondary captures. In the Z-Score Analysis window, click **Save As...** and select **Secondary Capture**. A capture of the z-score results is added to the Capture Gallery.

Save Your Session

Click the save  button in the MIM top toolbar and select **Save Session....** When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.



MIM Workflows[™]: Neuro HMPAO — SPECT Reconstruction

MIMTD-837 • 15 Dec 2023

Overview

Use the **Neuro HMPAO - SPECT Reconstruction** workflow for raw HMPAO studies, such as subtraction cases. This workflow reconstructs the series into an image that can be used for analysis.



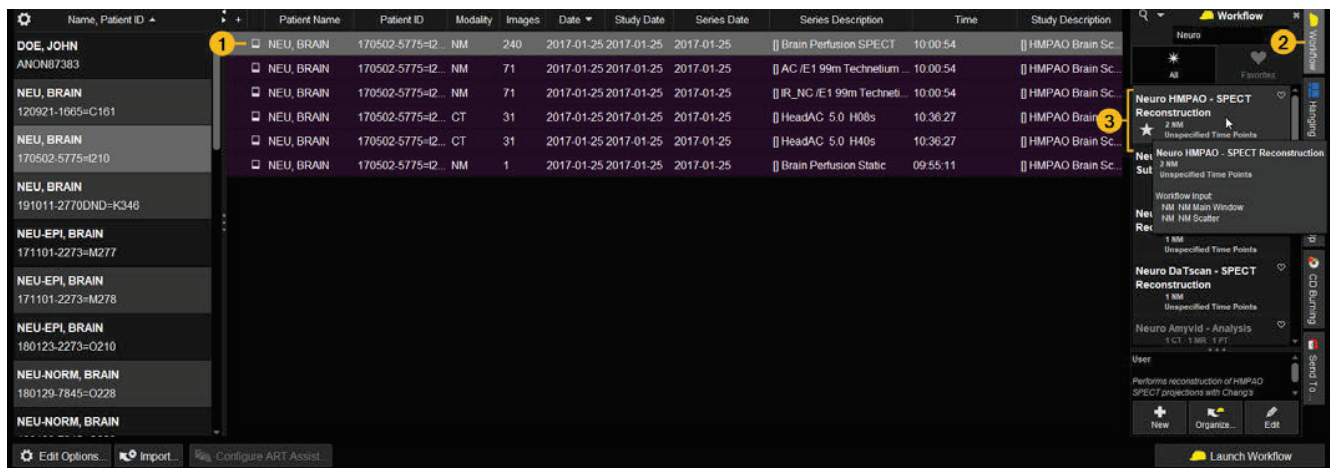
Important: This workflow requires a SPECTRA Recon[®] license in addition to a MIMneuro[®] license.







Related: Refer to [MIM Workflows[™]: Neuro HMPAO — Analysis](#) if your image has been reconstructed and you are ready for analysis.

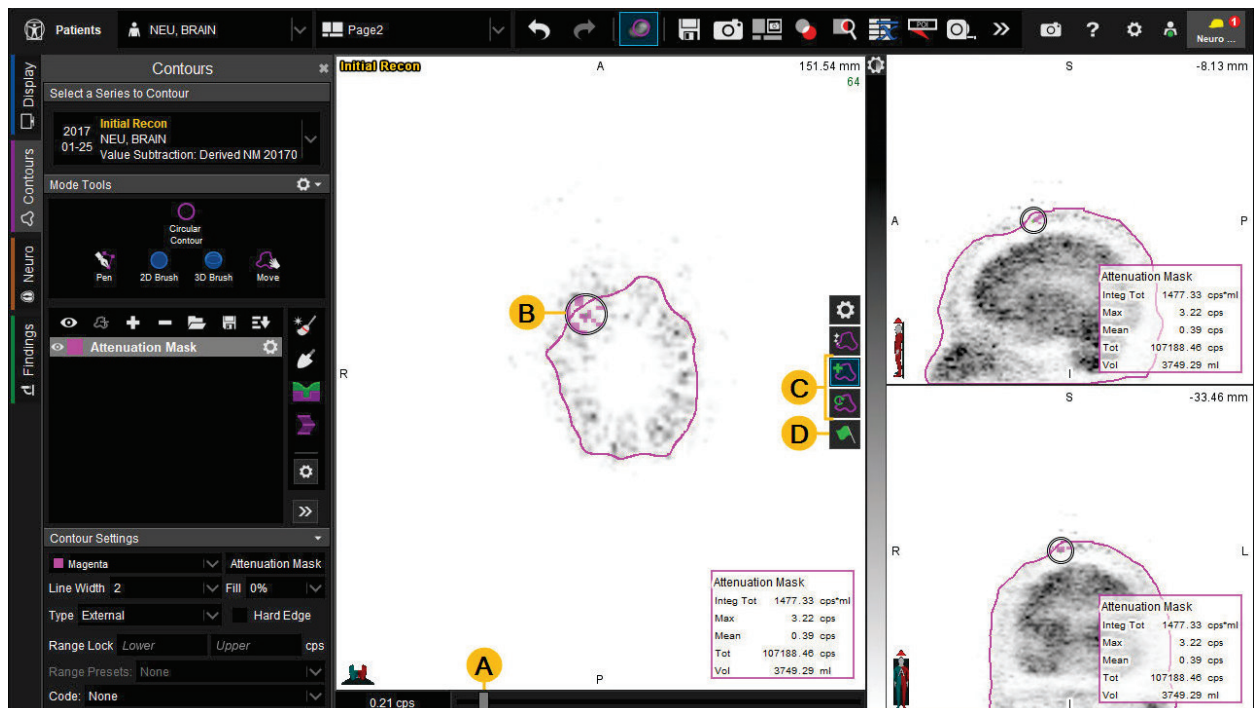
Run the Workflow

1. From the patient list, select the desired HMPAO projection image.
2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **Neuro HMPAO — SPECT Reconstruction** workflow from the list to launch it.



4. In the Confirm Selections window, ensure that the appropriate series have been assigned to the NM Main Window and NM Scatter workflow targets. If necessary, use the dropdowns to select the appropriate series for each target. Click **Confirm** to continue.

5. When prompted, review the region to be used for attenuation correction. The **Threshold**  tool is activated by default:
 - A. Use the slider at the bottom of the viewport to adjust the threshold.
 - B. Move the sphere to inspect the auto-generated contour. You can scroll between slices, and right-click drag up or down to resize the sphere. The area that is above the threshold appears with a color wash.
 - C. If necessary, click the append  button on the right side of the viewport if you need to add to the contour or the replace  button if you need to replace the contour.
 - D. Click the green flag  button to make your change.

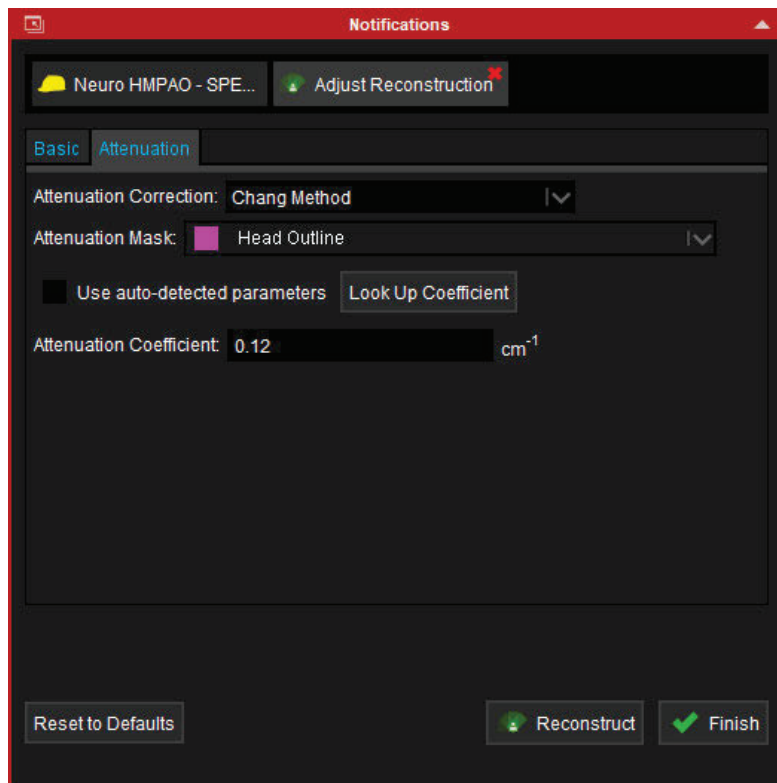


Related: See [Create Contours with the Threshold Tool](#) or click the question mark  in the upper-right corner of MIM for more information on using the Threshold tool.

When you are finished, return to the Notifications window and click **Resume Workflow**. The workflow performs attenuation correction and displays the reconstructed SPECT image.


6. Review the reconstructed image:
 - Typically, no changes are needed. In the Notifications window, click **Finish** to finish the reconstruction. Go to step 7 below.

- If necessary, adjust the reconstruction settings in the Notifications window and reconstruct the image.
 - i. Adjust settings as needed. For example:
 - On the **Basic** tab, select **Perform automatic motion correction** if there is a lot of motion in the image.
 - On the **Attenuation** tab, change the **Attenuation Correction** option to **None** if you do not want attenuation correction to be performed using the Chang Method.



- ii. After adjusting the reconstruction settings, you have two options:
 - Click **Reconstruct** if you would like to review the reconstruction again before proceeding to the next steps of the workflow. Repeat this step as necessary until you are satisfied with the reconstruction.
 - Click **Finish** to finalize the reconstruction with the settings as shown and immediately proceed to the next step of the workflow. If you made any changes to the reconstruction settings, the reconstruction is rerun before proceeding.
7. The workflow finishes processing and displays the reconstructed image. The series is automatically saved to your patient list.



Tip: Use the save  button in the top toolbar if you want to save additional copies of the reconstructed series or save to a different location.



Tip: You can use the saved series as the input for the HMPAO analysis workflow. Select the saved series from the patient list and run the Neuro HMPAO - Analysis workflow. Refer to [MIM Workflows[™]: Neuro HMPAO — Analysis](#) for more information.

MIM Workflows[™] : Neuro Amyvid — Analysis

MIMTD-827 • 07 Nov 2024



Important: This workflow has been replaced by the [Neuro Amyloid - Centiloid Analysis](#) workflow.

Overview

Use the **Neuro Amyvid - Analysis** workflow with amyloid studies using the Amyvid tracer. This workflow uses the Florbetapir (Clark, 2012) atlas to perform region-based analysis.



Related: Refer to [MIMneuro Atlases: Technical Details](#) for more information about the atlas used.

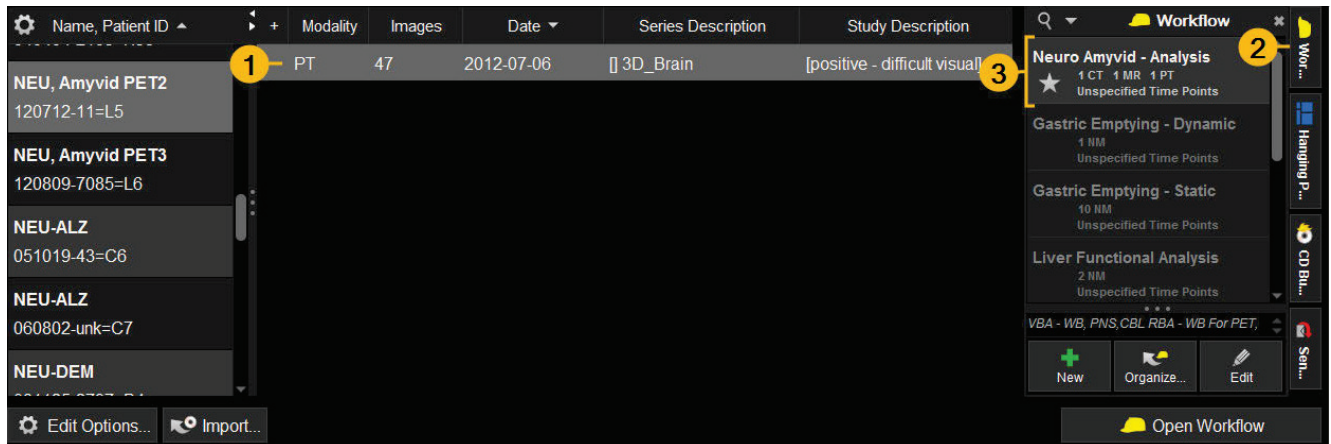
Contents


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- [Analyze the Results](#)
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 - [Review the Statistics Table](#)
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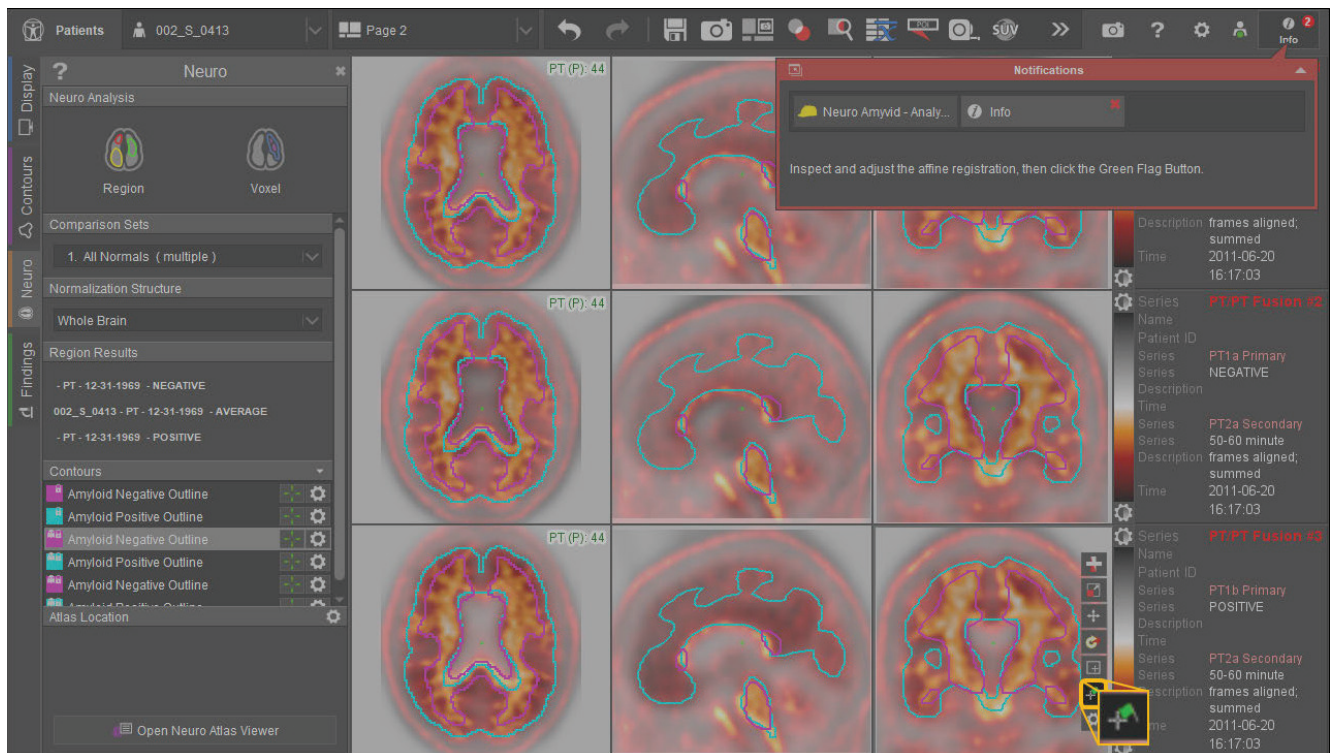
Run the Workflow

1. From the patient list, select the desired PET series. A CT or MR is optional for this workflow. You may select a CT or an MR series if you have one.
2. Select the **Workflow** tab in the patient list to expand it.

- Double-click the **Neuro Amyvid — Analysis** workflow from the list to launch it.



- If the workflow does not find the tracer in the DICOM data, answer the prompt to select the tracer (Amyvid) and click **OK** to continue. If the workflow finds the tracer in the DICOM data, the workflow proceeds immediately to the next step.
- The workflow performs an affine registration between your PET series (secondary series) and the average, negative, and positive templates (primary series). Check the registrations to make sure they align as accurately as possible. When you are ready, click the green flag button  to continue.



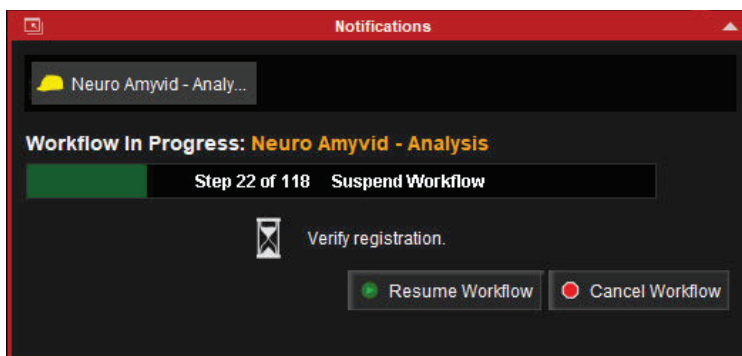


Tip: As indicated by the series information on the right side, the top row shows the average template space. The middle row shows the amyloid negative template, and the bottom row shows the amyloid positive template.



Tip: Affine registrations rarely require adjustment. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See [Adjust Affine Registration](#) for more information.

6. The workflow asks you to assess the quality of the registration. Generally, the amyloid tracer uptake in negative cases is contained in the white matter of the brain, outlined by the Amyloid Negative ROI.
 - *If the alignment is appropriate*, click **Resume Workflow** to continue.
 - *If the alignment is not satisfactory*, click **Cancel Workflow**. Run the workflow again and make additional adjustments at the affine registration step to produce a better match to the templates.



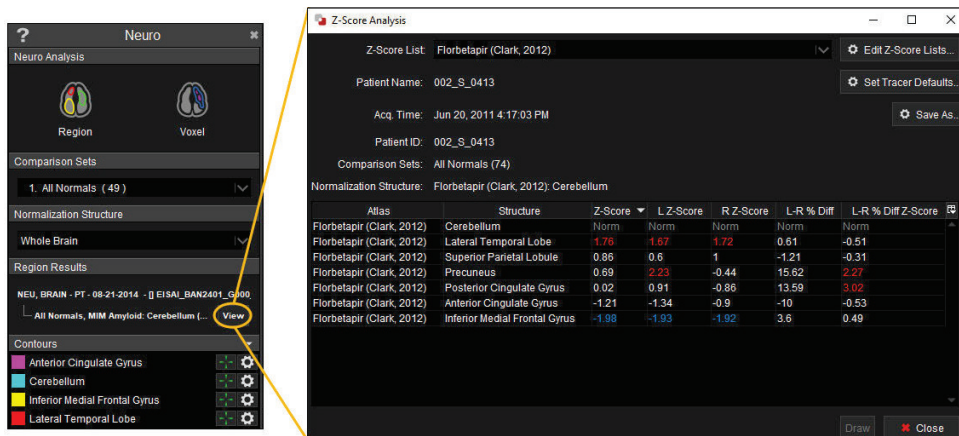
7. The workflow performs region-based analysis. The workflow finishes running and the Z-Score Analysis window opens.

Analyze the Results

When the workflow is complete, review the calculated results. If necessary, you can make adjustments and re-run region-based analysis for recalculation. Refer to [Review Region-Based Analysis](#) for more information.

Review Z-Scores

The Z-Score Analysis window opens by default. You can also open it by clicking the **View** button in the Region Results section of the Neuro sidebar.



The z-score for each structure listed in the Z-Score Analysis window is the number of standard deviations the structure is from the mean of the normal database for that structure. The cerebellum is listed as the normalization structure. The z-score for each structure is the average with respect to the number of normals in the database (e.g., 74 normals for Amyvid).

- *Areas of increased uptake* are statistically significant when they are +1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in **red**.
- *Areas of reduced uptake* are statistically significant when they are -1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in **blue**.



Related: Refer to [Review Results in the Z-Score Analysis Window](#) for more information about the Z-Score Analysis window.

Review the Statistics Table

The statistics table is included in the pages created by the workflow.



Tip: Use the left/right arrow keys to navigate between pages or use the page selector in the top toolbar.

Structure	SUVr	Normal Values Mean (Range)
Anterior Cingulate Gyrus	0.9	0.99 (0.84 - 1.14)
Inferior Medial Frontal Gyrus	0.8	0.91 (0.81-1.01)
Lateral Temporal Lobe	1.09	0.99 (0.88-1.11)
Posterior Cingulate Gyrus	0.94	0.94 (0.82-1.05)
Precuneus	1.04	1.00 (0.91-1.10)
Superior Parietal Lobule	1.02	0.97 (0.86-1.09)
Average	0.96	0.97 (0.89-1.04)
Reference Structure: Cerebellum		

The statistics table shows the SUV ratio (SUVr) for the PET image. The SUVr is the ratio of the average value for each brain region to the average value for the normalization structure (e.g., cerebellum). SUV ratios have been used for quantifying the amyloid plaque burden in the brain. For Amyvid PET, there are six analysis regions included in the Florbetapir (Clark, 2012) atlas.




Important: The Normal Values (Mean Range) is derived from the MIM Amyloid regions atlas.

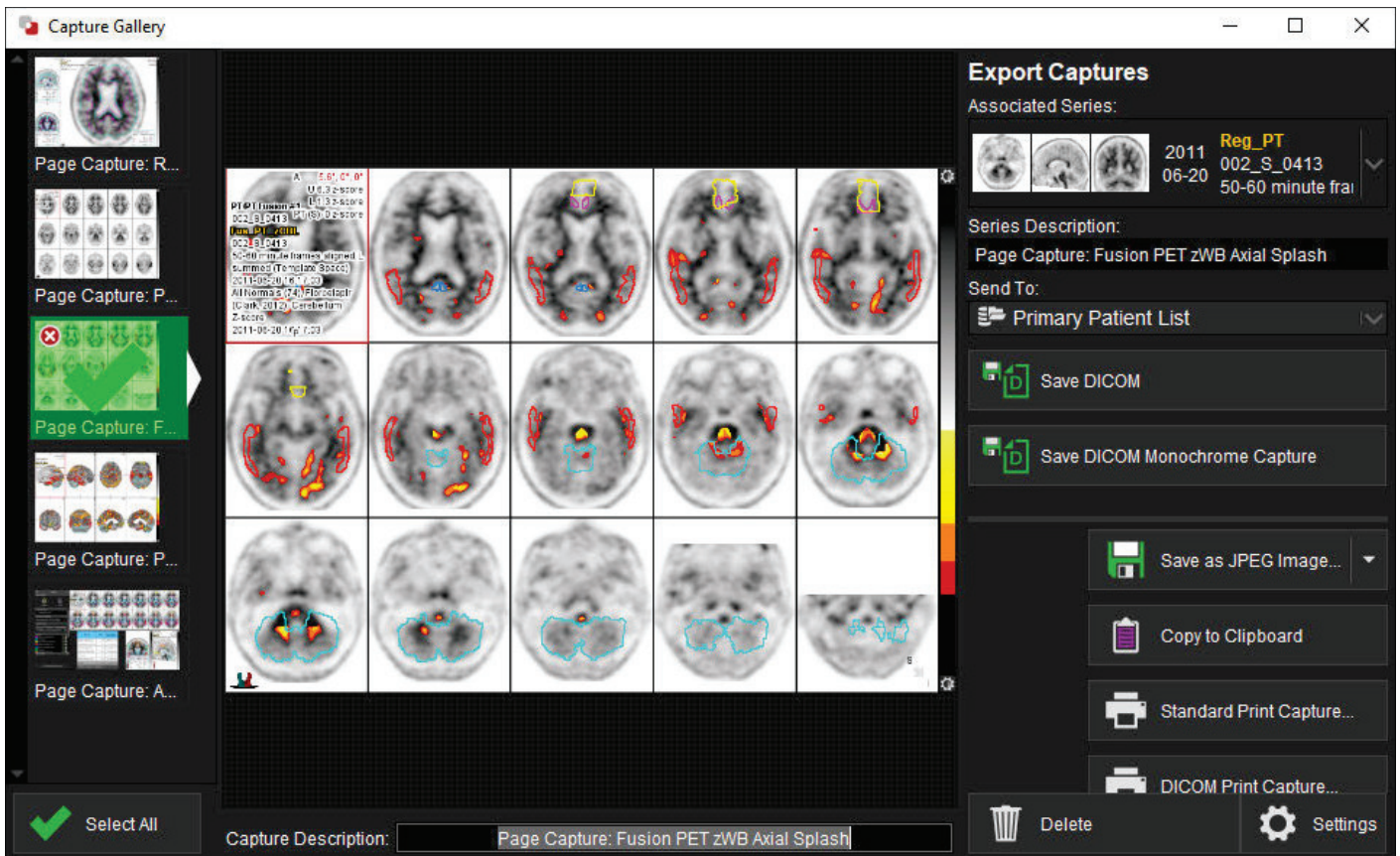
The SUVr is different from the region-based z-scores shown in the Z-score Analysis window because the z-scores are calculated from the mean of the intensity values of the region.

Save Results

Save your work so you can return to it later or share it with others.

Save Your Captures

Open the Capture Gallery  in the upper-right corner of MIM to save screen captures. You can send the screen captures to other physicians or store them in your PACS system for later review.




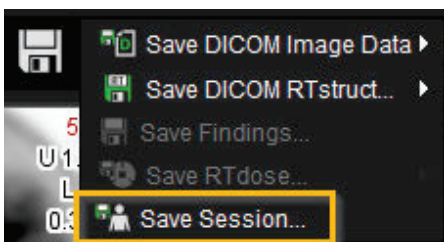
Refer to [Create and Save Secondary Captures](#) for more information about creating and saving captures.



Tip: You can also save Z-score windows as secondary captures. In the Z-Score Analysis window, click **Save As...** and select **Secondary Capture**. A capture of the z-score results is added to the Capture Gallery.

Save Your Session

Click the save  button in the MIM top toolbar and select **Save Session....** When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.



MIM Workflows[™] : Neuro Neuraceq[®] — Analysis

MIMTD-833 • 07 Nov 2024



Important: This workflow has been replaced by the [Neuro Amyloid - Centiloid Analysis](#) workflow. Note that the Neuro Amyloid - Centiloid Analysis workflow uses Clark atlas regions. It may produce different results than the Neuro NeuraCeq - Analysis workflow, which used MIM Amyloid regions.

Overview

Use the **Neuro NeuraCeq - Analysis** workflow with amyloid studies using the Neuraceq tracer. This workflow uses the MIM Amyloid atlas to perform region-based analysis.



Related: Refer to [MIMneuro Atlases: Technical Details](#) for more information about the atlas used.

Contents

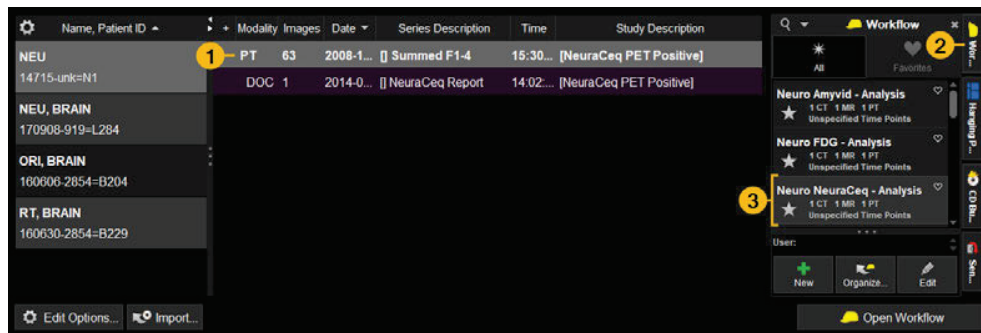
- [Run the Workflow](#)
- [Analyze the Results](#)
 - [Review Z-Scores](#)
 - [Review the Statistics Table](#)
- [Save Results](#)
 - [Save Your Captures](#)
 - [Save Your Session](#)


Run the Workflow

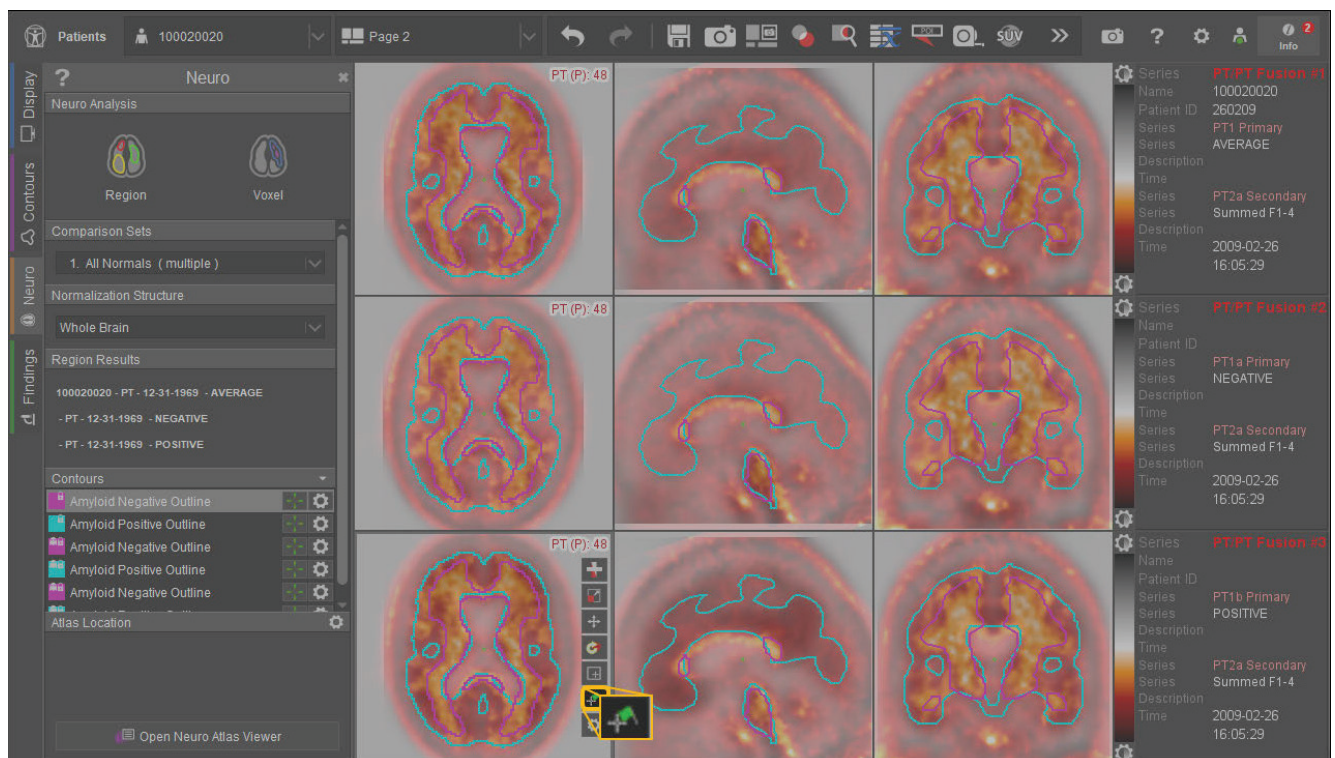
1. From the patient list, select the desired PET series. A CT or MR is optional for this workflow. You may select a CT or an MR series if you have one.



MIMneuro[®] User Guide



2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **Neuro NeuraCeq — Analysis** workflow from the list to launch it.
4. If the workflow does not find the tracer in the DICOM data, answer the prompt to select the tracer (NeuraCeq) and click **OK** to continue. If the workflow finds the tracer in the DICOM data, the workflow proceeds immediately to the next step.
5. The workflow performs an affine registration between your PET series (secondary series) and the average, negative, and positive templates (primary series). Check the registrations to make sure they align as accurately as possible. When you are ready, click the green flag button  to continue.





Tip: As indicated by the series information on the right side, the top row shows the average template space. The middle row shows the amyloid negative template, and the bottom row shows the amyloid positive template.



Tip: Affine registrations rarely require adjustment. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See [Adjust Affine Registration](#) for more information.

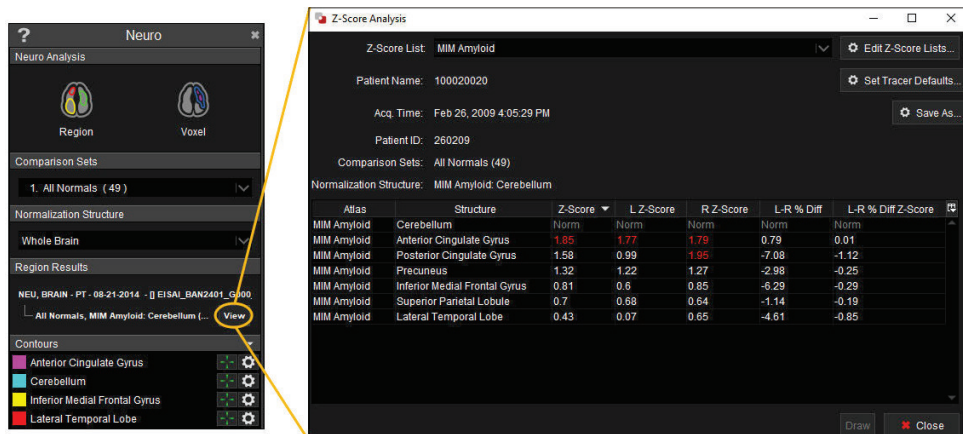
6. If you are prompted to confirm how to proceed with processing:
 - Select **Accept changes and perform registration** for MIM to accept your adjustments and perform a deformable registration between the template and the selected series. Statistics are calculated based on this deformable alignment.
 - Select **Accept changes as final registration** for MIM to accept your adjustments and use the current alignment to calculate statistics.
7. The workflow asks you to assess the quality of the registration. Generally, the amyloid tracer uptake in negative cases is contained in the white matter of the brain, outlined by the Amyloid Negative ROI.
 - *If the alignment is appropriate*, click **Resume Workflow** to continue.
 - *If the alignment is not satisfactory*, click **Cancel Workflow**. Run the workflow again and make additional adjustments at the affine registration step to produce a better match to the templates.
8. The workflow performs region-based analysis. The workflow finishes running and the Z-Score Analysis window opens.

Analyze the Results

When the workflow is complete, review the calculated results. If necessary, you can make adjustments and re-run region based analysis for recalculation. Refer to [Review Region-Based Analysis](#) for more information.

Review Z-Scores

The Z-Score Analysis window opens by default. You can also open it by clicking the **View** button in the Region Results section of the Neuro sidebar.



The z-score for each structure listed in the Z-Score Analysis window is the number of standard deviations the structure is from the mean of the normal database for that structure. The cerebellum is listed as the normalization structure. The z-score for each structure is the average with respect to the number of normals in the database (e.g., 49 normals for Neuraceq).

- *Areas of increased uptake* are statistically significant when they are +1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in red.
- *Areas of reduced uptake* are statistically significant when they are -1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in blue.



Related: Refer to [Review Results in the Z-Score Analysis Window](#) for more information about the Z-Score Analysis window.

Review the Statistics Table

The statistics table is included in the pages created by the workflow.



Tip: Use the left/right arrow keys to navigate between pages or use the page selector in the top toolbar.

Structure	SUVR	Normal Values Mean (Range)
Anterior Cingulate Gyrus	1.34	1.14 (0.93 - 1.35)
Inferior Medial Frontal Gyrus	1.14	1.07 (0.91 - 1.23)
Lateral Temporal Lobe	1.13	1.09 (0.92 - 1.26)
Posterior Cingulate Gyrus	1.32	1.19 (1.02 - 1.36)
Precuneus	1.23	1.10 (0.90 - 1.29)
Superior Parietal Lobule	1.23	1.14 (0.93 - 1.35)
Average	1.23	1.12 (0.98 - 1.26)
Reference Structure: Cerebellum		


The statistics table shows the SUV ratio (SUVR) for the PET image. The SUVR is the ratio of the average value for each brain region to the average value for the normalization structure (e.g., cerebellum). SUV ratios have been used for quantifying the amyloid plaque burden in the brain.

