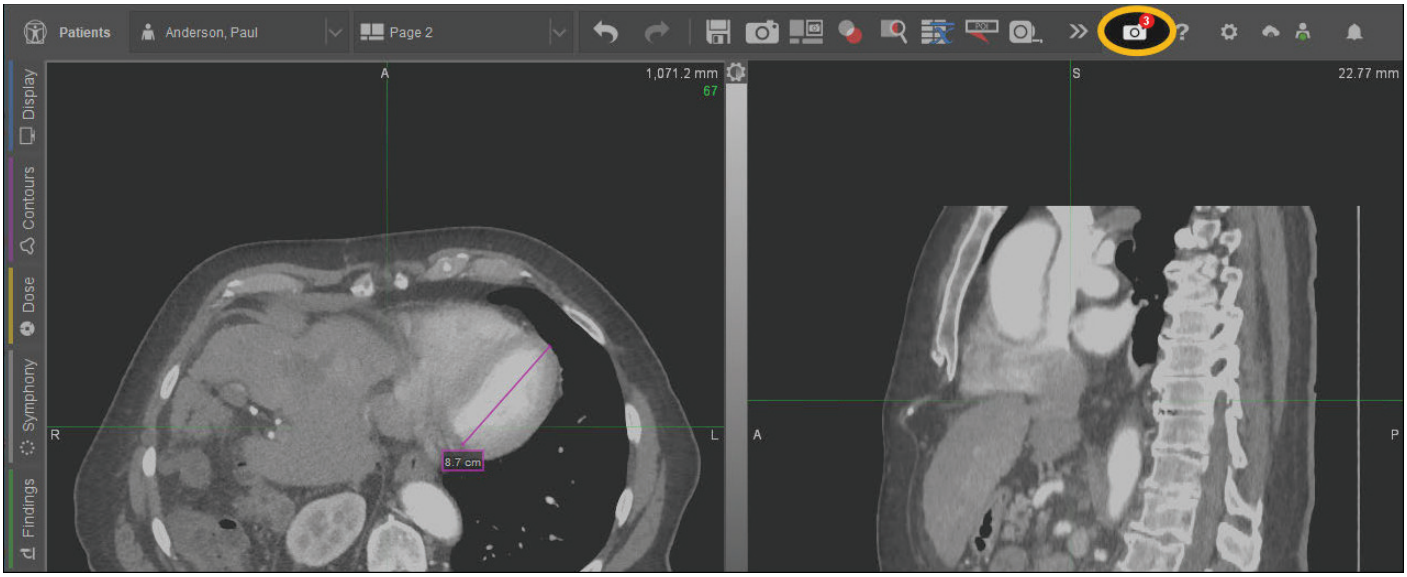
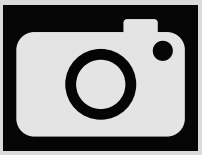
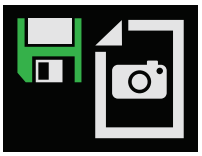
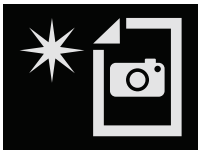
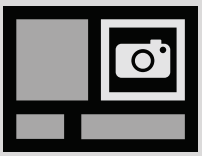
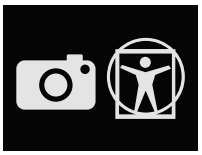
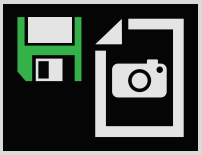


Tip: The number in red indicates how many captures have been taken and are in the gallery for the session.

Capture Tools

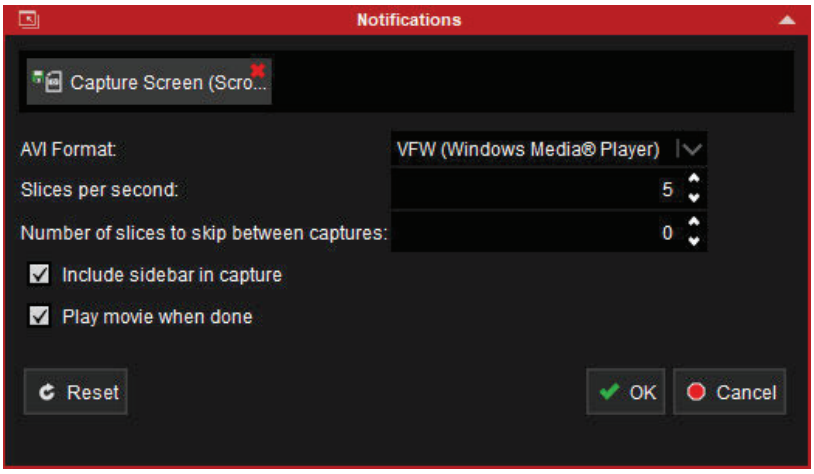
Capture Tool	What It Does	Scenario
	**Capture Screen** Takes a screenshot of the page you currently see. View the screenshot in the Capture Gallery.	Default tool. Save the image for your own future reference or to send to another system.
	**Capture and Save Current Page** Takes a screenshot of the page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

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

Scrollable Captures

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

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



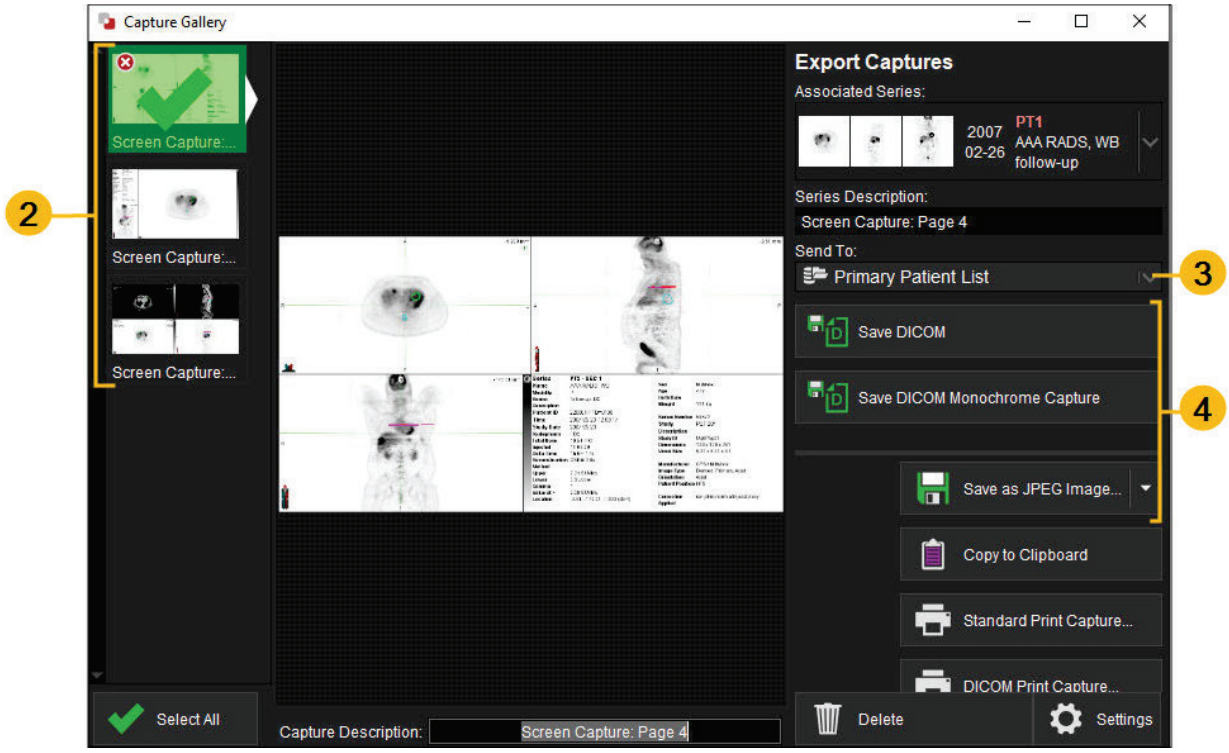
4. Click **OK**.
5. Choose the location on your workstation for the movie to save.
6. Click **Save**.

Save Secondary Captures

You can save secondary captures from the Capture Gallery.

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

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



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

Search Quickly with Saved Searches

MIMTD-619 • 12 Sep 2023

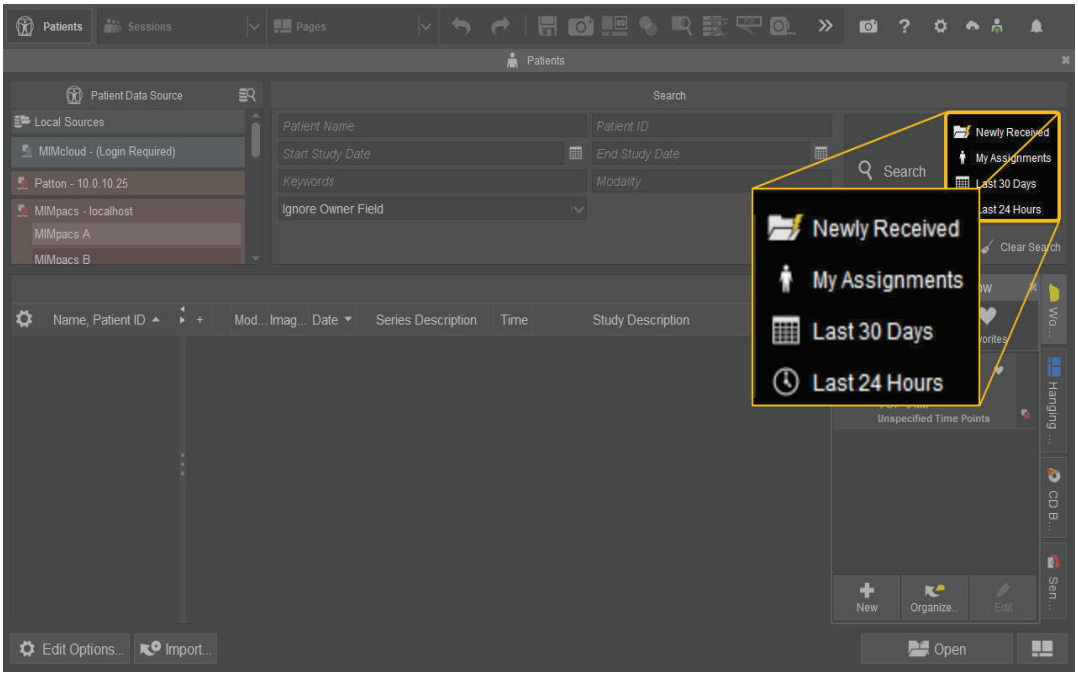
Overview

Saved searches let you find patient data in one click. Use MIM®'s default saved searches, or add your own.

Contents

Use MIM's Default Saved Searches

Click one of the default saved search buttons to find data that match pre-set parameters.



Default Saved Searches

- **Newly Received** — Find the most recent 100 series based on the MIMDateAdded tag.
- **My Assignments** — Find series that are owned by the logged-in user. This button only appears if user logins are enabled and you are searching a MIMpacs™ patient list.
- **Last 30 Days** — Find series that have a StudyDate DICOM tag within the last 30 days.
- **Last 24 Hours** — Find series that have a StudyDate DICOM tag of today or yesterday. For more information, see Search for Today's Series.

Default Radiology and Nuclear Medicine Saved Searches

- **Today's PET/CTs** — Find PET/CTs with today's date, and associated priors.
- **Today's NMs (SPECT/CT)** — Find NMs with today's date, and any SPECT/CTs with today's date that are also available.
- **Today's NMs** — Find only NMs with today's date.
- **Today's NM Sessions** — Find NM sessions that were created today.

Enable or Restore Default Searches

Important: Changing the default radiology and nuclear medicine saved searches is not recommended because clicking the **Restore Radiology and Nuclear Medicine Searches** or **Restore Default Searches** button undoes any changes that you made. Please add new saved searches instead. For instructions, see Save Your Frequently Used Searches.

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

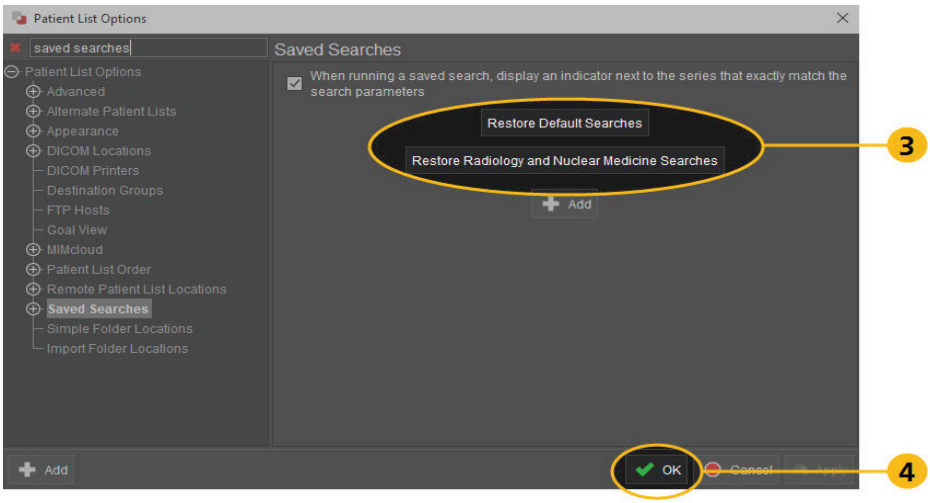
1. Click the Settings button in the upper-right corner of MIM.
2. Go to **Patient List Options** and search for "**saved searches**". Select **Saved Searches** on the left side.
3. Enable or restore default searches.
   - *If you need to enable Radiology and Nuclear Medicine Searches,* click **Restore Radiology and Nuclear Medicine Searches**.

     Important: If the Radiology and Nuclear Medicine Searches are already enabled, clicking this button undoes all previous edits to these search parameters.

   - *If you need to restore Radiology and Nuclear Medicine Searches,* click **Restore Radiology and Nuclear Medicine Searches**.
   - *If you need to restore Default Searches,* click **Restore Default Searches**.

4. Click **OK** in the lower-right corner. Radiology and nuclear medicine saved search buttons now appear in the upper-right corner of the patient list.



Save Your Frequently Used Searches

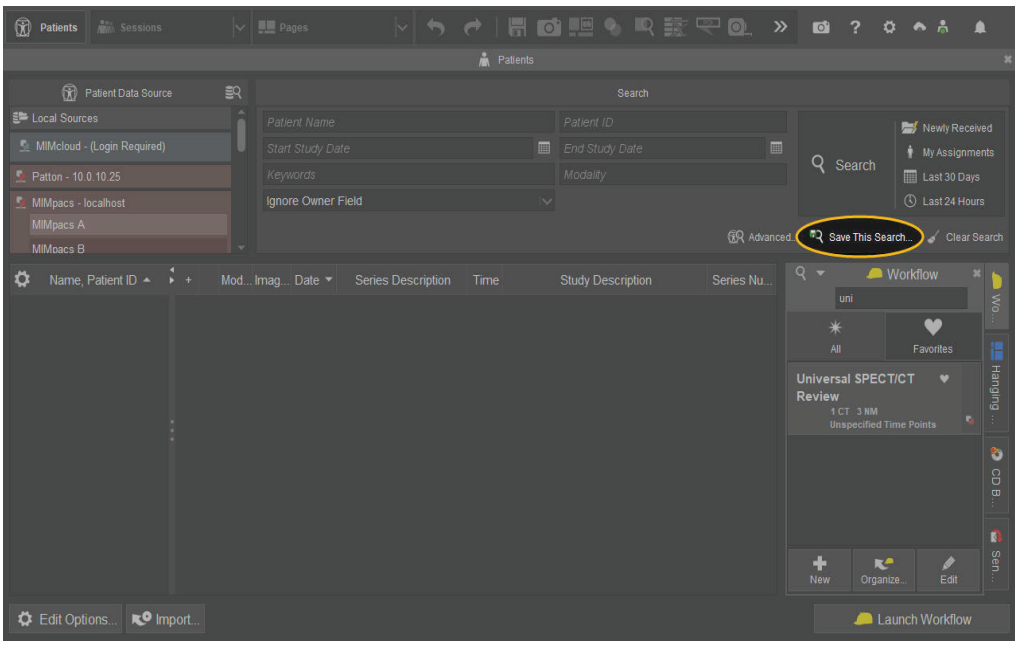
> **Tip**: If you want to share and standardize these settings across your institution, a MIM administrative user should make these additions or updates while logged into the **Edit Site Defaults** login mode. See Update Default Settings for Users for prerequisites and instructions.

To save frequently used searches:

1. In the patient list, enter the search parameters that you want to save.

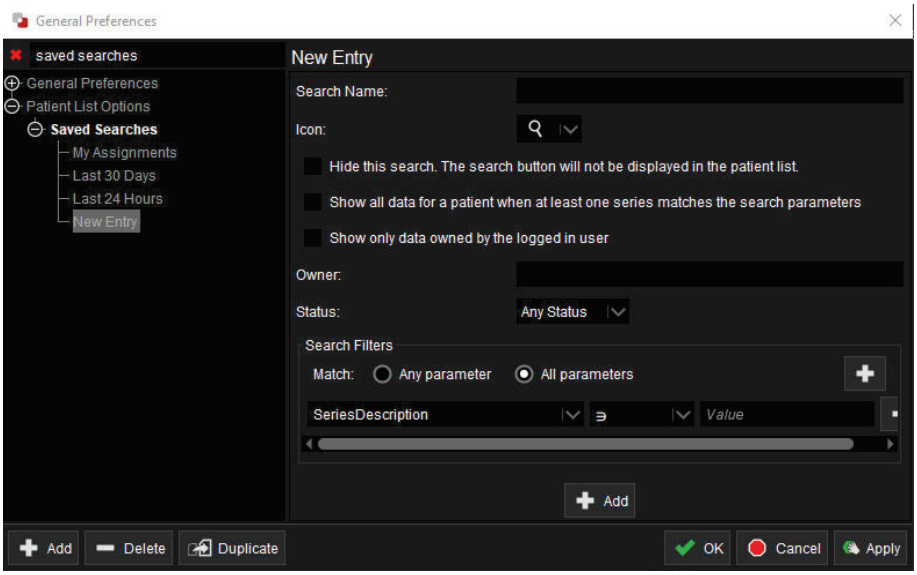
> **Related:** For detailed instructions on searching for patient data, see Find and Open Patient Data.

2. Click the **Save This Search...** button below the **Search** button.



A settings window appears.

3. Review and adjust the settings for the saved search as necessary.



- **Search Name** — Enter the name that will appear on the button for this saved search.
- **Icon** — Select the icon that will appear on the button for this saved search.
- **Hide this search. The search button will not be displayed in the patient list.** — Select this option to prevent the saved search from appearing in the patient list. This is useful if you are working on a search that is not yet ready for other users.

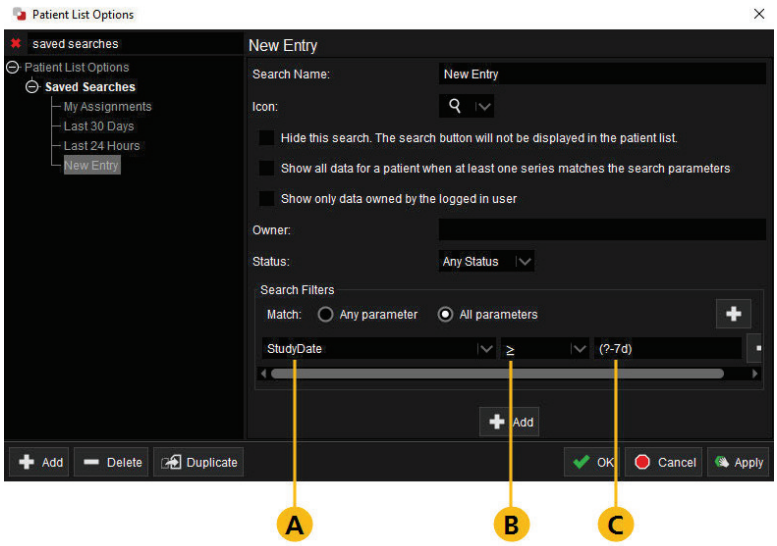
- **Show all data for a patient when at least one series matches the search parameters** — Select this option to show all of the patient's series in the results, even if some of the series do not match the search parameters.
    - This setting automates the right-click **Search for This Patient** option that you may be familiar with.

Related: For more information, see Find and Open Patient Data.

    - For instructions on enabling an indicator next to the results that are exact matches, see Indicate Exact Matches.

- **Show only data owned by the logged in user** — Select this option to only show results that are owned by the logged in user.
    - When this option is selected, the **Owner** field below it is disabled.
    - If user logins are not enabled in MIM, saved searches that have this option selected are disabled and do not appear in the search field.

- **Owner** — Enter a username to search by an owner that is not the logged in user. User logins must be enabled to use this feature.
- **Status** — Select an option to find series that have a specific status.
- **Search Filters** — Add DICOM-tag based filters using the ✚ button. Choose whether to match **Any parameter** or **All parameters**. This selection only affects whether the search matches any or all of the DICOM tag search filters; any search parameters configured above this section are always applied.



A. Select a DICOM tag (e.g., StudyDate) for the filter that you added. Scroll through the dropdown menu to see common tags, or start typing to find other tags.

B. Select an operator (e.g., ≥). To see an explanation of what the operator does, select the operator and hover your cursor over the field.

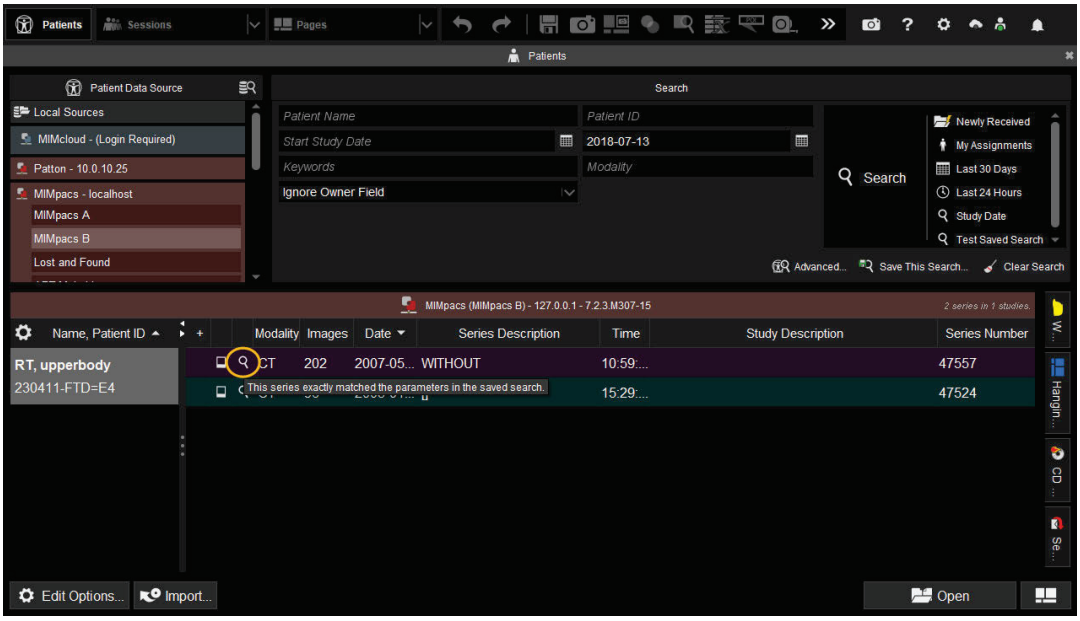
C. Enter a value (e.g., (?-7d)). For more information on the date format used in this example, see Search with Relative Date Ranges.

Indicate Exact Matches

When saved searches are set up to show all data for a patient, you may still want to see which results match the search parameters exactly.

To display an indicator next to exact matches:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **Patient List Options** and search for "**saved searches**". Select **Saved Searches** on the left side.
3. Select **When running a saved search, display an indicator next to the series that exactly match the search parameters**.
4. Click **OK** in the lower-right corner. An indicator now appears next to exact matches.



For more information on setting up saved searches to show all data for a patient, see Save Your Frequently Used Searches.

Search with Relative Date Ranges

Relative date ranges let you set up saved searches that do not need to be updated in the future. For example, your search can find studies that are older than the current date instead of studies that are older than the absolute date of 1 January 2021.

To configure relative date ranges in search filter fields:

1. Enter a question mark (?) as the variable that stands for "today."
2. Enter a plus (+) or minus (-) sign to offset the time from today.
    - Plus (+) — After today.
    - Minus (-) — Before today.
3. Enter an integer followed by a single character ("d" for days, "m" for months, or "y" for years) to indicate the amount of offset.
4. Place parentheses around the entire text.

Examples:

(?-5d)	Five days before today.
(?-6m)	Six months before today.
?-2d	This example is invalid because it lacks parentheses.

Search for Today's Series

MIM's default **Last 24 Hours** saved search finds series with a StudyDate of today or yesterday. It uses two search filters: StudyDate ≥ (?-1d) and StudyDate ≥ (?-0d)

If you would like to find only series with a StudyDate of today, set up a saved search that uses one filter: StudyDate ≥ (?-0d).

For more information on relative date ranges, see Search with Relative Date Ranges.

Create Structured Reports

Create and Modify Structured Reports

MIMTD-618 • 01 Sep 2023

Overview

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

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

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

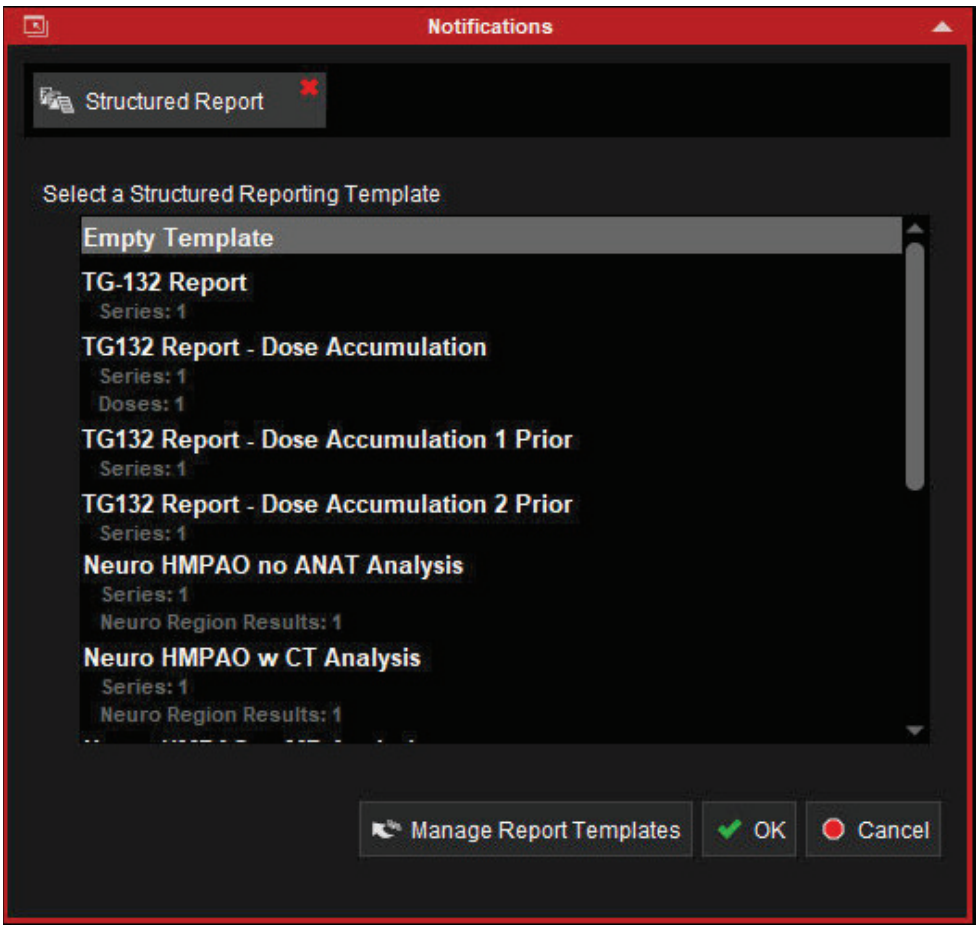
Contents

Create a Structured Report

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

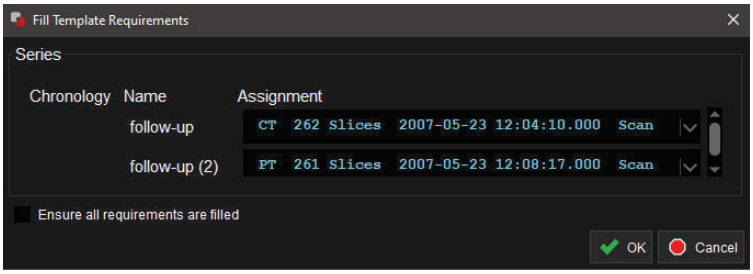
1. In an open MIM session, click the **Create Structured Report** tool in the toolbar, in the radial menu, or via keyboard shortcut.

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



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

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



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

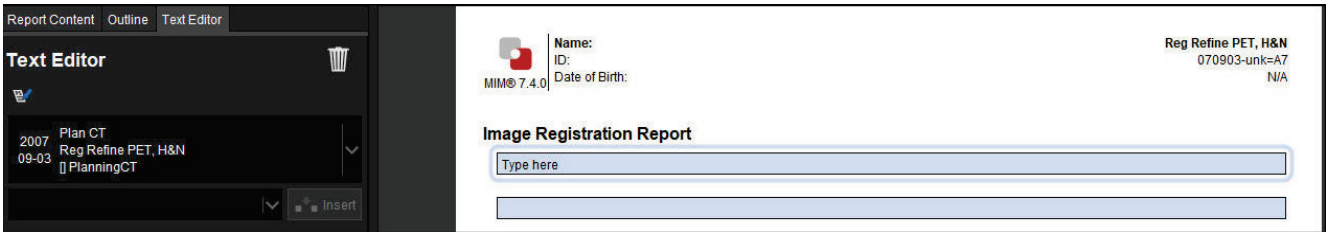
Modify Structured Report Content

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

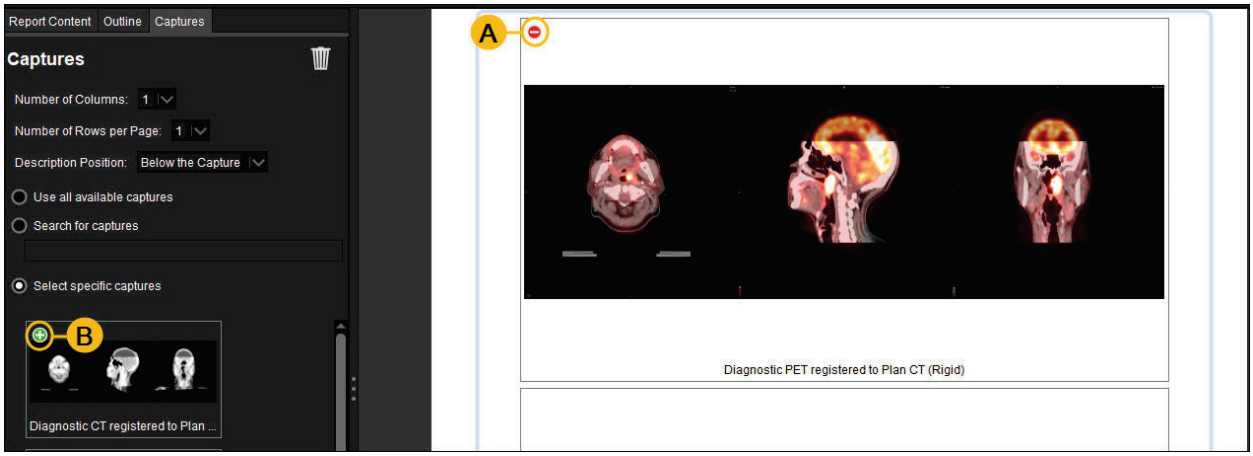
Make Common Updates

Review the report preview:

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



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



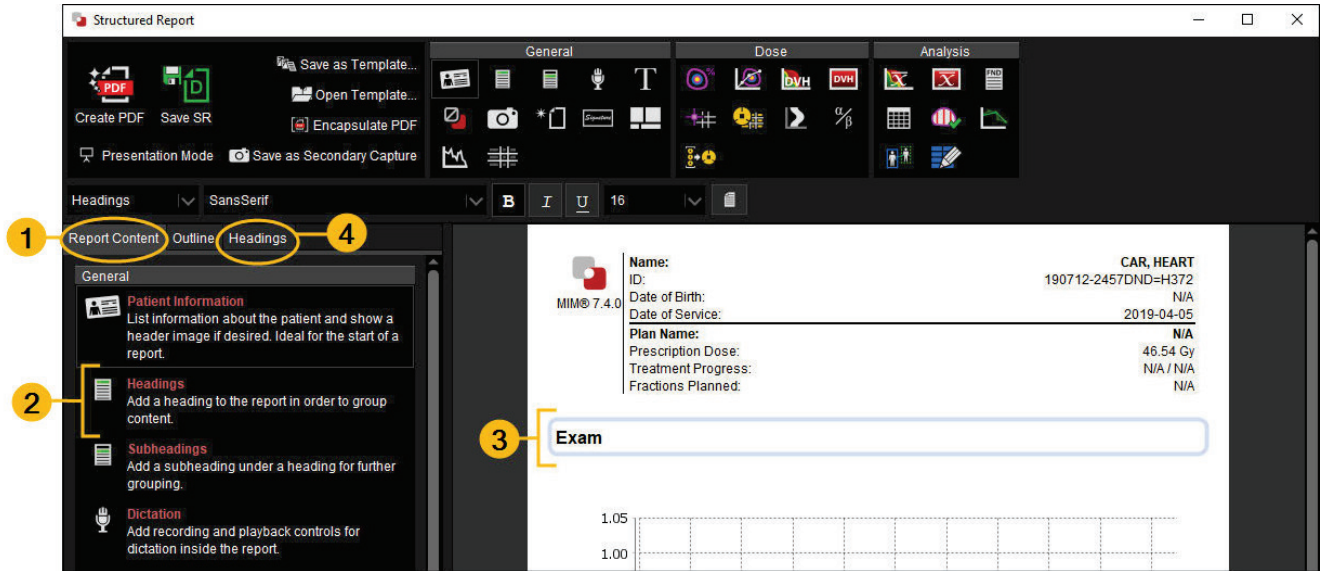
Add, Edit, and Delete Content

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

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

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

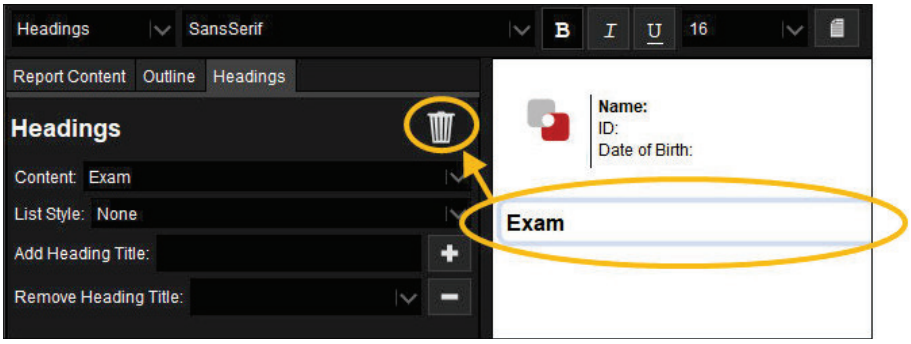
3. View the selected content type that appears in the report preview.
4. Go to the new tab for that content to edit it.



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

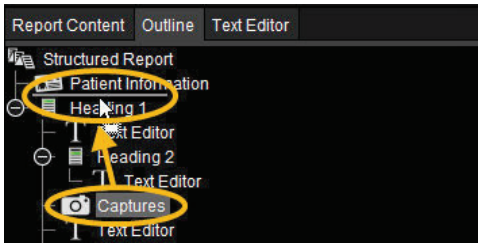
- Use Headings, Layouts, and Page Breaks to Organize Structured Report Content
- Add Secondary Captures to Structured Reports
- Add Statistics to Structured Reports

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



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

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



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

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

Save Structured Reports

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

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

Create Structured Report Templates

MIMTD-1435 • 01 Sep 2023

Overview

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

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

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

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

Contents

Design a Structured Report

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

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

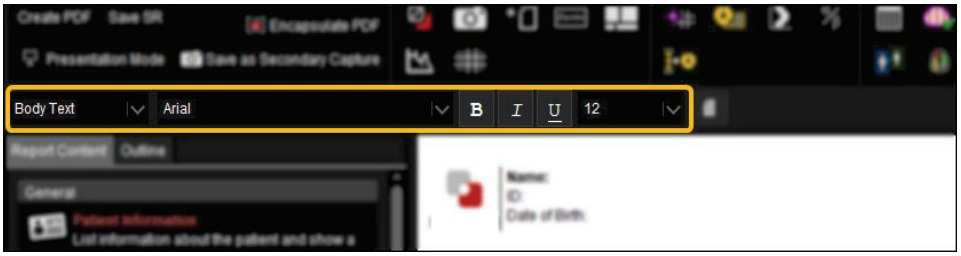
1. In an open MIM session, click the **Create Structured Report** tool in the toolbar, in the radial menu, or via keyboard shortcut.
2. In the Notifications window, either select the structured report template that you want to modify or select **Empty Template** to begin from a blank page. Click **OK**.

