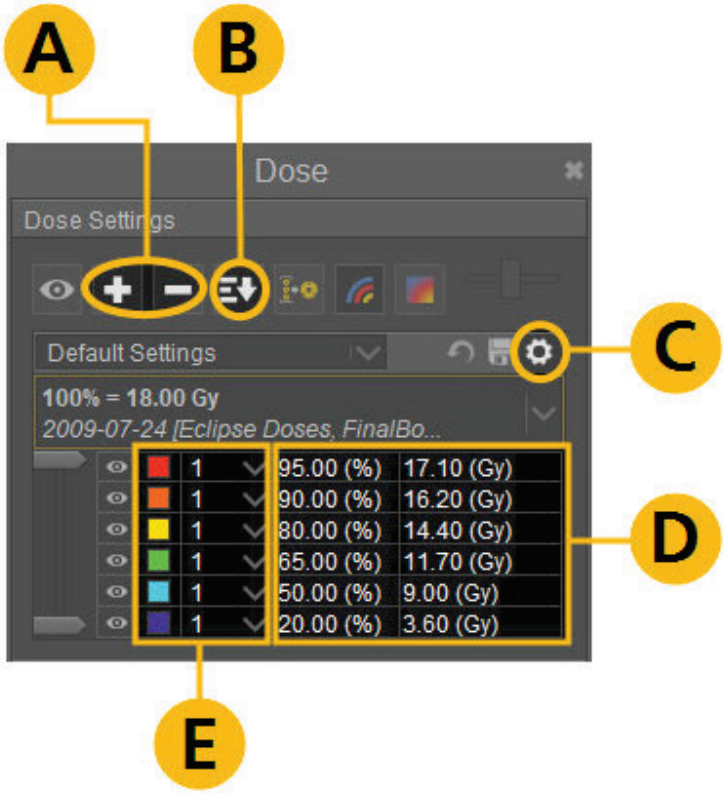


A. To add or delete lines, use the add ✚ and delete ▬ buttons.

B. *MIM 7.2 and later:* To sort the isodose lines, use the sort button.
MIM 7.1 and earlier: Isodose lines are sorted from high to low automatically.

C. To customize a variety of other dose display settings, click the gear ⚙ button in the Dose sidebar. From the gear ⚙ menu, you can:

- *MIM 7.3 and later:* Choose whether doses are displayed as **Absolute Dose and % Normalization Value** or **Absolute Dose Only**.
- *MIM 7.2 and earlier:* Choose whether doses are displayed as **Absolute Dose and % Rx Value** or **Absolute Dose Only**.

Tip: In MIM 7.2 and earlier, "normalization value" was known as "Rx dose" or "prescription dose." A normalization value may be a prescription dose, max dose, or user-entered value. Therefore, in MIM 7.3 and later, "Rx dose" and "prescription dose" were changed to "normalization dose" to be inclusive of all possibilities.

- Create a set of isodose lines based on a maximum and minimum value
- Space isodose lines uniformly
- Manage your isodose settings
- Choose whether to display a key to isodose line values in the viewports
- Choose whether to display dose values on isodose lines
- Apply a color table to your isodose lines

D. To enter a new value for a line, click inside a % or Gy cell in the table.

E. To change the color for an isodose line, click the colored square. To change the line thickness, use the dropdown menu.

Tip: If needed, use the undo button at the top of MIM to undo a single change. Or, use the revert button in the **Dose** sidebar to undo all changes you've made to the current isodose setting.

4. Click the Save button next to the setting name.
5. Select **Save Isodose Setting...**.
6. In the Isodose Setting Name window, enter a name for the new isodose setting.
7. Click **OK**.

If you would like to update an existing setting, instead of creating a new setting, follow steps 1-3 above. Then, click the Save button and choose **Overwrite Isodose Setting (*Setting Name*)**.

Default Isodose Setting

When you change the isodose setting selected in the Dose sidebar, MIM automatically makes that setting the default setting. To change this behavior:

1. Click the Settings button in the upper-right corner of MIM.
2. In the Settings menu, select **General Preferences**.
3. In the General Preferences window, search for "**dose**" and select **Dose** from the menu on the left side of the window.
4. On the Dose page, deselect **Automatically update the default isodose setting when the isodose setting in the Dose sidebar changes**.
5. Click **Apply**.

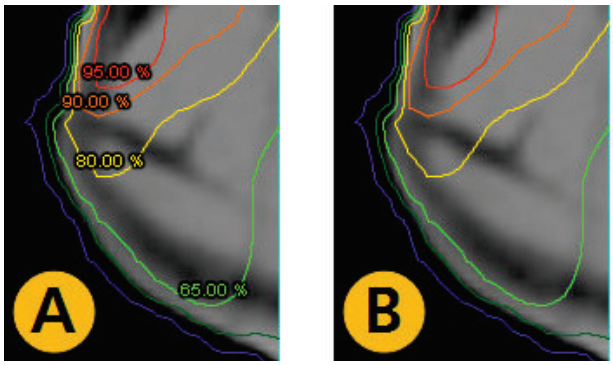
Then, set a default isodose setting using the **Default Isodose Setting** and/or **Default Brachy Isodose Setting** dropdowns.

Additional Isodose Preferences

Dose Values Displayed on Series

If desired, you can hide the values displayed on isodose lines on the series.

- To always hide the values:
  1. Click the Settings button in the upper-right corner of MIM.
  2. In the Settings menu, select **General Preferences**.
  3. In the General Preferences window, search for "**dose**" and select **Dose** from the menu on the left side of the window.
  4. On the Dose page, deselect **Dose values on isodose lines**.
  5. Click **OK** to save your change and close the window.
- To hide the values in a session, click the gear button in the upper-right corner of the Dose sidebar and deselect **Dose values on isodose lines**.



A. Dose values displayed on isodose lines
B. No dose values displayed on isodose lines

Color Wash Display

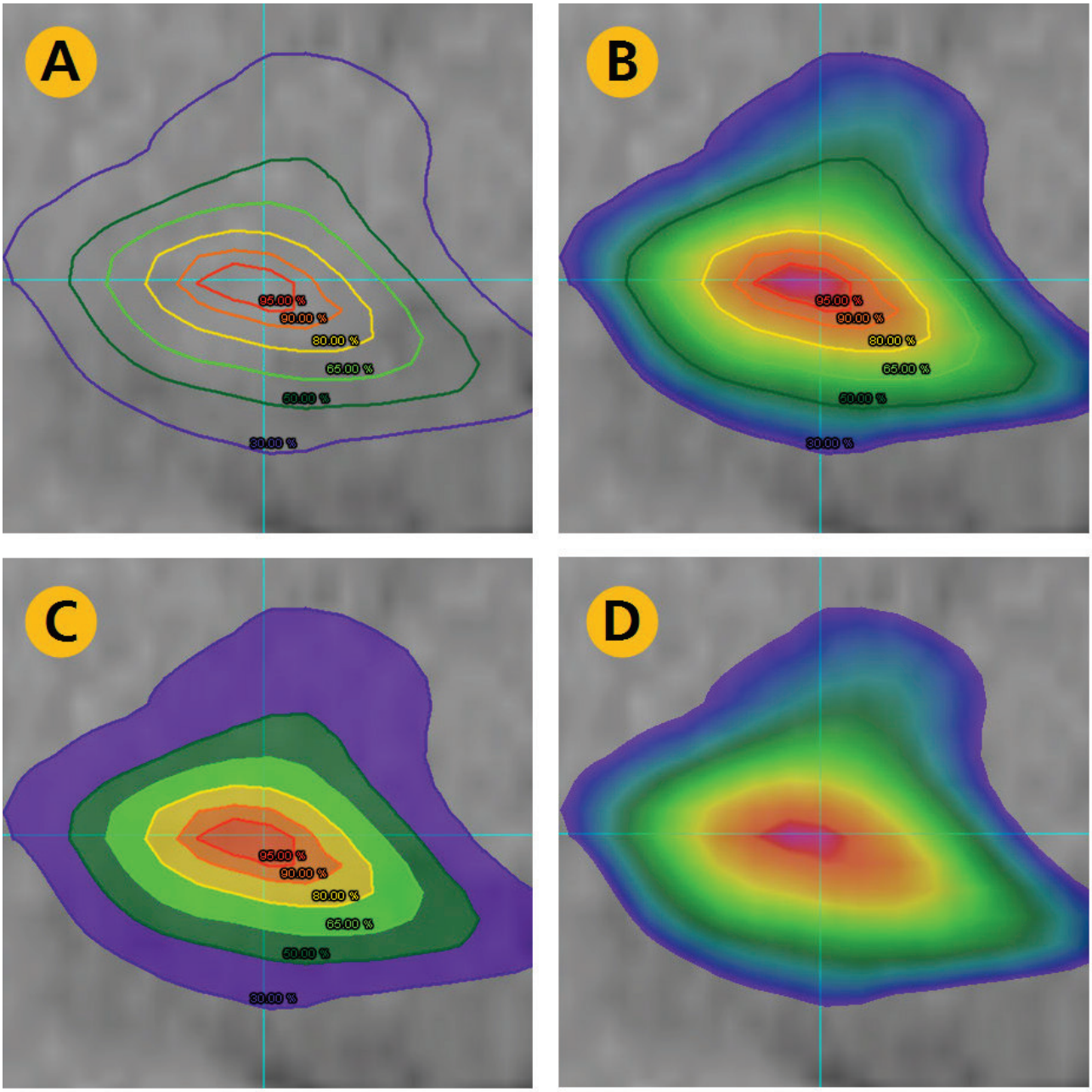
You can choose to display isodose lines, a color wash, a banded color wash, or both isodose lines and a color wash. To configure your color isodose display:

1. Click the Settings button in the upper-right corner of MIM.
2. In the Settings menu, select **General Preferences**.
3. In the General Preferences window, search for "**dose**" and select **Dose** from the menu on the left side of the window.

4. On the Dose page, choose your desired option from the **Display** dropdown.

> **Tip:** By default, the color wash interpolates the colors between isodose lines. To prevent colors from interpolating between the lines select **Display dose with banded color wash** on this page as well.

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



A. Isodose lines, no color wash
B. Isodose lines with color wash
C. Isodose lines with banded color wash
D. Color wash (not banded), no isodose lines

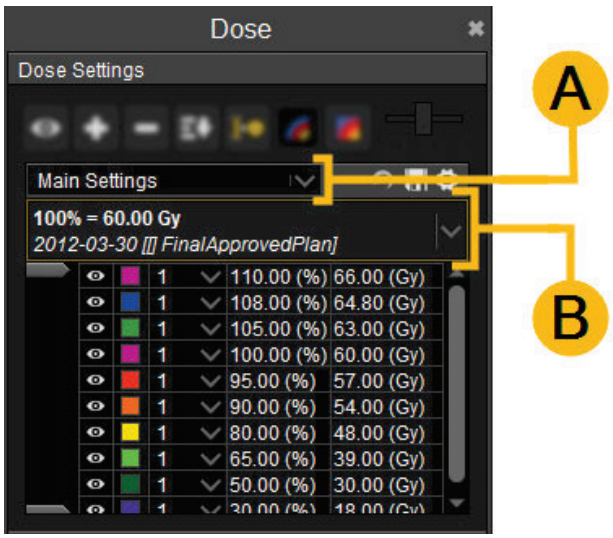
Manage or Delete Isodose Settings

To delete settings, create copies of settings, or rename settings, click the gear button and select the **Manage Isodose Settings...** option.

Dose Display

Dose Sidebar: Isodose Display

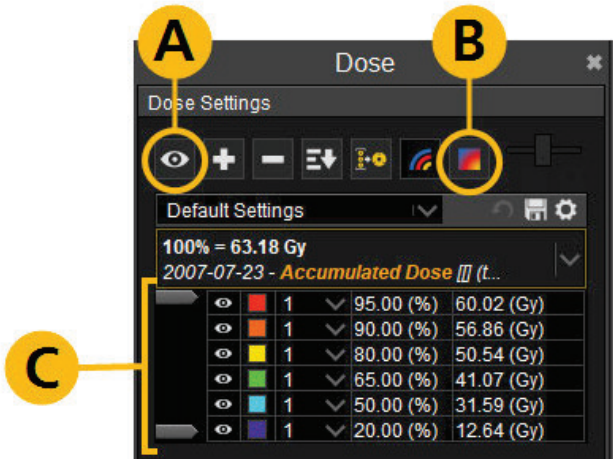
The **Dose Settings** section of the sidebar displays the isodose settings and the normalization value.



A. The selected isodose setting appears in the first dropdown menu. As desired, you can select another setting or edit the lines. See Create, Edit, and Save Isodose Settings above.
B. The normalization dose determines which values are associated with each percentage.

Tip: If multiple doses are open in your session, the normalization dose is also outlined with a thin gold box in the **Doses** section of the sidebar.

Adjust the view of isodose lines from the top of the sidebar.



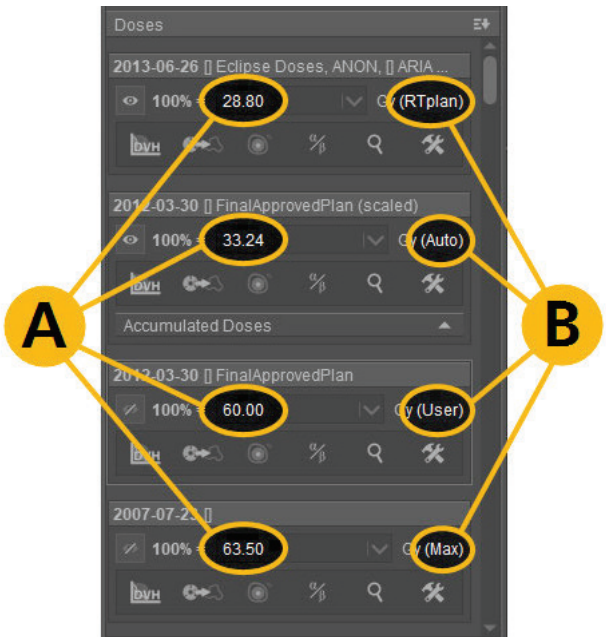
A. Toggle all isodose lines on or off using the open eye button.

B. Toggle the color wash on the series using the toggle color wash button.

C. Use the slider bar or the open eye and closed eye buttons to the left of the individual dose lines to toggle visibility.

Dose Sidebar: Normalization Value and Normalization Source

For each dose, MIM indicates the normalization value and the source of this value in the Doses section of the sidebar.



A. **Normalization Value** — See below for more information.

B. **Normalization Source** — The label in parentheses indicates where the normalization value comes from. See below for definitions of each possible label.

Normalization Value

- The normalization value normalizes the percentage-based isodose lines rendered for that dose.
  - The normalization value corresponds to the 100% isodose line for that dose.
  - If absolute-value isodose lines are displayed, then the normalization value has no effect on the display.
- The normalization value also normalizes dose constraints that utilize the "% norm" value.

Normalization Source Definitions

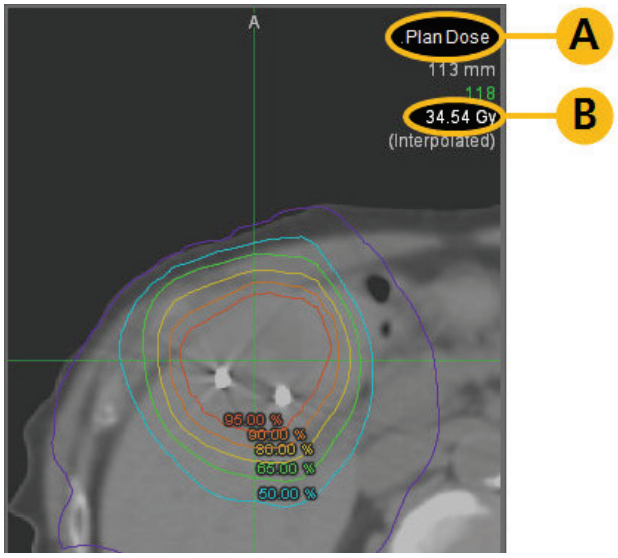
- **(Max)** — This is the max point dose value of the entire dose volume. This is shown if a prescription dose was not entered in the RTplan file.
- **(RTplan)** or **(Site)** — This is the prescription dose pulled from the RTplan file, if one exists.
  - When **(Site)** is displayed, it indicates that this is the overall prescription dose for the clinical site.
  - The value could also be followed by a set of coordinates (e.g., for a calculation point or off-axis point) if a point was specified while creating the RTplan.
- **(User)** — This label is applied when the dose value is manually changed by the user. For example, if MIM displays the max dose, you may wish to enter the plan dose value.

Important: Manually changing the dose value only affects how the dose is displayed on the series. Manually changing the dose value does not scale the dose, nor does it affect the dose values used during dose accumulation processing. Dose accumulation uses the underlying voxel values of the doses, regardless of the selected normalization doses.

- **(Auto)** — This indicates MIM computed a value for the dose (e.g., after scaling a dose).

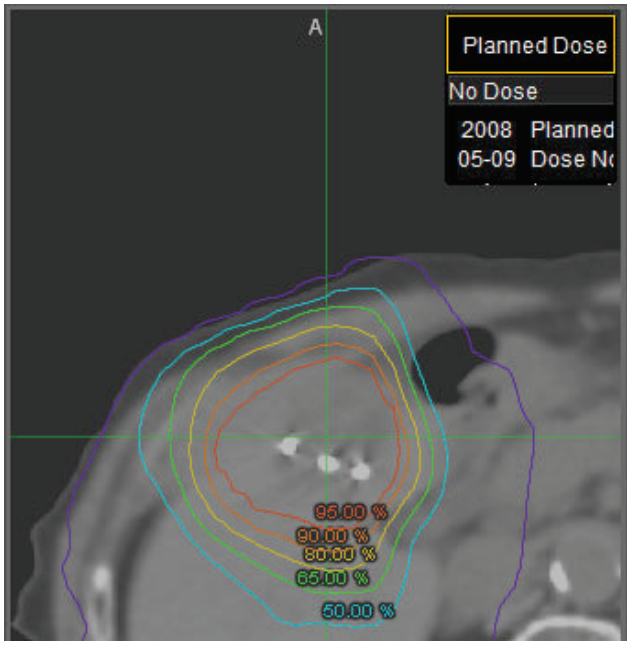
Dose Display on Series

MIM displays dose information in the upper-right corner of the left-most viewport.



A. The name of the dose displayed on this viewport.

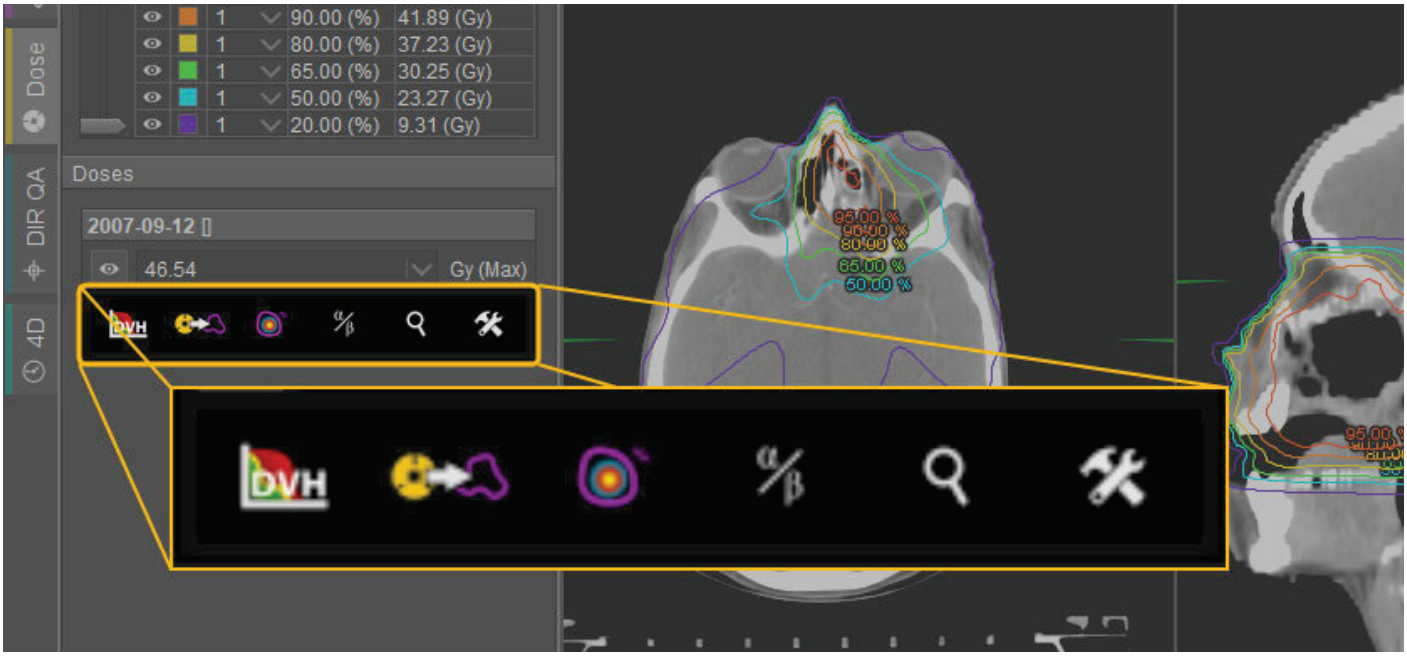
B. The dose value at the crosshair.



- To hide the dose display, click the name of the dose, and then select **No Dose** from the dropdown.
- You can also set a keyboard shortcut to toggle dose visibility. See Set Keyboard Shortcuts for more information.

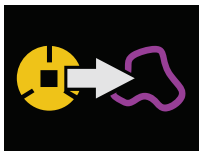
Additional Dose Tools

Additional tools are found below the listed dose value. Hover over each tool to see a tooltip.



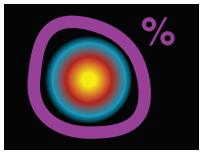
DVH — Lets you choose how to generate a dose volume histogram (DVH). See Dose Volume Histogram (DVH) for more information.

Important: You must have contours (an RTstruct) present in the session in order to generate a DVH.



Create Contours from Isodose Curves — Lets you create contours from selected isodose curves.

Important: The contours and isodose lines are not linked after the contours are created. If you adjust the isodose curves after creating contours, use this tool again to generate new contours.



Dose Constraints — Lets you select a dose constraint set to apply.

Highlight Series — Briefly highlights the series viewports that the dose is currently displayed on.

Additional Tools — Displays the following options:

- **Rename...** — Rename the dose. Enter the new name in the Notifications window.
- **Use global isodose settings** — This option is selected by default. The dose display uses the isodose settings selected at the top of the Dose sidebar. See Dose Sidebar: Isodose Display.
- **Individual Isodose Settings** — Deselect **Use global isodose settings** to access individual settings. Then, hover over **Individual Isodose Settings** and select a new setting.
- **Transfer Dose** — Hover over **Transfer Dose** and then select the series to transfer the dose to.

> **Tip:** Transferring a dose requires an existing link between the two series (e.g., a fusion link).

- **Localize to Max Dose** — Localize to the max dose for the entire dose or a specified contour. Select the contour in the Notifications window.
- **Save RTdose...** — Save a DICOM RTdose file. Follow saving instructions in the Notifications window.
- **Close RTdose** — Close the dose. Any displayed isodose lines disappear.
- **Scale Dose** — Scale the dose by entering the correct value in the Notifications window.
- **Clip Dose Display to Contour** — Select a contour from the Notifications window. MIM restricts the isodose display to the selected contour.

Dose Volume Histogram (DVH)

MIMTD-704 • 20 Jun 2024

Overview

MIM® provides a highly flexible interface for creating and evaluating Dose Volume Histograms (DVHs). You can use the DVH viewer or create a custom DVH display to view dose statistics for any ROI, evaluate dose constraints, calculate tumor control probability, and more.

Contents

Create a DVH

To create a DVH in MIM, follow these steps:

1. Open a series with at least one dose and at least one contour.
2. Open the **Dose** sidebar. Find the dose you want to evaluate in the list of doses.
3. Click the DVH button below that dose. The Notifications window opens with the option for **MIM-Generated DVH from Selected Contours** selected by default.

> **Tip:** If you want to view a DVH generated by another system that is part of the RTdose file, you can change the option to **Saved DVH from RTdose**. Note that calculations on these DVHs may differ from MIM-generated DVHs.

4. Use the checkboxes in the Notifications window to select which contours to include on the DVH.

> **Tip:** Use the **Select All** or **Deselect All** buttons to quickly add or remove all contours.

5. Click **OK** to create the DVH. The Dose Volume Histogram window opens.

> **Tip:** Click the **Hide Options Panel** button in the lower-left corner to view the graph in the full window.

6. If desired, make adjustments to the display. See DVH Tab below for more information.

To add another dose to the DVH, follow these steps:

1. Minimize the DVH viewer.
2. In the **Dose** sidebar, click the DVH button below another dose.
3. Use the checkboxes in the Notifications window to select which contours to include.
4. Click **OK**. The DVH window reopens with information from both doses.
5. If desired, make adjustments to the display. See DVH Tab below for more information.

Save a DVH

To save and export a DVH, click the **Save As...** button in the lower-left corner of the DVH window.

> **Caution**: When exporting a DVH to a CSV file, the dose unit will always be Gy, regardless of cGy preferences you or your organization may have set. Additionally, a point, not a comma, will be used as a decimal separator in the CSV file, regardless of language preferences you or your organization may have set.

DVH Viewer

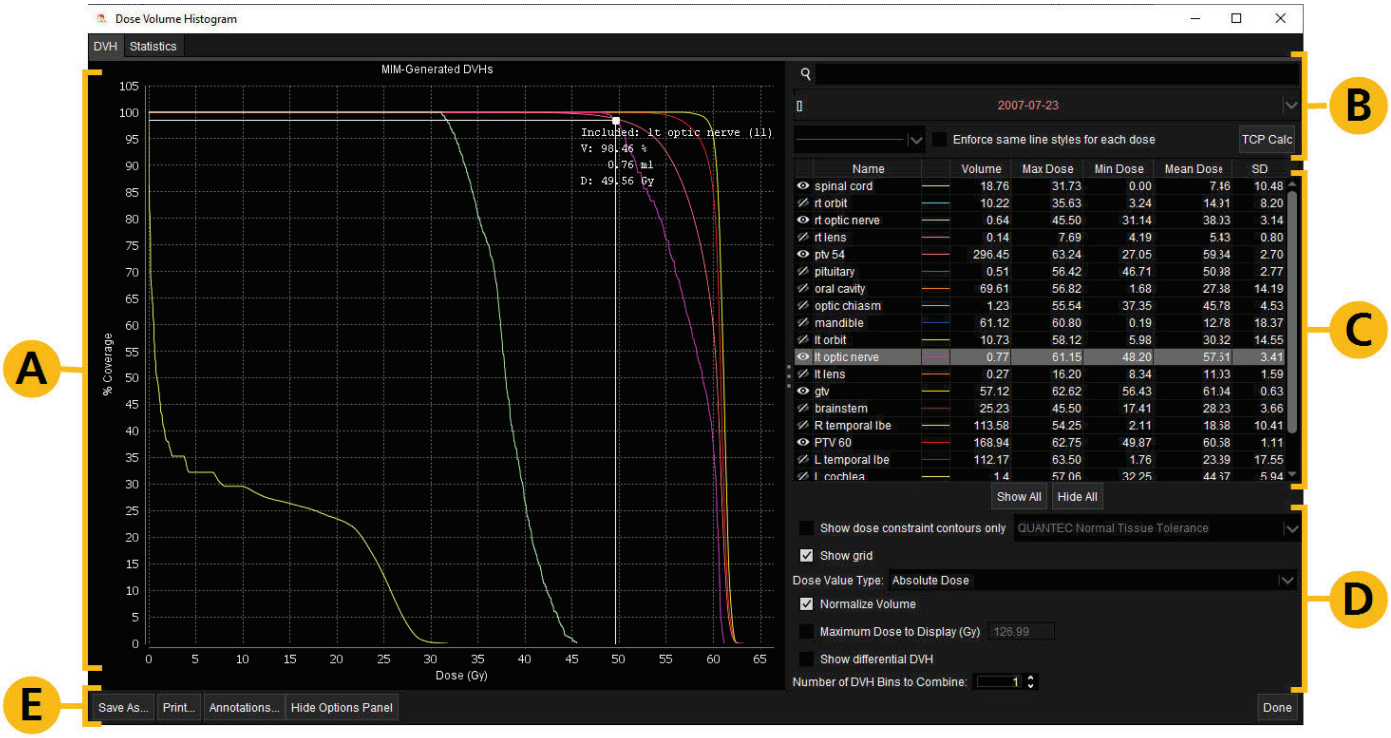
The DVH viewer contains a DVH tab and a Statistics tab. You can adjust preferences and the information displayed in both.

DVH Tab

When the DVH viewer opens, you see the **DVH** tab.

- See the annotated screenshot below for additional information.
- If necessary, expand the options panel by clicking the **Show Options Panel** button in the lower-left corner of the viewer.

To view additional information, click on the **Statistics** tab in the upper-left corner of the Dose Volume Histogram window. See DVH Viewer: Statistics Tab below for details.



A. The DVH itself makes up the largest portion of the main page of the DVH viewer.
   - To view statistics for the active contour (the one highlighted in the contour list to the right), hover over its line in the histogram.
   - To switch to a different active contour, click its name in the contour list to the right, or click directly on its line on the DVH.

B. In the upper-right section of the DVH window, you can do the following:
   - Search for a contour.
   - Toggle between doses if more than one dose is present in the DVH.
   - Change the line style for the DVH.
   - Perform TCP Calculations.

C. The list on the right side shows all of the contours that are included in the DVH and important statistics for each contour.

- To show or hide specific contours, click the eye button to the left of the contour name.
- To show or hide all contours, click the **Show All** or **Hide All** button below the list.
- To make a contour active (so you can view more detailed statistics by hovering over it on the graph), click on its name.

D. The lower-right corner of the DVH viewer window provides additional options for customizing the DVH display.

- **Show dose constraint contours only** — Limit the contour list and display to contours included in the dose constraint set. Select this option, and then select a dose constraint set from the dropdown to the right.
- **Show grid** — Show or hide the grid background.
- **Dose Value Type** — The type of dose to display on the x-axis of the DVH.
  - **Absolute Dose** — The default option. Displays absolute dose values.
  - **Normalized Dose (Dose Max)** — Displays percentages of the maximum dose contained in the DVH.
  - **Normalized Dose (Contour Max)** — Displays percentages of the maximum dose for each contour, so that 100% is the largest dose value within each ROI.
  - *MIM 7.3 and later:* **Dose Normalization Value (Gy)** — Displays percentages of the entered normalization value. Enter the normalization value to the right.
  - *MIM 7.2 and earlier:* **Prescription Dose** — Displays percentages of the entered prescription dose value. Enter the prescription dose value to the right.