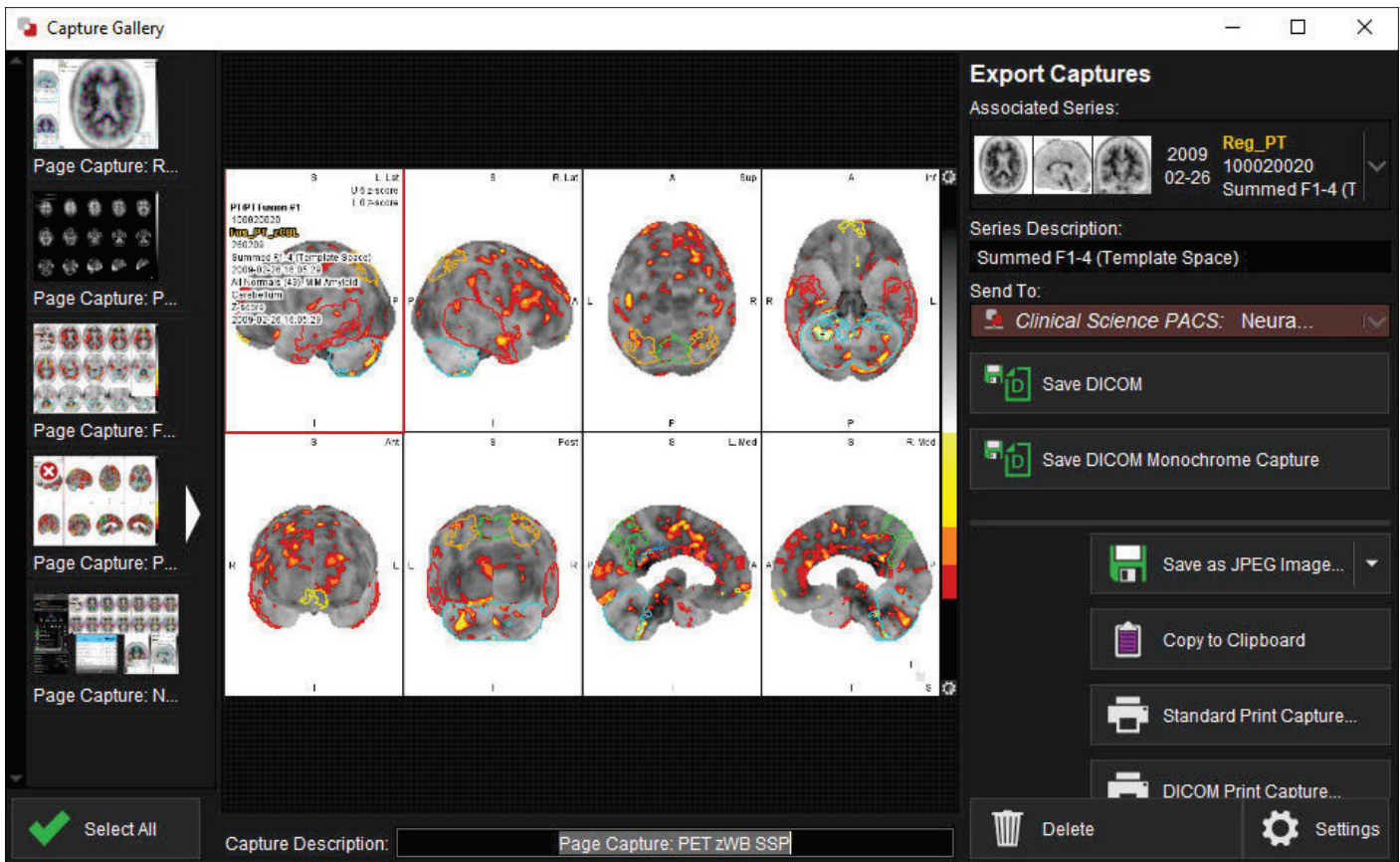
The SUVR is different from the region-based z-scores shown in the Z-score Analysis window because the z-scores are calculated from the mean of the intensity values of the region.

Save Results

Save your work so you can return to it later or share it with others.

Save Your Captures

Open the Capture Gallery  in the upper-right corner of MIM to save screen captures. You can send the screen captures to other physicians or store them in your PACS system for later review.




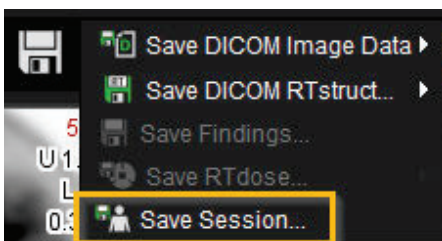
Refer to [Create and Save Secondary Captures](#) for more information about creating and saving captures.



Tip: You can also save Z-score windows as secondary captures. In the Z-Score Analysis window, click **Save As...** and select **Secondary Capture**. A capture of the z-score results is added to the Capture Gallery.

Save Your Session

Click the save  button in the MIM top toolbar and select **Save Session....** When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.



MIM Workflows[™] : Neuro Vizamyl — Analysis

MIMTD-835 • 07 Nov 2024



Important: This workflow has been replaced by the [Neuro Amyloid - Centiloid Analysis](#) workflow. Note that the Neuro Amyloid - Centiloid Analysis workflow uses Clark atlas regions. It may produce different results than the Neuro Vizamyl - Analysis workflow, which used MIM Amyloid regions.

Overview

Use the **Neuro Vizamyl - Analysis** workflow with amyloid studies using the Vizamyl tracer. This workflow uses the MIM Amyloid atlas to perform region-based analysis.



Related: Refer to [MIMneuro Atlases: Technical Details](#) for more information about the atlas used.

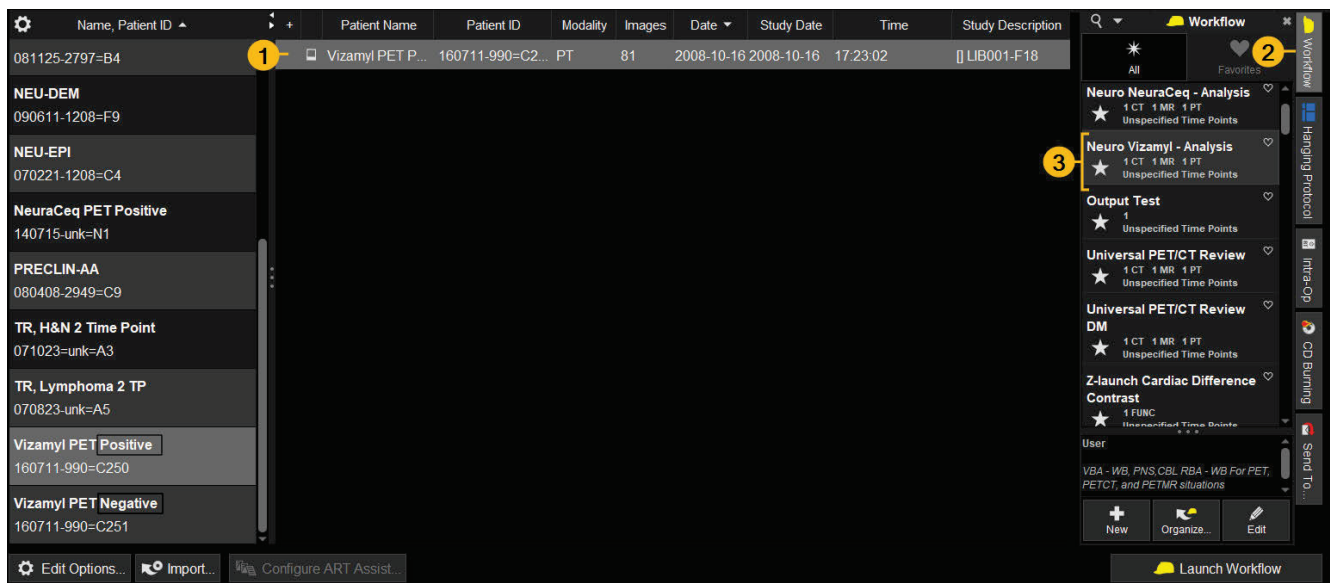
Contents


- [Run the Workflow](#)
- [Analyze the Results](#)
 - [Review Z-Scores](#)
 - [Review the Statistics Table](#)
- [Save Results](#)
 - [Save Your Captures](#)
 - [Save Your Session](#)

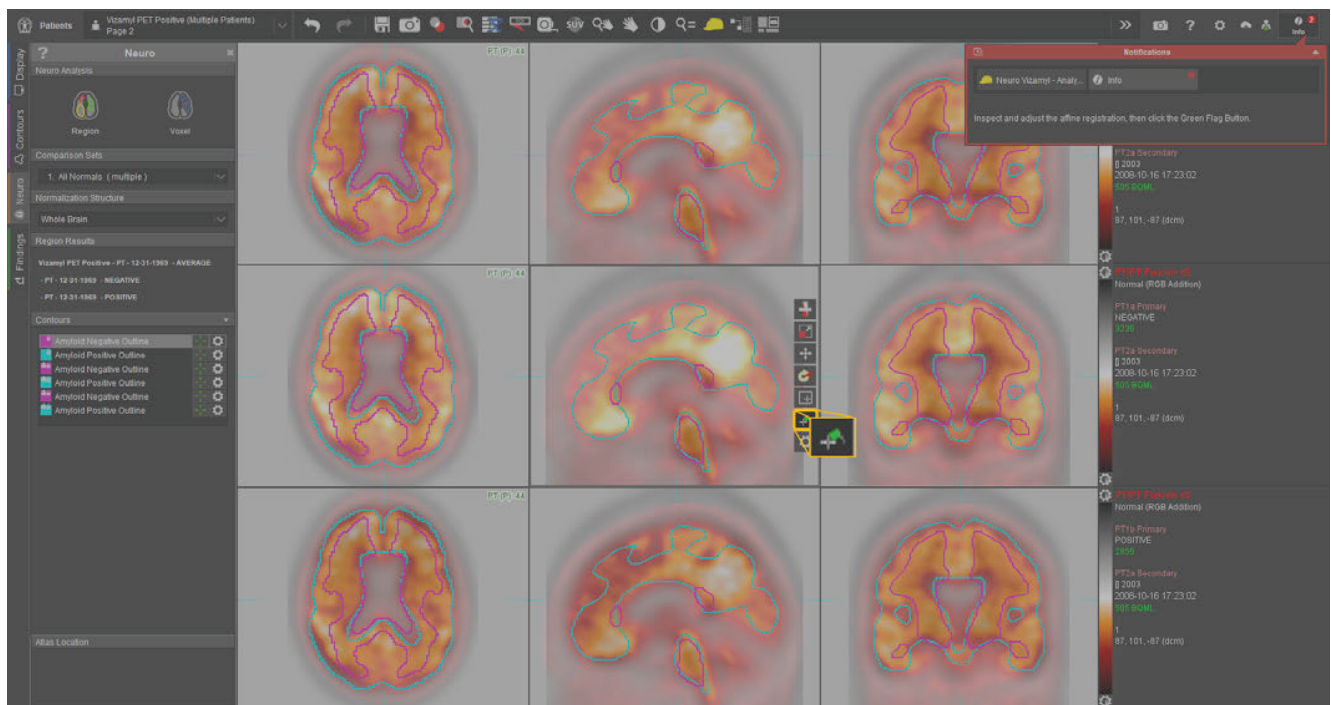
Run the Workflow

1. From the patient list, select the desired PET series. A CT or MR is optional for this workflow. You may select a CT or an MR series if you have one.
2. Select the **Workflow** tab in the patient list to expand it.

- Double-click the **Neuro Vizamyl — Analysis** workflow from the list to launch it.



- If the workflow does not find the tracer in the DICOM data, answer the prompt to select the tracer (Vizamyl) and click **OK** to continue. If the workflow finds the tracer in the DICOM data, the workflow proceeds immediately to the next step.
- The workflow performs an affine registration between your secondary series (PET series) and the primary series (average, negative, and positive templates). Check the registrations to make sure they align as accurately as possible. When you are ready, click the green flag button  to continue.





Tip: As indicated by the series information on the right side, the top row shows the average template space. The middle row shows the amyloid negative template, and the bottom row shows the amyloid positive template.



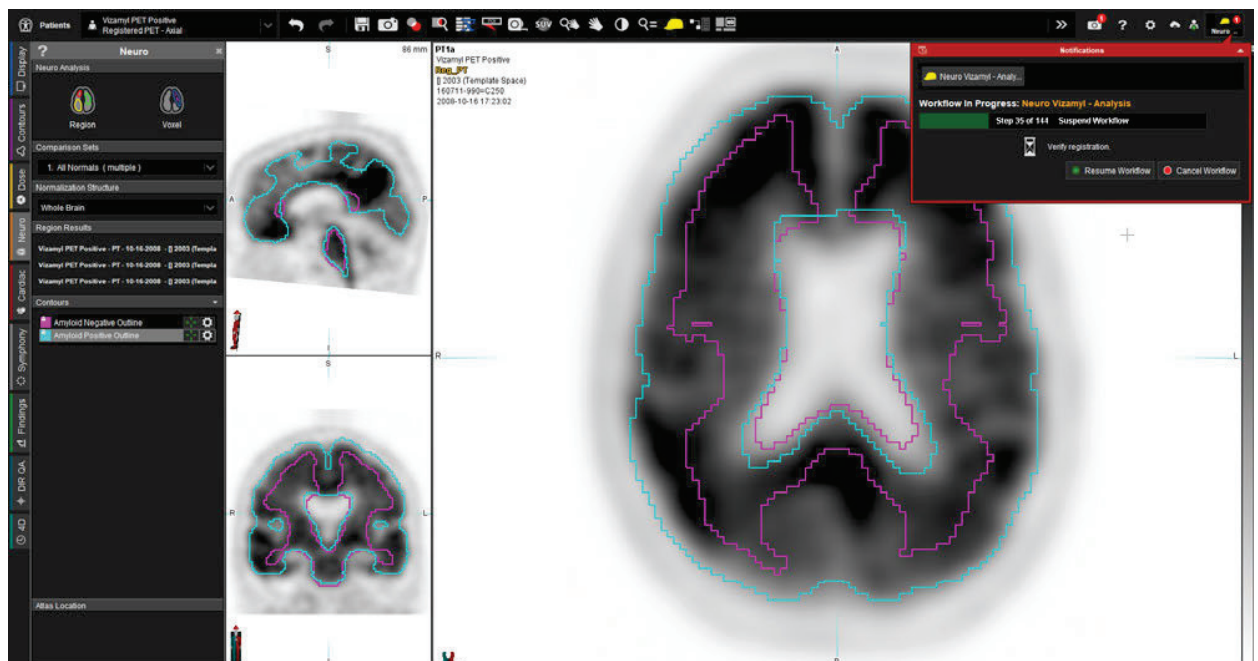
Tip: Affine registrations rarely require adjustment. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See [Adjust Affine Registration](#) for more information.

6. If you are prompted to confirm how to proceed with processing:

- Select **Accept changes and perform registration** for MIM to accept your adjustments and perform a deformable registration between the template and the selected series. Statistics are calculated based on this deformable alignment.
- Select **Accept changes as final registration** for MIM to accept your adjustments and use the current alignment to calculate statistics.

7. The workflow asks you to assess the quality of the registration. Generally, the amyloid tracer uptake in negative cases is contained in the white matter of the brain, outlined by the Amyloid Negative ROI.

- *If the alignment is appropriate*, click **Resume Workflow** to continue.
- *If the alignment is not satisfactory*, click **Cancel Workflow**. Restart the workflow and make more adjustments at the affine registration step to produce a better match to the templates.



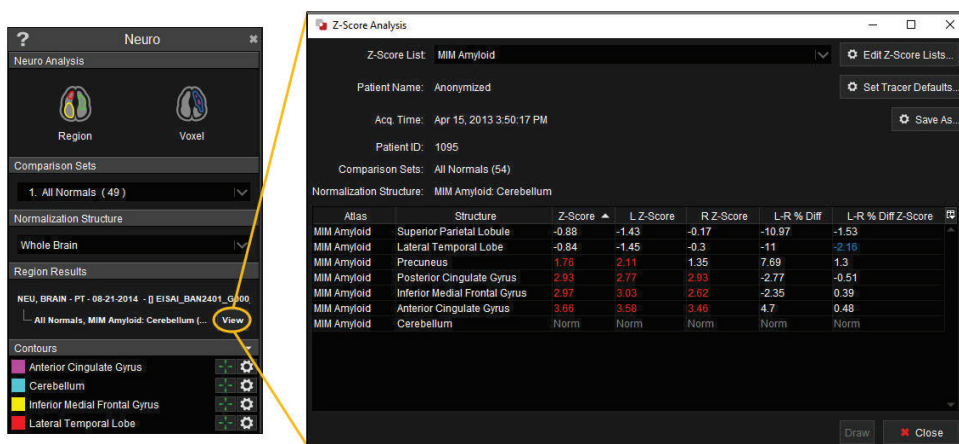
- The workflow performs region-based analysis. The workflow finishes running and the Z-Score Analysis window opens.

Analyze the Results

When the workflow is complete, review the calculated results. If necessary, you can make adjustments and re-run region based analysis for recalculation. Refer to [Review Region-Based Analysis](#) for more information.

Review Z-Scores

The Z-Score Analysis window opens by default. You can also open it by clicking the **View** button in the Region Results section of the Neuro sidebar.



The z-score for each structure listed in the Z-Score Analysis window is the number of standard deviations the structure is from the mean of the normal database for that structure. The cerebellum is listed as the normalization structure. The z-score for each structure is the average with respect to the number of normals in the database (e.g., 54 normals for Vizamy).

- Areas of increased uptake* are statistically significant when they are +1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in **red**.
- Areas of reduced uptake* are statistically significant when they are -1.65 standard deviations or further from the mean of the normals (corresponding to a 95% statistical significance level). These values display in **blue**.



Related: Refer to [Review Results in the Z-Score Analysis Window](#) for more information about the Z-Score Analysis window.

Review the Statistics Table

The statistics table is included in the pages created by the workflow.



Tip: Use the left/right arrow keys to navigate between pages or use the page selector in the top toolbar.

Structure	SUVR	Normal Values Mean (Range)
Anterior Cingulate Gyrus	1.63	1.14 (0.88 - 1.40)
Inferior Medial Frontal Gyrus	1.41	1.09 (0.89 - 1.30)
Lateral Temporal Lobe	1.07	1.15 (0.97 - 1.34)
Posterior Cingulate Gyrus	1.56	1.22 (1.00 - 1.45)
Precuneus	1.31	1.11 (0.88 - 1.34)
Superior Parietal Lobule	1.07	1.16 (0.98 - 1.34)
Average	1.34	1.15 (0.99 - 1.30)
Reference Structure: Cerebellum		


The statistics table shows the SUV ratio (SUVR) for the PET image. The SUVR is the ratio of the average value for each brain region to the average value for the normalization structure (e.g., cerebellum). SUV ratios have been used for quantifying the amyloid plaque burden in the brain.

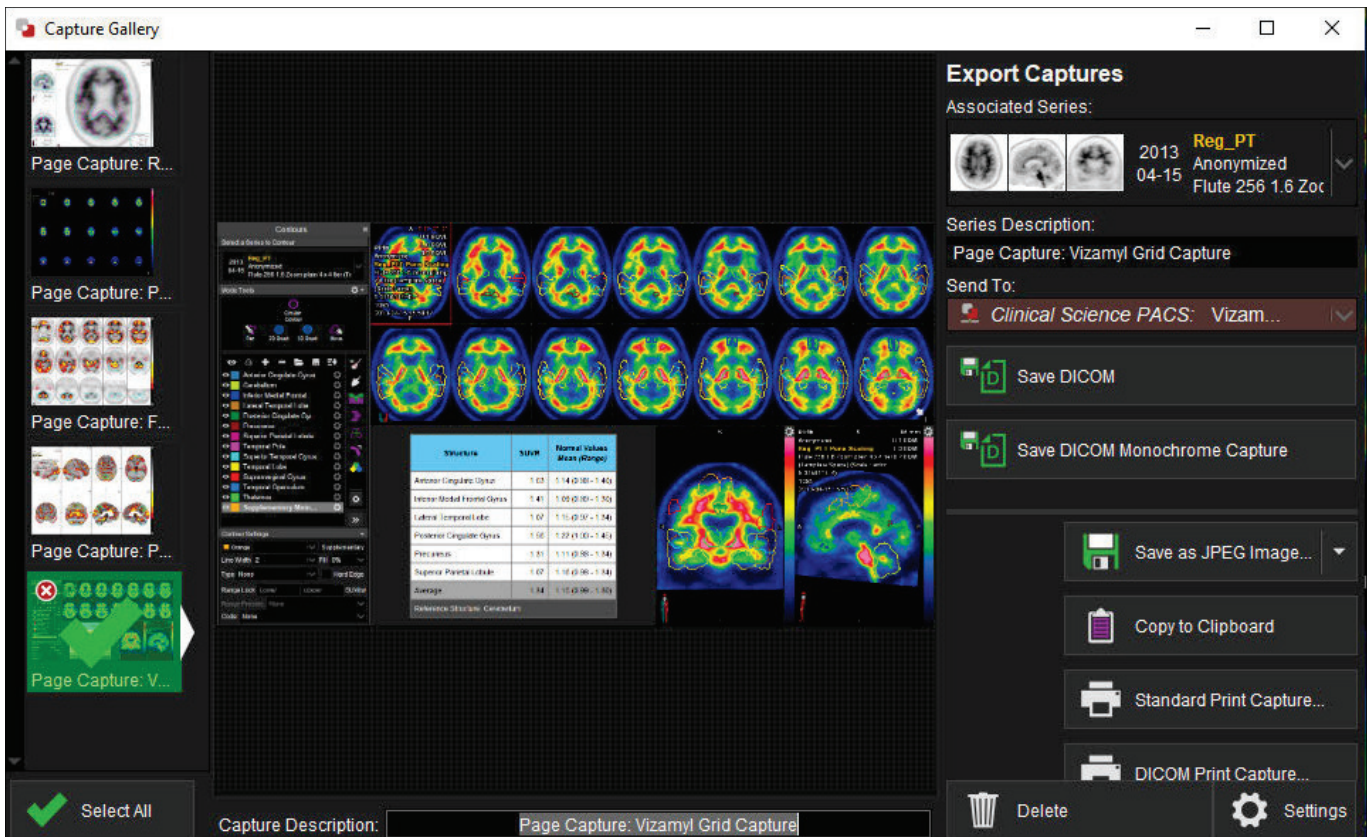
The SUVR is different from the region-based z-scores shown in the Z-score Analysis window because the z-scores are calculated from the mean of the intensity values of the region.

Save Results

Save your work so you can return to it later or share it with others.

Save Your Captures

Open the Capture Gallery  in the upper-right corner of MIM to save screen captures. You can send the screen captures to other physicians or store them in your PACS system for later review.




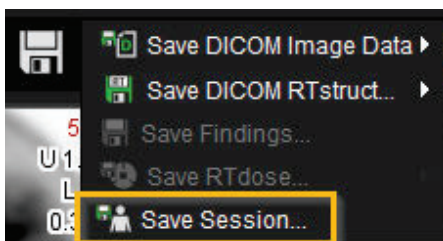
Refer to [Create and Save Secondary Captures](#) for more information about creating and saving captures.



Tip: You can also save Z-score windows as secondary captures. In the Z-Score Analysis window, click **Save As...** and select **Secondary Capture**. A capture of the z-score results is added to the Capture Gallery.

Save Your Session

Click the save  button in the MIM top toolbar and select **Save Session...** When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.



MIM Workflows[™]: Neuro PET/SPECT — Subtraction

MIMTD-834 • 03 Jan 2024

Overview

Use the **Neuro PET/SPECT - Subtraction** workflow to subtract a comparison image from a baseline image. This workflow performs a cluster analysis to identify voxels where z-scores indicate a different level of uptake.



Related: Refer to [Cluster Analysis: Technical Details](#) for more information about how cluster analysis is performed.

Contents

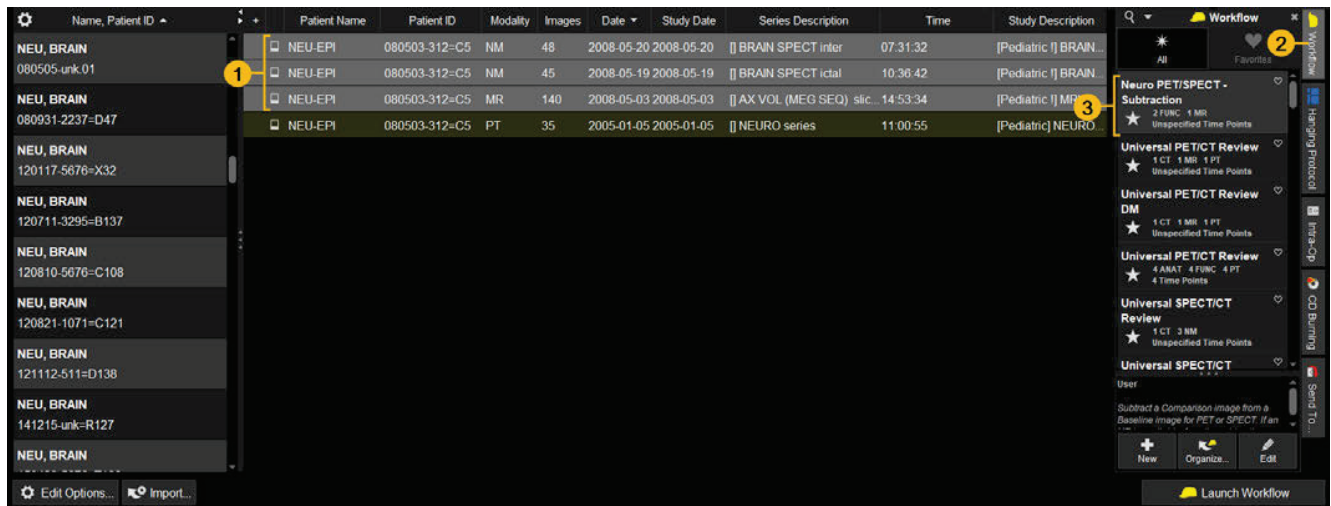
- [Run the Workflow](#)
 - [Launch the Workflow](#)
 - [Register the Series](#)
 - [Review Auto-Normalization](#)
 - [Perform Subtraction Cluster Analysis](#)
- [Analyze the Results](#)
 - [Review Brain Displays](#)
 - [Review the Structured Report](#)
- [Save Your Results](#)
 - [Save Your Captures](#)
 - [Save Your Session](#)
- [\(Optional\) Determine Which Region to Use for Analysis](#)

Run the Workflow

The workflow automates much of the processing. Follow the prompts in the Notifications window as the workflow runs.


Launch the Workflow

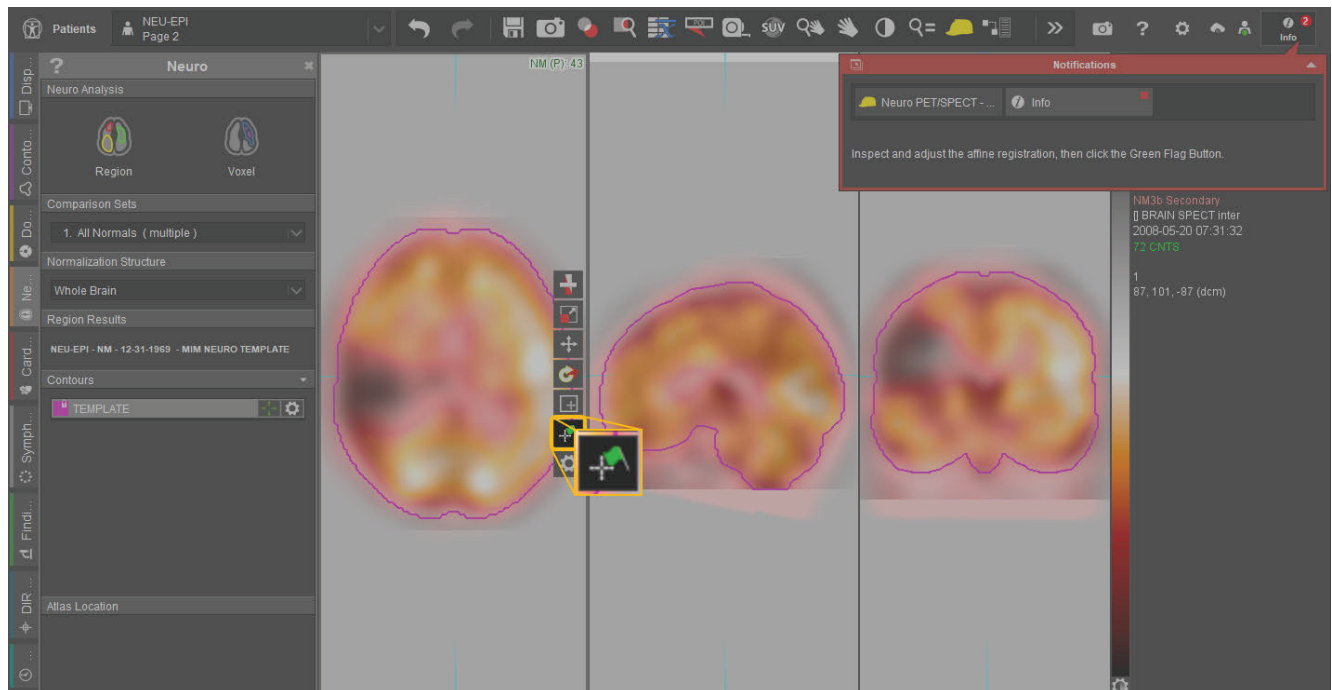
1. Select a pair of PET or SPECT series that includes a baseline and a comparison from the patient list. If there is an MR for the patient, select it as well.
2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **Neuro PET SPECT — Subtraction** workflow from the list to launch it.



4. In the Confirm Selections window, 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.
5. If the workflow does not find the tracer in the DICOM data, answer the prompt to select the tracer and click **OK** to continue. If the workflow finds the tracer in the DICOM data, the workflow proceeds immediately to the next step.

Register the Series

1. The workflow performs an affine registration. Check the registration to make sure the majority of the SPECT or PET series fits within the pink Template contour. When you are ready, click the green flag button  to continue.



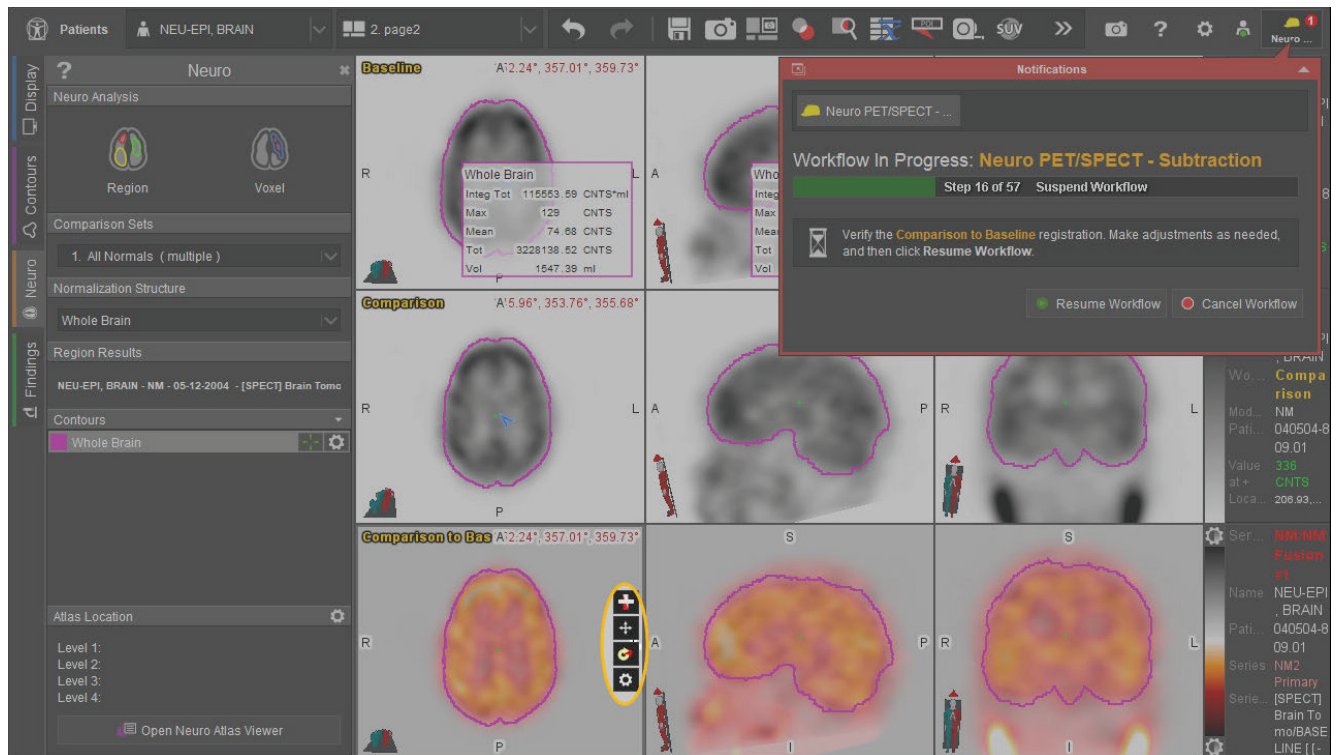
Tip: Affine registrations rarely require adjustment. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See [Adjust Affine Registration](#) for more information.

2. If an MR is present, the workflow pauses and asks you to verify the registration between the MR and the baseline registration. If adjustments need to be made to the image alignment, use the fusion adjustment tools to the right of the fused image. After verifying the registration, click **Resume Workflow**.



Related: Refer to [Adjust Fusions Manually](#) for more information about the adjustment tools.

3. The workflow fuses the comparison image to the baseline image. The workflow pauses and asks you to verify the registration between the baseline image and the comparison image. If adjustments need to be made to the image alignment, use the fusion adjustment tools to the right of the fused image.



After verifying the registration, click **Resume Workflow**.



Related: Refer to [Adjust Fusions Manually](#) for more information about the adjustment tools.

Review Auto-Normalization

The workflow normalizes the comparison image to the baseline image. The workflow pauses and prompts you to verify the auto-normalization it performed.



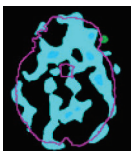
Follow the onscreen instructions to review the normalization and, if necessary, to make adjustments.



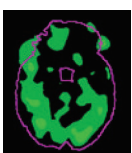
Tip: To hide the Notifications window, click the arrow in the upper-right corner of the Notifications window. To expand the Notifications window again, click the flashing notification symbol in the upper-right corner of MIM.

The auto-normalization algorithm seeks to minimize the differences between voxels in the two PET or SPECT scans. If the algorithm finds a local minimum, manually adjust the contrast of either scan until the desired normalization is achieved.

Focus on the bottom **Comparison to Baseline** row, which overlays the comparison image to the baseline image.



- More blue indicates that the baseline image is appearing more strongly. Left-click drag down on the contrast bar on the **Baseline** image (top row).



- More green indicates that the comparison image is appearing more strongly. Left-click drag down on the contrast bar on the **Comparison** image (middle row).

When you are ready, click **Resume Workflow** to continue.