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

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

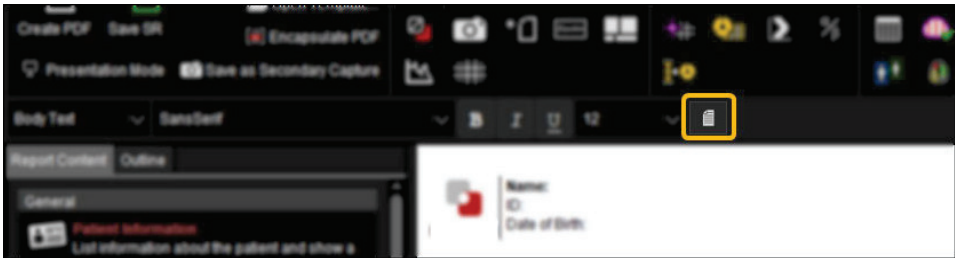
Change the Font, Font Style, and Font Size

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



Change the Page Orientation

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



Add Content to the Report

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

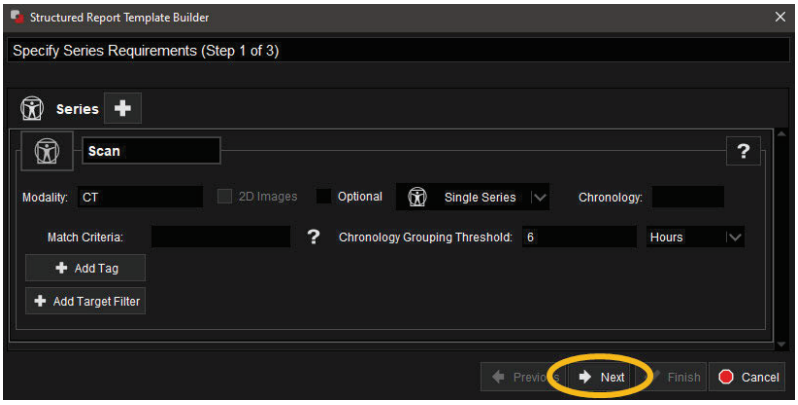
Review the following for more information about specific types of content that you can add:

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

Save the Report As a Report Template

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

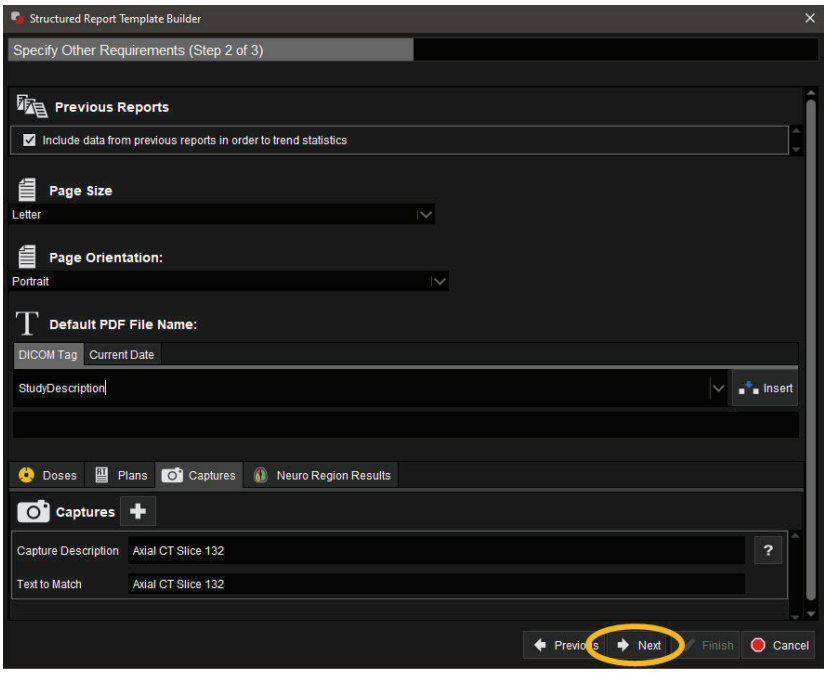
1. Click the **Save as Template...** button in the upper-left corner of the Structured Report Builder. The Structured Report Template Builder opens.
2. If desired, adjust the information in the **Specify Series Requirements** step. The information in this step is autofilled based on the study in your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



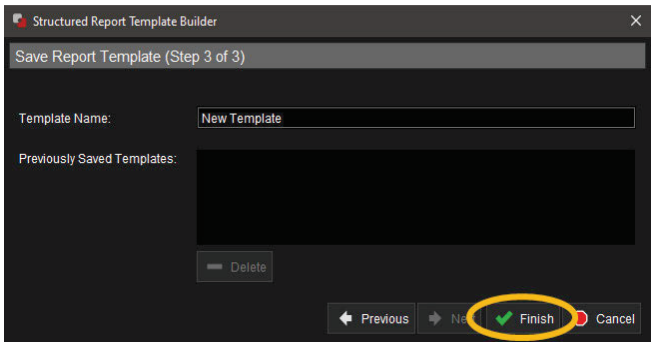
4. If desired, adjust the information in the **Specify Other Requirements** step:
   - To compare data across structured reports from multiple time points, select **Include data from previous reports in order to trend statistics**. MIM trends data using any existing DICOM structured reports (i.e., structured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

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

5. Click **Next**.



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



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

Distribute the Report Template

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

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

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

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

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

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

MIMTD-1436 • 14 Sep 2023

Overview

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

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

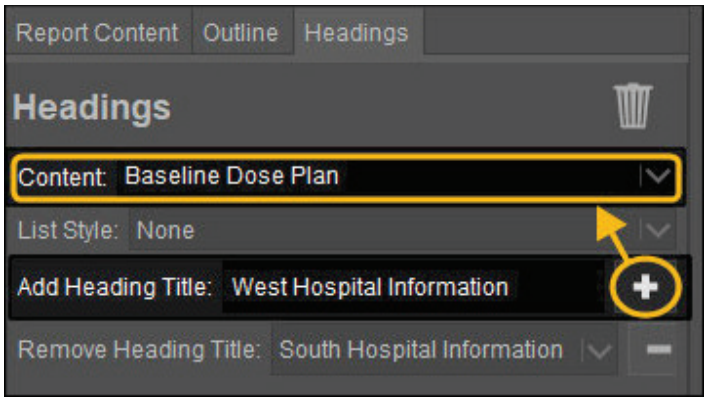
Contents

Use Headings and Subheadings

Add headings and subheadings to your report:

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

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



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

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

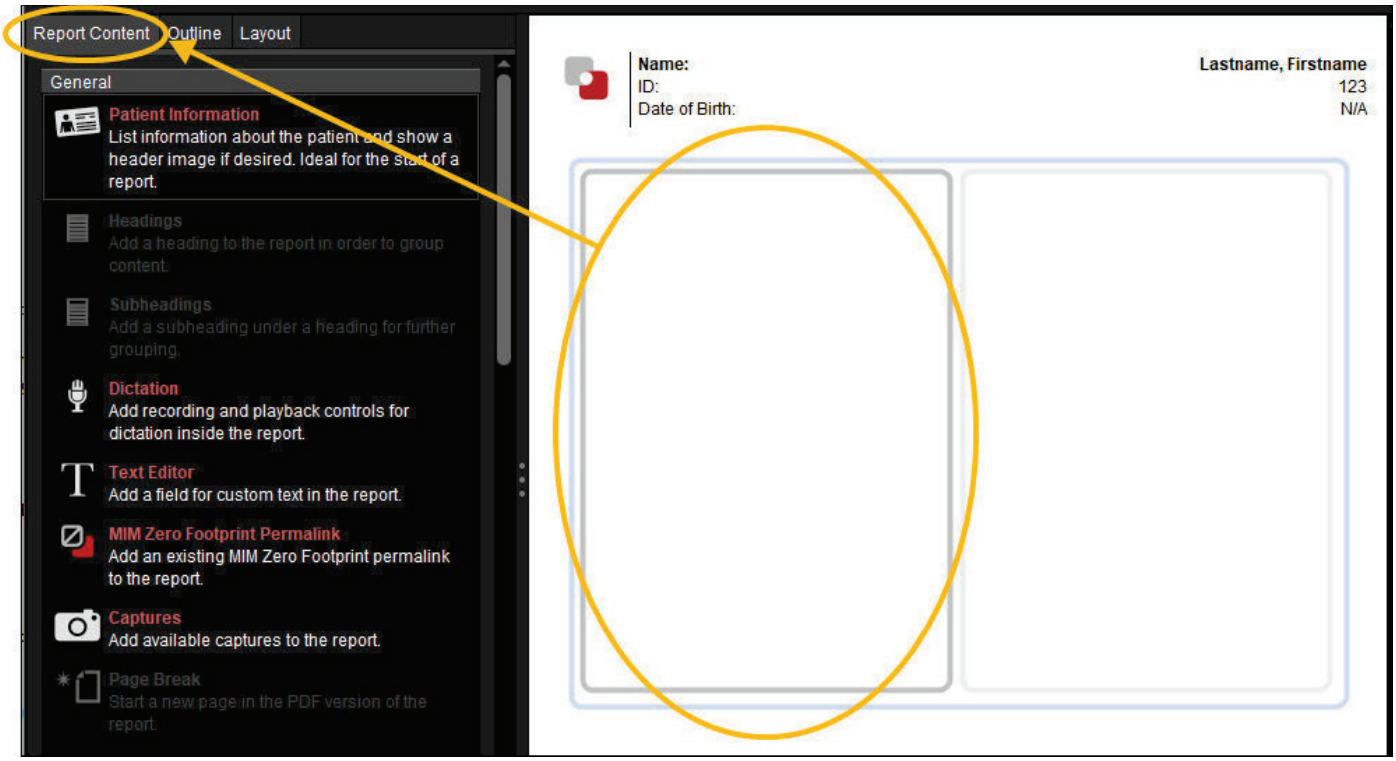
Arrange Content in Layouts

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

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

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

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

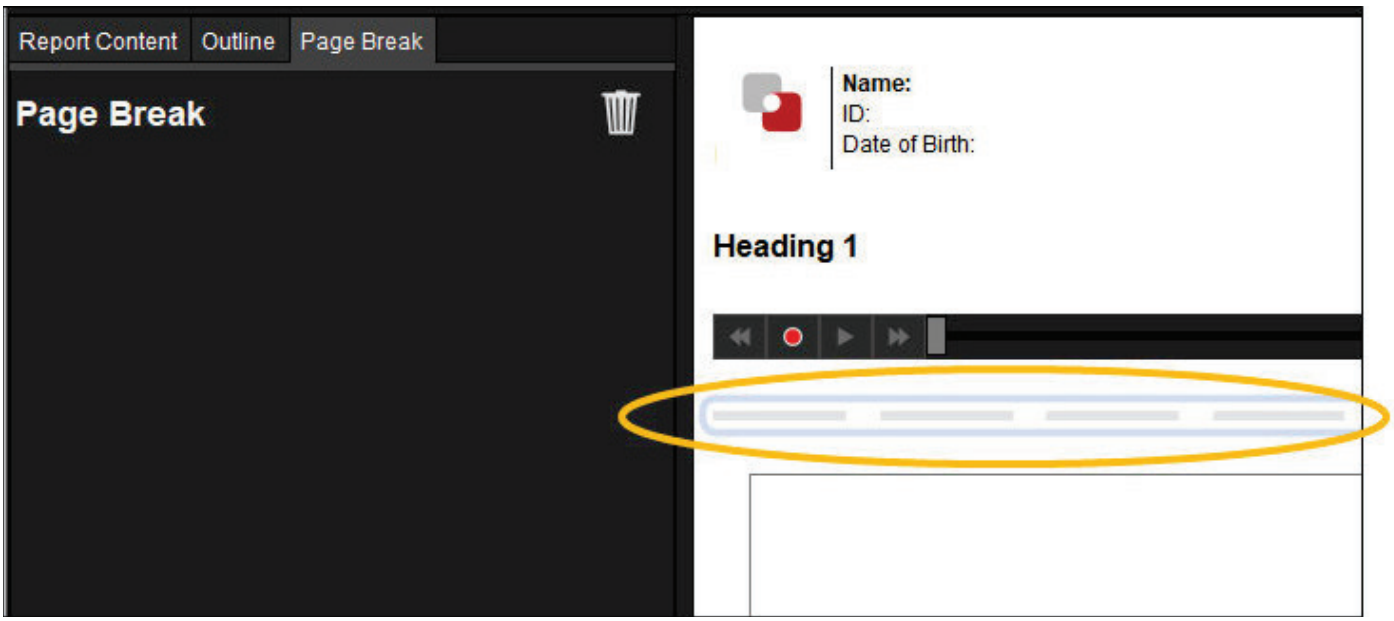


Important: If you delete a layout, all content within that layout is also deleted. You can see which items are within the layout on the **Outline** tab.

Insert Page Breaks

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

saved PDF version of the structured report.



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

Add Secondary Captures to Structured Reports

MIMTD-1437 • 13 Sep 2023

Overview

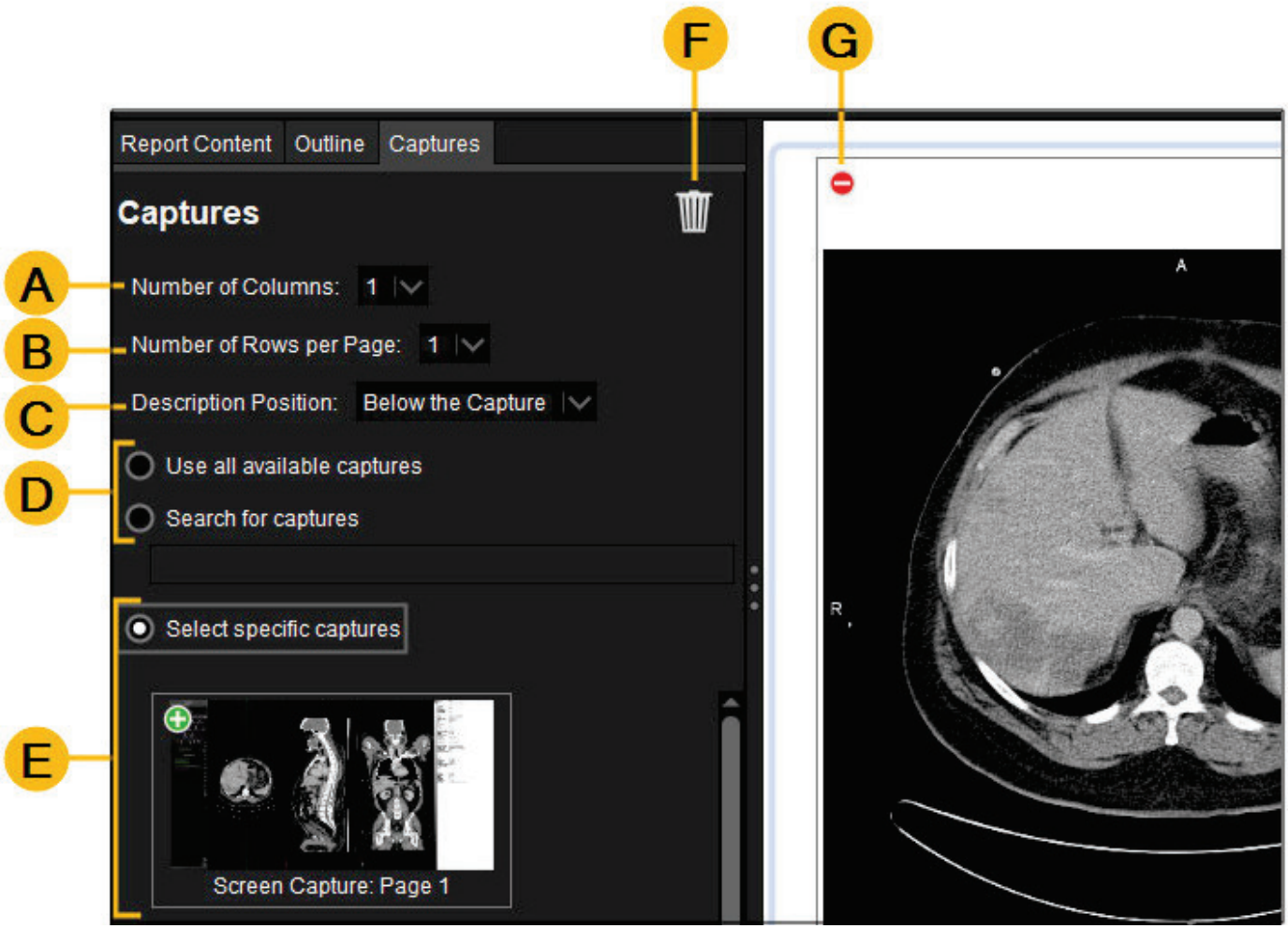
You can add screen captures to structured reports. Use the steps below if you are building a report template or if you want to add a Captures section to an existing report.

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

Add Capture Content

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

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



A. Choose the number of columns that captures appear in.
B. Choose the number of rows per page that captures appear in.
C. Choose whether the description appears above or below captures.
D. Add all available captures from your MIM session, or search for captures.
E. Select from a list of captures that are available in your MIM session. Click the add ⊕ button to add a capture.
F. Delete the captures from the structured report.
G. Click the remove ⊖ button to remove a specific capture from the structured report preview.

Add Statistics to Structured Reports

MIMTD-1438 • 13 Sep 2023

Overview

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

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

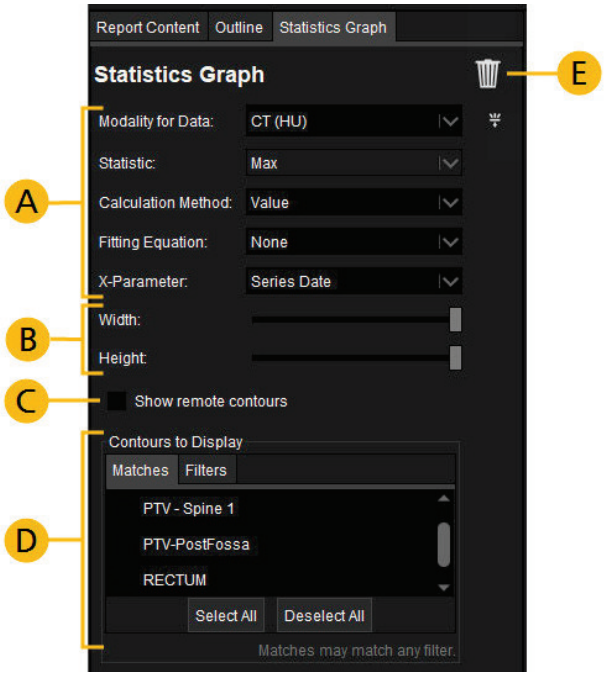
Related: For more information about designing structured report templates, see Create Structured Report Templates.

Contents

Add a Statistics Graph

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

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



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

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

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

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

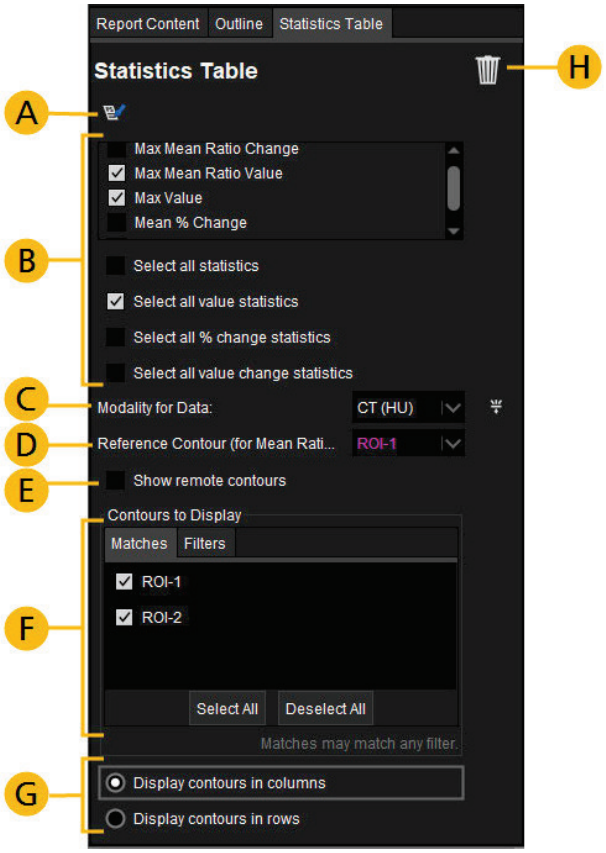
E. Delete the statistics graph from the structured report.

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

Add a Statistics Table

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

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



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

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

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

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

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

F. Choose which contours to display in the table.

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

H. Delete the table from the structured report.

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

Use Macros to Insert Frequently Used Text into Structured Reports

MIMTD-1440 • 21 Feb 2023

Overview

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

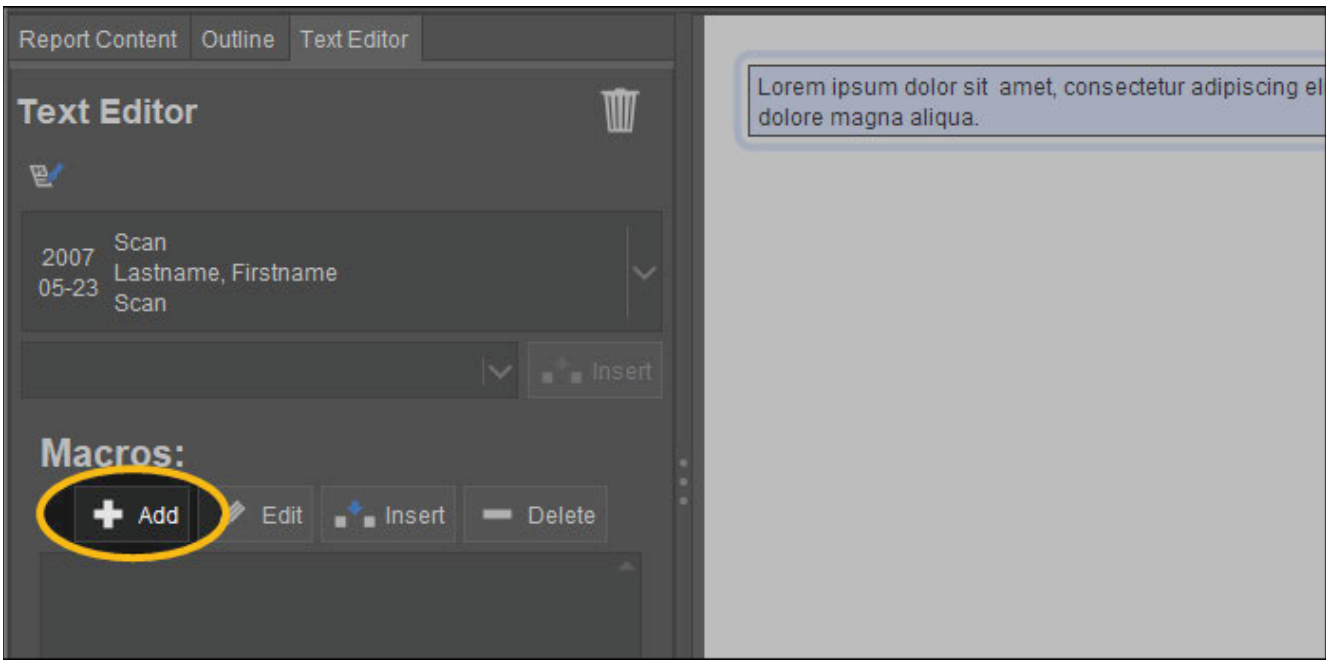
Related: For more information about using report templates to create reports, see Create and Modify Structured Reports.

Contents

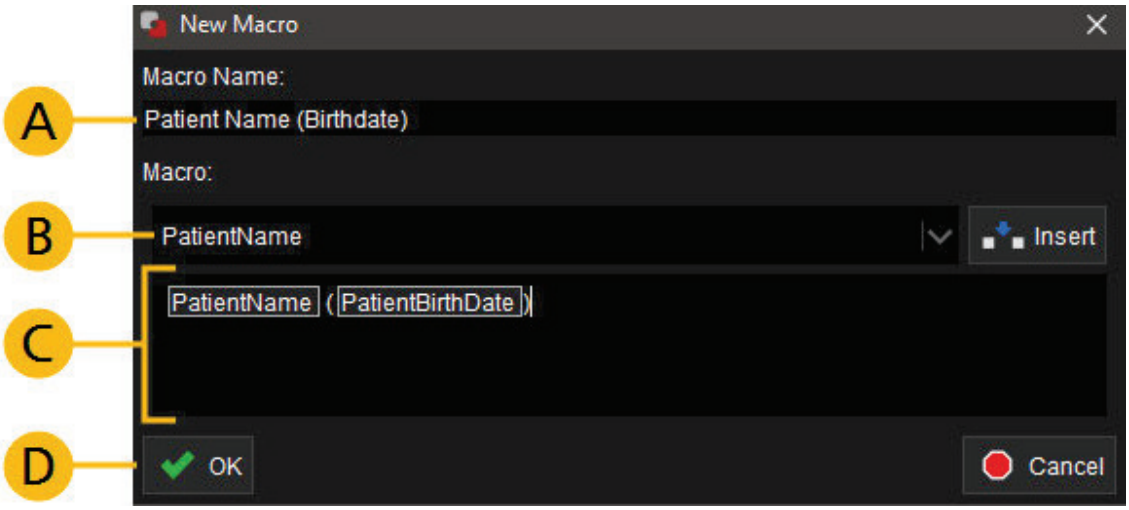
Create and Insert Macros

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

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



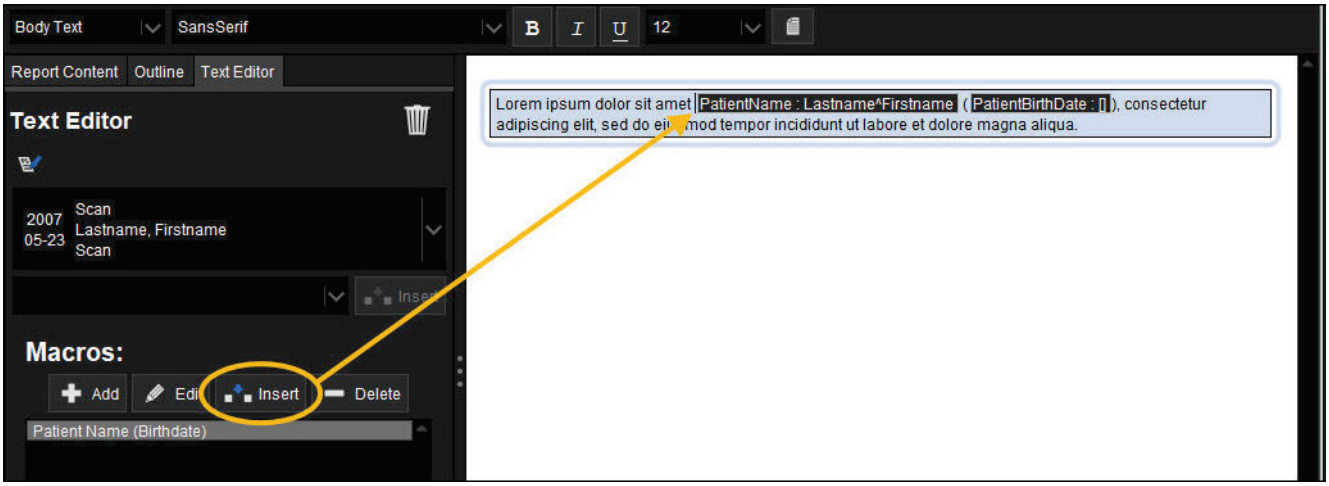
3. Create a new macro:



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

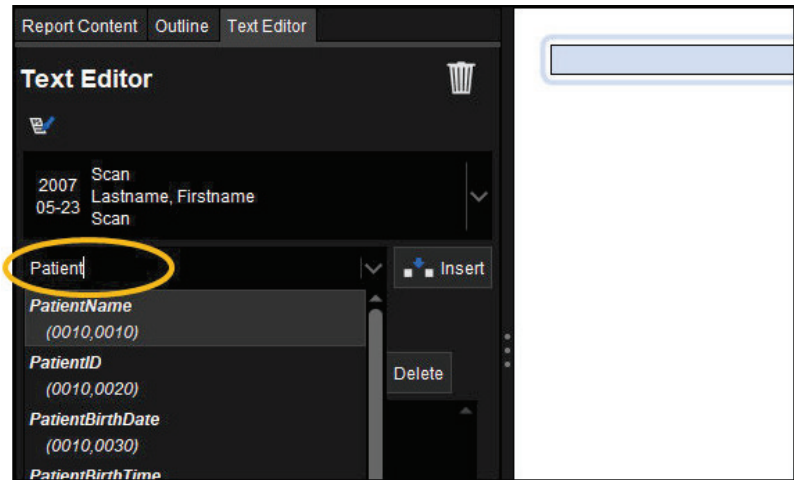
4. Place the cursor in the Text Editor field where you want the macro to appear.

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



Add Dynamic DICOM Information Directly into Text Editor Fields

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



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

4. Click the desired DICOM tag from the dropdown of search results that appears.

5. Click the **Insert** button on the right side of the search box to add the DICOM information to the Text Editor field.

Advanced Data Management

Manage Patient Data

MIMTD-626 • 07 Sep 2023

Overview

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

Contents

Data Management Options

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

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

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

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

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

- **Create New DICOM...** — There are multiple selections under this option.

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

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

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

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

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

  Important: Series deleted in MIM cannot be recovered.

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

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

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

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

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

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

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

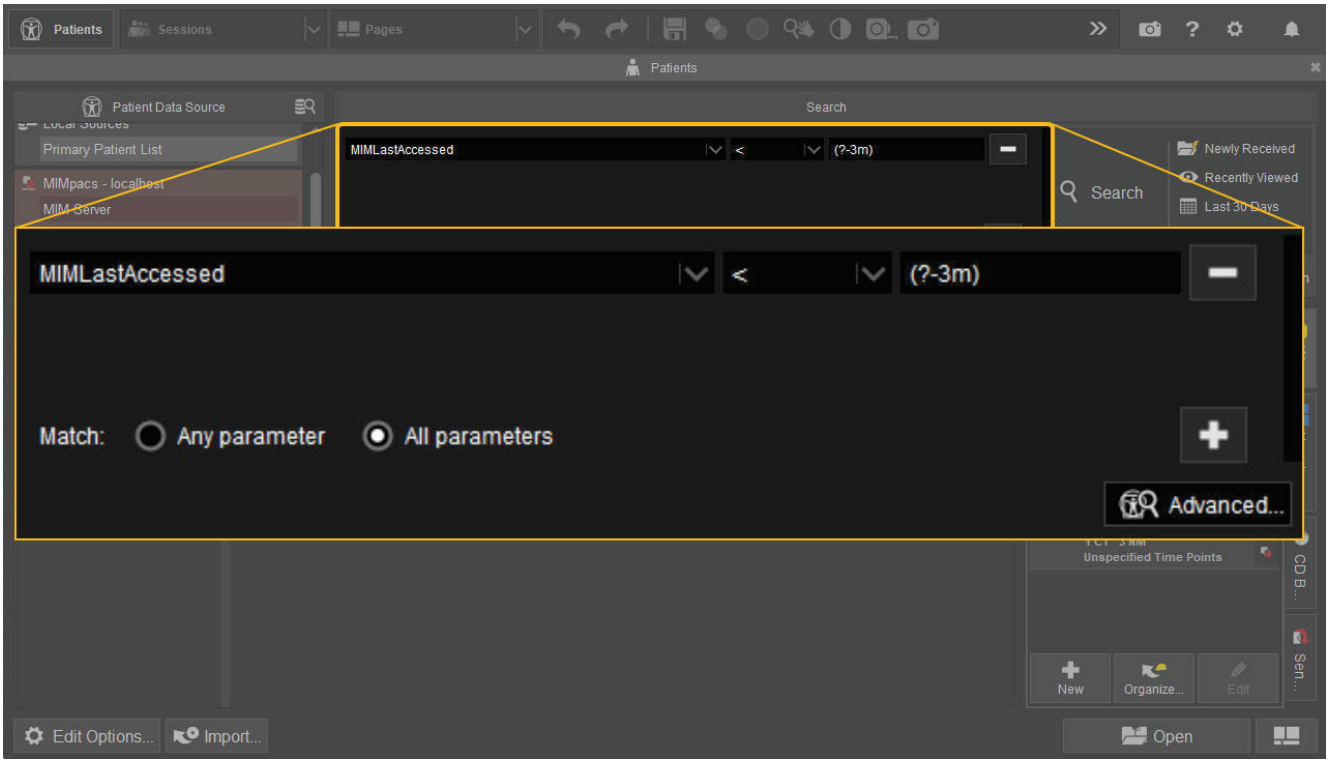
Delete Old Data to Manage Drive Space

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

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

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

1. Choose an appropriate patient list for your search. If you are on a client machine, this is most likely the Primary Patient List. If you are on the MIMpacs™ server, you may have many lists of locally stored data to choose from.
2. Click **Advanced...** in the MIM search area.
3. Enter search parameters as shown below, ensuring that the second dropdown contains the < symbol:



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

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

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

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

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

Set Owners on Series or Sessions

MIMTD-1107 • 24 Jul 2023

Overview

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

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

Contents

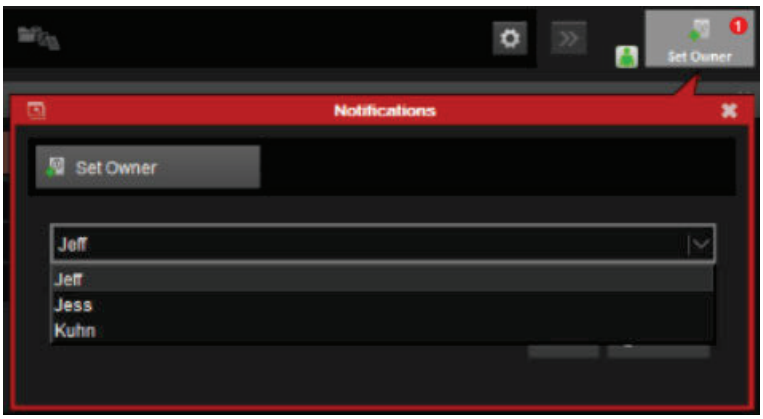
Prerequisites

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

Assign an Owner from the Patient List

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

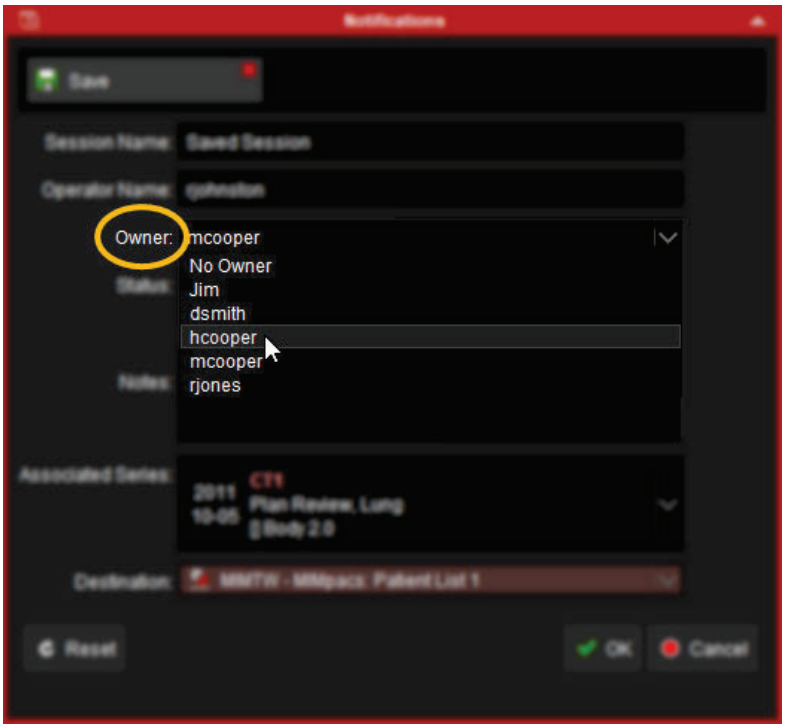
3. In the **Set Owner** field, select the person or group to own the series.



4. Click **OK**.

Assign an Owner when Saving a Session

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

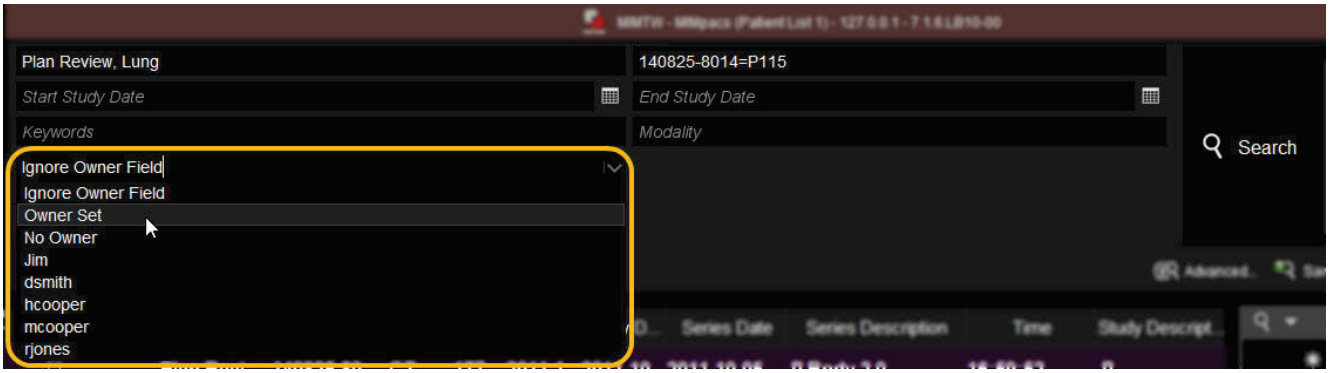


Search from the Patient List

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

Choose one of the following search options:

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



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

Anonymize Data

MIMTD-624 • 27 Jul 2023

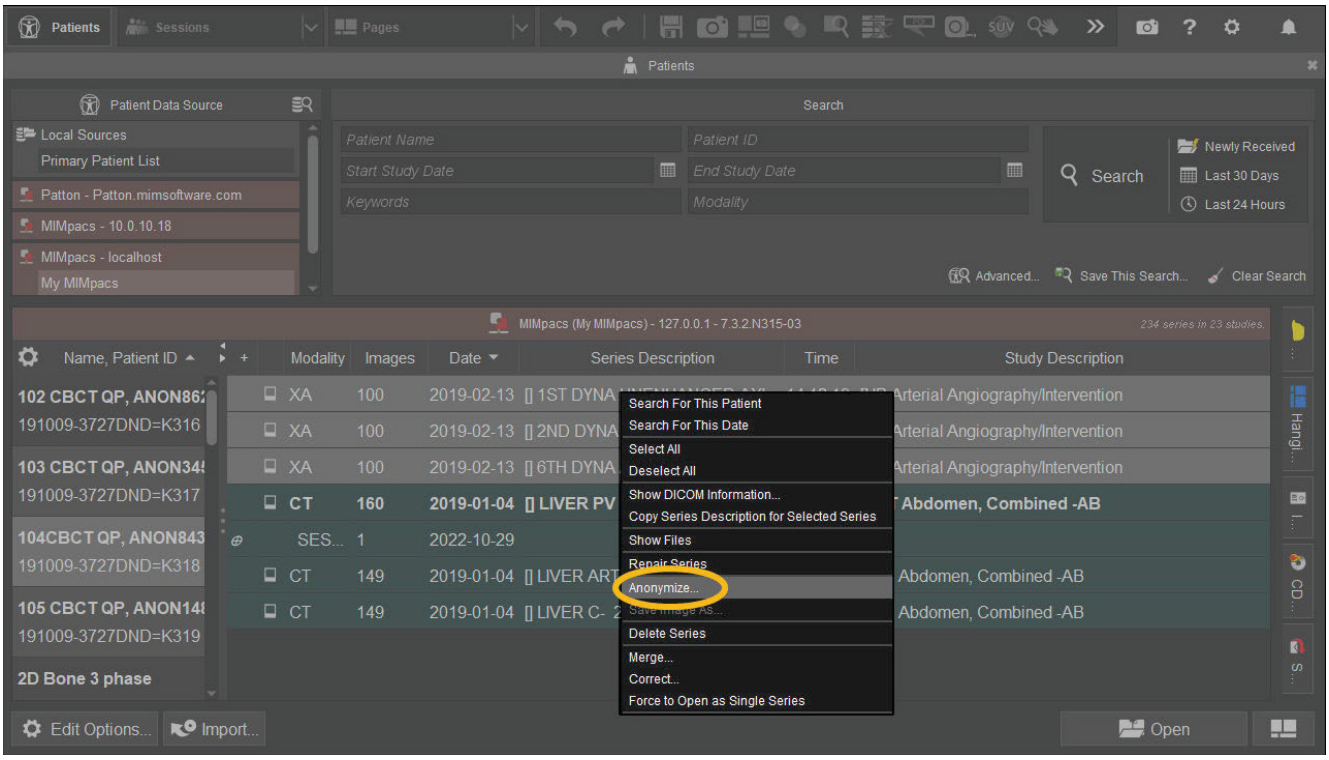
Overview

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

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

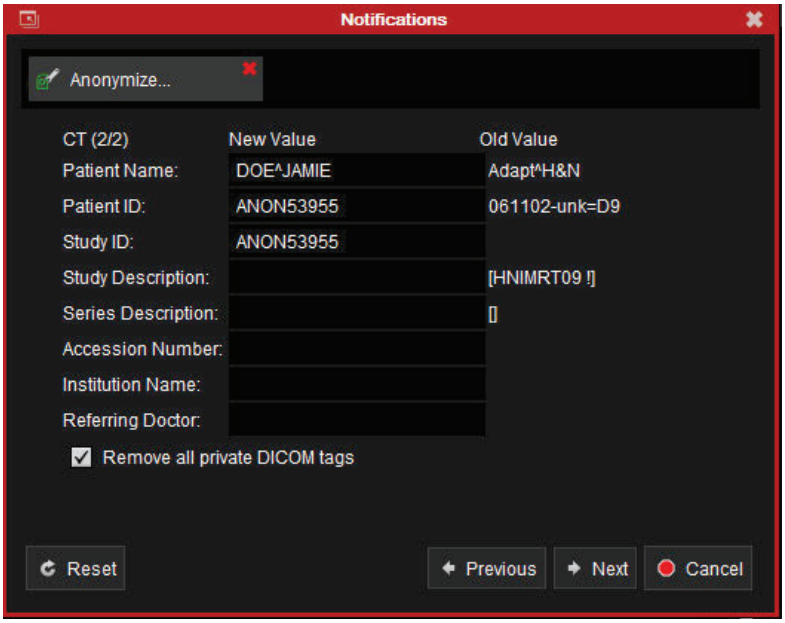
Anonymize Data

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



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

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



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

Correct Patient Data

MIMTD-625 • 07 Aug 2023

Overview

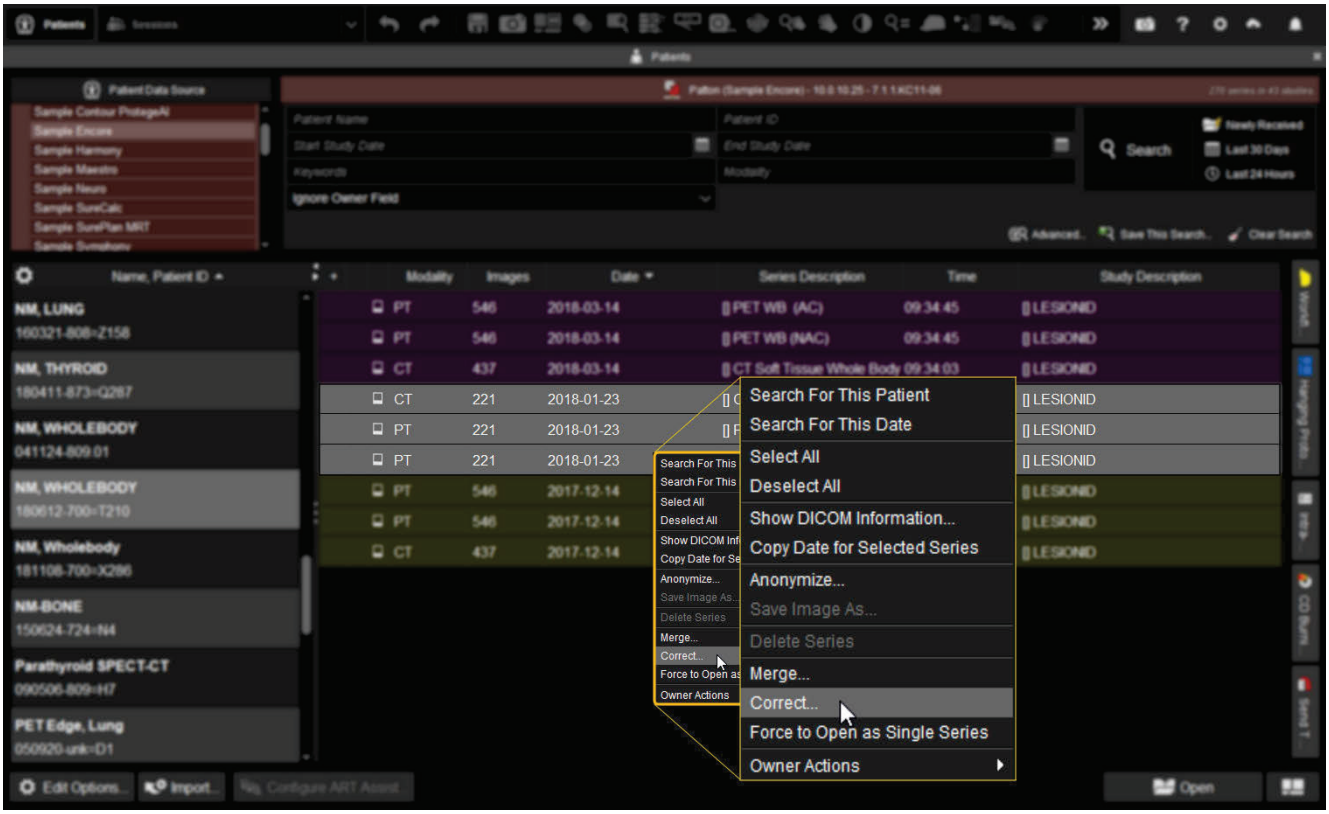
If the patient ID, patient name, or other data has been incorrectly or inconsistently entered, you can correct it in MIM®.