Tip: In MIM 7.2 and earlier, "normalization value" was known as "Rx dose" or "prescription dose." A normalization value may be a prescription dose, max dose, or user-entered value. Therefore, in MIM 7.3 and later, "Rx dose" and "prescription dose" were changed to "normalization dose" to be inclusive of all possibilities.

- **Normalize Volume** — By default, the DVH shows percent coverage on the y-axis, from 0% to 100% of the volume of each region of interest. To display cubic centimeters (within the region of interest) instead, uncheck **Normalize Volume**.
- **Maximum Dose to Display (Gy)** — Limit the display to a maximum Gy value. Select this option, and then enter a maximum dose value to display.
- *MIM 7.2 and later:* **Show differential DVH** — Display a differential DVH instead of the default cumulative DVH. *MIM 7.1 and earlier*: Differential DVH is not available.

- *MIM 7.3 and later:* **Number of DVH Bins to Combine** — Choose the number of DVH bins to combine to control the granularity of the DVH graph. *MIM 7.2 and earlier*: This option is not available.

E. Use the buttons in the lower-left corner of the window to save, print, add annotations to the DVH, or hide the options panel.

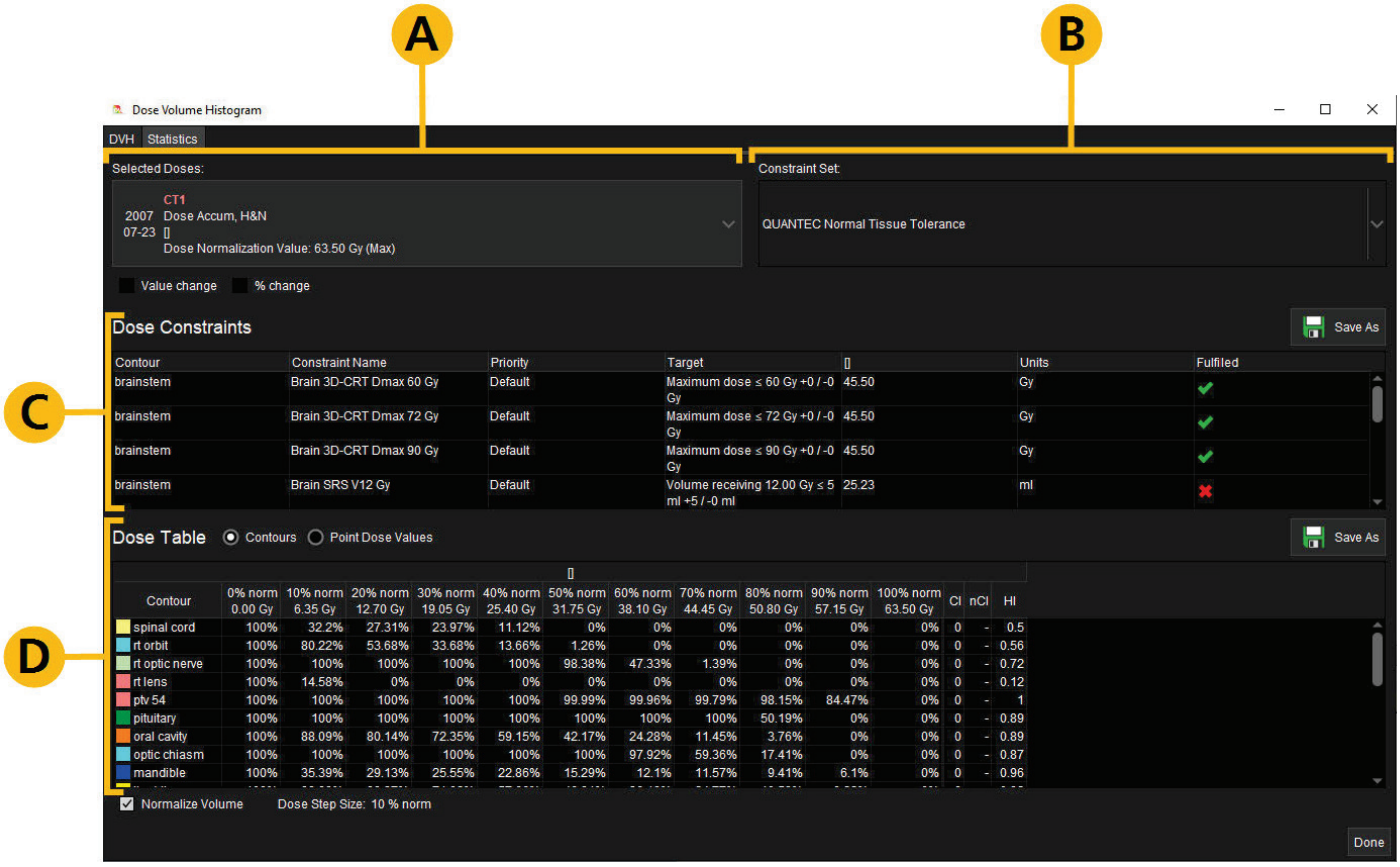
Tip: Annotations are included in secondary captures.

- Select **Annotations...** >> **Add...** to create a point at a user-defined dose value or a percent coverage of the volume.
- Select **Annotations...** >> **Load** to select dose constraints to view on the graph. You can create annotations for Dose, Volume, and Volume Spared constraints.
- Select **Annotations...** >> **Clear All** to remove any annotations on the DVH.

Caution: When exporting a DVH to a CSV file, the dose unit will always be Gy, regardless of cGy preferences you or your organization may have set. Additionally, a point, not a comma, will be used as a decimal separator in the CSV file, regardless of language preferences you or your organization may have set.

Statistics Tab

The Statistics tab of the DVH viewer lets you compare doses and evaluate dose constraints. See the annotated screenshot below for additional information.



A. Use the **Selected Doses** dropdown to choose a dose for evaluation.

> **Tip:** If you selected **Saved DVH from RTDose** when opening the DVH viewer, the dose constraints table in the Statistics tab is based on the DVH embedded in the RTdose.
>
> To double-check whether you're using the MIM-generated DVH or the DVH embedded in the RTdose, open the **Selected Doses** dropdown and confirm whether the **Use Saved DVH from RTdose** option is enabled.

- If there are multiple doses in your session, you can select multiple doses for comparison.
- If there are multiple doses in your session, choose a base dose.

B. Use the **Constraint Set** dropdown to choose a dose constraint set to evaluate the dose against.

C. Based on your selections at the top of the screen, the Dose Constraints section of the DVH Statistics tab populates with information about whether your base and comparison doses meet the specific dose constraints.

D. The Dose Table at the bottom of the window displays statistics for each contour. To change the **Dose Step Size**, follow these steps:

1. Click on "10% norm" (*MIM 7.3 and later*) or "10% Rx" (*MIM 7.2 and earlier*) and then make adjustments in the editable fields.

> **Tip:** In MIM 7.2 and earlier, "normalization value" was known as "Rx dose" or "prescription dose." A normalization value may be a prescription dose, max dose, or user-entered value. Therefore, in MIM 7.3 and later, "Rx dose" and "prescription dose" were changed to "normalization dose" to be inclusive of all possibilities.

2. Click the green checkmark ✅ to apply the changes.

Adjust DVH Preferences

Some aspects of the DVH Viewer, including the background and text colors of the viewer, are customizable. To make changes, follow these steps:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**DVH**". Select **DVH** on the left side.
3. Make changes to any settings.

Customizable preferences include:

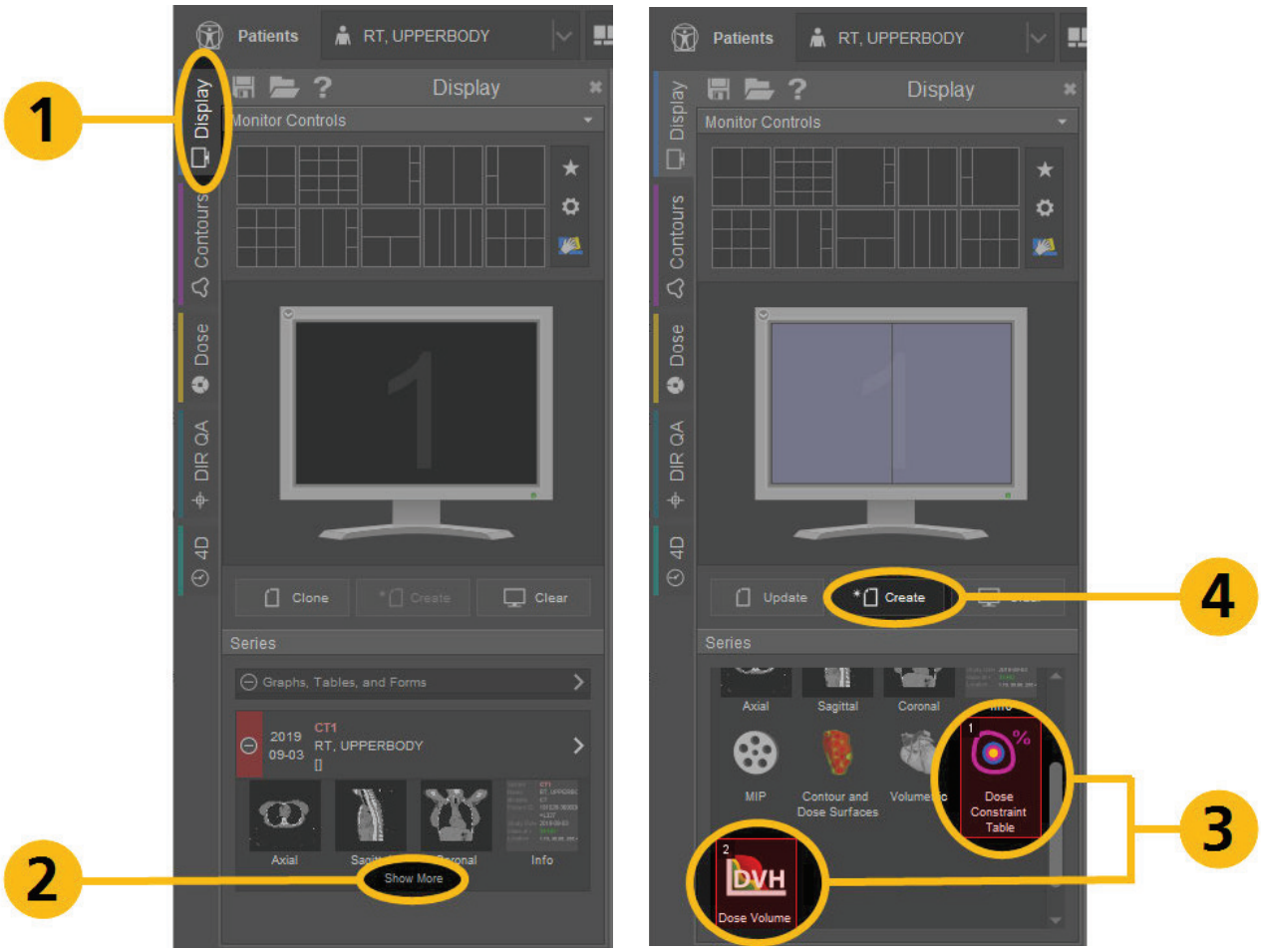
- The background color and the text color of the viewer.
- The max dose to display (as a percentage of the normalization value).
- The contours to exclude from the DVH Viewer by default.
- The max dose percentage to show on the viewer by default.
- Bin sizes for CSV outputs.

Create a DVH and Dose Comparison Page

MIM provides the ability to add a DVH and dose constraint table to a custom display page within a MIM session.

To add a DVH and/or dose constraint table to a MIM session, follow these steps:

1. Open the **Display** sidebar.
2. Find the series associated with the dose and structure set and click **Show More**.



3. Select **Dose Volume Histogram** and **Dose Constraint Table** from the thumbnail options.
4. Click the **Create** button below the preview monitor.

View DVHs in Structured Reports

You can add DVHs to a structured report. See Create and Modify Structured Reports for additional information.

Work with Multiple Doses

MIMTD-1767 • 15 Dec 2023

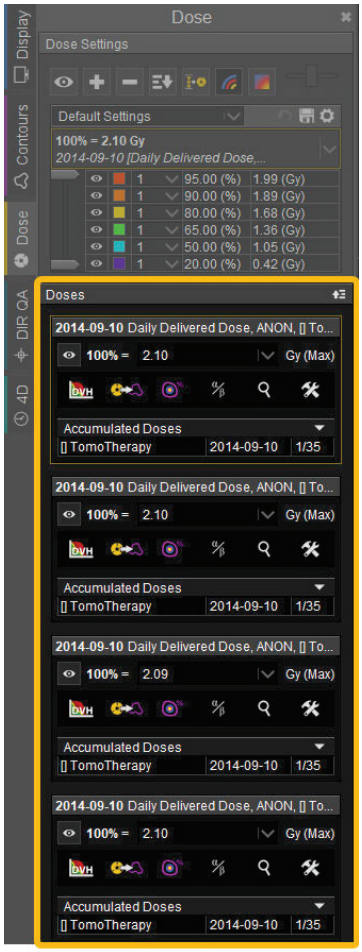
Overview

The Dose sidebar has a number of features that help you work efficiently in sessions where multiple doses are present.

Contents

Identify Multiple Doses in the Dose Sidebar

When multiple doses are open in a session, MIM®'s default behavior is to list them in the Dose sidebar sorted from oldest to newest. Click the sort button in the upper-right corner of the **Doses** section to reverse this order.



Alternatively, you can configure MIM to sort doses based on the order of the images on your screen. The doses in the sidebar update as you move between pages in your session.

To enable this preference:

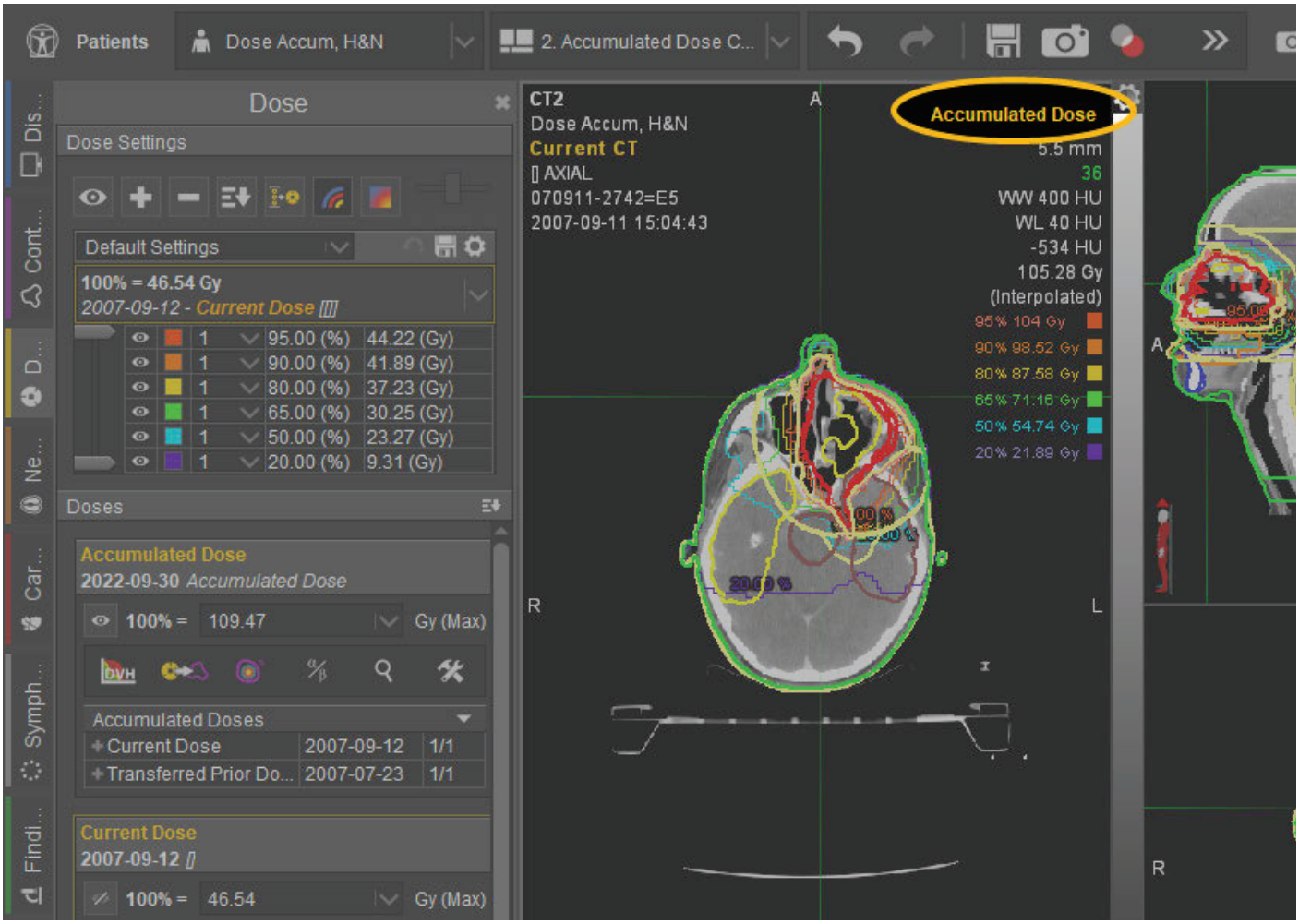
1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**Dose**." Select **Dose** on the left side.
3. Select **Sort doses in the Dose sidebar based on the order of images in the display**.
4. Click **OK** to apply the preference and close the window.

Determine Which Dose Is Shown on an Image

MIM 7.3 and Later

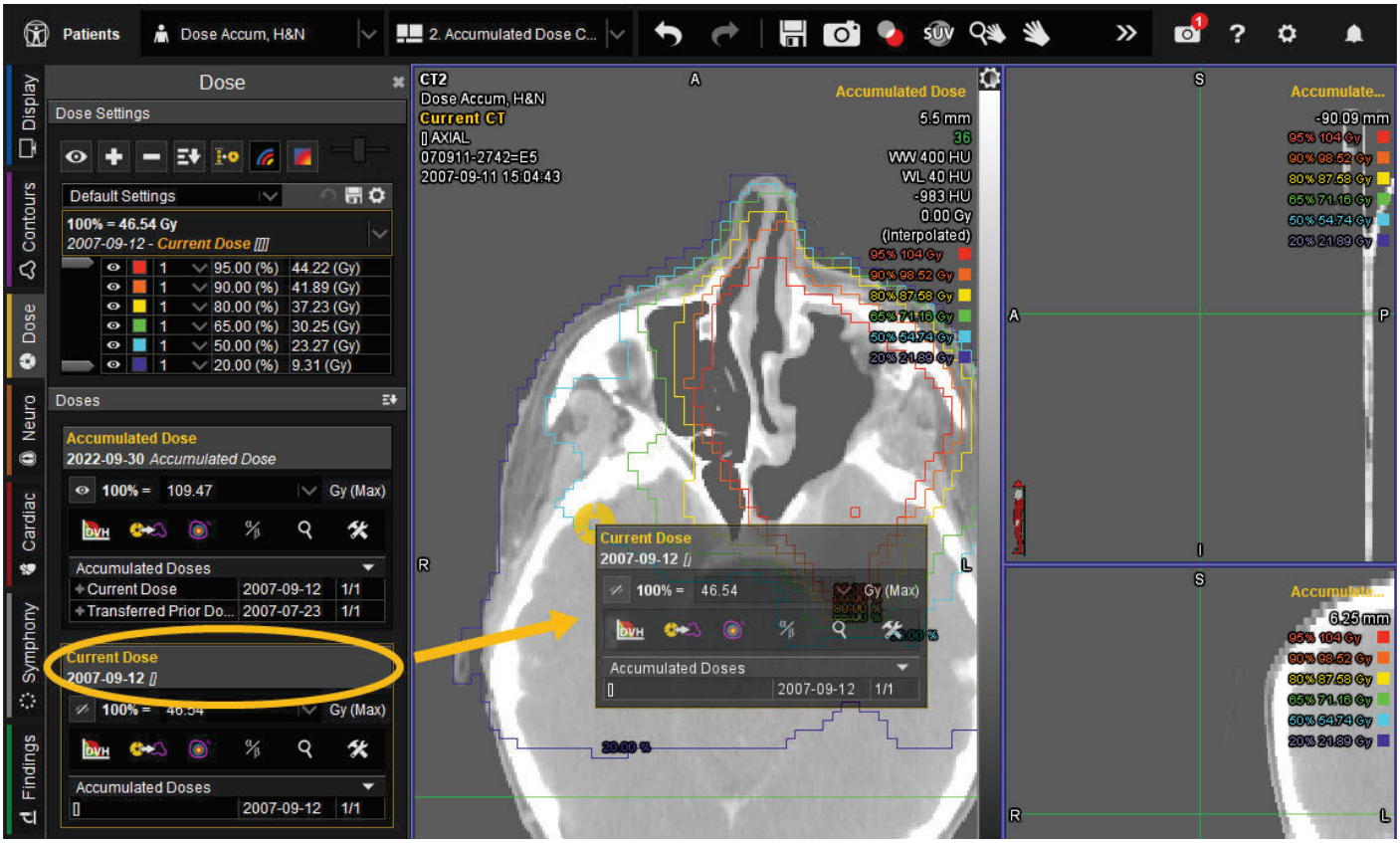
The dose currently displayed on a series is indicated in the upper-right corner of each viewport.

Tip: The name of the dose appears in gold if it was manually named in the session or by a MIM workflow.



If there are multiple doses that could be displayed on a series, click the name of the dose to view a dropdown that lists the other doses. Select a dose from the dropdown to update the display.

You can also drag a dose from the sidebar onto a viewport to replace the dose that is visualized on a series.

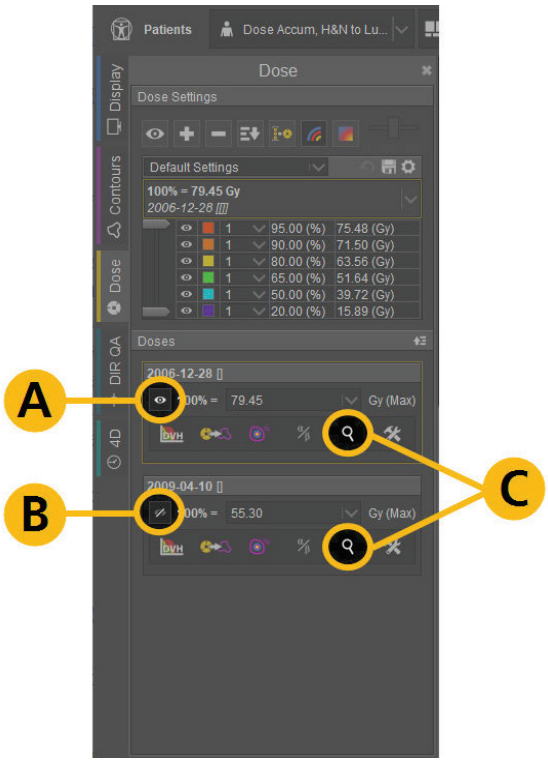


Tip: If a dose does not exist on a series, dragging it onto the series is not allowed and does not transfer the dose. See Additional Dose Tools for information on transferring doses.

All MIM Versions

Identify Doses

1. In the Dose sidebar, find the dose you would like to view.
2. Locate a  or  button, immediately below the dose name.
   A. The open eye  indicates that the dose is currently displayed on the page.
   B. The closed eye  , which is grayed out with a slash through it, indicates that the dose is not currently displayed on the page.
   C. Click the spyglass  button underneath a displayed dose to briefly highlight the series that the dose is displayed on. If the dose is not currently visible, this button has no effect.

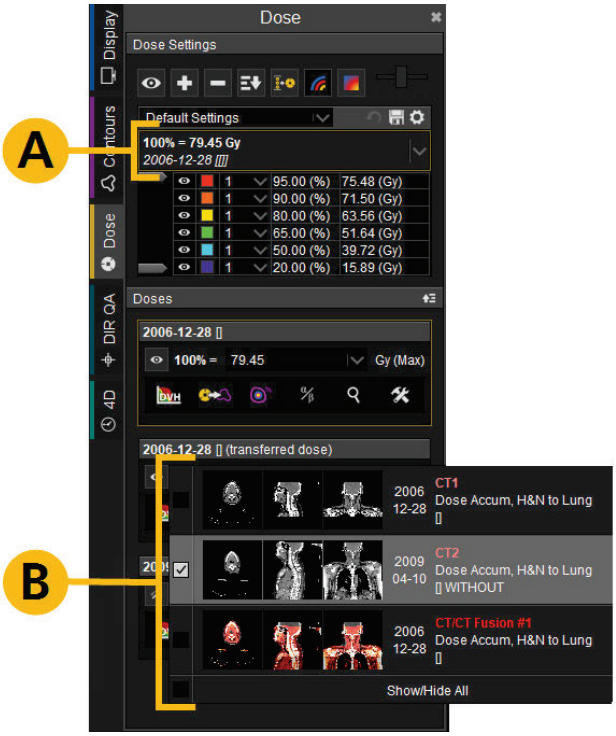


Change Displayed Doses

Tip: Changing a displayed dose does not automatically change the normalization dose (A). After changing the displayed doses, you may also want to change the normalization dose.

- For currently displayed doses, click the open eye button. The menu that opens (B) indicates which series the dose is displayed on (look for the check to the left of the image thumbnails).

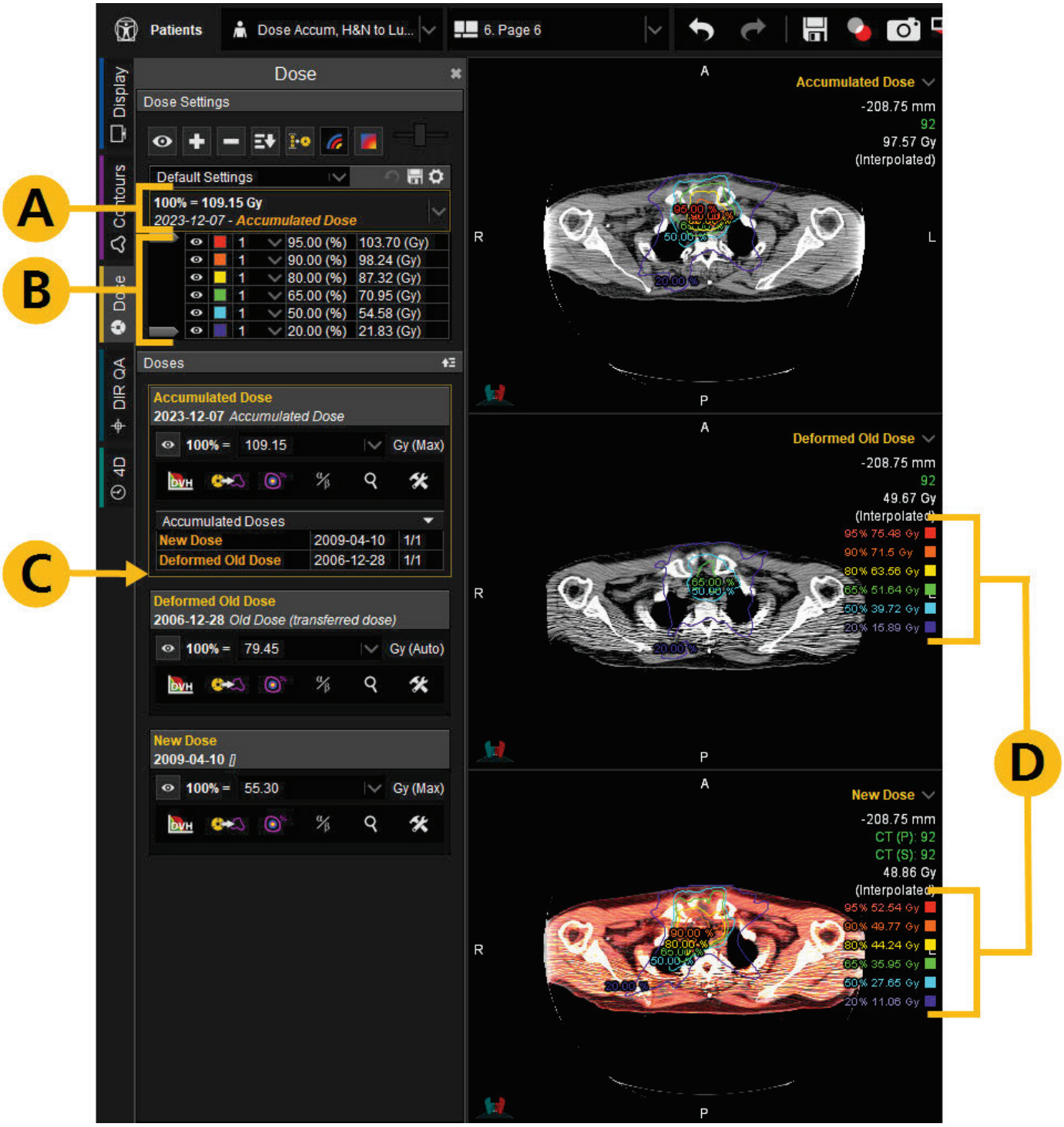
  To display the dose on a different series, select the checkbox on a different series in the menu.
- For the doses that are not displayed, click the closed eye button to see a list of series that the dose could be displayed on. Select the series you want to display the dose on.



Tip: You can only display one dose per CT, but you can display multiple CTs on a page, each with its own dose.