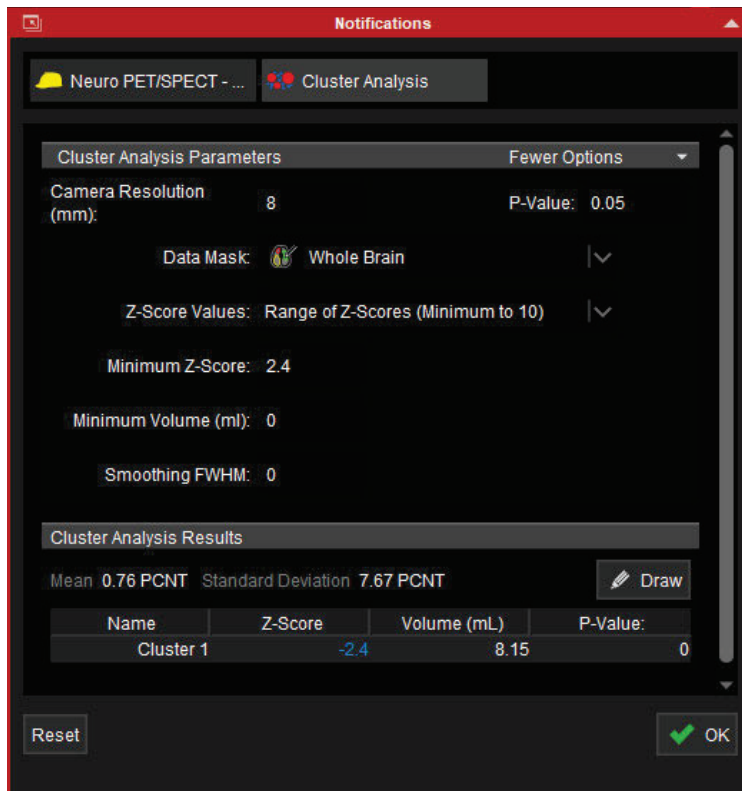


Tip: For more information on MIM's auto-normalization method, refer to [Fusion Image Subtraction Formulas: Technical Details](#).

Perform Subtraction Cluster Analysis

A new tab opens in the Notifications window for subtraction cluster analysis:

1. If necessary, enter or edit the **Camera Resolution** used for the PET or SPECT scans and the cluster **P-Value**.



The screenshot shows the 'Notifications' window with the 'Cluster Analysis' tab selected. The 'Cluster Analysis Parameters' section is expanded, showing settings for Camera Resolution (8 mm), P-Value (0.05), Data Mask (Whole Brain), Z-Score Values (Range of Z-Scores (Minimum to 10)), Minimum Z-Score (2.4), Minimum Volume (ml) (0), and Smoothing FWHM (0). The 'Cluster Analysis Results' section shows a Mean of 0.76 PCNT and Standard Deviation of 7.67 PCNT. A table below lists the results for Cluster 1.

Name	Z-Score	Volume (mL)	P-Value:
Cluster 1	-2.4	8.15	0

Buttons for 'Reset' and 'OK' are visible at the bottom.

2. Optionally adjust additional cluster analysis settings. Click the **Cluster Analysis Parameters** title bar to expand or collapse additional parameters.
 - **Data Mask** — By default, the Whole Brain atlas is used. See [\(Optional\) Determine Which Region to Use for Analysis](#) below for more information if you want to limit analysis to a different region.
 - Use the **Z-Score Values** dropdown menu to choose how to show clusters by z-score:
 - **Minimum Value Only** — Shows clusters that contain z-scores that are greater than or equal to the minimum value entered.

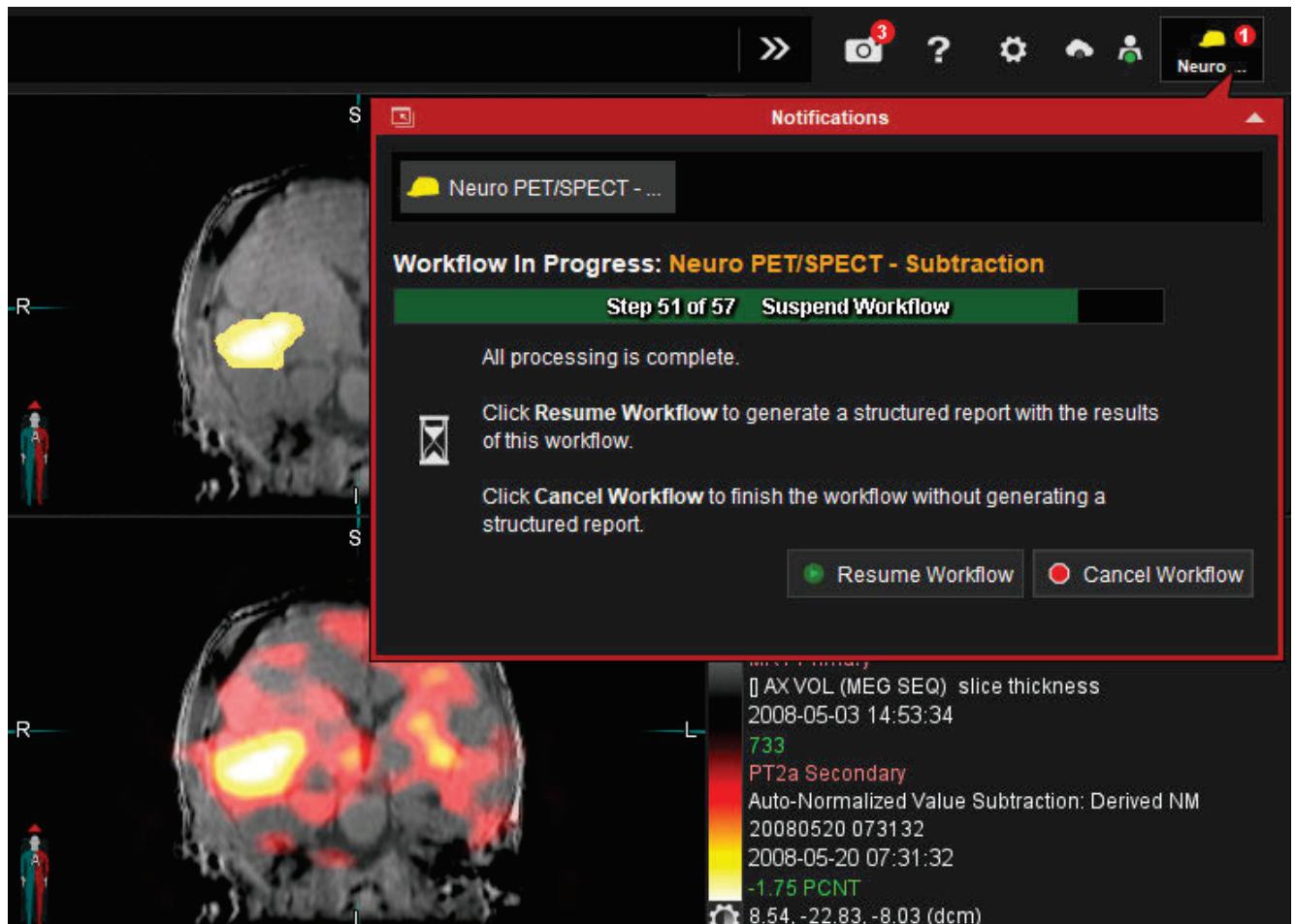


- **Range of Z-Scores (Minimum to 10)** — Shows a range of z-scores from 10 to the minimum z-score entered, moving in .5 z-score increments. This range is two-tail, meaning if the minimum z-score entered was 2.4, the range extends from 2.4 to 10 and -10 to -2.4.
 - **Minimum Z-Score** — Determines the minimum z-score value to show.
 - **Minimum Volume (ml)** — Determines the minimum size to show. For example, increase this value to show only larger volumes.
 - **Smoothing FWHM** — This value is typically 0. If needed, increase the smoothing factor to reduce noise within the image.
3. Cluster analysis results appear in the table below the cluster analysis parameters and update automatically as you edit parameters:
- i. Click any of the clusters in the table to localize to that cluster on the image.
 - ii. Click the **Draw** button to draw the cluster on the image.



Tip: The cluster results depend on the entered p-value, minimum volume, and minimum z-score value. If a cluster falls into the range of z-scores but is out of the range of the p-value, or is at the minimum volume or lower, it is not displayed.

4. After you have completed cluster analysis, click **OK** to continue the workflow.
5. Follow the prompt in the Notifications window to determine whether the workflow produces a structured report. This is the final step of the workflow.



Tip: If you do not want to be prompted to create a report, please contact MIM Software Support at support.mimsoftware.com to remove this step of the workflow.

Analyze the Results


When the workflow is complete, review the image display and the cluster analysis results.

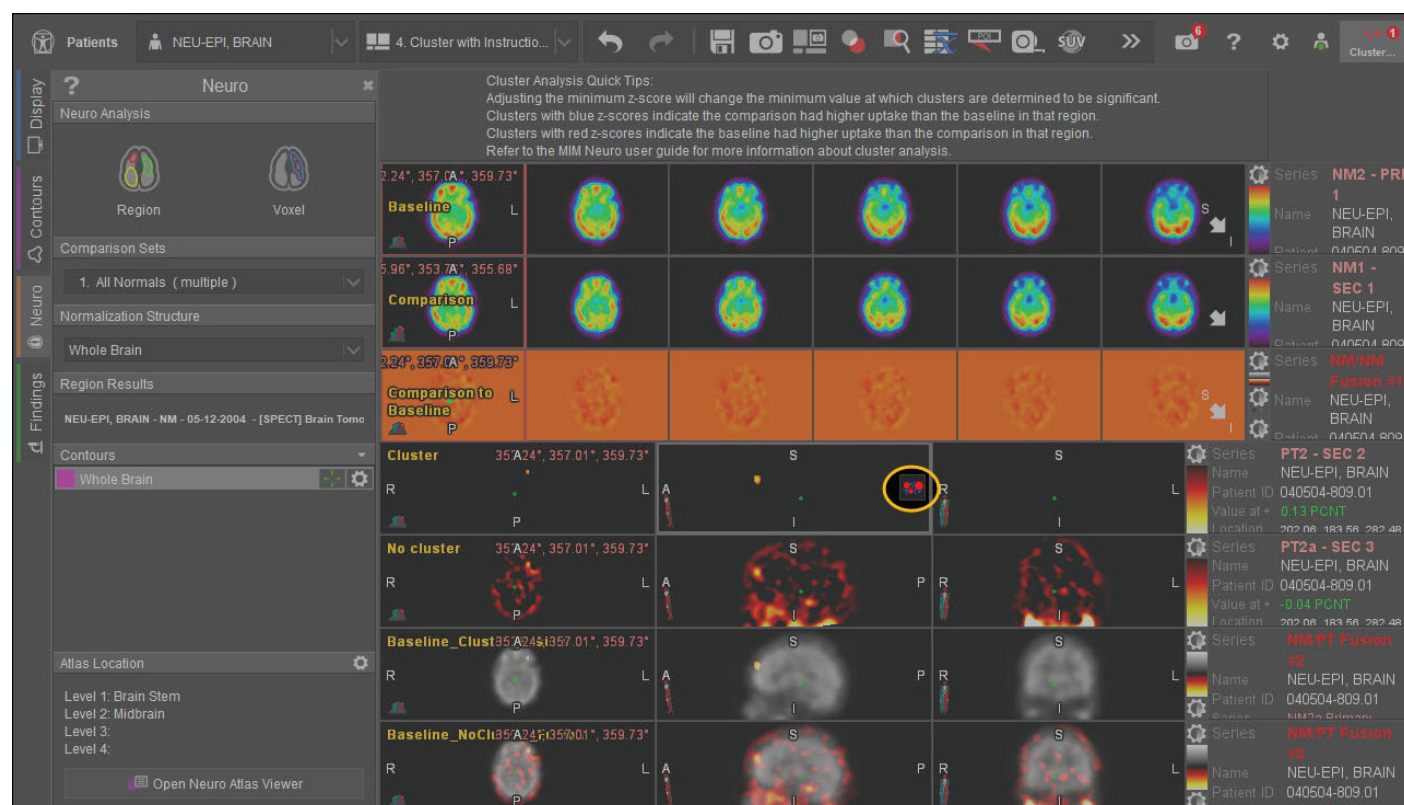
Review Brain Displays

The final display shows the following images:

- PET or SPECT fused to an image showing clusters only.
- PET or SPECT fused to the full subtraction image without cluster analysis.

- PET or SPECT baseline image.
- PET or SPECT comparison image.

To reopen the Cluster Analysis window, go to the page with the Cluster Analysis Quick Tips at the top. Hover over the cluster series and click the cluster analysis  button that appears on the right side of the viewport.

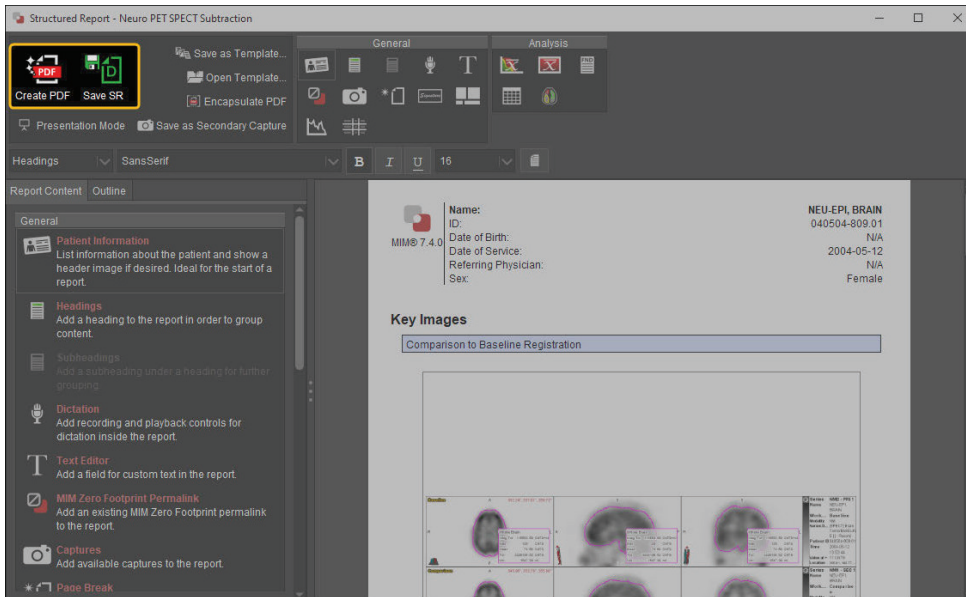


Review the Structured Report

If desired, you can have the workflow generate a structured report. The report includes a screen capture of each generated image display.

Save the report using in the buttons in the upper-left corner:

- Click **Create PDF** to download the structured report as a PDF, such as to share with other clinicians.
- Click **Save SR** to save the structured report as a DICOM object in MIM that you can access from your patient list.




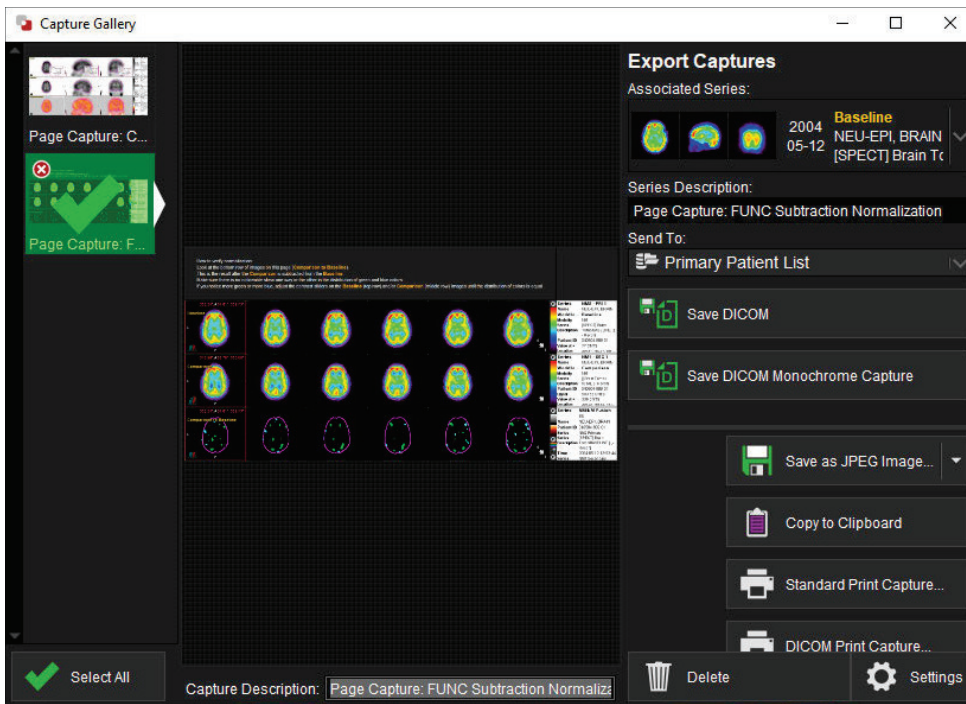
Related: Refer to [Create and Modify Structured Reports](#) for more information about working with structured reports.

Save Your Results

Save your work so you can return to it later or share it with others.


Save Your Captures

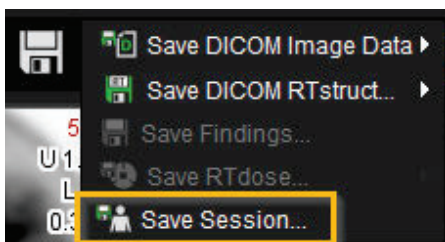
Open the Capture Gallery  in the upper-right corner of MIM to save screen captures. You can send the screen captures to other physicians or store them in your PACS system for later review.



Refer to [Create and Save Secondary Captures](#) for more information about creating and saving captures.

Save Your Session

Click the save  button in the MIM top toolbar and select **Save Session....** When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.





(Optional) Determine Which Region to Use for Analysis

The cluster analysis tool uses the Whole Brain atlas by default to restrict the part of the image being used for the calculation of significant clusters. If desired, you can choose a different area of the image instead.

For example, you may want to use a custom data mask region if one scan is missing part of the brain that is present in the other scan (e.g., if the patient had surgery between the time of the two scans).

To use a custom region instead of the whole brain, follow these steps:



1. Launch the workflow and register the series, as described above.
2. While on the normalization step, go to the **Contours** sidebar.
3. Click the plus  to add a new contour and use the **2D Brush**  or another contouring tool of your choice to contour the area that you want to be included in the analysis.
4. Resume the workflow.
5. In the Cluster Analysis notification, use the **Data Mask** dropdown to select the contour that you drew. The Cluster Analysis Results at the bottom of the Notifications window update for the contour that you selected.

MIM Workflows™ : Neuro SPECT

MIMTD-1798 • 04 Jan 2024

Overview

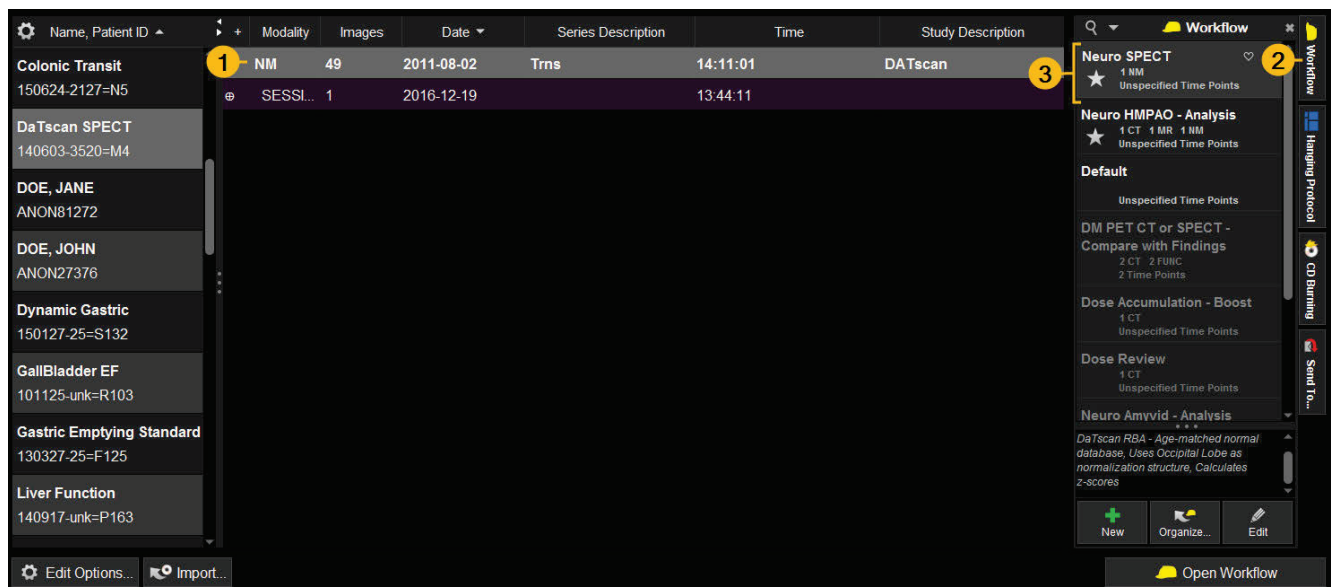
Use the **Neuro SPECT** workflow to generate a viewing display for neuro NM studies. This workflow registers the image and applies a color table to aid in visualization but does not perform any analysis.

Contents

- [Run the Workflow](#)
- [Review the Display](#)
- [Save the Session](#)


Run the Workflow

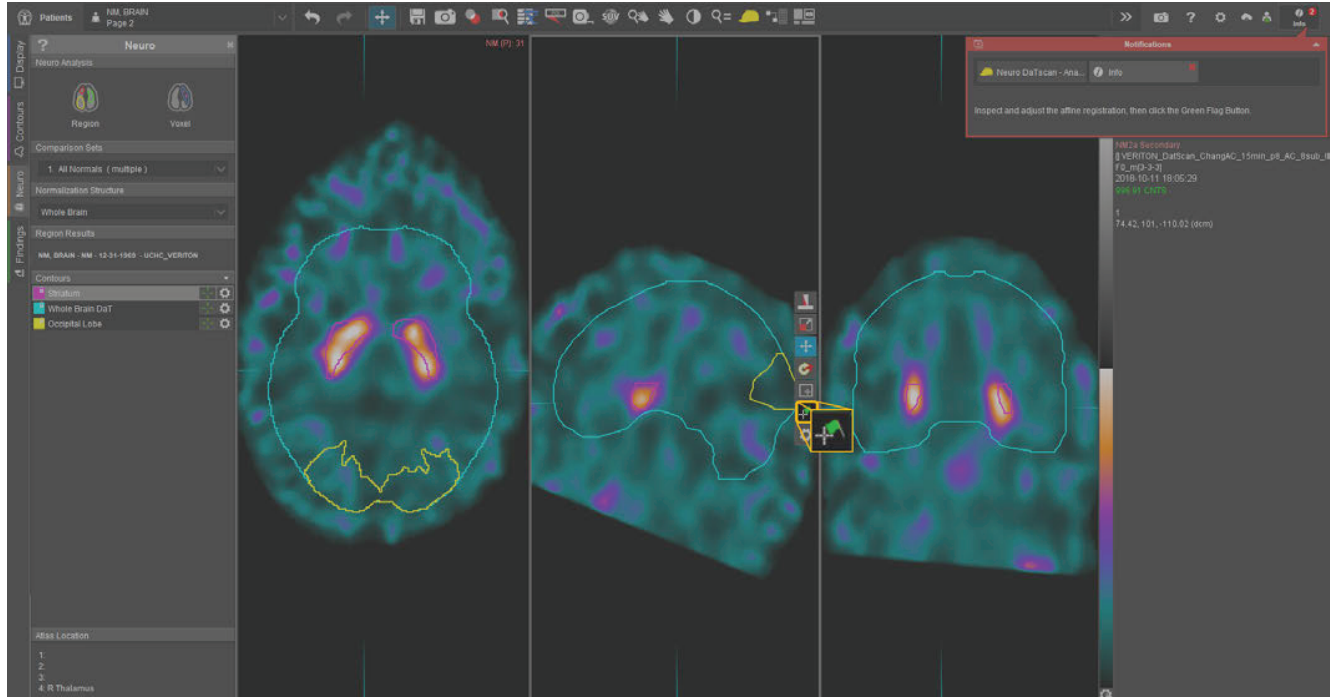
1. From the patient list, select the desired SPECT series.
2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **Neuro SPECT** workflow from the list to launch it.




4. If the workflow does not find the tracer in the DICOM data, answer the prompt to select the tracer and click **OK** to continue. If the workflow finds the tracer in the DICOM data, the workflow proceeds immediately to the next step.



- The workflow performs an affine registration between your SPECT series (secondary series) and the template space (primary series). Check the registration to make sure it aligns as accurately as possible. When you are ready, click the green flag button  to continue.



Tip: If adjustments are necessary, use the tools to the right of the image to correct the alignment. See [Adjust Affine Registrations](#) for more information.

- The workflow then prompts you to inspect and adjust the affine registration for each side of the brain separately. Aligning the two hemispheres independently helps account for atrophy or asymmetry that may make it difficult to align both sides at once. When you are ready, click the green flag button  to continue.



Tip: If adjustments are necessary, use the tools to the right of the image to correct the alignment. See [Adjust Affine Registrations](#) for more information.

- If you are prompted to confirm how to proceed with processing:
 - Select **Accept changes and perform registration** for MIM to accept your adjustments and perform a deformable registration between the template and the selected series. Statistics are calculated based on this deformable alignment.

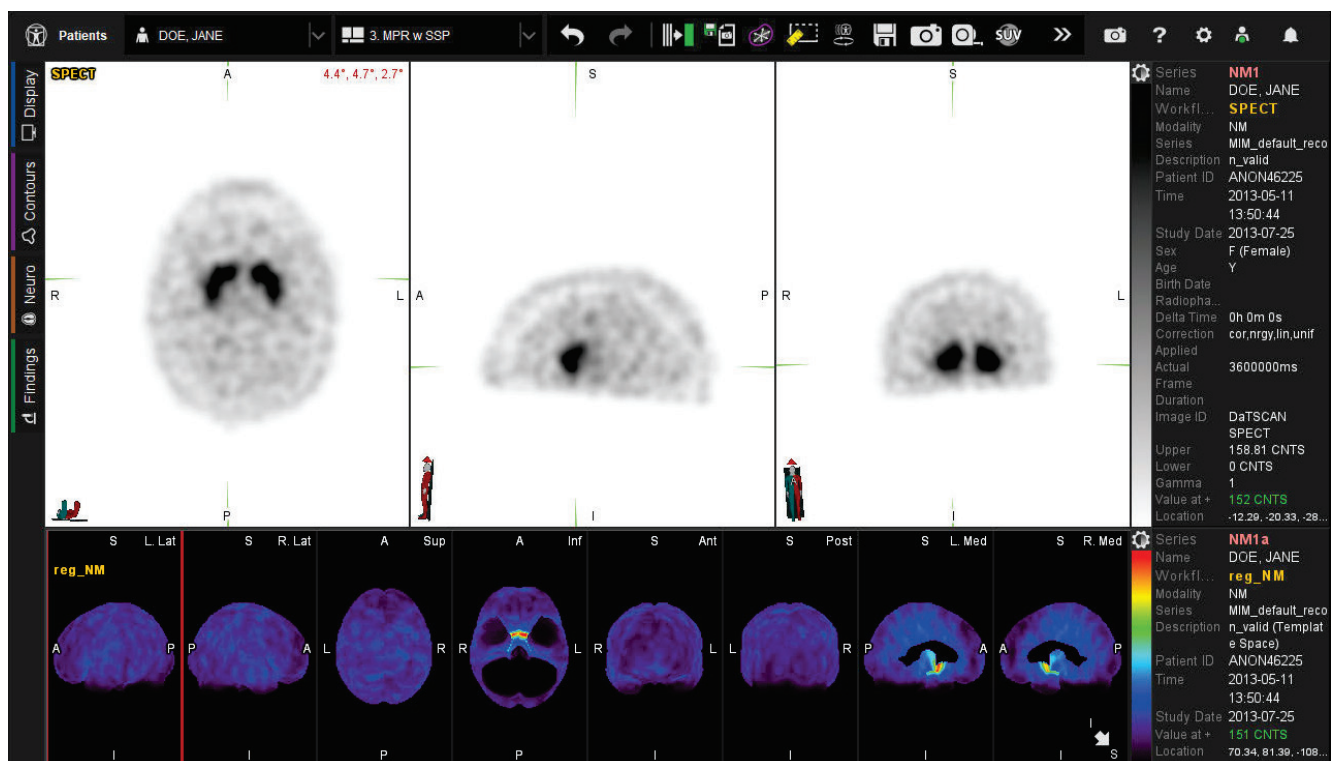
- Select **Accept changes as final registration** for MIM to accept your adjustments and use the current alignment to calculate statistics.

8. The workflow finishes running and displays the images.

Review the Display

The workflow produces the following pages:

- Ax Grid w SSP — Shows multiple axial slices with a SSP.
- MPR w SSP — Shows the axial, sagittal, and coronal planes with a Stereotactic Surface Projection (SSP).




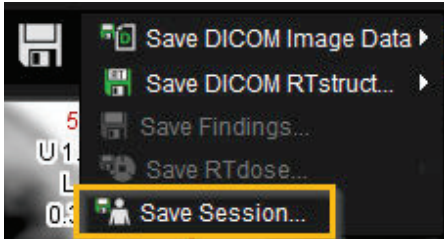
Tip: Use the left/right arrow keys or the page selector in the top toolbar to move between pages.



Related: Refer to [View Color Scales and Stereotactic Surface Projections](#) for more information about MIMneuro[®] displays.

Save the Session

Click the save  button in the top toolbar and select **Save Session....** When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.



MIM Workflows[™] : Neuro DIAMOX — Subtraction

MIMTD-1799 • 04 Jan 2024

Overview

Use the **Neuro DIAMOX - Subtraction** workflow to subtract a comparison DIAMOX image from a baseline image. This workflow performs a cluster analysis to identify voxels where z-scores indicate a different level of uptake.



Related: Refer to [Cluster Analysis: Technical Details](#) for more information about how cluster analysis is performed.

Contents

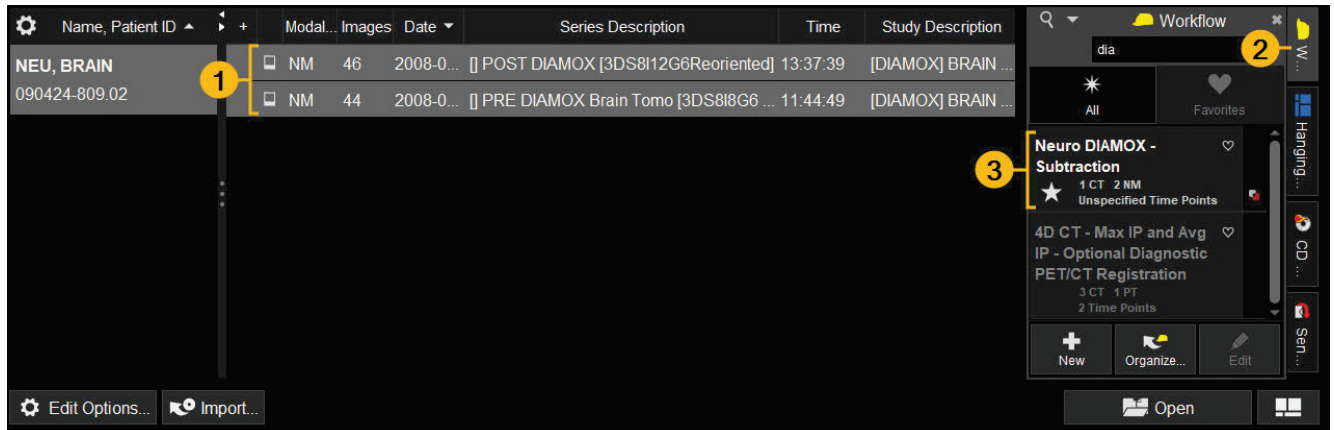
- [Run the Workflow](#)
 - [Launch the Workflow](#)
 - [Register the Series](#)
 - [Review Auto-Normalization](#)
 - [Perform Subtraction Cluster Analysis](#)
- [Analyze the Results](#)
 - [Review Brain Displays](#)
 - [Review the Structured Report](#)
- [Save Your Results](#)
 - [Save Your Captures](#)
 - [Save Your Session](#)
- [\(Optional\) Determine Which Region to Use for Analysis](#)

Run the Workflow

The workflow automates much of the processing. Follow the prompts in the Notifications window as the workflow runs.


Launch the Workflow

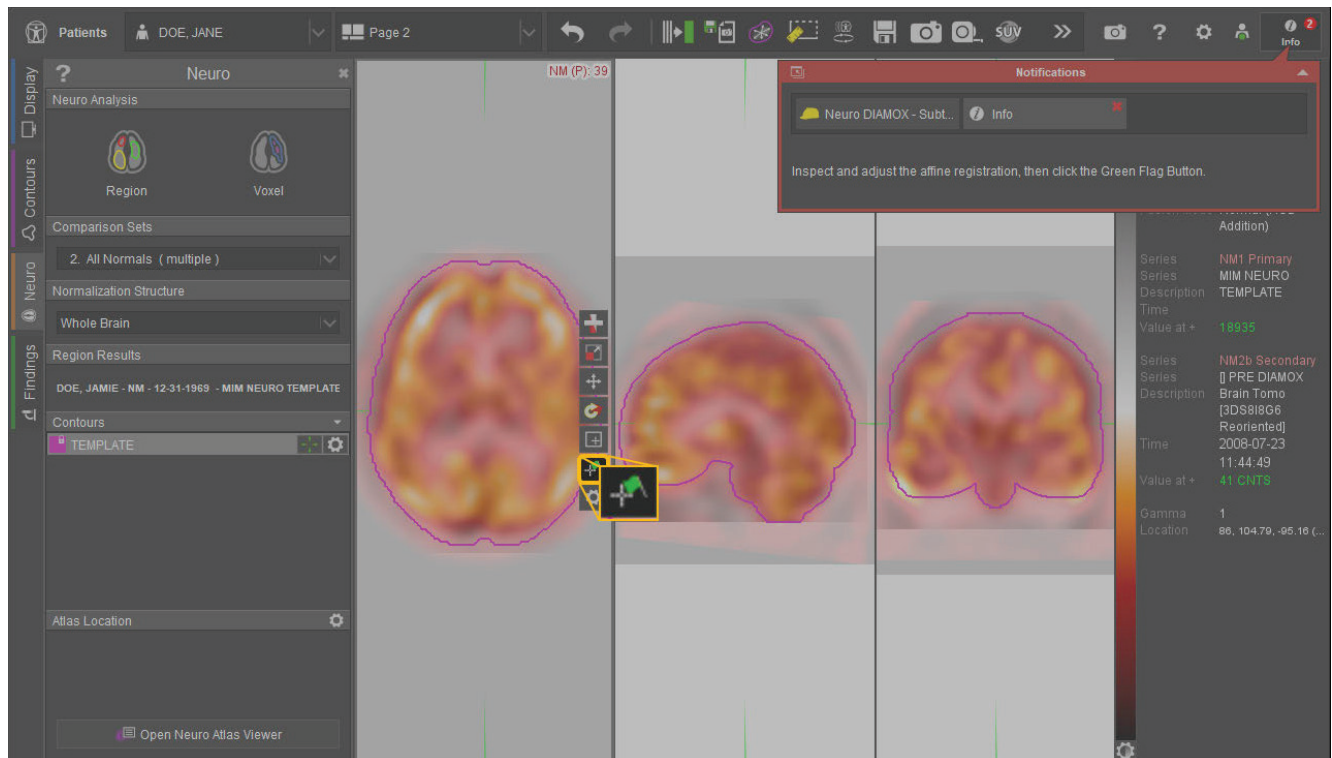
1. Select a pair of SPECT series that includes a baseline and a comparison from the patient list. If there is a CT for the patient, select it as well.
2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **Neuro DIAMOX — Subtraction** workflow from the list to launch it.



4. In the Confirm Selections window, 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.

Register the Series

1. The workflow performs an affine registration. Check the registration to make sure the majority of the SPECT series fits within the pink Template contour. When you are ready, click the green flag button  to continue.