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

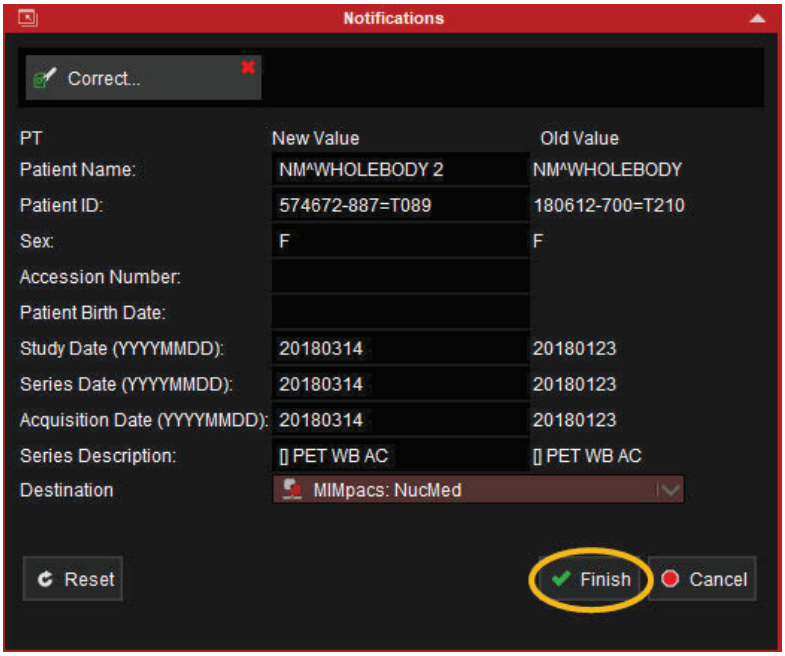
Important: If a patient is listed multiple times in MIM due to different names, spellings, patient IDs, or other issues, see Merge Patients instead to align the data for all images.

Correct Data

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



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



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

Merge Patients

MIMTD-628 • 07 Aug 2023

Overview

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

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

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

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

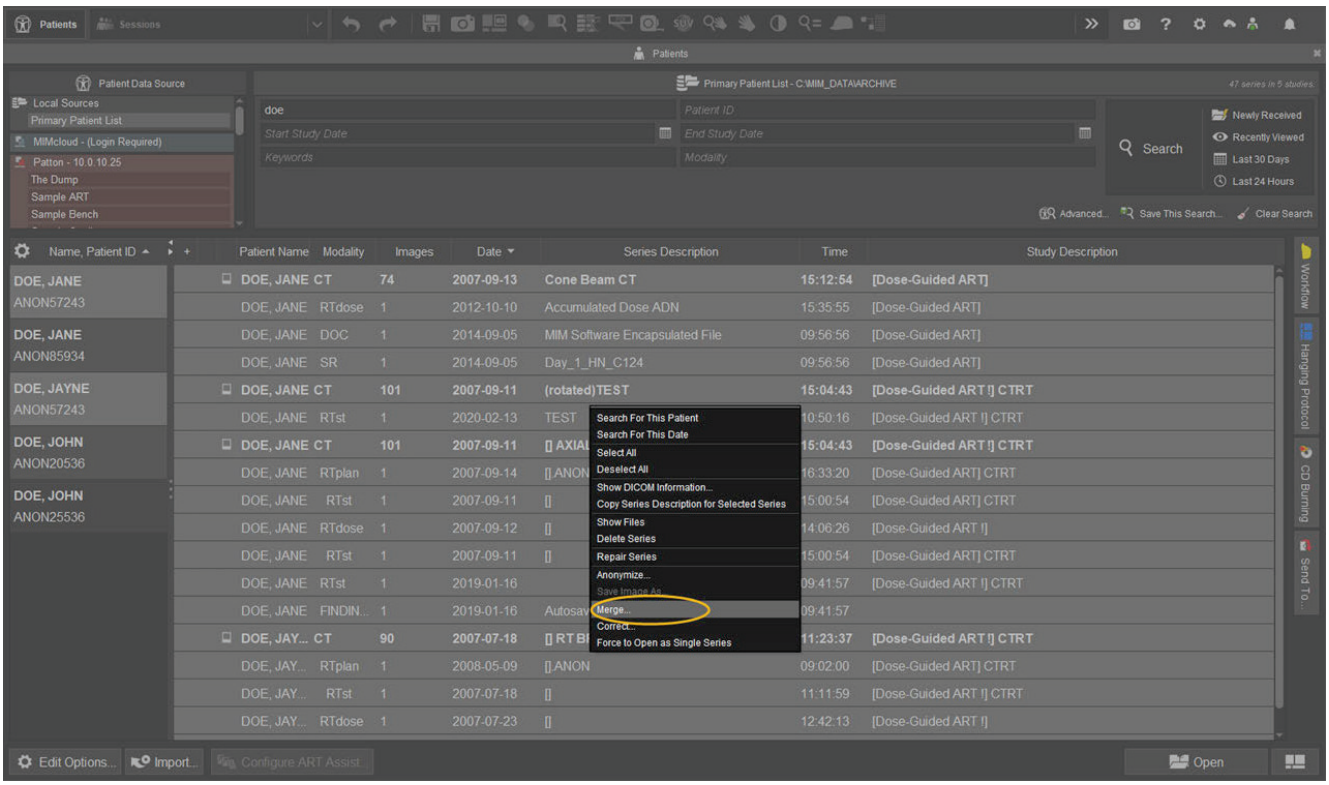
Combine Patient Records

To merge data:

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

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

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



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

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

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

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

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

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

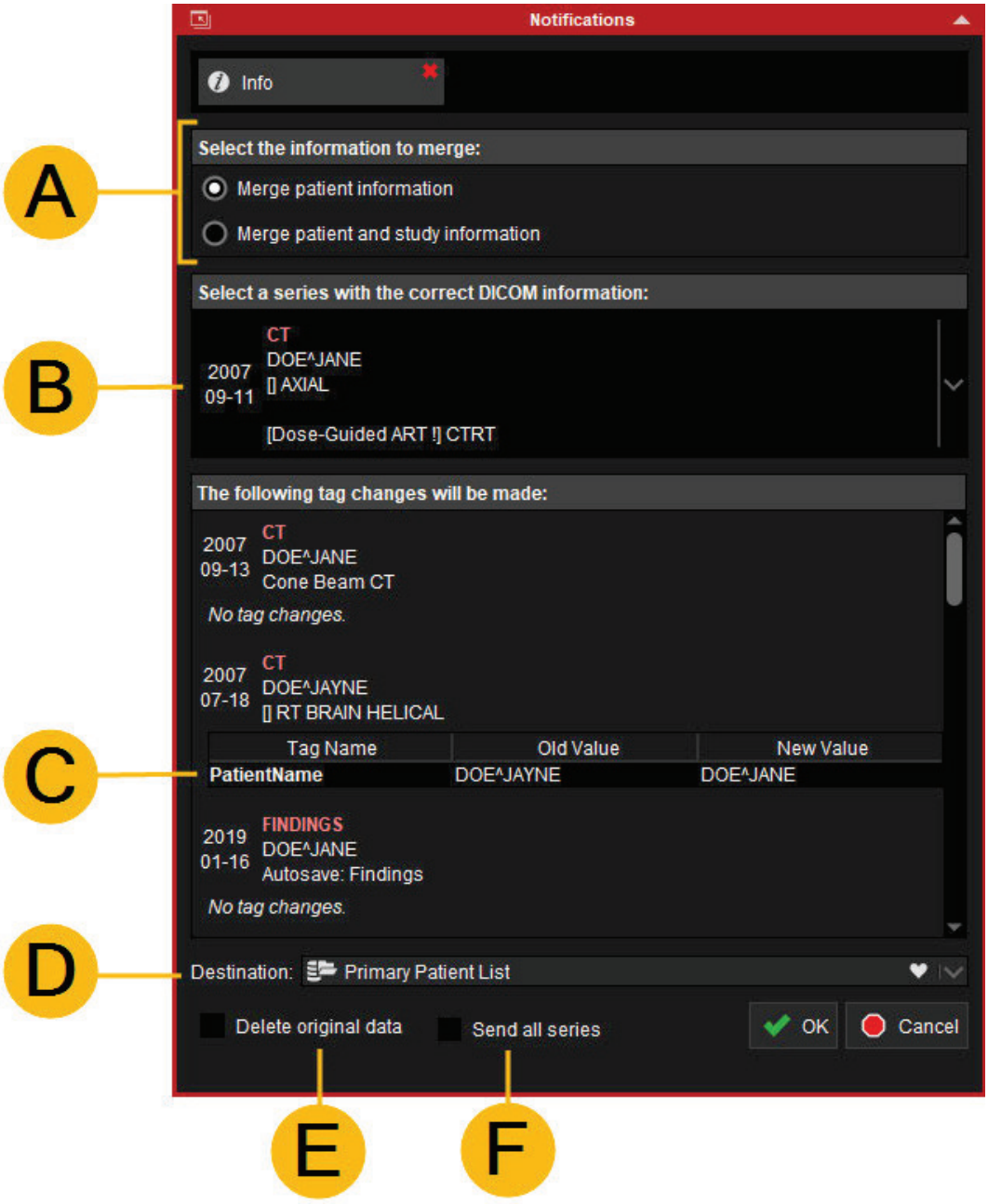
   C. **The following tag changes will be made** — Review the changes that will be made (you might need to scroll down). For each series that will be updated, review the **Tag Name**, **Old Value**, and **New Value**.

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

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

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

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



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

View and Edit DICOM Information

MIMTD-627 • 27 Jul 2023

Overview

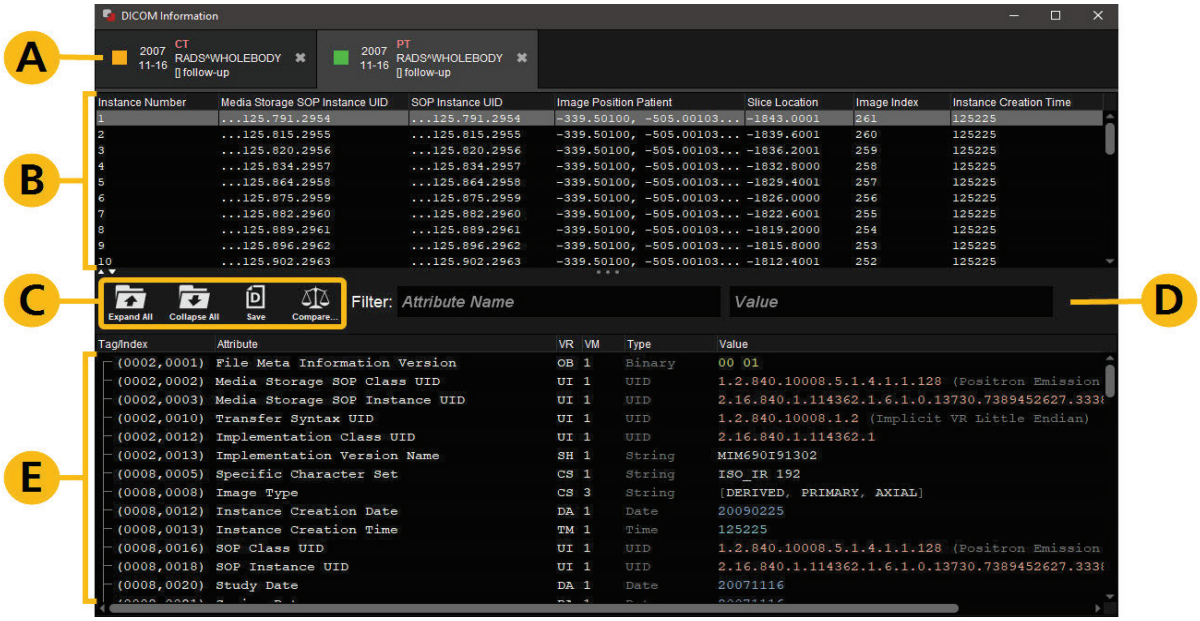
View and edit DICOM information for any series in MIM®. You can also compare DICOM files from the same series, or compare different series.

Contents

Open the DICOM Information Viewer

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

Navigate the DICOM Information Viewer



A. *Series Tabs*

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

B. *File List*

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

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

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

Tip: To expand just one sequence and view its children, go to section **E** and click the + button for the individual sequence.

MIM 7.4 and later: To fully expand an individual sequence and see all of its children, plus their children attributes, press the Ctrl or Cmd key and click the + button. This Ctrl/Cmd functionality is not available in MIM 7.3 and earlier.

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

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

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

Compare DICOM

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

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

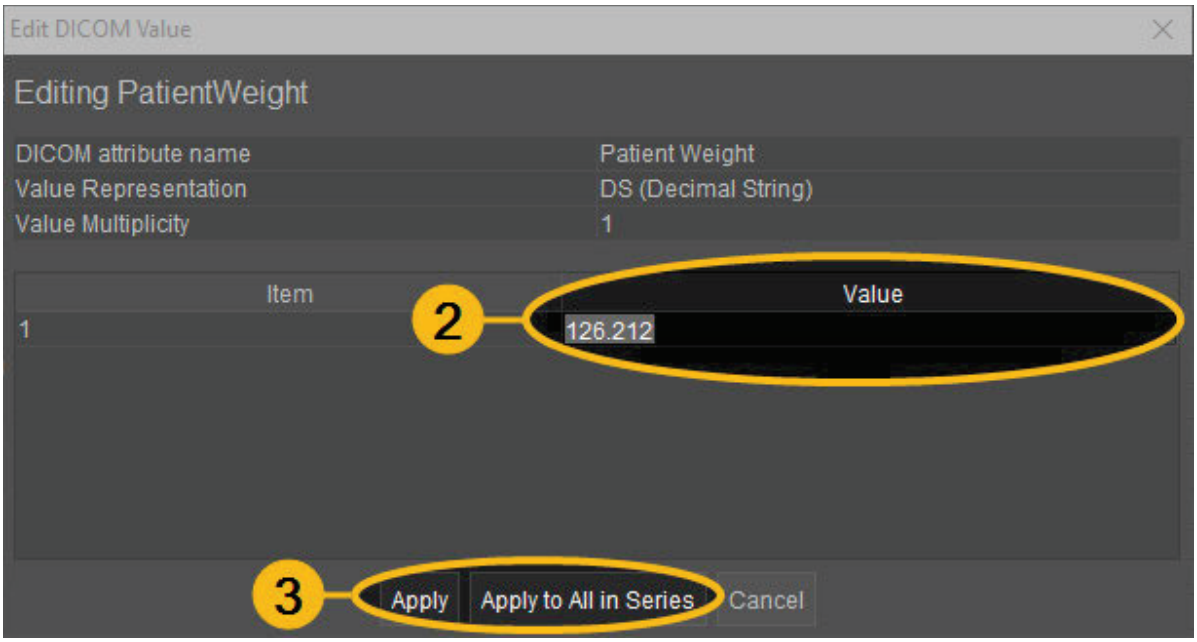
Edit DICOM

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

To edit DICOM values:

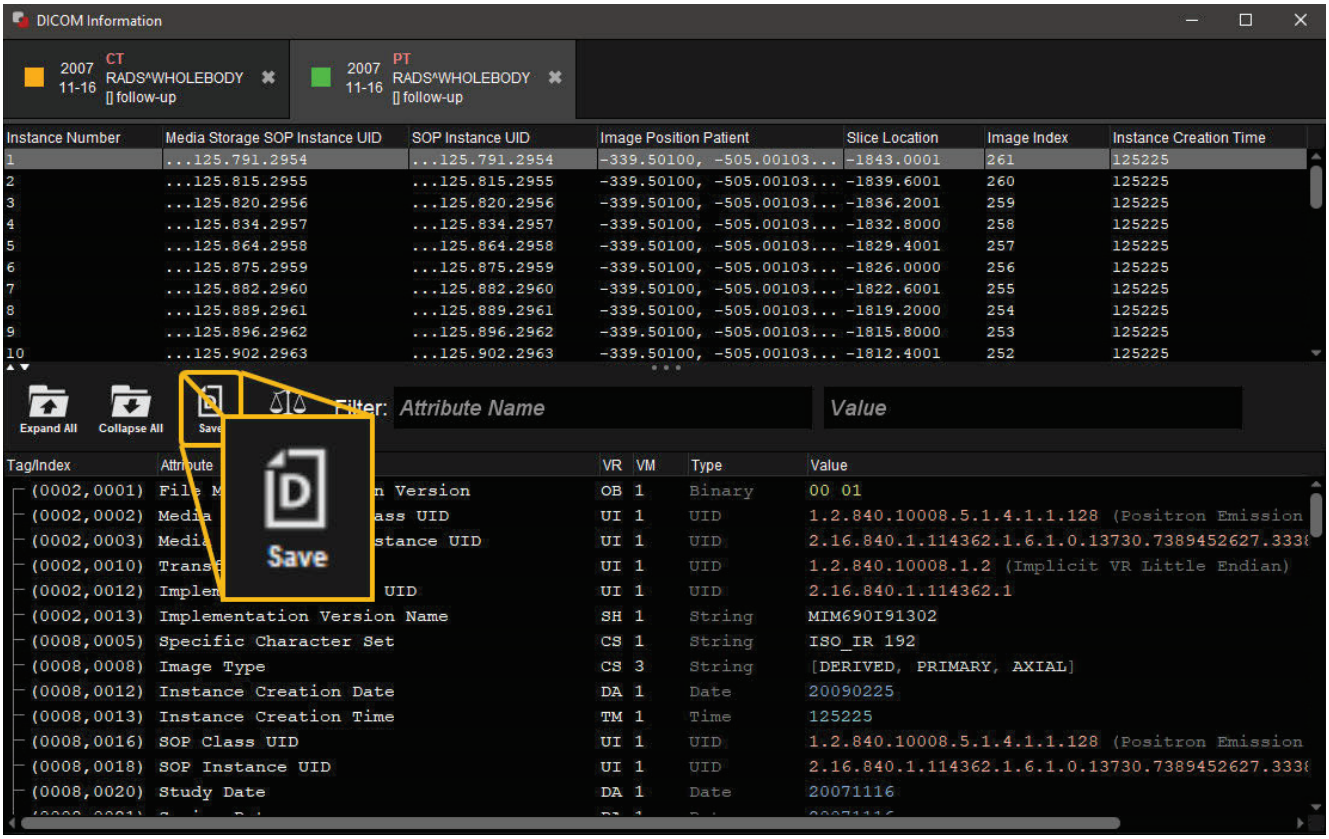
1. Double-click any value in the DICOM Information viewer. The Edit DICOM Value window opens.
2. Change the value.

3. Select **Apply** to change the value for the individual file (i.e., slice) or **Apply to All in Series** to change the value for all files of the series.



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

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


DICOM Information
2007 11-16 CT RADS^WHOLEBODY [] follow-up
2007 11-16 PT RADS^WHOLEBODY [] follow-up
Instance Number | Media Storage SOP Instance UID | SOP Instance UID | Image Position Patient | Slice Location | Image Index | Instance Creation Time
1 ...125.791.2954 ...125.791.2954 -339.50100, -505.00103... -1843.0001 261 125225
2 ...125.815.2955 ...125.815.2955 -339.50100, -505.00103... -1839.6001 260 125225
3 ...125.820.2956 ...125.820.2956 -339.50100, -505.00103... -1836.2001 259 125225
4 ...125.834.2957 ...125.834.2957 -339.50100, -505.00103... -1832.8000 258 125225
5 ...125.864.2958 ...125.864.2958 -339.50100, -505.00103... -1829.4001 257 125225
6 ...125.875.2959 ...125.875.2959 -339.50100, -505.00103... -1826.0000 256 125225
7 ...125.882.2960 ...125.882.2960 -339.50100, -505.00103... -1822.6001 255 125225
8 ...125.889.2961 ...125.889.2961 -339.50100, -505.00103... -1819.2000 254 125225
9 ...125.896.2962 ...125.896.2962 -339.50100, -505.00103... -1815.8000 253 125225
10 ...125.902.2963 ...125.902.2963 -339.50100, -505.00103... -1812.4001 252 125225
Expand All
Collapse All
Save
Filter: Attribute Name
Value
Tag/Index | Attribute | VR | VM | Type | Value
(0002,0001) File M n Version OB 1 Binary 00 01
(0002,0002) Media ass UID UI 1 UID 1.2.840.10008.5.1.4.1.1.128 (Positron Emission
(0002,0003) Medi stance UID UI 1 UID 2.16.840.1.114362.1.6.1.0.13730.7389452627.333
(0002,0010) Trans UI 1 UID 1.2.840.10008.1.2 (Implicit VR Little Endian)
(0002,0012) Implem UID UI 1 UID 2.16.840.1.114362.1
(0002,0013) Implementation Version Name SH 1 String MIM690I91302
(0008,0005) Specific Character Set CS 1 String ISO_IR 192
(0008,0008) Image Type CS 3 String [DERIVED, PRIMARY, AXIAL]
(0008,0012) Instance Creation Date DA 1 Date 20090225
(0008,0013) Instance Creation Time TM 1 Time 125225
(0008,0016) SOP Class UID UI 1 UID 1.2.840.10008.5.1.4.1.1.128 (Positron Emission
(0008,0018) SOP Instance UID UI 1 UID 2.16.840.1.114362.1.6.1.0.13730.7389452627.333
(0008,0020) Study Date DA 1 Date 20071116
Save

MIMneuro®

Process a Neuro Study

MIMTD-823 • 06 Dec 2023

Overview

Users typically use a MIMneuro® workflow to process neuro cases. The workflow automates most of the processing and prompts you when action is needed.

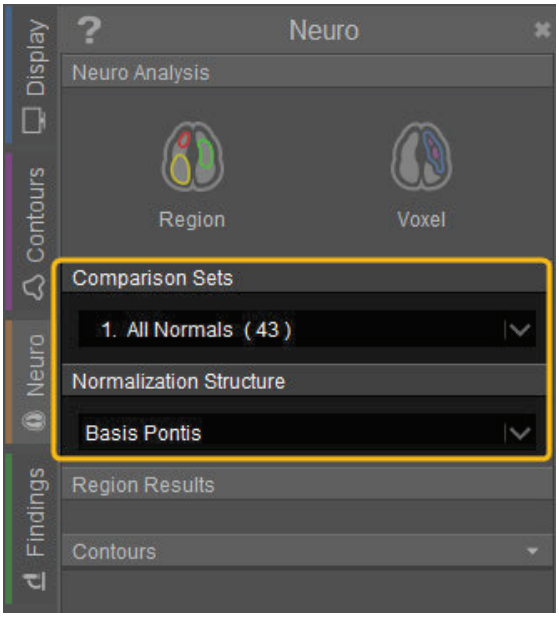
After a workflow runs, or if you open a neuro study without using a workflow, use the Neuro sidebar for processing and analysis.

Related: Refer to MIMneuro Workflows for more information about available workflows.

Contents

Determine Normals for Processing

A case is processed based on the comparison set and normalization structure. If you run a workflow and the results do not appear as expected, you may want to update these settings.



- The **Comparison Set** determines which normals to use as a baseline for the study. For example, you might want to use Age Matched Normals so that only normals from patients with a similar age are included. Refer to Compare Studies with Matched Normals for more information or if you want to edit a comparison set.
- The **Normalization Structure** determines which MIMneuro atlas region is used to register the series in the template space. For example, choose the region of interest from the single brain atlas as the normalization structure to improve registration in that area for a FDG PET.

Important: Tracer-specific atlas regions were validated for their corresponding neuro template. The spatial accuracy of regional contours may not be reliable when using a specific radiotracer atlas on an image not acquired using that radiotracer.

Run Neuro Analysis

You can run or rerun neuro analysis to use the comparison set and normalization structure that you selected.

Neuro analysis compares the patient scan to the comparison set of normal controls. Z-scores are calculated based on the number of standard deviations from the mean of the normals.

You have two options for neuro analysis:

6.1.9

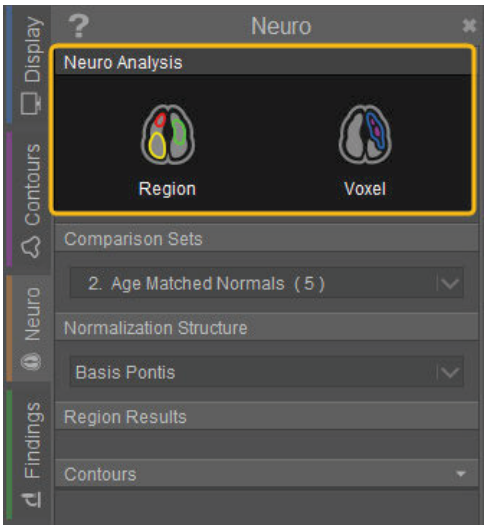
Analysis Options	Output	How It Works
Region-Based Analysis	• Structures drawn based on the atlas • Z-Score tables in the Z-Score Analysis window	Atlases are applied to contour regions. Z-scores and asymmetry measurements are calculated for the regions compared to the normals. These calculations are displayed in the Z-Score Analysis window.

6.1.9

Analysis Options	Output	How It Works
Voxel-Based Analysis *Not available for DaTscans*	• Stereostatic surface projections (SSPs) • Optional z-score cluster analysis	Z-scores are calculated on a voxel-by-voxel basis. Intensity data from the patient brain scan is compared to the normals. These calculations are then projected to the brain surface to create a visual display (SSP).

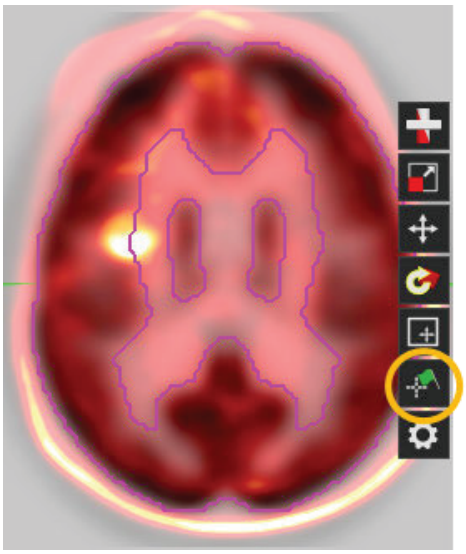
To run neuro analysis, follow these steps:

1. With a brain series open in MIMneuro, click the **Region** button or the **Voxel** button at the top of the **Neuro** sidebar.



2. If the tracer is not found in the series DICOM, you are prompted to manually select the tracer used for the series. Select the tracer in the Notifications window and click **OK**.
3. Inspect the registration to the atlas template and make adjustments as needed using the tools described in Adjust Affine Registrations.

4. Click the green flag button to continue.



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

6.1.8

- 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.

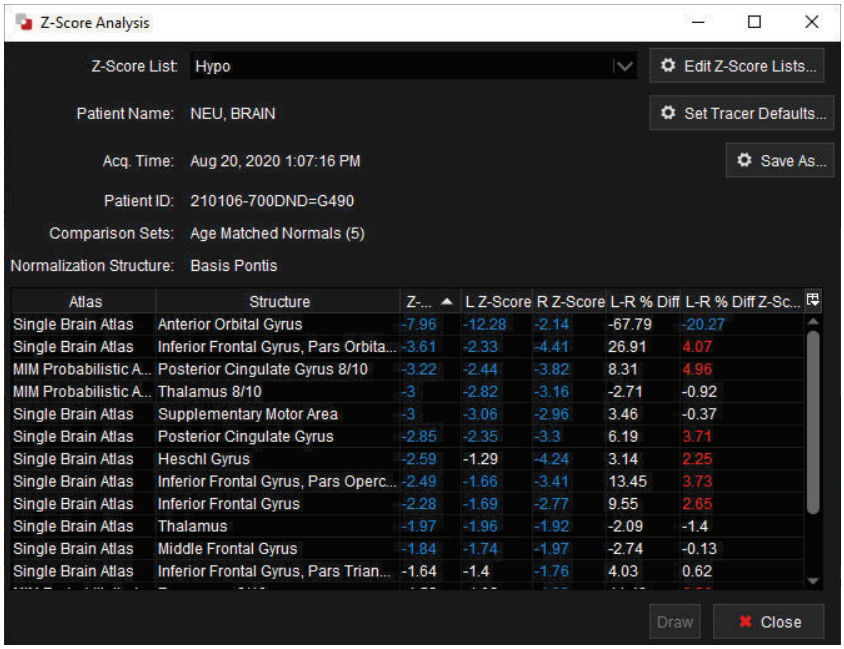
6. Verify that the analysis completes.

Review the Neuro Analysis Results 6.1.8

The page display may vary based on the study and whether you were using a workflow. Depending on whether you used region-based or voxel-based analysis, the following results are generated.

Results for Region-based Analysis

- Contours are drawn based on atlases. The structures are shown on the series and also appear listed in the Neuro sidebar. Refer to Review Region-Based Analysis for more information.
- Z-scores are calculated and displayed in the Z-Score Analysis window. You can see the results listed in the Region Results section of the Neuro sidebar. Click **View** if you need to reopen the Z-Score Analysis window. Refer to Review Results in the Z-Score Analysis Window for more information.



Atlas	Structure	Z-...	L Z-Score	R Z-Score	L-R % Diff	L-R % Diff Z-Sc...
Single Brain Atlas	Anterior Orbital Gyrus	-7.96	-12.28	-2.14	-67.79	-20.27
Single Brain Atlas	Inferior Frontal Gyrus, Pars Orbita...	-3.61	-2.33	-4.41	26.91	4.07
MIM Probabilistic A...	Posterior Cingulate Gyrus 8/10	-3.22	-2.44	-3.82	8.31	4.96
MIM Probabilistic A...	Thalamus 8/10	-3	-2.82	-3.16	-2.71	-0.92
Single Brain Atlas	Supplementary Motor Area	-3	-3.06	-2.96	3.46	-0.37
Single Brain Atlas	Posterior Cingulate Gyrus	-2.85	-2.35	-3.3	6.19	3.71
Single Brain Atlas	Heschl Gyrus	-2.59	-1.29	-4.24	3.14	2.25
Single Brain Atlas	Inferior Frontal Gyrus, Pars Operc...	-2.49	-1.66	-3.41	13.45	3.73
Single Brain Atlas	Inferior Frontal Gyrus	-2.28	-1.69	-2.77	9.55	2.65
Single Brain Atlas	Thalamus	-1.97	-1.96	-1.92	-2.09	-1.4
Single Brain Atlas	Middle Frontal Gyrus	-1.84	-1.74	-1.97	-2.74	-0.13
Single Brain Atlas	Inferior Frontal Gyrus, Pars Trian...	-1.64	-1.4	-1.76	4.03	0.62

The z-score displays for each structure. It includes the total z-score as well as the separate left and right z-scores, as applicable.

Results for Voxel-based Analysis

A new row of images appears that shows z-scores fused to the brain series for easy visualization. Z-scores are represented by a default color table that is dependent on the type of tracer used for the study. For more information, refer to View Color Scales and Stereotactic Surface Projections.

Tip: For a subtraction case, you might also want to view the cluster analysis results produced by voxel-based analysis. Click the eye by the Clusters Analysis section of the sidebar to view these results. Refer to MIM Workflows™: Neuro PET/SPECT — Subtraction for more information.

Review Region-Based Analysis

MIMTD-1773 • 07 Dec 2023

Overview

Region-based analysis applies atlas contours to the patient brain and runs an analysis with these regions. This processing often occurs during a MIMneuro® workflow, or you can run or rerun region-based analysis manually.

The MIMneuro atlases used for contouring and normalization are developed by MIM Software® and verified by expert physicians in the field.

Related: Refer to Process a Neuro Study for more information about region-based analysis.

Related: Refer to MIMneuro Atlases: Technical Details for more information about MIM's atlases that are used for processing.

Contents

Begin Region-Based Analysis

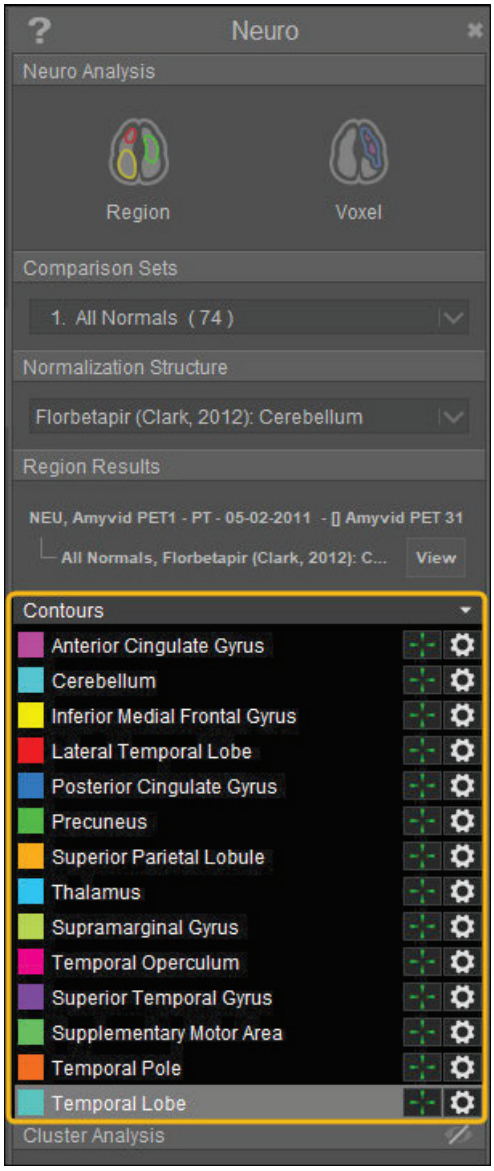
Follow the steps in Process a Neuro Study to launch region-based analysis:

1. In the Neuro sidebar, select the comparison sets and normalization structure in the Neuro sidebar.
2. Click **Region** .

3. Follow the prompts to register the series to the template space. If you needed, you can make adjustments using the tools described in Adjust Affine Registrations.

Review Contours in the Neuro Sidebar

MIMneuro detects the tracer in the study or prompts you to select a tracer. Based on the tracer, structures from the applicable atlas are drawn.



Structures that have been drawn are listed in the Contours section of the Neuro sidebar.

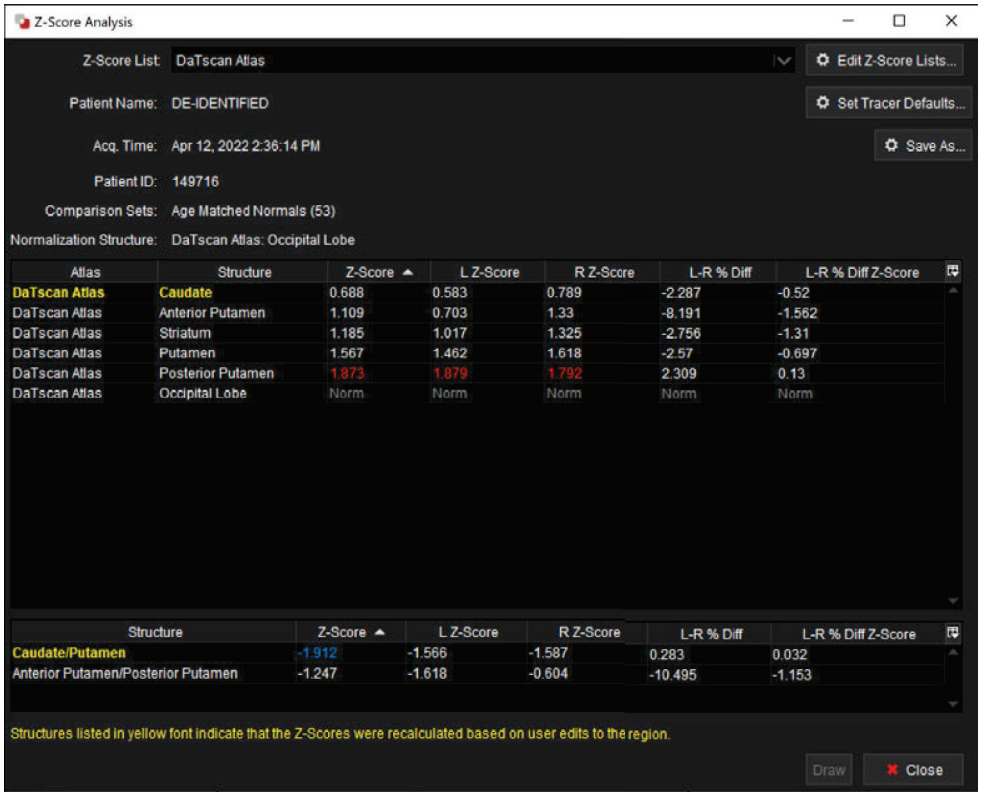
You can:

- Click the crosshairs to localize on the structure.
- Hover over a contour color box and scroll to change the contour color.
- Click the gear to see further options, including deleting, mirroring, or splitting the contour.

Modify a Structure

If needed, you can adjust a neuro atlas region.

1. Use the steps in the previous section to draw a structure.
2. Select a contouring tool, such as the **2D Brush** .
3. Edit the structure as needed.
4. Review the updated results:
    - *MIM 7.2 and later:* Check the Z-Score Analysis window. Region-based z-scores are automatically recalculated based on the edited region. The structure name appears as yellow text if the values have been recalculated.



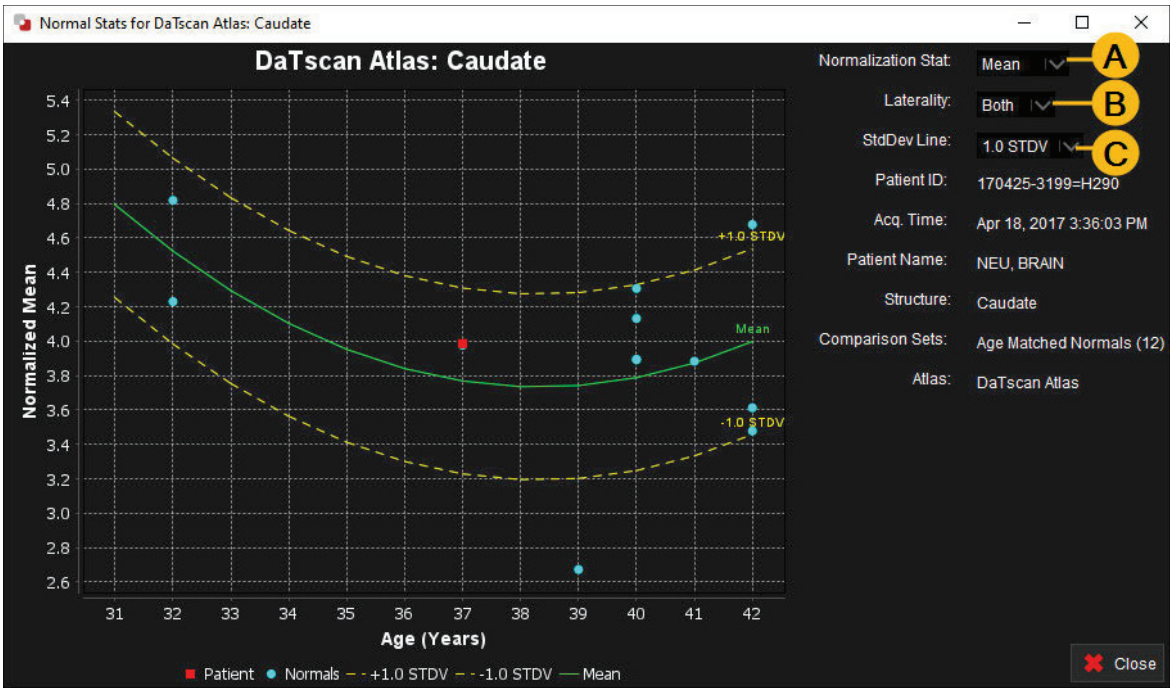
    - *MIM 7.1 and earlier*: Click **Region** to rerun region-based analysis. Updated results are calculated based on the edited region.