Isodose Lines and Multiple Doses

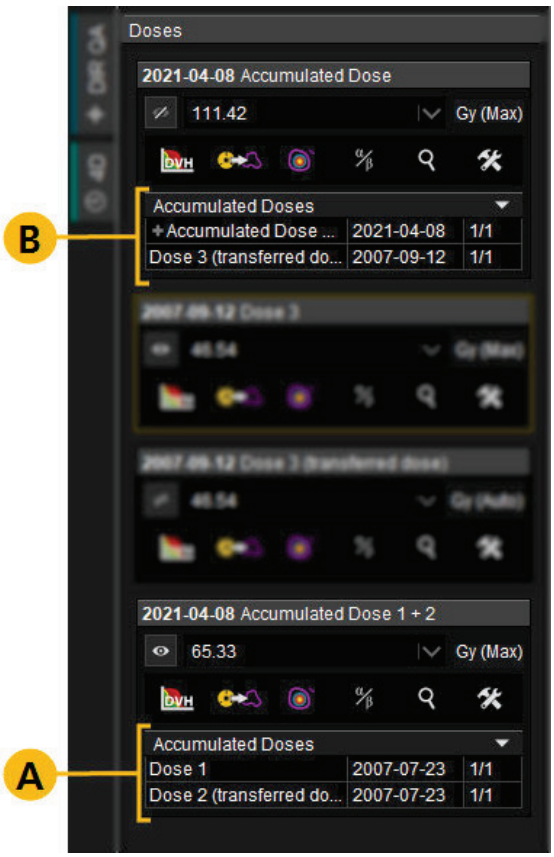
If multiple doses are displayed and you are using both percent and absolute value isodose display, MIM shows an isodose key for each dose.



- The key for the normalization dose (A) is shown via the isodose settings at the top of the Dose sidebar (B). This dose also has a thin gold outline in the list of all doses (C).
- The key for other doses is displayed in the corner of the viewport (D). Note that the image in the top viewport does not have a key. This is because this image is displaying the normalization dose, which corresponds to the isodose setting as described above.
    - *MIM 7.3 and later:* The key is shown in the upper-right corner.
    - *MIM 7.2 and earlier:* The key is shown in the upper-left corner.

Accumulated Doses

Use the following tips to identify and distinguish between accumulated doses in the Dose sidebar.



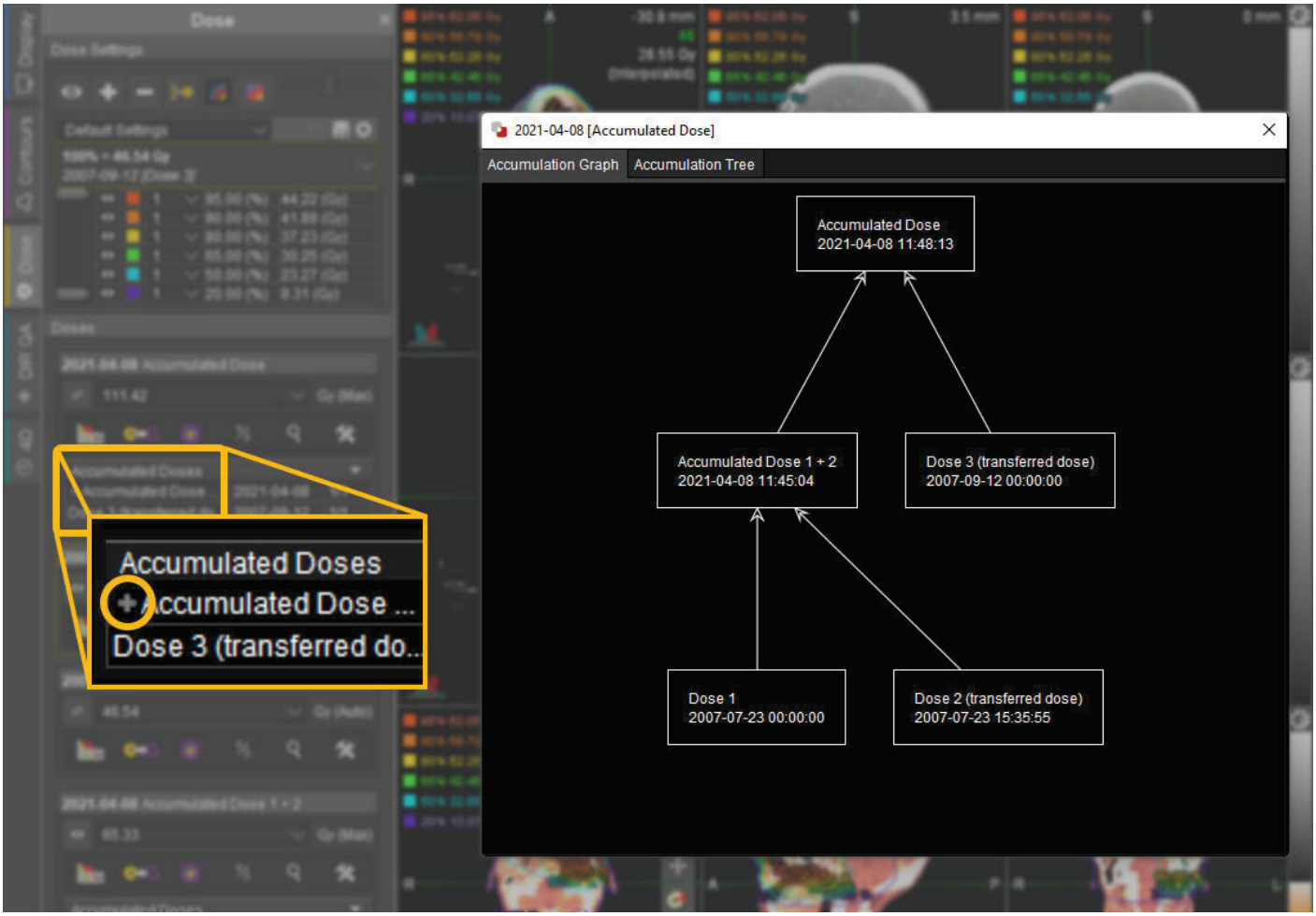
When a dose is accumulated in MIM, the component doses are listed below the dose value and dose tools, under an **Accumulated Doses** heading.

For example:

A. The 65.33 Gy dose consists of Dose 1 + Dose 2.

B. The 111.42 Gy dose consists of another Accumulated Dose + Dose 3.

When an accumulated dose is used in a subsequent dose accumulation, you can click the plus sign (+) to the left of the Accumulated Dose in the list. MIM opens an **Accumulation Graph** that indicates how each component dose was summed. If the component doses were scaled, the scaling information is also displayed in the graph. The **Accumulation Tree** tab presents similar information in a table.


2021-04-08 [Accumulated Dose]
Accumulation Graph
Accumulation Tree
Accumulated Dose
2021-04-08 11:48:13
Accumulated Dose 1 + 2
2021-04-08 11:45:04
Dose 3 (transferred dose)
2007-09-12 00:00:00
Dose 1
2007-07-23 00:00:00
Dose 2 (transferred dose)
2007-07-23 15:35:55
Accumulated Doses
Dose 3 (transferred do..

Save a Dose File (RTdose)

MIMTD-664 • 19 Dec 2023

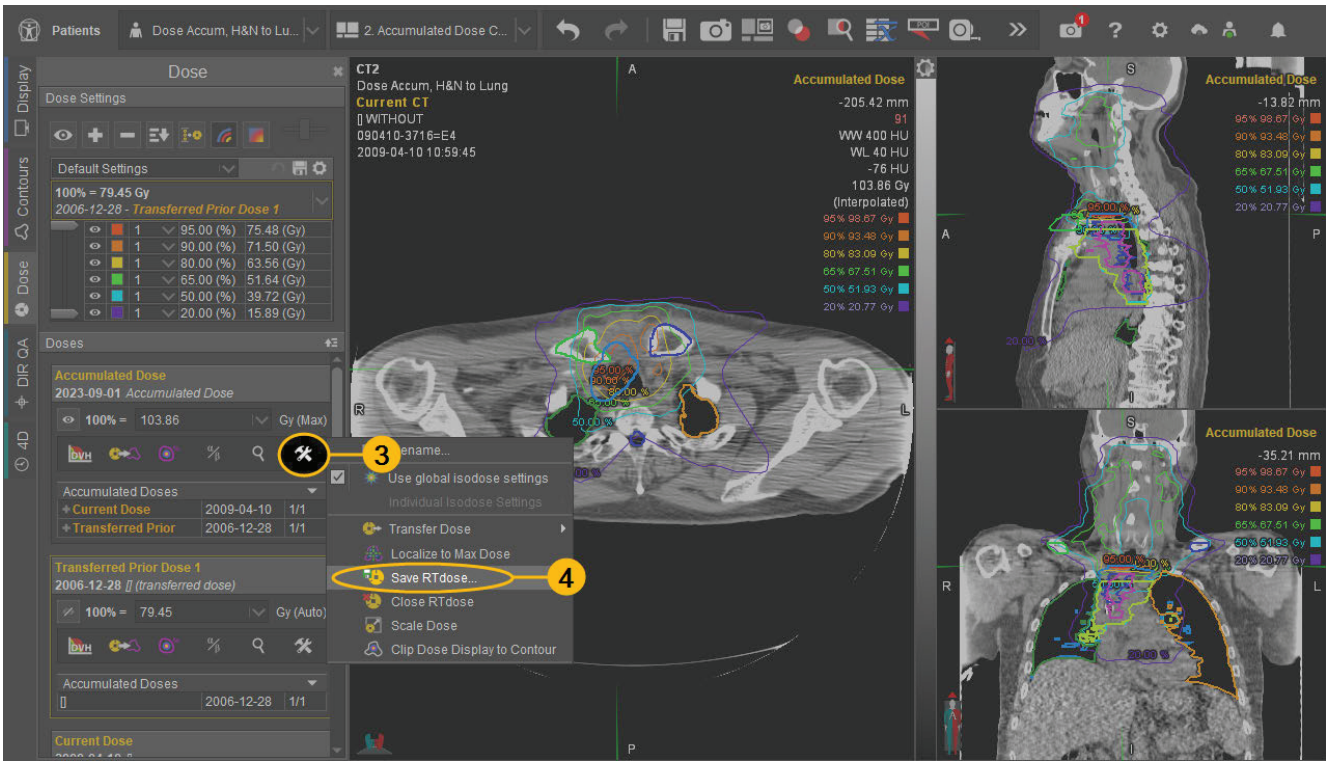
Overview

MIM® provides you with the option to save individual RTdose files. You may need to separately save an individual RTdose (e.g., after accumulating or transferring a dose) outside of a session save or in order to send an RTdose file to another system.

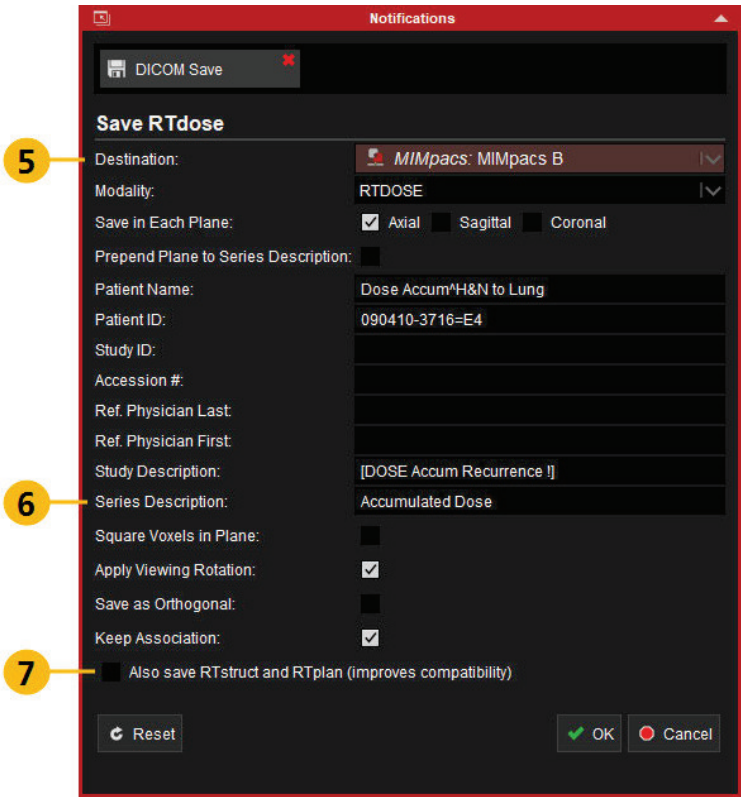
Save an RTdose

To save an RTdose, follow these steps:

1. Go to the **Dose** sidebar on the left side of MIM.
2. Find the dose that you would like to save in the **Doses** section.
3. Click the dose tools button.
4. Select **Save RTdose...**.



5. In the Save RTdose Notifications window, ensure that the **Destination** is correct or update it to save the file to another location.



6. Enter a **Series Description** for the RTdose.
7. If necessary, select **Also save RTstruct and RTplan (improves compatibility)**.

Tip: Treatment planning systems (TPSs) have different ways of associating a dose to an image series. Some TPSs require a dose to be associated with an RTplan, which then uses an RTstruct to reference the image series that the dose is associated with. If you are sending to one of these TPSs, you can select this preference to generate a basic RTplan and an RTstruct that links the dose to the appropriate image series. This RTplan does not actually contain any information about how the treatment should be delivered.

Important: If you select this option when saving an RTdose and plan on exporting the RTdose to a TPS, ensure that you also export the newly generated basic associated RTstruct and RTplan at the same time.

8. Click **OK**.

9. If you selected **Also save RTstruct and RTplan (improves compatibility)**, save an additional RTplan and RTstruct.
    i. Save the RTplan.
        a. In the Save DICOM RTplan Notifications window, ensure that the **Destination** is the same as the destination for the RTdose.
        b. Enter a **RTplan Description** for the RTplan.
        c. Click **OK**.
    ii. Save the RTstruct.
        a. In the Save DICOM RTstruct Notifications window, ensure that the **Destination** is the same as the destination for the RTdose.
        b. Enter a **Series Description** for the RTstruct.
        c. Click **OK**.

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.

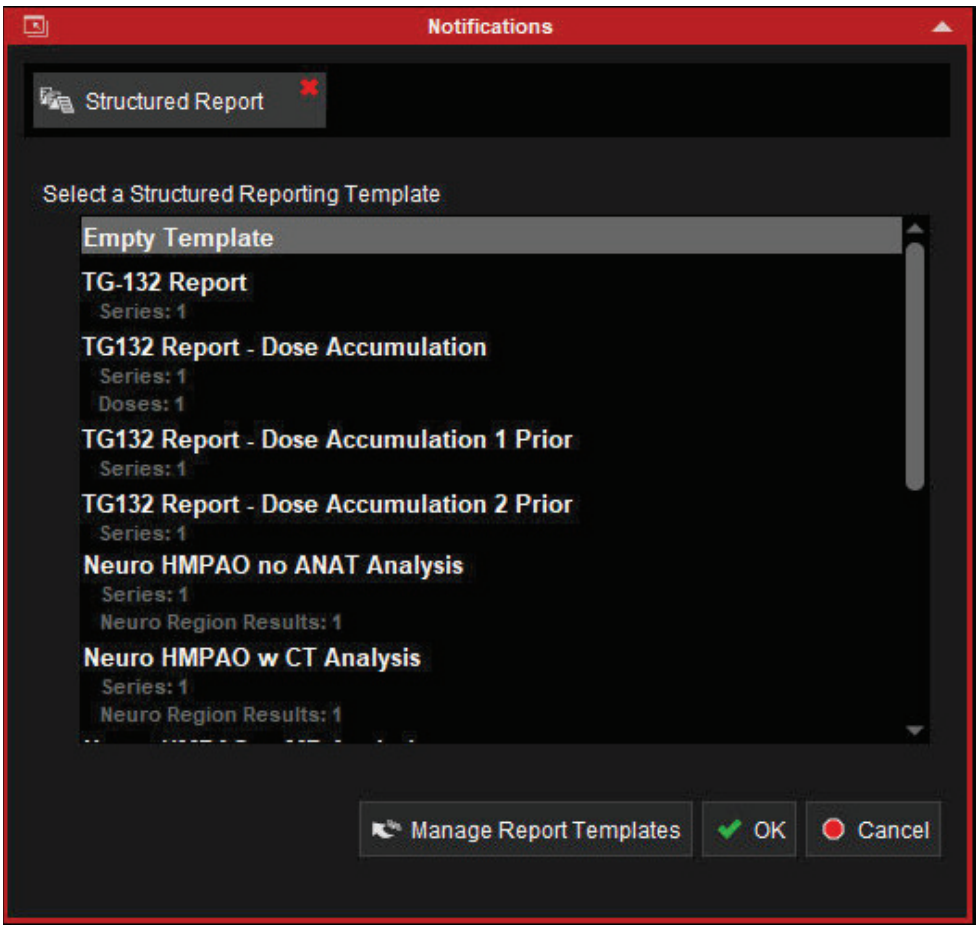
Contents

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:

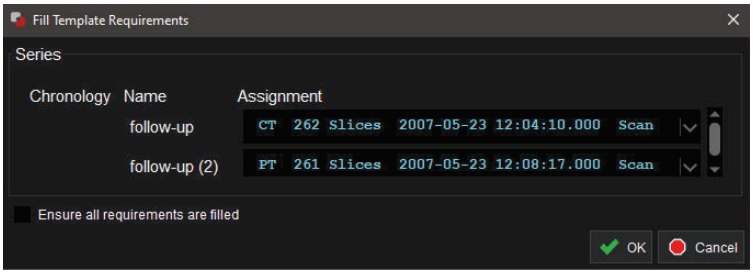
1. In an open MIM session, click the **Create Structured Report** tool in the toolbar, in the radial menu, or via keyboard shortcut.

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.

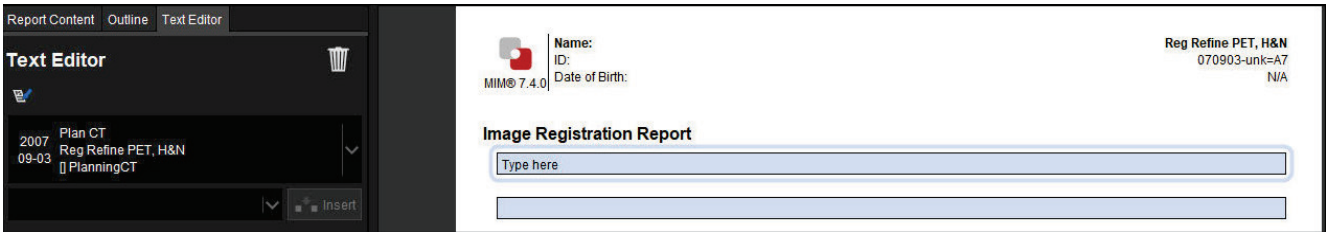
Modify Structured Report Content

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

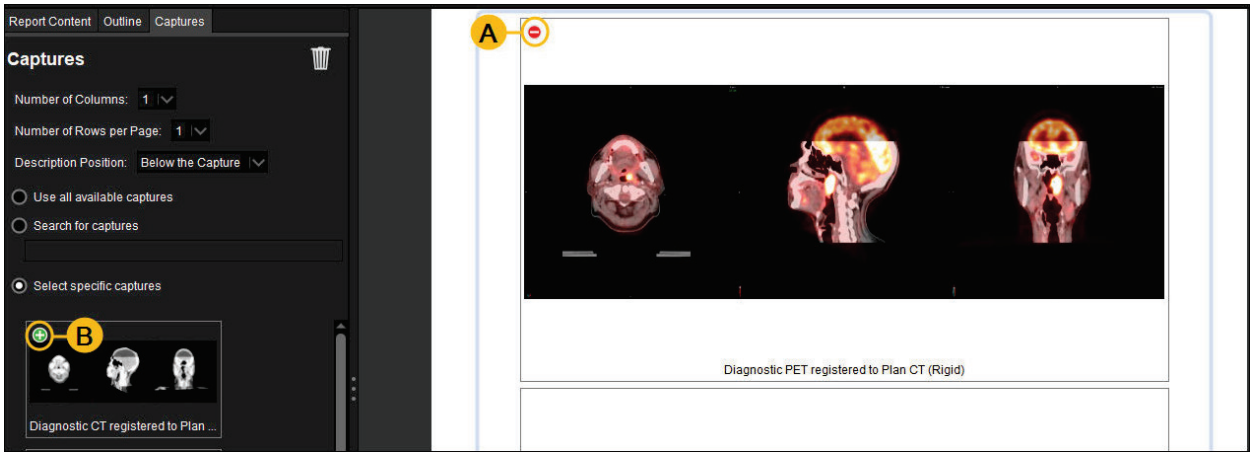
Make Common Updates

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.



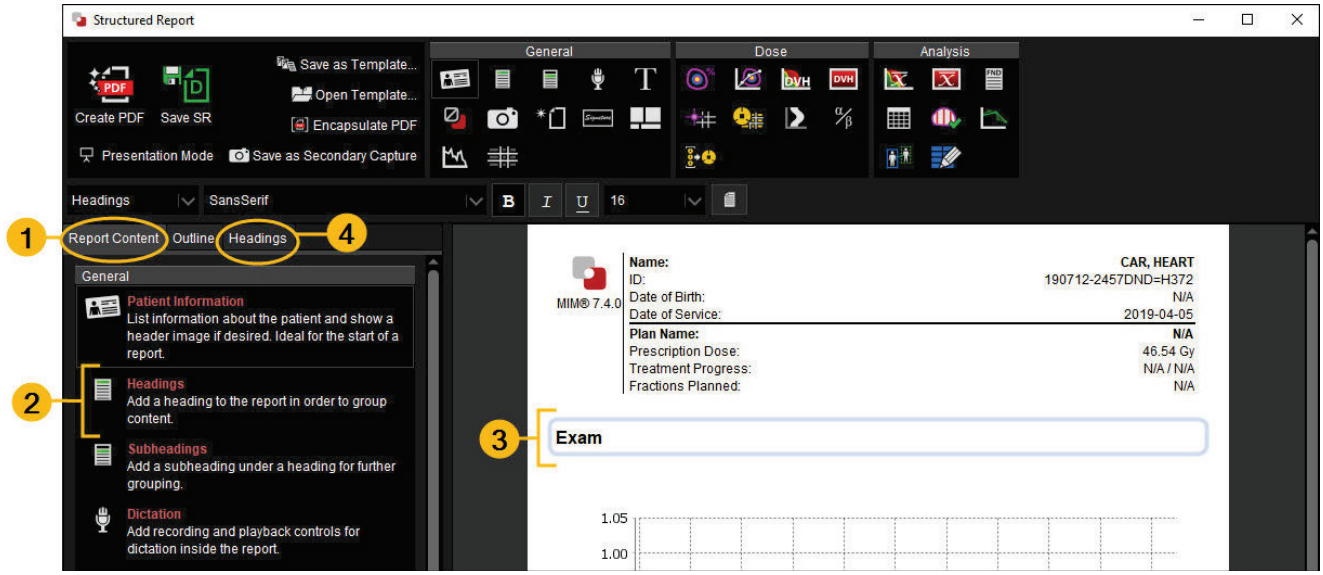
Add, Edit, and Delete Content

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.

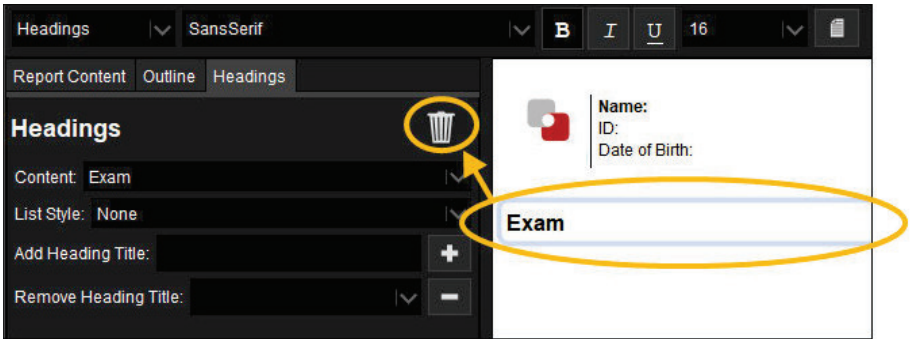
3. View the selected content type that appears in the report preview.
4. Go to the new tab for that content to edit it.



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

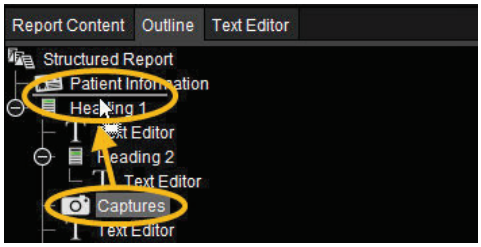
- Use Headings, Layouts, and Page Breaks to Organize Structured Report Content
- Add Secondary Captures to Structured Reports
- Add Dose Information to Structured Reports
- Add Statistics to Structured Reports

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.

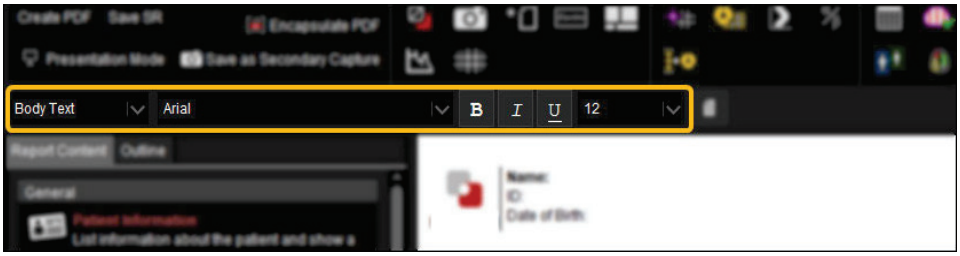
1. In an open MIM session, click the **Create Structured Report** tool in the toolbar, in the radial menu, or via keyboard shortcut.
2. In the Notifications window, either select the structured report template that you want to modify or select **Empty Template** to begin from a blank page. Click **OK**.

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.

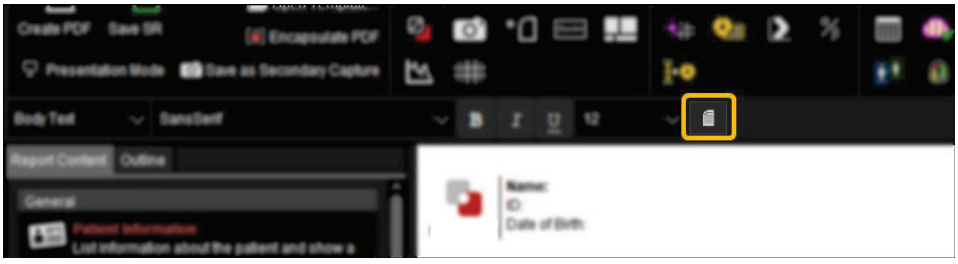
Change the Font, Font Style, and Font Size

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.

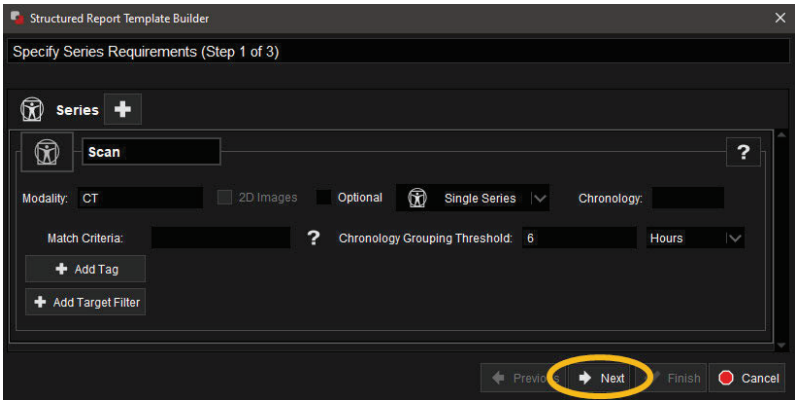
Review the following for more information about specific types of content that you can add:

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

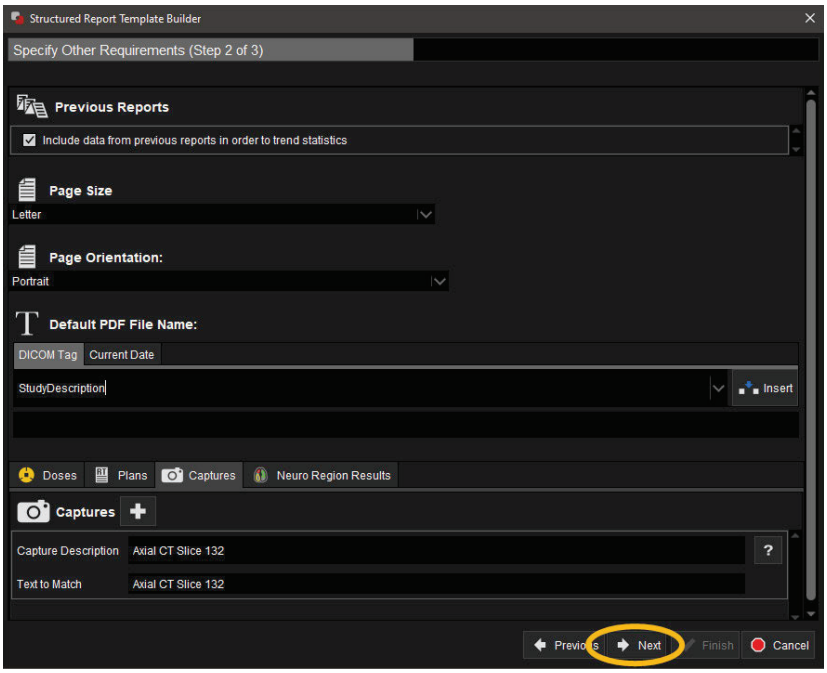
1. Click the **Save as Template...** button in the upper-left corner of the Structured Report Builder. The Structured Report Template Builder opens.
2. If desired, adjust the information in the **Specify Series Requirements** step. The information in this step is autofilled based on the study in your 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**.



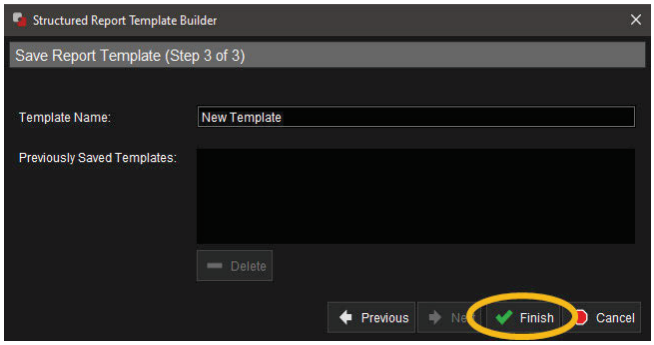
4. If desired, adjust the information in the **Specify Other Requirements** step:
   - To compare data across structured reports from multiple time points, select **Include data from previous reports in order to trend statistics**. MIM trends data using any existing DICOM structured reports (i.e., structured 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.