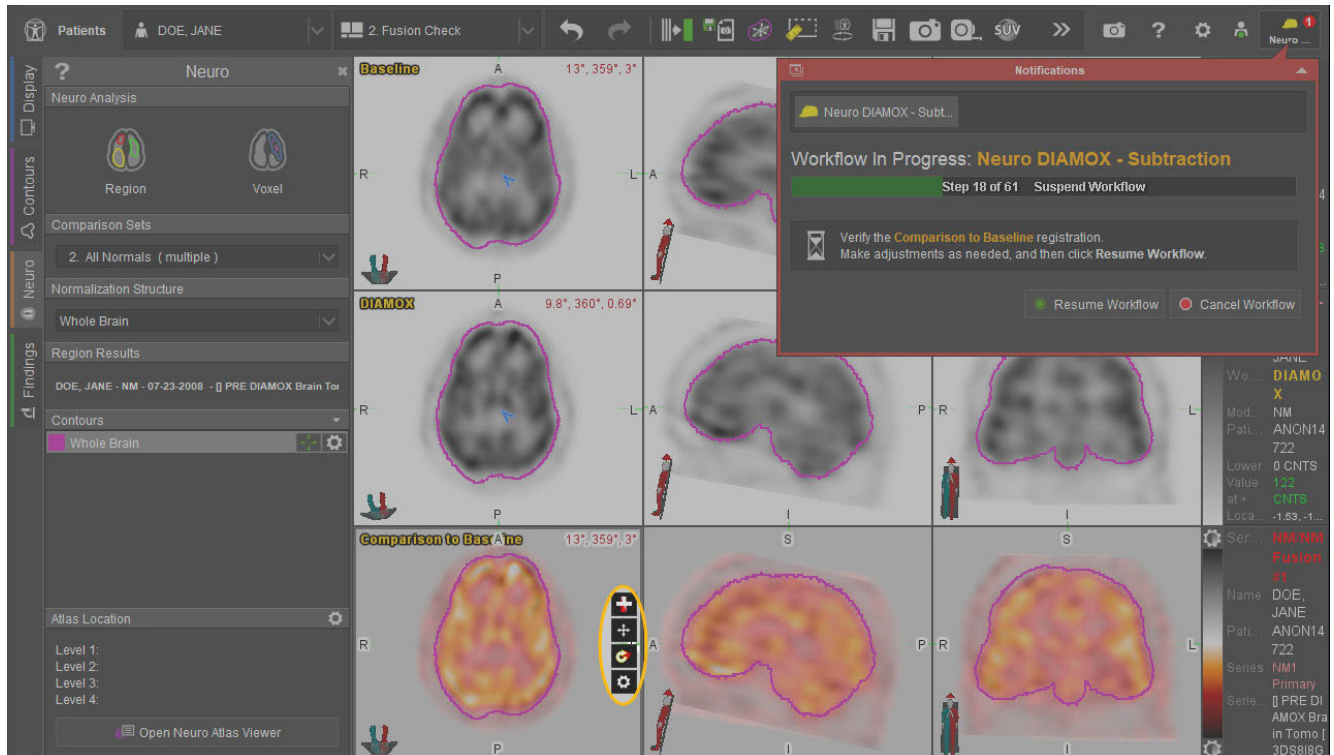
Tip: Affine registrations rarely require adjustment. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See [Adjust Affine Registration](#) for more information.

2. If you are prompted to confirm how to proceed with processing:
 - Select **Accept changes and perform registration** for MIM to accept your adjustments and perform a deformable registration between the template and the selected series. Statistics are calculated based on this deformable alignment.
 - Select **Accept changes as final registration** for MIM to accept your adjustments and use the current alignment to calculate statistics.
3. If a CT is present, the workflow pauses and asks you to verify the registration between the CT and the baseline registration in the bottom row. If adjustments need to be made to the image alignment, use the fusion adjustment tools to the right of the fused image. After verifying the registration, click **Resume Workflow**.



Related: Refer to [Adjust Fusions Manually](#) for more information about the adjustment tools.

- The workflow fuses the comparison image to the baseline image. The workflow pauses and asks you to verify the registration between the baseline image and the comparison image in the bottom row. If adjustments need to be made to the image alignment, use the fusion adjustment tools to the right of the fused image.



After verifying the registration, click **Resume Workflow**.



Related: Refer to [Adjust Fusions Manually](#) for more information about the adjustment tools.

Review Auto-Normalization

The workflow normalizes the comparison image to the baseline image. The workflow pauses and prompts you to verify the auto-normalization it performed.



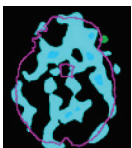
Follow the onscreen instructions to review the normalization and, if necessary, to make adjustments.



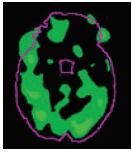
Tip: To hide the Notifications window, click the arrow in the upper-right corner of the Notifications window. To expand the Notifications window again, click the flashing notification symbol in the upper-right corner of MIM.

The auto-normalization algorithm seeks to minimize the differences between voxels in the SPECT scans. If the algorithm finds a local minimum, manually adjust the contrast of either scan until the desired normalization is achieved.

Focus on the bottom **Comparison to Baseline** row, which overlays the comparison image to the baseline image.



- More blue indicates that the baseline image is appearing more strongly. Left-click drag down on the contrast bar on the **Baseline** image (top row).



- More green indicates that the comparison image is appearing more strongly. Left-click drag down on the contrast bar on the **Comparison** image (middle row).

When you are ready, click **Resume Workflow** to continue.

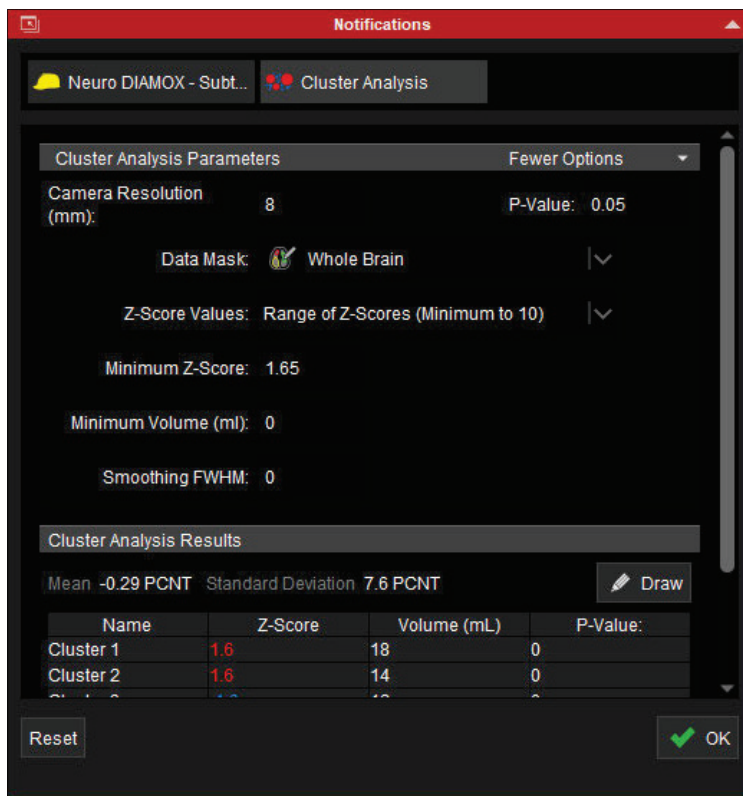


Tip: For more information on MIM's auto-normalization method, refer to [Fusion Image Subtraction Formulas: Technical Details](#).

Perform Subtraction Cluster Analysis

A new tab opens in the Notifications window for subtraction cluster analysis:

1. If necessary, enter or edit the **Camera Resolution** used for the SPECT scans and the cluster **P-Value**.



The screenshot shows the 'Notifications' window with the 'Cluster Analysis' tab selected. The 'Cluster Analysis Parameters' section is expanded, showing settings for Camera Resolution (8 mm), P-Value (0.05), Data Mask (Whole Brain), Z-Score Values (Range of Z-Scores (Minimum to 10)), Minimum Z-Score (1.65), Minimum Volume (ml) (0), and Smoothing FWHM (0). The 'Cluster Analysis Results' section shows a table with columns for Name, Z-Score, Volume (mL), and P-Value. The table lists Cluster 1 and Cluster 2, both with a Z-Score of 1.6 and a P-Value of 0. A 'Draw' button is next to the results. At the bottom, there are 'Reset' and 'OK' buttons.

Name	Z-Score	Volume (mL)	P-Value
Cluster 1	1.6	18	0
Cluster 2	1.6	14	0

2. Optionally adjust additional cluster analysis settings. Click the **Cluster Analysis Parameters** title bar to expand or collapse additional parameters.
 - **Data Mask** — By default, the Whole Brain atlas is used. See [\(Optional\) Determine Which Region to Use for Analysis](#) below for more information if you want to limit analysis to a different

region.

- Use the **Z-Score Values** dropdown menu to choose how to show clusters by z-score:
 - **Minimum Value Only** — Shows clusters that contain z-scores that are greater than or equal to the minimum value entered.
 - **Range of Z-Scores (Minimum to 10)** — Shows a range of z-scores from 10 to the minimum z-score entered, moving in .5 z-score increments. This range is two-tail, meaning if the minimum z-score entered was 2.4, the range extends from 2.4 to 10 and -10 to -2.4.
 - **Minimum Z-Score** — Determines the minimum z-score value to show.
 - **Minimum Volume (ml)** — Determines the minimum size to show. For example, increase this value to show only larger volumes.
 - **Smoothing FWHM** — This value is typically 0. If needed, increase the smoothing factor to reduce noise within the image.
3. Cluster analysis results appear in the table below the cluster analysis parameters. The results update automatically as you edit parameters.
- i. Click any of the clusters in the table to localize to that cluster on the image.
 - ii. Click the **Draw** button to draw the cluster on the image.



Tip: The cluster results depend on the entered p-value, minimum volume, and minimum z-score value. If a cluster falls into the range of z-scores but is out of the range of the p-value, or is at the minimum volume or lower, it is not displayed.

4. After you have completed cluster analysis, click **OK** to continue the workflow.
5. Follow the prompt in the Notifications window to determine whether the workflow produces a structured report. This is the final step of the workflow.



Tip: If you do not want to be prompted to create a report, please contact MIM Software Support at support.mimsoftware.com to remove this step of the workflow.

Analyze the Results

When the workflow is complete, review the image display and the cluster analysis results.

Review Brain Displays

The final display shows the following images:

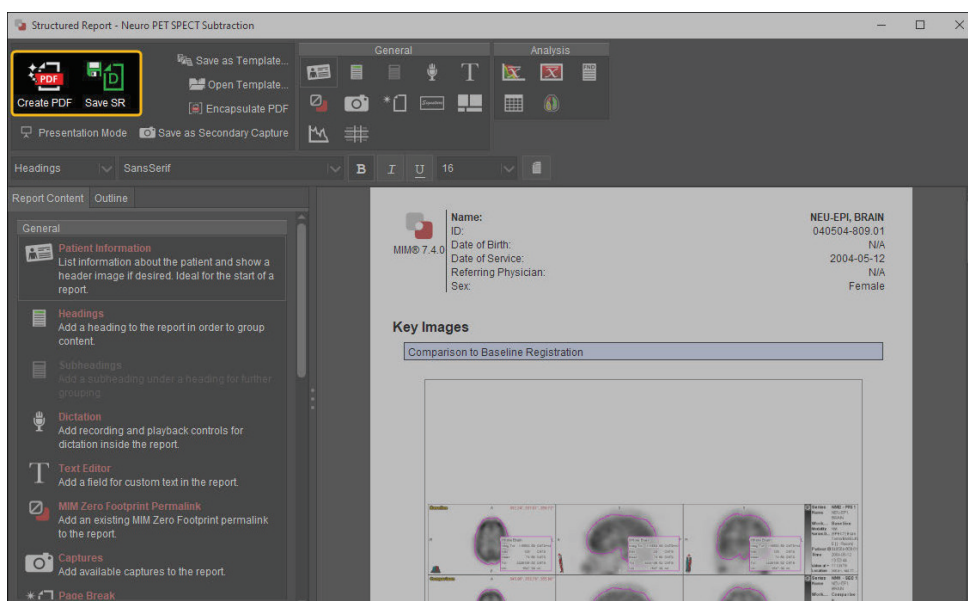
- SPECT fused to an image showing clusters only.
- SPECT fused to the full subtraction image without cluster analysis.
- SPECT baseline image.
- SPECT comparison image.

Review the Structured Report

If desired, you can have the workflow generate a structured report. The report includes a screen capture of each generated image display.

Save the report using in the buttons in the upper-left corner:

- Click **Create PDF** to download the structured report as a PDF, such as to share with other clinicians.
- Click **Save SR** to save the structured report as a DICOM object in MIM that you can access from your patient list.




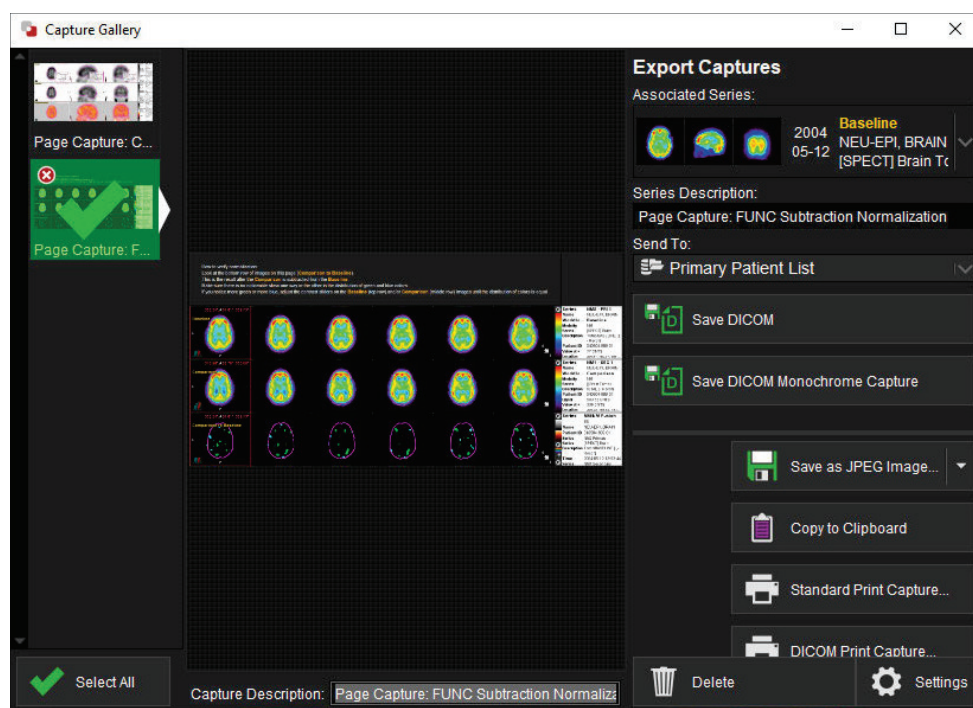
Related: Refer to [Create and Modify Structured Reports](#) for more information about working with structured reports.

Save Your Results

Save your work so you can return to it later or share it with others.


Save Your Captures

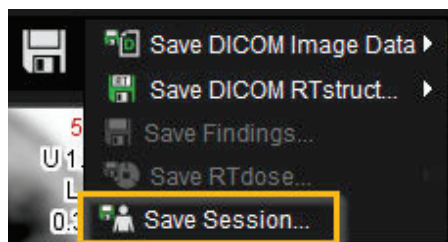
Open the Capture Gallery  in the upper-right corner of MIM to save screen captures. You can send the screen captures to other physicians or store them in your PACS system for later review.



Refer to [Create and Save Secondary Captures](#) for more information about creating and saving captures.

Save Your Session

Click the save  button in the top toolbar and select **Save Session...** When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.





(Optional) Determine Which Region to Use for Analysis

The cluster analysis tool uses the Whole Brain atlas by default to restrict the part of the image being used for the calculation of significant clusters. If desired, you can choose a different area of the image instead.

For example, you may want to use a custom data mask region if one scan is missing part of the brain that is present in the other scan (e.g., if the patient had surgery between the time of the two scans).

To use a custom region instead of the whole brain, follow these steps:

1. Launch the workflow and register the series, as described above.
2. While on the normalization step, go to the **Contours** sidebar.
3. Click the plus  to add a new contour and use the **2D Brush**  or another contouring tool of your choice to contour the area that you want to be included in the analysis.
4. Resume the workflow.
5. In the Cluster Analysis notification, use the **Data Mask** dropdown to select the contour that you drew. The Cluster Analysis Results at the bottom of the Notifications window update for the contour that you selected.

MIM Workflows[™]: Neuro Tauvid — Contrast Display

MIMTD-1800 • 19 Dec 2023

Overview

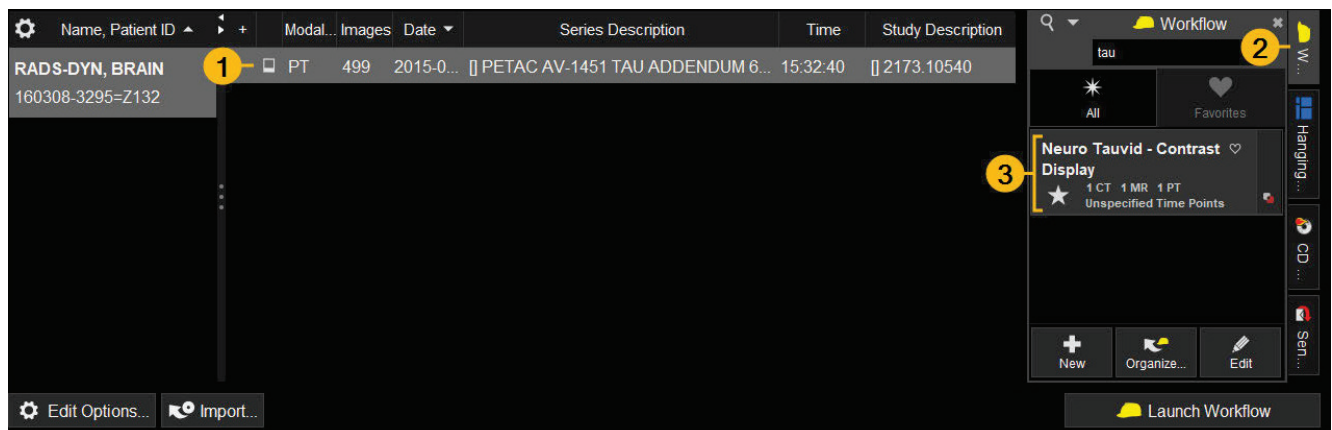
Use the **Neuro Tauvid - Contrast Display** workflow to generate a viewing display for Tauvid studies. This workflow registers the image and applies a color table to aid in visualization but does not perform any analysis.


Contents

- [Run the Workflow](#)
- [Review the Display](#)
- [Save the Session](#)

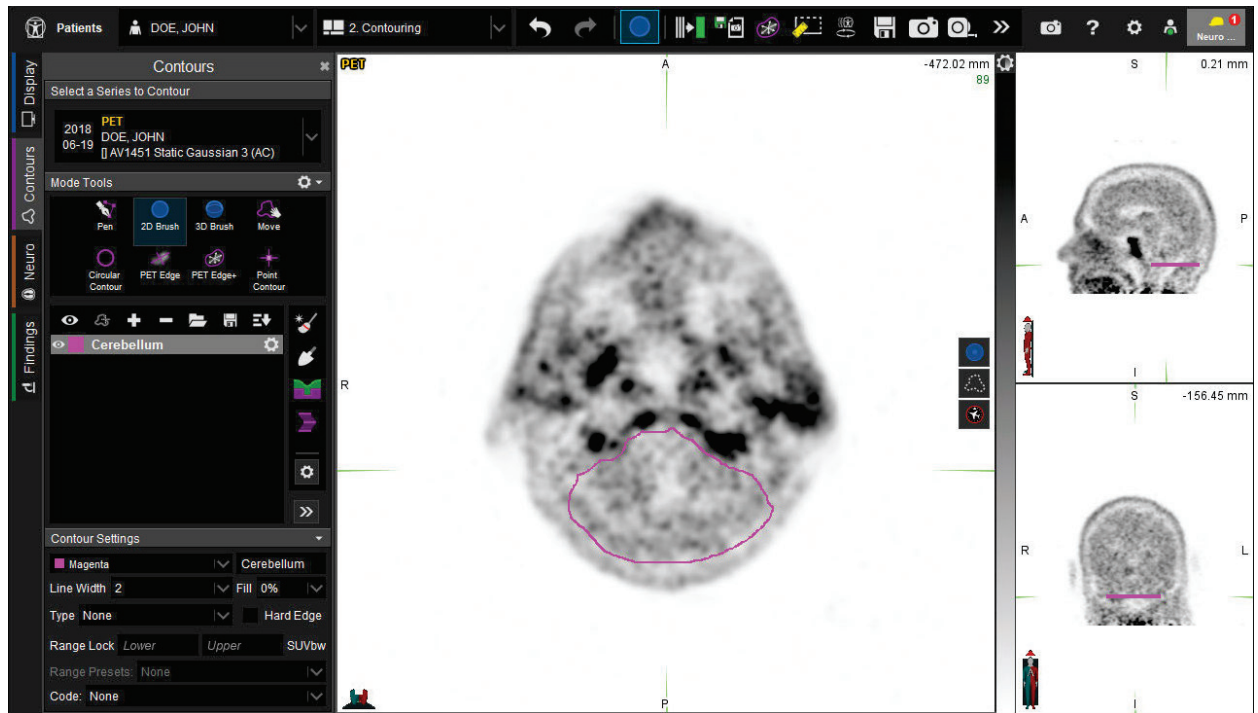
Run the Workflow

1. From the patient list, select the desired PET series. A CT or MR is optional for this workflow. You may select a CT or an MR series if you have one.
2. Select the **Workflow** tab in the patient list to expand it.
3. Double-click the **Neuro Tauvid - Contrast Display** workflow from the list to launch it.



4. The workflow activates the 2D Brush and prompts you to contour the cerebellum:
 - i. Scroll to the axial slice where the cross-section of the cerebellum is at its maximum.
 - ii. Use the **2D Brush**  to contour the cerebellum.

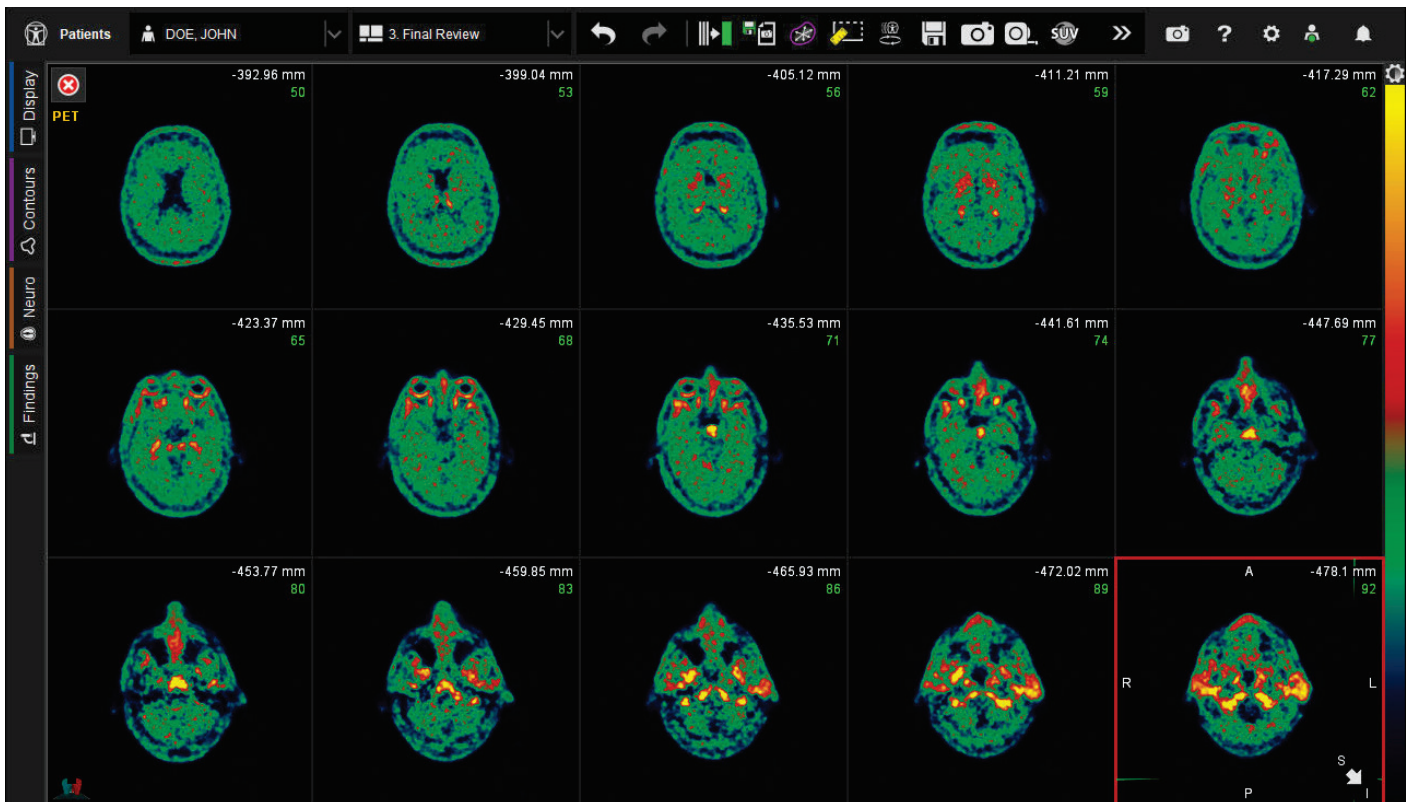
- iii. When you are ready, click **Resume Workflow** in the Notifications window.



5. The workflow finishes running and displays the images.


Review the Display

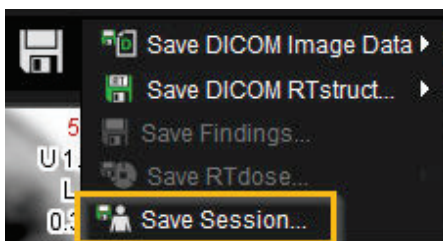
The workflow produces a display with contrast settings and a color table applied. It uses the cerebellum region that you contoured for normalization. Areas of higher uptake appear in red and orange, and areas of lower uptake appear in green and blue.



Related: Refer to [View Color Scales and Stereotactic Surface Projections](#) for more information about MIMneuro® displays.

Save the Session

Click the save  button in the top toolbar and select **Save Session...**. When you save a session, it is like putting a bookmark in the session at its current state. You can reopen the session at the same place at a later time or to share the results with colleagues.



Appendix

Default Keyboard Shortcuts

MIMTD-1363 • 26 Jul 2023


Overview

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



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



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



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

Contents

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

General

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

Viewing, Localizing, and Scrolling

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

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

Zoom

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

Contrast

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

Annotations, Measurements, and SUV

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

Contouring

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

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

Fusions

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

Nuclear Medicine Processing

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

Screen Captures

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

Series Resolution

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

Neuro Analysis: Technical Details

MIMTD-857 • 06 Dec 2023

PET and SPECT brain image volumes normally have different intensities based on anatomic location. In order to compare intensities between brain image volumes, the brains are mapped to a standard space, or template space. Ideally, all similar structures would be mapped to the same location in this standard space.

Registration to a Template Space

MIMneuro® maps a brain image volume into template space in a two-step process.¹

1. In the first step, the brain is automatically translated, rotated, and independently scaled in three independent orthogonal directions to provide the optimum mapping to template space.
2. In the second step, the brain is warped into template space using a Thin Plate spline technique and automatically determined control points that are defined to be at the same anatomic location in the patient and image space volumes.

Determination of a Comparison Set

Persons defined as having normal brain function are all mapped to template space and the mean and standard deviation of normalized count levels are determined for each location in this standard space. These mean and standard deviation count levels are used to define a comparison set that is then used for comparison to an individual patient's count levels in template space.

Differences between the patient and the template can be determined at the following levels:

- For each voxel in template space
- For a group of voxels that defines an anatomic brain region in template space
- For an operator-defined cluster size of contiguous voxels that are outside of a defined normal limit

Evaluation with Multiple Templates

For patients imaged with highly targeted radiotracers, such as approved amyloid agents, MIM® provides multiple templates for mapping the patient's brain into template space:

- A template expressing the target
- A template not expressing the target
- A combination of the two templates

In this case, the basic two-step registration process stays the same. The difference is that for each step MIM tries to match the patient's image to multiple templates simultaneously, either via affine or deformable

registration. At the end, there is a registered image in template space that closely spatially matches all of the templates at the same time.

¹Piper JW. Quantitative Comparison of Spatial Normalization Algorithms for 3D PET Brain Scans. J Nucl Med 2007; 48 Suppl 2:S403.

Z-Score Calculation: Technical Details

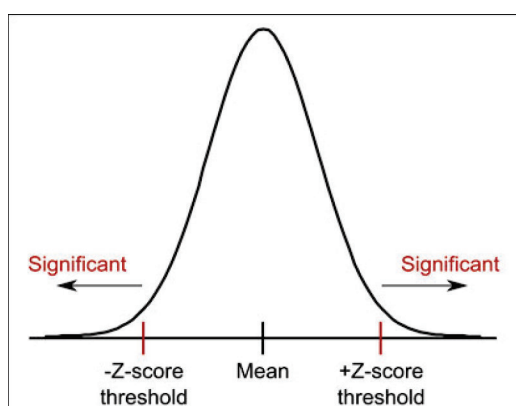
MIMTD-853 • 19 Jul 2024

A z-score is defined as the number of standard deviations from the mean of a data point. In the case of MIMneuro® statistical analysis, the mean is defined by the normals. When comparing a patient brain to the normals for a specific tracer, MIM will notify you of regions that are significantly different through z-scores.

MIM's default z-score threshold is ± 1.65 . This value can be interpreted differently depending on whether you are interested in a one-tailed test or a two-tailed test.

A one-tailed test (common for DaTscan® analysis, FDG analysis, amyloid tracer analysis, and HMPAO imaging) means you are only concerned with z-scores in a specific direction from the mean (negative OR positive z-scores). In a one-tailed test, the default z-score threshold of ± 1.65 equates to a 95% confidence in the output.

A two-tailed test (common in subtractions) means you are interested in z-scores in both directions from the mean (negative AND positive z-scores). In this case, the default z-score threshold of ± 1.65 equates to a 90% confidence in the output.



Given a true mean and a distribution of measurements, significant differences from the mean lie outside of the z-score thresholds. The desired confidence interval and the type of test (one-tailed or two-tailed) determine the threshold. Examples are included in the table below.

Confidence Interval for Mean	Z-score Threshold	
	Two-tailed	One-tailed
99%	± 2.58	2.33 (+ or -)
95%	± 1.96	1.65 (+ or -)
90%	± 1.65	1.28 (+ or -)

Cluster Analysis: Technical Details

MIMTD-858 • 23 Jul 2020

In statistics, an observation is typically considered significant only if the null hypothesis — which proposes that the observation was due to random processes — can be rejected with an acceptable level of certainty.

The probability that the null hypothesis is true is referred to as the p-value. When considering a large sample size, such as in voxel-based z-score or subtraction analysis, reasonable p-values will still yield significant results for some voxels, even for normal images. For example, when using a p-value of 0.01, 1% of voxels will be considered significant in a normal image. In a scan with only random variation, these significant voxels should be randomly distributed throughout the image. The resolution of the camera and the individual voxel p-value threshold will determine the size of spatially correlated voxels, or clusters, which could be due to random variation. Gaussian Random Field Theory uses these inputs to compute a size which would constitute a spatially significant cluster, given some cluster p-value.

Cluster analysis in MIM takes a reasonable estimation of the resolution of the image, in addition to user input for the individual voxel z-score (or standard deviation) threshold and cluster p-value, and filters out any voxels which are not part of a cluster of voxels which are individually more significant than the threshold. At higher z-score thresholds clusters can be smaller and still be statistically significant since the magnitude of the activity difference between the images is larger. At lower z-score thresholds clusters need to be larger in order to be statically significant since the magnitude of differences between the images is less.

For a more detailed explanation, see: Brett M., Penny W., and Kiebel S. An Introduction to Random Field Theory, <http://www.fil.ion.ucl.ac.uk/spm/doc/books/hbf2/pdfs/Ch14.pdf>.

MIMneuro Atlases: Technical Details

MIMTD-859 • 05 Jan 2024

MIM Single Brain Atlas

The MIM Single Brain Atlas was developed from a high-resolution T1-weighted MR scan obtained on a 1.5 Tesla magnet defined on an asymptomatic 57-year-old male subject with no evidence of neuropsychiatric disease and no significant past medical history. The MR scan was reviewed by a radiologist for suitability. Regions were defined in conjunction with a neuroanatomist and expert physicians in the field using MIM standard contouring tools.

The atlas was defined on four levels:

- First level — Lobe-level structures
- Second level — Sublobar structures
- Third level — Gyral-level structures
- Fourth level — Individual structures that did not fall into the previous three levels (e.g., hippocampus and amygdala)

MIM Probabilistic Atlas

The MIM Probabilistic Atlas was created to aid in quantitative region-based analysis by accounting for intersubject anatomic variability.¹ The goal was to create a probabilistic human brain atlas that would allow for more precise and flexible region-based comparison.

The MIM Probabilistic Atlas was developed from T1-weighted MR scans obtained on a 1.5 Tesla magnet for 10 subjects using standard MIM contouring tools. The subjects included 5 males (ages 53, 57, 64, 67, 70) and 5 females (ages 53, 55, 60, 67, 80). The subjects included in the atlas were reviewed by a radiologist for suitability and were without neuropsychiatric symptoms. Four of the subjects also received 11C-DTBZ PET scans and 6 also received FDG-PET scans. The MR scans were fused to the PET brain volumes and the PET volumes were registered using MIMneuro software to bring the atlas into the standard template space.

Ten levels of probability can be chosen for the region-based analysis based on desired sensitivity or specificity. A more sensitive region would be one that encompasses as much of the structure as possible while a more specific region may be smaller and encompasses fewer voxels from other surrounding structures. The levels of probability run from 10% to 100% at 10% increments.

- A 10% probability level would give a region made up of all of the voxels that represented the structure in at least 10% (1/10) of the subjects.
- A 50% probability level would give a region made up of all of the voxels that represented the structure in at least 50% (5/10) of the subjects.

- A 100% probability level would give a region made up of all of the voxels that represented the structure in all (10/10) of the subjects.

A user desiring to include as much of a structure as possible in their region would choose a lower probability level (higher sensitivity). A user desiring that as little as possible of other structures be included in the region (even though less of the actual structure may be included as well) would choose a higher probability level (higher specificity).

¹Nelson AS, Piper JW, Friedland RP, Freeman B. Probabilistic Human Brain Atlas for Functional Imaging: Comparison to Single Brain Atlases. J Nucl Med 2007; 48 Suppl 2:S403.

MIM Amyloid Atlas

The MIM Amyloid brain atlas regions were defined on 10 high-resolution MR scans and a single probabilistic brain atlas region was generated from these. MIM contoured the anatomical brain structures corresponding to the 6 analysis regions that Avid Radiopharmaceuticals[®] used. It is important to note that the Avid brain regions were derived from areas that were significantly different between AD and normal control groups and therefore do not define the entire anatomical structure.

MIM DaTscan[™] Atlas

The MIM DaTscan atlas is a probabilistic atlas that was created by defining volumes of interest (VOIs) on 10 high-resolution T1-weighted MR scans of the brain. Each of the 10 MR scans was registered to template space using their co-registered SPECT scans. The brain regions were then transformed to template space and combined into probabilistic brain regions using majority vote. A default level of 5/10 overlap was chosen. The brain regions were smoothed to account for the lower resolution of a SPECT scan.

Analysis regions were created for the putamen, anterior putamen, posterior putamen, and caudate. The boundary between the anterior and posterior putamen was defined at the level of the anterior commissure. An occipital lobe region was created for use as the reference in region-based analysis.

Florbetapir (Clark 2012) Atlas

The Florbetapir (Clark 2012) Brain Atlas was provided by Avid Radiopharmaceuticals and contains 6 analysis regions and the whole cerebellum for reference. The atlas was developed from a group comparison of Alzheimer's disease (AD) patients to age-matched normal controls. Regions were created that highlighted the largest differences between the two groups.^{1,2} The atlas regions have been registered to the MIMneuro Amyvid PET template space for use in SUVR and region-based analysis with z-scores.