Tip: The image above shows z-score results for a DaTscan® series. The section at the bottom of the z-score window that shows Caudate/Putamen and Anterior Putamen/Posterior Putamen z-scores is specific to DaTscan cases. This section does not appear for scans that use other tracers.

View the Stats Graph for a Structure

You can view data for a structure on a graph along with the distribution of normal data.

1. In the Z-Score Analysis window, right-click on the desired structure.
2. Select **Stats Graph...**.
3. Review the results in the Stats Graph window:



   A. Use the **Normalization Stat** option to show either the normalized mean or median over a range of subject ages. By default, the mean is shown.

   B. Specify **Laterality**.

   C. *MIM 7.4 and later*: Use the **StdDev Line** option to choose which standard deviation lines appear on the graph.
   MIM 7.3 and earlier: Fitting lines appear based on 5%, 50%, and 95% of the normals data range.

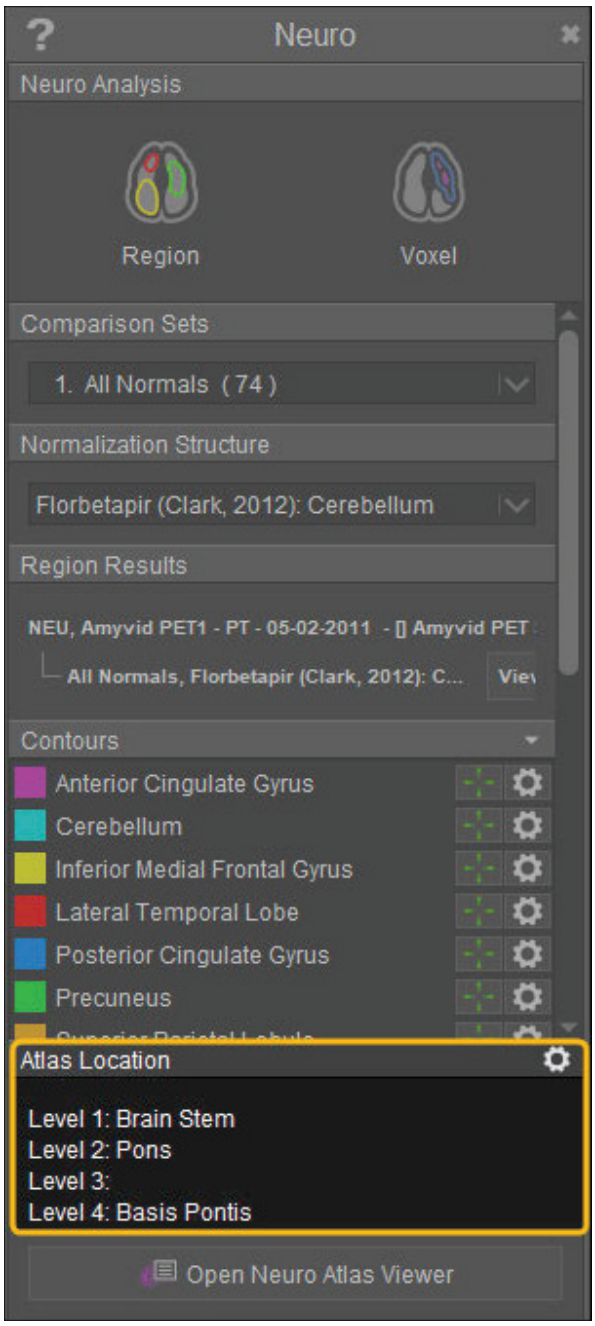
4. Click **Close** to exit the window.

View the Atlas Location

After region-based analysis runs, either manually or as part of a workflow, the Atlas Location section appears at the bottom of the Neuro sidebar. This section shows the region in the atlas that maps to your current localization point.

For example, to confirm your visual identification of the basis pontis, click on that point in the scan. Verify that the Atlas Location shows that point is mapped to the basis pontis in the atlas.

MIM 7.3 and later: You can choose which atlas the location is displayed from. Click the gear ⚙ in the Atlas Locations heading and choose an atlas. *MIM 7.2 and earlier*: Only regions from the Single Brain Atlas are displayed.



The Single Brain Atlas identifies the region in four levels of increasing specificity, as applicable:

- Level 1: Lobe-level structures
- Level 2: Sublobar structures
- Level 3: Gyral-level structures
- Level 4: Individual structures not included in the previous three levels (e.g., hippocampus and amygdala)

Tip: Optionally, the atlas location can appear when you hover over a region in the image. Go to Settings >> **General Preferences** >> **Imaging** >> **Neuro** and select **Display Atlas Location on Hover** to enable this feature.

Draw Additional Structures

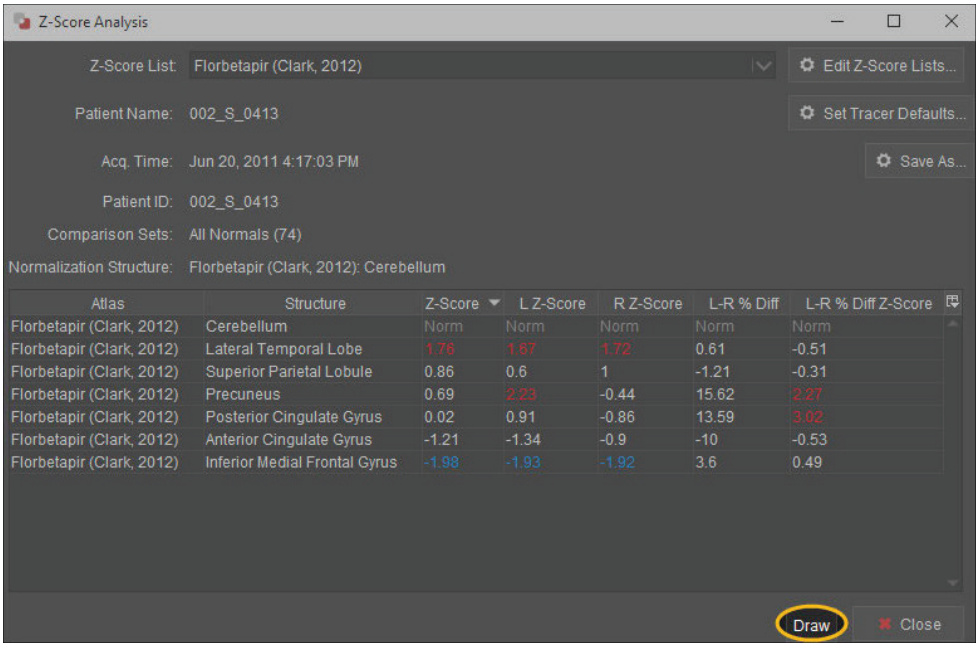
After structures are initially drawn, you can choose additional areas for the system to contour based on the selected atlas.

Draw from the Z-Score Analysis Window

1. Open the Z-Score Analysis window.
2. Select a structure.

> **Tip:** Select multiple structures at once by left-click dragging or by holding Shift or Ctrl while you select structures.

3. Click **Draw** in the lower-right corner.



The structure from the atlas is drawn on the series and appears in the Neuro sidebar.

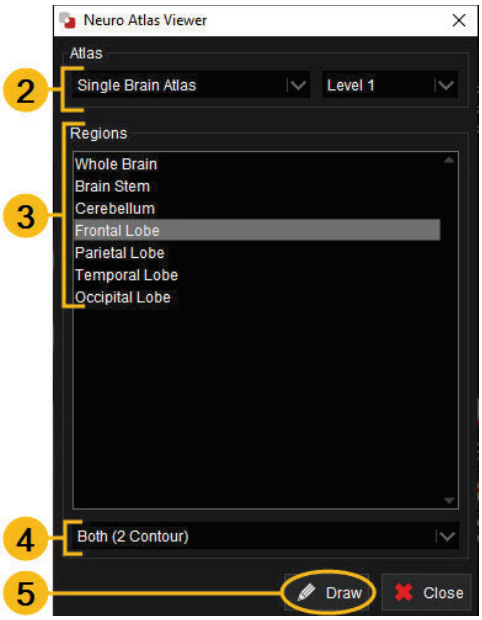
> **Related:** Refer to Review Results in the Z-Score Analysis Window for more information about the structures listed in Z-Score Analysis window.

Use the Neuro Atlas Viewer (MIM 7.2 and Later)

MIM 7.2 and later: You can add structures using the Neuro Atlas Viewer. *MIM 7.1 and earlier:* This functionality is not available.

To use the Neuro Atlas Viewer, follow these steps:

1. At the bottom of the Neuro sidebar, click **Open Neuro Atlas Viewer**.
2. In the Neuro Atlas Viewer window, select an **Atlas**:
   - If you select **Single Brain Atlas**, use the second dropdown to select a level, as described above.
   - If you select **MIM Probabilistic Atlas**, use the second dropdown to select a level of probability.
   - If you select **Custom Regions**, use the second dropdown to select the region set that you want to use.
3. Select a region (or use Ctrl+Click or Shift+Click to select multiple regions).
4. As applicable, use the dropdown at the bottom of the window to choose whether to draw contours on only the left or right sides, or on both sides.
5. Click **Draw** to draw the structure on the image.



The structure from the atlas is drawn on the series and appears in the Neuro sidebar.

Review Results in the Z-Score Analysis Window

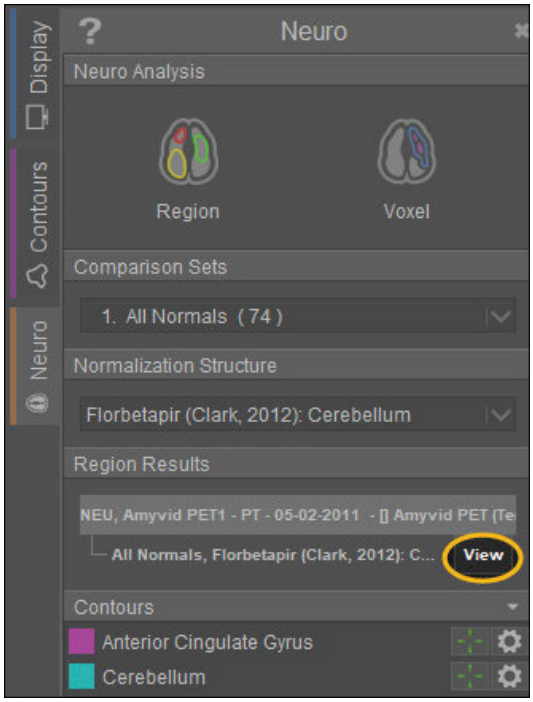
MIMTD-824 • 29 Nov 2023

Overview

Z-scores are available after running region-based analysis. This processing often occurs during a MIMneuro® workflow, or you can run or rerun region-based analysis manually.

Related: Refer to Review Region-Based Analysis for more information about region-based analysis.

The Z-Score Analysis window shows z-score statistics and asymmetry measurements. Z-scores are calculated based on the number of standard deviations from the mean of the normals.



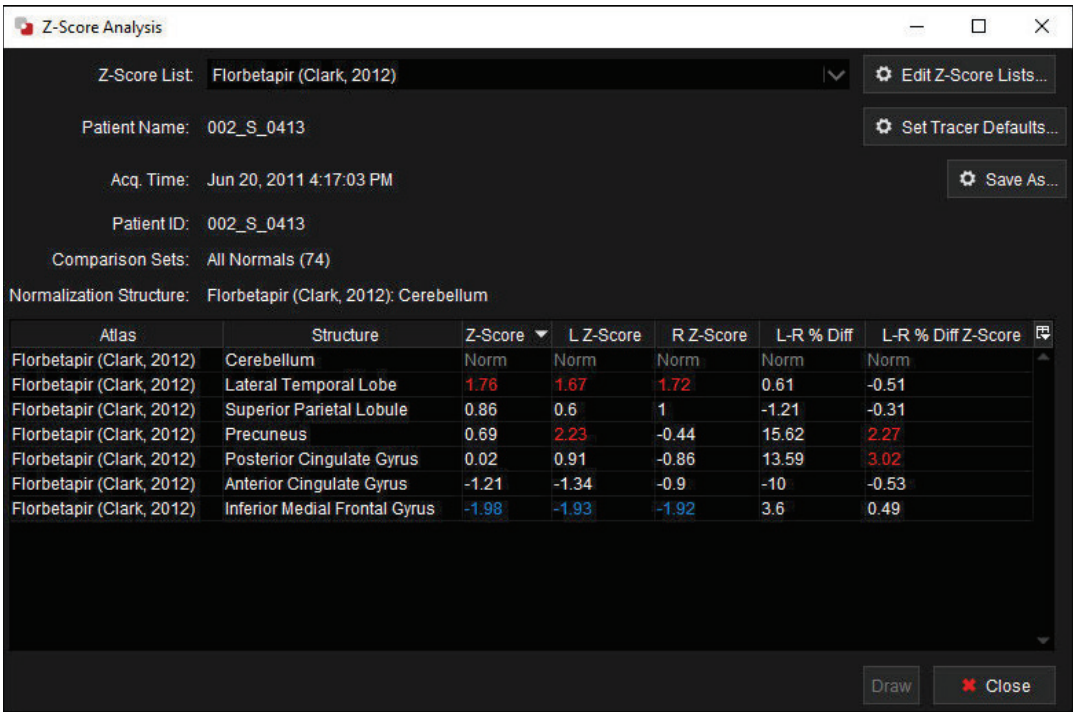
Depending on the workflow, the Z-Score Analysis window may open by default. You can also open or reopen it at any time by clicking the **View** button in the Region Results section of the Neuro sidebar. The name indicates both the comparison set and the normalization structure used for calculation.

If you change the comparison set or normalization structure and rerun region-based analysis, the updated z-score results are also listed in the Region Results section.

Contents

Review Results in the Z-Score Analysis Window

Region-based analysis draws structures (also called regions) from an atlas. The Z-Score Analysis window shows results calculated at the structure level.



For each structure, you can see the calculated z-score:

- Regions with increased uptake/perfusion (hyper) appear in red text. Hyper is defined as a z-score above 1.65.

6.1.9

- Regions with low uptake/perfusion (hypo) appear with blue text. Hypo is defined as a z-score below -1.65.

6.1.9

> **Tip:** You can select a structure in the Z-Score Analysis window and click **Draw** in the lower-right corner. The structure from the atlas is drawn on the series and appears in the Neuro sidebar. Refer to Review Region-Based Analysis for more information about working with structures.

Note that the window shows a filtered list of structures from an atlas that are determined by the Z-Score List. Refer to Edit Region Results Included for Z-Score Lists below for more information about configuring Z-Score List options. For example, you could create a list that excludes certain structures that you don't want to be included.

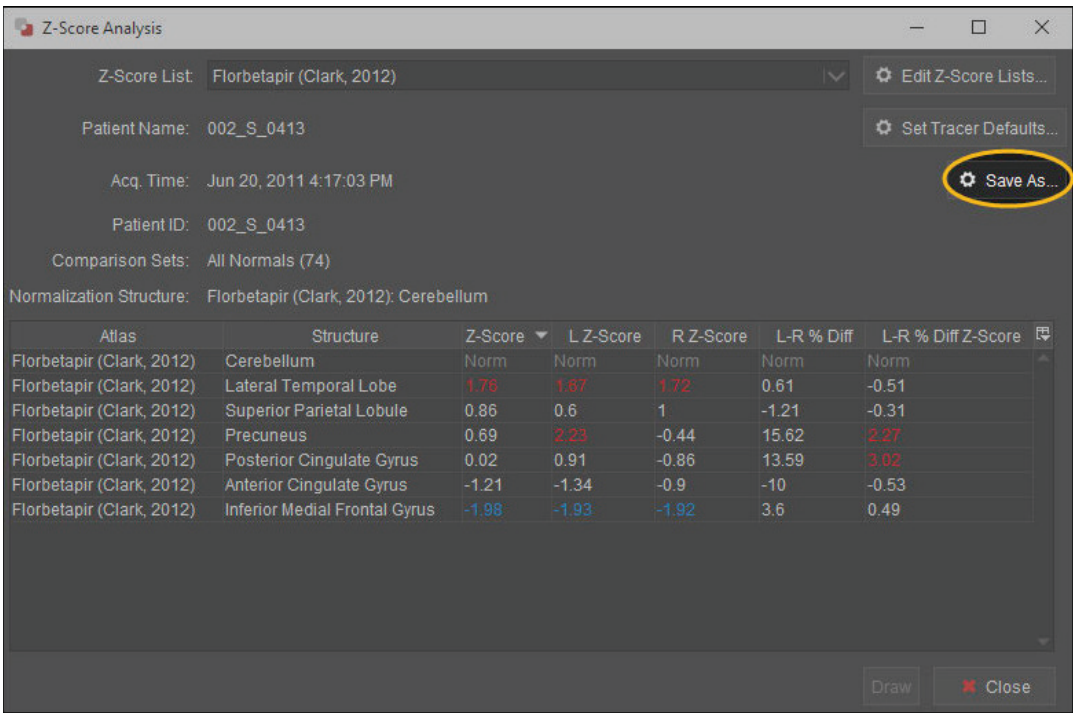
> **Tip:** Change the **Z-Score List** dropdown at the top of the Z-Score Analysis window to Hyper to see only hyper regions or to Hypo to see only hypo regions. Regions are displayed in the hyper or hypo z-score lists if the region is unilaterally hyper or hypo, even if the entire bilateral region is not hyper or hypo.

Save Z-Scores

You can save the results from the Z-Score Analysis window in a few ways. If desired, you can update the display before saving, as described in Tips for Adjusting Z-Score Display below.

Save a Secondary Capture or Spreadsheet

1. In the Z-Score Analysis window, click **Save As...**.



2. Choose how to save the results:
   - Select **Secondary Capture** to save a capture of the z-score results. View and save the capture from the Capture Gallery. For more information, refer to Create and Save Secondary Captures.
   - Select **Spreadsheet** to save the z-score results to your workstation as a CSV file.

Copy Lines

You can copy lines from the z-score table so that you can paste them into a different application.

1. In the Z-Score Analysis window, select one or more lines.

> **Tip:** Select multiple lines at once by left-click dragging or by holding Shift or Ctrl while you select lines.

2. Right-click and select **Copy to Clipboard**. Note that the column headers are not copied.
3. Paste the copied lines into your desired application.

Tips for Adjusting Z-Score Display

If desired, you can update the Z-Score Analysis window display before you take a screen capture or save the results.

You can:

- Add or remove columns by clicking the column button on the far right side of the z-score table and selecting which columns to add or remove.

> **Tip:** If you are working with a limited window size, select **Horizontal Scroll** to enable a horizontal scroll bar. Alternatively, select **Pack All Columns** to remove horizontal scrolling and pack all the columns to fit within the window's dimensions.

- Sort a column by clicking the column header.
- Adjust column width by left-click dragging on the side of the column.
- Hide a structure. Right-click on one or more structures and select **Hide Structure Temporarily**. The structures no longer appear in the window. To show the structures again, right-click anywhere in the Z-Score Analysis window list of regions and select **Show All Structures**.

Determine Z-Score Analysis Settings

The default settings generally accommodate most scenarios. If needed, you can update the following based on your organization's preferences or unique needs.

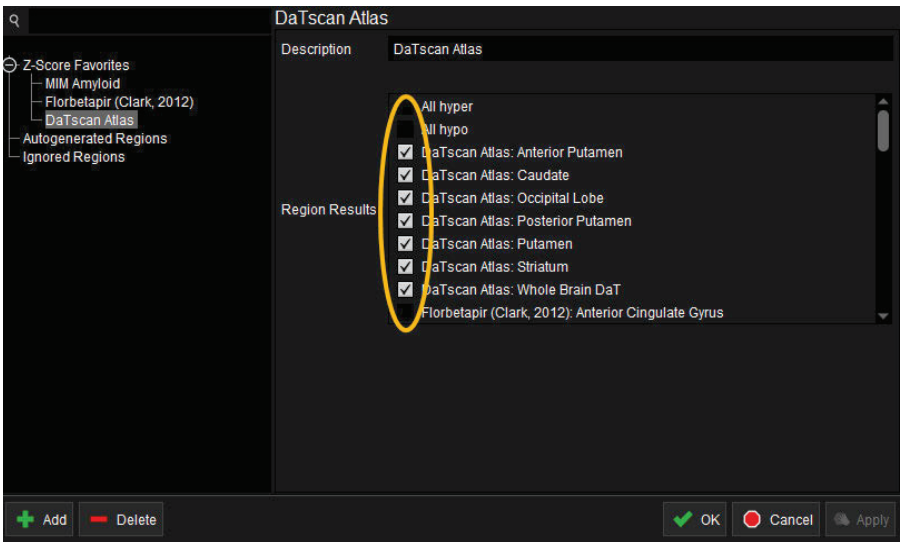
> **Tip:** By default, regions with z-scores above 1.65 are considered hyper and regions with z-scores below -1.65 are considered hypo. If needed, you can edit this threshold. Refer to Use MIMneuro® for Research for more information.

Edit Region Results Included for Z-Score Lists

The Z-Score List option is at the top of the Z-Score Analysis window. It defines which structures to show. For example, the DaTscan Atlas list includes DaTscan regions and should be used with DaTscan images. If necessary, you can edit which structures are included in a Z-Score List, such as removing a region that you don't want to be included.

1. In the Z-Score Analysis window, click **Edit Z-Score Lists...**.
2. In the new window, select the Z-Score List that you want to edit.

3. Select or deselect regions in the list of Region Results.



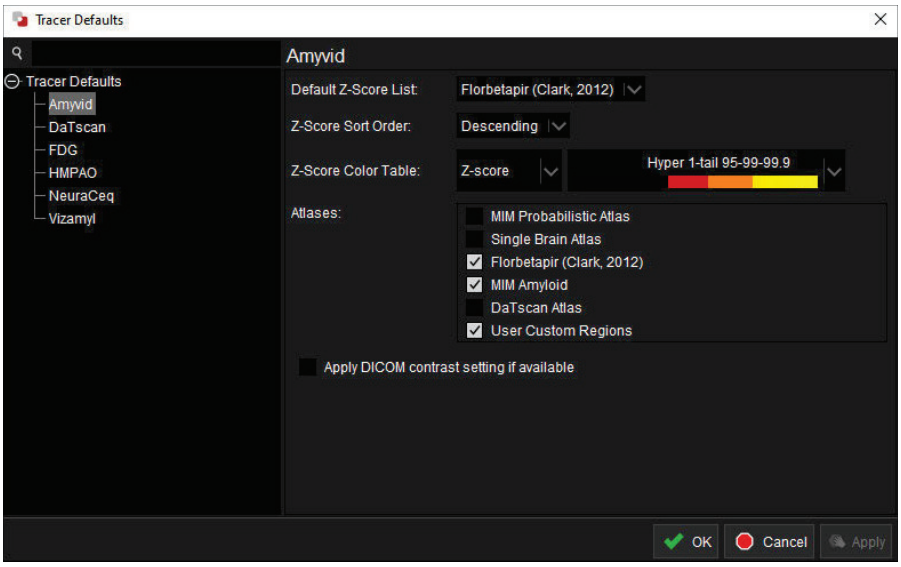
4. If desired, select other Z-Score Lists and update the included regions.
5. If desired, click **Add** and create your own Z-Score List with the region results that you want to include.
6. Click **OK** to save the changes and close the window.

Adjust Default Settings for a Tracer

You can adjust default settings for specific tracers.

1. In the Z-Score Analysis window, click **Set Tracer Defaults...**.
2. In the new window, select the tracer that you want to edit.

3. Adjust the display using the **Z-Score Sort Order**, **Z-Score Color Table**, and **Apply DICOM contrast setting if available** options.



4. If needed, update the **Default Z-Score List** that appears when the Z-Score Analysis window opens for that tracer.

> **Tip:** If you created your own Z-Score List using the steps above, you might want to set it as the new default.

5. If needed, update the **Atlases**. This setting determines from which atlases structures should be shown. For example, if you use the Hypo Z-Score List, it includes only hypo structures based on the atlases selected here.
6. If desired, configure settings for additional tracers.
7. Click **OK** to save the changes and close the window.

View Color Scales and Stereotactic Surface Projections

MIMTD-825 • 04 Jan 2024

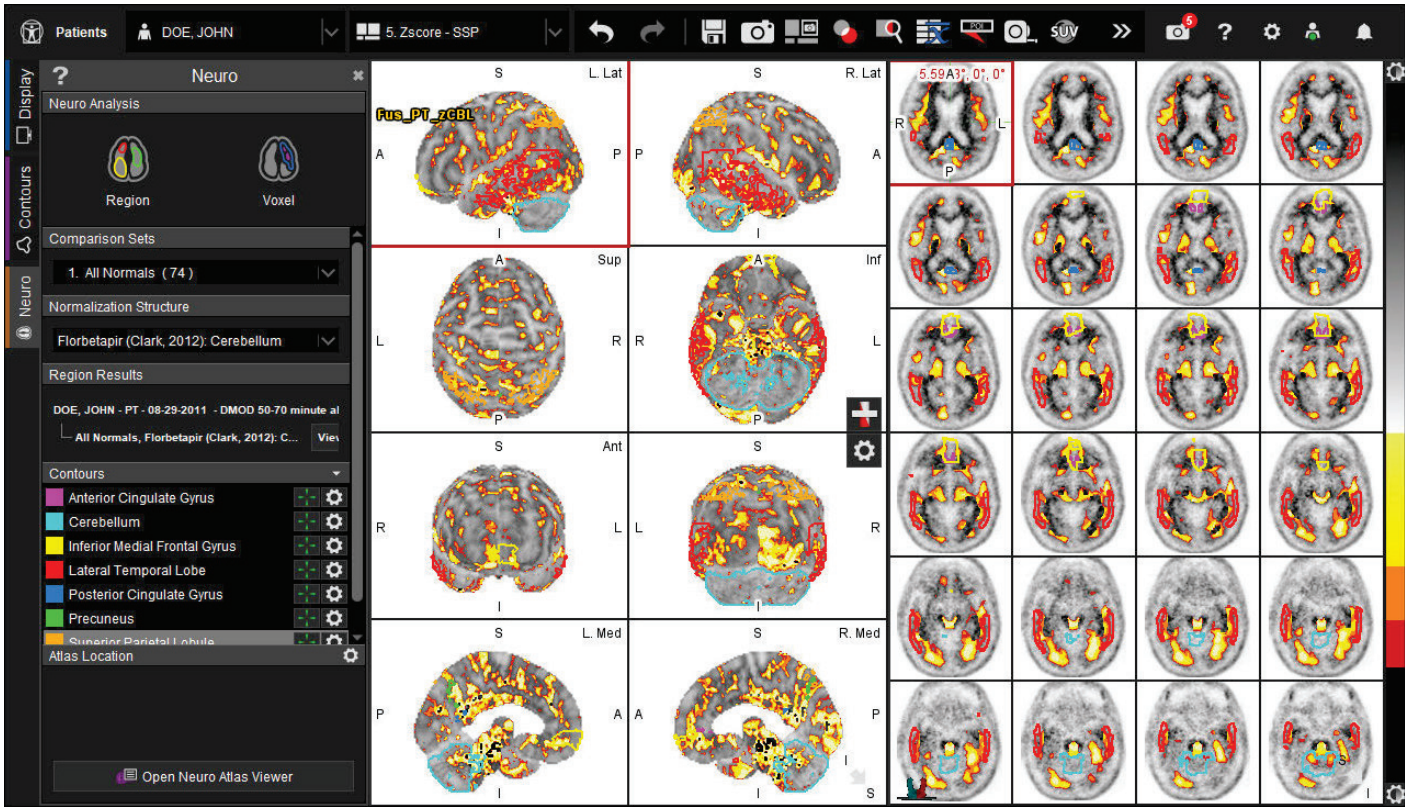
Overview

MIMneuro® includes views to help you visualize z-score results.

When voxel-based analysis has been performed, the voxel-analysis results are fused as a secondary image to the registered SPECT or PET image.

You can see:

- Z-score color scaling. The z-scores fused to the image are displayed with a color table. You can scroll through slices and see the coloring reflect the z-score in a given region.
- Sterotactic surface projections (SSPs). You can see static views of an intensity-based SSP. The maximum z-score values are projected to the surface.



Amyvid scan with a hyper z-score color scale applied. Left side: SSPs. Right side: Gridded axial image.

Depending on the workflow you are using, these views may be automatically created. You can also manually create or update these views as needed.

Contents

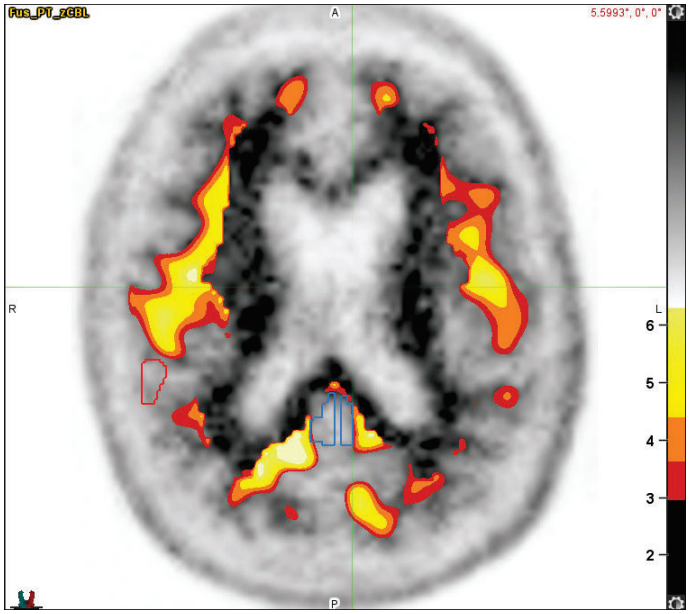
Use Z-Score Color Scaling

When voxel-based analysis is performed on an image, z-scores are fused to the image and displayed with a default color table. These color tables differ depending on the workflow that is run and whether you are looking for increased or decreased uptake in the brain.

View the Z-Score Range by Color

The color tables use significance bands within the z-score ranges to show voxels of increased or decreased uptake. Increased or decreased uptake is defined as above or below the default z-score threshold of +/- 1.65.

Hover over the vertical color bar to see the z-score ranges indicated by each color.

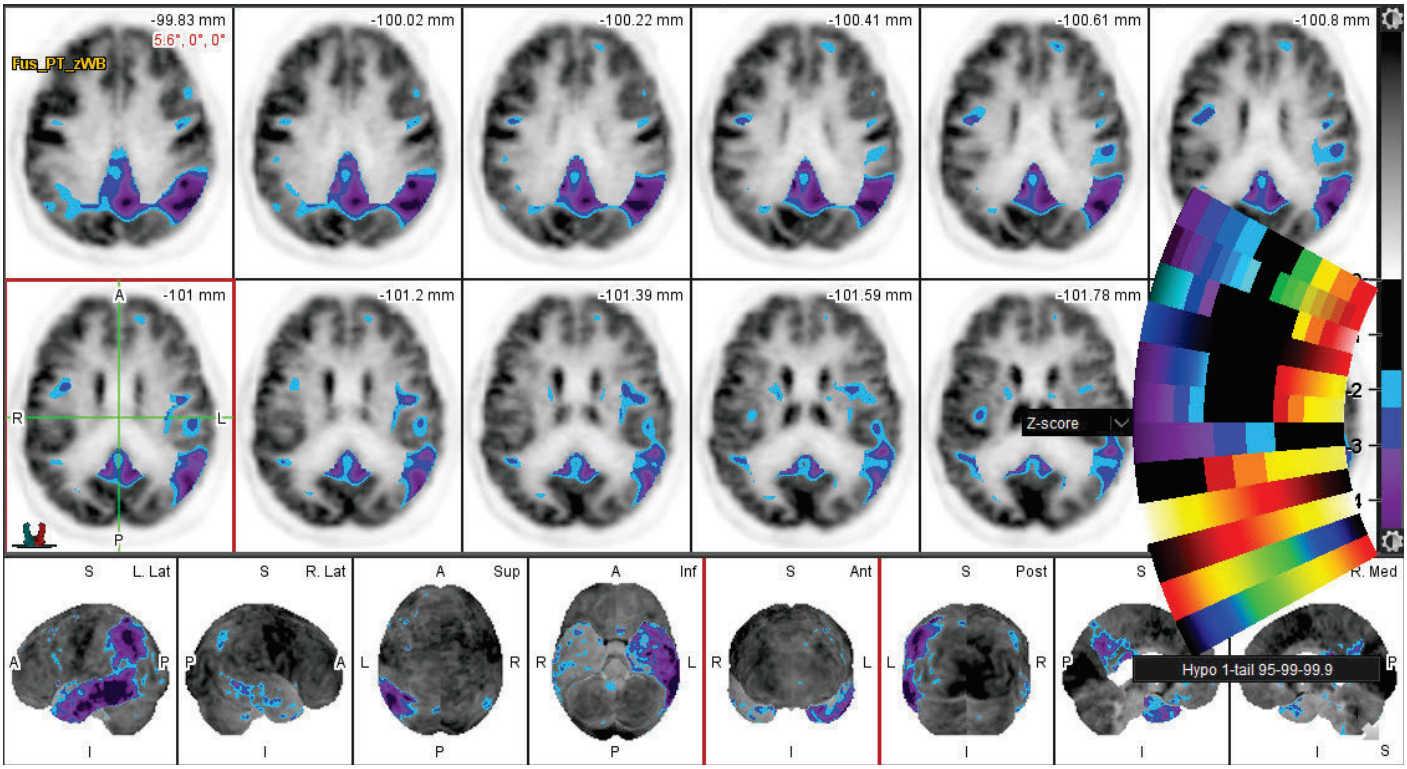


In this Amyvid scan example, hyper regions are shown. Looking at the scale by the color bar, z-scores that are +3 to +3.5 are red. Orange indicates the next range of z-scores. Z-scores above +4.5 are an increasingly lighter yellow.

Choose a Different Color Scale

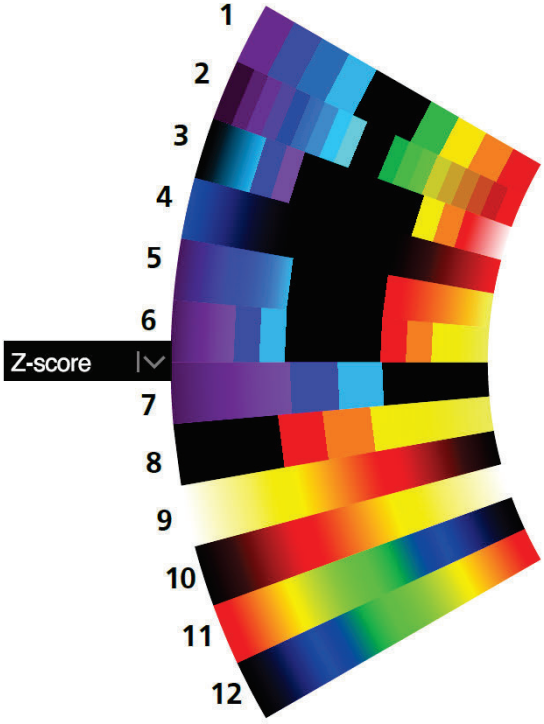
Color scales are visible on series where a normalization structure has been applied.

To view a color scale or change which color scale is used, click on the contrast bar on the far right side of the viewport.



Below is a list of available color scales in the z-score color table grouping (numbers match with the corresponding image to the right):

1. 5 Unit
2. 10 Unit
3. 2-tail 95-99-99.9
4. 1-tail Blue/Red 95+
5. 1-tail Smooth 95+
6. 1-tail 95-99-99.9
7. Hypo 1-tail 95-99-99.9
   (default for FDG/HMPAO)
8. Hyper 1-tail 95-99-99.9
   (default for Amyvid/NeuraCeq/Vizamyl)
9. Red/Yellow Negative
10. Red/Yellow Positive
11. Quad-prism Negative
12. Quad-prism Positive



Change the Default Color Scale

Instead of manually changing the color scale used, you can set your desired color scale as the default. A different color scale can be selected as applicable for each tracer.

To update a default color scale:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"tracer defaults"**. Select a tracer on the left side.
3. Update the **Z-Score Color Table** for that tracer.
4. If desired, repeat these steps to update the default color table for additional tracers.
5. Click **OK** to save the changes and close the window.

Update the Color Scale

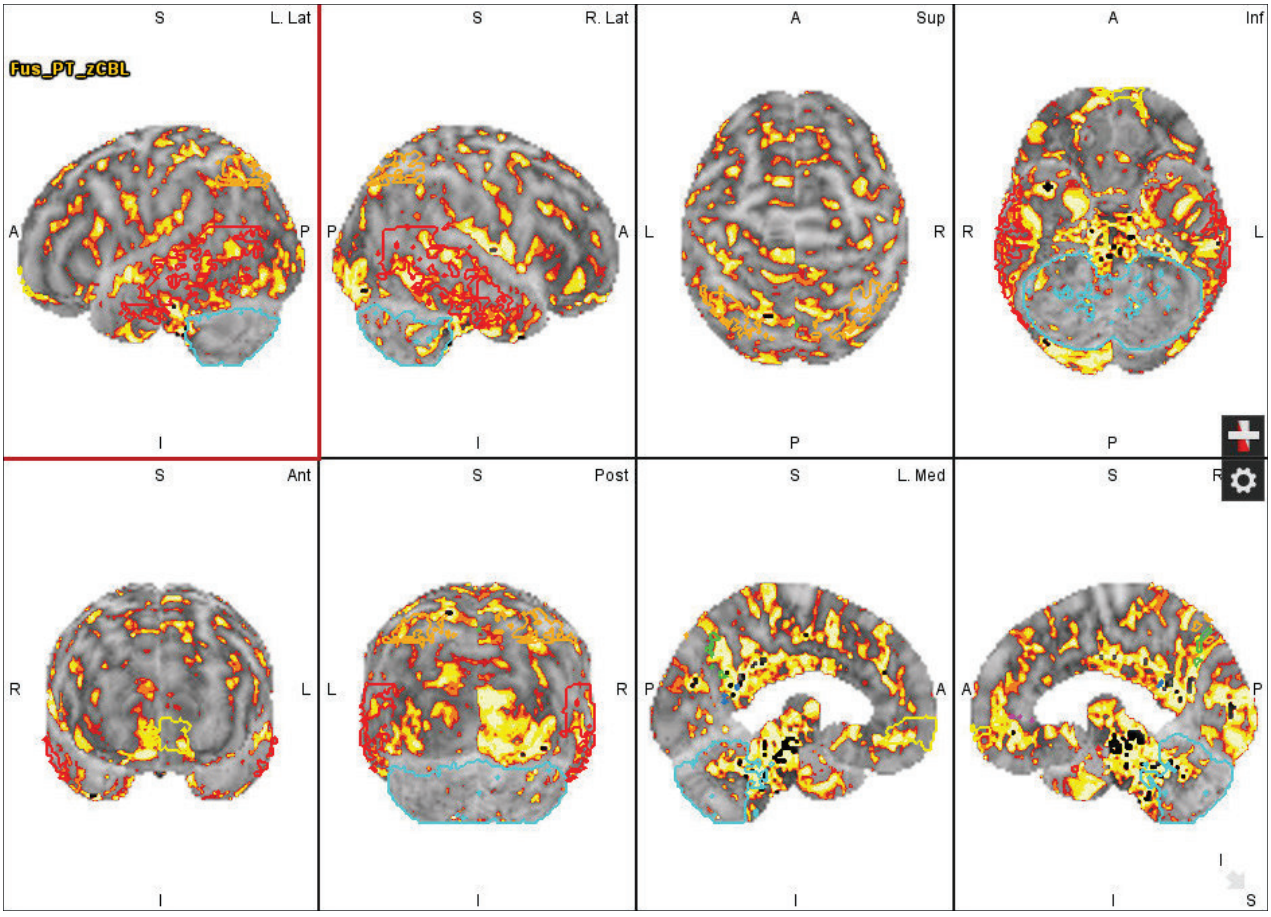
If needed, you can modify the z-score range that is reflected by each color.

Important: If you update the color scale, make sure to communicate the change to other users who may see the results. Modifications are saved for the current session but not for future sessions.

1. Select the **Contrast** tool from the top toolbar or radial menu.
2. In the contrast histogram that appears in the bottom of the viewport:
    - Left-click drag the far right dot to adjust the scale upward.
    - Click a yellow dot so it turns red and locks that position.
3. When you are finished, exit the Contrast tool.

View Stereotactic Surface Projections (SSPs) 6.1.8

Some workflows include the display of Stereotactic Surface Projections (SSPs). When a PET or SPECT brain volume is registered, eight views of an intensity-based SSP can be displayed.