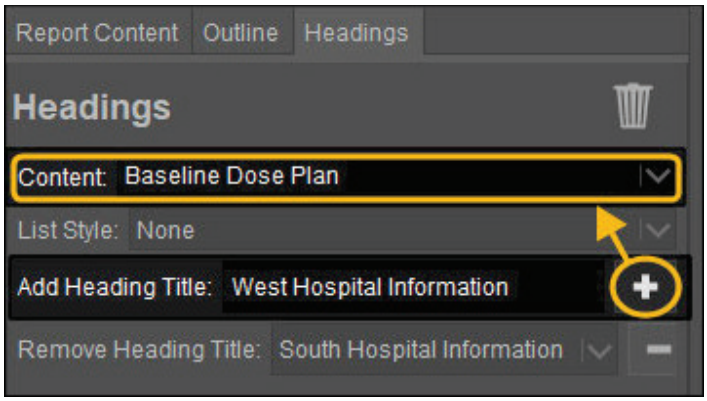
Contents

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.

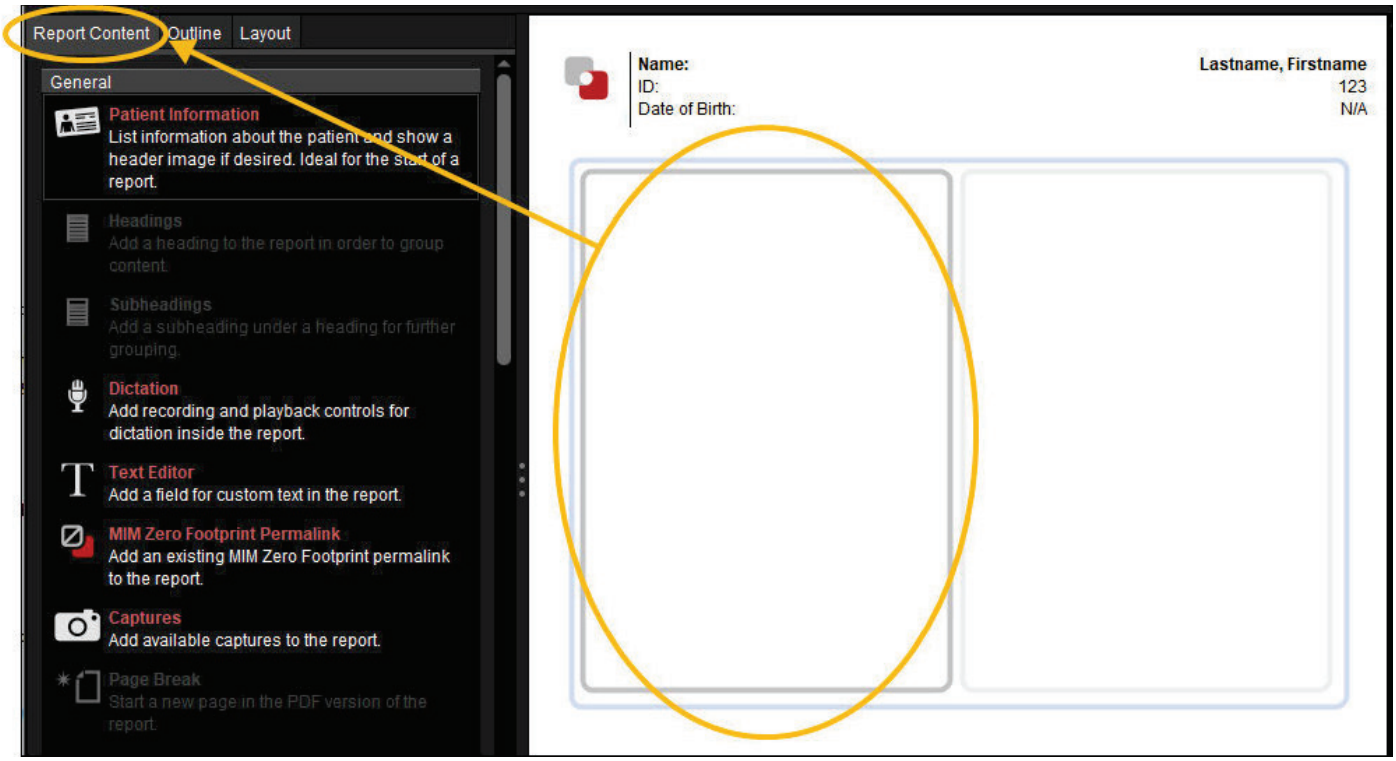
Arrange Content in Layouts

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.

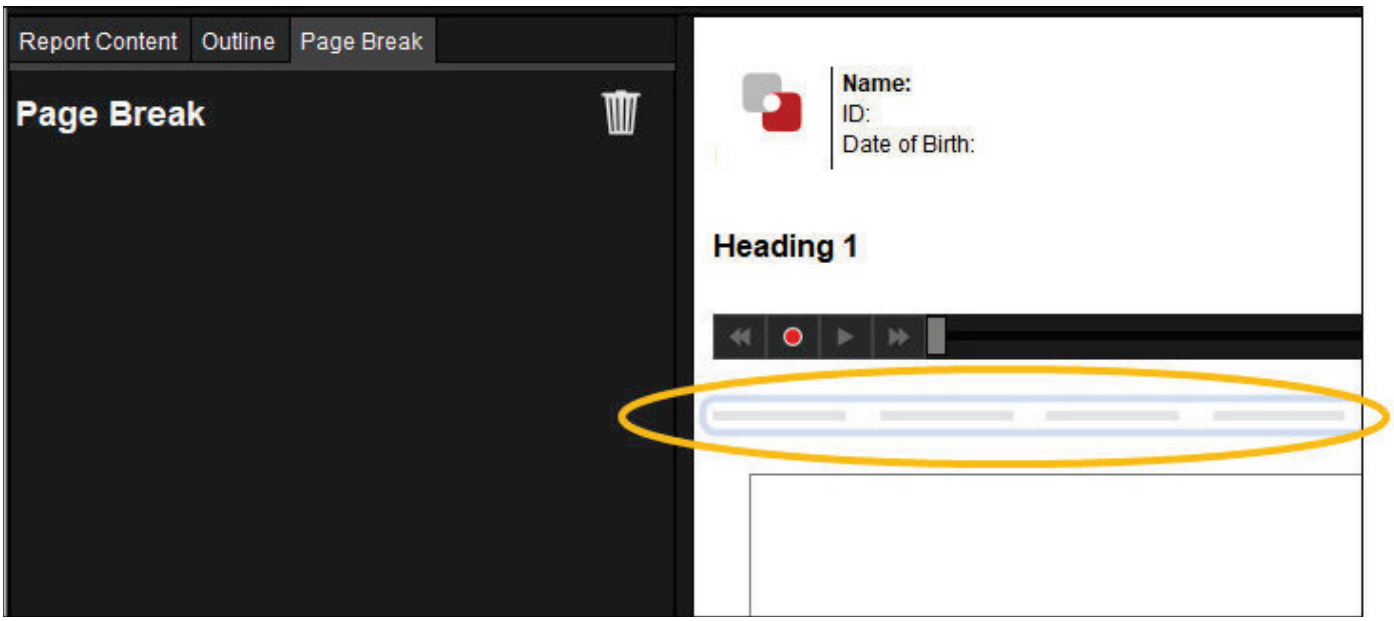


Important: If you delete a layout, all content within that layout is also deleted. You can see which items are within the layout on the **Outline** tab.

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

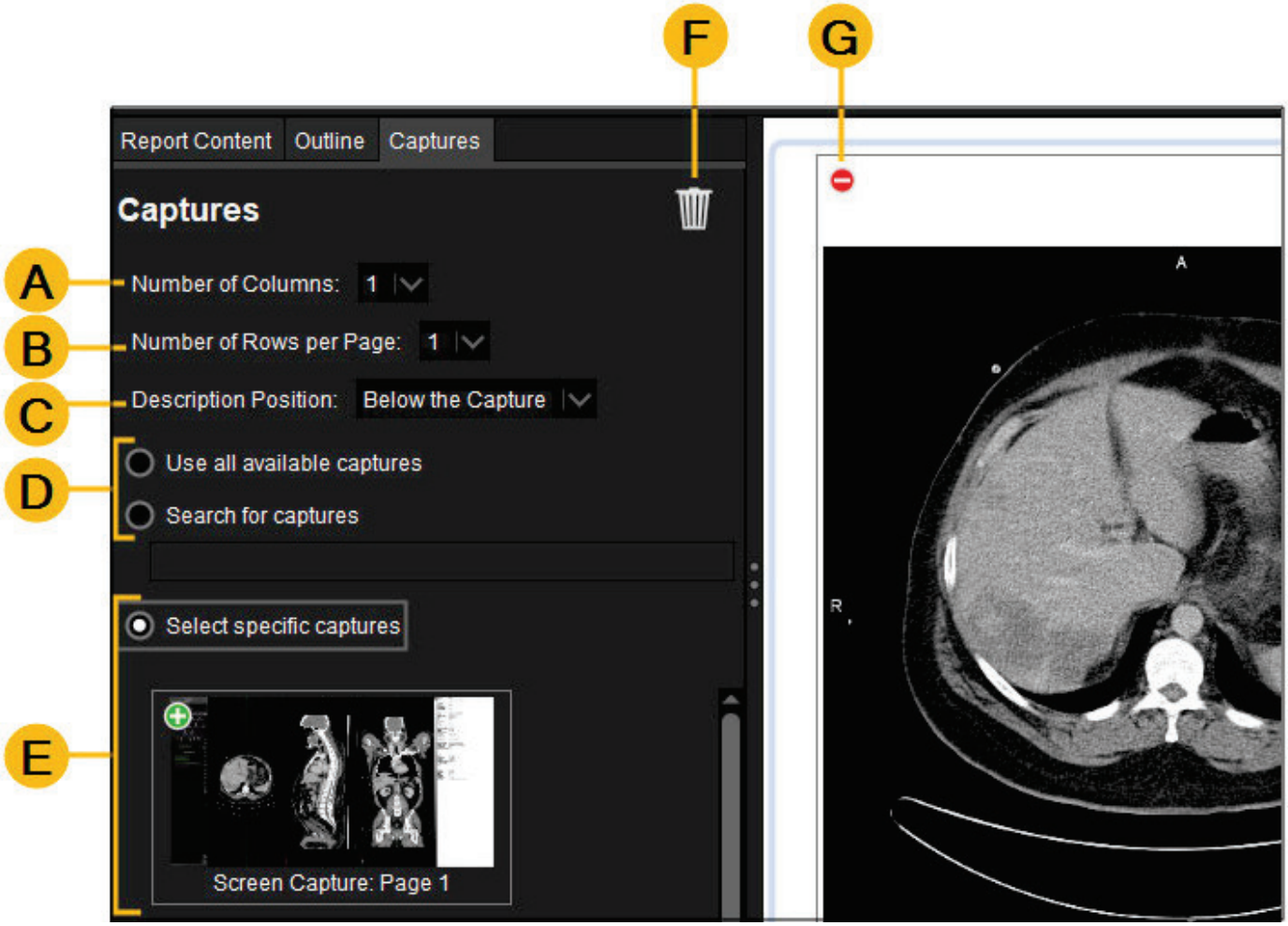
You can add screen captures to structured reports. Use the steps below if you are building a report template or if you want to add a Captures section to an existing report.

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.

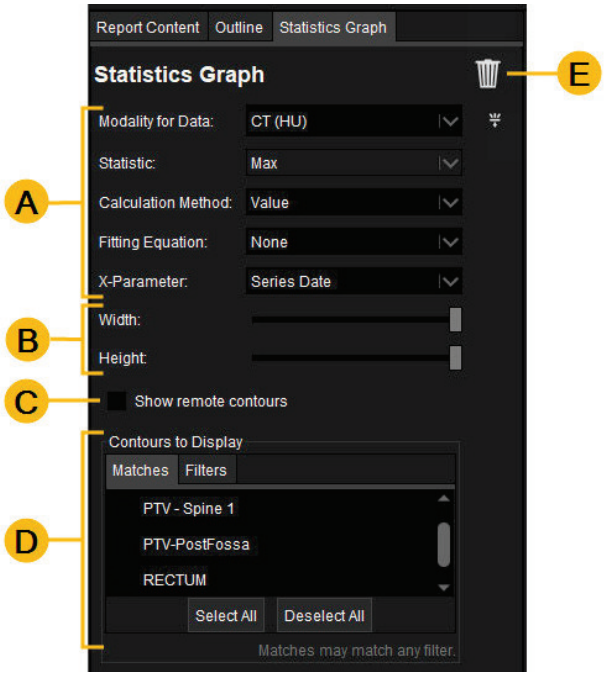
Related: For more information about designing structured report templates, see Create Structured Report Templates.

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.

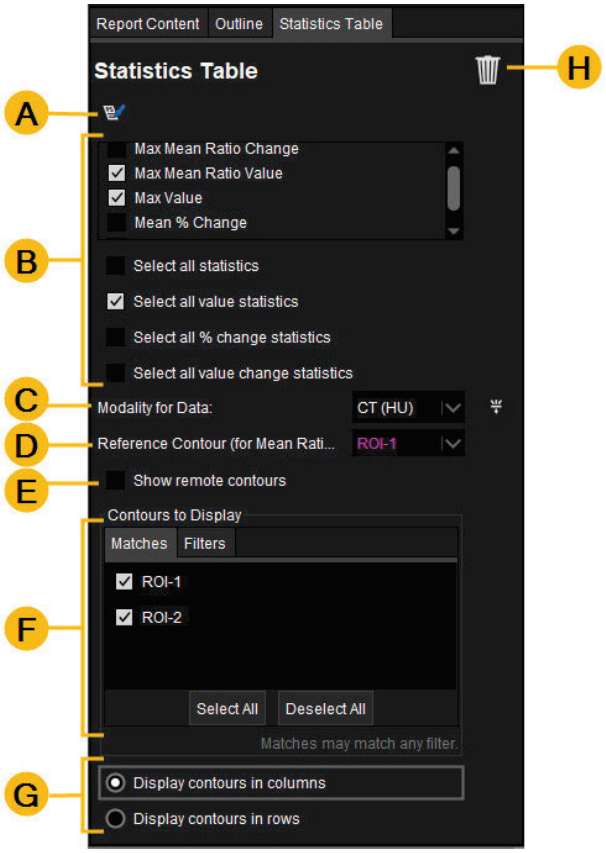
E. Delete the statistics graph from the structured report.

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.

Add Dose Information to Structured Reports

MIMTD-1439 • 02 Jul 2024

Overview

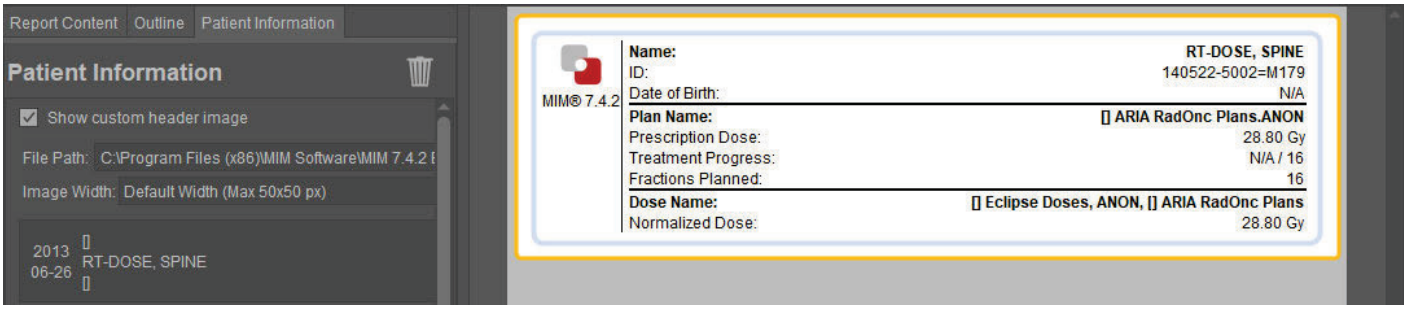
You can include dose constraint and DVH information from a session in the structured report that you create.

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

Contents

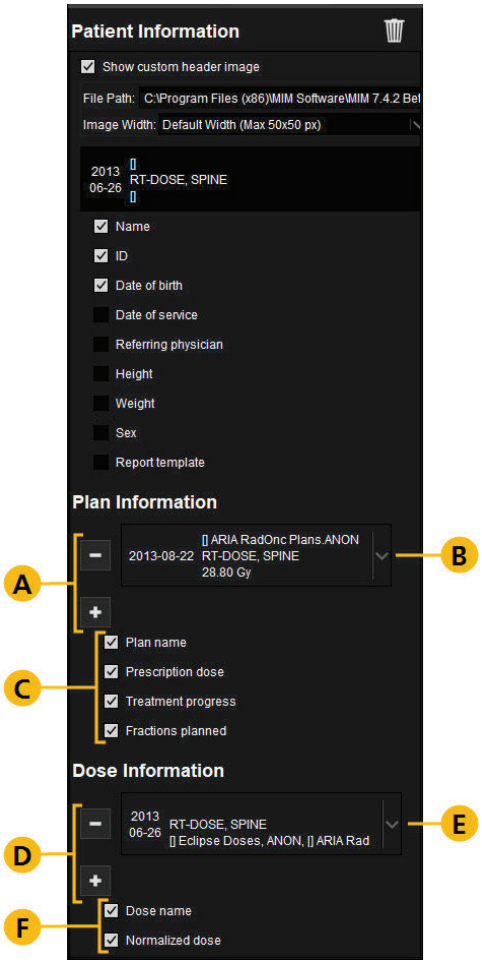
Add Plan and Dose Information to the Patient Information Header

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



Add Plan and Dose Information to the Patient Information Header (MIM 7.4 and Later)

Use these tips to make adjustments in the Patient Information tab:

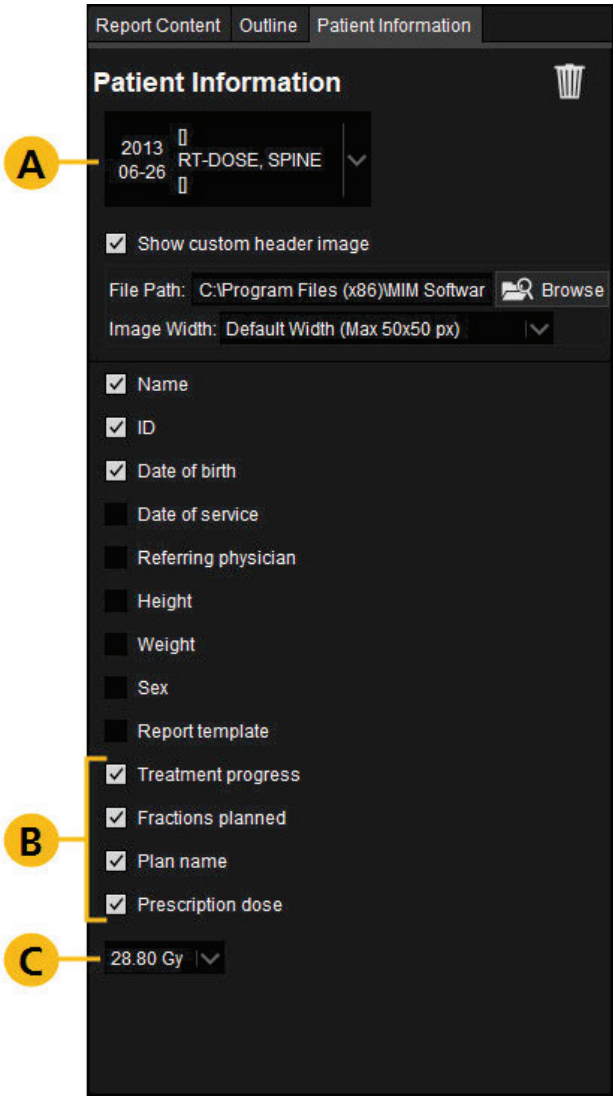


A. To add a plan to the patient information header, click the add ✚ button. To remove a plan from the patient information header, click the remove ▬ button.
B. Use the dropdown to choose from the available plans.
C. Select which plan information to include in the patient information header.
D. To add a dose to the patient information header, click the add ✚ button. To remove a dose from the patient information header, click the remove ▬ button.
E. Use the dropdown to choose from the available doses.
F. Select which dose information to include in the patient information header.

Add Plan and Dose Information to the Patient Information Header (MIM 7.3 and Earlier)

Caution: In MIM 7.3 and earlier, only dose values are shown in the patient information header. These doses are not labeled. Consider opening a session with a single dose before creating a structured report to ensure you include the desired dose in the patient information header. Or, upgrade to MIM 7.4, where dose labels provide clarity.

Use these tips to make adjustments in the Patient Information tab:



A. Select the series with the associated plan or dose information that you want to include in the patient information header.

B. Select which plan and dose information to include in the patient information header.

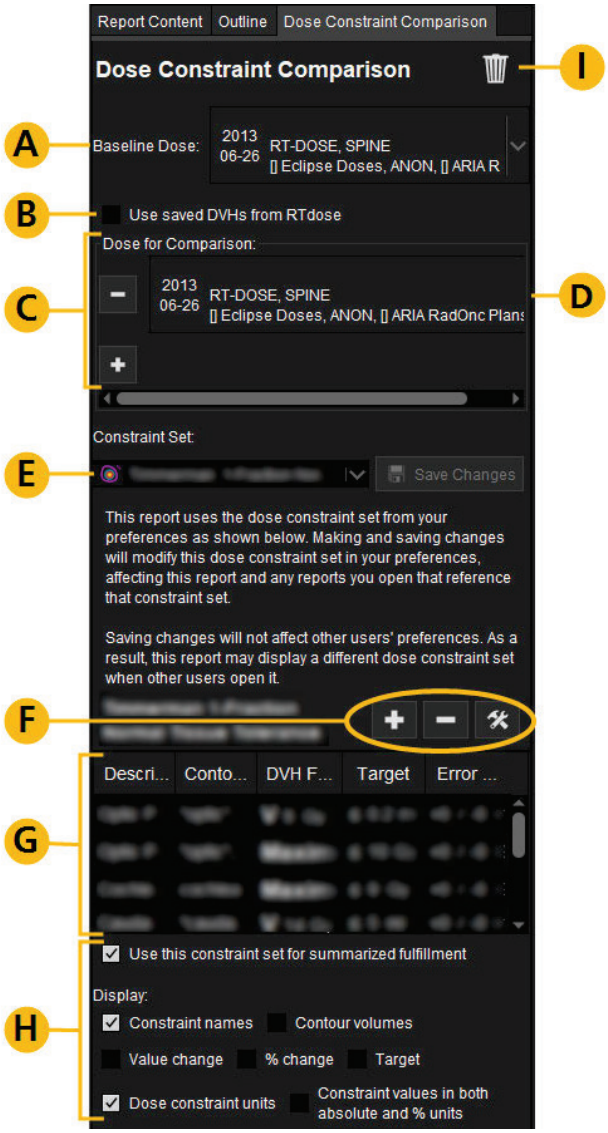
C. Select the dose to include in the patient information header.

Important: When choosing a dose to include in the Patient Information header, only the dose values are displayed. Refer to doses included in the Dose sidebar to ensure that the desired dose matches the dose value selected.

Add a Dose Constraint Comparison

Click **Dose Constraint Comparison** in the **Report Content** tab or the top toolbar of the Structured Report Builder.

Use these tips to make adjustments in the **Dose Constraints Comparison** tab:



A. Select the dose that the constraints will be compared to.

B. Choose whether to use saved DVHs from the RTdose instead of MIM-generated DVHs.

C. To add a dose to compare to the baseline dose, click the add button. To remove a comparison dose, click remove button.

D. Select which dose to compare to the baseline dose.

E. Select the constraint set to use for the comparison. See the note below about saving changes.

F. To add a new constraint to the set, click the add button. To delete a constraint from the set, click a constraint from the list and click the delete button. For editing options, select a constraint on the list and click the tools button.

G. View and adjust the constraints in the selected dose constraint set.

H. Select additional information to include in the dose constraint comparison table.

I. Delete the dose constraint comparison from the structured report.

Structured reports use the selected dose constraint set from your MIM preferences. If you make changes to the dose constraint set (D in the image above), you are prompted to save your changes:

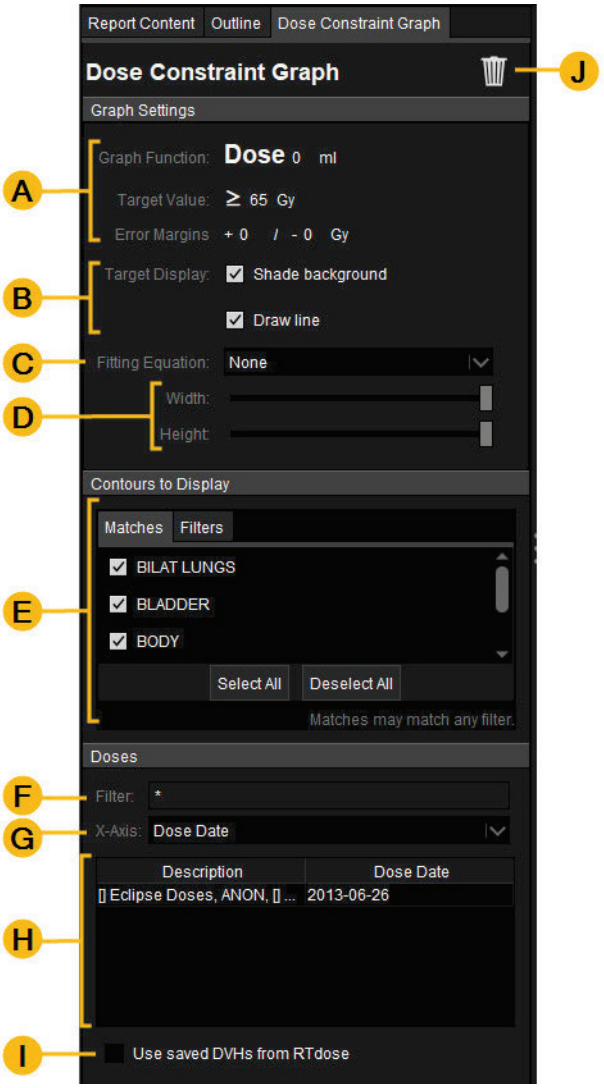
- **Save Changes** — Updates the dose constraint set in your MIM preferences. These changes affect this structured report and any reports that reference this constraint set.
- **Set as Report-Specific Constraint Set** — Updates the dose constraint set for this structured report only. No changes are made to your MIM preferences or other reports.

Important: Neither save option affects other users' preferences. As a result, this structured report may display a different dose constraint set when other users open it based on the other users' MIM preferences.

Add a Dose Constraint Graph

Click **Dose Constraint Graph** in the **Report Content** tab or the top toolbar of the Structured Report Builder. The graph lets you compare contours against a dose constraint and plot the comparison over time.

Use these tips to make adjustments to graph in the **Dose Constraint Graph** tab:



A. Click any value to select a different option or type a new value. For example, click **Dose** and select a different graph function from the dropdown. Or, highlight the error margin values and type new numbers.

B. Choose whether to indicate the target value and error margins on the graph with shading and/or lines.

C. Choose a fitting equation to apply to the graph.

D. To adjust the width and height of the graph, drag the sliders.

E. Select the contours to display in the graph.

F. Type to filter the list of doses to display on the graph.

G. Choose what displays on the x-axis of the graph.

H. View the list of doses that are linked to the current study.

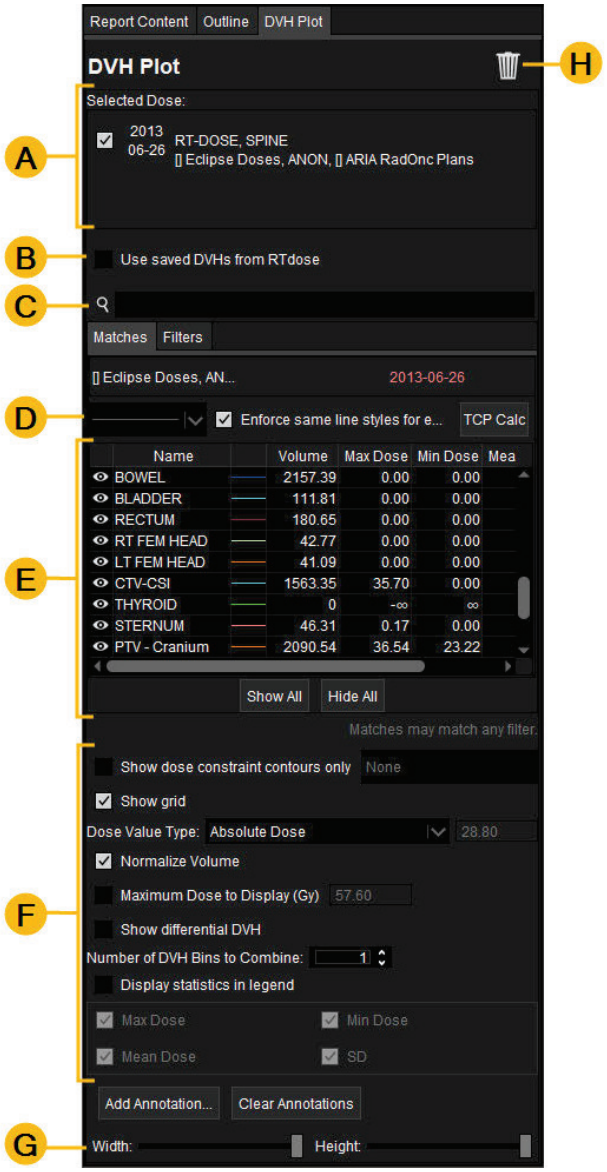
I. Choose whether to use saved DVHs from the RTdose instead of MIM-generated DVHs.

J. Delete the dose constraint graph from the structured report.

Add a DVH Plot

Click **DVH Plot** from the **Report Content** tab or the top toolbar of the Structured Report Builder.

Use these tips to make adjustments in the **DVH Plot** tab:



A. Select the dose or doses to display on the DVH plot.

B. Choose whether to use saved DVHs from the RTdose instead of MIM-generated DVHs.

C. Type keywords to search through a list of contours.

D. Choose a line style for the contours that are displayed on the DVH plot. To calculate tumor control probability for a specific contour, click the **TCP Calc** button.

E. Choose which contours to show on the DVH Plot.

F. Adjust the value types displayed in the DVH plot. For more details about these options, see Dose Volume Histogram (DVH).