The following is an excerpt from Fleisher et al 2011² describing how the regions were generated:

The ROIs were defined from 11 patients with AD and 15 age-matched healthy controls participating in an early phase I study, all of whom underwent 90-minute dynamic florbetapir-PET acquisitions (images excluded from our analysis) and structural magnetic resonance imaging. The whole-cerebellar reference ROI was hand-drawn from mean group magnetic resonance imaging scans after they were spatially normalized to MNI atlas space. Flow maps from the first 10 minutes of PET data acquisition and a voxelwise comparison of between-

group activity in patients with AD vs. controls were used to identify key cortical regions of increased PET signal in MNI brain atlas space. After gray or white matter and cerebrospinal fluid space segmentation, by use of participants' MRI scans registered in MNI space, 6 cortical gray matter ROIs were defined from the Automated Anatomic Labeling Atlas³ or were manually delineated in gray matter regions that had prominent PET activity in patients with AD compared with controls: medial orbital frontal (Automated Anatomic Labeling), temporal, anterior, and posterior cingulate; parietal lobe; and precuneus.⁴ The average of these 6 regions was evaluated as a measure of global mean cortical florbetapir F 18 binding and was used as the primary outcome measure for ROI analyses.

¹Clark CM, Pontecorvo MJ, Beach TG, et al. Cerebral PET with florbetapir compared with neuropathology at autopsy for detection of neuritic amyloid-Beta plaques: a prospective cohort study. *Lancet Neurol* 2012; 11(8):669-678.

²Fleisher AS, Chen K, Liu X, et al. Using Positron Emission Tomography and Florbetapir F 18 to Image Cortical Amyloid in Patients with Mild Cognitive Impairment or Dementia Due to Alzheimer's Disease. *Arch Neurol* 2011; 68(11):1404-1411.

³Tzourio-Mazoyer N, Landeau B, Papathanassiou D, et al. Automated anatomical labeling of activations in SPM using a macroscopic anatomical parcellation of the MNI MRI single-subject brain. *Neuroimage* 2002;15(1):273-289.

⁴Clark CM, Schneider JA, Bedell BJ, et al. Use of Florbetapir-PET for Imaging B-Amyloid Pathology. [Published correction appears in *JAMA* 2011; 305(11):1096]. *JAMA* 2011; 305(3):275-283.

MIMneuro[®] Normals Databases: Technical Details

MIMTD-860 • 02 Apr 2024

Overview

MIMneuro workflows compare data against normals databases. Refer to [Import MIMneuro Normals](#) for more information about importing the normals into MIM[®]. Review the information below for more details about the normals.

Contents

- [Validate Normals](#)
- [MIM FDG \(Fluorodeoxyglucose 18F\) PET Normal Database](#)
- [MIM 99mTc HMPAO SPECT Normal Database](#)
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- [MIM Amyvid[™] \(Florbetapir 18F\) PET Normal Database](#)
- [MIM NeuraCeq[™] \(Florbetaben 18F\) PET Normal Database](#)
- [MIM VizamyI[™] \(Flutemetamol 18F\) PET Normal Database](#)
- [MIM FDG \(Fluorodeoxyglucose 18F\) Digital PET Normal Database](#)

Validate Normals



Important: Validate normal images from your institution against the MIMneuro normals before clinical use.

To validate normal images, it is recommended that you compare at least five normal scans acquired from each relevant camera to the MIMneuro normals database to ensure that your images are sufficiently similar to the MIM normal data. If a discrepancy is found, you may need to adjust reconstruction settings to appropriately match the MIMneuro normal data.

Alternatively, you may need to create a custom normal database of images from your institution. Each scan added to the new normal database should be compared to an appropriate normal database prior to inclusion. Refer to [Create a Custom Neuro Normals Database](#) for more information.

MIM FDG (Fluorodeoxyglucose ¹⁸F) PET Normal Database

Database Composition

The FDG PET brain database is comprised of 43 individuals (19 females, 24 males) ages 41–80. The breakdown into age ranges is as follows:

- 6 subjects ages 40–49
- 8 subjects ages 50–59
- 14 subjects ages 60–69
- 14 subjects ages 70–79
- 1 subject ages 80–89

The mean age and standard deviation of the group of 43 individuals is 63.79 \pm 9.98 years.

Eligibility Criteria

The database of FDG PET brain scans is comprised of volunteers who met the eligibility criteria for inclusion as determined by an expert neurologist. To be included, the subjects needed:

- To be ambulatory
- In general good health
- Score within normal ranges for standard neuropsychiatric testing

Subjects could not have any of the following: brain tumors, brain metastases or metastases in or near the head, history of a stroke, history of radiation treatment in or near the head, poorly controlled diabetes, chemotherapy, drug abuse, alcoholism, medications which could affect cerebral metabolism, leukemia, history of significant head trauma, kidney failure, severe chronic obstructive pulmonary disease, severe cardiac disease, or a disease which would compromise the immune system (such as HIV).

All brain scans were reviewed by a radiologist to confirm normalcy prior to inclusion into the database.

Protocol for FDG PET Brain Acquisition

The subjects were required to be isolated in a quiet, dimly lit room for a minimum of 20 minutes after the injection of FDG, to remain awake during the PET scan. At least 30 minutes were required to pass after the time of injection before the brain PET acquisition could be started. The PET brain acquisitions were at least 5 minutes in duration for a 3D acquisition and 10 minutes for a 2D acquisition.

The PET brain scans were obtained with the subject's arms down, and the entire brain was included in the scan. A head immobilization device was recommended to be used during the PET acquisition.

The PET brain scans were attenuation corrected and iteratively reconstructed to an in-plane voxel size of approximately 2.5 mm or less. The slice separation for these scans was allowed to be slightly larger than the voxel size, but could not exceed 3.3 mm. The resultant FDG PET brain scans were registered to a common template space using both a linear and nonlinear registration for inclusion into the database.

MIM ^{99m}Tc HMPAO SPECT Normal Database

Database Composition

The database of ^{99m}Tc HMPAO (hexamethylpropylene amine oxime) SPECT brain scans is comprised of 90 healthy volunteers (51 females and 39 males). The breakdown into age ranges is as follows:

- 3 subjects ages 10–19
- 17 subjects ages 20–29
- 15 subjects ages 30–39
- 23 subjects ages 40–49
- 17 subjects ages 50–59
- 11 subjects ages 60–69
- 3 subjects ages 70–79
- 1 subject ages 80–89

The mean age and standard deviation of the group of 90 individuals is 43.88 +/- 15.48 years.

Protocol for SPECT Brain Acquisition

The following is an excerpt from Barnden et al 2015¹ describing image acquisition and reconstruction:

Following injection of 500 MBq of ^{99m}Tc hexamethylpropylene amine oxime (^{99m}Tc-HMPAO) all participants underwent cerebral SPECT scanning using a tripleheaded Irix gamma camera system (Philips Medical Systems, Cleveland, Ohio, USA) with high resolution parallel-hole collimators. HMPAO was administered through a brachial vein cannula at least 5 minutes after local discomfort from its insertion had abated and with the subject lying undisturbed in low light with eyes closed. A 30 minute supine SPECT scan was commenced within 1 hour of injection. Photopeak (126–154 keV) and scatter (111–125 keV) projections were acquired at 120 angles into 128x128 arrays of 3.50mm square pixels.

The scatter projections were smoothed with a Butterworth pre-filter (cut-off 0.25 cycle/pixel, order 3.0), multiplied by 1.3 and subtracted from the photopeak projections. The resulting projections were then Butterworth smoothed (cut-off 0.5 cycle/pixel, order 5.0) and reconstructed using filtered backprojection with slice specific Chang attenuation correction (attenuation coefficient 0.12 cm⁻¹). Care was taken to ensure consistent specification (across subjects) of the scalp edge during attenuation correction. The values for the scatter window multiplier and attenuation coefficient were optimized by comparing reconstructions of the physical Hoffman phantom to its numerical template.²

¹Barnden LR, et al. Age related preservation and loss in optimized brain SPECT. Nucl Med Comm. 2005, 26:497-503.

²Barnden LR, Hatton RL, Behin-Ain S, Hutton BF, Goble EA. Optimization of brain SPET and portability of normal databases. *Eur J Nucl Med Mol Imag* 2004; 31:378–387.

DaTscan[™] (Ioflupane ¹²³I) SPECT Normal Database

Database Composition

Regional statistics (mean and standard deviations) were generated from ¹²³I Ioflupane DaTscan SPECT scans for 209 normal controls (73 females, 136 males) from the Parkinson's Progression Markers Initiative (PPMI) as part of an investigation into DaTscan quantification.

The breakdown into age ranges is as follows:

- 10 subjects ages 30–39
- 23 subjects ages 40–49
- 53 subjects ages 50–59
- 76 subjects ages 60–69
- 41 subjects ages 70–79
- 6 subjects ages 80–89

The mean age and standard deviation of the group of 209 individuals is 61+/- 11 years.

Protocol for DaTscan SPECT Acquisition

Each patient underwent a 30- to 45-minute SPECT scan beginning 4 ± 0.5 hours after the time of (max) injection of 185 MBq (5 mCi) of DaTscan.

Images were acquired into a 128x128 matrix and reconstructed using the OSEM method with 8 subsets, 8 iterations, 6mm Gaussian smooth, and Chang's attenuation correction using a site specific mu-map determined by doing a phantom study. No scatter correction was applied. Visual interpretation by experienced nuclear physicians was performed at the PPMI Core lab as the final criterion for inclusion.

For more information regarding the acquisition and reconstruction of data within the PPMI database, refer to the PPMI Imaging Technical Operations Manual, which can be found at <http://www.ppmi-info.org/>.

An abstract showing the results obtained by using MIMneuro with the PPMI data can be found at http://jnm.snmjournals.org/content/57/supplement_2/1827.short?utm_source=TrendMD&utm_medium=cpc&utm_campaign=J_Nucl_Med_TrendMD_0

MIM Amyvid[™] (Florbetapir ¹⁸F) PET Normal Database

Database Composition

The database of Amyvid-PET brain scans is comprised of 74 individuals (48 males, 26 females) ages 18–50 who met the eligibility criteria for inclusion.

Eligibility Criteria

To be included subjects needed to be:

- In general good health
- Score within normal ranges for standard clinical neurologic and cognitive testing
- Have a negative amyloid scan upon visual assessment

Clinical inclusion criteria included scoring within normal ranges for the MMSE and Weschler memory test. The mean and standard deviation for these clinical tests were 29.7 +/- 0.57, and 15.4 +/- 3.46 respectively.

Genetic testing for the allele ApoE 4 was also considered. Of the 74 healthy participants included in the database, 47 had genotyping that was negative for the ApoE 4 allele.

Visual assessment of PET images was based on the median readings of three Nuclear Medicine physicians using a score ranging from 0 (no amyloid) to 4 (high levels of cortical amyloid). All 74 had an Amyvid-PET image rated as amyloid negative, with strong agreement amongst physicians (91–99% pairwise agreement).

Protocol for Amyvid PET Brain Acquisition

Each patient underwent a 10-minute PET scan beginning 50 minutes after the time of injection of 370 MBq (10 mCi) of Amyvid.

Images were obtained using a 128x128 matrix and reconstructed using iterative or row action maximization likelihood algorithms.

Clark C, Schneider J, Bedell B, et al. Use of Florbetapir-PET for Imaging -Amyloid Pathology. *JAMA* 2011; 305 (3):275-283.

MIM NeuraCeq[™] (Florbetaben ¹⁸F) PET Normal Database

Database Composition

The database of NeuraCeq brain scans is comprised of 49 individuals (19 males, 28 females, 2 unspecified) ages 57–84 who met the eligibility criteria for inclusion.

Eligibility Criteria

To be included, subjects needed to be:

- 55 years or older
- Have had completed at least 6 years of education
- Clear of any physical or imaging findings characteristic of another neurological or psychiatric illness or a history of such illness
- Clear of present or recent drug or alcohol use or dependence, or any other relevant disease or unstable medical disorder

All participants underwent a comprehensive clinical and neuropsychiatric examination, including the clinical dementia rating (CDR), the Consortium to Establish a Registry for Alzheimer's Disease (CERAD) test battery (which included the mini-mental state examination; MMSE), and other cognitive tests. Brain MRIs

were acquired for each subject to exclude cerebral lesions or major cerebrovascular disease, both of which constituted exclusion criteria.

The clinical diagnosis based on the NINCDS–ADRDA criteria and on the revised Diagnostic and Statistical Manual of Mental Disorders IV criteria served as the standard to which findings were compared. The florbetaben (¹⁸F) PET data were visually assessed during a centralized masked read at the imaging core laboratory by three independent brain PET experts who were masked to the clinical diagnosis and all other clinical findings. All images included in the database were considered PET amyloid negative by consensus read and were acquired within 4 weeks from the initial screening.

Protocol for NeuraCeq PET Brain Acquisition

Subjects were administered a single dose of 300 MBq (equivalent to a mass dose ≤ 5 mg) \pm 20% florbetaben (¹⁸F) in a maximum volume of 10 ml as a slow intravenous bolus injection and then a 10 ml saline flush. Brain PET images were acquired in three-dimensional mode with either a stand-alone PET or a PET/CT scanner from 45 to 60 min and from 90 to 130 min post-injection. To minimize motion artifacts, the participants' heads were immobilized with the institution's head holder and fixation equipment.

The PET data obtained were corrected for radioactive decay, dead time, measured attenuation, and scatter. The resulting image data were reconstructed by iterative reconstruction algorithms. The four 5-minute frames (90–110 min) were then aligned to frame one to remove any motion and summed together to create a summed image of 20-minute duration to be included in the normal database.

Barthel, H et al. Cerebral amyloid- PET with florbetaben (¹⁸F) in patients with Alzheimer's disease and healthy controls: a multicentre phase 2 diagnostic study. *The Lancet Neurology* 2011; 10(5):424-435.

Acquisition Parameters

The acquisition parameters of the Ph2A data to which MIM had access were as follows:

- A 3D Hoffmann brain phantom was acquired prior to subject enrollment in order to establish a standardized acquisition and reconstruction method for ensuring comparability of quantitative PET between sites.
- All subjects underwent a 20-minute PET scan (4 \times 5 min dynamic frames) starting at 90 min after intravenous injection of 300 MBq \pm 20% of FBB followed by a 10 mL saline flush.
- PET scans were reconstructed using Ordered Subsets Expectation Maximization (OSEM) algorithm using 4 iterations and 16 subsets (zoom =2) or comparable reconstruction as guided by the phantom. Corrections were applied for attenuation, scatter, randoms, and dead time.

Bullich, S et al. Optimized classification of ¹⁸F-Florbetaben PET scans as positive and negative using an SUVR quantitative approach and comparison to visual assessment. *NeuroImage: Clinical* 2017; 15: 325-332

MIM Vizamyl[™] (Flutemetamol ¹⁸F) PET Normal Database

Database Composition

The database of Vizamyl PET brain scans consists of 54 normals (25 males, 29 females) ages 60–84 who met the eligibility criteria for inclusion.

Eligibility Criteria

To be included, subjects needed to be:

- Classified as normal according to AIBL criteria
- Have a negative amyloid scan upon visual assessment

Visual assessment of PET images was based on one expert reading by a Nuclear Medicine physician who determined all normals included to have Amyloid negative scans.

Protocol for Vizamyl PET Brain Acquisition

All PET images were obtained from AIBL (<https://aibl.csiro.au/adni/imaging.html>) and acquired on GE and Philips scanners. Each patient underwent a 20-minute PET scan beginning 90 minutes after the time of injection of approximately 185 MBq (5 mCi) of Vizamyl. Images were obtained using a 128x128 or 256x256 matrix and reconstructed using iterative or row action maximization likelihood algorithms.

MIM FDG (Fluorodeoxyglucose ¹⁸F) Digital PET Normal Database

Available in MIM 7.3.6 and later. This database is not available in earlier versions of MIM.

Database Composition

The database of digital FDG PET brain scans consists of 67 normals (34 males, 33 females) ages 22–87 who met eligibility criteria for inclusion.

Eligibility Criteria

To be included, subjects needed to be:

- Healthy
- Have a brain ¹⁸F-FDG PET scan for cognitive assessment that returned normal by careful visual analysis
- Had a neuropsychological assessment that was not consistent with a neurodegenerative disorder:
 - Normal neuropsychological tests (i.e. MMSE≥27, FAB≥15) and no major depressive disorders
 - A clinical follow-up, of longer than 1 year, which showed a stabilisation and/or improvement of cognitive symptoms.

Protocol for Digital FDG PER Brain Acquisition

Subjects were administered a single dose of 2–3 MBq/kg of ¹⁸F-FDG. All subjects had fasted at least 6 hours prior to receiving the injection and had blood glucose levels < 10 mmol/L. The brain ¹⁸F-FDG PET scan was recorded over 15 minutes (1 bed position), 45–50 min after injection.

All PET images were reconstructed with iterative OSEM methods, as performed in routine clinical practice. Correction was performed for scatter, random, and attenuation with a CT scan. Reconstructed parameters



included 3 iterations and 15 subsets, PSF, subsequently displayed in a 256×256 matrix with $1 \times 1 \times 1$ mm³ voxels for the digital PET camera.

Images were acquired on a digital camera (Vereos, Philips®) at Centre Hospitalier Régional Universitaire (CHRU) of Nancy, France.


Mairal E, Doyen M, Rivasseau-Jonveaux T, et al. Clinical impact of digital and conventional PET control databases for semi-quantitative analysis of brain ¹⁸F-FDG digital PET scans. *EJNMMI Res* 2020; 10(144):1-10.

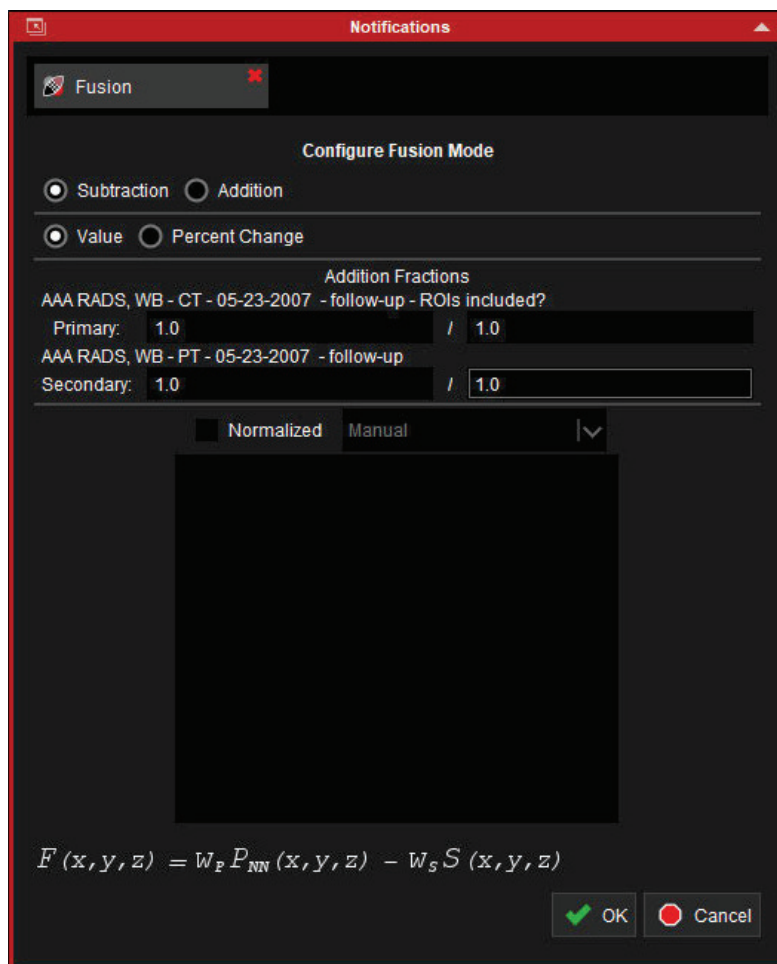
Fusion Image Subtraction Formulas: Technical Details

MIMTD-623 • 30 Aug 2023

Overview

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

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



Notifications

Fusion

Configure Fusion Mode

☒ Subtraction ☐ Addition

☒ Value ☐ Percent Change

Addition Fractions

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

Primary: 1.0 / 1.0

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

Secondary: 1.0 / 1.0

Normalized **Manual**

$$F(x, y, z) = w_P P_{NN}(x, y, z) - w_S S(x, y, z)$$

OK Cancel

You can choose:

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



Related: Refer to [View Images with Various Fusion Modes](#) for more information about working with fusions.

Formulas Used for Subtraction

In the equations below:

- F is the voxel value of the output image
- (x, y, z) are the image coordinates
- $P(x, y, z)$ is a sampling function of the primary image (uses nearest neighbor interpolation)
- $S(x, y, z)$ is a sampling function of the secondary image (uses linear interpolation)
- W_p and W_s are values based on the intensity scaling controls (see [Addition Fractions](#))
- U_p and U_s are normalization factors (see [Contrast](#))

Value Subtraction

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

Value Subtraction - Normalized

(see [Apply Normalization](#))

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

Percent-Change Subtraction

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

Percent-Change Subtraction - Normalized

(see [Apply Normalization](#))

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

Addition Fractions

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

Contrast

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

Apply Normalization

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


There are three options for normalization:

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

The scaling factor for the secondary image is determined by applying a linear curve fit (iteratively reweighted least squares algorithm¹). MIM uses the image's contrast to scale its intensity data. All intensity data that is lower than or equal to the image contrast lower bound is set to 0. All intensity data that is greater than or equal to the image contrast upper bound is set to 100. This scaling minimizes the mismatch between the series.

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

Interpolation Levels

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



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

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



Version 7.1 - 7.4

Have questions about MIM Software?
Contact MIM Software Support for technical assistance:
support.mimsoftware.com



MIM SurePlan™ MRT for Molecular Radiotherapy
Dosimetry
User Guide

Version 7.1 - 7.4

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Symbols Used in Documentation



Caution: Indicates potential hazards or restrictions on use that are critical for safe use of the product or for compliance with legal or regulatory standards.



Important: Indicates information that must be read and understood to successfully complete a task. Failure to review and act on important information may result in unexpected system behavior.



Tip: A helpful hint related to system behavior or usability. Tips are not required for task completion.



Related: Introduces a link to additional optional information that may be relevant or helpful when learning about a topic or completing a task.

Regulatory Information

MIMTD-759 • 24 Mar 2025

US Federal law and other national laws restrict this medical device to sale to, or use by, or on the order of a physician.



Important: This product may not yet be commercially available in some countries. Please contact your local MIM Software representative for further details.



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Caution: The following intended uses and indications apply to MIM in its entirety. Depending on your specific licenses and functionality, and the region where you use the software, some indications may not apply to your use of MIM.

Intended Use

MIM software is intended for trained medical professionals including, but not limited to, radiologists, oncologists, physicians, medical technologists, dosimetrists, and physicists.

MIM is a medical image and information management system that is intended to receive, transmit, store, retrieve, display, print, and process digital medical images, as well as create, display, and print reports from those images. The medical modalities of these medical imaging systems include, but are not limited to, CT, MR, CR, DX, MG, US, SPECT, PET, and XA as supported by ACR/NEMA DICOM 3.0.

MIM provides the user with the means to display, register, and fuse medical images from multiple modalities. Additionally, it evaluates cardiac left ventricular function and perfusion, including left ventricular end-diastolic volume, end-systolic volume, and ejection fraction. The Region of Interest (ROI) feature reduces the time necessary for the user to define objects in medical image volumes by providing an initial definition of object contours. The objects include, but are not limited to, tumors and normal tissues.

MIM provides tools to quickly create, transform, and modify contours for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.

MIM aids in the assessment of PET/SPECT brain scans. It provides automated quantitative and statistical analysis by automatically registering PET/SPECT brain scans to a standard template and comparing intensity values to a reference database or to other PET/SPECT scans on a voxel by voxel basis, within stereotactic surface projections or standardized regions of interest.

MIM allows the dose distribution of an implant to be individually shaped for each patient and is a general purpose brachytherapy planning system used for prospective and confirmation dose calculations for patients undergoing a course of brachytherapy using permanent implants of various radioisotopes (not including radioactive microspheres).

MIM allows voxel-based dose calculations for patients who have been administered radioisotopes or radioactive microspheres.

MIM assists with the planning and evaluation of ablation procedures by allowing the energy zone that comprises the ablation zone to be visualized on medical imaging through the placement of virtual ablation devices for the purpose of confirming ablation zone placement.

Indications for Use

MIM software is used by trained medical professionals as a tool to aid in evaluation and information management of digital medical images. The medical image modalities include, but are not limited to, CT, MR, CR, DX, MG, US, SPECT, PET, and XA as supported by ACR/NEMA DICOM 3.0. MIM assists in the following indications:

- Receive, transmit, store, retrieve, display, print, and process medical images and DICOM objects.
- Create, display, and print reports from medical images. **6.1.12**
- Registration, fusion display, and review of medical images for diagnosis, treatment evaluation, and treatment planning.
- Evaluation of cardiac left ventricular function and perfusion, including left ventricular end-diastolic volume, end-systolic volume, and ejection fraction.
- Localization and definition of objects such as tumors and normal tissues in medical images.
- Creation, transformation, and modification of contours for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.
- Quantitative and statistical analysis of PET/SPECT brain scans by comparing to other registered PET/SPECT brain scans.
- Planning and evaluation of permanent implant brachytherapy procedures (not including radioactive microspheres).
- Calculating absorbed radiation dose as a result of administering a radionuclide. **6.1.12**
- Assist with the planning and evaluation of ablation procedures by providing visualization and analysis, including energy zone visualization through the placement of virtual ablation devices validated for inclusion in MIM-Ablation. The software is not intended to predict specific ablation zone volumes or predict ablation success.

When using this device clinically within the United States, the user should only use FDA-approved radiopharmaceuticals. If used with unapproved ones, this device should only be used for research purposes.

Lossy compressed mammographic images and digitized film screen images must not be reviewed for primary image interpretations. Images that are printed to film must be printed using a FDA-approved printer for the diagnosis of digital mammography images. Mammographic images must be viewed on a display system that has been cleared by the FDA for the diagnosis of digital mammography images. The software is not to be used for mammography CAD.

When used for diagnostic purposes, the mobile thin client is not intended to replace a full workstation and should only be used when there is no access to a workstation.

Use of MIM on Mobile Devices

MIM Software Inc. has previously worked with board certified radiologists to evaluate mobile devices for diagnostic reading. Devices tested included Apple iPad, Kindle Fire HDX, Samsung Galaxy Note Pro, and Microsoft Surface. In these cases, testers affirmed that the devices they evaluated were capable of displaying images at diagnostic quality.

Due to the number of available mobile devices, and the frequency with which new mobile devices are released, MIM cannot evaluate all available mobile devices for diagnostic reading. However, displays have dramatically increased in quality (e.g., resolution, contrast) since these earlier devices were tested. It is at the discretion of the user and their employer to determine which mobile devices are acceptable for diagnostic reading, and to ensure that these devices are properly calibrated.



Caution: All treatment plan reports shall be approved by a qualified person before the information in them is used for radiotherapy treatment purposes. The responsible organization shall ensure that individuals authorized to perform treatment planning functions are appropriately trained for the functions they perform, and the operator shall always be aware that the quality of the output depends critically on the quality of the input data. Any irregularities or uncertainties about input data units, identification, or quality of any other nature shall be thoroughly investigated before the data are used.



Caution: Any health professional having a complaint or grounds for dissatisfaction relating to the identity, quality, durability, reliability, safety, effectiveness, or performance of a device should notify MIM Software. Moreover, if a device has malfunctioned, MIM Software or its representative must be informed immediately. If a MIM Software product could have caused or contributed to the death or serious injury of a patient, MIM Software or its representative must be informed immediately. These serious incidents must also be reported to the Competent Authority of the European Member State or, when applicable, the equivalent regulatory authority, where the user and/or patient is established.



Caution: Users must perform validation when developing their own extensions or workflows and when modifying any default extensions or workflows that MIM Software provides. For extensions and workflows developed or modified by the user or provided by a third-party, MIM Software (i) does not endorse, control, monitor, or verify the contents, (ii) does not provide any warranty; and (iii) is not liable for any loss, damage, or injury sustained resulting from downloading, installing, accessing, integrating, supporting, or using the extension or workflow.



Caution: Due to the inherent nature of medical images, with their variable characteristics (e.g., level of noise and artifacts), the degree of accuracy may be variable as well. These limitations must be considered before making any decision based on images and quantitative values. It is recommended that acceptance testing be performed prior to use. This testing should include, at a minimum, all representative data sets (images) intended for transfer, all types of transfers desired for a type of data set, and clinical evaluation of each representative data set on the receiving end after each desired type of transfer.

For more information on accuracy details, see appendix or white paper information.

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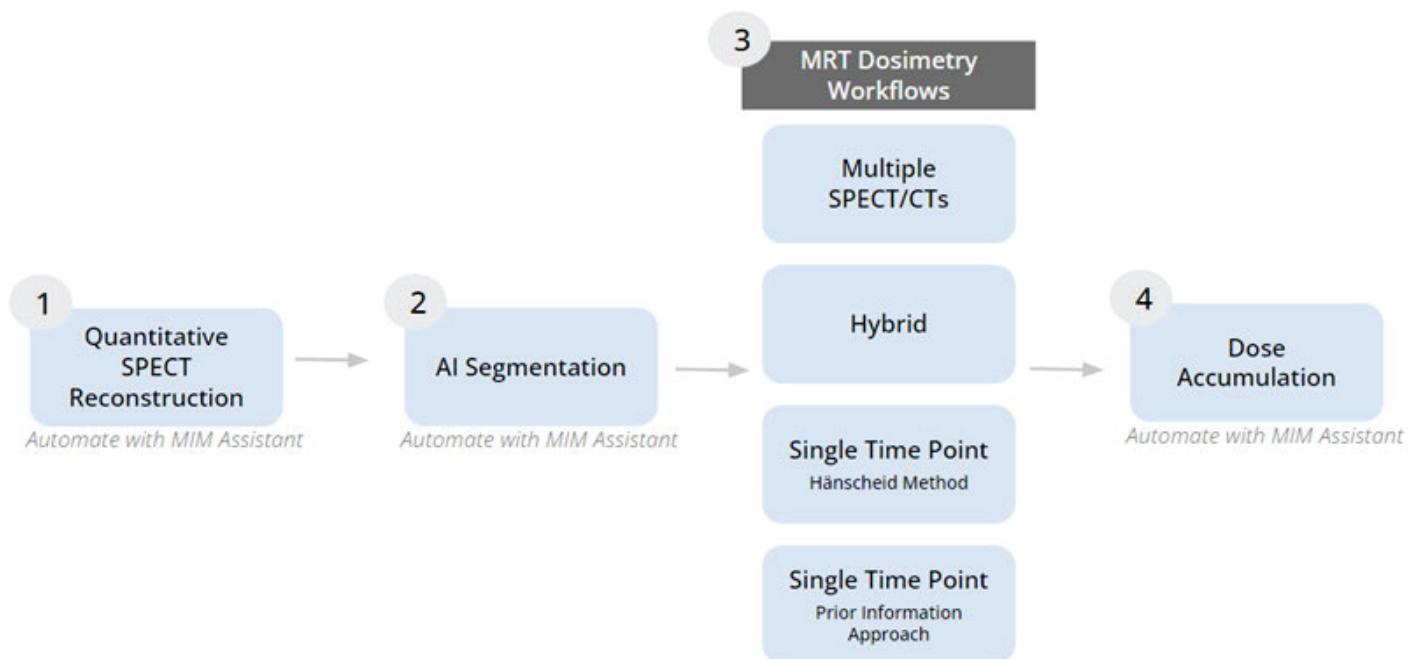
Get Started with MIM SurePlan™ MRT

MIM SurePlan™ MRT Feature Overview

MIMTD-700 • 20 Jun 2024

Overview

MIM SurePlan MRT has many features to assist with voxel-based dosimetry and related imaging work. See an overview of the steps below.



Contents

- [Quantitative SPECT Reconstruction](#)
- [AI Segmentation](#)
- [Dosimetry](#)
- [Absorbed Dose Accumulation](#)
- [Supported Isotopes](#)
- [Additional Resources](#)
 - [Reporting](#)
 - [User Logins/LDAP](#)



- [Increased Automation](#)

Quantitative SPECT Reconstruction

MIM SurePlan MRT includes MIM's quantitative reconstruction tool, SPECTRA Quant®. SPECTRA Quant reconstructs 2D SPECT images as 3D quantitative images in units of Bq/ml.

For a list of supported isotopes, see [Supported Isotopes](#).



Important: Scanner commissioning and calibration is essential for accurate reconstruction and quantification. Ask your MIM Software® representative for the SPECTRA Reconstruction Welcome Packet for more information about implementation steps.

MIM SurePlan MRT includes SPECTRA Quant support for one SPECT camera. There is no limit to the number of isotopes supported for a camera set up with SPECTRA Quant. Multiple cameras can be commissioned if desired. Ask your MIM Software representative for more information.



Tip: MIM SurePlan MRT supports zero-click processing for automatic SPECT reconstruction through MIM's automation solution, MIM Assistant®. Ask your MIM Software representative for more information.

SPECTRA Quant is not required for MIM SurePlan MRT processing if either of the following is true:

- You have another quantitative SPECT reconstruction package that is able to export data in units of Bq/mL with proper DICOM.
- You are only interested in dosimetry for PET/CTs.

AI Segmentation

MIM SurePlan MRT includes a dedicated segmentation model in MIM's auto-contouring solution, Contour ProtégéAI+™. The model is designed to segment the most common organs of interest in MRT dosimetry.

For a list of available structures, see the [Contour ProtégéAI+](#) home page.



Tip: Contour ProtégéAI+ can be run either locally or via MIM's cloud solution, MIMcloud®.



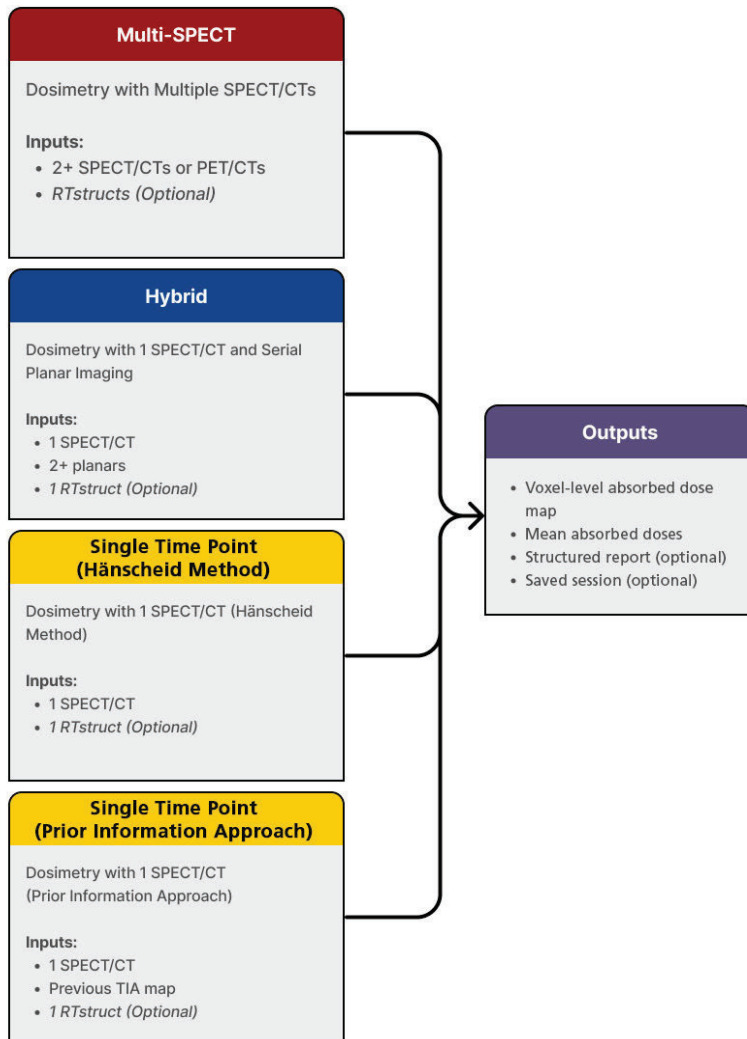
Tip: MIM SurePlan MRT supports zero-click processing for automatic organ segmentation through MIM's automation solution, MIM Assistant. Ask your MIM Software representative for more information.