MIM calculates SSPs using Minoshima's method.[1]. The algorithm projects z-scores to the SSP brain surface by searching along vectors from the brain surface into the brain. It locates maximum z-scores, which are then projected to the brain surface. Note that a different method is used for mapping activity to the surface for Amyloid scans because of high white matter uptake.

[1]Minoshima, Satoshi, et al. 1995. "A Diagnostic Approach in Alzheimer's Disease Using Three-Dimensional Stereotactic Surface Projections of Fluorine-18-FDG PET." *The Journal of Nuclear Medicine* 36, no. 7 (July): 1238-1248.

The same z-score color tables described above are then applied to the SSPs.

Tip: SSPs are static projections. You cannot use them to scroll through slices.

Work with SSPs

If region-based analysis has been performed, structures appear on the SSPs.

- Any modifications that you make to the structures are reflected on the SSP.
- You can hide the structures that are visible on the SSPs and other images. Go to the **Contours** sidebar and click the eye next to a structure to hide it.
- You can click anywhere on an SSP image to localize to that location on the PET or SPECT brain volume.

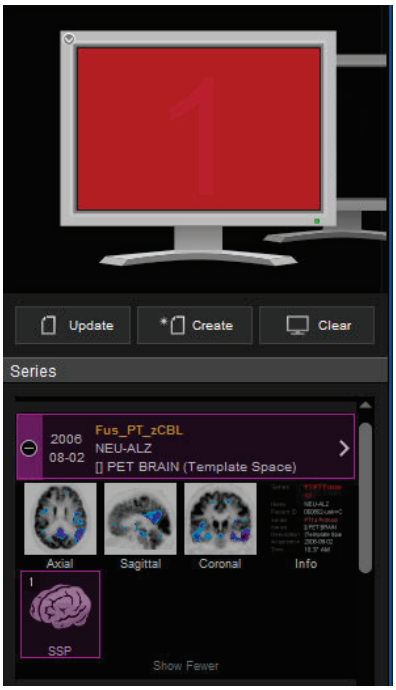
For example, Amyloid scans have high white matter uptake. You can confirm that an area is within the gray matter or within the white matter. Localize on the SSP and then view the corresponding location in the axial, sagittal, or coronal views of the image.

Add SSPs to Your Display

If SSPs are not displayed by default after running a workflow, you can add them using the Display sidebar.

1. Go to the **Display** sidebar.

2. In the **Series** section, find the PET or SPECT series and click **Show More** below the thumbnail pictures of the brain image.



3. Select SSP and then click the **Create** button below the picture of the monitor.

> **Related:** Refer to Create and Modify Display Layouts for more information about working with displays

Compare Studies with Matched Normals

MIMTD-826 • 04 Dec 2023

Overview

6.1.8

By default, MIMneuro® uses all normals in the database for analysis. You can use a dynamic comparison set to match a study with only a subset of normals instead. The comparison set selects which normals to use based on the current patient's demographics and study information.

For example, the default Age Matched Normals comparison set uses normals that are within five years of the patient's age. This means that older patients are matched with different normals than younger patients.

Complete the steps below to create a comparison set and apply the set to a study.

Related: Alternatively, you can use static comparison sets to make sure that the same subset of normals is always used. This can be helpful for research studies. Refer to Use MIMneuro® for Research for more information.

Related: To get started with normals, refer to Import MIMneuro Normals.

Contents

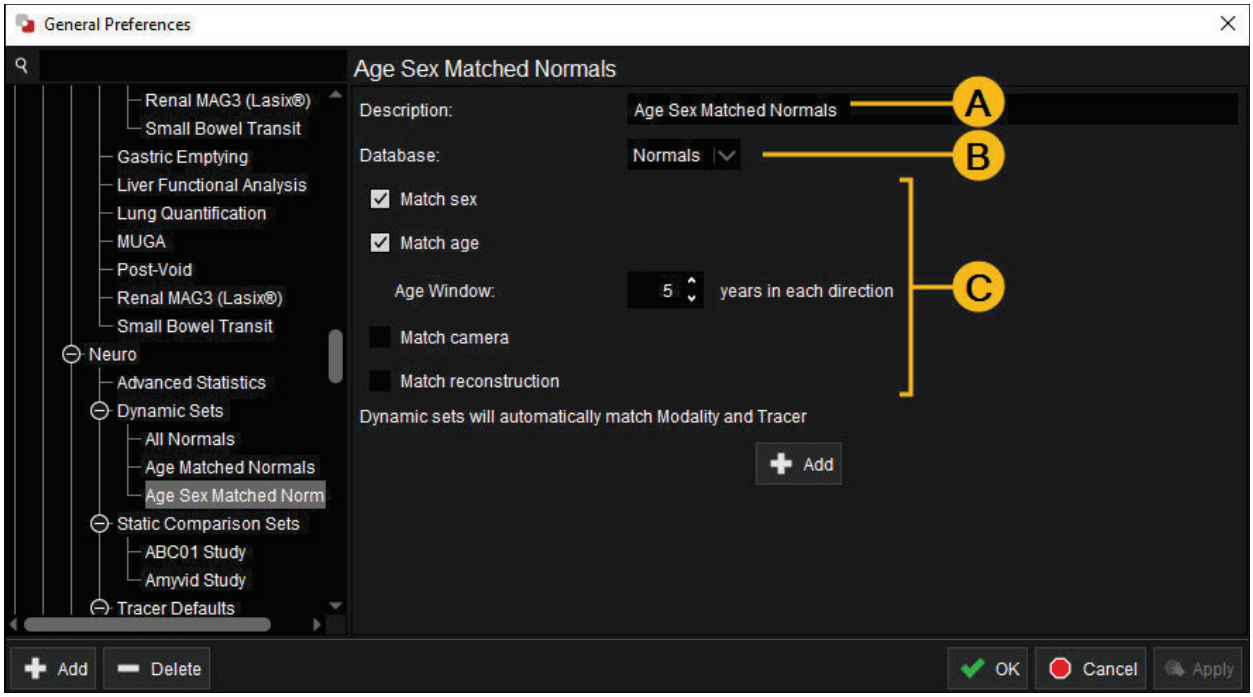
Create Dynamic Comparison Sets

Tip: Dynamic sets automatically match by modality and tracer (e.g., only normal controls with PET FDG brain volumes are used if the study being evaluated is a PET FDG brain volume).

To create your own dynamic comparison set, follow these steps:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**dynamic sets**". Select **Dynamic Sets** on the left side under Neuro.

3. Click **Add** to create a dynamic comparison set or select an existing dynamic set on the left side that you want to edit.
4. Configure the following:
   A. In the **Description** field, enter a name.
   B. In the **Database** field, select either the default Normals database or a custom normals database that you've created.
   C. Determine the criteria to use for matching. For example, you might want to make a new comparison set that matches on both patient age and sex.



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

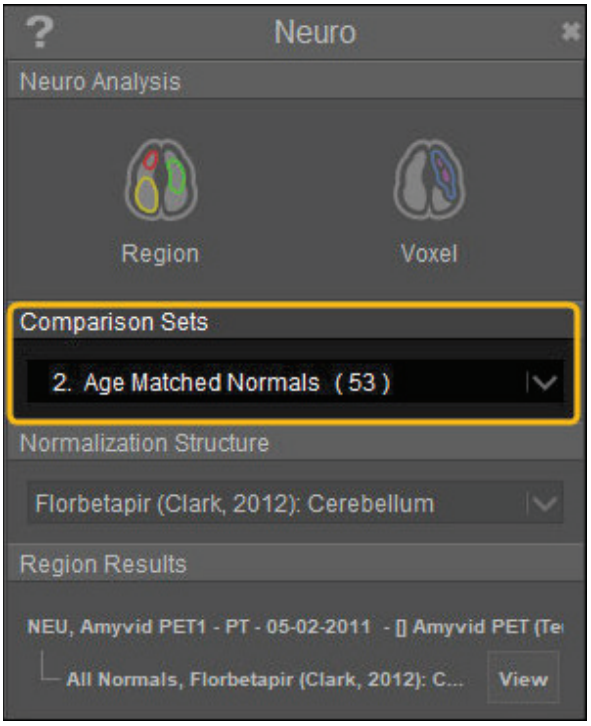
Apply Comparison Sets

By default, workflows run using all normals. You can select a comparison set for neuro analysis after the workflow runs.

> **Tip:** Please contact MIM Software Support at support.mimsoftware.com if you would like to update the default behavior for a neuro workflow to use a comparison set instead of all normals.

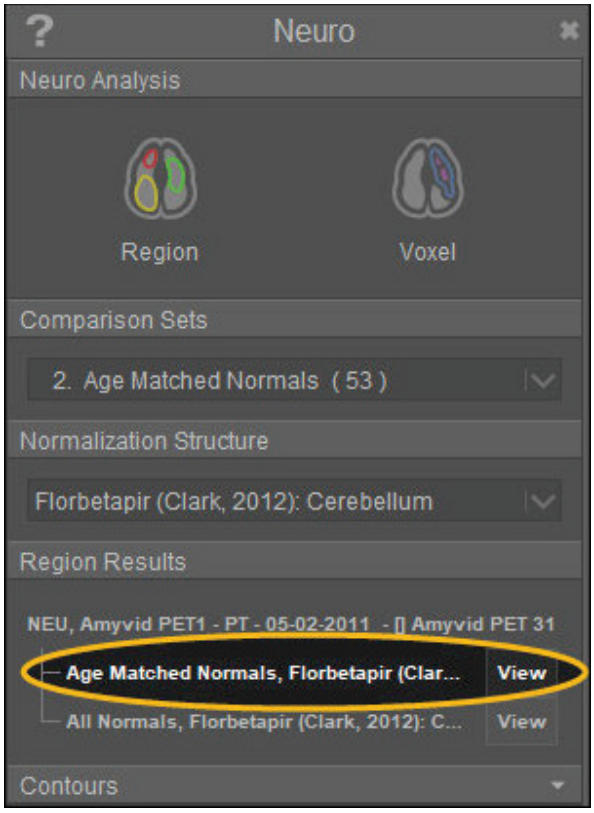
To select a comparison set, follow these steps:

1. When the workflow completes, go to the Neuro sidebar.
2. In the Comparison Sets section, use the dropdown to select a comparison set.



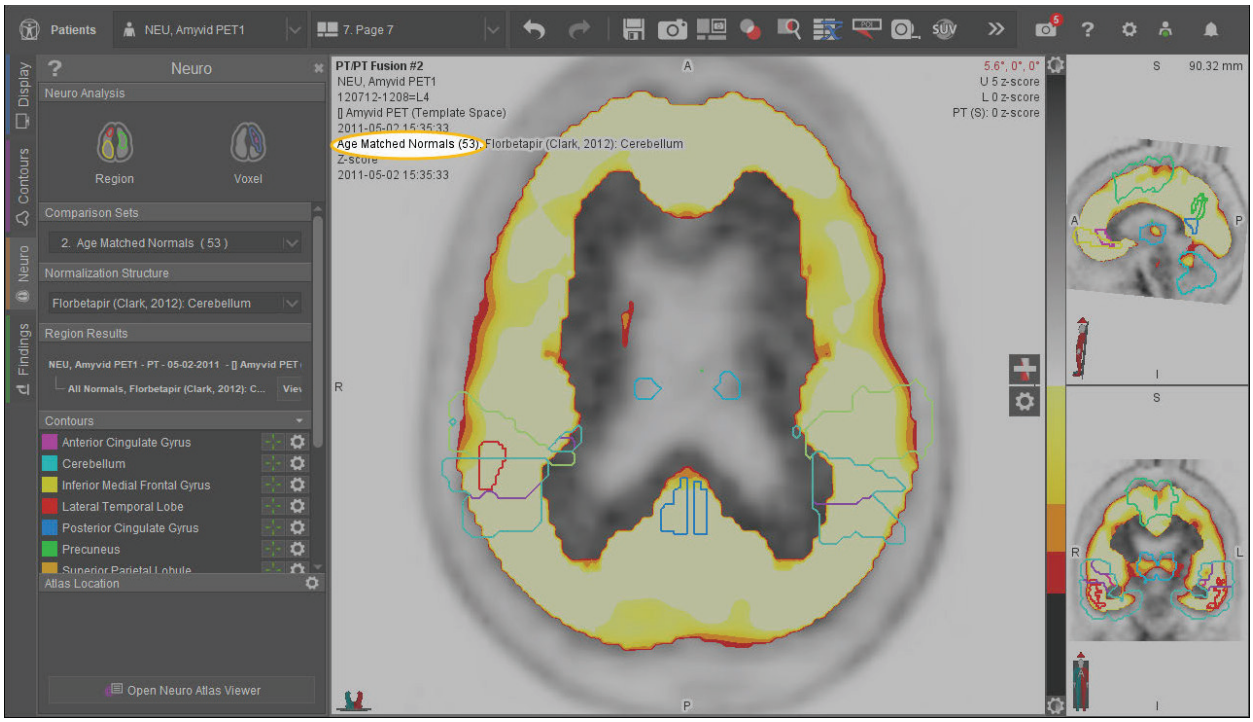
> **Tip**: In the dropdown menu, the number in parentheses indicate how many normals in the comparison set match the current study.

3. In the Neuro Analysis section, click either **Region** to run a region-based analysis or **Voxel** to run a voxel-based analysis. The processes run using the normals in the selected comparison set.
4. Review the results:
   - *If you ran a region-based analysis*, the results for the comparison set are listed in the Region Results section. Click **View** to open the Z-Score Analysis window.



Related: For more information about the Z-Score Analysis window, refer to Review Results in the Z-Score Analysis Window.

- *If you ran a voxel-based analysis*, a new fusion series is created. Note the Comparison Set listed in the series information in the left corner of the viewport.



Use MIMneuro® Processing Results with Other Systems

MIMTD-889 • 06 Dec 2023

Overview

Cases processed in MIMneuro can be used outside of the MIM® environment. Many systems, such as Brainlab®, can read and display RTstruct files generated in MIMneuro.

For systems that cannot read MIMneuro's RTstruct files, you can use the Voxel Burn tool or the Mask tool:

- Use the Voxel Burn tool to burn the edges of a selected regions of interest (ROIs) into the voxel data of the image.
- Use the Mask tool to modify the voxel values of the internal volume of an ROI. This tool modifies voxels where the centroid is within the contour.

Contents

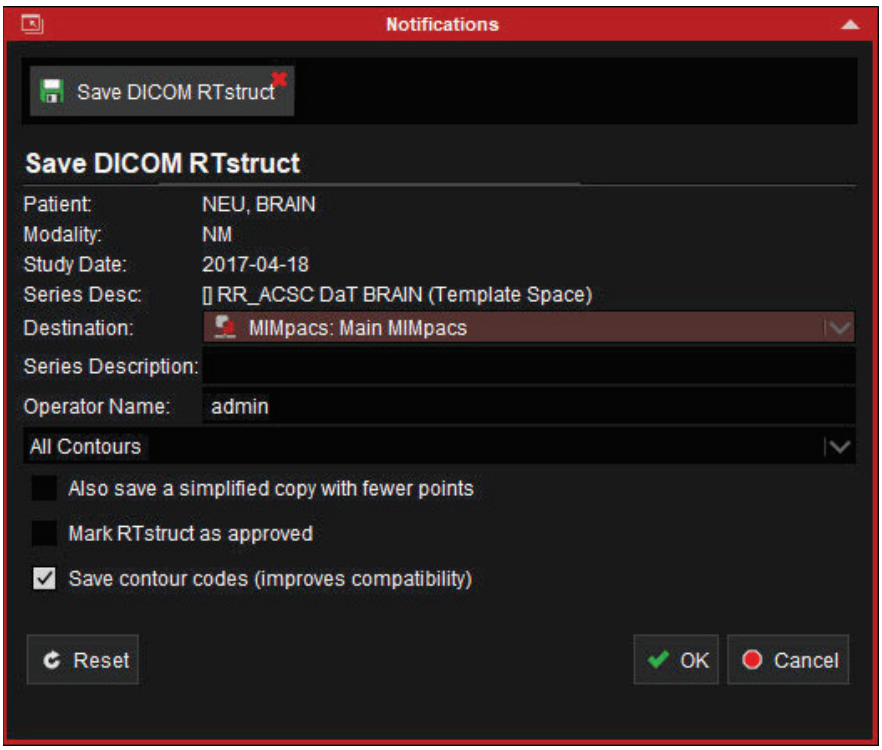
Save an RTstruct Set

Saving data as an RTstruct set should be used when possible. RTstructs follow DICOM standards and preserve the SeriesInstance UID to facilitate DICOM association.

To save a neuro study as RTstruct data, follow these steps:

1. Complete your processing in MIMneuro as usual.
2. When you are finished, click the save tool in the top toolbar.
3. Select **Save DICOM RTstruct** and select the series to save.
4. If you are prompted to save out the derived series along with the RTstruct, click **Yes** to save the associated series.

5. In the Notifications window, enter save information for the DICOM RTstruct and click **OK**.

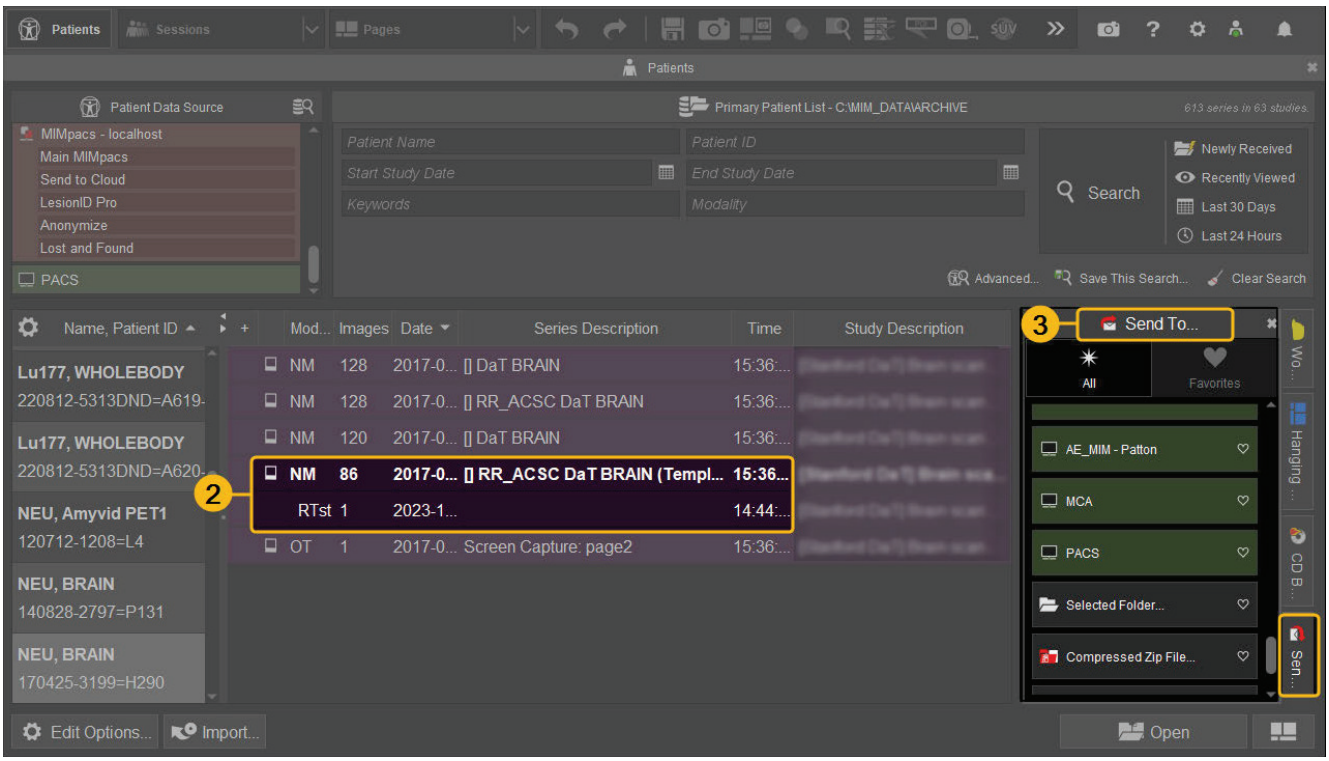


6. If you are saving the derived series too, continue to follow the prompts in the Notifications window:
    i. Select **Save DICOM Image Data**.
    ii. Enter save information for the DICOM image data and click **OK**.

Follow your organization's processes to send the saved files to the other system. If, for example, you manually send files, you may use the following steps:

1. Return to the patient list.
2. Select the series and the RTst file listed with it.

3. Go to the **Send To...** tab on the right side and select a recipient.



Use the Voxel Burn Tool

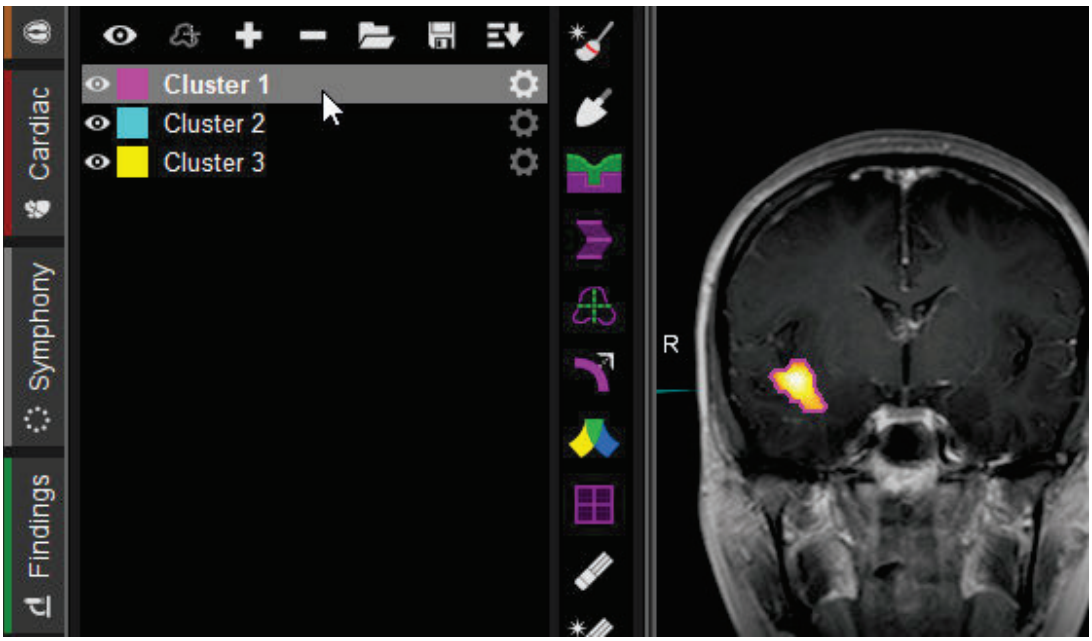
> **Important:** This tool is intended for use with other systems that do not accept an RTstruct set. Re-saving the image with burned contours creates a new Series Instance UID, which may interfere with DICOM association.

The Voxel Burn tool attempts to approximate the surface of the ROI as closely as possible. The edges of the contour are burned into the voxel data of the image.

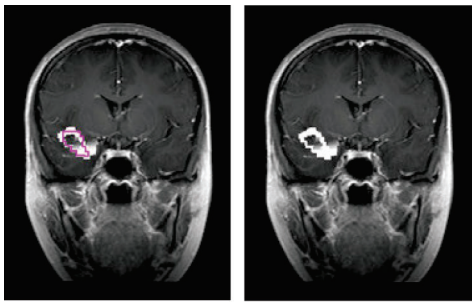
If you need to use the Voxel Burn tool, follow these steps:

1. Complete your processing in MIMneuro as usual.
2. On the left side of the screen, click the **Contours** tab to open the Contours sidebar.

3. In the list of contours, click on the contour that you want to burn into the image.



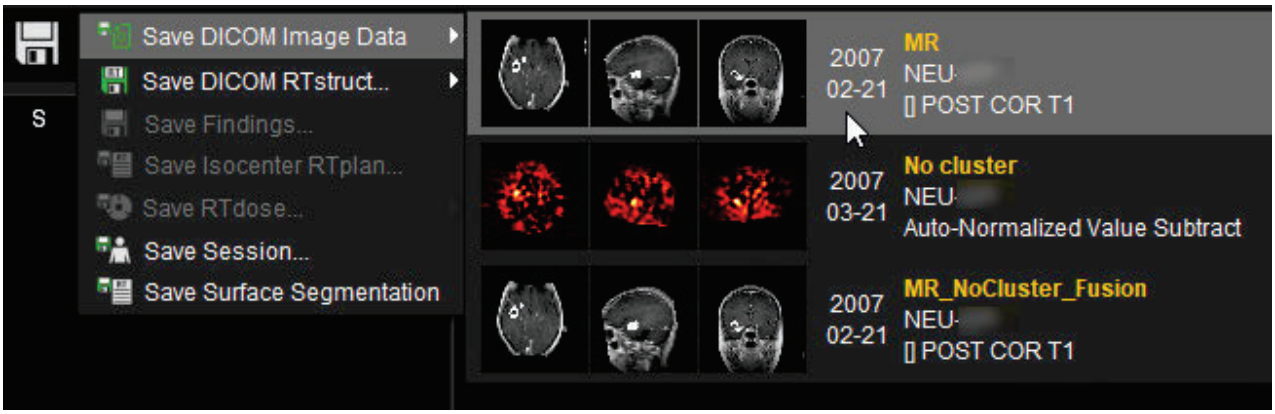
4. Click the double arrow button near the bottom of the Contours sidebar to open the full list of contouring tools.
5. Click the **Voxel Burn** tool to burn the contour into the image's voxel data.



Left: Contour that appears after using the Voxel Burn tool. Right: Same image with the contour hidden to show the result of the voxel burn.

6. Repeat this process for any additional contours you want to burn into the image.

7. When you are finished, click the save button at the top of the screen and use the **Save DICOM Image Data** option to save a copy of the image series with the burned-in voxel data.



Use the Mask Tool

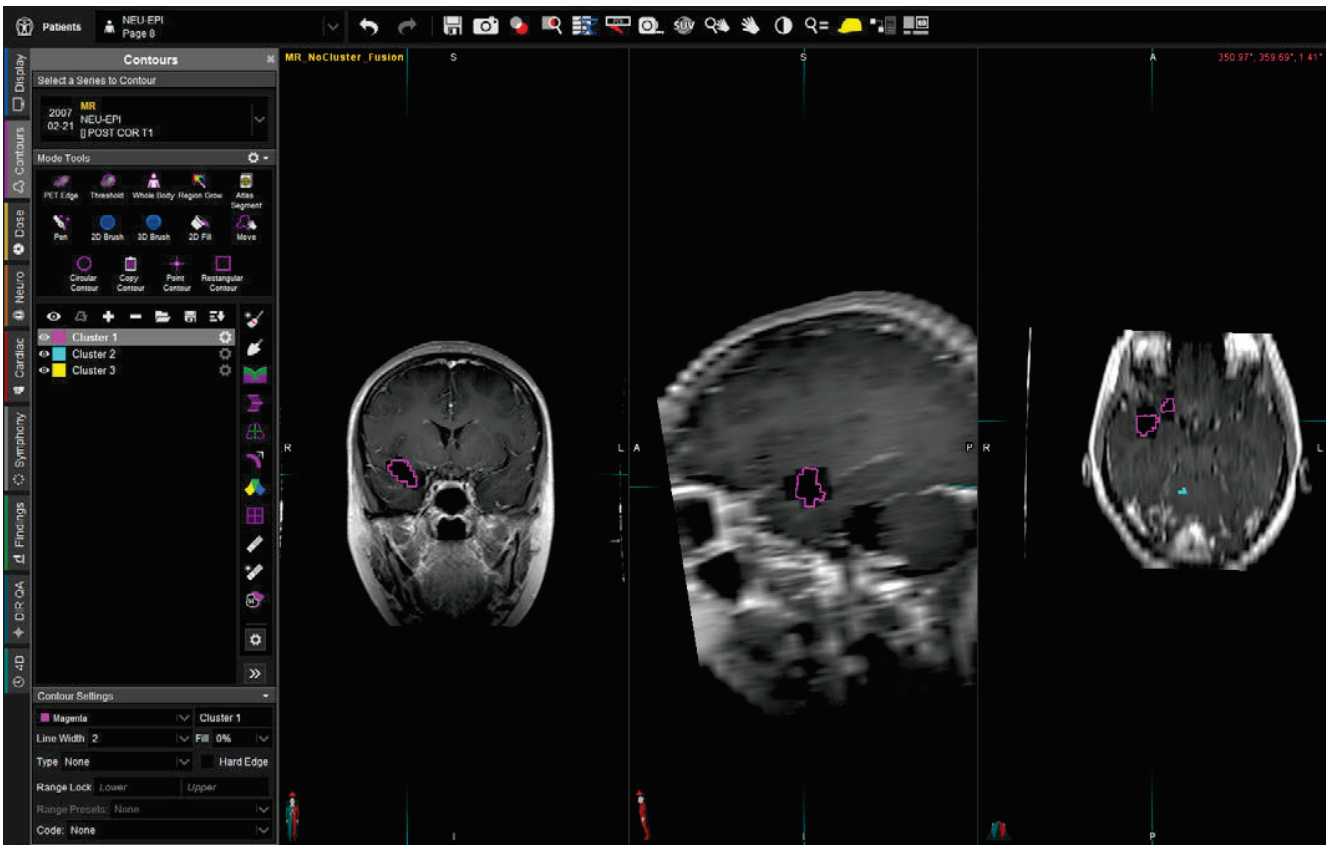
> **Important:** This tool is intended for use with other systems that do not accept an RTstruct set. Re-saving the image with masked contours creates a new Series Instance UID, which may interfere with DICOM association.

With the Mask tool, you can set a specific value for the internal voxels of a region of interest.

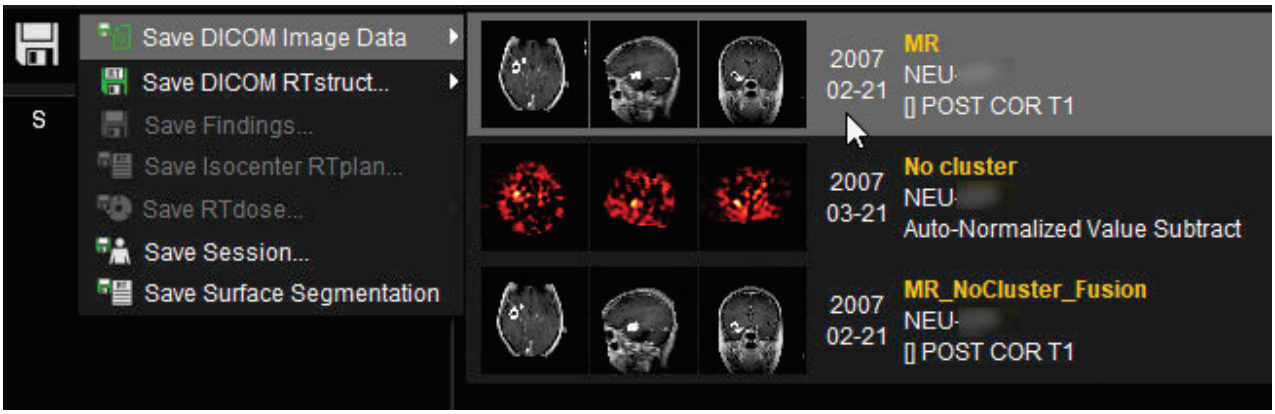
If you need to use the Mask tool, follow these steps:

1. Complete your processing in MIMneuro as usual.
2. On the left side of the screen, click the **Contours** tab to open the Contours sidebar.
3. In the list of contours, click on the contour that you want to use as a mask.
4. Click the double arrow button near the bottom of the contours sidebar to open the full list of contouring tools.
5. Click the **Mask** tool.
6. Review the mask parameters shown in the Notifications window and make adjustments as desired. To set a specific intensity value for the voxels in the ROI, use the **Mask to value** field.

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



8. Repeat this process for any additional contours you want to use to mask the image.
9. When you are finished, click the save button at the top of the screen and use the **Save DICOM Image Data** option to save a copy of the image series with the masked voxel data.



Create a Custom Neuro Normals Database

MIMTD-846 • 04 Dec 2023

Overview

Organizations typically use the neuro normals database provided with MIMneuro®. Refer to Import MIMneuro Normals for more information about installing this database.

If desired, you can use the steps below to create your own database of neuro normals.

Contents

Prepare for Your Project

Plan sufficient time to create a normals database. This project includes the following tasks:

- Collect patient normals scans
- Create the database in MIM®
- Set up a comparison set in MIM that determines when your normals database should be used
- Validate the database

Important: You are responsible for validating the database according to your organization's policies. Ensure studies have undergone appropriate analysis and validation before being added as normals to your custom database.

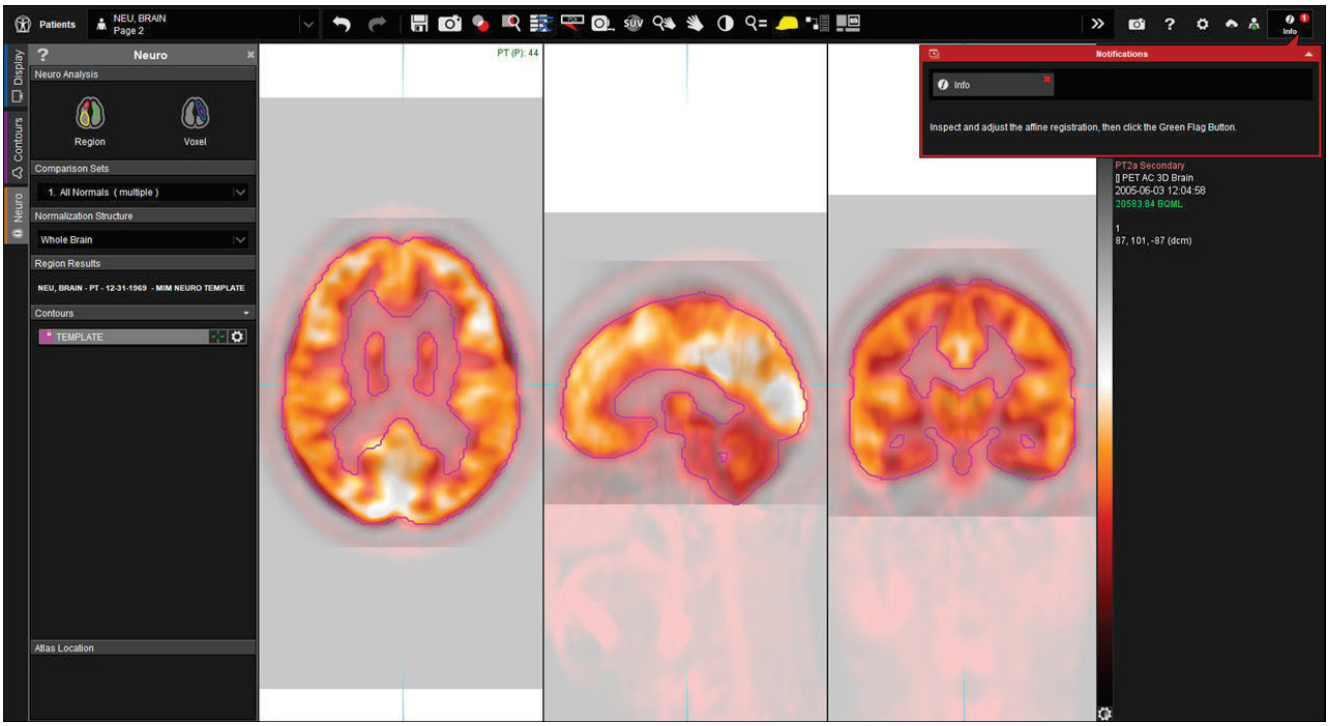
Before you continue to creating the database, make sure that all of the scans that you want to include are saved to a MIM patient list.

Create a Normals Database 6.1.9

Follow these steps to register images and save them to your own normals database:

1. From the MIM patient list, select the PET or SPECT image you want to add to your normal database and click **Open**.
2. Click the double arrow ⏩ button on the right side of the MIM toolbar and select the **Neuro Registration** tool. This tool registers the patient to the MIM Neuro Normal template.
3. If the tool 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 tool proceeds immediately to the next step.
4. Inspect the affine registration and, if necessary, make adjustments for proper alignment.

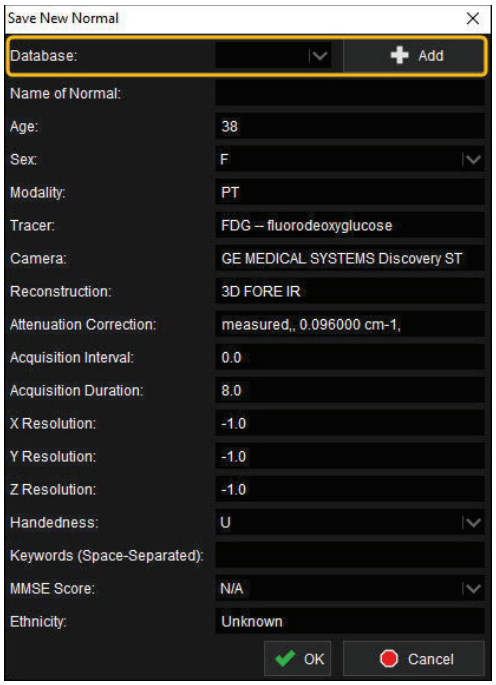
> **Tip:** Affine registrations rarely require adjustment. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See Adjust Affine Registration for more information.



5. Click the double arrow ⏩ button again and select the **Save As Neuro Normal** tool.
6. When the **Select a series for this action** prompt appears, locate the series that was created by the Neuro Registration tool. Click the **Select this series** button on the series.

> **Tip:** This series has "(template space)" in its description. It is likely to be the bottom series on the page.

7. The **Save New Normal** window opens.
    - *If this is the first study that you are adding to your database*, you need to create the database. Click the **Add** button in the upper-right corner and enter a name for the new database.
    - *If you are adding more studies to a database that you've already created*, select the database from the **Database** dropdown menu.



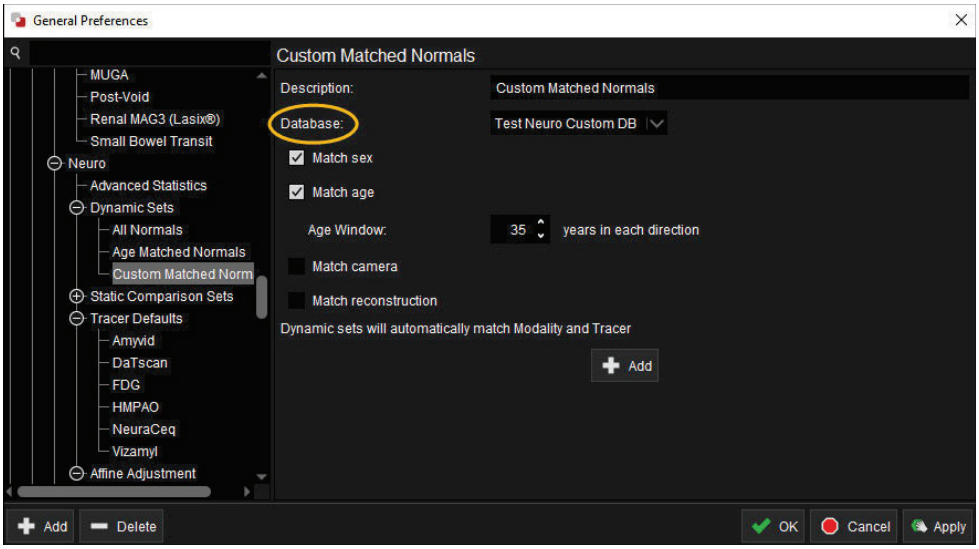
8. Enter known information for this patient in the Save New Normal window. Click **OK**.
9. If you are prompted to confirm this action, click **Yes**.
10. Repeat the steps above for additional studies that you want to include in the database.

Use a Comparison Set with Your Custom Normals Database 6.1.9

To use your custom normals database for processing, you need to create a comparison set that references the database. The comparison set determines with which studies the database can be used.

Use a Dynamic Comparison Set

Follow the steps in Compare Studies with Matched Normals to create a dynamic set. As you configure the criteria for the dynamic set, make sure to select your custom normals database in the **Database** field.



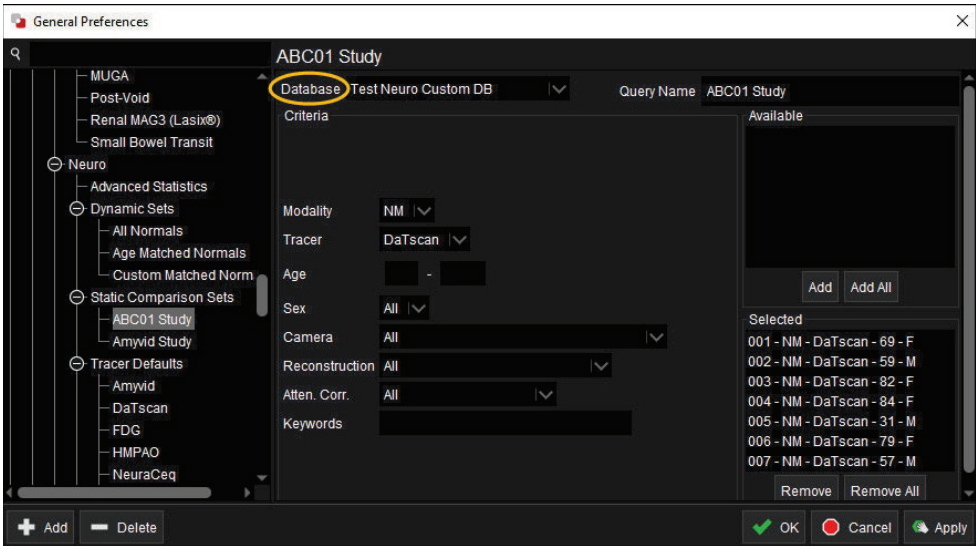
Tip: If you add normals to your database in the future, they are automatically included as part of the dynamic comparison set.