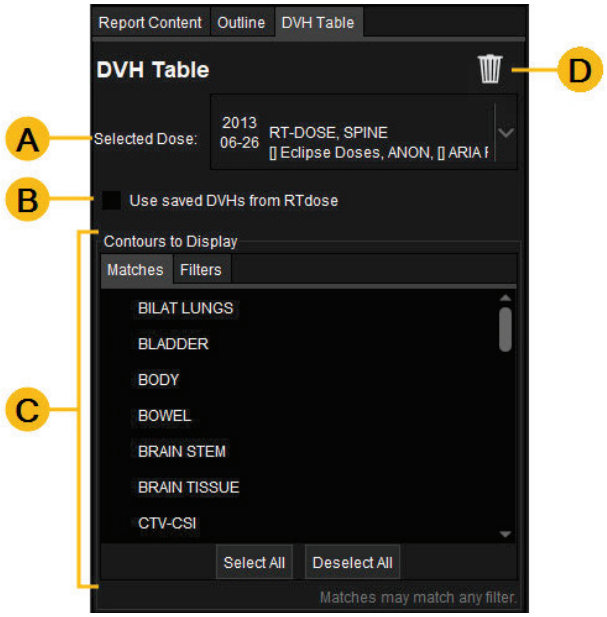
G. To adjust the width and height of the DVH plot, drag the sliders.

H. Delete the DVH plot from the structured report.

Add a DVH Table

Click **DVH Table** from the **Report Content** tab or the top toolbar of the Structured Report Builder.

Use these tips to make adjustments in the **DVH Table** tab:



A. Select the dose information to display.

B. Choose whether to use saved DVHs from the RTdose instead of MIM-generated DVHs.

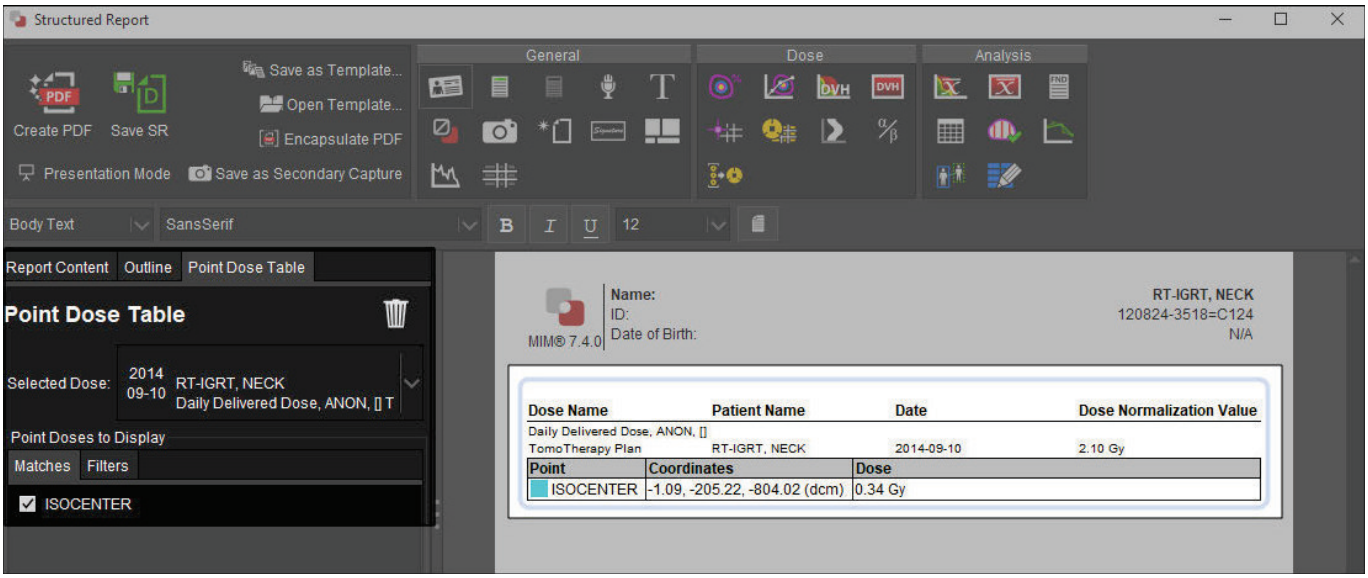
C. Select the contours to display.

D. Delete the DVH table from the structured report.

Add a Point Dose Table

Click **Point Dose Table** from the **Report Content** tab or the top toolbar of the Structured Report Builder.

On the **Point Dose Table** tab, use the dropdown to select which point dose to include in the report. Optionally, if there are many doses, use filters to determine which point doses to display.

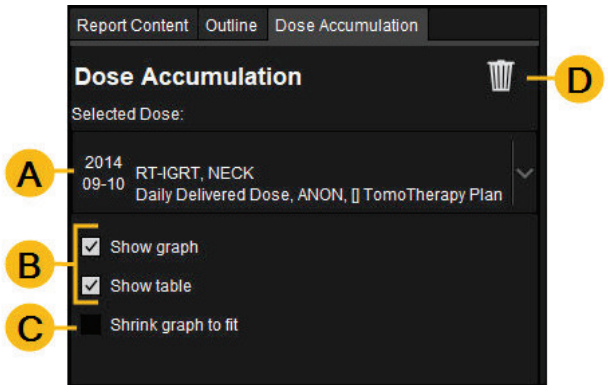


Add Dose Accumulation (MIM 7.3 and Later)

Click **Dose Accumulation** from the **Report Content** tab or the top toolbar of the Structured Report Builder. *MIM 7.2 and earlier*: This functionality is not available.

If you have a MIM-generated accumulated dose within the session, you can include an accumulation graph and/or accumulation tree in the structured report.

Use these tips to make adjustments in the **Dose Accumulation** tab:



A. Select the dose information to display.

B. Choose whether to show the dose accumulation graph, the table, or both.

C. If the graph would cover multiple pages, choose whether you want to shrink the graph to fit.

D. Delete the dose accumulation information from the structured report.

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.

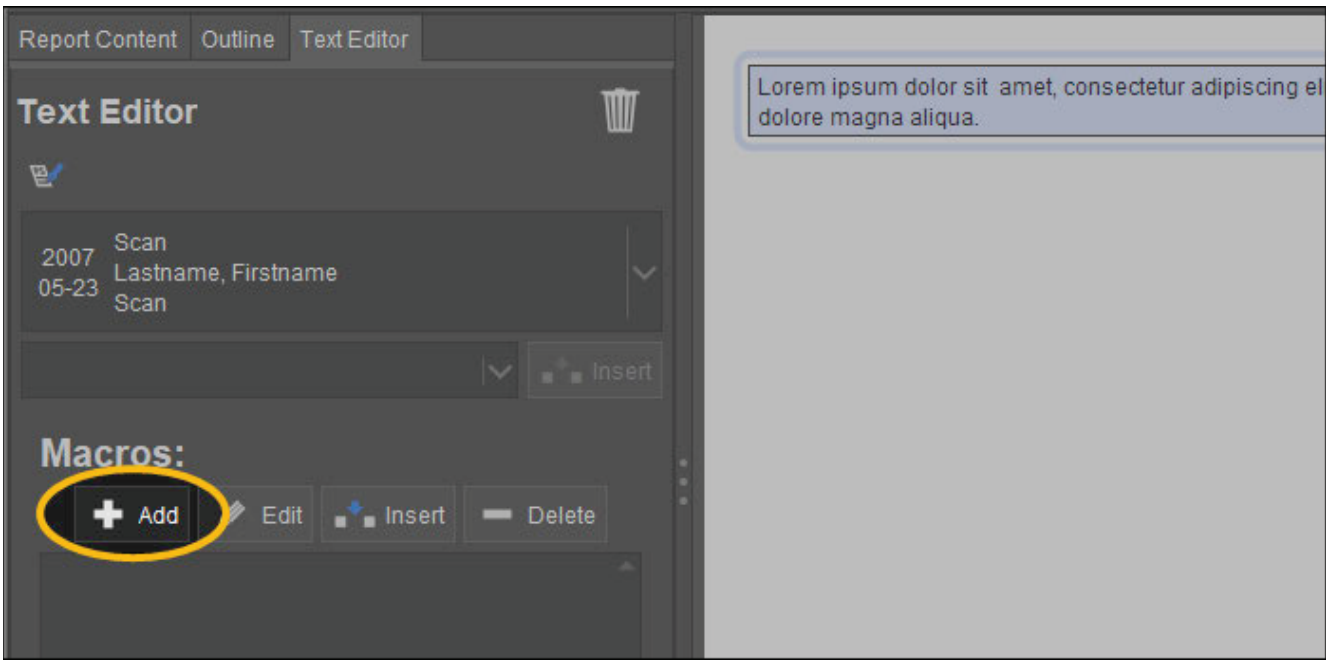
Related: For more information about using report templates to create reports, see Create and Modify Structured Reports.

Contents

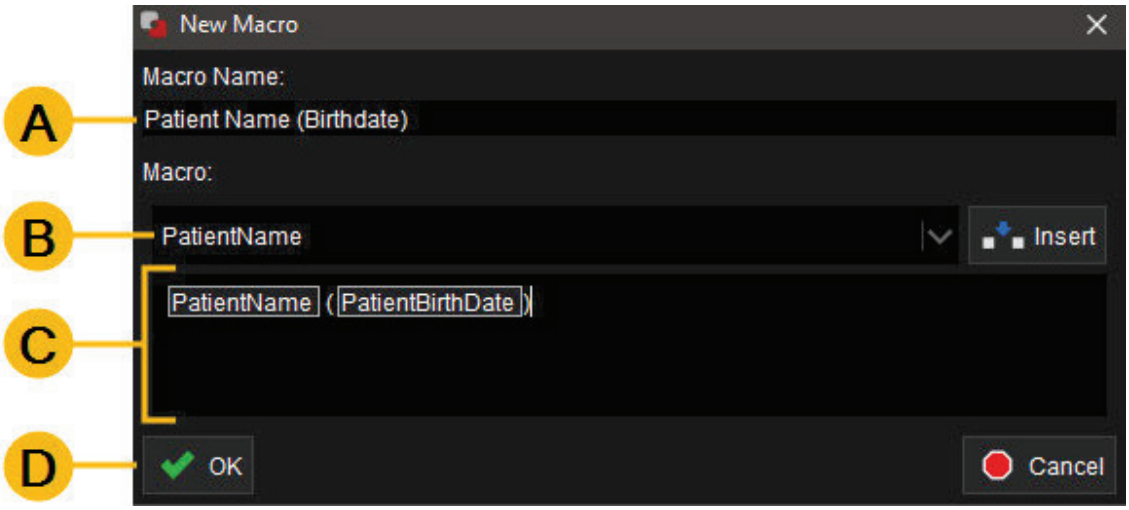
Create and Insert Macros

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.



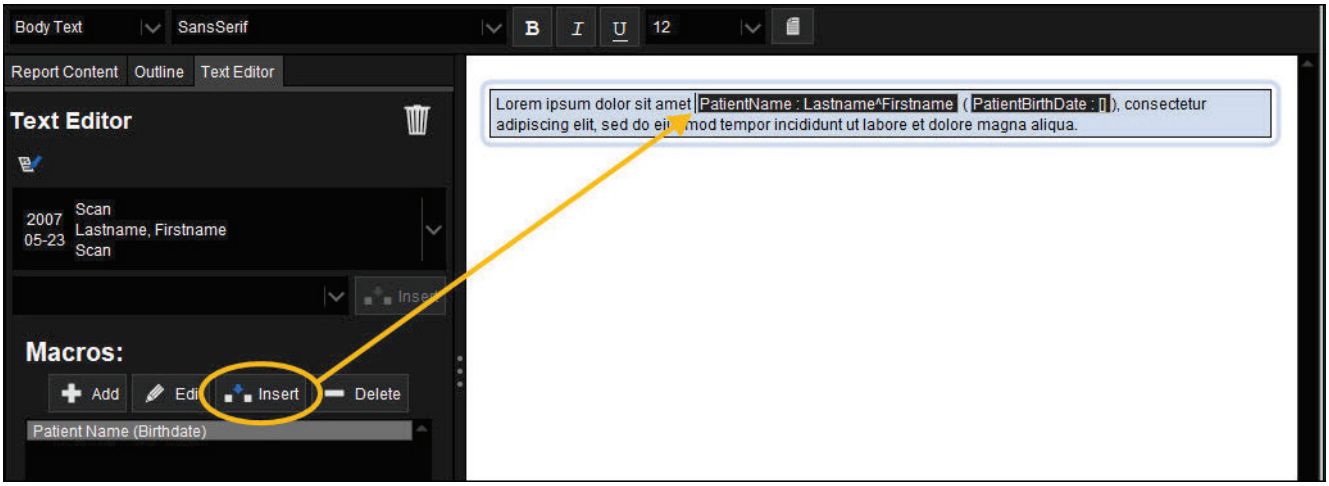
3. Create a new macro:



   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.

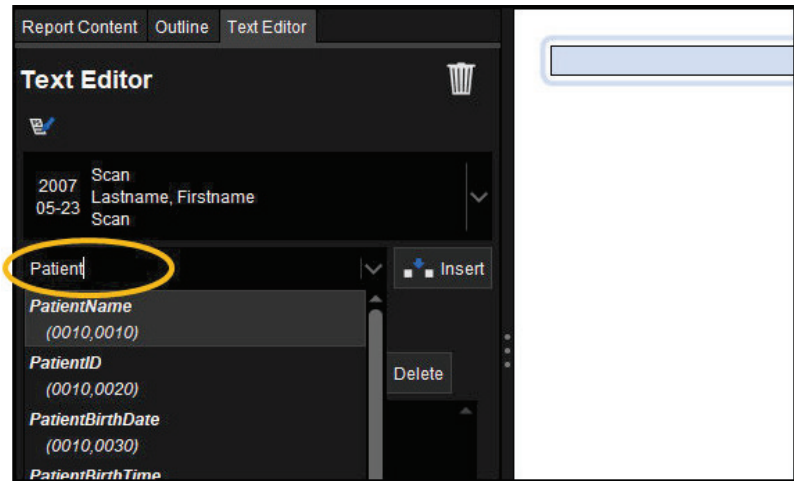
4. Place the cursor in the Text Editor field where you want the macro to appear.

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** 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.

Appendix

Default Keyboard Shortcuts

MIMTD-1363 • 26 Jul 2023

Overview

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

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

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

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

Contents

General

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

Viewing, Localizing, and Scrolling

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

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

Zoom

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

Contrast

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

Annotations, Measurements, and SUV

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

Contouring

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

Command	Windows Keyboard Shortcut	Mac Keyboard Shortcut
Fill Single Slice	F	F
Quick Save Contours	Ctrl+R	Cmd+R
Transfer All Contours	Ctrl+Shift+B	Cmd+Shift+B
Transfer Contour	Ctrl+Shift+T	Cmd+Shift+T

Fusions

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

Screen Captures

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

Series Resolution

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

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

MIMTD-656 • 24 Oct 2023

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

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

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

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

Dosimetry for Targeted Molecular Radiotherapy

A.S. Nelson, MD, D. Mirando, A. Kruzer, R. Niman, N.M. Cole, PhD, T. Stork
MIM Software Inc.

Introduction

Cancers have been treated with internally administered radionuclides since the 1940s.[1,2] This process has been described as Molecular Radiotherapy (MRT). MRT provides a targeted approach for treating cancer through the use of radioisotopes which emit particles (beta and alpha) to deliver dose directly to tumors while minimizing the exposure of healthy tissues.

These therapies have proven to be successful in treating an increasing number of oncologic disorders, including neuroendocrine,[3] prostate,[4] and thyroid cancers.[5]

Molecular radiotherapy is unique because the patient-specific biodistribution can be imaged using SPECT and PET cameras.[6,7] Quantitative images in units of radioactivity, such as Becquerels, can be used to calculate the total number of decays of a radionuclide over time, and application of algorithms such as Voxel S-Value kernel convolution[8] can convert this information into absorbed dose.

In the European Union, dosimetry for treatment planning and verification has been mandated by the European Council directive 2013/59/Euratom[9] which states in Chapter VII, Medical Exposures, Article 56:

"For all medical exposure of patients for radiotherapeutic purposes, exposures of target volumes shall be individually planned and their delivery appropriately verified taking into account that doses to non-target volumes and tissues shall be as low as reasonably achievable and consistent with the intended radiotherapeutic purpose of the exposure."

It is further stated in Chapter II, Definitions, Article 4, Definition 81 that: *"'radiotherapeutic' means pertaining to radiotherapy, including nuclear medicine for therapeutic purposes."*

MIM SurePlan™ MRT provides comprehensive tools needed to efficiently calculate absorbed dose from input imaging data, to aid clinicians in making treatment decisions.

Activity Quantification

The calculation of absorbed dose requires the determination of the total number of decays of a radioisotope. These values can be obtained using quantitative SPECT/CT images or quantitative planar scintigraphic images.[6,7]

Quantitative SPECT/CT

The Absolute quantification of SPECT requires correction for attenuation, scatter, and the conversion of counts to Bq/ml. MIM SurePlan MRT provides a SPECT reconstruction suite that includes Ordered Subset Expectation Maximization (OSEM) reconstruction, CT-based attenuation correction, energy window based scatter correction, depth dependent resolution recovery, and Bq/ml conversion. See the white paper *SPECT/CT Reconstruction with SPECTRA Quant*™ for more details.[10]

Determination of Time-Integrated Activity Concentration

The determination of the total number of decays (i.e., time-integrated activity concentration) for radioisotopes delivered as permanent implants, such as yttrium-90 microspheres, are accomplished by integrating the physical decay curve from the activity concentration image since these therapies do not have biologic clearance. Other radionuclide therapies, such as Lu-177 Peptide Receptor Radiotherapy or I-131 thyroid therapy, undergo both a physical decay and a biological decay since they are not permanently bound to targets in the body.

To capture the biokinetics of the radionuclides, multiple images must be acquired over time. A time-activity curve can be created from these images and integration of the time-activity curve provides an estimate of the total number of decays over time.[7]

These could be SPECT/CT images, a single SPECT/CT image with multiple planar images over time, or a single SPECT/CT image taken at an optimal time point for leveraging previous or population based time-activity information.

Here, we describe the MIM SurePlan MRT **3D Multiple SPECT/CT** Dosimetry Method. Our other white papers describe the Hybrid SPECT/Planar Dosimetry Method[11] and the Single Timepoint Dosimetry methods.[12]

3D Multiple SPECT/CT Method Overview

The 3D method of determining the time-integrated activity concentration is accomplished by modeling activity over time on a voxel or ROI level. In MIM SurePlan MRT, select organ ROIs can be defined using MIM's AI Segmentation tool, Contour ProtégéAI®.[13] Tumor ROIs can be quickly defined using PET Edge®+.[14]

MIM SurePlan MRT creates time-activity curves by aligning quantitative SPECT images from multiple time points with the SPECT/CT from the user-defined reference time point using multiple local rigid registrations[15] for each ROI. First, each time point is aligned to the reference time point. Then the SPECT intensity within a configurable expansion of each ROI is used to create multiple local rigid registrations. These are spliced together to generate a composite-aligned SPECT image for that time point.[16,17] Alternatively, organ-level curve fitting can be accomplished with user-defined regions on each time point, rather than using a reference time point for alignment.

The aligned images can then be used to calculate time-activity curves and absorbed dose. MIM SurePlan MRT allows for dose calculation with voxel-level or organ-level curve fitting. There are two methods of curve fitting and dose calculation; 1) Curve fitting of the time-activity curve generated from the quantitative SPECT activity (per voxel or per organ), time-integration of the curve, then absorbed dose calculation from the time-integrated activity concentration by convolution with a voxel S-value kernel; 2) Dose calculation for each time point to generate dose-rate maps in Gy/s (per voxel or per organ), curve fitting, then time-integration of the dose rate map curves.

The absorbed dose map is corrected for physical density by applying a physical density map (derived from the CT) in which Hounsfield unit (HU) values are mapped to physical density values using a bilinear fit curve.[18]

A line is fit for HU values above water density (HU = 0) and another line is fit for values below water density. The bi-linear fit curves are camera model and kVp specific and are obtained by scanning a CT density phantom.

Activity-Based Image Corrections

MIM SurePlan MRT offers correction methods to better approximate the true activity in ROIs on SPECT. A useful application of these features is to correct for partial volume effects.

Recovery Coefficient Scaling

ROI-Specific Scaling

Scale factors can be entered per region. These values represent the ratio of measured to true activity. For example, if the kidney activity in the image is estimated to be 80% of the true activity, the recovery coefficient would be 0.8.

Volume-Based Scaling

Scale factors per region are determined by an equation relating measured activity to true activity based on volume.

Volume-to-Surface-Area Ratio Scaling

Scale factors per region are determined by an equation relating measured to true activity base on the ratio of the volume and surface area of the region.

The recovery coefficient scaling equations are specific to each camera and can be derived from phantom scanning.

Dual contour approach

As an alternative to recovery coefficient scaling, individual ROIs can be corrected by defining two contours. One contour defines the anatomical volume for dose calculation and the other defines the activity for the dose calculation. This avoids decreasing the mean dose by defining a larger region in order to capture spill-out activity.

Time-Activity Curve Fitting and Area Under the Curve (AUC) Calculation

The AUC calculation method in MIM SurePlan MRT provides a per-region (voxel or ROI) curve fitting and integration. Curve fitting is performed by minimizing the squared differences between the curve from the user selected function and the observed data points. The curve fitting options are trapezoid + exponential, mono-exponential, bi-exponential, bi-exponential (force zero at uptake time 0), and auto-determined which finds the best fitting model from the mono-exponential and bi-exponential options.[19]

Trapezoid + Exponential for Extrapolation

Data is extrapolated from the first time point back to the time of injection using the physical decay of the isotope. The physical decay of the isotope is stored in a preference file. Decays were derived from ICRP Publication 107.[20] The data is extrapolated after the last time point by fitting the last two time points to a mono-exponential decay function.

If the decay is found to be less than the physical half-life of the isotope, then the physical half-life is used for the decay function after the final time point. The portions of the curve between the first and last time points are integrated using the trapezoidal rule.

Mono-Exponential

$$(K = 2) \quad f_2(t) = C_1 e^{-(\lambda_1)t}$$

Bi-Exponential

Useful for cases where there is rapid decay of radioisotope activity (perhaps due to excretion) that is followed by a period of prolonged decay.

$$(K = 4) \quad f_4(t) = C_1 e^{-(\lambda_2)t} + C_2 e^{-(\lambda_2)t}$$

Bi-Exponential (force zero uptake at time 0)

Bi-exponential function where the time-activity curve is forced to start at 0 at the time of injection. Thus, it is useful for cases where the radioisotope uptake cannot be assumed to be instantaneous.

$$(K = 3) \quad f_{4a}(t) = C_1[e^{-(\lambda_1)t} - e^{-(\lambda_2)t}]$$

Where C_1, C_2, λ_1, and λ_2 are model parameters, λ_{phys} is the physical decay constant, and K is the number of model parameters.

Auto-Determined Exponential

The best fit equation for each voxel is found by comparing the *Mono-exponential, Bi-exponential, and Biexponential (force zero uptake at time 0)* models with the limitation that there are enough time points to determine the model parameters (Either $K \leq$ # of time points, or $K <$ # of time points).[19]

The Akaike Information Criterion (AIC)[21] is used as the metric to evaluate each equation where the AIC evaluates the loss of information when a model is used to approximate a true distribution. The lowest AIC value corresponds to the lowest information loss and the model with the lowest AIC is chosen on a per-region (voxel or ROI) basis.

Dose Calculation

The time-integrated activity values generated from the AUC method are used for the calculation of absorbed dose.

Absorbed dose (Gy) is the amount of energy deposited in joules per unit mass of tissue in kilograms. Therefore, to calculate dose, the mass of the tissue in each voxel needs to be determined. The mass of each voxel can be found by creating a physical density map of the patient. See the CT-Based Density Calibration section of this white paper for a description of the procedure for generating the bilinear fit curves.

The Voxel S value convolution (VSV) method for dose calculation in MIM SurePlan MRT is an approach based on the schema in MIRD Pamphlet 17 for nonuniform distribution of radioactivity.[8]

MIRD Pamphlet 17 has applied Monte Carlo methods for radionuclide sources in water to calculate dose deposited in target voxels surrounding a uniform source of the radionuclide in the central voxel. MIM SurePlan MRT VSV kernels are sourced from a publicly available database of kernels simulated in this fashion.[22] These kernels are designed to capture 99% of the deposited energy from a central voxel, with matrix sizes comparable to the FOV of a SPECT. All dose kernels were validated by comparing total decay energy to published ICRP 107 values and dose calculation for generalized activity maps in Olinda EXM 1.1.

For alpha emitters, the VSV kernel is designed such that all energy is deposited in the source voxel with the assumption of local deposition.

Rather than creating a new Monte Carlo kernel for the voxel size of each image, the SPECT image is resampled to the size of the kernel using trilinear interpolation.

Trilinear interpolation is a commonly used method of approximating the value at a 3D coordinate located within a regular 3D grid of data points.[23,24]

CT-Based Density Calibration

The VSV kernels are simulated assuming a certain density, such as water.

Therefore, a correction is necessary for tissues with heterogeneous densities.[25, 26]

The absorbed dose map is corrected for physical density by applying a physical density map derived from the CT where HU values are mapped to physical density values using a bi-linear fit curve.[18]

A line is fit for HU above water density (HU = 0), and another line is fit for values below water density.

The bilinear relationship is derived from scanning a CT density phantom with various tissue-mimicking inserts of known physical density, and relating each physical density to a measured HU value.

The bi-linear fit curves are camera model and kVp specific. Therefore, this process needs to be repeated for different combinations of SPECT/CT cameras and CT imaging protocols.

The resulting dose maps are divided by the physical density map providing a density-corrected absorbed dose calculation.

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WHITE PAPER

Hybrid SPECT/Planar Dosimetry for Targeted Molecular Radiotherapy

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Introduction

Personalized dosimetry for Molecular Radiotherapy (MRT) is used for treatment planning, verification of dose delivery, and guiding subsequent treatment decisions[1]. Calculation of the absorbed dose to regions of interest requires quantification of the total number of decays of the radioisotope. As described in the white paper *Dosimetry for Targeted Molecular Radiotherapy*, these values can be determined using multiple imaging timepoints with quantitative SPECT/CT or planar scintigraphy.

MIM's hybrid dosimetry approach uses a combination of multiple planar imaging timepoints and a single SPECT/CT to calculate absorbed dose. The planar images are obtained over time to characterize the tracer biokinetics and provide the shape of the time-activity curve while the amplitude of the time-activity curve is determined by normalizing the planar activity with the more quantitatively accurate SPECT/CT activity[2,3,4]. This dosimetry approach may be more feasible in certain clinical settings than multiple SPECT/CT dosimetry due to logistical or cost limitations.

Hybrid SPECT/Planar Dosimetry Method

The Hybrid SPECT/Planar Method employs quantitative corrections for the SPECT and planar images. At least one time point with both SPECT and planar acquisitions is required. Regions of interest (ROIs) are created on the SPECT/CT due to the superior identification of organ boundaries on a 3D image.

The planar images are aligned to the SPECT/CT by creating anterior and posterior projections from the SPECT image and then performing a rigid alignment of the planar images from each time point back to the SPECT-derived projections. The ROIs from SPECT/CT are transferred to the planar images. Overlapping regions are determined on the planar images and calculations for mean regional activity are restricted to the non-overlapping source regions. The regional values in the planar image are normalized by the SPECT-to-planar activity ratio.

The spatially-aligned quantitative planar images are then used to calculate a time-activity curve with the mean activity for each ROI. A fit curve and integral of the fit are then calculated[5]. This results in a time-integrated activity value for each pixel as well as a total activity value for each region of interest.

These total regional values are then mapped back to a SPECT/CT to create a final 3D time-integrated activity image in which regional total values match the total values calculated by the integration process. This final image can then be used for dose calculation using the Voxel S-Value Kernel method[6]. Area under the curve (AUC) and absorbed dose calculation methods are detailed in the white paper *Dosimetry for Targeted Molecular Radiotherapy.*

Planar Corrections Method

Quantification of planar images may require corrections for background due to overlapping activity of background regions with the source ROI as well as corrections for scatter and attenuation. The Hybrid SPECT/Planar Dosimetry Method does not apply these corrections by default.

Corrections can be made for background activity using the conjugate-view methodology described in MIRD 16, the Kojima Method[8,9], or an expansion to the Kojima Method. Corrections for scatter are made using the Multiple-Energy Window Subtraction Method[10,11] and corrections for attenuation are made using a CT-derived attenuation map[12]. Conversion from counts to activity is performed by using a ratio of regional SPECT activity (Bq/ml) to planar counts per second derived from a SPECT and planar image obtained on the same day.

Scatter correction

Correction is employed independently for each pixel based on the following equation:

$$C_{sc} = C_p - \left(\frac{C_l}{w_l} + \frac{C_u}{w_u}\right) \times \frac{w_p}{2}$$

where w_p, w_l, and w_u are the widths (keV) of the primary, lower, and upper energy windows, respectively; C_p, C_l, and C_u are the recorded counts in the corresponding energy windows; and C_{SC} is the scatter corrected count value.

Background Correction

Background correction is applied independently for each source region. The CT is used to determine the thickness of the source region to generate an attenuation map and calculate the average attenuation in the background region for each source. Three-dimensional source regions are projected onto each set of planar images where the corresponding background regions are defined.

MIRD 16 background correction is applied to the anterior and posterior images with the following equation:

$$C_{BC} = C_{src} - \frac{T_{src}}{T} C_{bkg}$$

where C_{BC} is the background-corrected counts for a source region, C_{src} is the original counts for the source region, T_{src} is the thickness of the source, T is the thickness of the patient and C_{bkg} is the counts in a defined background region.

The Kojima Method background correction is applied to the anterior and posterior images with the following equations[8]:

$$C_{BC_A} = C_{src_A} - C_{bkg_A}\left(1 - \frac{\left(e^{-\mu_{bkg}L_A} - e^{-\mu_{bkg}(L_A+t)}\right)}{1 - e^{\mu_{bkg}T}}\right)$$

$$C_{BC_P} = C_{src_P} - C_{bkg_P}\left(1 - \frac{\left(e^{-\mu_{bkg}(T-L_A-t)} - e^{-\mu_{bkg}(T-L_A)}\right)}{1 - e^{\mu_{bkg}T}}\right)$$

where C_{BCA} and C_{BCP} are the background-corrected counts in the anterior and posterior planar images; C_{src_A} and C_{src_P} are the anterior and posterior source region detected counts; C_{bkg_A} and C_{bkg_P} are the detected counts within the background region in the anterior and posterior images; L_A is the distance between the anterior edge of the patient and the anterior edge of the source region; and T is the thickness of the patient. All non-background parameters are calculated on a per-pixel basis.