Dosimetry

After the reconstructed series and contours are saved to the patient list, you can run a dosimetry workflow. When the workflow completes, you can review the time-integrated activity (TIA) dose calculation and absorbed dose map. The workflow produces series to use for absorbed dose accumulation calculation. For a list of supported isotopes, see [Supported Isotopes](#).

There are various approaches to dosimetry in MIM SurePlan MRT. Dosimetry is performed with workflows with customizable preferences. You can control processing during the workflow, or configure processing at an organization level.

The following workflows are available:



Absorbed Dose Accumulation

The Absorbed Dose Accumulation workflow accumulates mean doses across cycles of therapy to generate cumulative absorbed dose results. This is most relevant to multi-cycle treatments such as ^{177}Lu -DOTATATE and ^{177}Lu -PSMA.



Tip: MIM SurePlan MRT supports zero-click processing for automatic absorbed dose accumulation through MIM's automation solution, MIM Assistant. Ask your MIM Software representative for more information.



Supported Isotopes

SPECTRA Quant

- ^{177}Lu
- ^{131}I
- $^{99\text{m}}\text{Tc}$
- ^{123}I
- ^{67}Cu
- ^{166}Ho
- ^{111}In
- ^{186}Re
- ^{188}Re
- ^{67}Ga
- ^{153}Sm
- $^{117\text{m}}\text{Sn}$
- ^{161}Tb
- ^{223}Ra
- ^{203}Pb
- ^{212}Pb

MIM SurePlan MRT

PET Isotopes

- ^{124}I
- ^{64}Cu
- ^{68}Ga
- ^{18}F
- ^{89}Zr
- ^{90}Y

Non-PET Isotopes

- ^{177}Lu
- ^{131}I
- ^{123}I
- ^{67}Cu
- ^{186}Re
- ^{188}Re
- ^{161}Tb
- ^{67}Ga
- ^{89}Sr
- ^{111}In
- $^{99\text{m}}\text{Tc}$
- ^{153}Sm
- $^{117\text{m}}\text{Sn}$
- ^{212}Pb
- ^{225}Ac
- ^{223}Ra

Workflow	Supported Isotopes
Dosimetry with Multiple SPECT/CTs or PET/CTs	All MIM SurePlan MRT isotopes
Dosimetry with 1 SPECT/CT and Serial Planar Imaging	MIM SurePlan MRT non-PET isotopes only
Dosimetry with 1 SPECT/CT or PET/CT (Prior Information Approach)	All MIM SurePlan MRT isotopes

Workflow	Supported Isotopes
Dosimetry with 1 SPECT/CT (Hänscheid Method)	¹⁷⁷ Lu-DOTATATE ¹⁷⁷ Lu-PSMA



Caution: When using the device clinically, within the United States, the user should only use FDA approved radiopharmaceuticals. If used with unapproved ones, this device should only be used for research purposes.

Additional Resources

Reporting

The dosimetry workflows include templated structured reports that can be saved as a PDF or DICOM secondary capture. These reports can be used for internal reference, for sharing with a referring physician, or for sharing with a patient.

Structured report customizations can be performed upon request during or after implementation of MIM SurePlan MRT. For more information, ask your MIM Software representative.

User Logins/LDAP

Integrate with your organizations's existing LDAP user logins. Alternatively, MIM-specific user logins may be used.

Increased Automation

MIM SurePlan MRT comes with specific functions of MIM's automation solution, MIM Assistant: Automatic SPECT reconstruction, automatic organ segmentation, and automatic absorbed dose accumulation.

If upgraded, MIM Assistant can be used to automate various other processes, such as fetching prior studies, launching additional workflows, and archiving data. For more information, ask your MIM Software representative.

MIM Basics

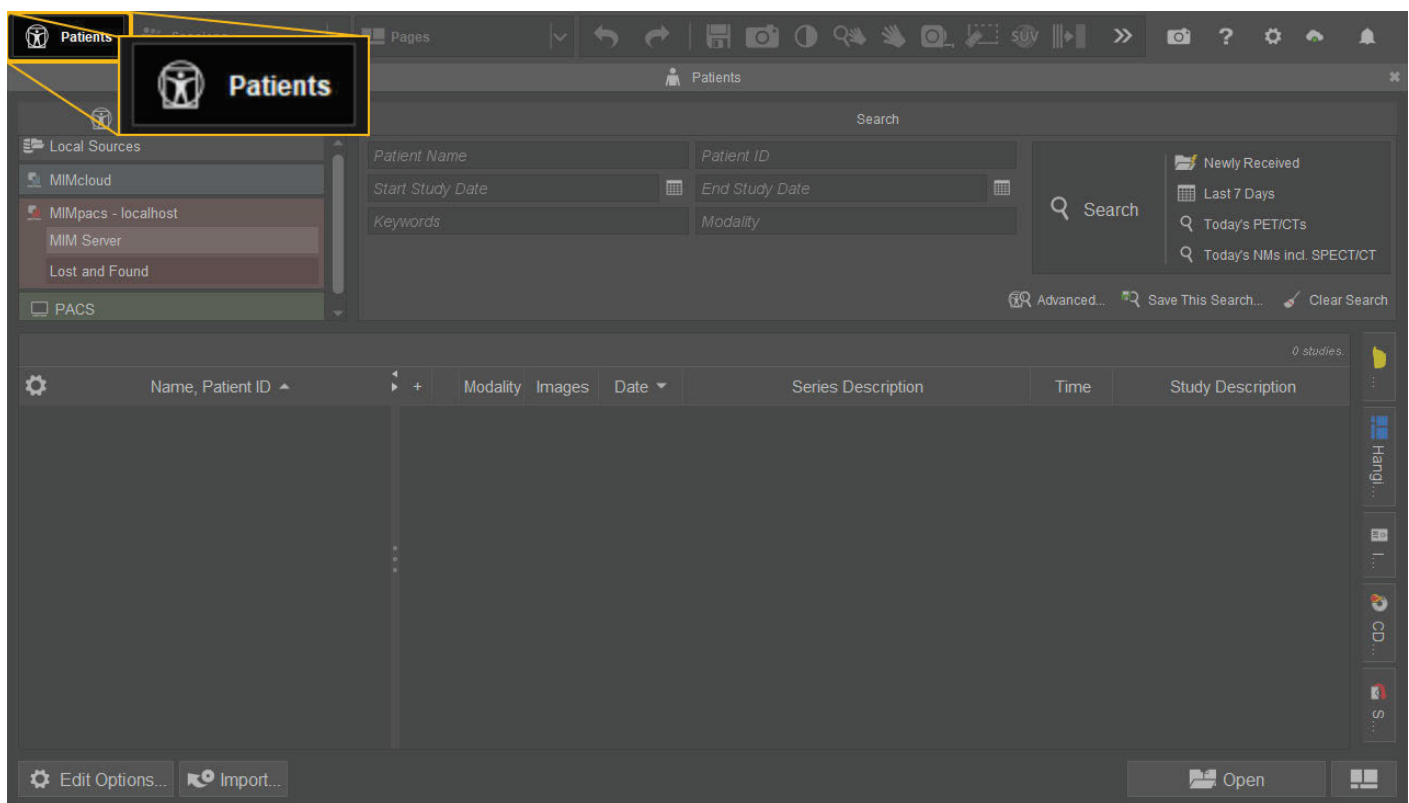
Find and Open Patient Data

MIMTD-1642 • 07 Sep 2023

Overview

Use the patient list to find and open patient data. When you launch MIM®, the patient list appears by default.

To return to the patient list anytime, click the **Patients** button in the upper-left corner.



Contents

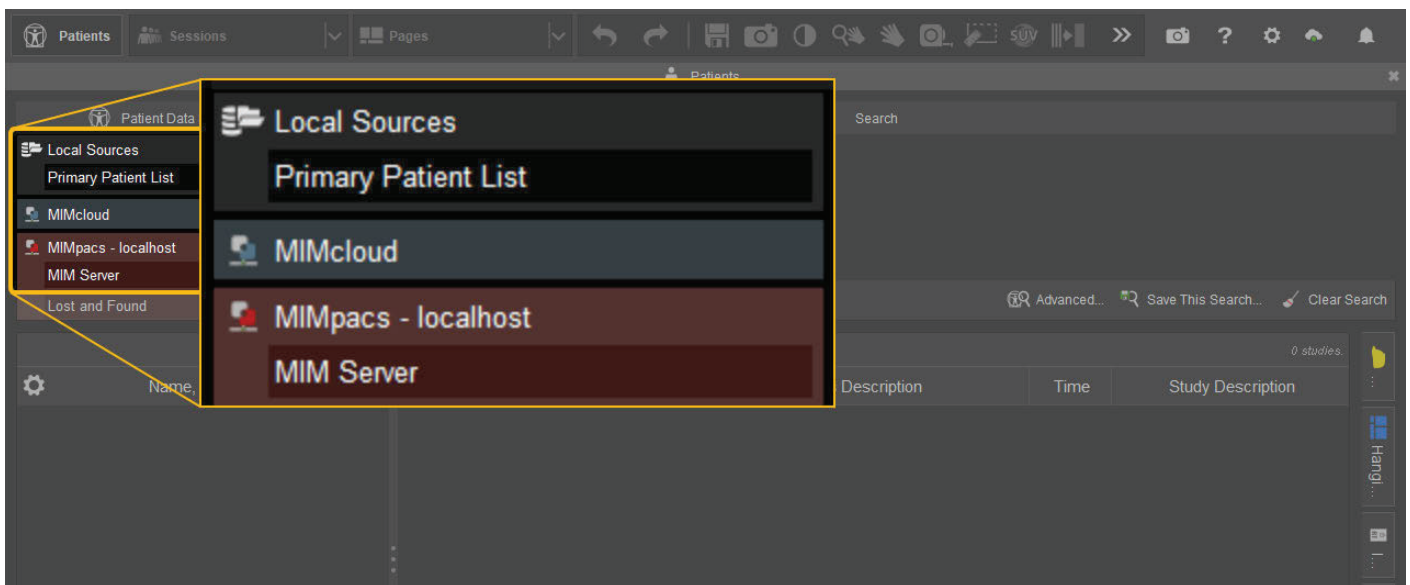
- [Find and Open Data](#)
- [Tips for Searching](#)
- [Do Advanced Searches](#)
- [Query and Retrieve from PACS](#)
- [Import Data from a Local File, Folder, or CD](#)



Find and Open Data

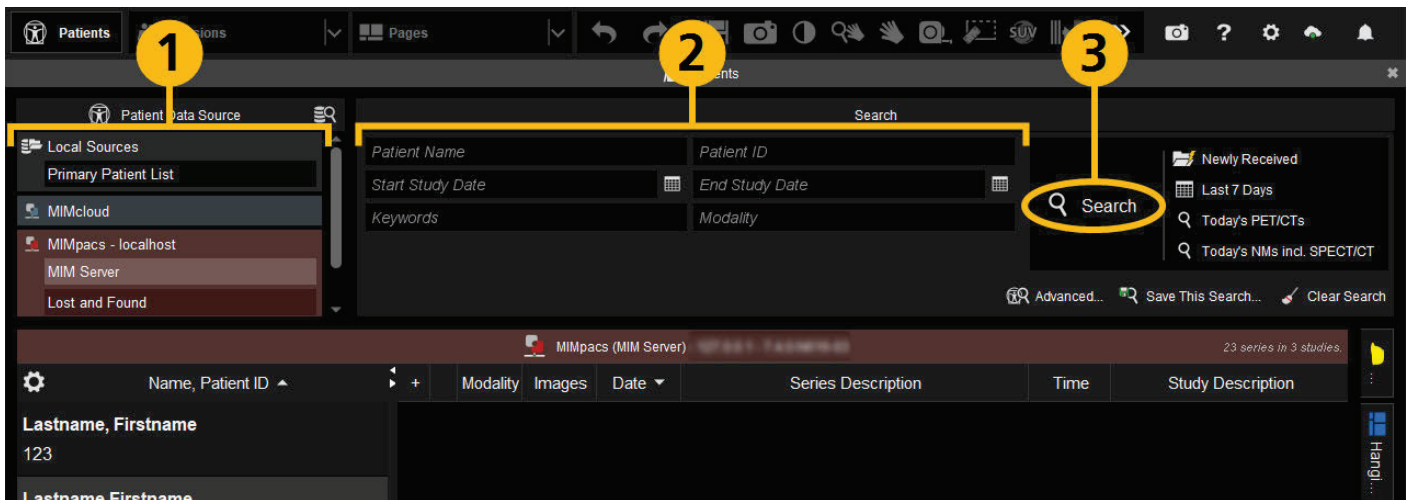
Patient data sources are in the upper-left corner. Search for patient data and open it directly from any of the following patient data sources:

- **Local Sources** (Gray) — Data in these sources is stored on your computer.
- **MIMcloud® Sources** (Blue) — Data in these sources is stored in MIMcloud. For more information about MIMcloud, go to mimcloud.com.
- **MIMpacs™ Sources** (Red) — Data in these sources is stored on your organization's MIM server.



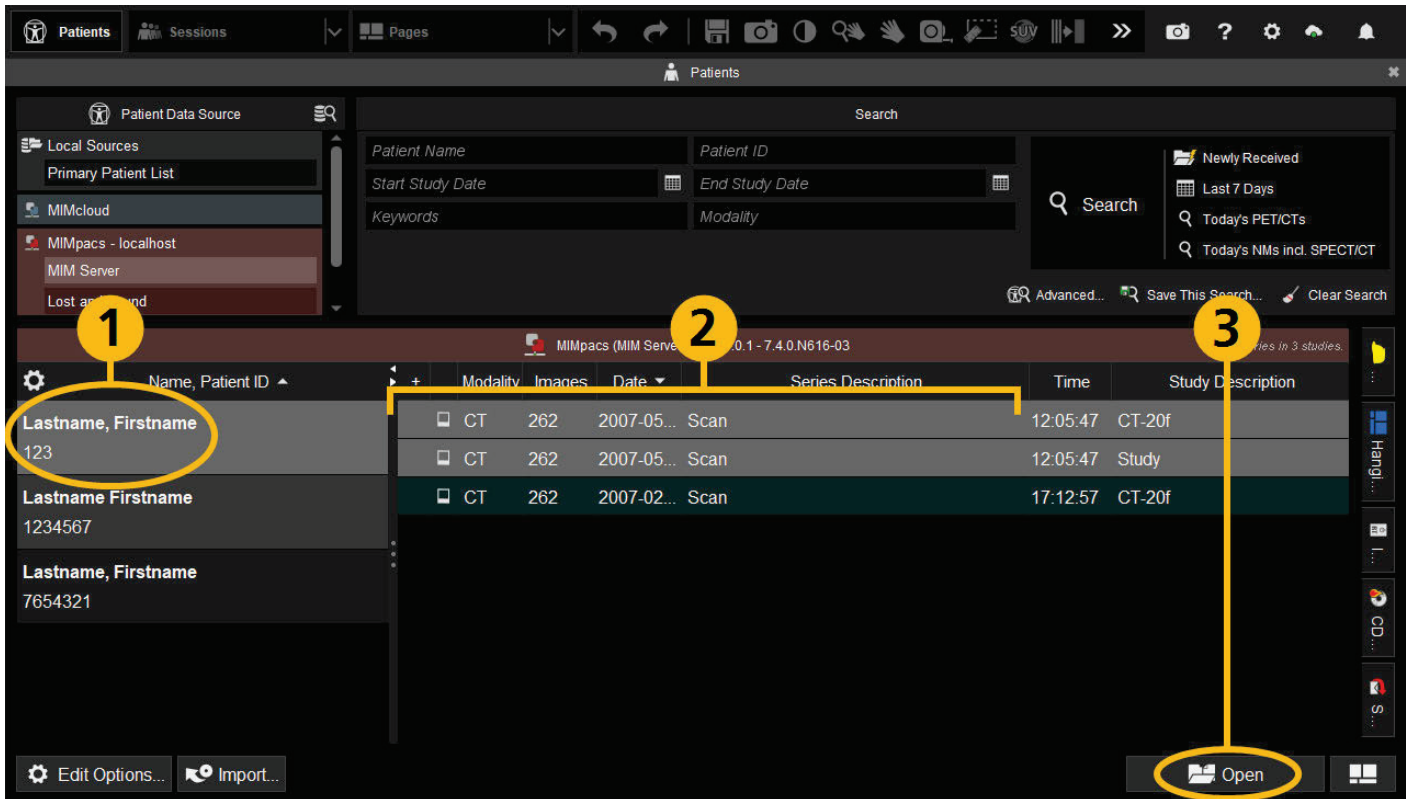
Important: If the data that you want to open is not in local sources, MIMcloud sources, or MIMpacs sources, you must first retrieve or import the data. Refer to [Query and Retrieve from PACS](#) or [Import Data from a Local File, Folder, or CD](#) below.

Find Data



1. Select the desired patient data source.
2. Enter search criteria as necessary. All search fields are optional.
3. Click the **Search** button. Search results appear below the data sources, in the column on the left side.

Open Data



The screenshot shows the MIM SurePlan MRT User Guide interface. The left sidebar contains a list of patient data sources, including 'Local Sources', 'MIMcloud', 'MIMpacs - localhost', 'MIM Server', and 'Lost and Found'. The central table displays a list of patient series with columns for Name, Patient ID, Modality, Images, Date, Series Description, Time, and Study Description. The right sidebar contains search filters and a search bar. Three yellow callouts with numbers 1, 2, and 3 indicate the steps: 1. Select a patient from the left sidebar. 2. Select one or more individual series from the central table. 3. Click the 'Open' button at the bottom right.

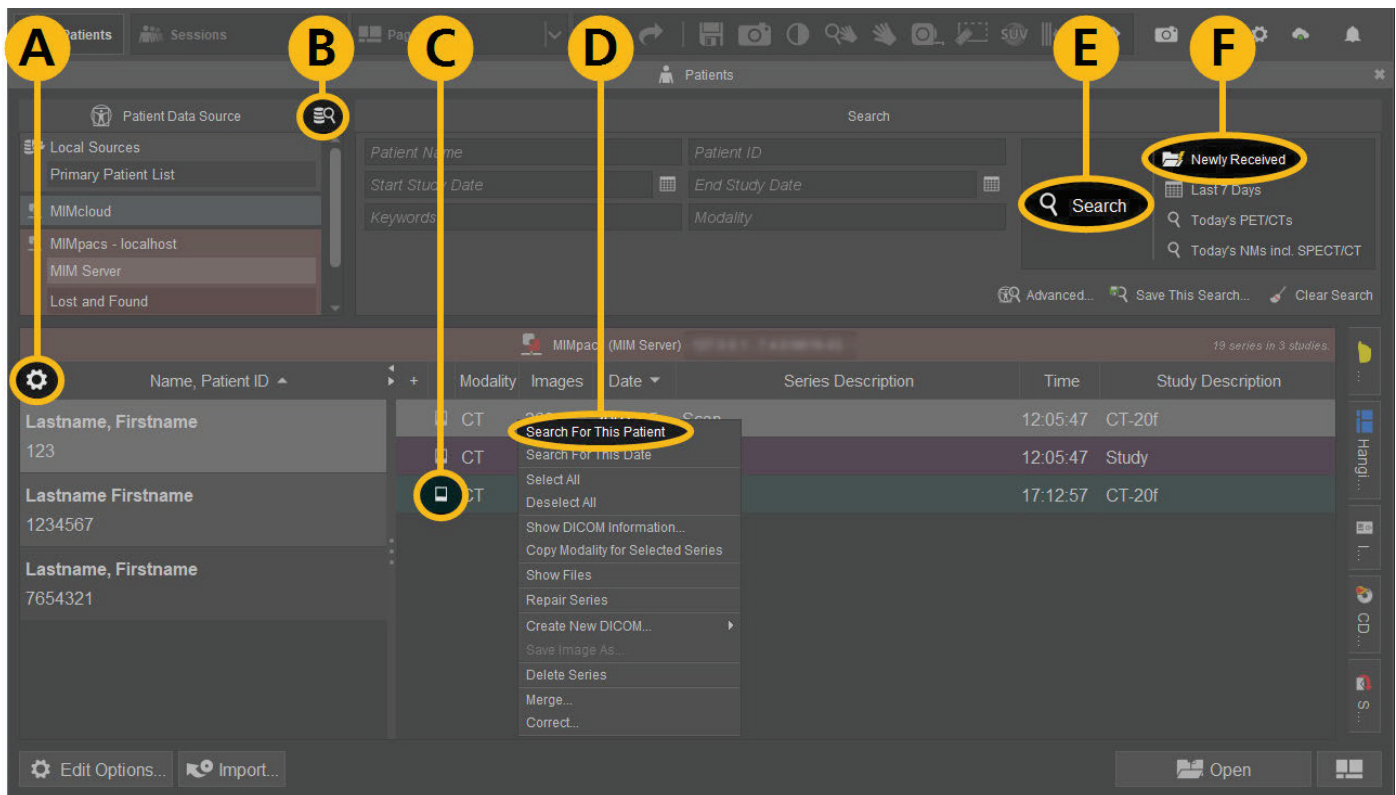
1. Select the desired patient from the column on the left side. Individual series appear in the center of the screen.
2. If you want to open only certain series, select one or more individual series. If you do not select individual series, all series for the patient will open.






Tip: To select multiple patients or series at a time, hold the Ctrl key while clicking, or left-click drag over multiple items.


3. To open the data into a MIM session, click the **Open** button. Or, to automate processing, launch a MIM Workflow™.

Tips for Searching



- To change how the search results are sorted, click the settings  button above the search results on the left side.
- MIM 7.2 and later:* To search for a specific patient data source, click the  button and start typing the name of the source. This is useful if one of your data sources has many individual patient lists.
MIM 7.1 and earlier: This functionality is not available.
- To preview an image before you open it, hover over the thumbnail  symbol on the left side of the series information.
- To see all series for a patient, instead of only those returned by the search criteria, right-click a search result and select **Search for This Patient**.
- To clear all search criteria, right-click the **Search** button.
- To show only newly received data, click **Newly Received** next to the **Search** button.

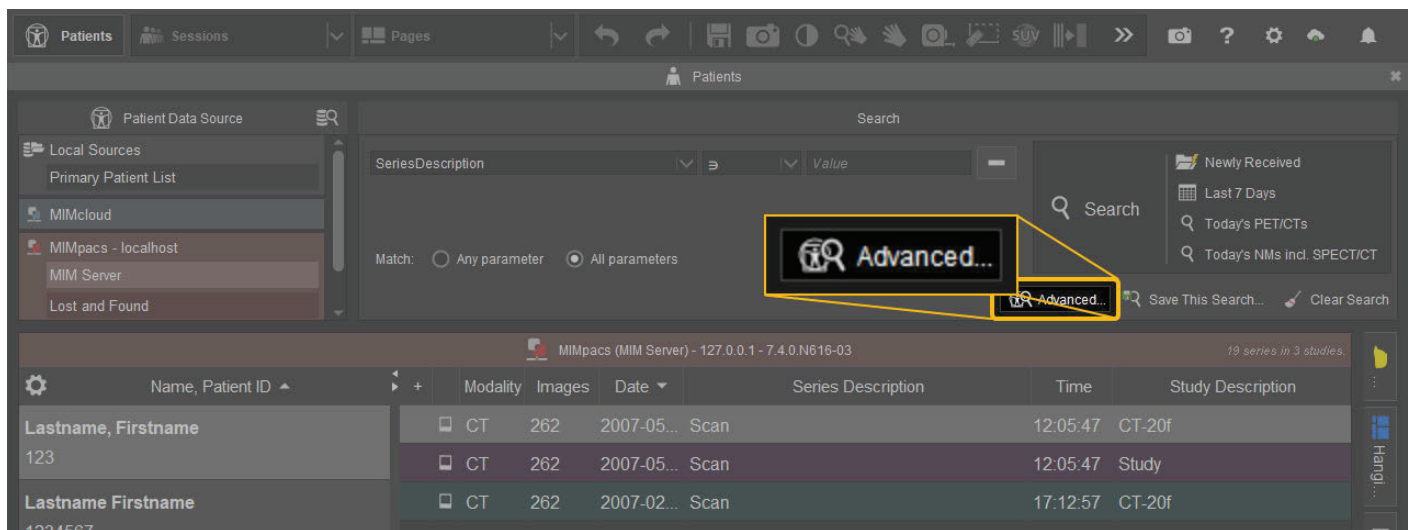
Adjust Patient List Options

To personalize a variety of patient list functions, go to Settings  in the upper-right corner of MIM and choose **Patient List Options**. Adjustments that you can make include the following:

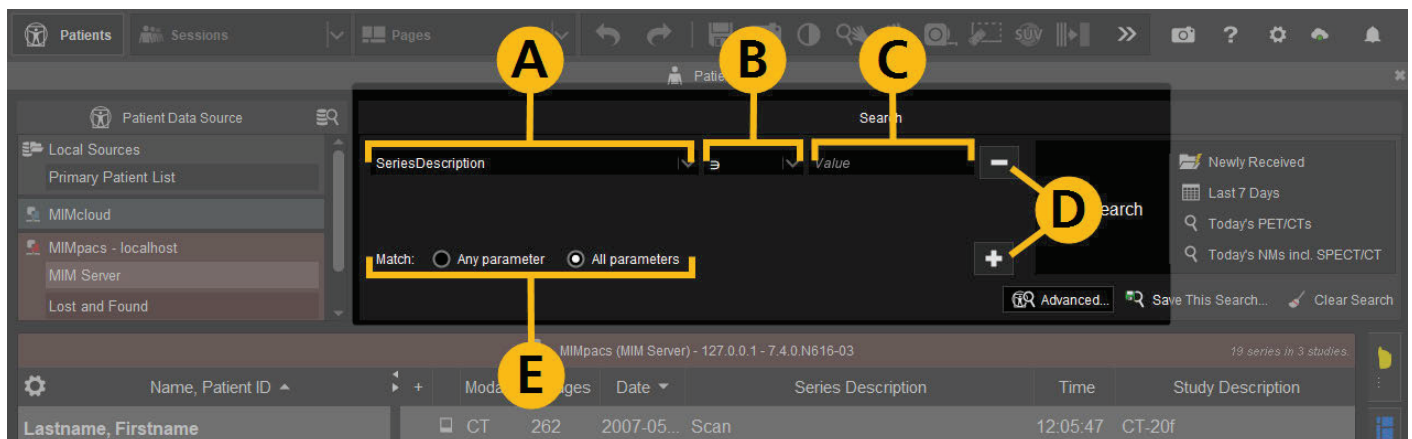
- Choose which series columns (e.g., Modality, Series Description, Time) are shown and in which order.
- Set the patient list view to show newly received series by default.
- Change the default sorting method for search results.

Do Advanced Searches



If desired, click the **Advanced...** button in the middle of the search panel to find data using DICOM tag-based search filters.



Follow these tips to use the advanced search options:

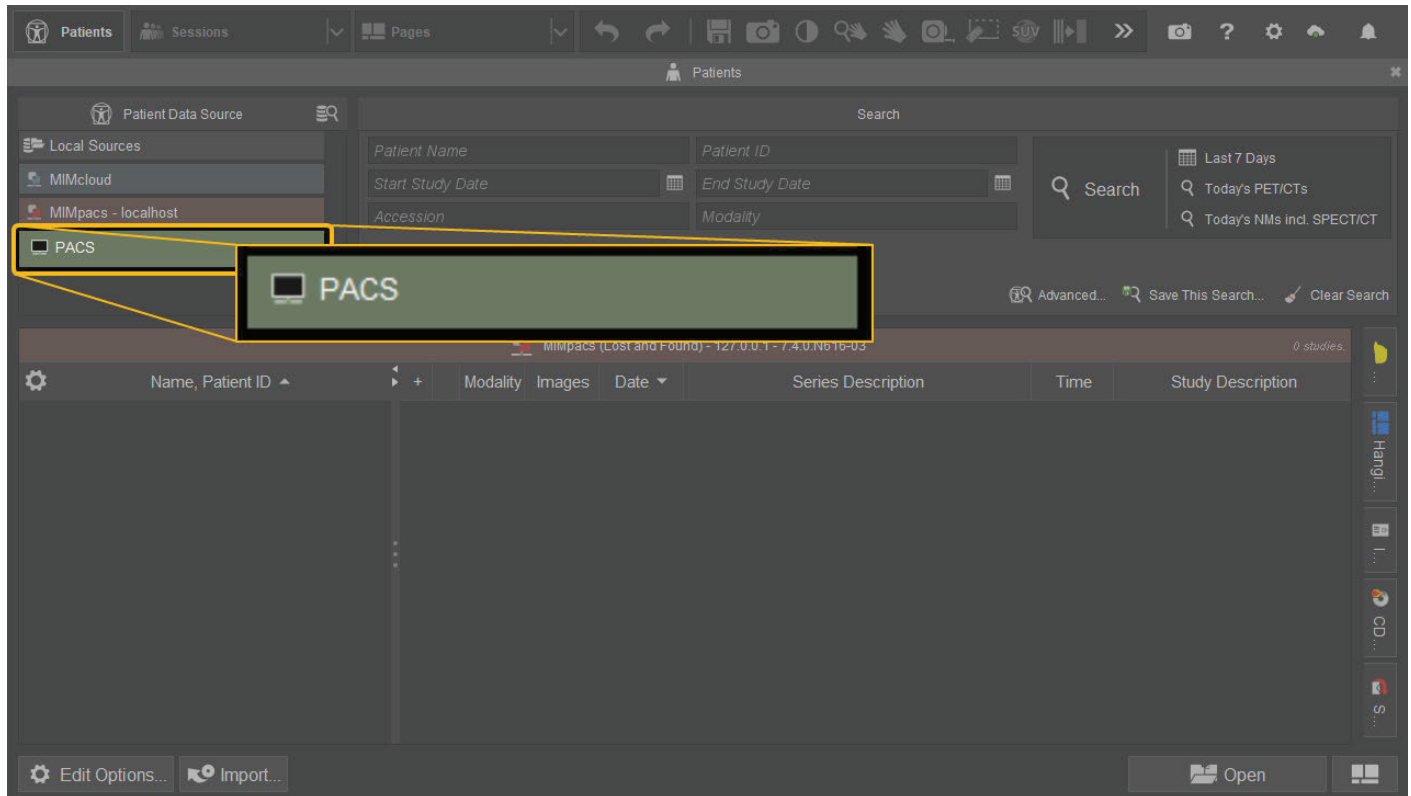


- Select a DICOM tag (e.g., SeriesDescription). Scroll through the menu to see common tags, or start typing to find other tags.
- Select an operator (e.g., =). To see an explanation of what the operator does, select the operator and hover over the field.
- Enter a value (e.g., WB AC).

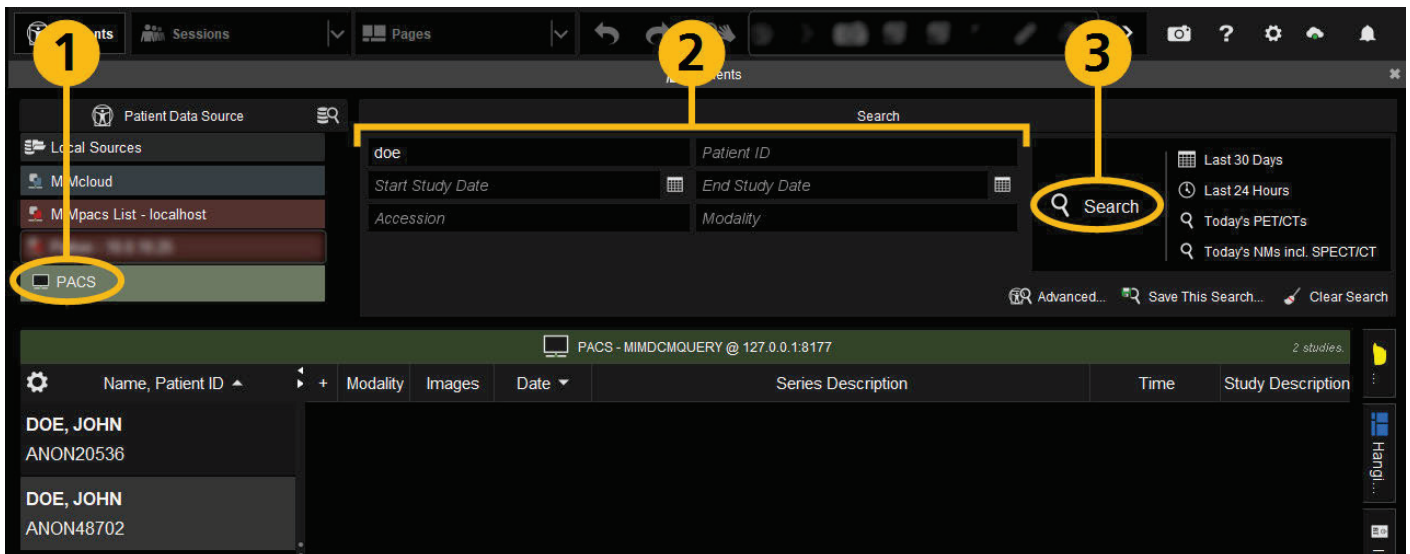
- D. To add a search filter, click the  button. To remove a search filter, click the  button.
- E. Select whether the search should return results that match any or all of the filters that you configure.

Query and Retrieve from PACS

PACS lists, or third-party DICOM locations, are highlighted in green and located under MIM patient lists. You can search for patient data in these data sources. To open the data, you must send it to a MIM patient list.



Search a PACS List



1. Select the desired PACS list.
2. Enter search criteria as necessary. All fields are optional.



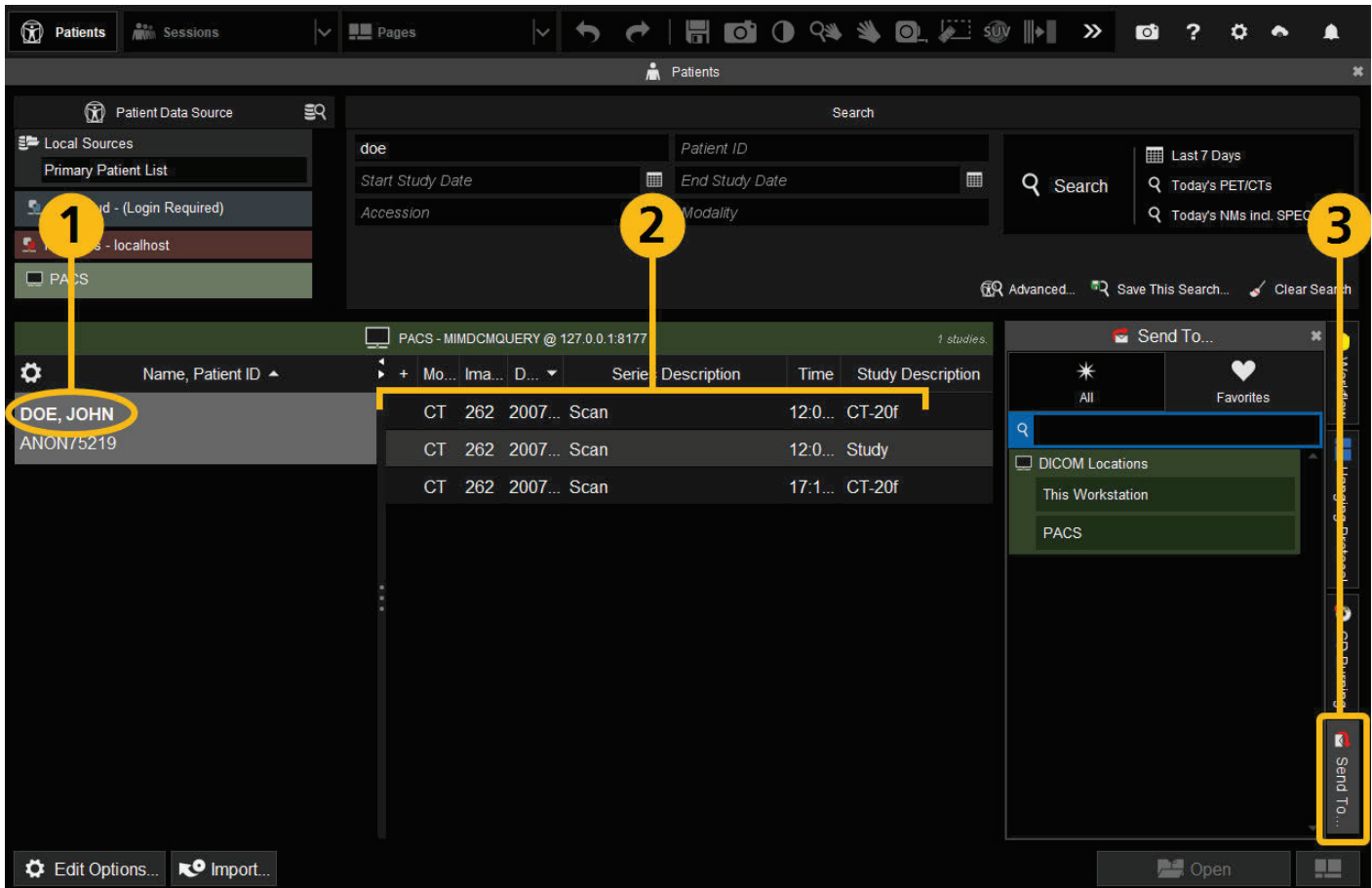
Important: Each PACS supports different search criteria when queried by another system such as MIM. Some search criteria may not return results.