Use a Static Comparison Set

Follow the steps in Use MIMneuro® for Research to create a static comparison set.

Make sure to do the following:

- Select your custom normals database in the **Database** field.



- Select which studies from your database to include in the comparison set.

Important: If you later add normals to your database, you need to update the static comparison set to include the new normals.

Use MIMneuro® for Research

MIMTD-1774 • 08 Jan 2024

Overview

MIMneuro includes several features that are specifically helpful in research scenarios.

> **Related**: If you want to make your own neuro normals database to support your research, refer to Create a Custom Neuro Normals Database for more information.

Contents

Use Static Comparison Sets

A static comparison set is a subset of normal controls based on predefined criteria (e.g., age, sex, camera, and reconstruction). A static comparison set ensures that the same normals are used from study to study. If you use a dynamic comparison set, as described in Compare Studies with Matched Normals, different normals could be matched to different studies.

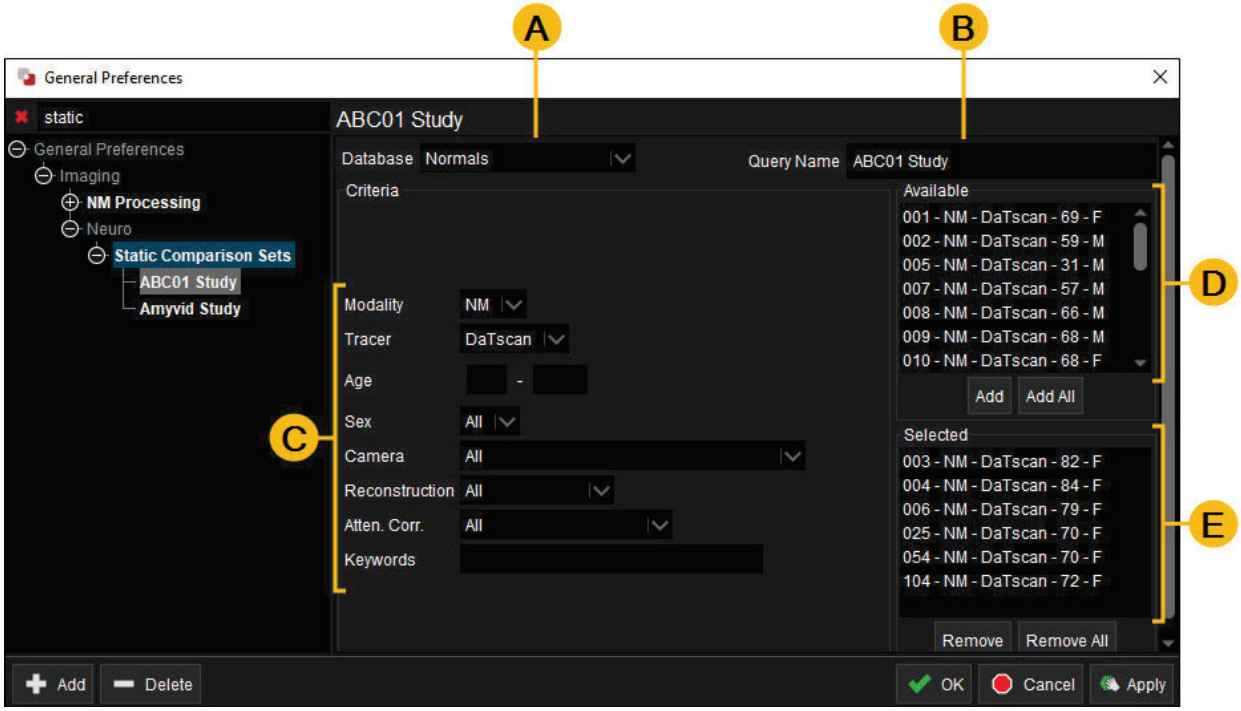
To create a static comparison set, follow these steps:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**static**". Select **Static Comparison Sets** on the left side.
3. Click **Add** to create a static comparison set.
4. Configure the following:
    A. In the **Database** field, select either the default Normals database or a custom normals database that you've created.
    B. In the **Query Name** field, enter a name.
    C. Determine the criteria for the normals that you want to include in the static set. Normals that match the criteria you configured appear in the Available pane.

D. In the Available pane, select normals to include and click **Add**.

> **Tip**: Press and hold Shift or Ctrl to select multiple normals at once or click **Add All**.

E. Verify that the normals you want to include in the static set appear in the Selected pane.



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

To use the static comparison set that you created, select your set from the Comparison Sets section of the Neuro sidebar. Refer to Apply Comparison Sets for more information.

Manually Position a Scan

A scan must be registered to the template space before an atlas can be applied. Registration is built in to MIMneuro workflows and region-based analysis.

If you are reviewing a study without automated processing, you can separately register the scan:

1. Open the series.
2. In the top toolbar, click the double arrows on the right side to see additional tools and find the **Neuro Registration** tool.
3. Follow the prompt in the Notifications window to adjust the series if needed. Click the green flag button to confirm the registration.

Related: Refer to Adjust Affine Registrations for more information about options for manual adjustment.

The registered series appears in the bottom row of the viewport. As desired, you can now use an atlas to auto-contour regions of the brain. Refer to Use the Neuro Atlas Viewer (MIM 7.2 and Later) for more information about how to select and draw structures (MIM 7.2 and later).

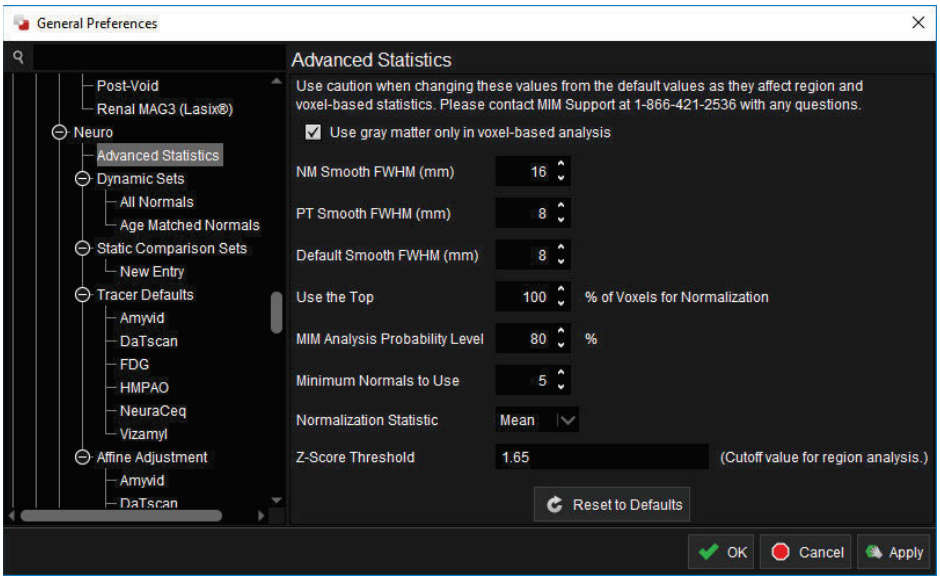
Tip: If you want to reorient the series along the AC-PC Line or the Hippocampal Plane, you can use the Neuro Reorientation tool. In the top toolbar, click the double arrows on the right side to find the **Neuro Reorientation** tool and follow the prompt in the Notifications window.

Configure Statistical Thresholds

If necessary, you can update statistical levels used for MIMneuro calculations.

To adjust statistic settings, follow these steps:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**advanced statistics**". Select **Advanced Statistics** on the left side.
3. Review the available settings and update as needed.



- **NM/PT/Default Smooth FWHM (mm)** — Adjust the smoothing factor (in mm) to be applied to images to reduce noise within the image.

- **Use the top __ % of voxels for normalization** — Change this percentage to exclude areas of low activity within your reference region. Excluding these portions from the analysis allows you to remove areas, such as cerebrospinal fluid, that may be contained within the reference region and could falsely lower the mean activity measured in that reference region.
- **MIM Analysis Probability Level** — Used with the MIM Probability Atlas. Enter the percentage of probability to use during analysis. For example, a 90% probability level would indicate that 9 out of 10 contours in the atlas overlapped on a particular brain structure.
- **Minimum Normals to Use** — Adjust the minimum number of normals to use when running a voxel- or region-based analysis.
- **Normalization Statistic** — Determine the value that is used for normalizing intensity levels in the image prior to z-score calculation.
- **Z-Score Threshold** — Set the cutoff value used in region-based analysis to determine which z-scores are significant. Refer to Review Results in the Z-Score Analysis Window for more information about z-score analysis.

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

Review Additional Statistics

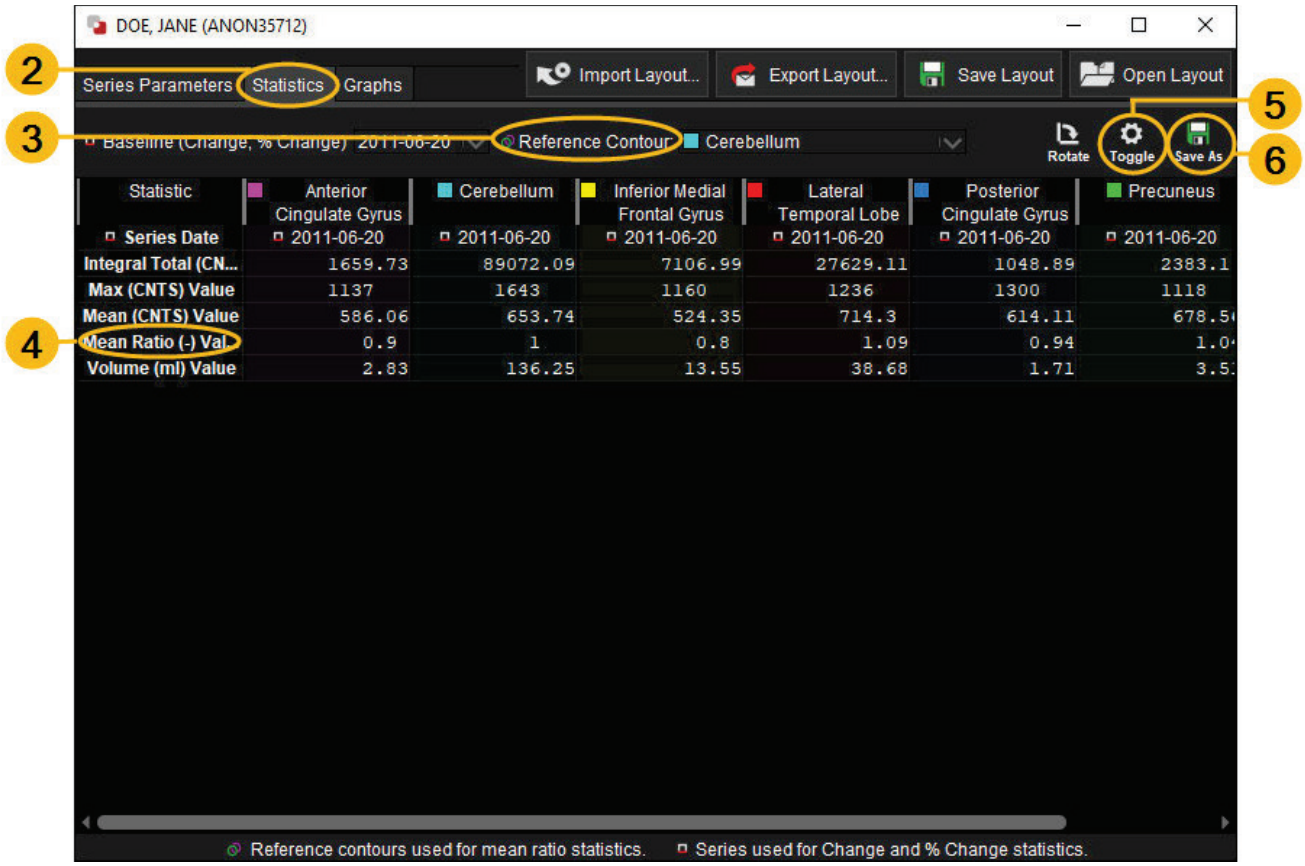
Depending on which MIMneuro workflow you run, you may see the Z-Score Analysis window or other calculated results. You can review additional statistics as needed using the Statistics Viewer.

1. In the top toolbar, click the **Statistics Viewer**  .
2. In the window that opens, go to the **Statistics** tab to view results for each structure.
3. Change the **Reference Contour** to Cerebellum or choose another structure as appropriate.
4. *If you are reviewing an amyloid PET study*, check the **Mean Ratio** (also called the SUV Ratio). This ratio is the average value for each brain region to the average value for the normalization structure (e.g., cerebellum).

Important: These results are different from the region-based z-scores shown in the Z-Score Analysis window where the z-scores are calculated from the mean intensity values of the region.

5. If you need to view more data, click the **Toggle**  button and go to the **Statistics** tab to select additional statistics to show.

6. To save the statistics, click the **Save As** button in the upper-right corner of the Statistics Viewer window. Select the format in which you want to save the results.



MIMneuro® Workflows

MIMneuro Workflows

MIMTD-1231 • 08 Nov 2024

Overview

MIMneuro® comes with workflows built to handle common processing requests.

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

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

Contents

Available Workflows

Neuro Amyloid - Centiloid Analysis — Perform amyloid quantification with SUVr and Centiloid processing for Amyvid®, Neuraceq®, and Vizamyl™. *MIM 7.2.3 and later.*

> **Related:** Go to Featured Workflow: Neuro Amyloid - Centiloid Analysis to learn more about this workflow.

Neuro DaTscan - Analysis — Compare tracer uptake in the striatum to normals. It includes regional comparisons, anterior/posterior ratios, and caudate/putamen ratio for loss of uptake.

Neuro DIAMOX - Subtraction — Subtract a comparison image from a baseline image for a DIAMOX SPECT. If a CT is available, it is registered to the subtraction results. This workflow runs cluster-based analysis.

Neuro Dynamic Analysis — Create up to 5 regions of interest on a static PET image, which are transferred to the dynamic PET image. The final results include a time activity curve and additional statistics for each region. This workflow does not include region-based or voxel-based analysis.

Neuro FDG - Analysis — Perform voxel-based analysis with normalization using the whole brain, pons, and cerebellum. Perform region-based analysis with normalization using the whole brain.

Neuro HMPAO - Analysis — Subtract a comparison image from a baseline image. If an MR is available, it is registered to the subtraction results.

Neuro PET/SPECT - Subtraction — Subtract a comparison image from a baseline image for PET or SPECT. If an MR is available, it is registered to the subtraction results. This workflow runs cluster-based analysis.

Neuro SPECT — View a cortical surface projection.

Neuro Tauvid - Contrast Display — Display a Tauvid PET for review. Contrast is set based on mean cerebellar counts with two color bars that transition at the 50% point.

Reconstruction Workflows

Neuro DaTscan - SPECT Reconstruction — Perform reconstruction of DaTscan® SPECT projections with Chang's attenuation correction.

Neuro HMPAO - SPECT Reconstruction — Perform reconstruction of HMPAO SPECT projections with Chang's attenuation correction.

Important: Reconstruction workflows require a SPECTRA Recon® license in addition to a MIMneuro® license. For more information, please contact MIM Software Support at support.mimsoftware.com.

Legacy Workflows

Important: These workflow has been replaced by the Neuro Amyloid - Centiloid Analysis workflow.

Neuro Amyvid - Analysis — Perform voxel-based and region-based analysis with the cerebellum as a normalization structure. It includes SUVr analysis for Florbetapir (Clark, 2012) amyloid regions.

Neuro NeuraCeq - Analysis — Perform voxel-based and region-based analysis with the cerebellum as a normalization structure. It includes SUVr analysis for MIM amyloid regions.

Neuro Vizamyl - Analysis — Perform voxel-based and region-based analysis with the cerebellum as a normalization structure. It includes SUVr analysis for MIM amyloid regions.

MIM Workflows™: Neuro Amyloid — Centiloid Analysis

MIMTD-1229 • 29 Jul 2024

Overview

Use the **Neuro Amyloid – Centiloid Analysis** workflow to provide a calibrated Centiloid quantification value. The workflow is designed for the following acquisition protocols:

- Florbetapir (Amyvid®): 2 x 5-minute frames 50-60 minutes post-injection
- Florbetaben (Neuraceq®): 4 x 5-minute frames 90-110 minutes post-injection
- Flutemetamol (Vizamyl™): 4 x 5-minute frames 90-110 minutes post-injection

The Global Alzheimer's Association Interactive Network (GAAIN) created a standardized scale for amyloid PET quantification called Centiloid. This scale can be calibrated for any PET quantification software using fixed anchor points at 0 and 100 derived from the average of young, cognitively normal controls, and Alzheimer's disease patients, respectively. The Centiliod scale can be used to compare quantification across multiple amyloid tracers.

For more information on the Centiloid project, see gaain.org/centiloid-project.

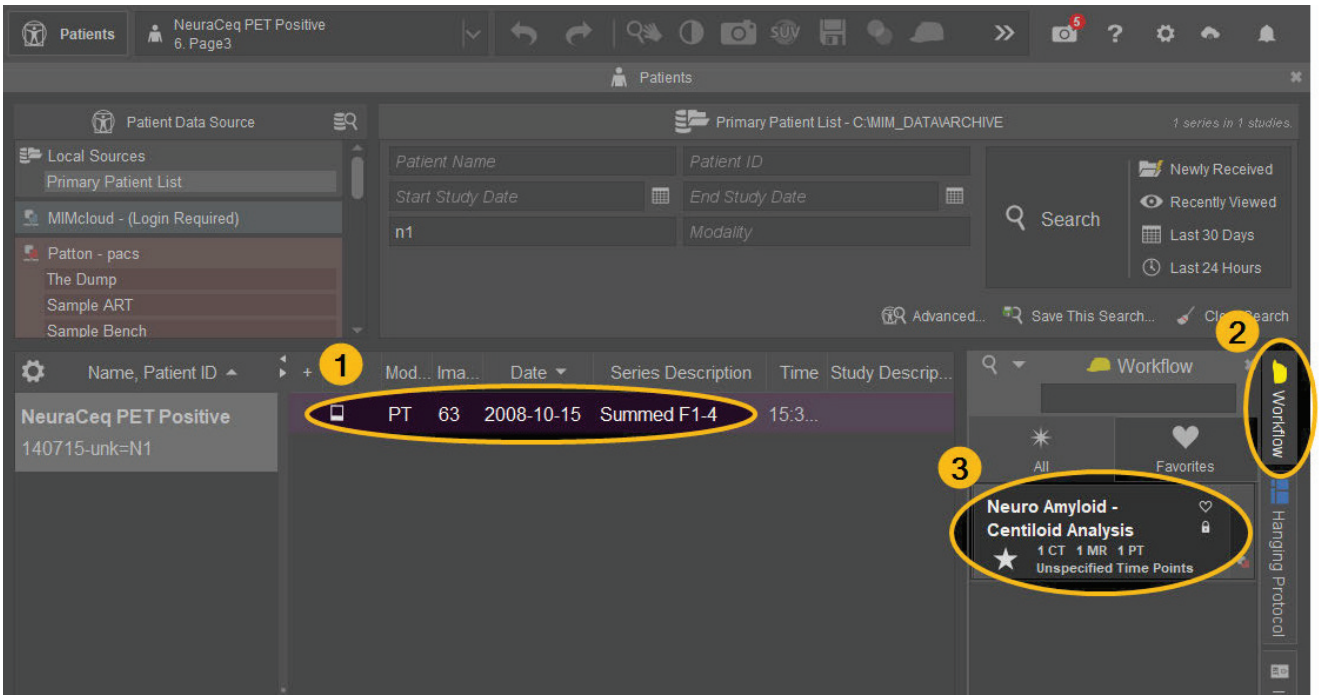
Contents

Run the Workflow

1. From the patient list, select the PET series. If desired, select an optional CT or MR.

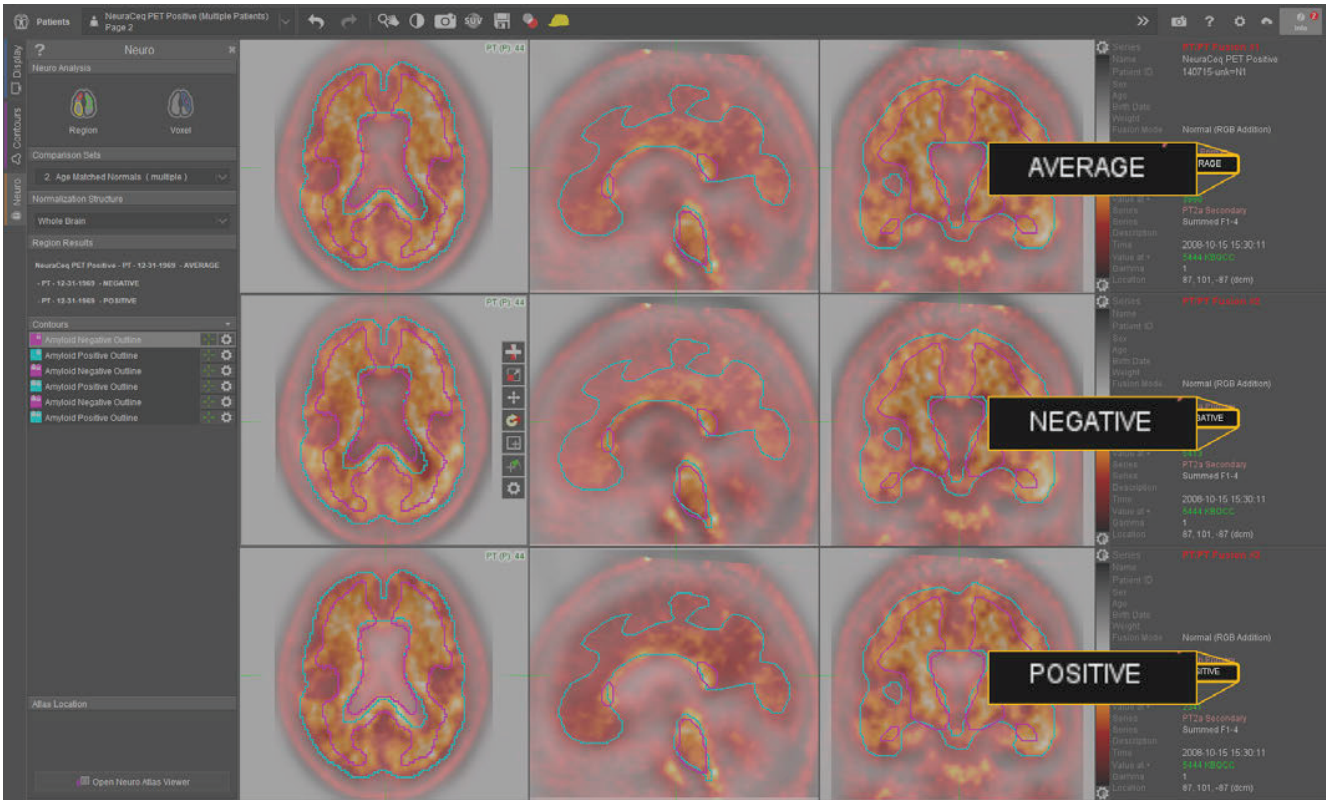
> **Important:** If you are using a dynamic scan, ensure each frame is 5 minutes long. Processing scans composed of frames acquired outside the recommended post-injection time window (above) may affect your results.

2. Click the **Workflow** sidebar on the right side of the patient list to expand it.
3. Select the **Neuro Amyloid – Centiloid Analysis** workflow and double-click to launch the workflow.



4. If prompted, in the Notifications window, select an image tracer from the dropdown.

5. Review the affine registration of the patient series to the template space.



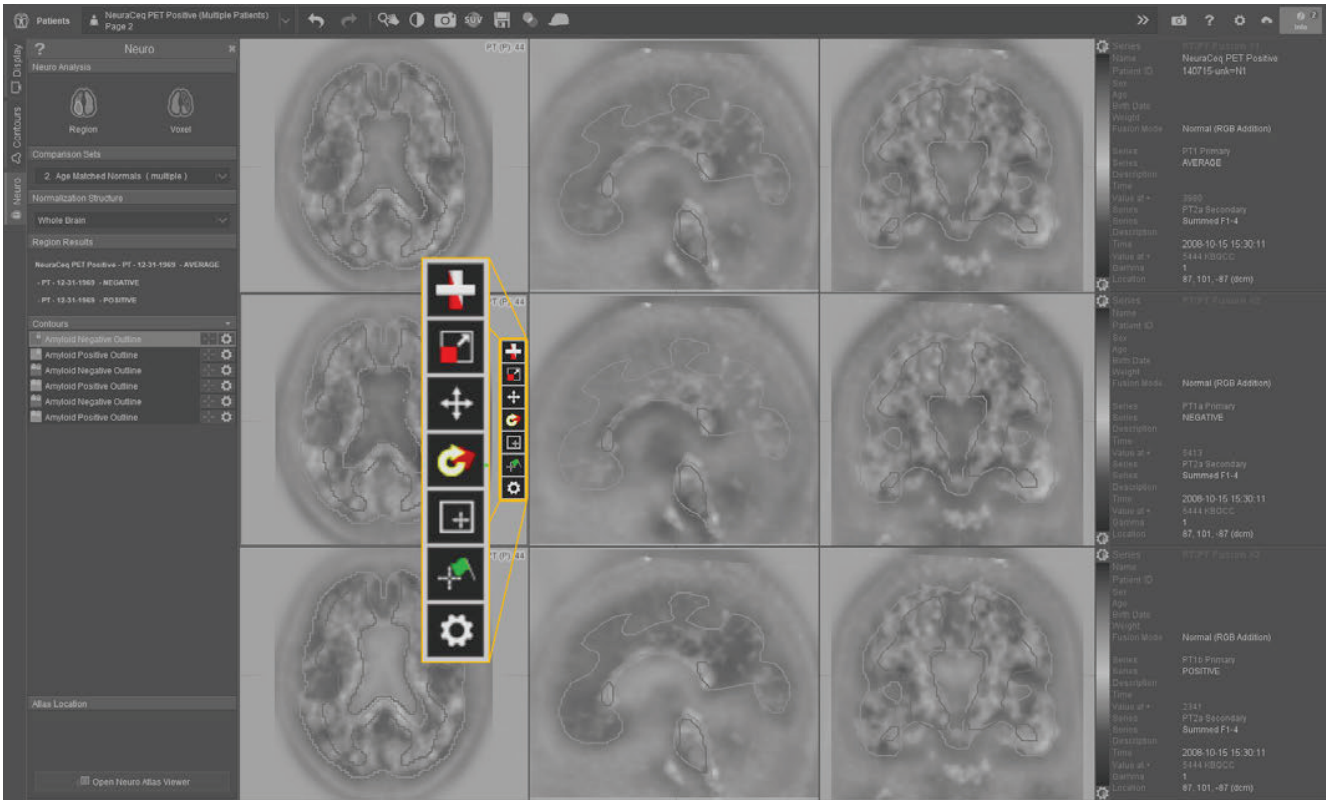
Because uptake can vary among patients, the patient image is fused to:

- The average of the negative and positive images (top row)
- A negative image in template space (middle row)
- A positive image in template space (bottom row)

Tip: Outlines derived from amyloid negative subjects and amyloid positive subjects are included for reference. The whole brain should be included in the cyan outline. The white matter should be included in the magenta outline. Refer to Registration Review below for more information.

Tip: Features in the PET image or patient anatomy can affect template registration. You may need to adjust the registration for images affected by the features described in Review Amyloid Image Quality below.

6. Use the fusion companion tools on the right side of the viewport to align the patient image to each of the three rows.



Related: Refer to Adjust Fusions Manually for more information about working with fusion tools.

7. When you have finalized the registration, click the green flag button. The workflow finishes running and creates the final page displays.

Review Results

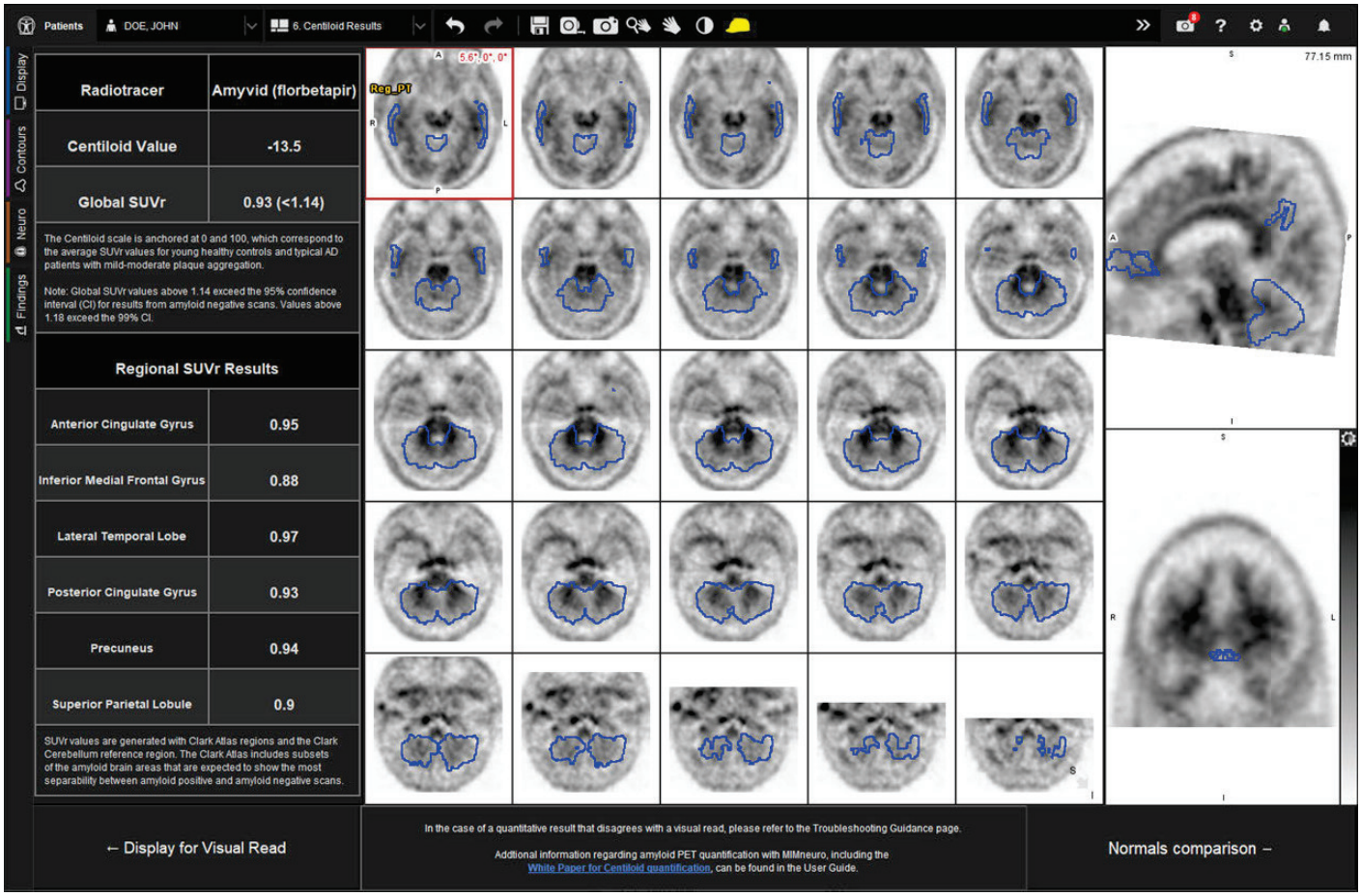
When you've finished running the workflow, review the output.

Tip: Use the left and right arrow keys or page dropdown in the top toolbar to move between pages and review results.

Caution: Quantitative results depend on several factors, including the regions and tracer used for analysis. Clinical review and interpretation is necessary to determine whether normal values are applicable to a study.

Centiloid and SUVr Results

On the Centiloid Results page, review the Centiloid value. The table includes the global SUVr, which is the average of the regional SUVr results.



Example of the Centiloid Results page.

Go to the Normals Comparison page to see how SUVr results per region compare to the reference range of mean normal values.

Z-Score Results

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 shows z-scores for the Clark atlas regions. The Clark Cerebellum is used to normalize patient values and normals values for comparison.

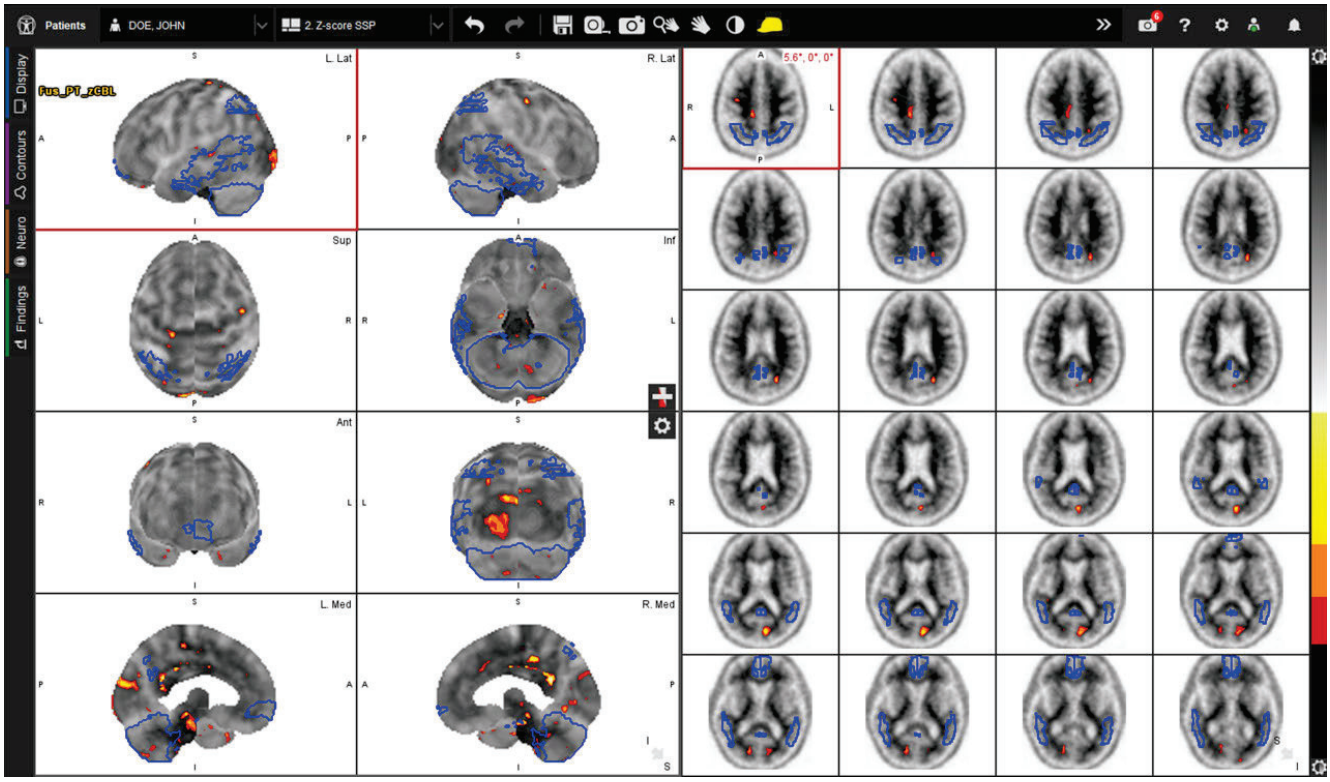
To review z-scores:

- Go to the Normals Comparison page to see a table of z-scores calculated based on the normals database.

ROI	Patient SUVr	Normal Values Mean (95% CI)	Z-score	Left Z-score	Right Z-score
Anterior Cingulate Gyrus	0.95	1.00 (0.89 - 1.12)	-0.73	-0.89	-0.48
Inferior Medial Frontal Gyrus	0.88	0.92 (0.85 - 1.00)	-0.91	-1	-0.77
Lateral Temporal Lobe	0.97	1.00 (0.91 - 1.10)	-0.56	-0.89	-0.23
Posterior Cingulate Gyrus	0.93	0.94 (0.84 - 1.04)	-0.09	0.17	-0.32
Precuneus	0.94	1.02 (0.95 - 1.10)	-1.79	0.39	-2.82
Superior Parietal Lobule	0.9	0.98 (0.89 - 1.07)	-1.51	-0.68	-2.21

- Go to the Z-score SSP page or the Z-score - ANAT Fusion page for a visual representation.
  - Red represents a lower z-score (closer to the mean).
  - Yellow represents a higher z-score (further away from the mean).

> **Tip:** Hover over the color scale on the right side of the viewport to see the z-score range represented by each color.

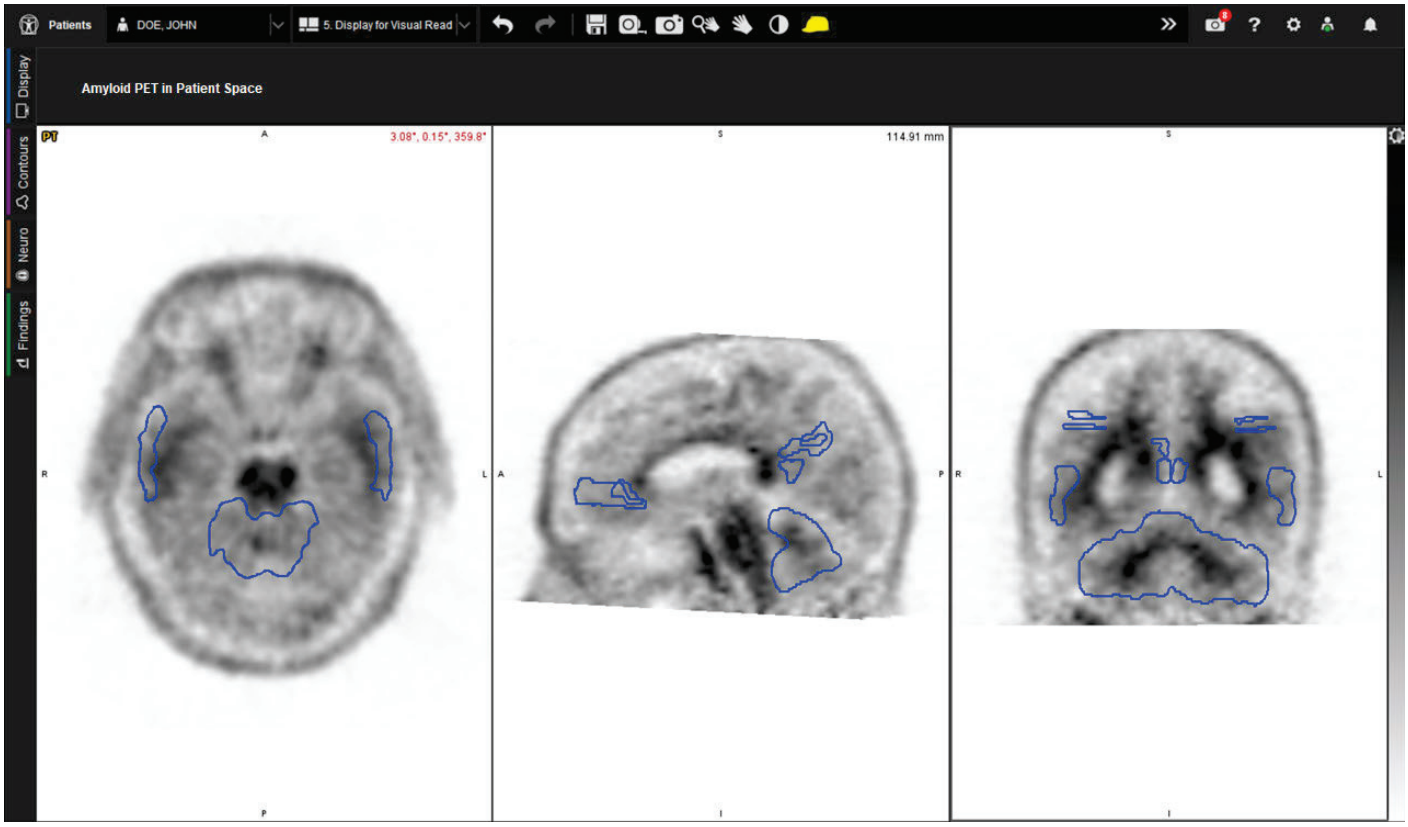


Example of the Z-score SSP page display.