The expanded Kojima's Method builds upon the concept of background correction to account for concave structures, such as the kidneys, allowing for disjointed volumes that contribute to the 2D ROI activity.

Attenuation Correction

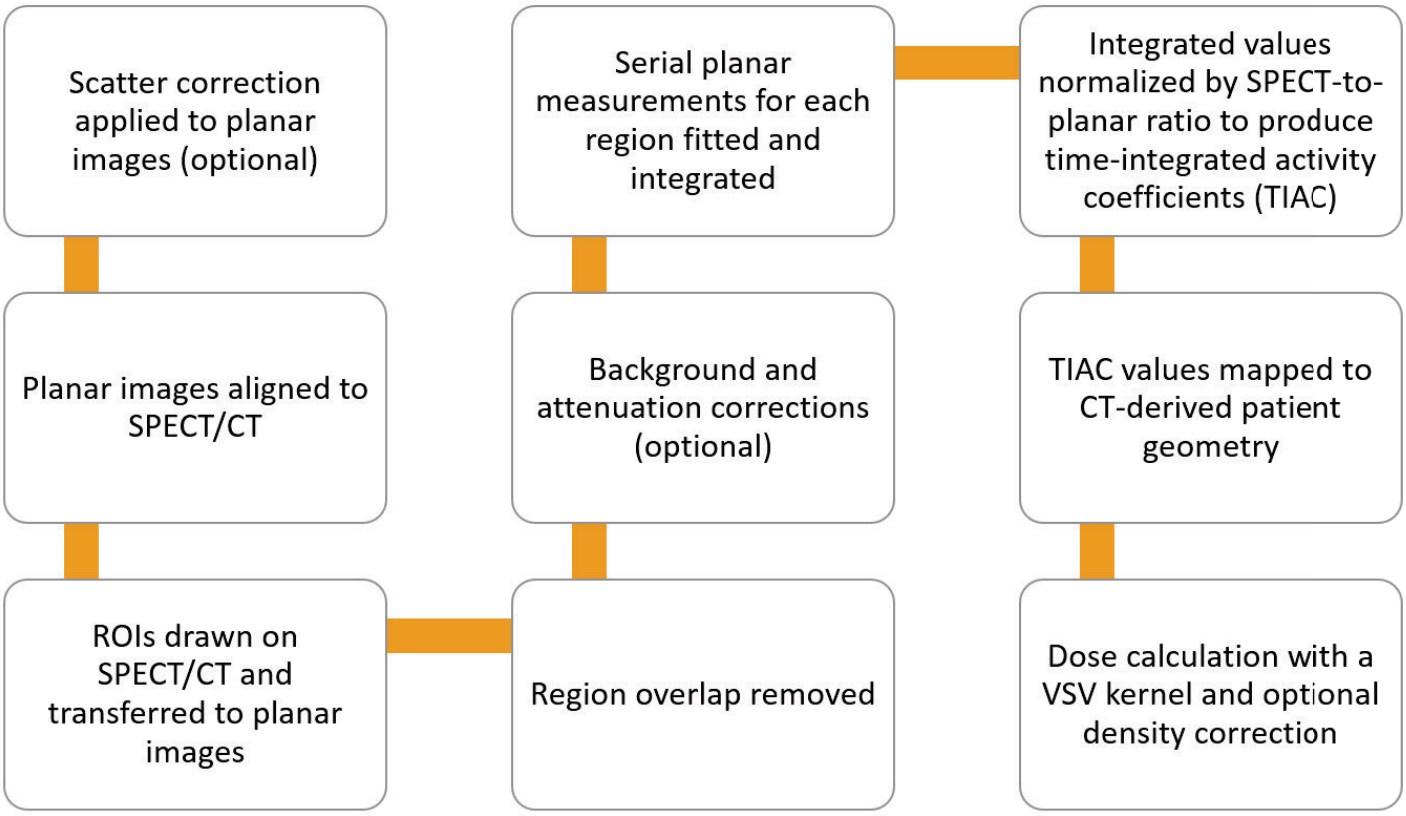
Attenuation correction is also applied independently for each source region. The geometric mean of the anterior and posterior images is then taken, and the per-pixel attenuation corrected counts value C_{AC} is calculated according to MIRD 16[7]:

$$C_{AC} = \frac{C_{GM}}{\sqrt{e^{-\mu_{sum}V_{AP}}}} f$$

Here, C_{AC} is the per-pixel attenuation-corrected counts, C_{GM} is the per-pixel geometric mean counts, μ_{sumV} is the summed projection of the attenuation map in the anterior direction, and V_{AP} is the voxel size in the anterior-posterior direction. The correction factor, f, is to account for attenuation within the source which is computed as:

$$f = \frac{\mu_{sum_{src}}V_{AP}/2}{\sinh\left(\mu_{sum_{src}}V_{AP}/2\right)}$$

See the following flow chart for a step-by-step description of the Hybrid SPECT/Planar Method.


Scatter correction applied to planar images (optional)
Planar images aligned to SPECT/CT
ROIs drawn on SPECT/CT and transferred to planar images
Region overlap removed
Background and attenuation corrections (optional)
Serial planar measurements for each region fitted and integrated
Integrated values normalized by SPECT-to-planar ratio to produce time-integrated activity coefficients (TIAC)
TIAC values mapped to CT-derived patient geometry
Dose calculation with a VSV kernel and optional density correction

Evaluation of Hybrid SPECT/Planar Dosimetry Method

Purpose

This test analyzed the consistency of dosimetry results between the 3D Multiple SPECT/CT Dosimetry Method and the Hybrid SPECT/Planar Dosimetry Method.

Methods

The SIMIND Monte Carlo program[13] was used to simulate anthropomorphic phantoms based on real anatomy. SPECT and planar images representing both Lu-177 and I-131 activity were generated. Poisson noise was added to the planar and projection data to model realistic noise characteristics. The SPECT images were reconstructed using an OSEM algorithm with 16 iterations and 8 subsets. CT-based attenuation correction, triple energy window-based scatter correction, and resolution recovery were applied. The energy windows used for the 3D Multiple SPECT/CT Method were as follows:

Lu-177 (20% primary, 10% scatter windows)
Lower: [166.4 - 187.2] keV
Primary: [187.2 - 228.8] keV
Upper: [228.8 - 249.6] keV

I-131 (15% primary, 15% scatter windows)
Lower: [282.1 - 336.7] keV
Primary: [336.7 - 391.3] keV
Upper: [391.3 - 445.9] keV

Both dosimetry methods were used to calculate dose to various structures, and mean doses were measured and compared.

Results

LU-177 Dosimetry Method Comparison

Region	SPECT/CT Method Mean (Gy)	Combined Method Mean (Gy)	% Difference Between Methods	Absolute Difference Between Methods (Gy)
Liver	20.97	18.66	-11.7	-2.3
Spleen	33.01	30.82	-6.9	-2.2
Lung_L	12.01	10.75	-11.1	-1.3
Lung_R	12.64	11.14	-12.6	-1.5
Kidney_L	17.92	15.65	-13.5	-2.3
Kidney_R	17.98	15.18	-16.9	-2.8

I-131 Dosimetry Method Comparison

Region	SPECT/CT Method Mean (Gy)	Combined Method Mean (Gy)	% Difference Between Methods	Absolute Difference Between Methods (Gy)
Lung_L	19.57	20.80	6.1	1.2
Lung_R	21.07	23.04	8.9	2.0
Thyroid	300.92	266.58	-12.1	-34.3

Discussion

The results for both Lu-177 and I-131 showed an acceptable level of difference when these two methods were compared. The differences that were seen were attributed to differences in quantitative accuracy between SPECT/CT and planar images.

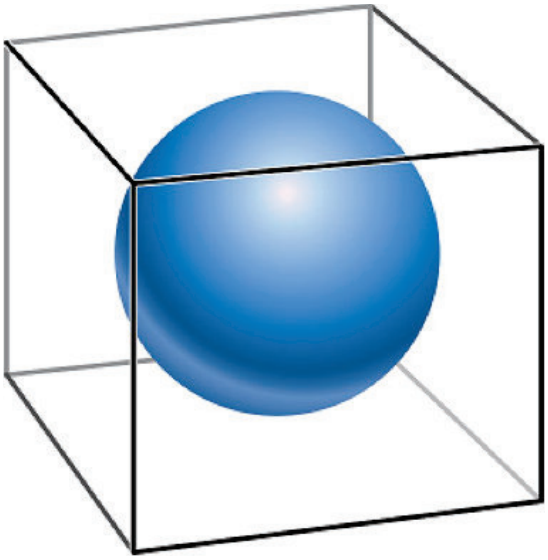
Validation of Planar Correction Methods for Image Quantification

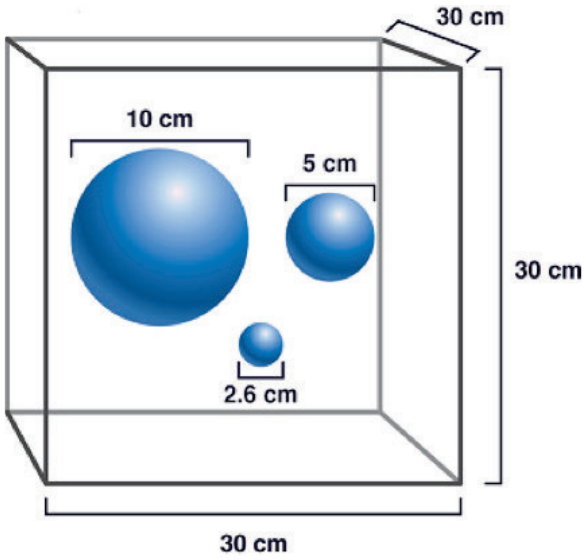
Purpose

The purpose of this test was to validate corrections applied to planar images in order to correct for scatter, background, and attenuation effects as a part of the Hybrid SPECT/Planar Method. Our methodology was chosen in an effort to ensure that organ and tumor statistics were maximally independent of the volume of the region, the source-to-background ratio, and the position of the region within the patient, all critical prerequisites for the use of derived time activity curves in absorbed dose calculations.

Methods

The accuracy of planar corrections for attenuation, scatter, and background (using the Kojima Method[8]) were verified in simulated phantoms. The average errors were less than 12% for all regions, except for the smallest region (2.6 cm) with 21% error for Lu-177 and 17% error for I-131 where the partial volume effect lowered accuracy as expected. In all cases, the software passed its performance requirements and met specifications. The SIMIND Monte Carlo program[13] was used to simulate planar anterior and posterior images of both Lu-177 and I-131 spheres of multiple sizes within a cubic background. The spheres were evaluated at both central and offset locations within the phantom. All images were generated with two different source-to-background ratios. For each test, a "gold standard" image was generated by simulating anterior and posterior planar images with no attenuation or scattering effects added and then creating a geometric mean from which reference counts could be measured. Images with and without the corrections applied were then compared to the "gold standard."





Results

Lu-177, Sources Centered

Total Counts Comparison in Source Regions (8:1 source to background ratio)						
		Total counts in source region			% Error between total counts	
	Source Diameter	Gold Standard (GS)	MIM No Corrections	MIM With Corrections	MIM No Corrections vs GS	MIM With Corrections vs. GS
Phantom 1	20 cm	4649123	1351854	5129947	-70.9	10.3
Phantom 2	10 cm	972730	353519	1104219	-63.7	13.5
	5 cm	105143	63469	114343	-39.6	8.7
	2.6 cm	10676	14862	7179	39.2	-32.8

Total Counts Comparison in Source Regions (4:1 source to background ratio)						
		Total counts in source region			% Error between total counts	
	Source Diameter	Gold Standard (GS)	MIM No Corrections	MIM With Corrections	MIM No Corrections vs GS	MIM With Corrections vs. GS
Phantom 1	20 cm	3323265	1167010	3579087	-64.9	7.7
Phantom 2	10 cm	534523	280863	593529	-47.5	11.0
	5 cm	58486	58526	57533	0.1	-1.6
	2.6 cm	6511	15162	4847	132.9	-25.6

Lu-177, Sources Offset Anteriorly

Total Counts Comparison in Source Regions (8:1 source to background ratio)						
		Total counts in source region			% Error between total counts	
	Source Diameter	Gold Standard (GS)	MIM No Corrections	MIM With Corrections	MIM No Corrections vs GS	MIM With Corrections vs. GS
Phantom 1	20 cm	4637319	1378932	5051053	-70.3	8.9
Phantom 2	10 cm	973233	367433	1078513	-62.2	10.8
	5 cm	104303	65945	109808	-36.8	5.3
	2.6 cm	11355	15377	11251	35.4	-0.9

Total Counts Comparison in Source Regions (4:1 source to background ratio)						
		Total counts in source region			% Error between total counts	
	Source Diameter	Gold Standard (GS)	MIM No Corrections	MIM With Corrections	MIM No Corrections vs GS	MIM With Corrections vs. GS
Phantom 1	20 cm	3312527	1200234	3543174	-63.8	7.0
Phantom 2	10 cm	530468	290669	556330	-45.2	4.9
	5 cm	58387	60205	59292	3.1	1.6
	2.6 cm	6667	15583	4877	133.7	-26.8

I-131, Sources Centered

Total Counts Comparison in Source Regions (8:1 source to background ratio)						
		Total counts in source region			% Error between total counts	
	Source Diameter	Gold Standard (GS)	MIM No Corrections	MIM With Corrections	MIM No Corrections vs GS	MIM With Corrections vs. GS
Phantom 1	20 cm	14807366	4909939	14717608	-66.8	-0.6
Phantom 2	10 cm	3097945	1305804	3186853	-57.8	2.9
	5 cm	322599	226958	321183	-29.6	-0.4
	2.6 cm	32111	52402	25365	63.2	-21.0

Total Counts Comparison in Source Regions (4:1 source to background ratio)						
		Total counts in source region			% Error between total counts	
	Source Diameter	Gold Standard (GS)	MIM No Corrections	MIM With Corrections	MIM No Corrections vs GS	MIM With Corrections vs. GS
Phantom 1	20 cm	10588143	4180673	10437834	-60.5	-1.4
Phantom 2	10 cm	1709137	1013879	1746004	-40.7	2.2
	5 cm	179022	205115	156743	14.6	-12.4
	2.6 cm	20858	53152	16620	154.8	-20.3

I-131, Sources Offset Anteriorly

Total Counts Comparison in Source Regions (8:1 source to background ratio)						
		Total counts in source region			% Error between total counts	
	Source Diameter	Gold Standard (GS)	MIM No Corrections	MIM With Corrections	MIM No Corrections vs GS	MIM With Corrections vs. GS
Phantom 1	20 cm	14781819	5013789	14740238	-66.1	-0.3
Phantom 2	10 cm	3077032	1344049	3164920	-56.3	2.9
	5 cm	322353	235699	325352	-26.9	0.9
	2.6 cm	27672	52211	23441	88.7	-15.3

Total Counts Comparison in Source Regions (4:1 source to background ratio)						
		Total counts in source region			% Error between total counts	
	Source Diameter	Gold Standard (GS)	MIM No Corrections	MIM With Corrections	MIM No Corrections vs GS	MIM With Corrections vs. GS
Phantom 1	20 cm	10592017	4283836	10332392	-59.6	-2.5
Phantom 2	10 cm	1694707	1040752	1694292	-38.6	0.0
	5 cm	182040	212028	162702	16.5	-10.6
	2.6 cm	18190	53640	12395	194.9	-31.9

Discussion

The results from both the Lu-177 and I-131 testing were found to be clinically acceptable. The % error after applying corrections improved significantly for both isotopes. Larger errors seen with the smallest source sphere (2.6 cm) were attributed to sub-optimal measurement of counts from the small source. Caution should be taken when evaluating small regions, especially if the source-to-background ratio is low.

Effect of Planar Correction Method on Absorbed Dose Calculation

Purpose

The purpose of this test was to determine the effect of background correction method on absorbed dose calculation with the Hybrid SPECT/Planar Dosimetry Method. We compared three methods for background correction as well as not employing planar corrections to the 3D Multiple SPECT/CT Dosimetry Method. Absorbed dose result accuracy was evaluated for liver, kidney, and tumor ROIs.

Methods

The effect of planar corrections on the accuracy of the absorbed dose calculated with the Hybrid SPECT/Planar Dosimetry Method was investigated with nine patients and 13 therapy cycles of ^{177}Lu-DOTATATE. The SPECT/CT used for the hybrid method was the ~96 hour timepoint due to the increased source to background ratio compared to earlier timepoints. Kidneys and livers were segmented on the CT using a convolutional neural network and subsequent manual adjustment. Up to three tumors were identified by a physician and segmented on the SPECT using a gradient and intensity-based algorithm.

Dosimetry was conducted with two timepoints (Earliest planar and ~96 hour SPECT/Planar) and three or four timepoints using the Hybrid SPECT/Planar Method and compared to multi SPECT/CT dosimetry with 3/4 timepoints as the "gold standard." Results are shown for dosimetry with no corrections and planar corrections employing each of the three methods for background correction described in the Planar Corrections Method section of this white paper.

Consistent planar/SPECT alignments and consistent overlap-removed and background regions were used to ensure the resultant dose changes were caused solely by the planar corrections.

Results

Differences in absorbed dose values were highly varied across all ROIs with large standard deviations. Absolute differences were the most consistent and the lowest for the liver ROIs with or without planar corrections. These results are summarized in Figure 1 for two and 3/4 timepoint curve fits. Mean (±SD) and median difference values for the 3/4 timepoint absorbed dose results are included in the table below.

Comparison of Absorbed Dose Values with 3/4 timepoint dosimetry						
	Liver		Kidneys		Tumors	
Planar Corrections Applied	**Average Absolute % Difference (±SD)**	**Median % Difference**	**Average Absolute % Difference (±SD)**	**Median % Difference**	**Average Absolute % Difference (±SD)**	**Median % Difference**
No Corrections	5.2 ± 6.8%	0.0%	9.3 ± 8.3%	-6.5%	15.1 ± 18.4%	-7.9%
MIRD 16 BC + SC	12.1 ± 15.7%	3.4%	19.7 ± 21.7%	-14.6%	18.4 ± 30.9%	-6.2%
Kojima's BC+ SC	9.5 ± 13.9%	1.0%	18.1 ± 19.8%	-14.3%	15.0 ± 20.2%	-9.3%
Extended Kojima's BC+ SC	6.5 ± 11.9%	-2.0%	16.8 ± 20.0%	-8.3%	14.6 ± 19.2%	-8.6%

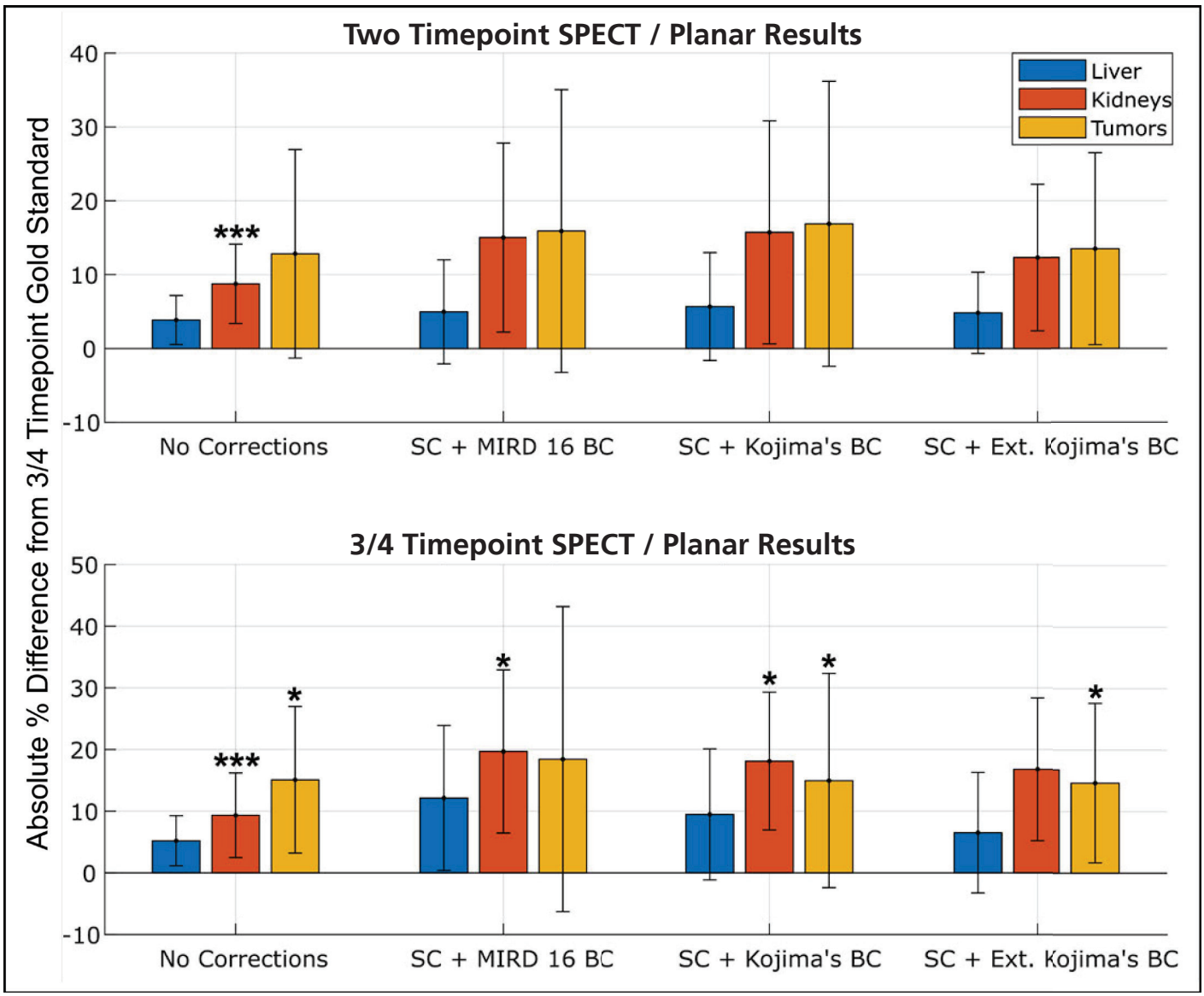


Figure 1. Dosimetry results with Hybrid SPECT/Planar approach using two or 3/4 timepoints compared to gold standard absorbed dose results with 3/4 timepoint multiple SPECT/CT dosimetry. Mean absolute % differences (± SD) are presented for each ROI. Using paired t-tests, significant differences were determined for each set of results and are denoted with (*) for $p<0.05$ or (***) for $p<<0.001$.

Discussion

Many factors affect the Hybrid SPECT/Planar Dosimetry Method and the effectiveness of planar corrections. However, based on these results and the way the planar images are incorporated into the hybrid method, we've determined that CT-based, planar attenuation correction and source self-attenuation correction don't affect dosimetry using the hybrid method. These are essentially scaling factors applied to each timepoint which would affect planar-only dosimetry. With the hybrid method, the planar activity is normalized by the SPECT-to-planar ratio. Thus any increase in counts from scaling would lead to a decrease in the SPECT-to-planar ratio and not affect the data on the time-activity curve (TAC). Effectively, the planar images only contribute to the shape of the TAC and the SPECT determines the activity values.

The need for scatter correction is also minimal. Because the amount of scatter is proportional to the amount of activity, the correction also approximates to a constant scaling factor applied to all planar images. Such scaling factors are canceled out when normalizing the planar images to the SPECT activity.

Background correction may be more effective for certain ROIs, particularly when there is a change in source-to-background ratios between timepoints. These results are based on consistently defined background regions, but it is important to note that defining the background region is difficult on a planar projection. For most source regions, the background is not homogeneous. Therefore, estimating the correct ratio of other structures anterior and posterior to the source region that contribute to the background activity is difficult. For some source regions, such as the right kidney or tumors within the liver, there is very little no-overlap volume.

Outside of planar corrections, the planar alignment to the SPECT/CT can also affect the calculated absorbed dose. Additionally, the timing of the SPECT/CT can have a large effect on the accuracy of the dosimetry method. Ideally, the SPECT/CT would be acquired ~96 hours post-injection due to the increase in source-to-background ratio at this later timepoint compared to earlier timepoints.

Based on the results of this investigation, we have determined that planar corrections will not be applied in the default Hybrid SPECT/Planar Dosimetry Method. The functionality is optional, given the possible need for background corrections for certain ROIs or scatter correction for noisy timepoints.

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Dosimetry for Targeted Molecular Radiotherapy Using a Single Measurement Timepoint

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Introduction

As described in the white paper **Dosimetry for Targeted Molecular Radiotherapy**, the ability to gather patient-specific biodistribution information is a unique feature of internally administered radiotherapies that can potentially be used for treatment planning and verification.

That article details how 3D patient-specific information about the total absorbed dose can be derived in MIM SurePlan™ MRT from imaging at multiple timepoints after the administration of a radionuclide. In particular, imaging at multiple timepoints allows for time-integration of measured rates of nuclear decay ("activities") to derive the total number of decays ("time-integrated activities"). Application of a voxel S-value kernel then allows the conversion of nuclear decays to 3D absorbed dose.

This need for information from multiple timepoints may be difficult for both clinics and patients. In order to calculate full dosimetry, a single patient may be imaged eight to 12 times over the course of treatment, which may be particularly challenging for patients who live far from the clinic. For patients with advanced disease, pain can limit the number of times they are able to undergo a scanning session [1].

To reduce these clinical requirements, several researchers in recent years have proposed methods for dosimetry using a single imaging timepoint. In all of these methods, assumptions are made to convert a single, sampled activity into a time-integrated total number of decays.

MIM SurePlan MRT includes two methods for dosimetry using a single imaging timepoint: the Hänscheid approach [2] and the prior-information approach [3-5]. These two methods provide estimates of the 3D patient-specific absorbed dose to aid clinical decision-making.

Theory

The Hänscheid Approach to Dosimetry

The formalism proposed by Hänscheid et al. [2] for single-timepoint dosimetry starts with the assumption of mono-exponential decay with a patient-specific effective half-life that incorporates both the physical decay of the radioisotope and biological decay of tracer concentration. While a patient-specific effective half-life would require multiple timepoints to measure, the proposed formalism simplifies the equation further by employing a property of mono-exponential equations: if the measurement time is between 75% and 250% of the effective half-life, the time-integral of the exponential equation can be approximated to within 10% of the true integral by using a simplification that eliminates the effective half-life term:

$$\tilde{A} = A(t_{meas}) \times (2^{t_{meas}/T_{eff}} \times T_{eff})/ln(2) \approx A(t_{meas}) \times (2 \times t_{meas})/ln(2)$$

where $\tilde{A}$ is the time-integrated activity, $A(t_{meas})$ is the activity at measurement time t_{meas}, and T_{eff} is the effective half-life.

This means if patient-specific effective half-lives for Molecular Radiotherapy do not vary greatly within a population, a measurement time can be defined such that time-integrated activities of individual patients can be estimated to a reasonable degree of accuracy. Even though bi-exponential modeling is often preferred for molecular radiotherapies, Hänscheid et al. demonstrate that this scheme nonetheless performs well compared to bi-exponential modeling.

They find that the optimal measurement time for ^{177}Lu-DOTATATE is at about 96 hours post-therapy, so measurement times should be close to 96 hours post-therapy when using this dosimetry scheme for ^{177}Lu-DOTATATE.

After time-integrated activity is calculated on a voxel level, dosimetry is performed using a voxel S-value kernel.

The Prior-Information Approach to Dosimetry

Several Molecular Radiotherapies, such as ^{177}Lu-DOTATATE, are delivered over the course of multiple therapy cycles. This creates an opening for a more patient-specific approach to dosimetry that still reduces imaging requirements.

In this prior-information approach, multiple SPECT/CTs are acquired after the first therapy cycle for dosimetry. From these multiple SPECT/CTs, mono-exponential or bi-exponential decay modeling is performed at the organ-level, according to the "Area Under the Curve Calculation" section of the **Dosimetry for Targeted Molecular Radiotherapy** white paper. For additional cycles of therapy, only one SPECT/CT image can be acquired, and the organ exponential equations from the first therapy cycle are then adapted to the current cycle according to the following equation:

$$\tilde{A} = A(t_{meas})/(C_1 e^{-\lambda_1 t_{meas}} + C_2 e^{-\lambda_2 t_{meas}}) \times (C_1/\lambda_1 + C_2/\lambda_2)$$

where C_1, λ_1, C_2, and λ_2 are parameters from a bi-exponential model fit to data from the first therapy cycle.

Propagating decay schemes from one cycle to future cycles assumes that there are no major physiological changes between these cycles that would dramatically change the patient-specific effective decay rate. Clinical biomarkers, such as those relating to kidney function, may help assess the applicability of this dosimetry scheme to individual patients [6]. Also, with this method, after time-integrated activity is calculated on a voxel level, dosimetry is performed using a voxel S-value kernel.

Defining an Optimal Imaging Timepoint

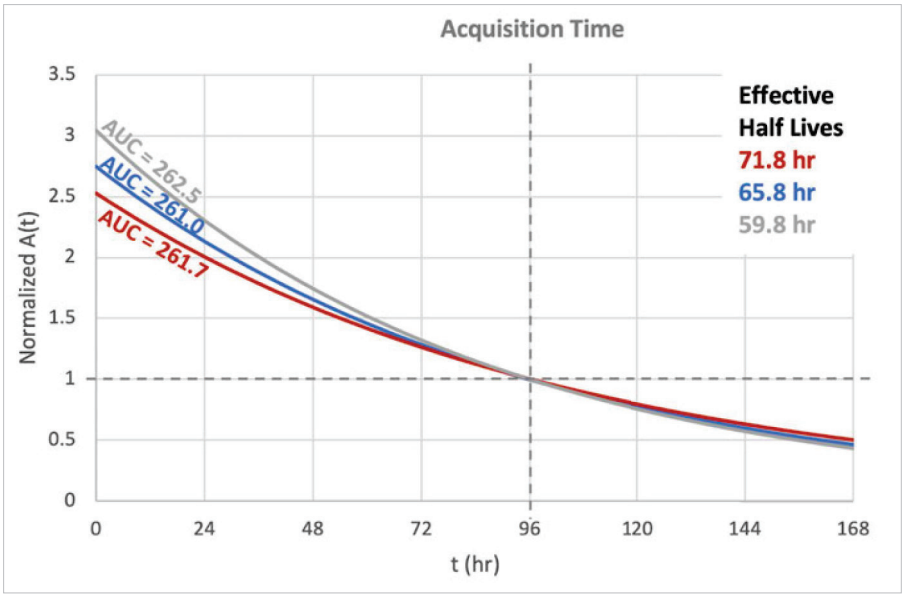
The Hänscheid et al. group found best agreement with multiple-timepoint dosimetry for ^{177}Lu-DOTATATE when imaging at 96 hours post-therapy. This is largely because imaging at this time allows estimation of the time-integrated activity to be robust against some uncertainty in the effective half-life. The average half-life over all organs reported by the Hänscheid et al. group was about 65.8 hours. Figure 1 below shows that fairly substantial deviations in the effective half-life near this value yield very small differences in the area under the time-activity curve ("AUC") when imaging at 96 hours post-therapy.