3. Click the **Search** button. Search results appear below the data sources, in the column on the left side.



Tip: For more details about search options, refer to [Tips for Searching](#) and [Do Advanced Searches](#) above.

Send Data from PACS to a MIM Patient List



The screenshot shows the MIM SurePlan MRT interface. On the left, under 'Local Sources', 'PACS' is selected (callout 1). The main area shows a search for 'doe' with a table of results. The first row is selected (callout 2):

Name, Patient ID	Mo...	Ima...	D...	Series	Description	Time	Study Description
DOE, JOHN ANON/5219	CT	262	2007...	Scan		12:0...	CT-20f
	CT	262	2007...	Scan		12:0...	Study
	CT	262	2007...	Scan		17:1...	CT-20f

On the right, the 'Send To...' panel is open (callout 3), showing 'DICOM Locations' with 'This Workstation' and 'PACS' as options.


1. Select the desired patient from the column on the left side.
2. If you want to send only certain series, select one or more individual series. If you do not select individual series, all series for the patient are sent.



Tip: To select multiple patients or series at a time, hold the Ctrl key while clicking, or left-click drag over multiple items.

3. Click the **Send To...** tab in the lower-right corner, then click the desired destination. The data is sent to the selected location.



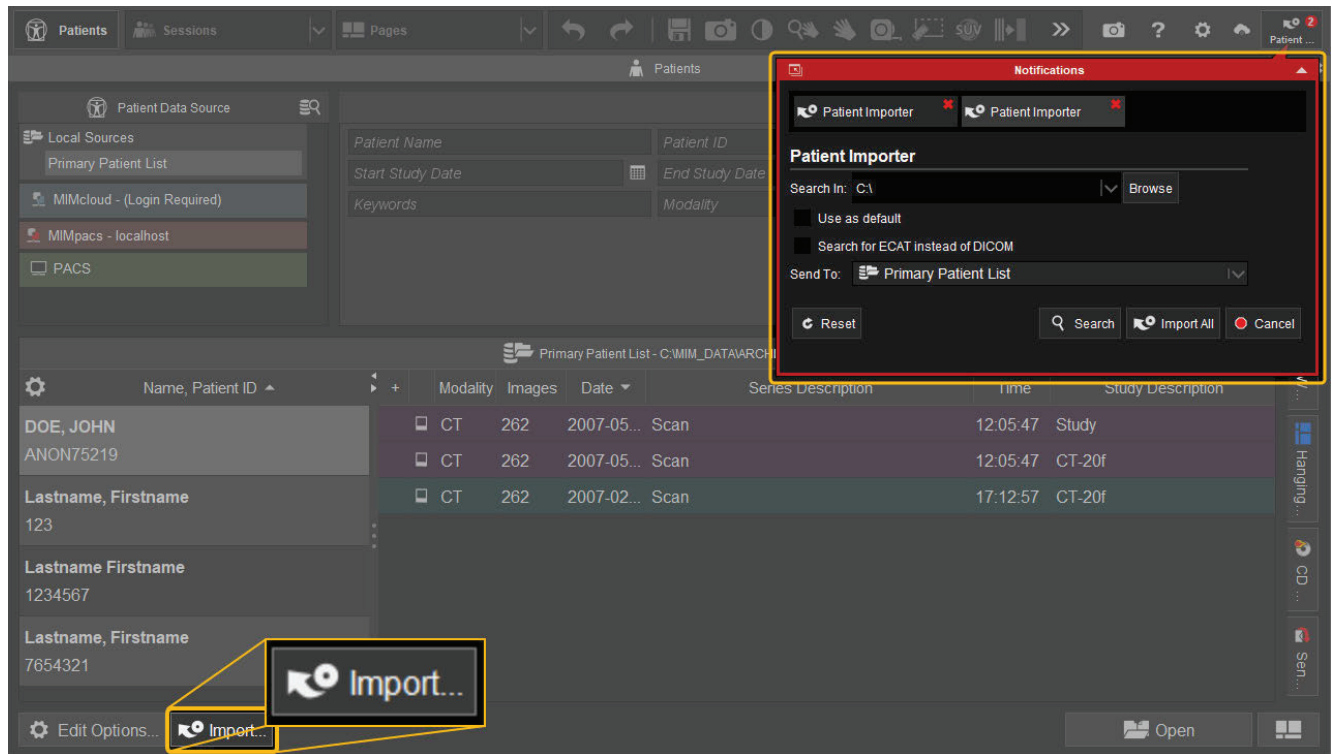
Tip: The **This Workstation** destination sends data to the MIMpacs patient list set up in Settings  >> **Network Services** >> **DICOM Store**.

To open the data, go to the patient list that you sent the data to. Follow the steps in [Find and Open Data](#) above.

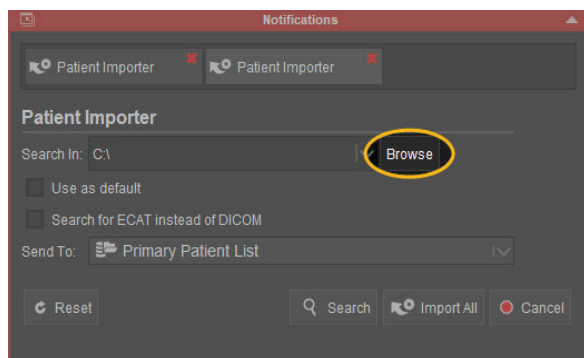
Import Data from a Local File, Folder, or CD

To import data from a local file, folder, or CD into a MIM patient list, follow these steps:

1. Click the **Import...** button in the lower-left corner. A Notifications window appears.



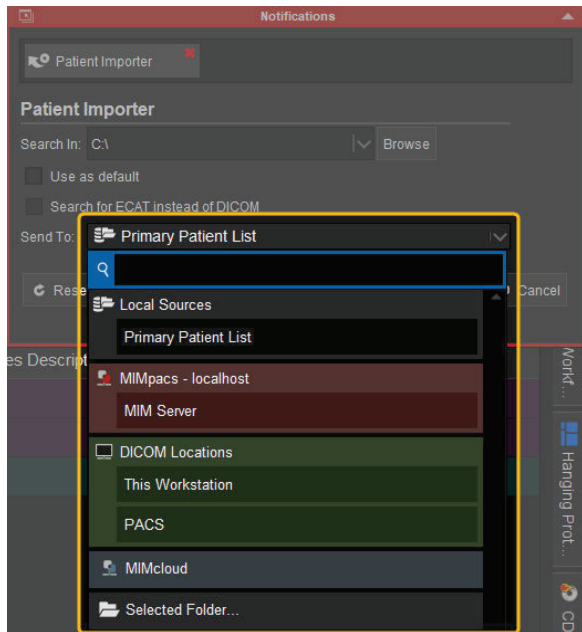
2. Click the **Browse** button in the Notifications window to find the filepath or drive where data is stored.



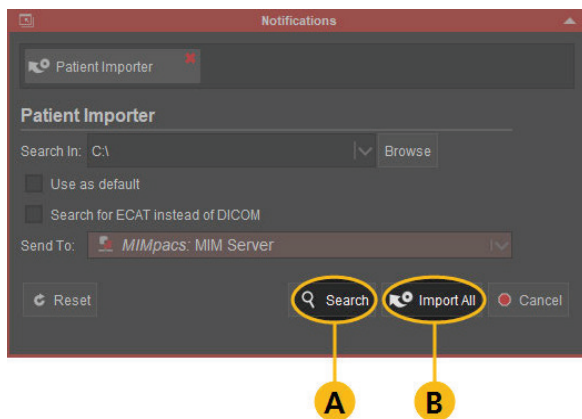


MIM SurePlan™ MRT User Guide

3. Choose a **Send To** location in the Notifications window dropdown.



4. Click **Search** or **Import All**:



- A. To select only some of the data to import, click the **Search** button.
 - i. In the **Patient Search** window that appears, check the individual series that you want to send to a MIM patient list.
 - ii. Click the **Import** button in the lower-right corner of the window.
- B. To import all of the data from the filepath or drive that you browsed to, click the **Import All...** button.

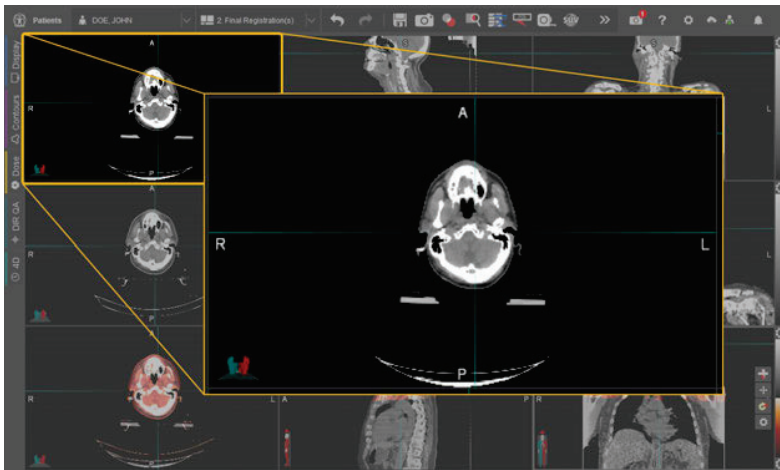
To open the data, go to the patient list that you imported the data into. Follow the steps in [Find and Open Data](#) above.

Work with Onscreen Information and Tools in MIM® Viewports

MIMTD-1592 • 06 Nov 2023

Overview

Each rectangular section of the MIM display is called a viewport. In addition to displaying images, viewports display patient and study information, provide options for adjusting viewing conditions, and display additional functionality for some MIM tools.



A viewport is considered active when your cursor is hovering in it or when the cursor was in it most recently. The active viewport has a slightly thicker border than other viewports.



Tip: Move your cursor back and forth between viewports to see how the border of the active viewport changes.

Contents

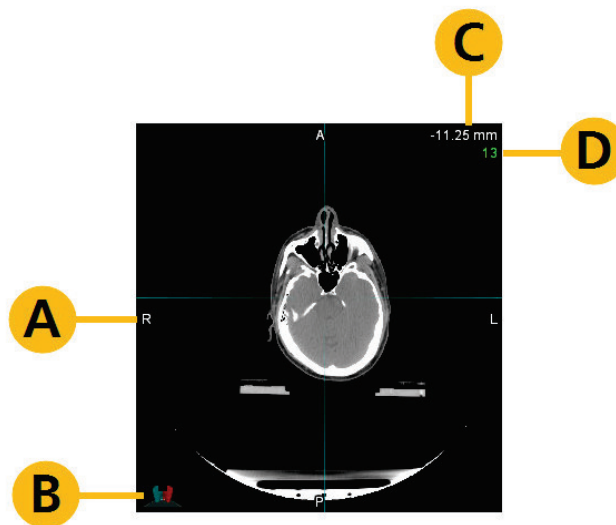
- [Default Viewport Information](#)
- [Information Displayed When the Info Panel Is Not in Use](#)
- [Hide Viewport Info](#)
- [Choose What Information Is Shown in Viewports](#)
- [Adjust Contrast and Color Tables in the Viewport](#)



- [Tool Menus in Viewports](#)
- [Dynamic Series Controls in Viewports](#)

Default Viewport Information

The information in the viewport varies based on your configured preferences, the type of image you are viewing, and whether or not a separate information panel is part of your display. At a minimum, you typically see the following:



- A. **Orientation Label** — Orientation labels indicate the patient's anterior, posterior, superior, inferior, left, and right.
- B. **Orientation Man** — The orientation man is an illustration that assists with determining patient position.
 - The figure has an **A** on its anterior and a **P** on its posterior.
 - The table in the illustration shows whether the patient was prone or supine.
 - An arrow at the figure's head or feet shows the direction the patient entered the scanner.
- C. **DICOM Position** — This is the DICOM position of the slice, as indicated in the Image Position (Patient) DICOM tag.
- D. **Slice Number** (In acquisition plane only) — MIM displays the slice number in the acquisition plane. This number comes from the Instance Number (0020, 0013) DICOM tag.
 - When the slice number is shown in green, it means you are looking at an actual slice of the image as it was acquired.





- When the slice number is shown in red, it means you are not localized directly in the "center" of a slice and some interpolation is occurring.
 - It is common to get into this state by localizing to a point in a reconstructed plane.
 - When you resume scrolling in the acquisition plane, MIM once again displays the actually acquired slices.
- If an image is the secondary in a , the slice number is replaced by its current rotation metrics.



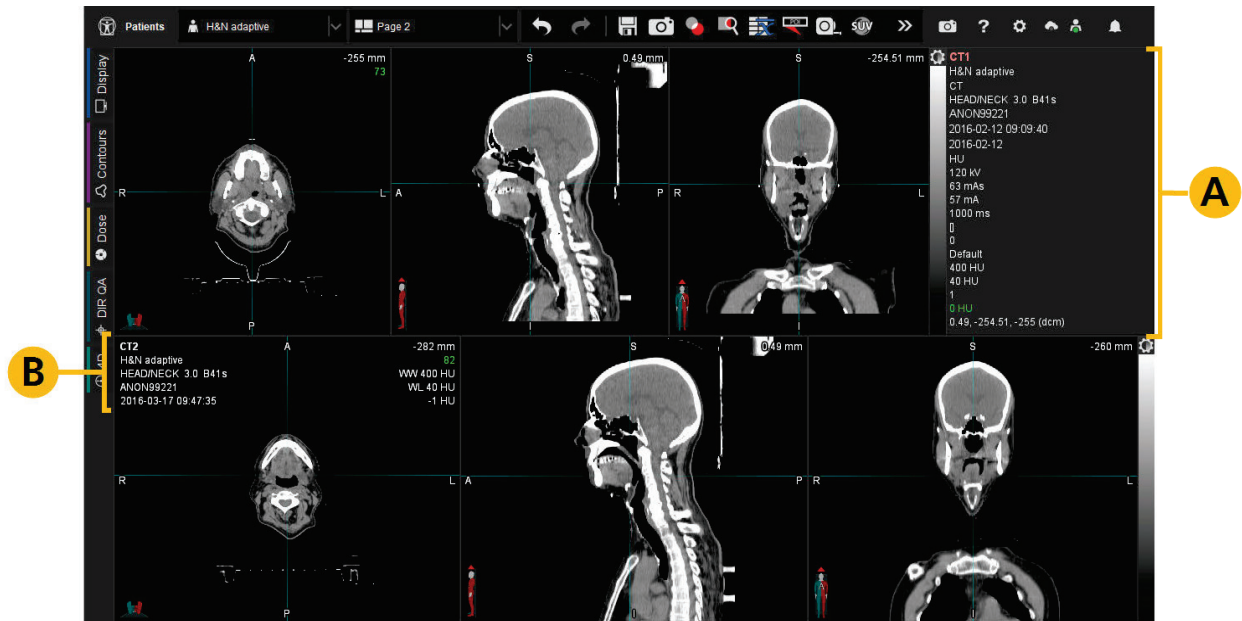
Tip: To see expanded series information in any viewport, press the space bar. The series information will be displayed over the image. Press the space bar again to hide this information.

The information shown in this view is adjustable via a JSON file. If you would like to change the information shown in this view, please contact MIM Software Support at support.mimsoftware.com.

Information Displayed When the Info Panel Is Not in Use

The info panel is a special viewport that appears on the right side of the screen when you open a series in MIM. The info panel displays detailed information from the series DICOM.

You can manually close the info panel. It may also be excluded when you create a new display page or run a workflow. When the info panel is not on the screen, some additional series information appears in the viewport.



In this two row display, the top row shows the info panel (A), which opens by default when you open a series in MIM. In the bottom row, the info panel has been closed. Note the additional information that is added to the top of the axial viewport when the info panel is not on screen (B).



When the info panel is not shown, the following information appears in the leftmost viewport for any series:



Upper Left

- Identifying information about the series
- Patient name
- Name assigned to the series by the user or workflow (if applicable)
- Patient ID
- Study date & study time (In a the study date and study time are shown for each series.)

Upper Right

- DICOM location
- Slice number (The slice number appears on the acquisition plane. The acquisition plane is often, but not always, the leftmost viewport of a series.)
- Window width
- Window level
- Voxel value at the localization point (In a the units are shown for the secondary image, which is indicated by the (S) annotation.)

Hide Viewport Info

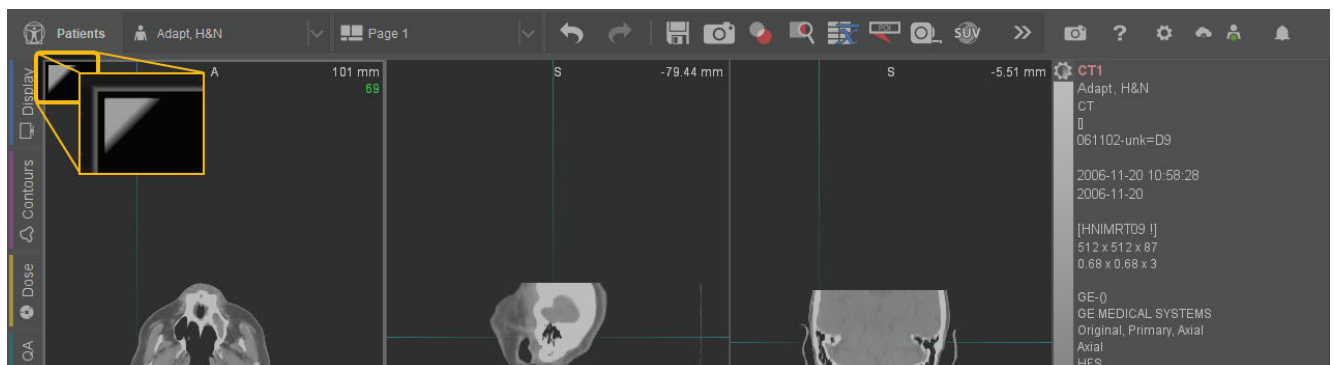
- To hide most viewport information, press i on your keyboard.
- The DICOM location and slice number are always visible. If a name has been assigned to a series by a user or workflow, this name is also always visible.

Choose What Information Is Shown in Viewports

Viewports can be personalized to show any information you would like. Several standard information layouts are available from a menu, and additional information layouts can be created using JSON files. To choose an alternative information layout, follow these steps:

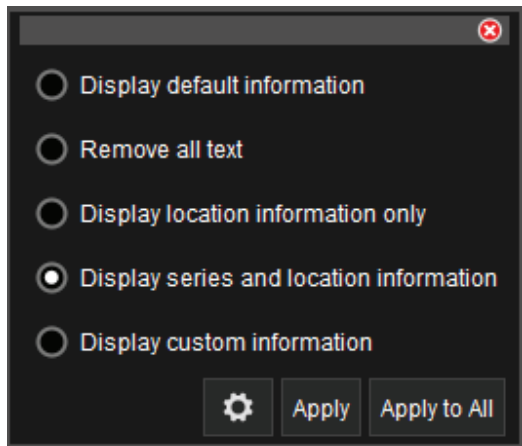
1. *MIM 7.3 and later:* Hover your cursor in the upper-left corner of a viewport until the corner turns gray.

MIM 7.2 and earlier: Hover your cursor in the upper-right corner of a viewport until the corner turns gray.






2. Click the gray corner of the viewport to open a menu of information layout options.



3. Select the information you would like to display.



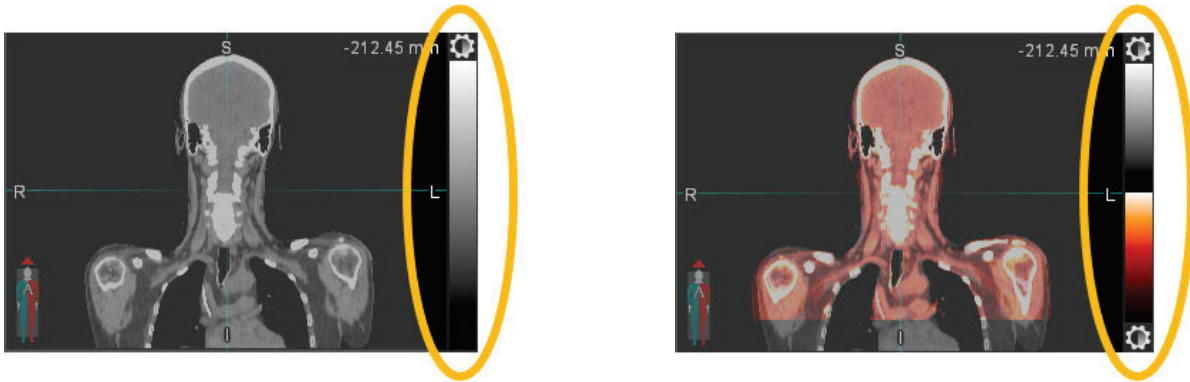
Important: The **Display custom information** option requires a JSON file to define the information layout. If you are interested in this option, please contact MIM Software Support at support.mimsoftware.com.

4. Optional: Click the gear  to adjust colors for the information display.
5. *If you would like to apply the information layout to only one viewport, click the **Apply** button.*

*If you would like to apply the information layout to all viewports on the current page, click the **Apply to All** button.*

Adjust Contrast and Color Tables in the Viewport

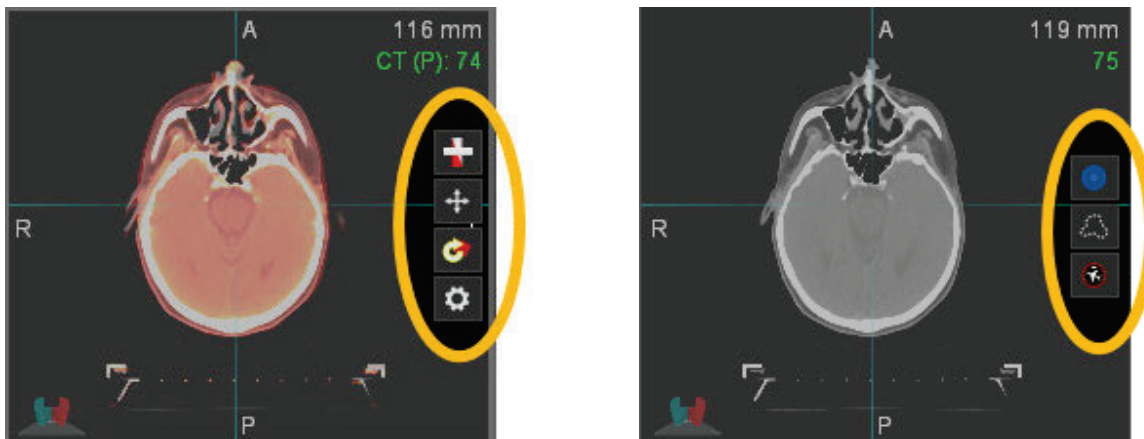
MIM provides onscreen tools for adjusting color tables and contrast. By default, these tools appear in the rightmost viewport for most image types. For detailed information, please see [Adjust Image Contrast](#).



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

Tool Menus in Viewports

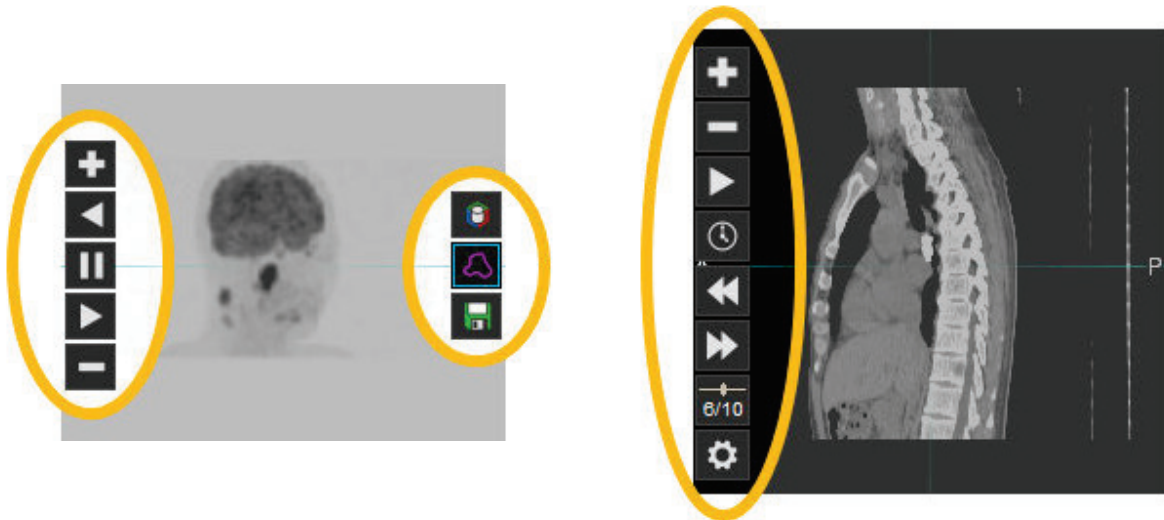
Many MIM tools have a menu of companion tools and options that appear along the right side of the active viewport. Hover over any tool in the menu for a brief description of what it does. Detailed information about specific tool menus is available in the user guide topics pertaining to each tool.



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

Dynamic Series Controls in Viewports

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



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

Localize and Scroll

MIMTD-606 • 25 Jul 2023

Overview

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

Contents

- [Localize](#)
- [Change the Appearance of the Crosshairs and Cursor](#)
- [Scroll](#)
 - [Fast Scroll \(MIM 7.2 and Later\)](#)
 - [Toggle Fast Scrolling in a Session with a Keyboard Shortcut \(MIM 7.2 and Later\)](#)


Localize

- Click within an image to localize on an area of interest in all planes.
- Left-click drag to gradually move the point of localization.
- Double-click in any plane to maximize the viewport. Double-click again to restore the viewport's original size.

Change the Appearance of the Crosshairs and Cursor

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

Crosshair Change	Keyboard Shortcut
Change Crosshair Style	=
Change Crosshair Color	Shift+=
Toggle Crosshair Visibility	Ctrl+=

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

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




Scroll

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

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




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

Fast Scroll (MIM 7.2 and Later)

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


Follow these steps to enable fast scrolling:

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

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

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

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

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



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

Access Tools: The Toolbar and the Radial Menu

MIMTD-1683 • 01 Nov 2023

Overview

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








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

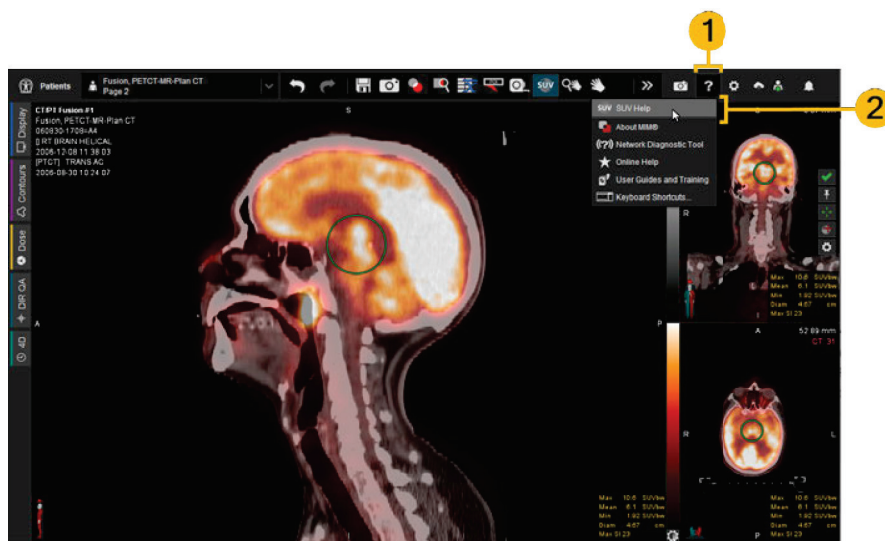
Contents

- [The Toolbar](#)
- [Customize the Toolbar](#)
- [The Radial Menu](#)
- [Customize the Radial Menu](#)

The Toolbar


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

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



Customize the Toolbar

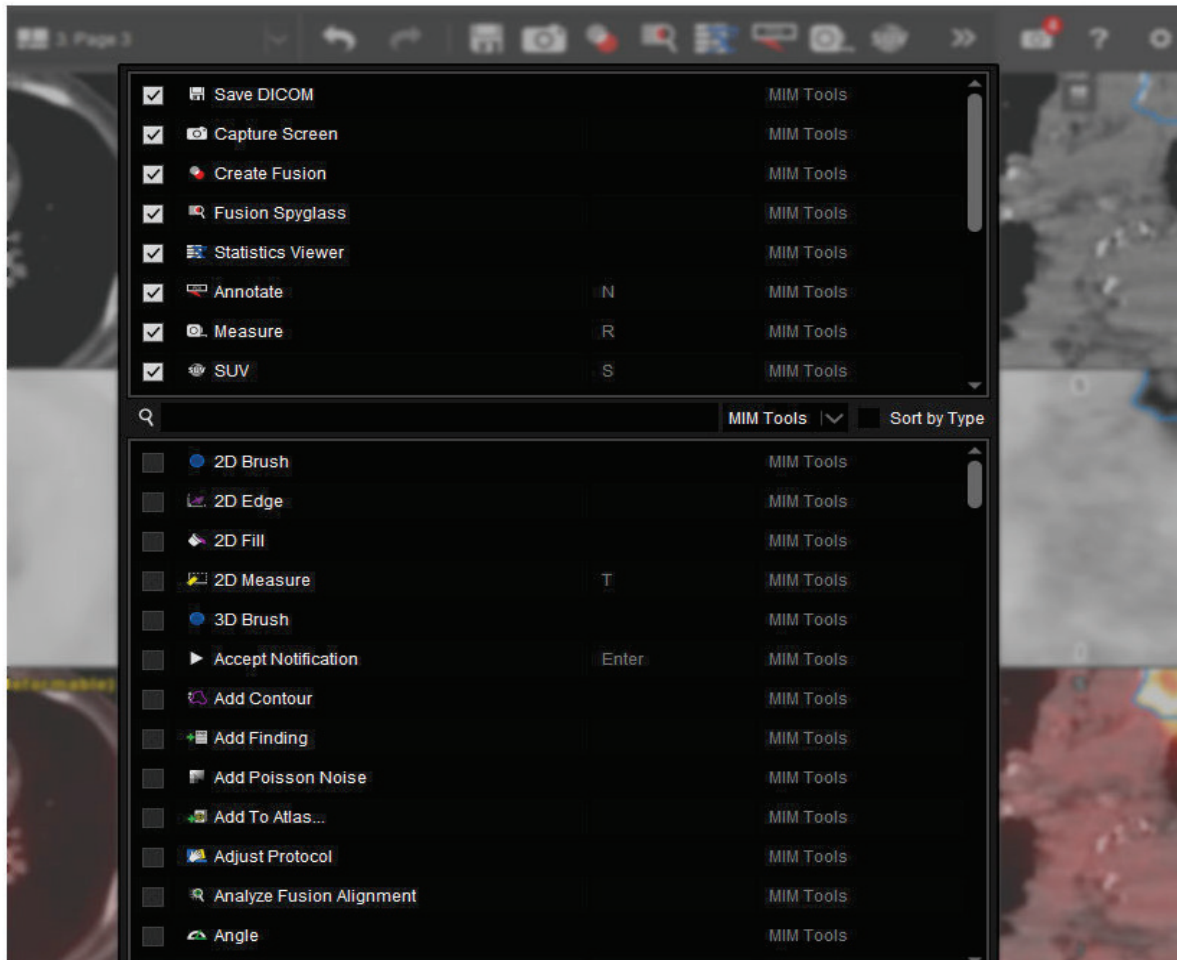
You can edit the toolbar to add tools you use frequently or remove tools you do not use:

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

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



them to the toolbar. Click tools in the top half of the window to remove them from the toolbar.



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

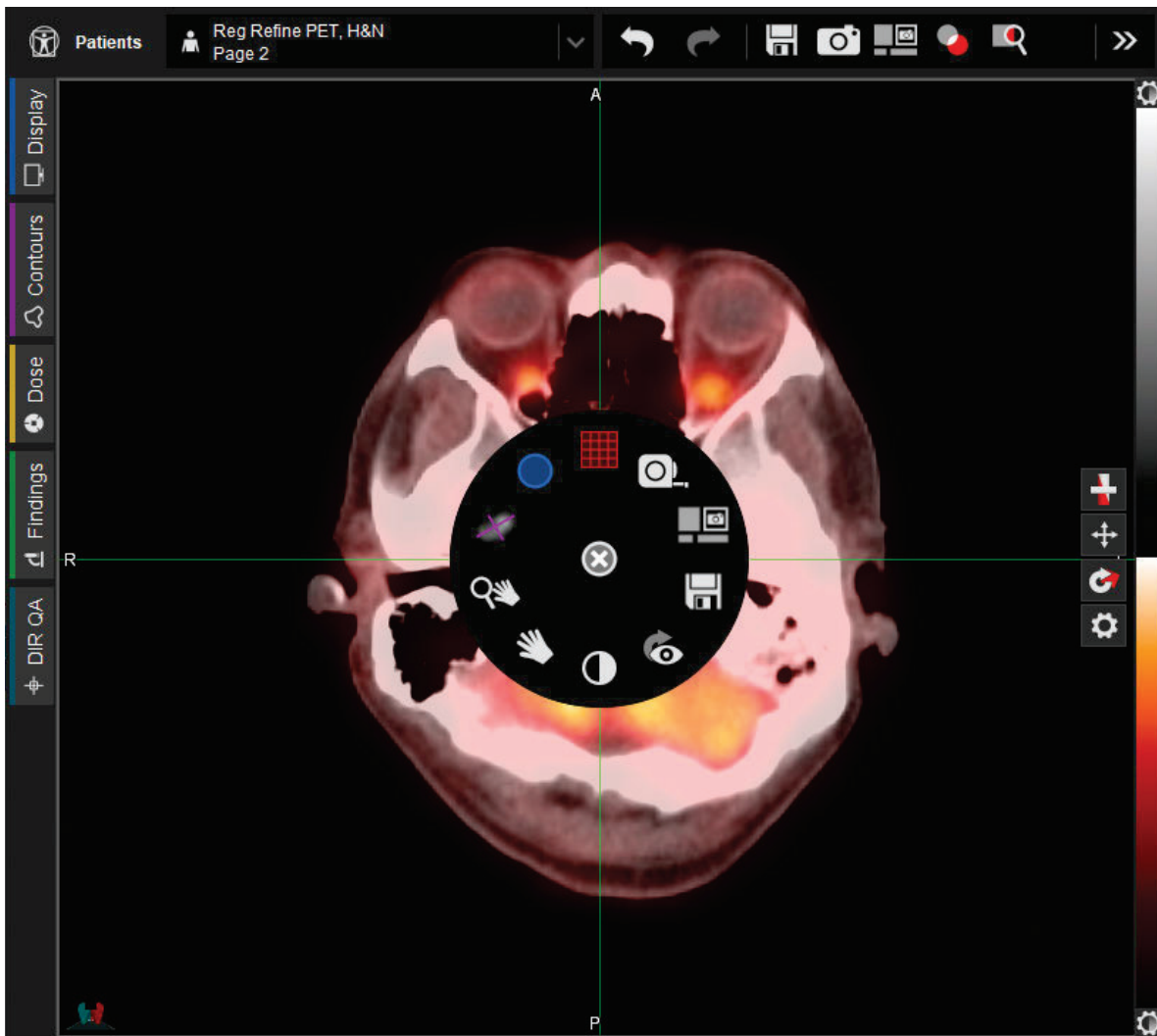
MIM 7.2 and earlier: Click the double arrow  button to close the menu.