Related: Refer to View Color Scales and Stereotactic Surface Projections for more information about MIMneuro® views.

Visual Read

You can use the Display for Visual Read page as you review and interpret the study. Use the instructions provided in the manufacturer's labels as you do your visual read.



Example of the Display for Visual Read page.

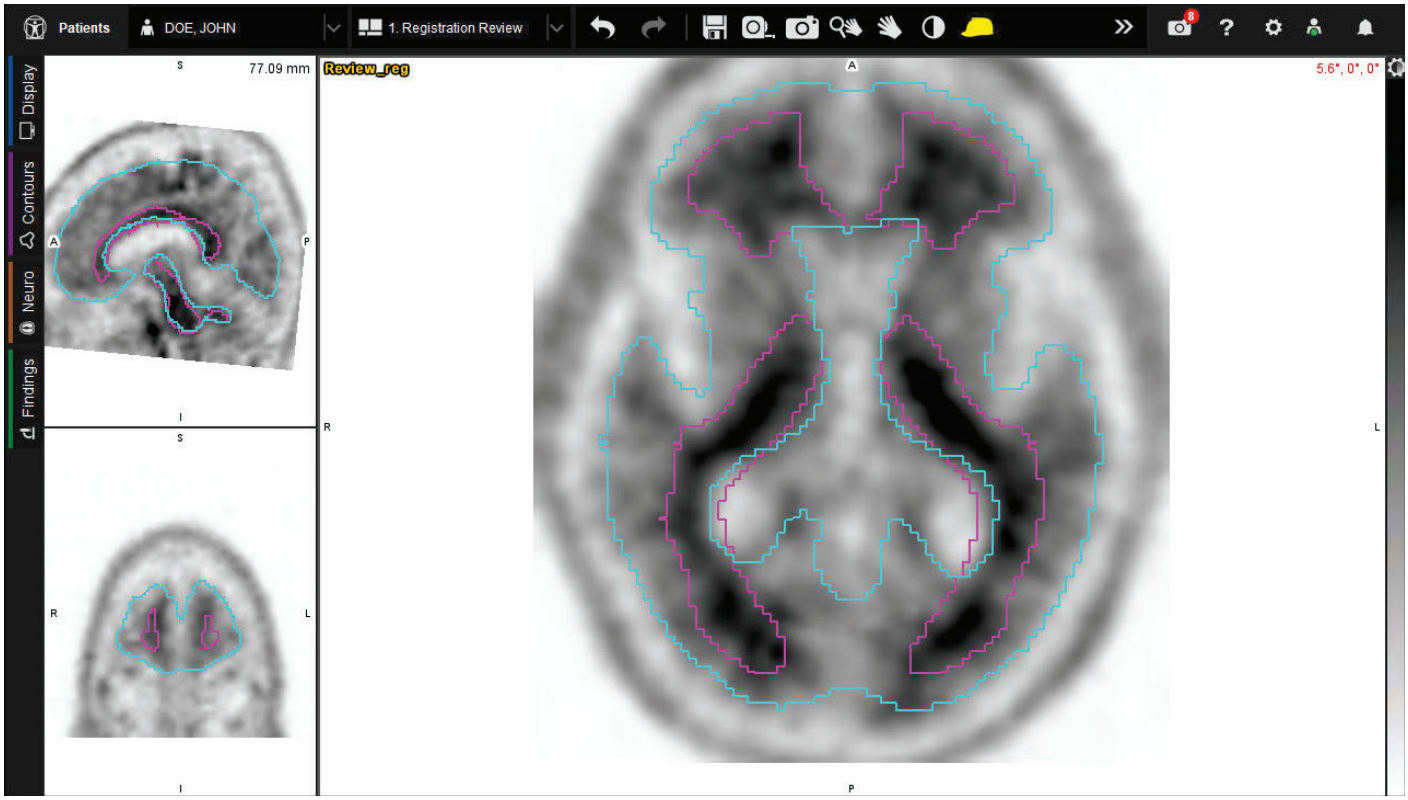
Tip: Optionally, you can enable the structure names to appear when you hover in the viewport. See Show Contour Names below for more information.

Tip: There may be several reason why your visual read differs from the quantitative results calculated by the workflow. See Troubleshoot a Disagreement with the Visual Read below for more information.

Registration Review

You can use the Registration Review page to double-check the image registration.

This page shows probabilistic white matter and gray matter contours to help you review the spatial normalization of the amyloid scan to the template. The area between the two sets of contours represents the gray matter, where an amyloid positive subject would have high uptake and an amyloid negative subject would have low uptake.



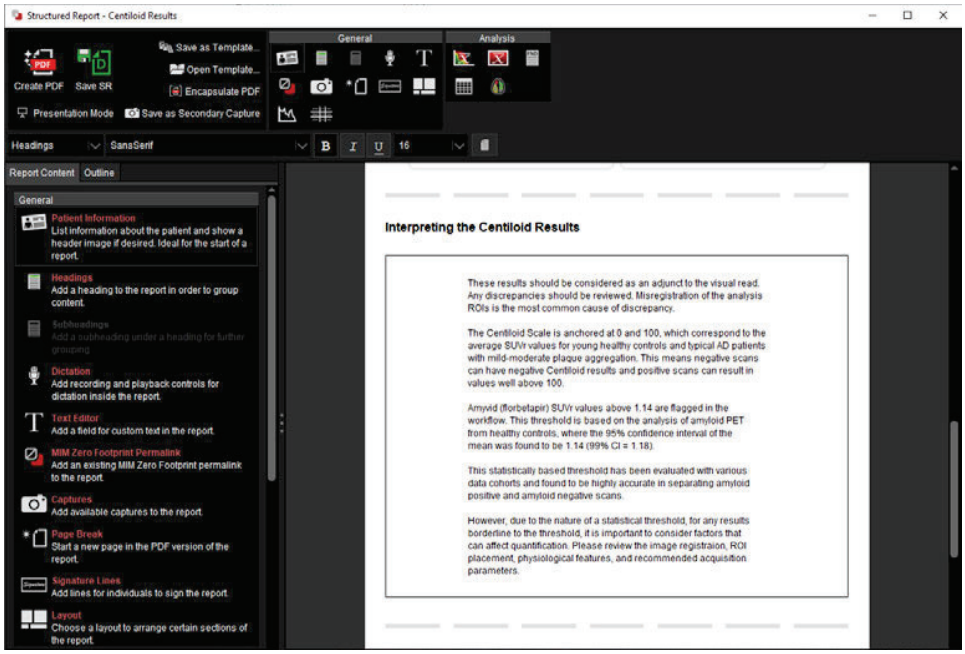
Example of the Registration Review page for a negative scan.

If the registration needs to be adjusted, close the session and relaunch the workflow. When the workflow prompts you to inspect and adjust the affine registration, adjust the registration of the image to the patient template space as needed.

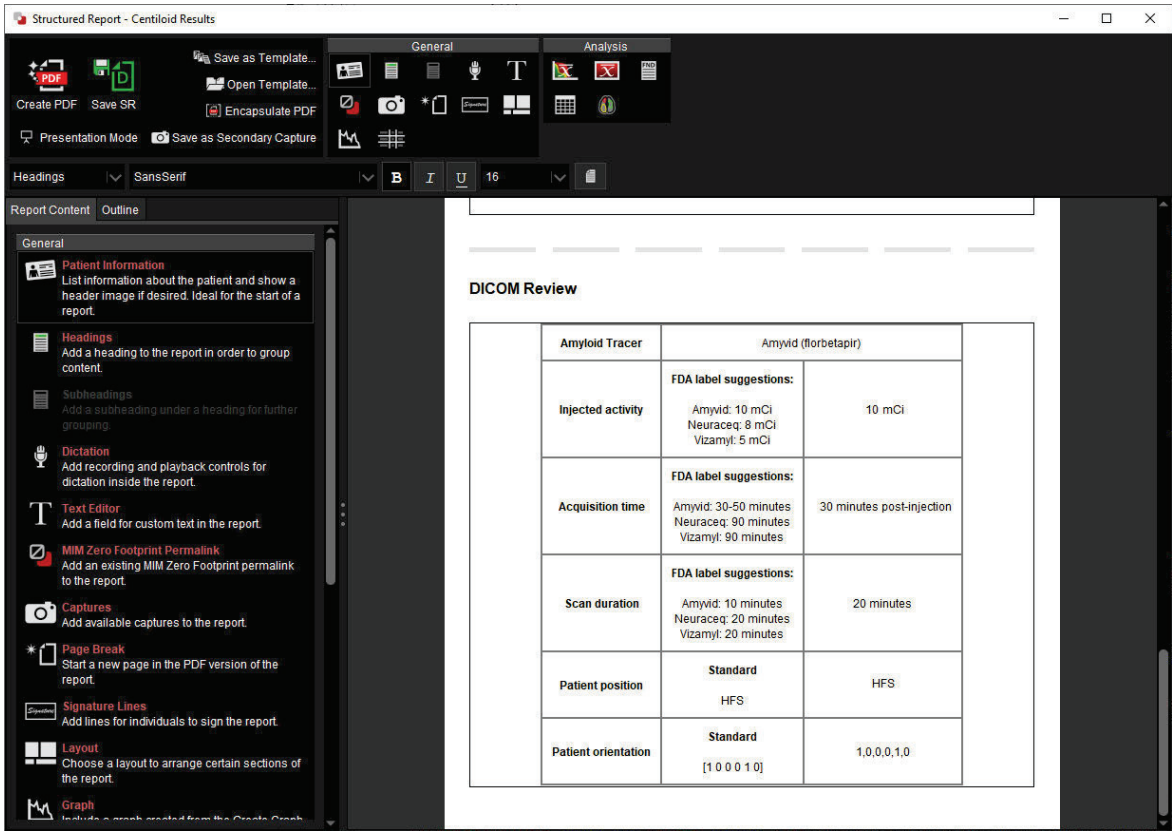
Structured Reporting

By default, the workflow creates a structured report that includes results tables and screen captures from the workflow. Additional information regarding Centiloid quantification is also provided, as well as DICOM tags for image quality review.

Click the **Create PDF** button in the upper-left corner to save the report as a PDF. Or, click the **Save SR** button to save the report as a DICOM object.



Information in the structured report about Centiloid results.

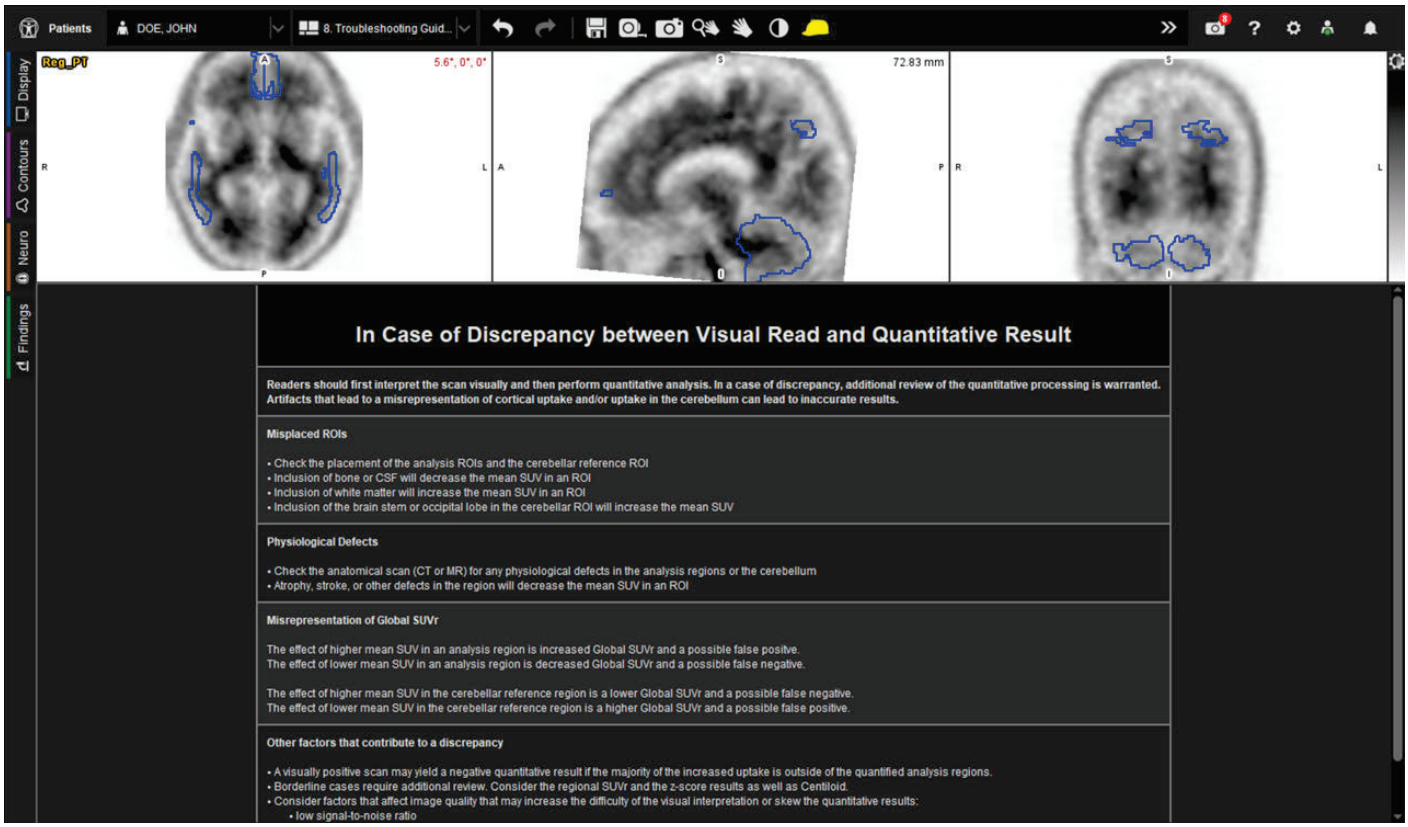


Information in the structured report showing series information from the image DICOM.

Workflow Tips and Additional Information

Troubleshoot a Disagreement with the Visual Read

If there is a discrepancy between your visual read and the quantitative results, there could be a few possible causes. Use the Troubleshooting Guide page in the workflow to review possible sources of error in the quantification or other causes of discrepancy.



Example of the Troubleshooting Guide page within the workflow results.

Review Amyloid Image Quality

Features in the PET image or patient anatomy can affect amyloid quantification. The main effect is in the template registration step. You may need to adjust the registration for an image affected by one or more of these features.

What to Look For	Details
Head position	Rotation in the axial plane can affect registration when greater than 10° in either direction. Head turning most directly affects this value; however, head tilt affects this measurement as well.
Total inclusion of the brain in the field of view	Missing brain areas affects image registration, contour placement, and, as a result, the final quantitative results. If less than 80% of the cerebellum is included, quantification results can differ up to 5% in SUVr.
Poor image quality	The following can affect quantification: • Motion artifacts • Poor gray/white matter contrast • Low signal-to-noise ratio
Physiological defects	Ventriculomegaly and severe atrophy can affect registration, contour placement, and, as a result, the final quantitative results. Stroke defects, atrophy, and other defects can affect quantification of the individual contours and/or the cerebellar reference region, which may affect the final results.
Unexpected tracer uptake	Scalp uptake can possibly affect image registration, contour placement, and, as a result, the final quantitative results.
Acquisition time	Follow manufacturer guidelines for acquisition time and scan duration when acquiring amyloid PET scans.
Radionuclide total dose	Follow manufacturer guidelines for radiopharmaceutical dosage when acquiring amyloid PET scans.

Show Contour Names

If desired, you can set the structure name to appear when you hover over the contour. Follow these steps:

1. Click the double arrow ⏩ button on the right side of the top toolbar to see all tools.
2. Search for "**toggle contour**" and select **Toggle Contour Selection in Viewport**.

3. Hover over a structure in any viewport and verify that the name appears.

Tip: Once enabled, this setting is automatically used for future sessions. If desired, you can disable it by re-selecting the same tool.

Use Results in the Workflow Output

When using the Neuro Amyloid – Centiloid Analysis workflow, the calculated results are displayed when the workflow completes, as described in Review Results above.

If you have previously used other MIMneuro® workflows, you may be familiar with using the Neuro sidebar for running calculations. The Neuro sidebar should not be used with the Neuro Amyloid – Centiloid Analysis workflow.

Region-based analysis from the Neuro sidebar produces slightly different results from what is calculated by the workflow. These differences are due to minimum contour resolution when calculating results for smaller structures.

Important: If you attempt to run region-based analysis for a Neuraceq or Vizamyl study, the Z-Score Analysis window shows the MIM Amyloid z-score list by default. You must use the dropdown at the top of the Z-Score Analysis window to change the z-score list to **Florbetapir (Clark, 2012)** instead.

Refer to the following white papers for more information about calculation:

- Standardizing Quantification of Amyloid PET Using the Centiloid Scale — Describes workflow calculations.
- Performance of a Statistically Based Centiloid Threshold Using MIMneuro — Describes how the MIMneuro Centiloid threshold was developed, along with performance data.

MIM Workflows™: Neuro Dynamic Analysis

MIMTD-1230 • 03 Jan 2024

Overview

6.1.9

The **Neuro Dynamic Analysis** workflow allows you to create up to 5 ROIs on a static PET image, which are then transferred to a dynamic PET image. The workflow calculates a time activity curve and statistics for each ROI.

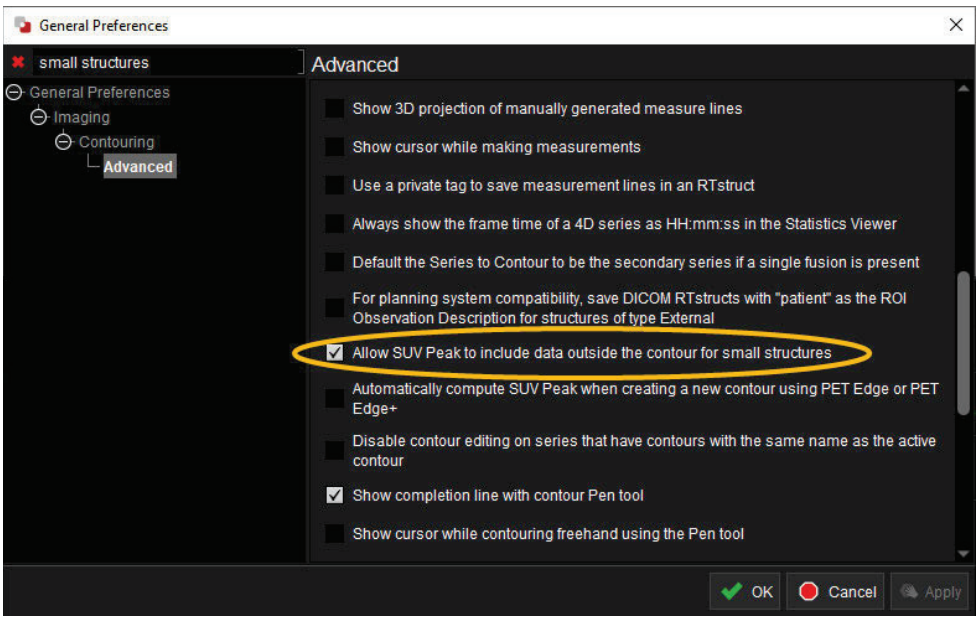
Contents

Prerequisites

Before you use this workflow, make sure that you've enabled calculations for small structures.

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

3. Select **Allow SUV peak to include data outside the contour for small structures**.



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

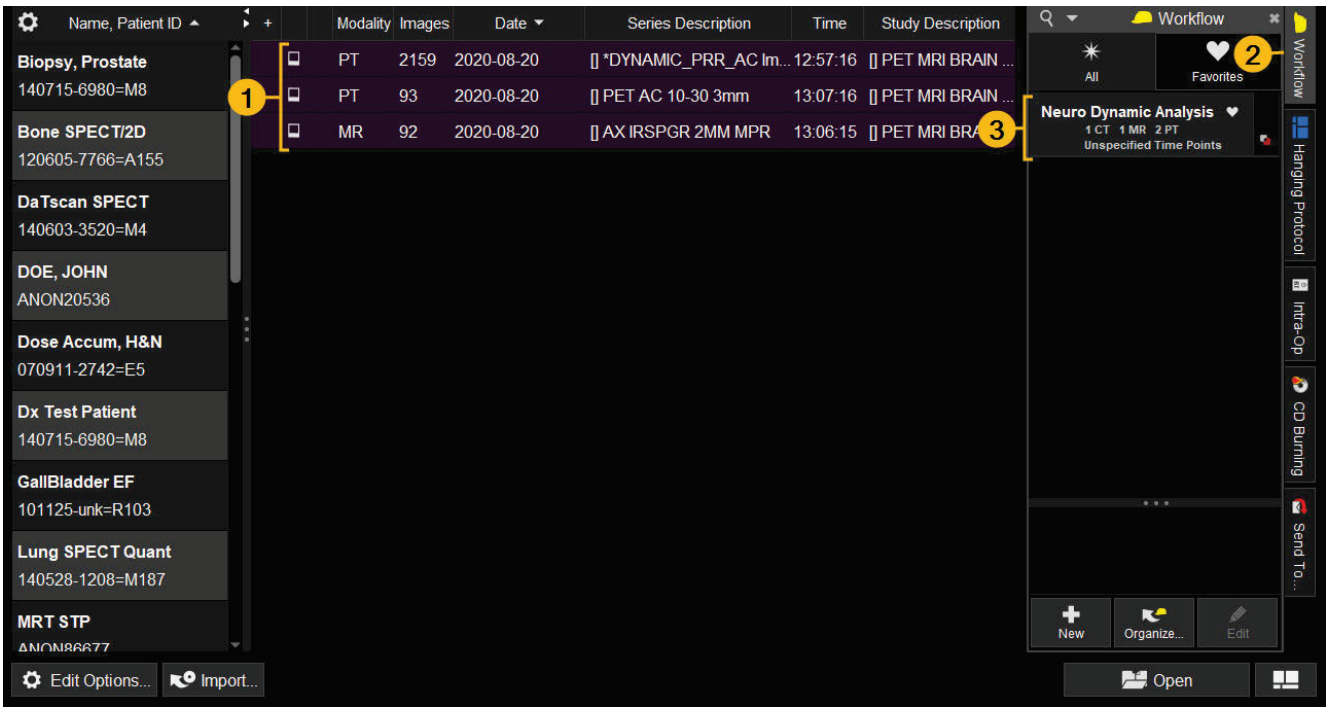
Run the Workflow

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

Launch the Workflow

1. From the patient list, select a dynamic PET and a static PET. If desired, select an optional MR or CT.
2. Select the **Workflow** tab in the patient list to expand it.

3. Double-click the **Neuro Dynamic Analysis** workflow from the list to launch it.



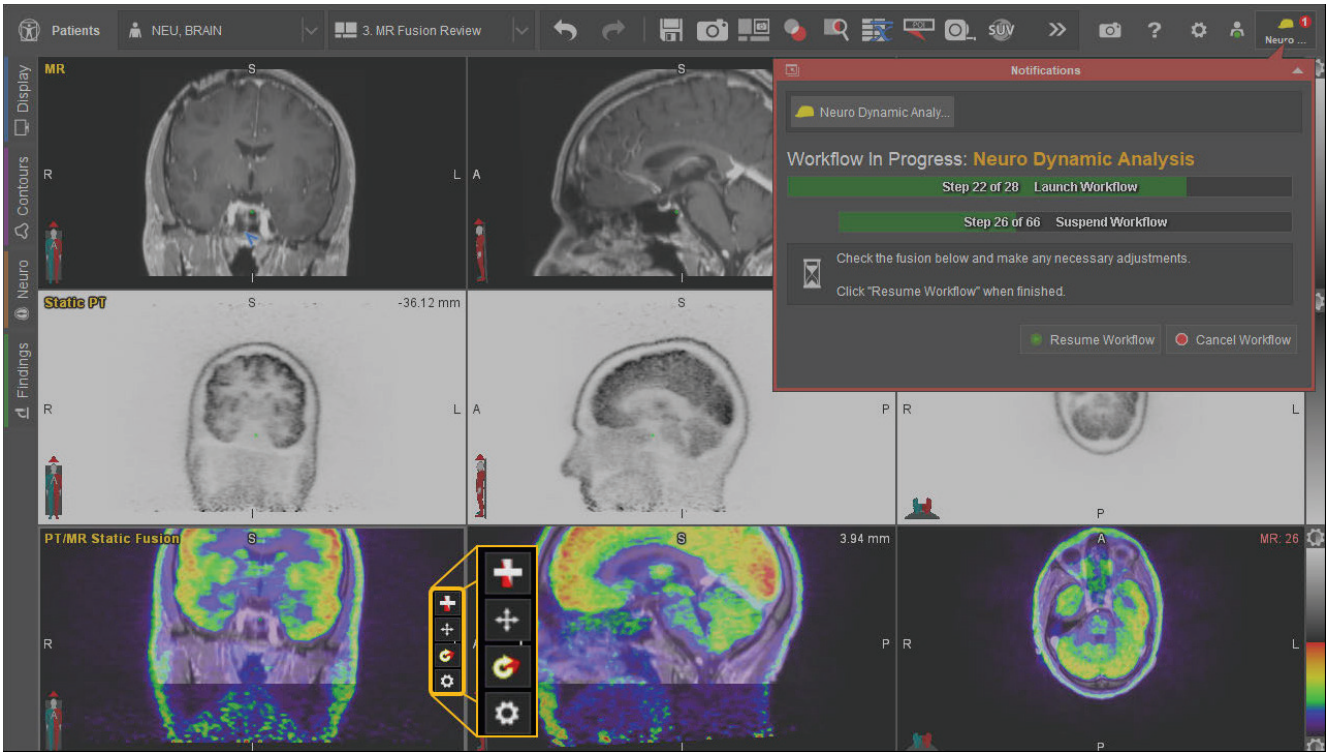
4. In the Confirm Selections window, ensure that the series are correctly assigned to the targets. If the series are not correctly assigned, click the dropdown under **Assignment** to choose the correct series for each target.
5. Click **Confirm**.

Review the Static PET Fusion

If you did not select an MR or CT, proceed to Segment the Tumors and Contralateral Side.

If you selected an MR or CT, review the fusion between the selected image and the static PET:

1. If adjustments need to be made to the image alignment, use the fusion adjustment tools to the right of the fused image.



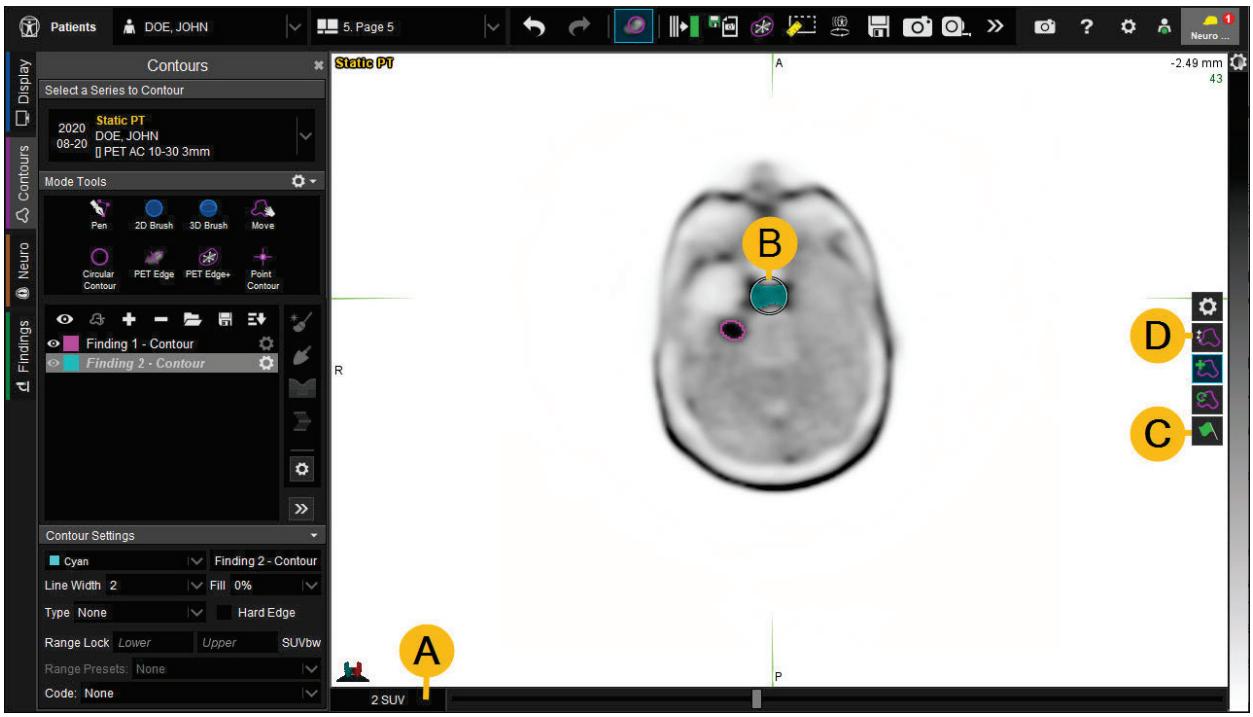
Related: Refer to Adjust Fusions Manually for more information about the adjustment tools.

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

Segment the Tumors and Contralateral Side

1. When prompted, segment up to 5 tumors on the static PET. The **Threshold** tool is activated by default:
   A. Use the slider at the bottom of the viewport to set the threshold.
   B. Move the sphere. 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. Click the green flag button on the right side of the viewport to create a contour of the area.

D. Click the new contour button to create another contour. Repeat these steps as needed.



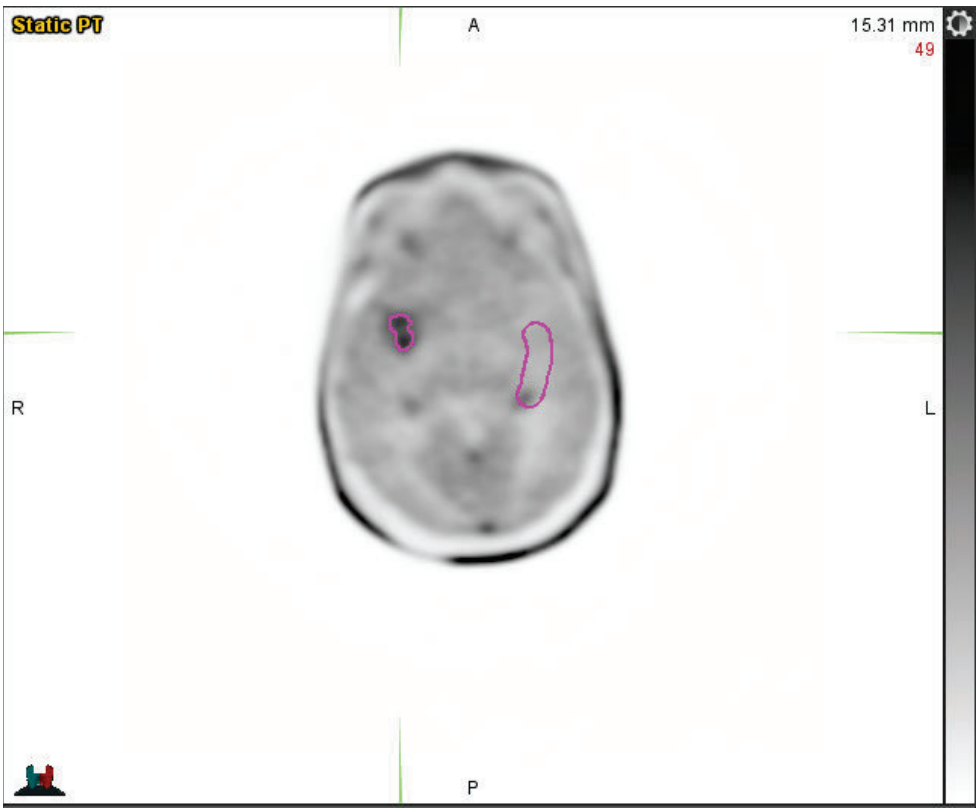
2. When you are finished, return to the Notifications window and click **Resume Workflow**.

Tip: If you selected an MR or CT when launching the workflow, you can also segment the tumors on the fusion.

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.

3. Click **Resume Workflow**.

4. Use the **3D Brush** to create a crescent-shaped contour on the contralateral side.



5. Click **Resume Workflow**.

Review the Max PET Fusion

If you did not select an MR or CT, proceed to Adjust the Dynamic Sphere ROI.

If you selected an MR or CT, review the fusion between the selected image and the max PET:

1. If adjustments need to be made to the image alignment, use the fusion adjustment tools to the right of the fused image.

> **Related:** Refer to Adjust Fusions Manually for more information about the adjustment tools.

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

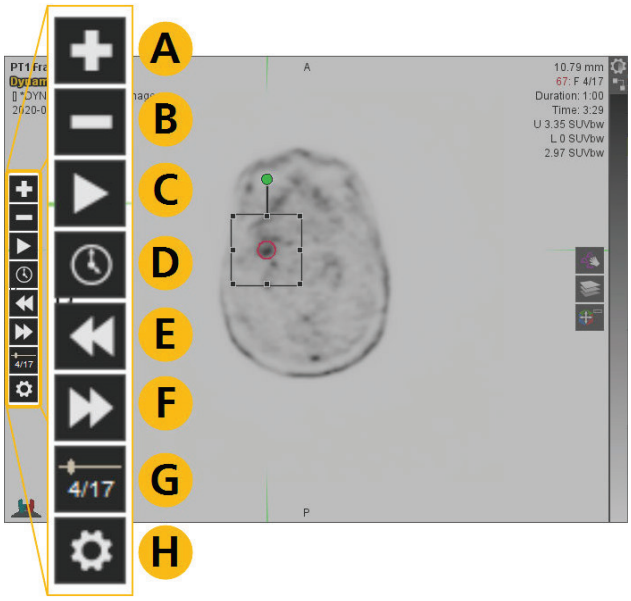
> **Tip:** The max PET is used to calculate the peak value.

3. Click **Resume Workflow**.

Adjust the Dynamic Sphere ROI

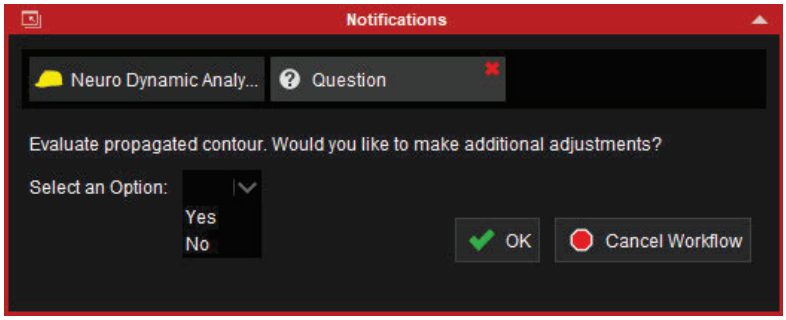
Follow these steps for each contour:

1. Use the dynamic frame tools to review the contours per frame.



A. Increase speed
B. Decrease speed
C. Play/Pause
D. Show/Hide dynamic series controls
E. Previous frame
F. Next frame
G. Current frame
H. 4D tools

2. Make adjustments per frame as desired by left-click dragging the points on the box encapsulating the tumor.
3. Click **Resume Workflow** to propagate the adjustment to subsequent frames.
4. At the prompt, choose whether to make additional adjustments:
   - Select **Yes** to make further adjustments before continuing the workflow.
   - Select **No** if you are satisfied with the adjustments and are ready to continue.



5. Click **OK**.
6. Repeat these steps as prompted in the Notifications window for each additional tumor that you contoured.

Analyze the Results

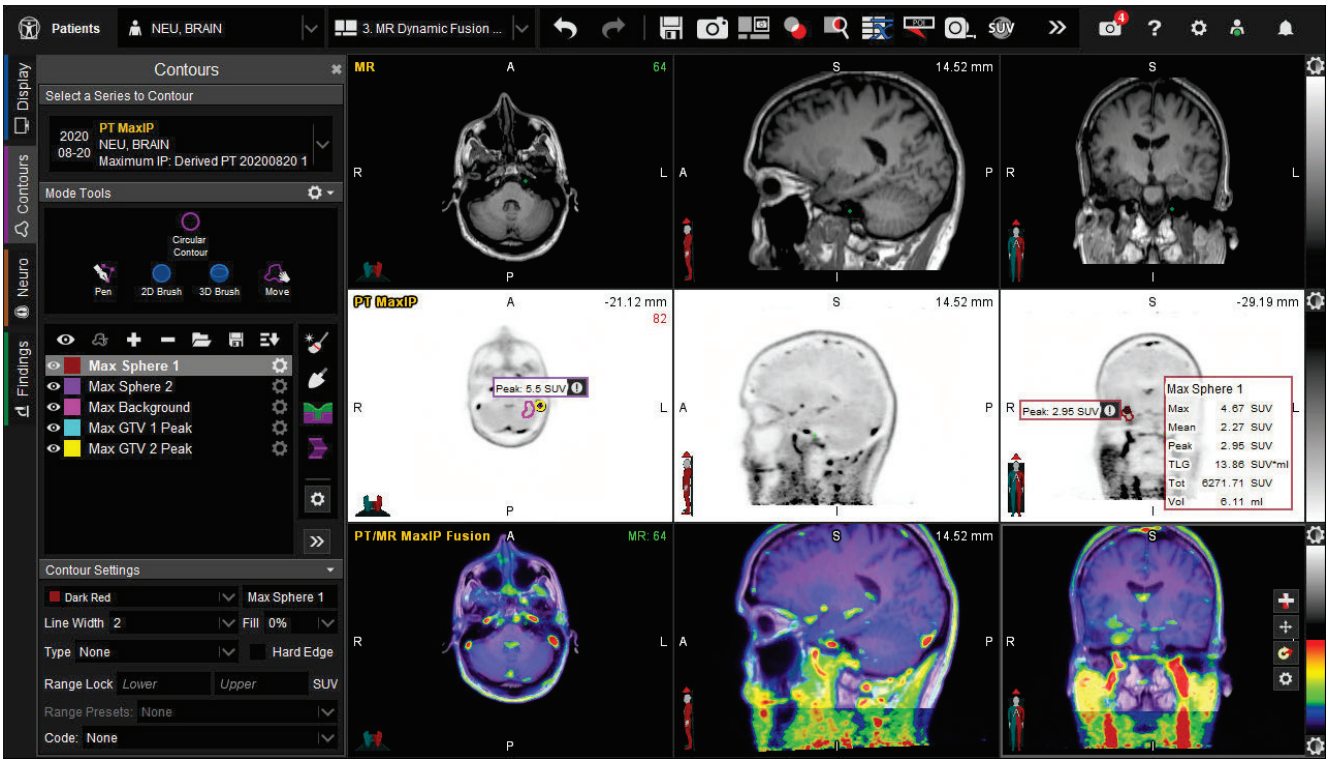
When the workflow is complete, review the image display and the results.

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

Review Displays

If you fused the PT images to a CT or MR, the workflow output includes MaxIP images.

- The middle row shows the SUV peak for each contour you drew.
- The bottom row shows the peak points projected on to a fusion image.

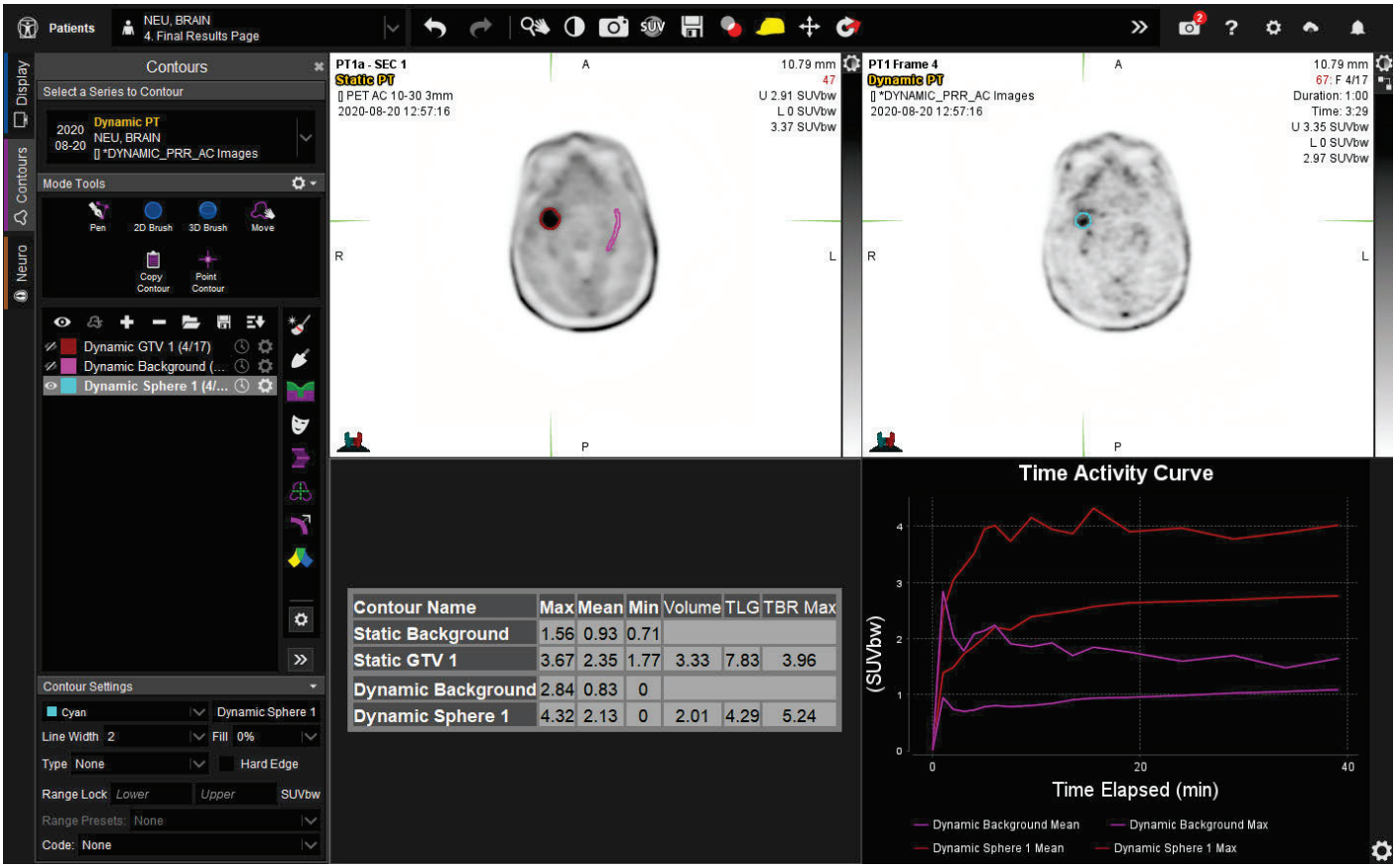


> **Tip:** If desired, click the color bar on right side of the far right viewport to choose a different color scale.