For the same reason, 96 hours post-therapy may also be an ideal timepoint for the prior-information method for ^{177}Lu-DOTATATE where physiological changes may occur between therapy cycles that affect the effective half-life. However, because not every organ experiences the same pharmacokinetics, it is likely that the optimal imaging timepoint will vary between organs.

This concept can be applied to other therapies, with particular attention paid to the effective half-lives of tumors and organs at risk. For example, Jackson et al. found that the optimal imaging time varied between organs when applying a single-timepoint dosimetry method to ^{177}Lu-PSMA-617, but that only imaging at around 70 hours post-therapy produced <10% error for tumors and most organs at risk [7].

We will see in the **Defining an Optimal Imaging Timepoint (Results)** section how this theory explains the accuracy of results at certain timepoints.

FIGURE 1. *Variations in the true patient effective half-life yield similar estimations in the area under the time-activity curve ("AUC") when imaging at 96 hours post-therapy, assuming mono-exponential decay.*



Evaluation Results

To evaluate the accuracy of single-timepoint dosimetry for ^{177}Lu-DOTATATE, organs-at-risk (OARs) and tumor absorbed doses were calculated for 23 patients from two cohorts across 73 cycles of therapy using both the Hänscheid approach and the prior-information approach. The regions of interest (ROIs) evaluated were the kidneys, liver, bone marrow, and up to five neuroendocrine tumors in the liver or abdomen. Segmented tumors were removed from the liver ROI for analysis.

Accuracy of Single-Timepoint Approaches to Dosimetry for 177Lu-DOTATATE

This section details the evaluation of the "optimal" imaging timepoints from those available in two patient cohorts. Cohort 1 datasets included images acquired around four, 24, or 72 hours post-injection and Cohort 2 datasets included images acquired around four, 24, 96, and 120 hours post-injection. Based on the existing evidence from literature, the 72 hour and 96 hour timepoints were considered the optimal acquisition times for single-timepoint dosimetry. We considered the absorbed dose calculations with multiple-timepoint dosimetry and per-ROI optimized exponential curve-fitting to be the gold standard for accuracy evaluation. Additionally, to understand the effect of acquisition time for OARs and tumors, we conducted another evaluation using each available timepoint as the single timepoint which is detailed in the **Defining an Optimal Imaging Timepoint (Results)** section.

Overall, the average error for the Hänscheid approach across all structures was -0.5 ± 18.5% for Cohort 1 and -1.3 ± 14.7% for Cohort 2. The average error for the Prior-Information approach across all structures was 6.4 ± 24.6% for Cohort 1 and -0.23 ± 14.3% for Cohort 2. Table 1 includes the average deviations of the single-timepoint doses from the multiple-timepoint dosimetry and the 95% confidence intervals for each ROI. Pearson correlation coefficients ranged from 80 – 99% across the OARs and tumors for both cohorts. Correlation plots for the multiple-timepoint and single-timepoint absorbed doses are displayed for each ROI in Figure 2, and Bland-Altman plots are shown in Figure 3.

For kidneys, liver, and tumors, we see that correlation plots closely follow the line of equivalence. There is a greater divergence for bone marrow ROIs, most of which had little uptake and may have been more influenced by noise than other regions. For tumor and liver (which contained unsegmented tumors in many cases), the Hänscheid approach using a 72 hour acquisition time systematically underestimated the multiple-timepoint dose results. Overall, imaging at 96 hours produced more accurate results for both the Hänscheid and prior-information methods than imaging at 72 hours.

CONCLUSION: For kidneys, liver, and tumors, single-timepoint dosimetry results compared well against multiple-timepoint results, with better results at 96 hous (mean error for each structure within 5%) than at 72 hours (mean error for each structure within 15%).

Previous Evidence for Single-Timepoint Dosimetry (Kidney)

There have been previous evaluations of single-timepoint dosimetry with the Hänscheid approach and variations of the prior-information approach. Table 2 is a comparison of kidney absorbed dose accuracy from these studies to our results. In Hänscheid et al., the Day 4 single-timepoint dose was compared to dosimetry using bi-exponential curve fitting for four or more whole-body planar timepoints (4-hour, 1, 2, and 4 day) [2]. In Del Prete et al., the Hänscheid approach (applied to a Day 3 SPECT/CT) and a prior-information approach with two timepoints were compared to a multiple-timepoint approach with piecewise curve fitting: constant activity from the time of administration to the 4-hour SPECT/CT (t1), a trapezoidal function from t1 to the Day 1 SPECT/CT (t2), and a monoexponential function fitted to t2 and the Day 3 SPECT/CT and extended out to infinity [5]. The prior-information approach was also evaluated in Willowson et al. where the curve fitting for three timepoints (4-hour, 1 and 4-5 day SPECT/CT) in the first cycle was used to calculate dose at the Day 1 acquisition in subsequent cycles [4]. The single-timepoint dosimetry was compared to multiple-timepoint dosimetry with mono-exponential curve fitting.

The results from previous evaluations show small average overestimations in the single-timepoint dose with data ranging -3% to 10% differences. Our results show small average overestimations with the 72 hour timepoint and small average underestimations with the 96 hour timepoint.

TABLE 1. *Average differences (± standard deviation) and 95% confidence intervals for each ROI and both cohorts.*

Cohort (timepoint)	ROI	Single-Timepoint Approach	Mean % Difference	95% Confidence Interval Lower Bound	Upper Bound
Cohort 1 (72hr)	Kidneys	Hänscheid	8.0 ± 2.7%	7.0%	9.1%
		Prior-Information	1.9 ± 3.6%	0.5%	3.3%
	Liver	Hänscheid	5.5 ± 12.0%	-1.3%	12.3%
		Prior-Information	5.3 ± 6.1%	1.8%	8.7%
	Bone Marrow	Hänscheid	32.9 ± 16.1%	22.9%	42.9%
		Prior-Information	51.9 ± 50.2%	20.8%	83.1%
	Tumors	Hänscheid	-12.2 ± 12.9%	-15.8%	-8.6%
		Prior-Information	-0.03 ± 15.2%	-4.2%	4.2%
Cohort 2 (96hr)	Kidneys	Hänscheid	-4.0 ± 10.7%	-8.7%	0.7%
		Prior-Information	-0.7 ± 9.2%	-4.9%	3.6%
	Liver	Hänscheid	1.0 ± 7.8%	-4.1%	6.1%
		Prior-Information	0.2 ± 6.5%	-4.4%	4.7%
	Bone Marrow	Hänscheid	-9.3 ± 21.5%	-42.3%	4.8%
		Prior-Information	-3.1 ± 14.7%	-41.3%	10.8%
	Tumors	Hänscheid	1.9 ± 11.6%	-1.3%	5.2%
		Prior-Information	1.8 ± 12.7%	-2.0%	5.5%

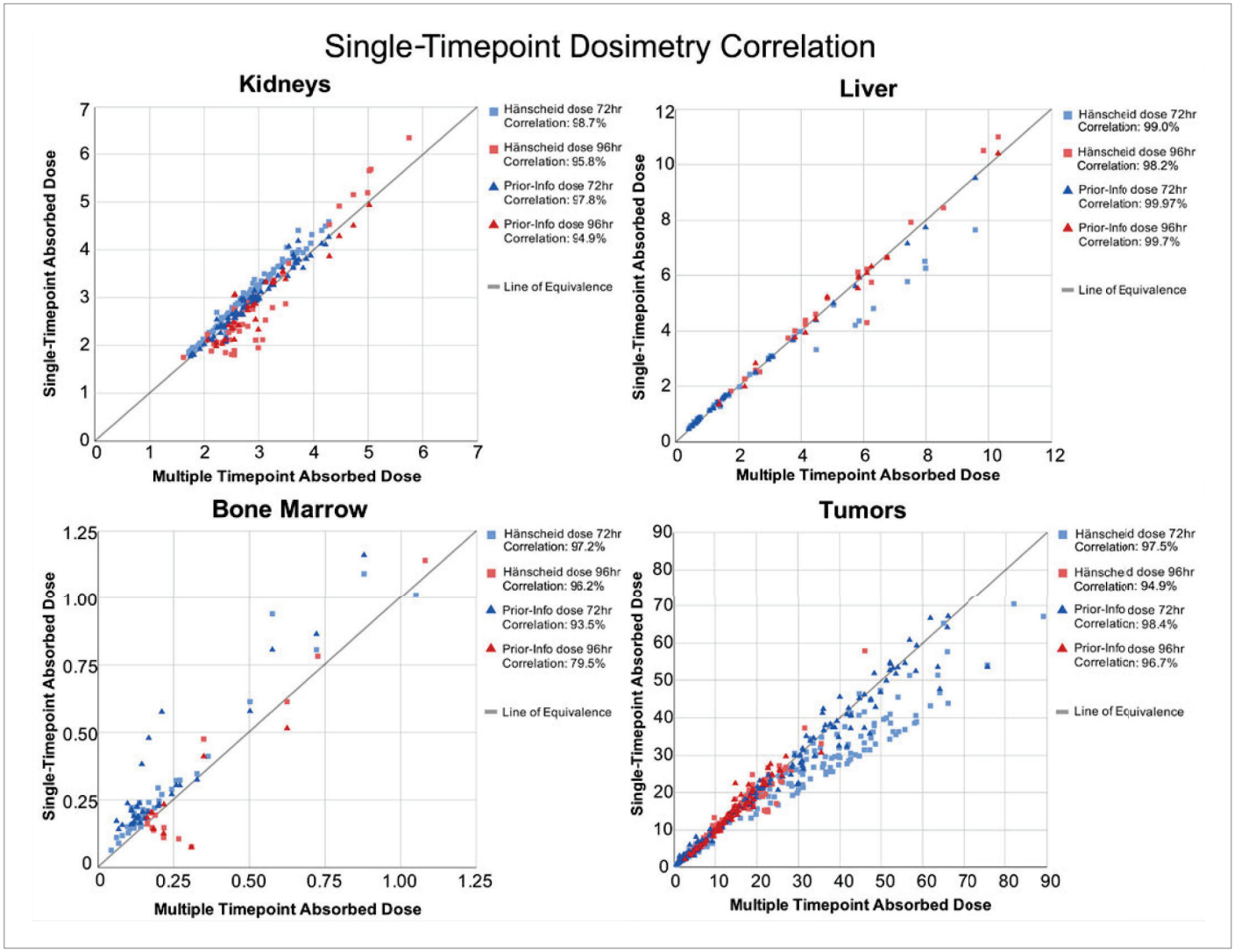


FIGURE 2. *Correlation between the single-timepoint approaches and the multiple-timepoint approach for each ROI. Cohort 1 (72hr STP) is plotted in blue, while Cohort 2 (96hr STP) is plotted in red. Pearson correlation factors are reported for each approach and cohort.*

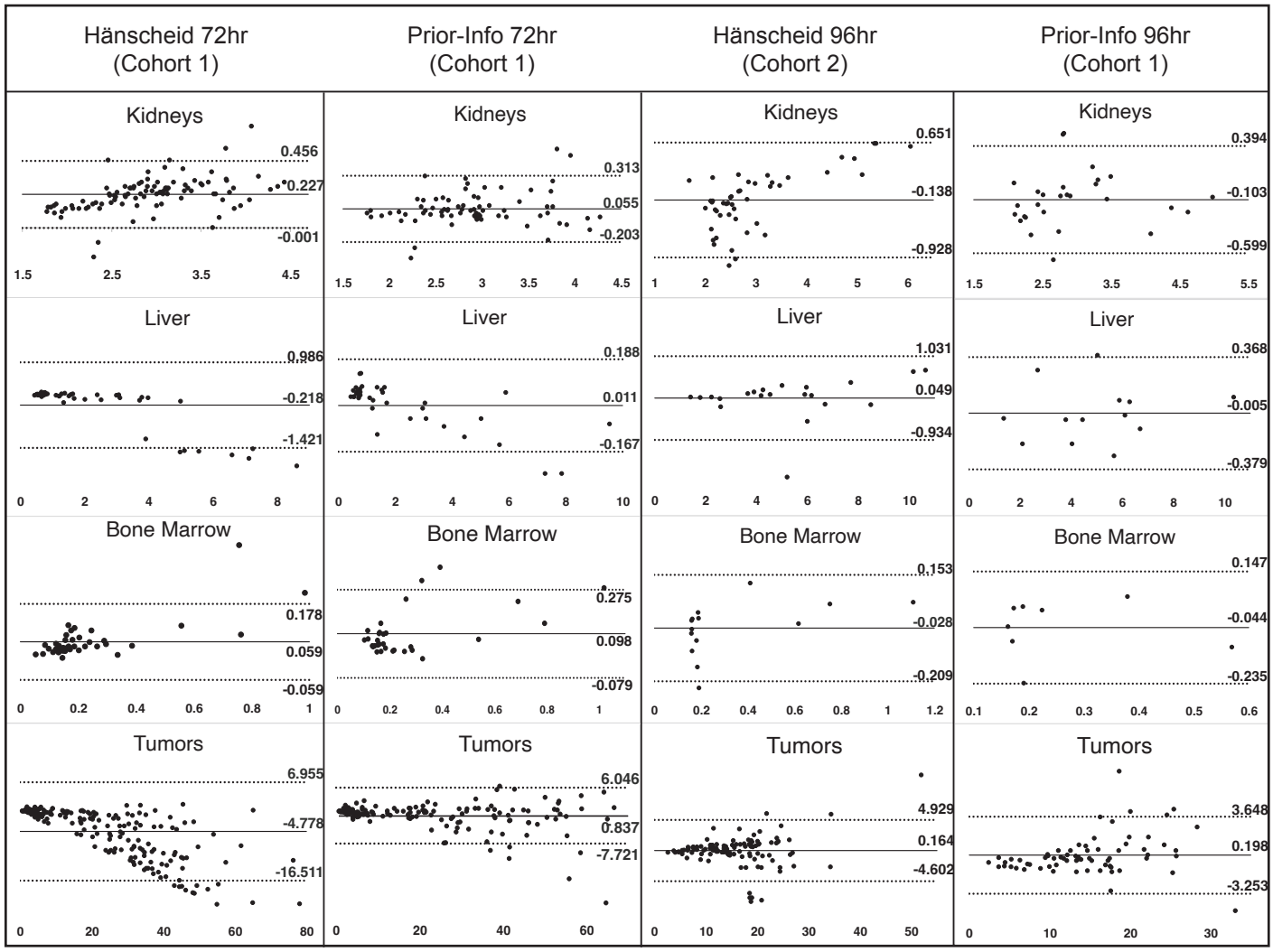


FIGURE 3. *Bland-Altman plots of agreement between the single-timepoint dosimetry approaches and the multiple-timepoint dosimetry approaches.*

TABLE 2. *Comparison of other single-timepoint evaluations to the present evaluation. Median deviations from the multiple-timepoint absorbed dose value for all kidneys are shown. The interdecile range for all results (various sample sizes) are also included. *Note: the Willowson evaluation results do not include the interdecile range of the data; the average difference was 2% with 16% standard deviation.*

Single-Timepoint Approach	#cycles/#patients	Acquisition Time	Median % Difference	Interdecile Range 10% | 90%	
Hänscheid *(this evalutation)*	52/13	72 hour	8.3%	3.5%	10.9%
Hänscheid *(this evalutation)*	24/10	96 hour	-3.8%	-16.3%	8.3%
Prior-Information *(this evalutation)*	39/13	72 hour	1.22%	-1.8%	6.9%
Prior-Information *(this evalutation)*	14/10	96 hour	-2.23%	-10.7%	10.4%
Hänscheid *(Del Prete et al.)*	279/81	72 hour	5.8%	-0.4%	9.2%
Prior-Information *(Del Prete et al.)*	279/81	72 hour	2.2%	-2.0%	7.4%
Hänscheid *(Hänscheid et al.)*	29/29	96 hour	5%	-3.0%	10.0%
Prior-Information *(Willowson et al.)*	80/18	24 hour	1%	N/A*	

Defining an Optimal Imaging Timepoint (Results)

We sought to determine the effect of acquisition time across various ROIs with both of our single-timepoint methods. The acquisition time is highly related to the decay rates of the monoexponential or biexponential fits applied to the activity maps during multiple-timepoint dosimetry. In order to simplify this discussion, we introduce the concept of a dominant half-life, which we take to be the longest half-life present in the multiple-timepoint fit curve. This is the half-life of the exponential component that typically contributes most to the time-integrated activity.

Hänscheid Approach

The theory behind the Hänscheid approach to single-timepoint dosimetry is that if mono-exponential decay is assumed, the error within a certain range of acquisition times $0.75T_{eff} \leq t_{acq} \leq 2.5T_{eff}$ is small. Taking the dominant half-life as T_{eff}, Figure 4 shows that the data generated by MIM is largely in agreement with the theory. Deviations can be primarily attributed to the effect of a second, non-negligible exponential and cross-talk from activity in nearby regions. In particular, some of the largest positive errors are in bone marrow regions that contain very little activity.

Because dominant effective half-lives from literature show prolonged half-lives in tumors and half-lives around 55 hours in kidneys, we can guess before even seeing the results that best results for kidneys will occur with an acquisition time of about $\frac{2.5+0.75}{2}$(55 hour)=89 hour and tumors with a significant permanent retention component (half-life = 159 hour) will produce most accurate results with acquisition times greater than 0.75(159 hour)=119 hour. Thus, compromise will be necessary.

Figure 5 below shows the results from this evaluation. The average absolute tumor error decreases with increasing acquisition time up to the 84-106 hour bin. It might be expected from the above discussion that this acquisition time may not be long enough for tumors, but many tumors investigated had dominant half-lives shorter than the physical half-life of Lu-177, suggesting that permanent retention was not significant based on the image data. Non-tumoral liver regions showed similar behavior to tumors, perhaps due to the effect of unsegmented or micrometastatic tumors in the liver. On the other hand, best results were achieved in kidneys in the 60-84 hour and 84-106 hour bins.

CONCLUSION: For most accurate results across these regions, it is therefore best to image around four days post-therapy. This result is in agreement with the data reported by Hänscheid et al. [2].

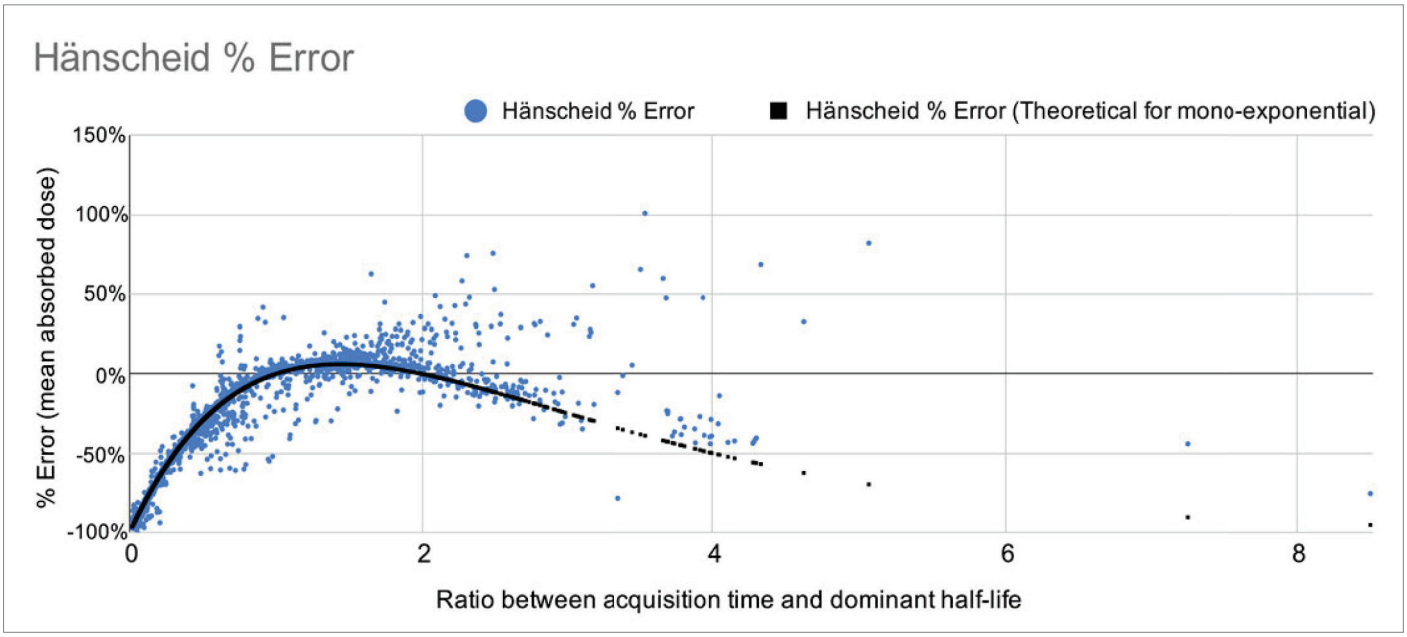


FIGURE 4. *Single-timepoint dose error as a function of tacq/Teff. Results across all ROIs, cycles, and patients from this evaluation are plotted in blue. The theoretical curve for a mono-exponential decay assumption is plotted in black.*

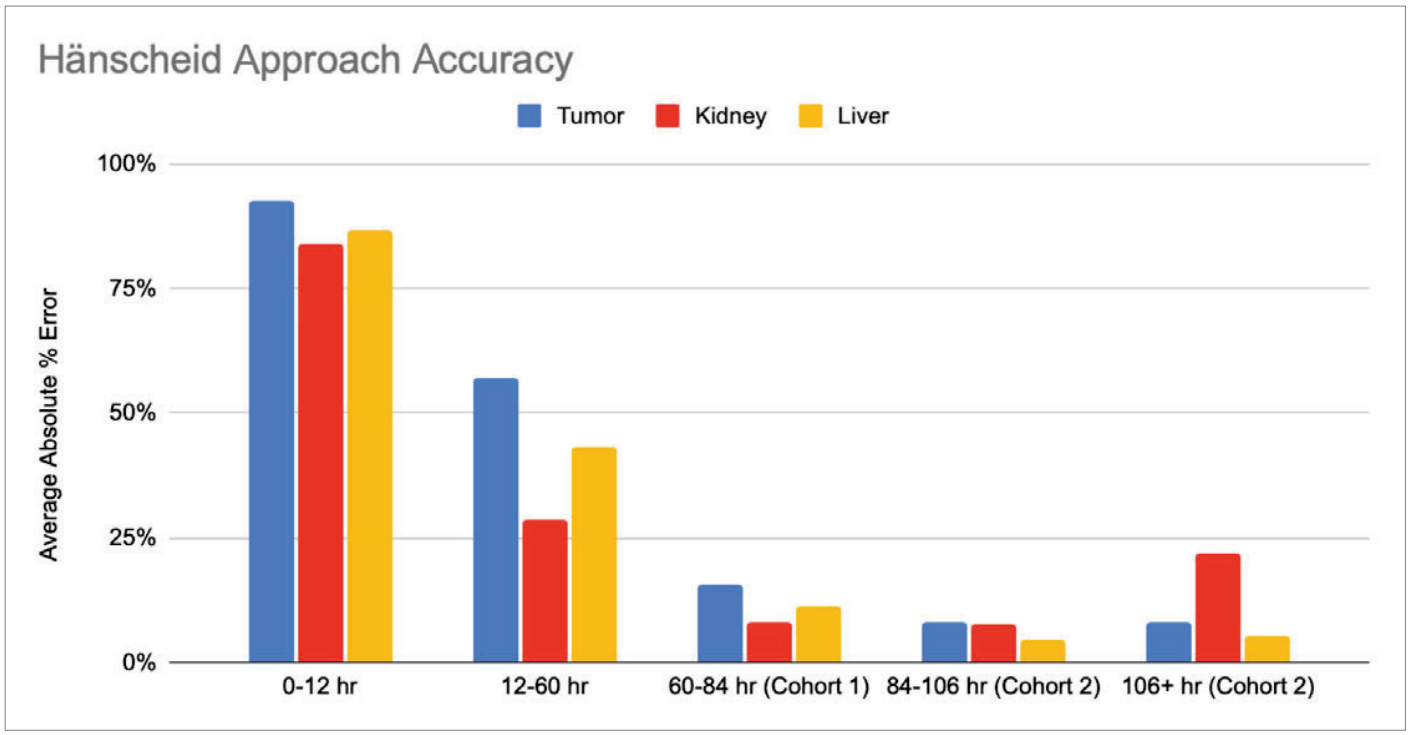


FIGURE 5. *Average absolute percent error in single-timepoint dosimetry with Hänscheid approach. Results are shown for kidney, liver, and tumor ROIs in bins for the acquisition time post-injection. Early timepoints from Day 0 or Day 1 include results from both patient cohorts.*

Comparison to Hänscheid et al. Evaluation Across Timepoints)

The original Hänscheid evaluation included liver and tumor ROIs as well as various single timepoints. Table 3 compares those results to our evaluation with both the Hänscheid and prior-information approaches. The estimations from a 24 hour acquisition were consistently poor using the Hänscheid approach, as expected. On the other hand, the Prior-Information approach utilizes patient-specific curve-fitting and is robust for OARs and tumors across timepoints. Median differences from this evaluation are mostly comparable to the Hänscheid et al. results, with somewhat higher median errors at 72 hours. This observation at 72 hours may reflect a cohort dependence in the accuracies reported in this evaluation, since those results were all from one cohort.

The higher range of errors for some structures in this evaluation is likely due to the differences from Hänscheid et al. in curve fitting for multiple-timepoint dosimetry. It was noted in the Hänscheid et al. evaluation that the short-lived time component in the bi-exponential models led to some deviation from a mono-exponential decay. The multiple-timepoint curve fitting method used in this evaluation automatically selects from mono-exponential, bi-exponential (four parameters), or bi-exponential (three parameters) fit models [8]. Therefore, larger differences in our results could be caused by larger effects of the second exponential in bi-exponential fits.

CONCLUSION: Results of the Hänscheid method in this evaluation compare reasonably well against the results reported in Hänscheid et al. across timepoints, while it is evident that the prior-information approach is more robust against the acquisition time. Interdecile ranges are generally wider for the Hänscheid approach in this evaluation, though it is predicted that this primarily reflects differences in the reference multiple-timepoint dosimetry method.

TABLE 3. *Comparison of the present evaluation to the Hänscheid et al. single-timepoint evaluation with liver, kidney, and tumor ROIs for various acquisition times. *Note: the 24hr results include the data from both patient cohorts while the 72hr results are from Cohort 1 and the two later timepoints are results from Cohort 2.*

ROI	STP Method	24 hr			72 hr			96 hr			120 hr		
		10%	Median	90%	10%	Median	90%	10%	Median	90%	10%	Median	90%
Liver	Hänscheid et al.	-52.0%	**-43.0%**	-37.0%	-4.0%	**-4.0%**	7.0%	3.0%	**6.0%**	9.0%	-1.0%	**3.0%**	8.0%
	Hänscheid (this eval)	-61.8%	**-40.5%**	-28.3%	-14.8%	**8.7%**	16.0%	-4.7%	**3.5%**	7.0%	-7.7%	**1.0%**	5.6%
	Prior-Information (this eval)	-15.6%	**-2.4%**	8.3%	-2.1%	**5.7%**	10.9%	-6.3%	**-0.3%**	7.7%	-10.6%	**-3.6%**	4.6%
Kidneys	Hänscheid et al.	-40.0%	**-33.0%**	-24.0%	4.0%	**6.0%**	16.0%	-3.0%	**5.0%**	10.0%	-16.0%	**-5.0%**	2.0%
	Hänscheid (this eval)	-39.7%	**-28.6%**	-14.3%	3.5%	**8.3%**	10.9%	-16.3%	**-3.7%**	8.3%	-39.6%	**-26.2%**	-6.5%
	Prior-Information (this eval)	-13.2%	**-2.3%**	-10.2%	-1.8%	**1.2%**	6.9%	-10.7%	**-2.2%**	10.4%	-10.5%	**3.9%**	22.2%
Tumor	Hänscheid et al.	-60.0%	**-49.0%**	-40.0%	-13.0%	**0.0%**	8.0%	-2.0%	**6.0%**	10.0%	2.0%	**5.0%**	10.0%
	Hänscheid (this eval)	-70.8%	**-54.9%**	-32.4%	-28.7%	**-10.0%**	5.0%	-14.9%	**3.6%**	12.1%	-14.5%	**3.6%**	9.1%
	Prior-Information (this eval)	-25.3%	**-6.9%**	20.0%	-14.0%	**-2.1%**	14.6%	-12.2%	**-0.3%**	17.9%	-15.3%	**-2.5%**	2.6%

Prior-Information Approach

Between the first cycle of therapy and future cycles, we can expect some changes in the pharmacokinetics of the radiopharmaceutical. In other words, the dominant half-life will change between cycles of therapy. Figure 1 tells us that we should expect best results for the acquisition time most robust against changes in this dominant half-life.

The sensitivities of the prior-information approach accuracy to changes in the dominant half-life are shown in Figure 6. For all regions acquired at early timepoints (<60 hour post-therapy), there is an inverse relationship between accuracy and the acquisition time. While the kidneys are most sensitive to these changes, the changes in dominant half-lives between cycles of therapy were much larger for tumors. The lowest sensitivity for kidneys occurs in the 60-84 hour and 84-106 hour bins, while the lowest sensitivity for tumors occurs at long acquisition times 106+ hour, reflecting the longer half-lives of tumors.