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

The Radial Menu


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



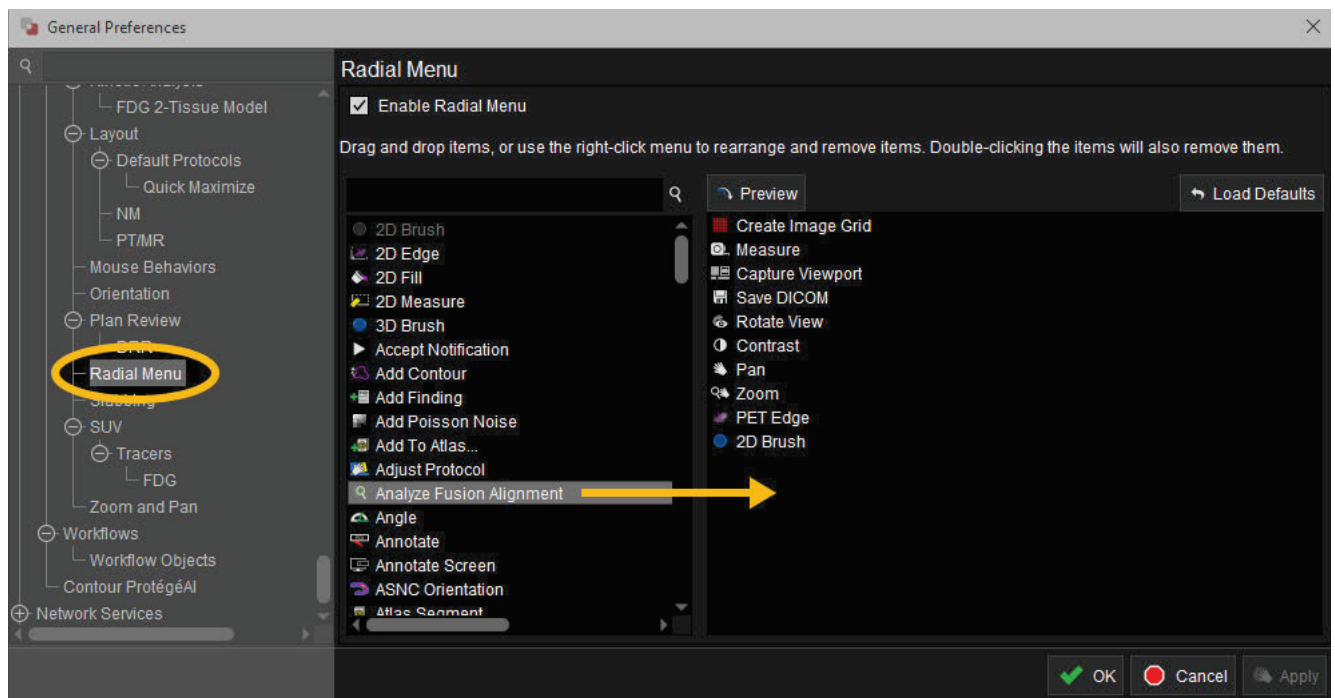
1. Access the radial menu by right-clicking on an image in an open session.
2. Click on a tool in the radial menu to activate it.
3. When you are finished using the tool, right-click again to access the radial menu. Select a new tool, or deactivate the current tool by clicking the X  button in the center.
4. Move the cursor away from the radial menu to hide it.

Customize the Radial Menu

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

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

4. Add items to your radial menu by dragging items from the left column to the right column.



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



Zoom and Pan

MIMTD-607 • 05 Oct 2023

Overview

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

Contents

- [Zoom](#)
- [Pan](#)

Zoom



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



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

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

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

1: Reset Zoom

2: Zoom In

3: Zoom In More

4: Zoom Out



Pan



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



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

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



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



Adjust Image Contrast

MIMTD-612 • 24 Aug 2023

Overview

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

Contents

- [Adjust Contrast with the Mouse \(MIM 7.3 and Later\)](#)
- [Adjust Contrast with the Contrast Bar](#)
- [Apply a Contrast Preset](#)
- [Adjust Contrast with the Contrast Tool](#)
 - [Read the Contrast Histogram](#)
 - [Adjust Contrast Bounds \(MIM 7.3 and Later\)](#)
- [Specify Manual Contrast Values](#)

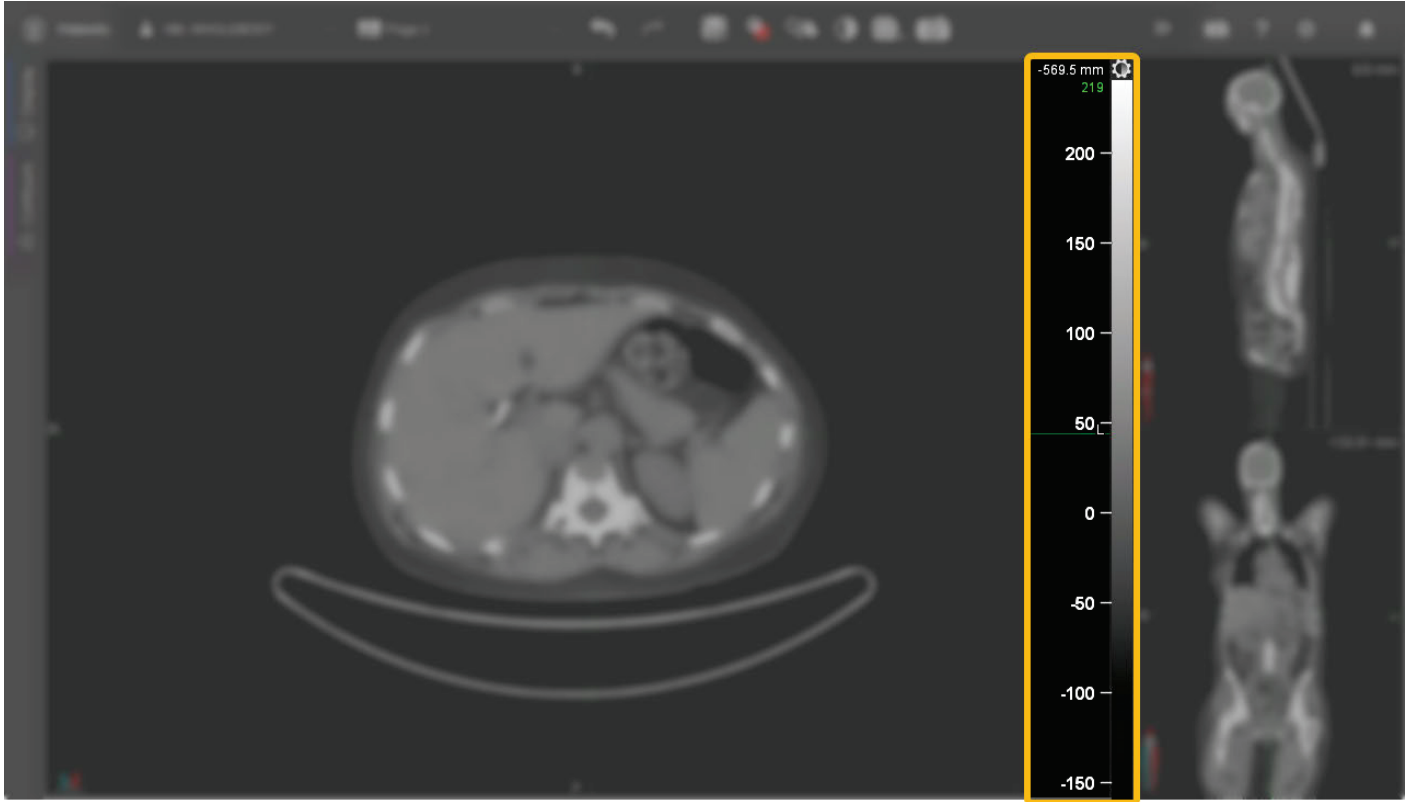
Adjust Contrast with the Mouse (MIM 7.3 and Later)

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

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

Adjust Contrast with the Contrast Bar

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

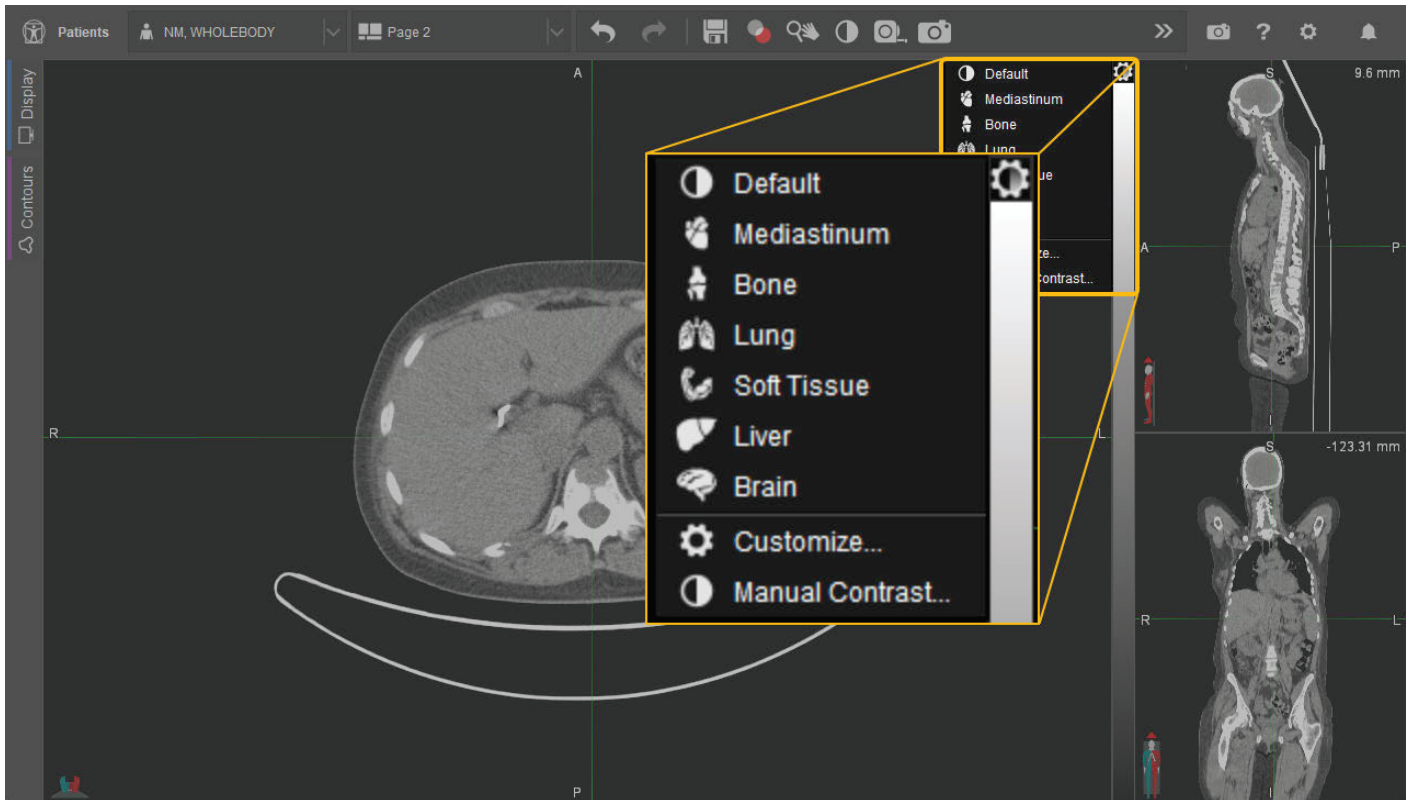


See the table below for possible contrast adjustments with the contrast bar:

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

Apply a Contrast Preset

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



Create Your Own Contrast Presets

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




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



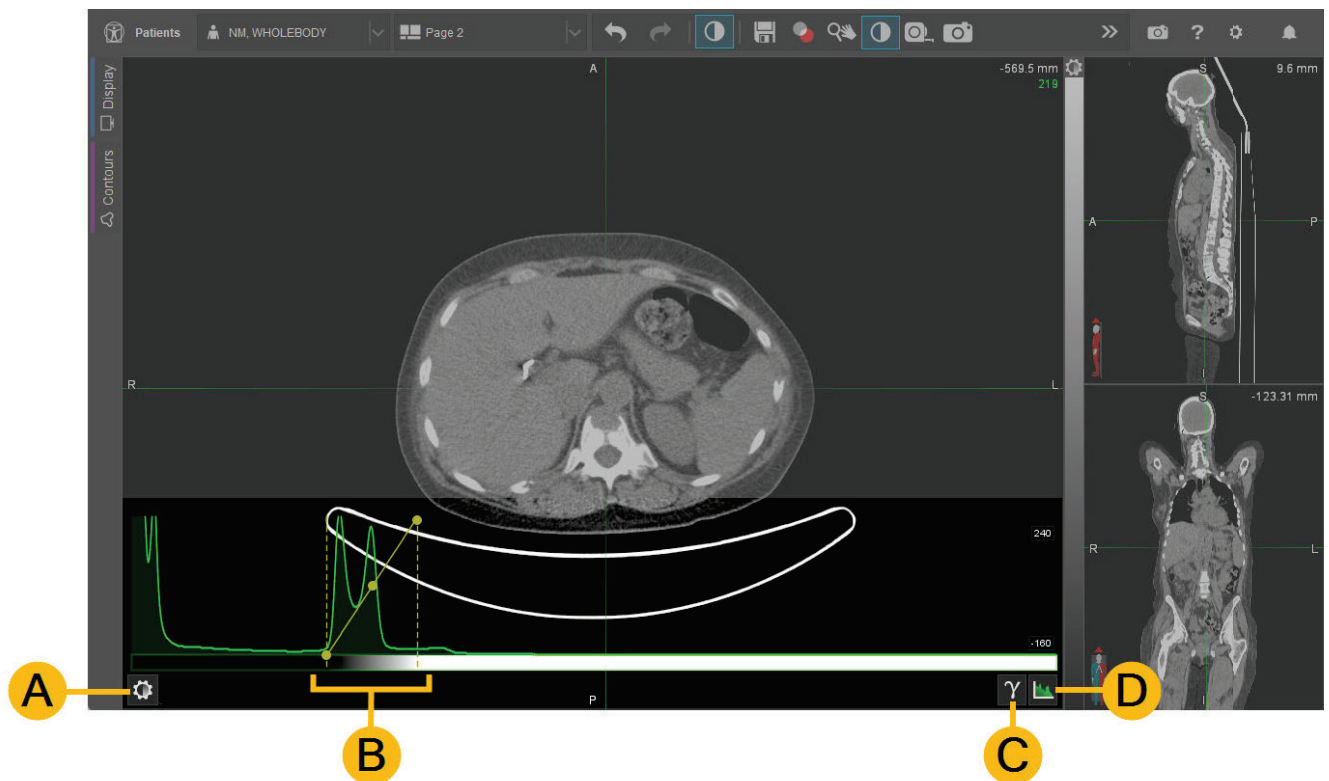
Tip: Image contrast, including presets, can also be applied in MIM Workflows™.

Adjust Contrast with the Contrast Tool

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

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

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



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

Read the Contrast Histogram

The green line shows the values present in the image.

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

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

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

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

Adjust Contrast Bounds (MIM 7.3 and Later)

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

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


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

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



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

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


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



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

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

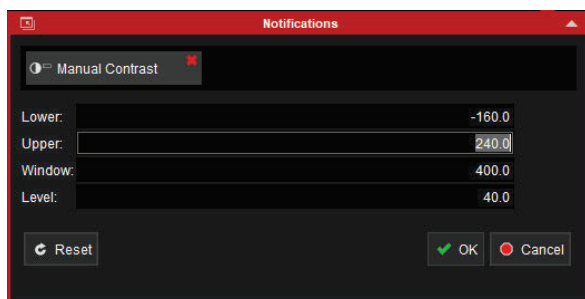
Specify Manual Contrast Values

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



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

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





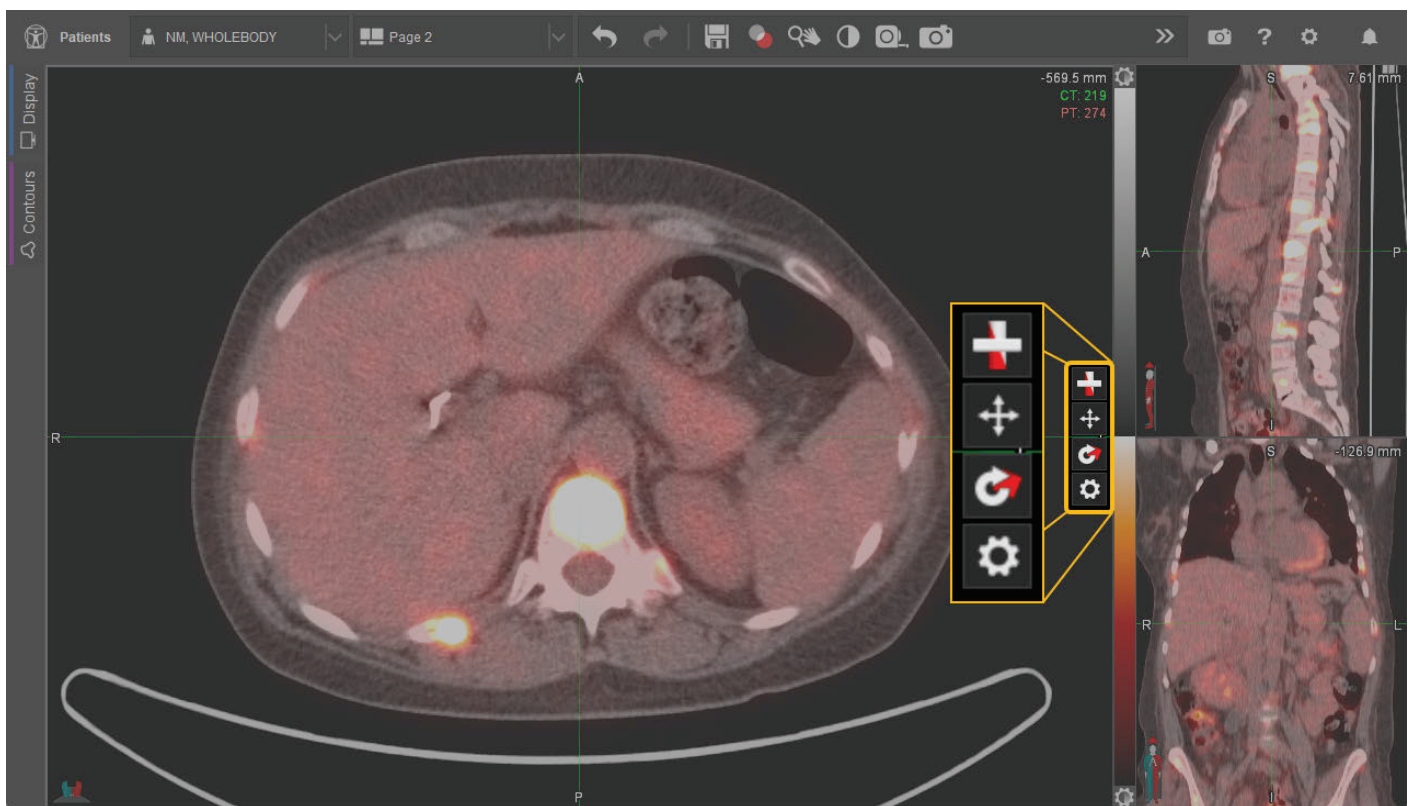
Tip: If you regularly set the contrast manually, the Manual Contrast tool can be set to a keyboard shortcut. For more information, see [Set Keyboard Shortcuts](#).

Adjust Fusions Manually

MIMTD-621 • 02 Jan 2024

Overview

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



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

Contents


- [Blend](#)
- [Translate](#)



- [Rotate](#)
- [Scale \(MIM 7.2 and Later\)](#)



Blend



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



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



Translate

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

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



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




Rotate

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



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



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

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






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



Scale (MIM 7.2 and Later)

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





MIM 7.3 and later:

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



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

In MIM 7.2:

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



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



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

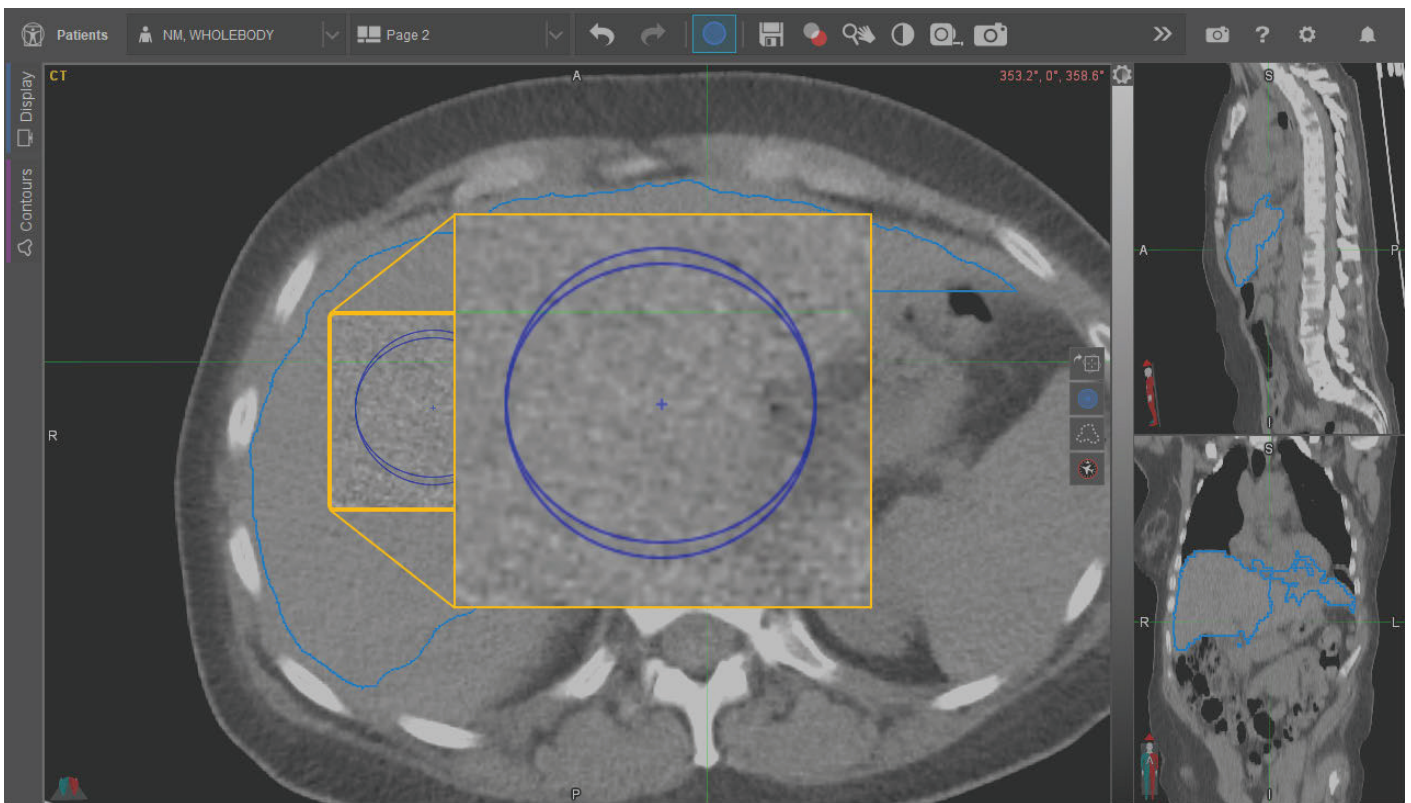


such as pelvic nodes.



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.

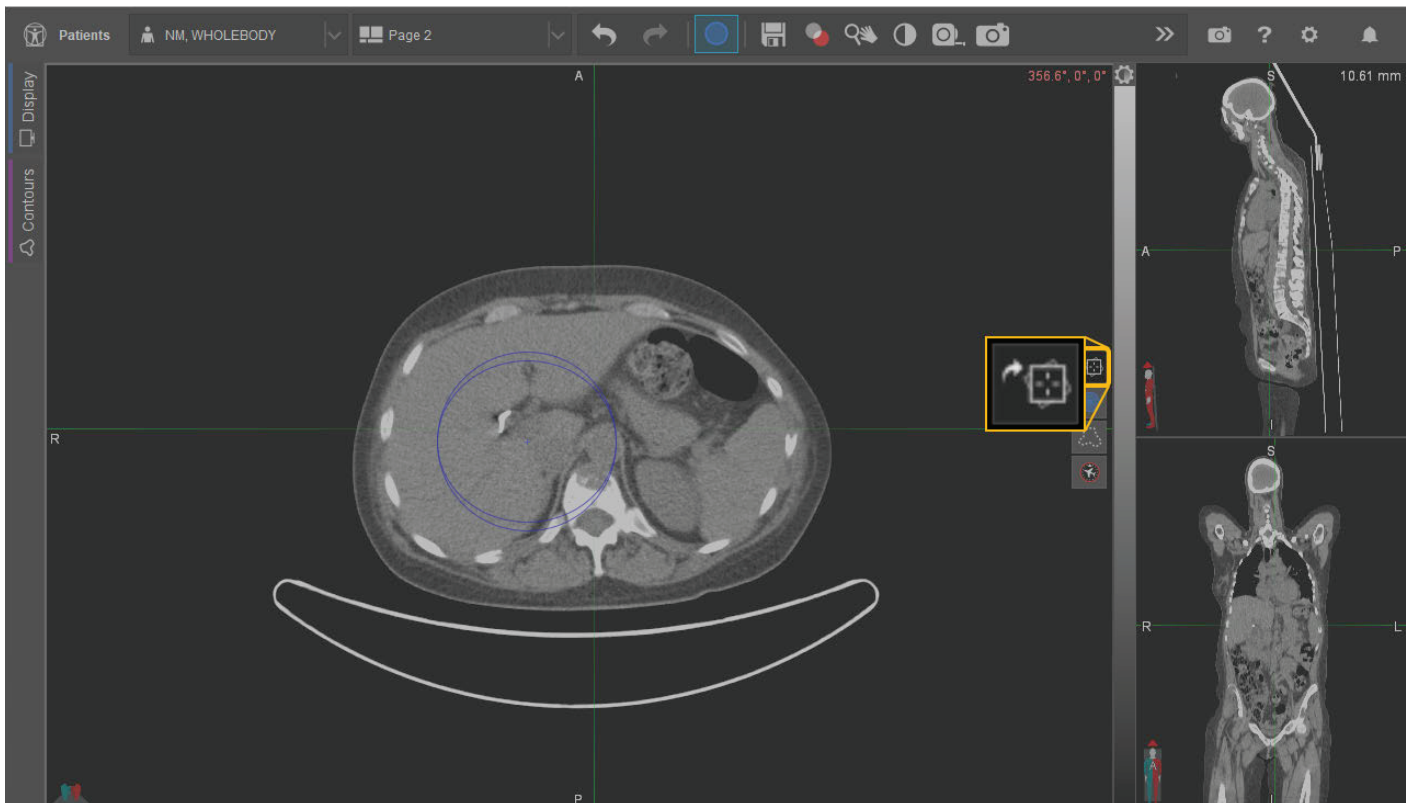
If you see the double 2D Brush, first rule out other issues by confirming the following:

- 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.



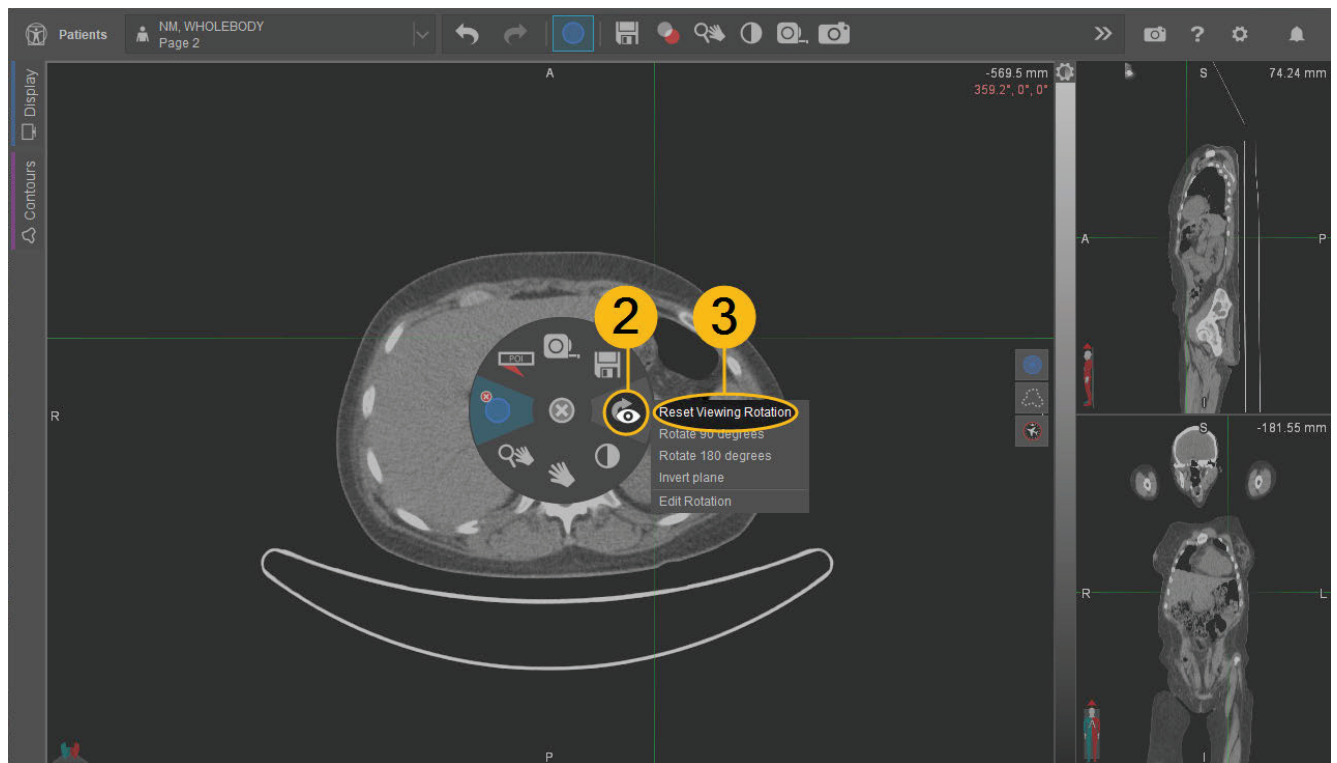
Tip: If desired, click this button again after contouring to return to the rotated view.

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

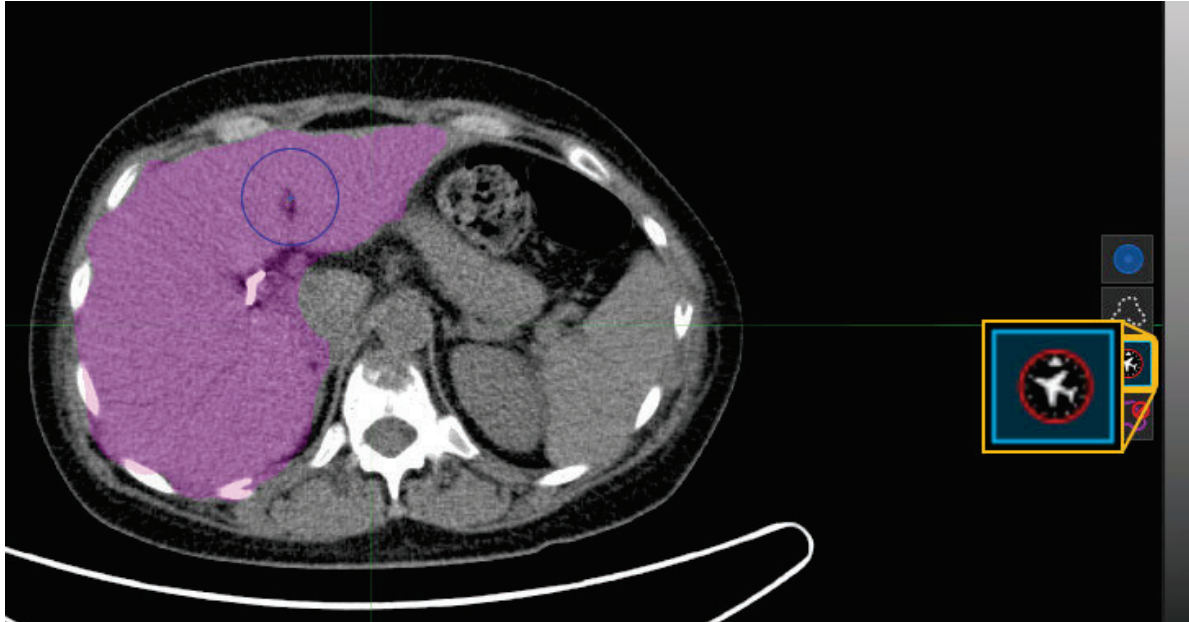
Companion tools offer additional or enhanced functionality to the primary tool.

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.



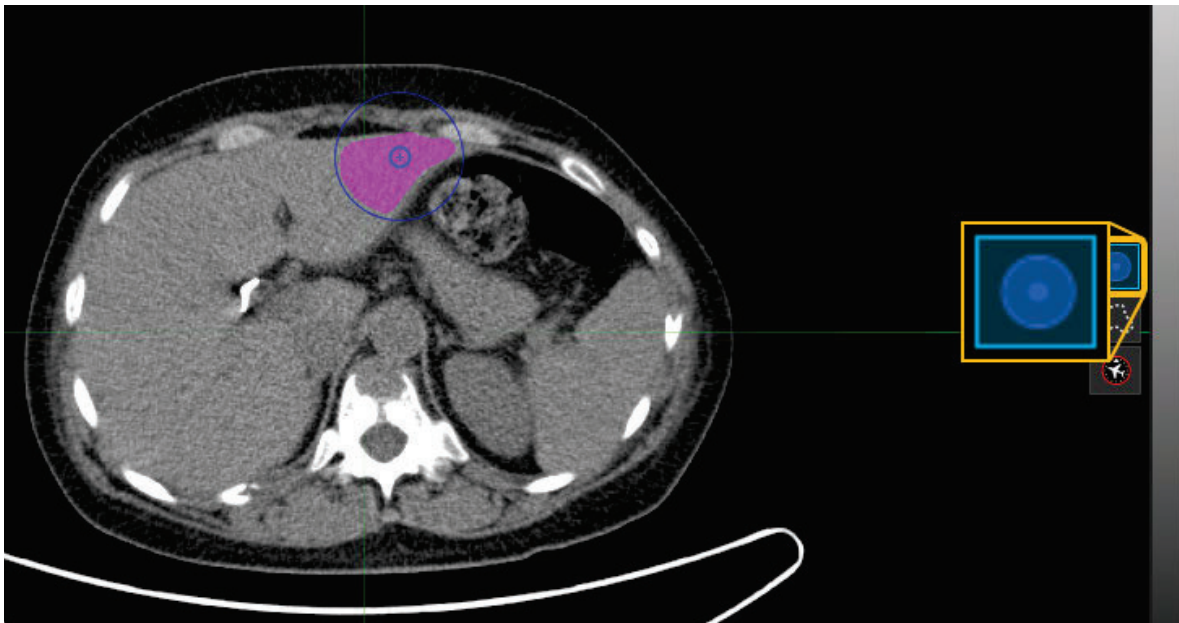
3. Scroll to another slice. A candidate contour automatically appears as a color wash on the visible slice.
4. To accept the contour, click within the viewport. If desired, continue to make edits manually with the 2D Brush.




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.