Review Results

The workflow creates the Final Results Page.

- The table shows the maximum, mean, and minimum SUV for each tumor. It also shows the volume, TLG, and TBR max values for each tumor.
- The graph shows the time activity curve color-coded for each tumor.



Contour Name	Max	Mean	Min	Volume	TLG	TBR Max
Static Background	1.56	0.93	0.71			
Static GTV 1	3.67	2.35	1.77	3.33	7.83	3.96
Dynamic Background	2.84	0.83	0			
Dynamic Sphere 1	4.32	2.13	0	2.01	4.29	5.24

Tip: Click the gear ⚙ in the lower-right corner of the graph to choose which contours to include and to save the graph.

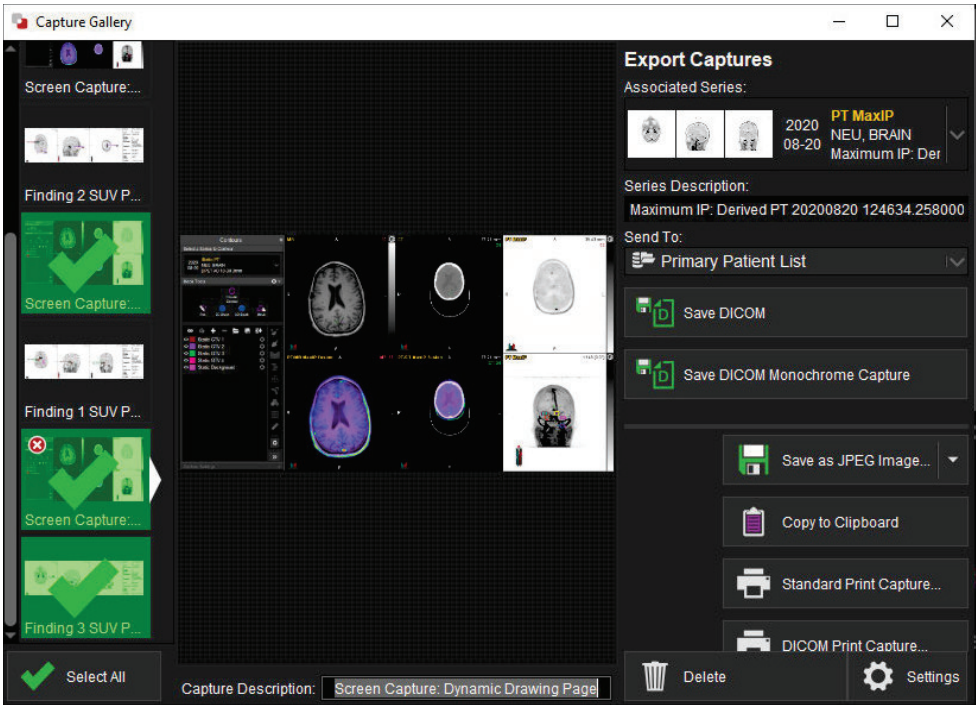
Tip: To view SUV information per frame, select the **Findings** sidebar on the left side of the screen.

Save Your Results

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

Save Your Captures

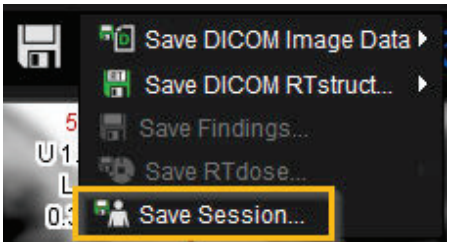
Open the Capture Gallery in the upper-right corner of MIM to save screen captures. You can send the screen captures to other physicians or store them in your PACS system for later review.



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.



MIM Workflows™: Neuro DaTscan™ — Analysis

MIMTD-828 • 22 Oct 2024

Overview

Use the **Neuro DaTscan - Analysis** workflow with DaTscan studies. This workflow uses the DaTscan atlas to perform region-based analysis.

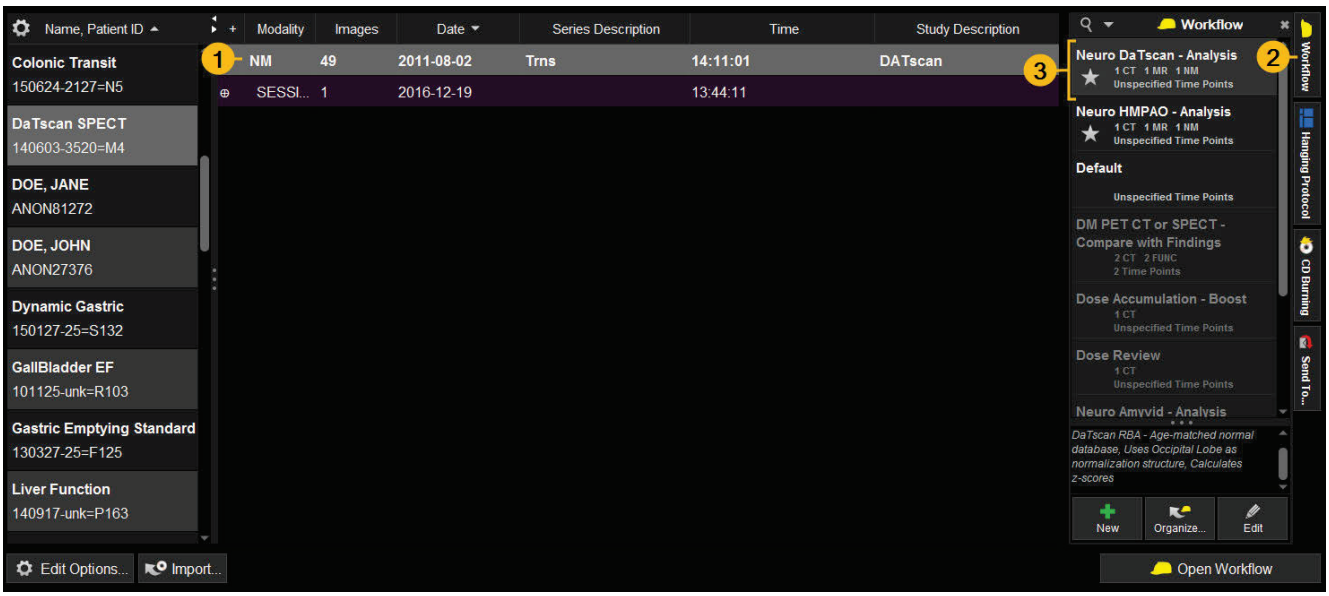
Related: Refer to Review Region-Based Analysis for more information about MIMneuro® processing.

Contents

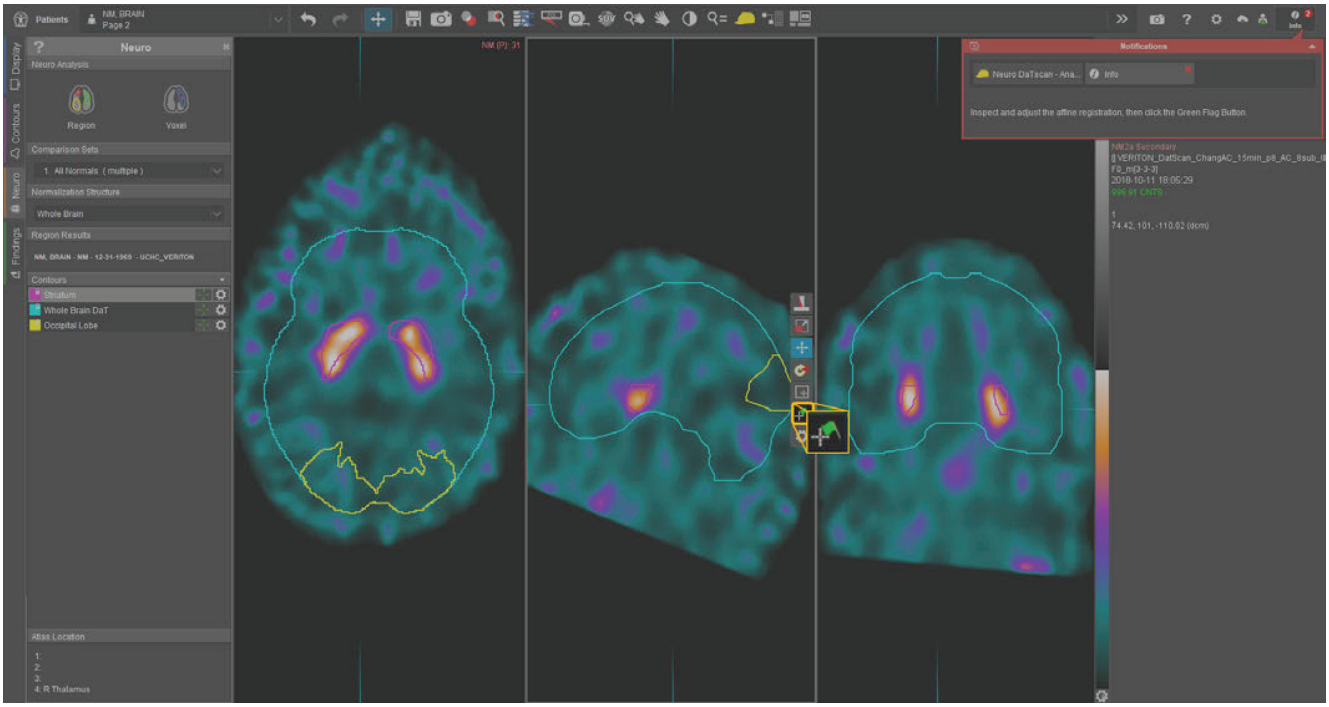
Run the Workflow

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.

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

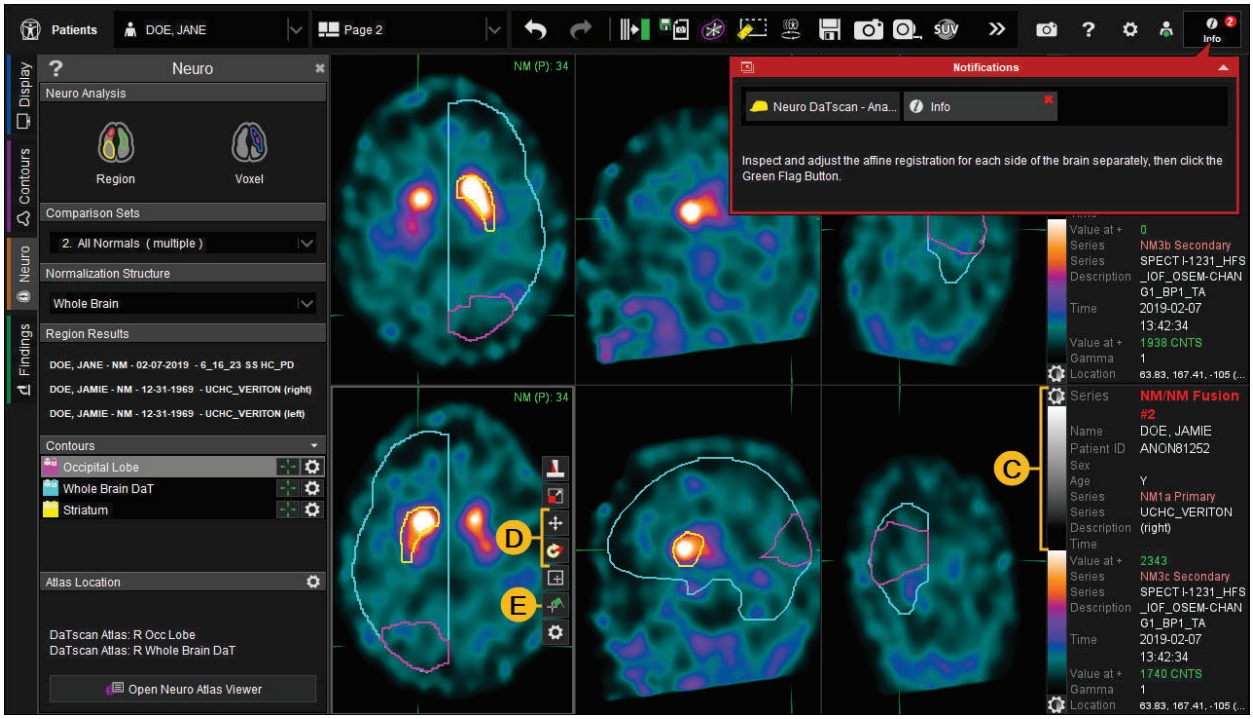


4. The workflow performs an affine registration between your SPECT series (secondary series) and the template space (primary series). Check the registration to make sure it aligns as accurately as possible. Pay special attention to the alignment of the occipital lobe at this step. When you are ready, click the green flag button to continue.



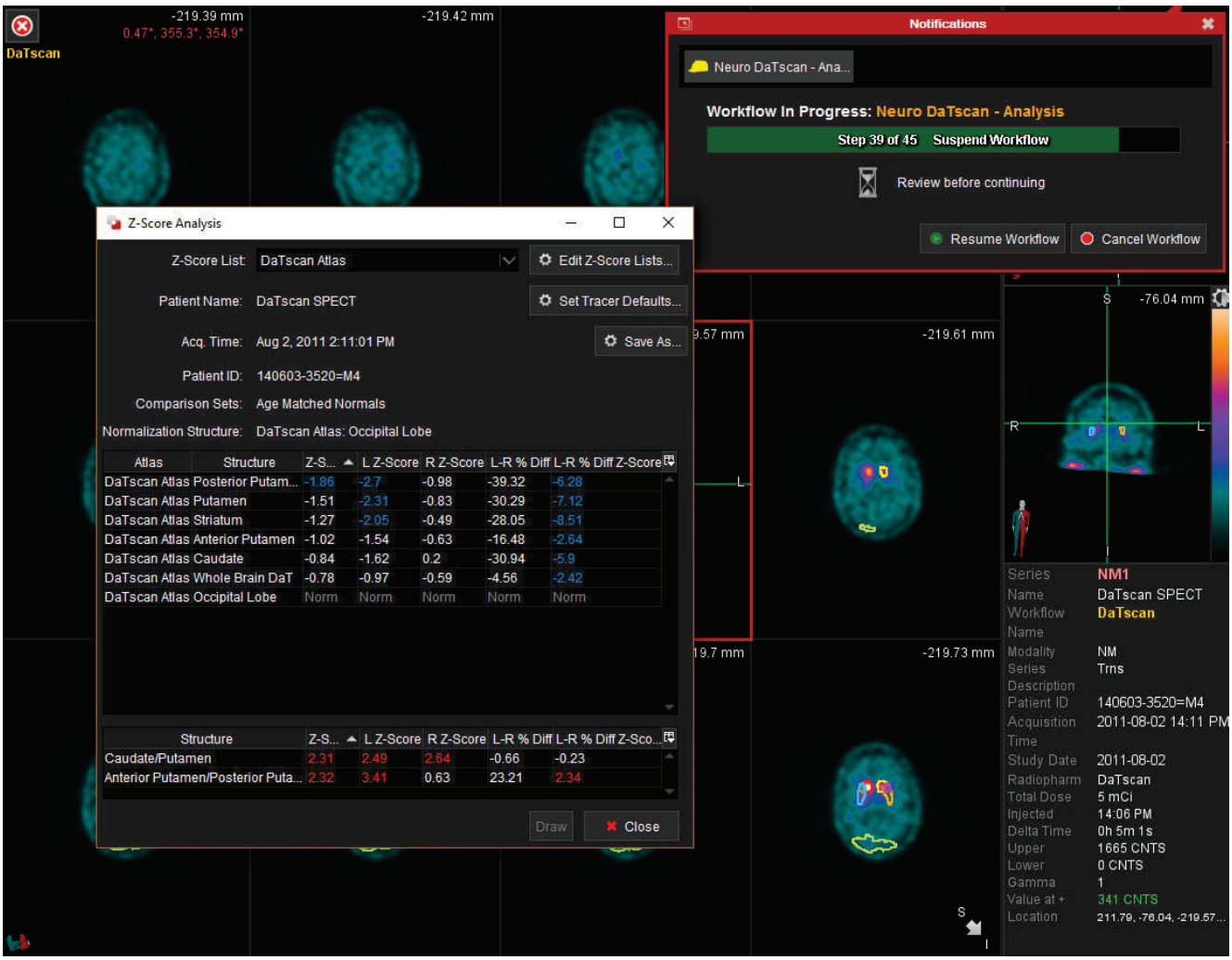
Tip: If adjustments are necessary, use the tools to the right of the image to correct the alignment. See Adjust Affine Registrations for more information.

5. 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.
   A. Localize to the Striatum contour by clicking in the head of the caudate, for both the left caudate and right caudate.
   B. Check that the activity in the striatum, especially in the caudate, is centered on both hemispheres.
   C. If needed, adjust the contrast of the image to better visualize the activity.
   D. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See Adjust Affine Registrations for more information.
   E. When you are ready, click the green flag button to continue.



6. The workflow begins region-based analysis and then pauses when the Z-Score Analysis window opens. See more information about z-scores below. When you are finished reviewing the z-scores,

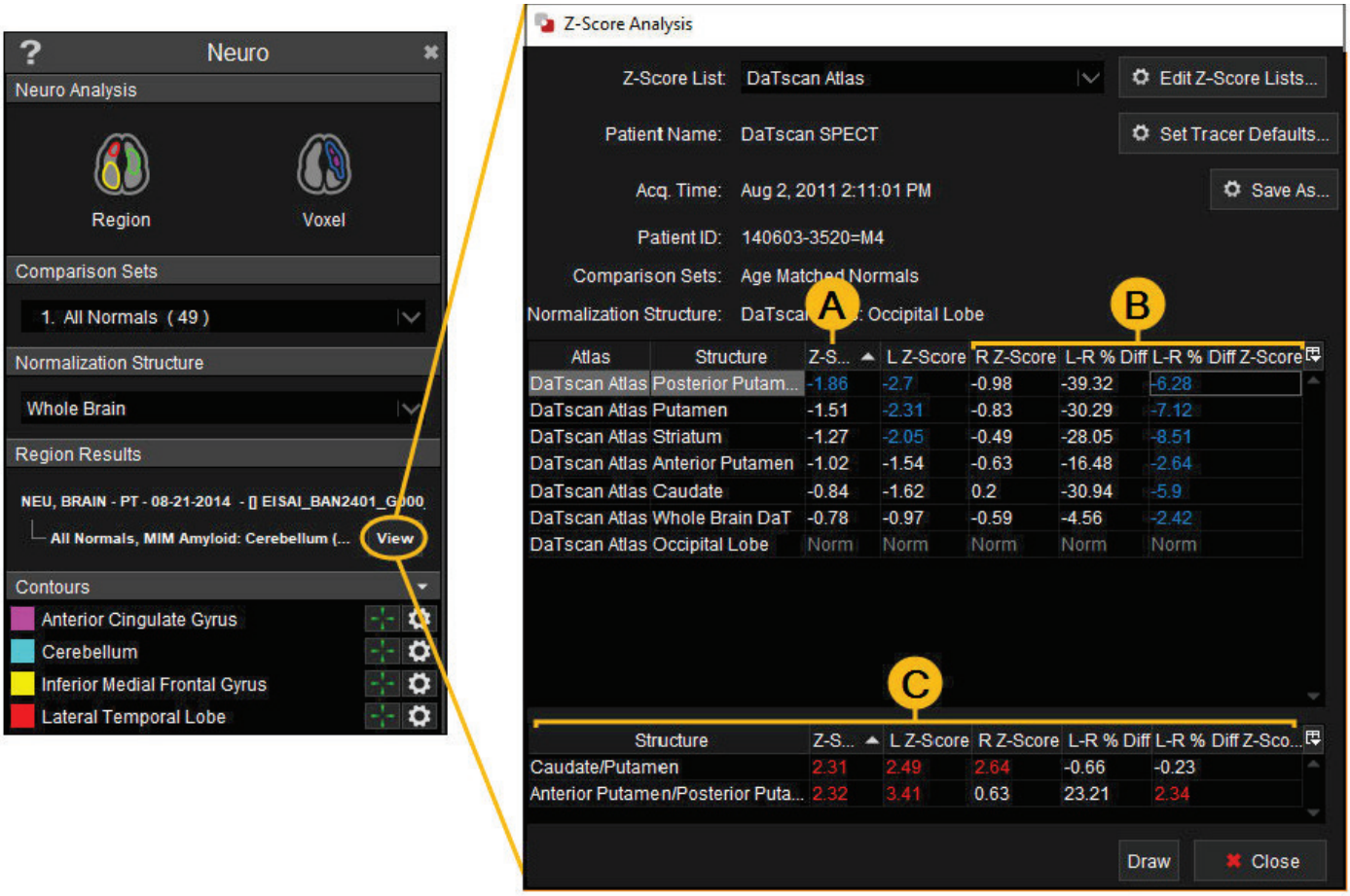
click **Resume Workflow** to continue.



7. The workflow finishes running and saves a session to your patient list.

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.



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.

- *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.

C. View the ratio scores. The ratio indicates the relative difference in uptake of a posterior structure (e.g., putamen) compared to an anterior structure (e.g., caudate). If the putamen had a decrease in uptake relative to the caudate, the result is a larger ratio value.

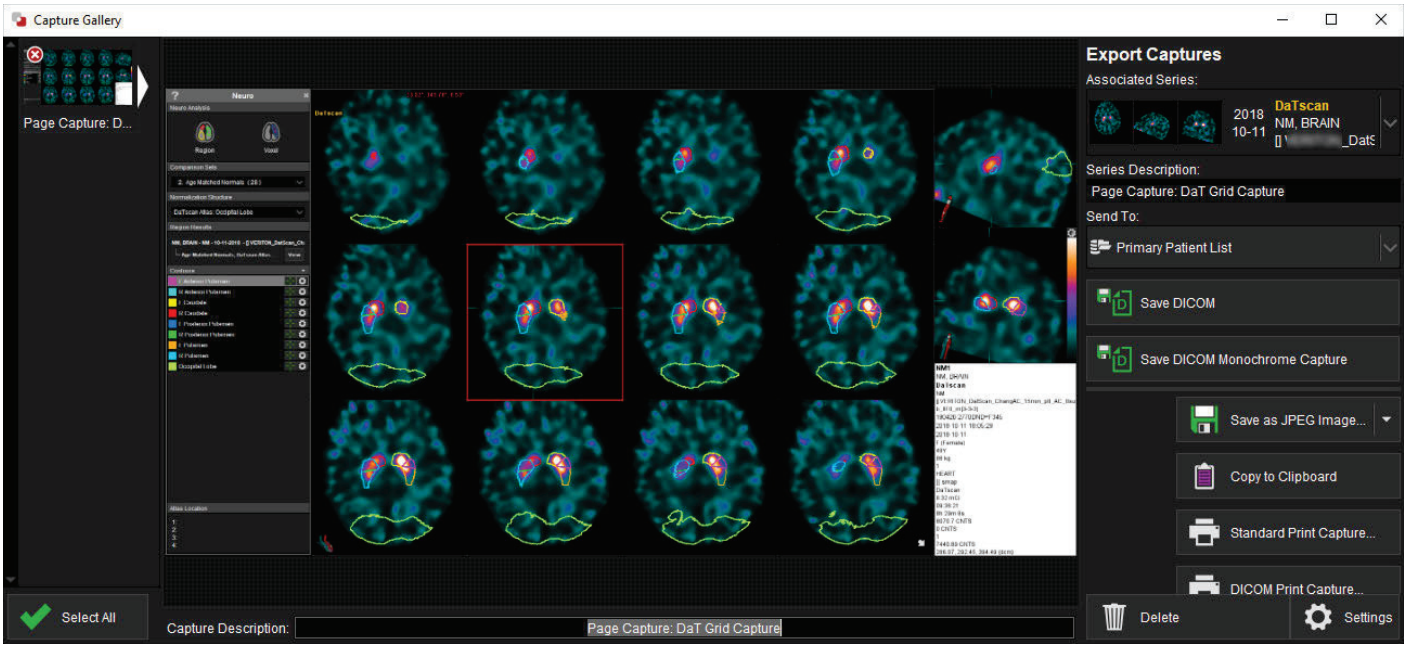
Related: Refer to Review Results in the Z-Score Analysis Window for more information about the Z-Score Analysis window.

Save the 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.

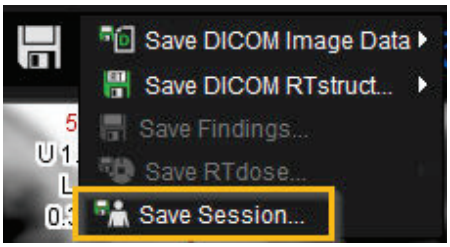


Refer to Create and Save Secondary Captures for more information about creating and saving captures.

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 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 DaTscan™ — SPECT Reconstruction

MIMTD-836 • 18 Dec 2023

Overview

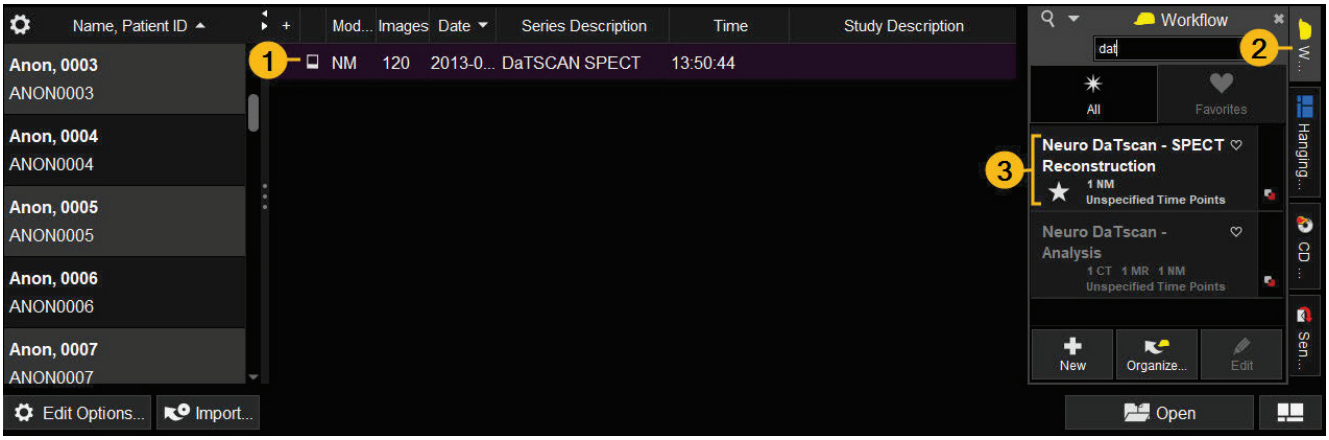
Use the **Neuro DaTscan - SPECT Reconstruction** workflow for raw SPECT series for DaTscan studies. This workflow reconstructs the series into an image that can be used for analysis.

Important: This workflows requires a SPECTRA Recon® license in addition to a MIMneuro® license.

Related: Refer to MIM Workflows™: Neuro DaTscan™ — Analysis if your image has been reconstructed and you are ready for analysis.

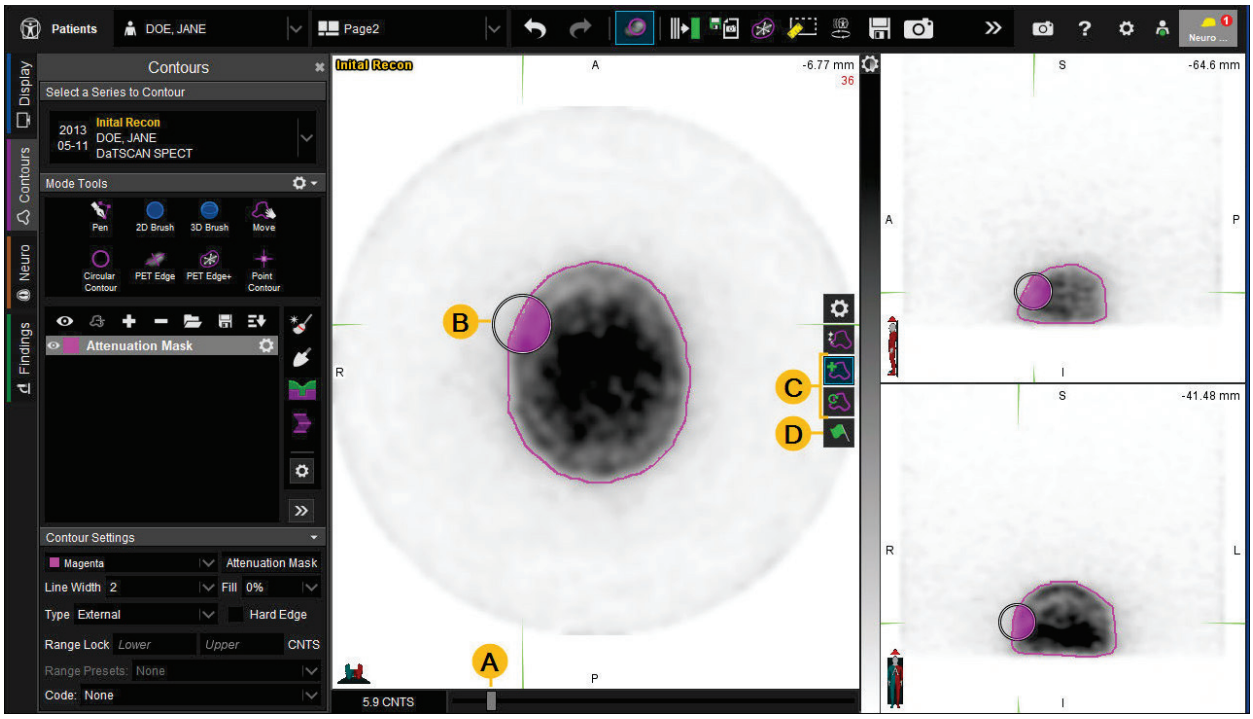
Run the Workflow

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



Tip: This workflow does most of its processing in the background with limited user interaction.

4. When prompted, review the region to be used for attenuation correction (Chang's method). 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.

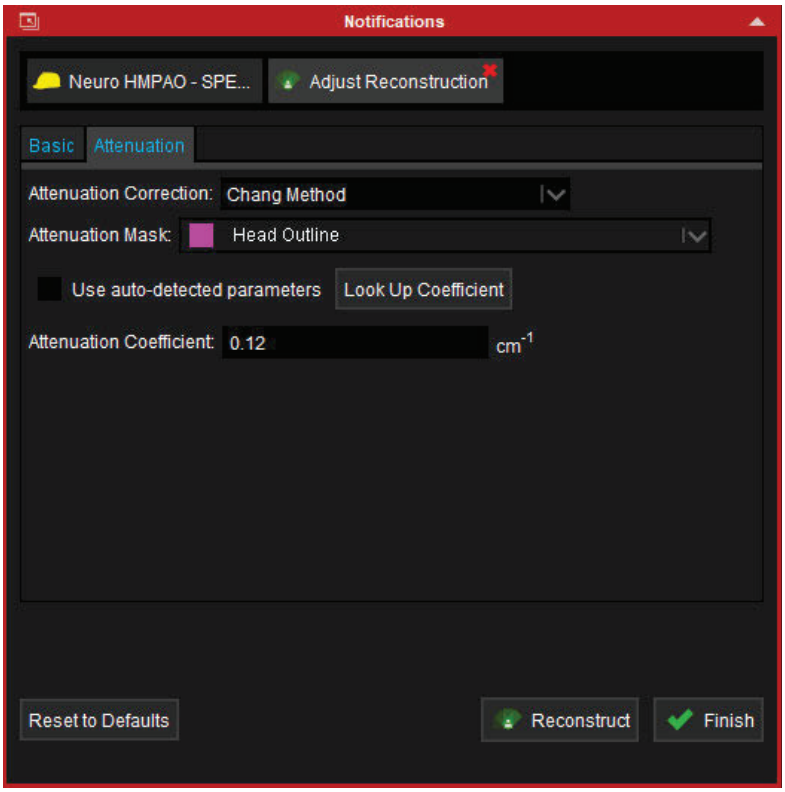


Related: See Create Contours with the Threshold Tool or click the question mark in the upper-right corner of MIM for more information on using the Threshold tool.

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

5. 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.

6. 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 DaTscan analysis workflow. Select the saved series from the patient list and run the Neuro DaTscan - Analysis workflow. Refer to MIM Workflows™: Neuro DaTscan™ — Analysis for more information.

MIM Workflows™: Neuro FDG — Analysis

MIMTD-829 • 15 Mar 2024

Overview

Use the **Neuro FDG - Analysis** workflow for neuro FDG studies. This workflow performs both voxel-based analysis and region-based analysis. 6.1.8

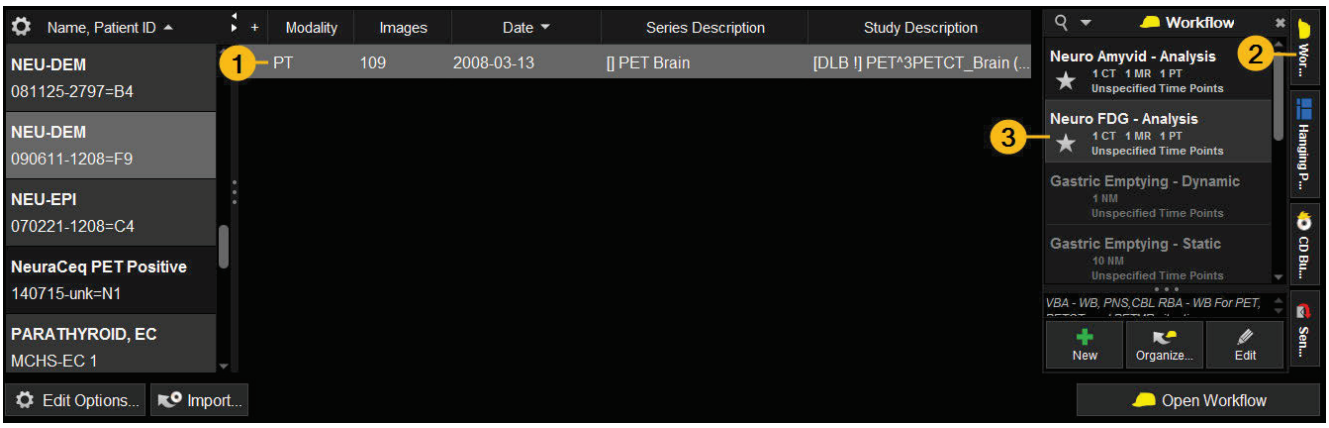
MIM 7.3.6 and later: If your organization is using high-resolution digital PET cameras, you can run this workflow with digital FDG normals. Contact your MIM Site Development Manager or MIM Software Support at support.mimsoftware.com if you are interested in using digital normals. *MIM 7.3.5 and earlier:* This functionality is not available.

Contents

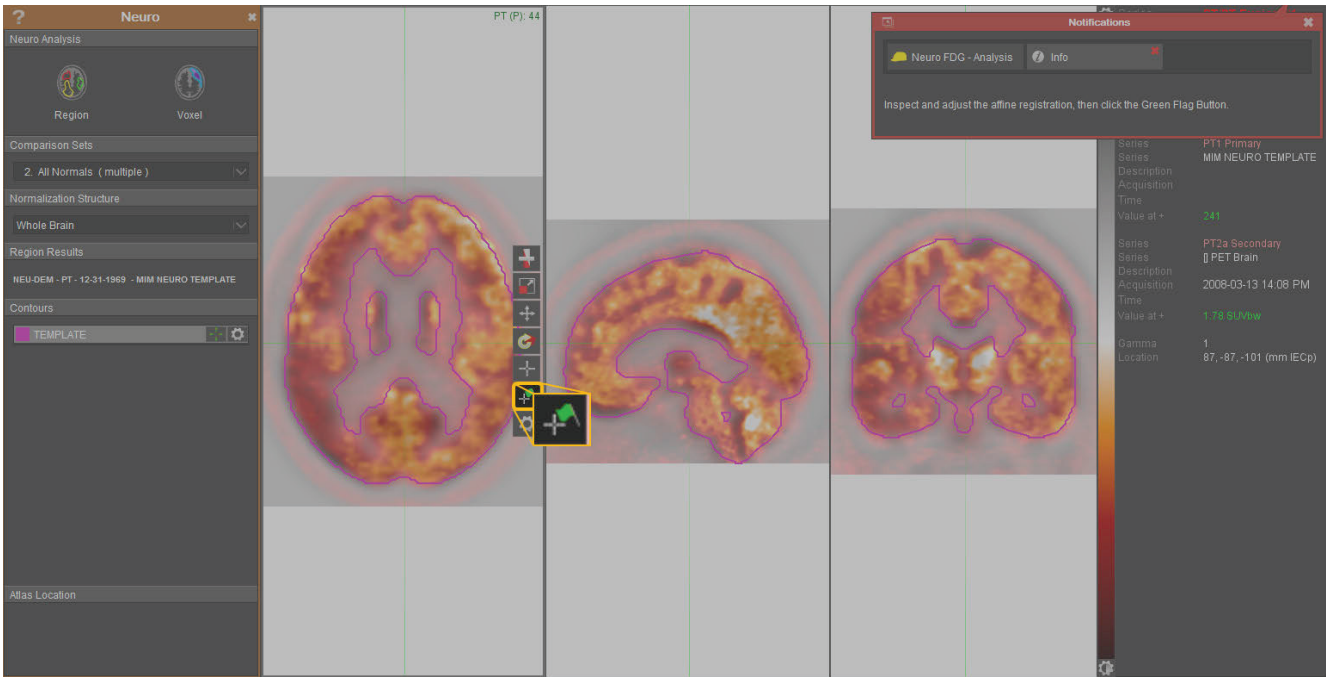
Run the Workflow

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 FDG — Analysis** workflow from the list to launch it.



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

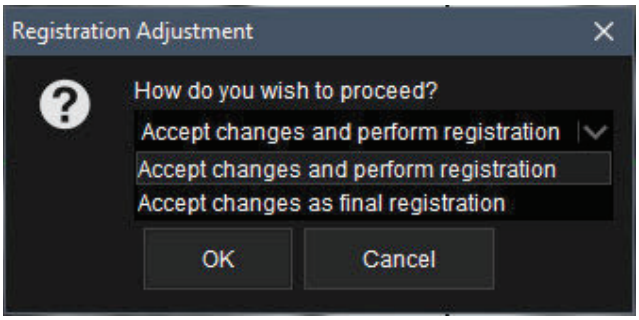


Tip: Affine registrations rarely require adjustment. If adjustments are necessary, use the tools to the right of the image to correct the alignment. See Adjust Affine Registration for more information.

5. After verifying the registration, the **Registration Adjustment** window appears and asks you how you would like to proceed:

- **Accept changes and perform registration** performs a deformable registration. The deformable registrations uses the affine registration, including any adjustments you have made, as a starting point.
- **Accept changes as final registration** proceeds with processing, using the current alignment.

Select the appropriate option from the dropdown and then click **OK**.



6. 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 Brain 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 PET brain.
  - Row 2 displays the z-score results fused to the stereotactic surface projections (SSPs) of the PET brain normalized to the whole brain.
  - Row 3 displays the z-score results fused to the SSPs of the PET brain normalized to the pons.
  - Row 4 displays the z-score results fused to the SSPs of the PET brain normalized to the cerebellum.
- **Whole Brain 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 whole brain.
- **Pons 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 pons.