Average absolute errors for this approach are shown in Figure 7 below. As expected, the optimal results for tumors are found in the 106+ hour bin, while for kidneys, the 60-84 hour and 84-106 hour bins are best. The differences between the 60-84 hour and 84-106 hour bins for kidneys may be due to effects of cohort on the dominant half-lives observed. There was not as significant an impact of acquisition time on non-tumoral liver accuracy, but best results were seen in the 60-84 hour and later bins.

CONCLUSION: If tumor dosimetry is prioritized, it is better to image at late timepoints 5-8 days post-therapy. If kidney dosimetry is prioritized, it is better to image 3-4 days post-therapy. With the prior-information approach, reasonable kidney and liver absorbed dose estimates can be observed with acquisition times as early as 4 hour.

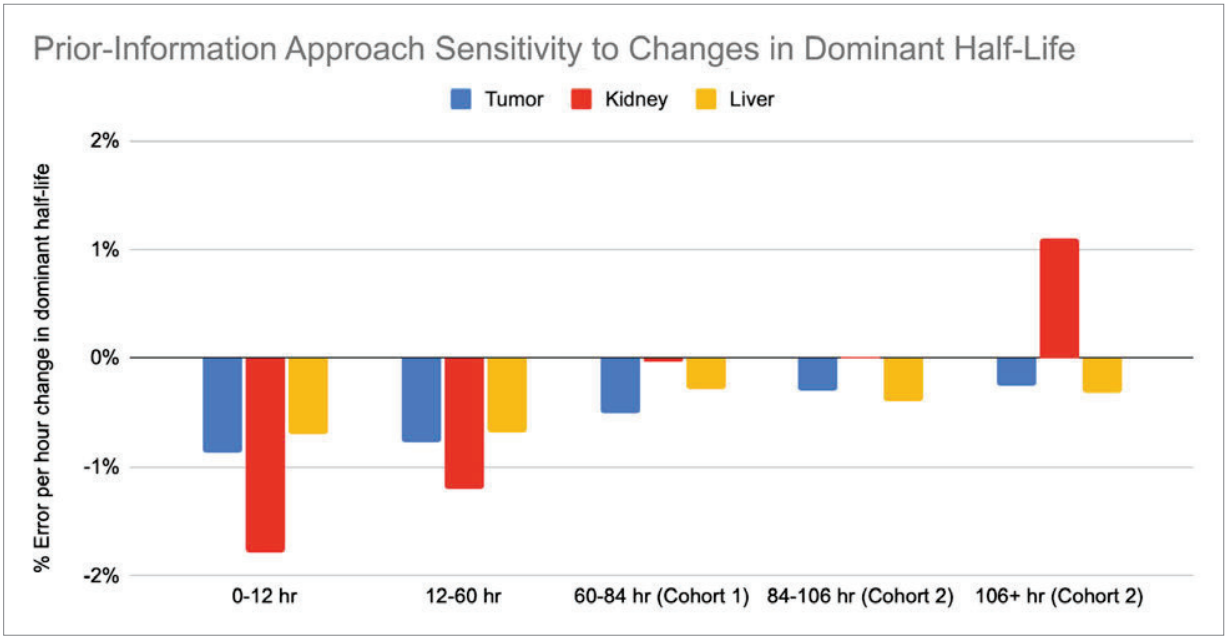


FIGURE 6. *Error in single-timepoint dosimetry with the prior-information approach in proportion to change in dominant half-life. Results are shown for kidney, liver, and tumor ROIs in bins for the acquisition time post-injection. Early timepoints from Day 0 or Day 1 include results from both patient cohorts.*

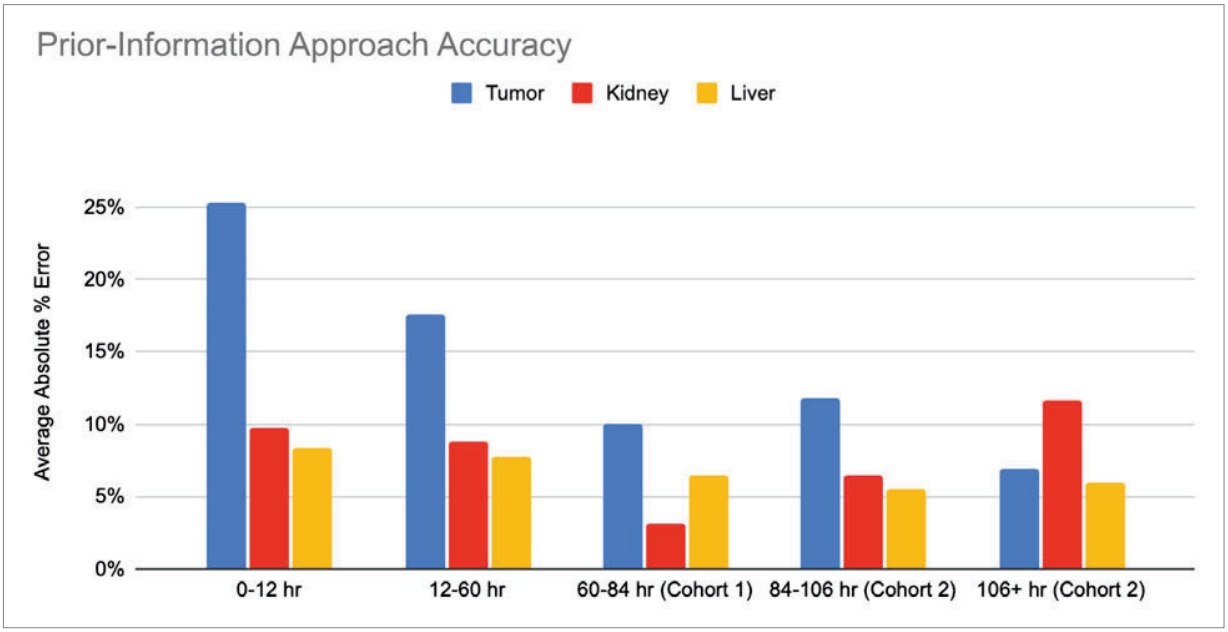


FIGURE 7. *Average absolute percent error in single-timepoint dosimetry with the prior-information approach. Results are shown for kidney, liver, and tumor ROIs in bins for the acquisition time post-injection. Early timepoints from Day 0 or Day 1 include results from both patient cohorts.*

Literature Supporting Single-Timepoint Dosimetry for ^{177}Lu-PSMA

Because ^{177}Lu-PSMA is a new radiotherapy, the evidence supporting single-timepoint dosimetry is limited. Evidence from ^{177}Lu-DOTATATE suggests it should perform well if the half-lives have similar variability, but the optimal acquisition timepoint may be different.

A summary of literature evaluating single-timepoint dosimetry for ^{177}Lu-PSMA can be found in Table 3. This includes studies for both ^{177}Lu-PSMA-617 and ^{177}Lu-PSMA-I&T, which may have different pharmacokinetic behavior to some degree. The Jackson et al. publication [7] uses a population-based approach, where pharmacokinetic information is averaged across a population and applied to individual patients. Because inter-patient variability is at least comparable to, if not greater than, intra-patient variability between cycles of therapy, these differences can be considered upper limits on results from the prior-information approach.

Based on current literature, there is a tradeoff between accuracy for normal organs and tumors. The optimal acquisition timepoint for kidneys and parotid glands seems to be 48 hours post-therapy across single-timepoint dosimetry methods. However, there may be a ~14% underestimation in tumor dose when imaging at this timepoint. The most accurate dosimetry for tumors may be found using a later acquisition timepoint at 96 hours or later.

CONCLUSION: Based on sparse literature, it can be deduced that using a timepoint 2 days post-therapy is best for normal organ dosimetry including kidneys and parotid glands. However, a later timepoint at 4 days may be best for tumors. To generate reasonable results for both tumor and organ dosimetry, a single-timepoint at 3 days is likely a reasonable compromise.

TABLE 4. *A summary of mean (± standard deviation) differences from a reference multiple-timepoint dosimetry method across several articles: Rinscheid et al. [9], Kurth et al. [10], and Jackson et al. [7].*

ROI	Source	STP Method	Tracer	Median differences from multiple-timepoint dosimetry			
				24 hr	48 or 52 hr	72 hr	96 hr
Kidneys	Rinscheid et al.	Hänscheid	PSMA-I&T	--	-2.8% ± 6.4%	--	--
	Kurth et al.	Prior-information approach	PSMA-617	7.9% ± 30.4%	1.6% ± 9.1%	0.2% ± 12.9%	--
	Jackson et al.	Population-based approach	PSMA-617	*(absolute)* 11.2%	*(absolute)* 7.5%	*(absolute)* 10.2%	*(absolute)* 15.8%
Parotids	Kurth et al.	Prior-information approach	PSMA-617	4.9% ± 31.1%	-0.6% ± 8.6%	1.2% ± 13.5%	--
	Jackson et al.	Population-based approach	PSMA-617	*(absolute)* 10%	*(absolute)* 3.9%	*(absolute)* 7.8%	*(absolute)* 16.7%
Tumors	Rinscheid et al.	Hänscheid	PSMA-I&T	--	-14% ± 7.6%	--	--
	Jackson et al.	Population-based approach	PSMA-617	*(absolute)* 19.4%	*(absolute)* 14.3%	*(absolute)* 9.3%	*(absolute)* 5.1%

References

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A GE HealthCare company

Version 7.1 - 7.4

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

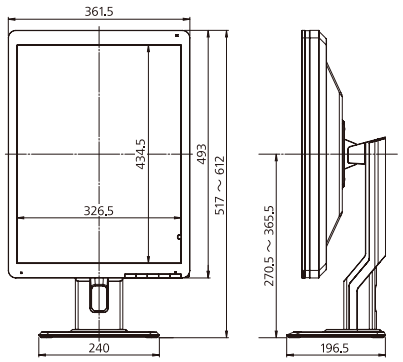
Config ID	Config Name	KMAT
NA	HP Z2 Tower G9 Workstation	M85349-999

Description	[redacted]	Qty
HP Z2 TWR Base Unit G9 700W RCTO	[redacted]	5
Windows 11 Pro 64	[redacted]	5
OS Localization	[redacted]B	5
Intel Core i5-13500 2.50G 24MB 14 cores 65W CPU	[redacted]	5
16GB (1x16GB) DDR5 4800 UDIMM NECC Memory	[redacted]	5
N-Vidia Quadro P400	[redacted]	5
Operating System Load to M.2	[redacted]	5
HP 512GB PCIe-4x4 2280 Value M.2 Solid State Drive	[redacted]	5
HP USB Business Slim Wired SmartCard CCID Keyboard	[redacted]	5
HP Wired 128 LSR Mouse	[redacted]	5
9.5mm SuperMulti DVDRW	[redacted]	5
HP Z2 G9 TWR Country Kit	[redacted]	5
C13 1.83m Sticker Conventional Desktop Power Cord	[redacted]	5
3/3/3 (material/labor/onsite) Warranty	[redacted]	5
Single Unit (Tower) Z2 Packaging	[redacted]	5
No Load Flex Port	[redacted]	5
Door/dock delivery workstations ZD081AA	[redacted]	5

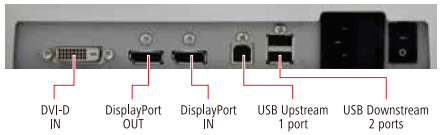
Specifications

		CL-S200BF : Protective Filter CL-S200BN : No Protective Filter	CL-S300BF : Protective Filter CL-S300BN : No Protective Filter
LCD Panel	Technology	21.3" color TFT IPS technology	21.3" color TFT IPS technology
	Display Area	324 mm × 432 mm	324.86 mm × 433.15 mm
	Pixel Pitch	0.270 mm × 0.270 mm	0.2115 mm × 0.2115 mm
	Contrast Ratio	1800 : 1 (typ.)	1500 : 1 (typ.)
	Maximum Luminance	1000 cd/m² (typ.) 410 cd/m² / 500 cd/m² (calibrated)	1000 cd/m² (typ.) 410 cd/m² / 500 cd/m² (calibrated)
	Viewing Angle	178° vertical and horizontal	178° vertical and horizontal
Visual Performance	Native Resolution	1200 × 1600	1536 × 2048
	Display Colors	16.77 million colors from a palette of 68 billion colors 1.07 billion colors with DisplayPort and 10-bit viewer	16.77 million colors from a palette of 68 billion colors 1.07 billion colors with DisplayPort and 10-bit viewer
Interface	Input Signal	DVI-D (DVI 1.0 compliant) DisplayPort (DisplayPort 1.2a compliant)	DVI-D (DVI 1.0 compliant) DisplayPort (DisplayPort 1.2a compliant)
	Output Signal	DisplayPort (DisplayPort 1.2a compliant)	DisplayPort (DisplayPort 1.2a compliant)
	Plug and Play	DDC2B compliant	DDC2B compliant
Input Power Supply	Input Power Supply	100 V - 240 V 50 / 60Hz	100 V - 240 V 50 / 60Hz
	Maximum Power Consumption	65 W (typ.)	95 W (typ.)
Features	Calibration Control	Luminance, Gamma, Color temperature Capable of storing 3 sets of LUT (Optional Calibration Kit is required)	Luminance, Gamma, Color temperature Capable of storing 3 sets of LUT (Optional Calibration Kit is required)
	OSD Information Display	Model name, Serial No., Total operating time,Calibration settings (Operating time since last calibration, Luminance, Gamma), Current luminance, Color temperature and Ambient light, DICOM conformance	Model name, Serial No., Total operating time, Calibration settings (Operating time since last calibration, Luminance, Gamma), Current luminance, Color temperature and Ambient light, DICOM conformance
	USB Hub	USB Rev.2.0 compliant, Self-powered USB upstream connector (x1), USB downstream connector (x2)	USB Rev.2.0 compliant, Self-powered USB upstream connector (x1), USB downstream connector (x2)
	Other Features	Uniformity Equalizer, Hardware pivot, LED indicator, Advanced power management, Human Presence Sensor, Dynamic Gamma, Auto Text Mode, Luminance stabilization, Multiple LUT, Self DICOM check, Self-calibration	Uniformity Equalizer, Hardware pivot, LED indicator, Advanced power management, Human Presence Sensor, Dynamic Gamma, Auto Text Mode, Luminance stabilization, Multiple LUT, Self DICOM check, Self-calibration
Approvals		ANSI/AAMI ES60601-1 (2005) + A1 (2012), CAN/CSA-C22.2 No. 60601-1 (2014), CE (EN60601-1, EN60601-1-2), RCM, FCC Part15 subpart B Class B , ICES-003-B, VCCI-B, FDA510(k), J-Moss, RoHS	ANSI/AAMI ES60601-1 (2005) + A1 (2012), CAN/CSA-C22.2 No. 60601-1 (2014), CE (EN60601-1, EN60601-1-2), RCM, FCC Part15 subpart B Class B , ICES-003-B, VCCI-B, FDA510(k), J-Moss, RoHS
Physical Characteristics	Dimensions (W × H × D)	Landscape : 493 mm × 451.3 / 546.3 mm × 196.5 mm Portrait : 361.5 mm × 517 / 612 mm × 196.5 mm	Landscape : 493 mm × 451.3 / 546.3 mm × 196.5 mm Portrait : 361.5 mm × 517 / 612 mm × 196.5 mm
	Weight	approx. 9 kg	approx. 10 kg
	Tilt Stand	Tilt, Swivel, Portrait / Landscape	Tilt, Swivel, Portrait / Landscape
	Mount	VESA standard (100 mm × 100 mm)	VESA standard (100 mm × 100 mm)
	Security Slot	Anti-theft security slot	Anti-theft security slot
Accessories		Power cord, DVI cable, DisplayPort cable, USB cable, Operation manual, Installation manual, Software (QA Medivisor Agent LE)	Power cord, DVI cable, DisplayPort cable, USB cable, Operation manual, Installation manual, Software (QA Medivisor Agent LE)

Dimensions (mm)



Interface



Options

Calibration Kit CAL-016

- Software
- Color Sensor

Safety Precautions

●Please read the user's manual for safe and proper use.
●Do not expose the product to dust, moisture, steam, or oily smoke. It could cause fire, electric shock, or a failure.

Please contact our distributor below with inquiries and orders.

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JVCKENWOOD Corporation
3-12, Moriya-cho, Kanagawa-ku, Yokohama-shi, Kanagawa, 221-0022, JAPAN
TEL: +81-45-450-1908 FAX: +81-45-450-1926
E mail : medical-display.j@jvckenwood.com
JVC Healthcare Website : http://healthcare.jvc.com/

JVCKENWOOD Corporation 3-12, Moriya-cho, Kanagawa-ku, Yokohama-shi, Kanagawa, 221-0022, Japan **www.jvckenwood.com/en/** K/HCTJE806010B Jun 2018

JVC

2 Megapixel 21.3" Color Monitor

CL-S200

3 Megapixel 21.3" Color Monitor

CL-S300

7.7.4, 7.7.5 6.4.1, 6.4.2 6.5.1 6.5.3 6.4.4, 6.5.2 6.4.3

Unparalleled Innovation in Diagnostic Imaging

i3 for Medical Imaging SERIES

21.3" | 1000 cd/m² | CL-S200 1800:1 | CL-S300 1500:1 | 16Bit LUT | DisplayPort & DVI-D | Calibration Function | Color Front Sensor | Uniformity Equalizer | Dynamic Gamma | Auto Text Mode | Human Presence Sensor | LED Backlight

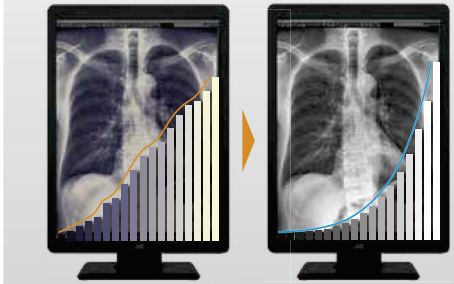
Providing the Best Diagnostic Environment

Fully redesigned hardware and software bring innovation in multi-modality image reading.

Pursuing an Effective Diagnostic Reading Environment

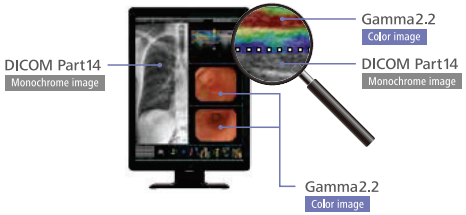
Clearly Defined Diagnostic Images

The new i3 color series render more precise color and monochrome modality images. One of its unique technologies the built-in self-calibrating sensor ensures that the monitor constantly performs at its best.



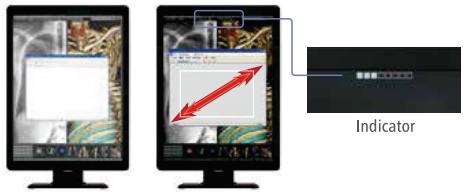
Dynamic Gamma

Color Images are automatically recognized to provide optimized contrast, brightness and gamma. No user intervention is required.



Auto Text Mode

Brightness is automatically adjusted on patient lists and reporting applications to reduce eye strain.



Quality Assurance Made Easy and Cost Effective

Integrated QA Solution QA Medivisor Agent (Option)

QA Medivisor Agent providing calibration and QA standard testing capabilities through an intuitive and easy to navigate user interface makes it effective to manage day-to-day operation in the radiology department. Simplified calibration scheduling tool QA Medivisor Agent LE is included.

*Optional calibration kit CAL-016 is required for standard QA testing.

Self-calibration

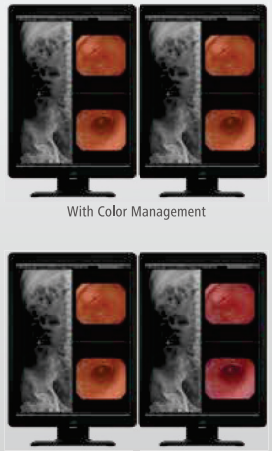
With the integrated color front sensor, the CL-S200 / CL-S300 self-calibrates to the DICOM Part 14 Standard on a regular schedule.

6.4.5

Schedule Setting (QA Medivisor Agent)

Razor-sharp Color Precision

Utilizing its unique X, Y, Z, color level tracking and color management technologies, any of the i3 model perfectly color-matches one another.



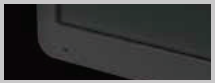
i3 for Medical Imaging SERIES

Advanced Features

- Premium Design
- LED Indicator / Front Buttons
- Built-in Sensor
- Space Saving
- Two-tone Color
- Wire Management / DisplayPort Daisy Chains

Premium Design

A simple and slim design for a modern look



LED Indicator / Front Buttons

The soft LED light indicator and front buttons are streamlined for intuitive operation.

6.4.5

Built-in Sensor

Ambient Light Sensor

Detects the level of ambient light to offset the effect for optimal calibration.

Color Front Sensor

Stabilizes luminance and color for consistent image quality.

Human Presence Sensor

Automatically switching to power save mode when sensor does not detect human presence.

Space Saving

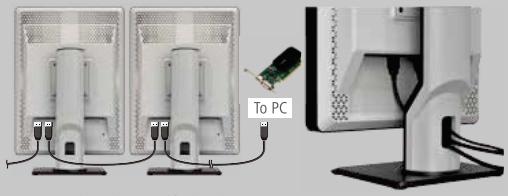
The new design of the CL-S200 / CL-S300 reduces 25% of the stand footprint compared to the conventional models.

Two-tone Color

The back side features a stylish gray-white tone color.

Wire Management / DisplayPort Daisy Chains

With the DisplayPort 1.2, the use of daisy chains allows for easier wiring connections.



Optional graphic card is required for daisy chains connections.

LONG DESCRIPTIONS

All pictures featured are for illustration purposes only, and do not necessarily relate to products or services mentioned in the text.

[redacted] Omni Legend 32cm AFOV for Fixed Install - Equipment Only

Omni Legend is built on a new scalable digital BGO detection technology, combining GE HealthCare generation 3 of digital detection technology, state of the art silicon photomultiplier technology and electronics with the outstanding stopping power of BGO, allowing tremendous gains in sensitivity, spatial resolution, and energy resolution achieved by 30 mm-thick crystals cut to 4.1x4.1 mm, ultra-high NEMA sensitivity per FOV length, of 46 cps/kBq for the 32 cm.

The technological advancements achieved by Omni Legend don't stop with hardware. Omni Legend is the first PET/CT system in the industry with Precision DL, a deep-learning processing method for images enhancement.

Omni Legend also delivers vast improvements to the entire PET/CT scanning process for more comfortable user and patient experience including smart and faster workflow, bore pattern and bore light.

Omni legend includes diagnostic CT innovations from our Revolution Maxima CT.

The Omni Legend 32 cm consists of an integrated gantry containing:

- Revolution Maxima CT 64 channel, 64 slice, 72KW CT 4.3
- dBGO detector composed of 32cm PET Field of View (6 rings)

CT Key Features: The Omni Legend platform can be operated as a standalone CT scanner (without gantry tilt). GE's Revolution Maxima is a new standard computed tomography, powered by artificial intelligence technology that delivers a streamed line workflow for better ease of use and operational efficiency.

- 40 mm coverage Clarity Detector /DAS
- 0.35 sec maximum rotation speed
- High Voltage Generation:
  - kV: 80, 100, 120, 140 4.10
  - mA range at 120 kV: 10 to 600 mA, 5 mA increment 4.11
- ASiR-V, up to 82% dose reduction relative to FBP at the same image quality

Key technologies enablers include:

- Clarity imaging chain with X-ray tube, Detector, and Iterative reconstruction technologies to overcome Image performance challenges such as noise, spatial resolution, low contract detectability and/or artifact.
- Performix 40 Plus X-ray tube with a liquid bearing tube enables 0.35 sec gantry rotation speed for routine use and with high helical pitch (1.531) enables a 1000 mm scan to be in 6 seconds.
- ASiR-V* combines the speed of ASiR while leveraging design elements found in VeoTM, GE's full model-based iterative reconstruction technology. By applying more advanced modeling and optimization technologies in projection- and image-space as part of the iterative reconstruction process.
- SnapShotTM* Freeze is designed to reduce blurring artifacts due to motion in coronary vessels that cannot be addressed by gantry speed alone, providing up to a 6X improvement, while maintaining high spatial resolution.

- SnapShot Puls* mode is for lower dose imaging of the coronary arteries. SnapShot Pulse can also be used to image structures that are near to the heart and may be affected by heart motion such as thoracic aorta's or pulmonary arteries.
- Volume Helical Shuttle* is a continuous scan technique that is a bi-directional scan mode and covers up to 312.5 mm for 4D imaging.
- Smart MAR helps reduce photon starvation artifacts, such as beam hardening and streak artifacts, caused by metal in the body, such as hip implants.
- Overlapped Recon* -for the 64-slice configuration, the overlapped reconstruction feature enables 128 slices per rotation in axial scanning modes to be produced. This reconstruction technique is intended to improve Z-axis visualization.

PET/CT Operators Console Key Features: 7.1

- Precision DL* is a deep-learning method for images enhancement. More than a new image processing method, it is a sophisticated neural network algorithm trained with thousands of images reconstructed with a variety of different reconstruction techniques, including ToF bringing image quality performance comparable to a TOF system with 385 ps.
- Prospective Reconstruction
    - VUE Point HD utilizes a fully 3D iterative reconstruction technique with all corrections within the loop, enhanced resolution with detector geometry modeling, model-based 3D scatter correction inside and scatter estimation outside the field of view, exclusive randoms corrections based on singles and dead-time correction with pile-up estimates providing high image quality and patient throughput.
    - SharpIR, Point Spread Function reconstruction, enhances visual contrast and resolution in both whole-body and brain PET images. SharpIR provides uniform High Definition resolution over a 70 cm PET FOV.
    - WideView - PET reconstructed transaxial Field of View coverage of 70cm diameter with CT based PET attenuation correction and CT wide-FOV Display.
- Motion Management (*) tools enable the reduction of motion artifacts caused by patient breathing and cardiac movement by acquiring motion information during the scan and incorporating it into motion related PET/CT applications.
- RAD Rx allows your own PET/CT protocol from any CT protocol. Automated CTAC creation from CT acquisitions, including contrast enhanced, perfusion and gated CTs (when equipped with the required CT options). Integrated Average Cine CT protocol for improved attenuation correction 6.1.4
- Auto Positioning* - AI based automatic patient positioning is an innovative, next generation technology. It is powered by Xtream camera that enables automatic landmark detection and auto patient centering. This GE' unique technology provides better patient throughput, optimize the CT radiation dose, ease of use, consistent image quality, standardization, and less error.
- Remote Auto Positioning*- Combined with GE Remote Control Suite and AI technology, it helps technologist to use auto patient positioning function remotely from operator room, to realize the auto scout scan range, anatomical reference detecting and centering by specifying the position and shape in three dimensions.
- Automatic ACQC* - An easy automated and advanced workflow correcting for any attenuation map misregistration using flexible geometrical transforms and enabling quality control, fully integrated in the patient scan workflow.

Features marked (*) are not part of the basic configuration.

7.3

Freedom Workspace: Innovative hardware and software creates a convenient, ergonomic working environment. It offers sit/stand and horizontal/vertical monitor flexibility. It can also help reduce noise and heat with remote location of the console.

- Two 19 -inch diagonal width high-resolution color monitors for image display, analysis, processing, and management of PET, CT, and PET/CT images.

PET/CT Service Features:

Each system is supported by GE's InSite™ remote diagnostics, iLinq™, and TiP Virtual Assist.

InSite broadband – all hardware and software required to remotely connect this PET/CT system to GE's InSite On-Line Center via secure VPN high-speed Internet connections. Enables access to services designed to reduce downtime, improve quality, enhance performance, increase productivity, and expand imaging capabilities.

[redacted] Base configuration of Omni Legend 7.1

Base configuration, mandatory selectable, which includes the following features:

- Q.Clear - Full convergence iterative reconstruction technology for accurate PET quantitation and high image quality, to help with fast and efficient reading and confident diagnosis.. Q.Clear controls
  the amount of noise allowing full convergence of reconstruction without compromising signal and giving great image quality.
- SmartMAR - Metal Artifact reduction (MAR) helps reduce photon starvation, beam hardening and streak artifacts caused by high Z materials in the body, such as hip implants. The clarity of MAR images is addressing the challenges posed by metal artifacts, helping clinicians accurately contour targets and critical organs.

  MAR offers:
  - Exceptional image quality. MAR is based on the latest in GE Healthcare smart technology, which uses a novel three-step, sinogram-based iterative algorithm.
  - Streamlined workflow. MAR requires only one scan, making the process of obtaining a corrected image fast and efficient. Dose conscious. MAR requires only one acquisition.
  - Patient comfort. The efficient, single-scan process helps to reduce patient time inside the scanner.
  - Versatility. MAR is designed to enhance clarity across a range of images including scans of hip implants, dental fillings, screws and other metal objects.

[redacted] Plus Package 7.1

Omni "Plus" configuration. Selectable option bundle adding the following functionality:

- Motion Free - software-only solution to derive a respiratory signal from the acquired PET data as an alternative to existing device-based respiratory gating options. It generates a respiratory signal which can be used to automate motion correction of PET images with respiratory motion.
- Q.Static - Represents a starting point for adding motion correction techniques to your facility and the opportunity to build towards a full 4D phase-matched workflow. The result is a single image series with reduced blurring from organ motion and therefore more consistent quantitation compared to a static image.
- Q. Freeze - is designed to combine the quantitative benefits of 4D phase- matched PET/CT imaging into a single static image. Resulting image has the dual benefit of frozen patient motion and reduced image noise
- Auto Positioning - AI based automatic patient positioning is an innovative, next generation technology. It is powered by Xtream camera that enables automatic landmark detection and auto patient centering. This GE' unique technology provides better patient throughput, optimize the CT radiation dose, ease of use, consistent image quality, standardization, and less error
- Q.AC - Our Q.AC algorithm helps to ensure that the attenuation coefficients used in image reconstruction are accurate in ultra-low-dose, non-diagnostic CT protocols.
- Overlap Recon - for the 64-slice configuration, the overlapped reconstruction feature enables 128 slices per rotation in axial scanning modes to be produced. This reconstruction technique is intended to improve Z-axis visualization.
- ASIR-V - combines the speed of ASiR while leveraging design elements found in VeoTM, GE's full model-based iterative reconstruction technology. By applying more advanced modeling and optimization technologies in projection- and image-space as part of the iterative reconstruction process.

[redacted] Deep Learning Technology (DLT)

7.1

Deep Learning Technology (DLT), an advanced image generation algorithm enhanced by deep learning-based technology. More than a new reconstruction technique, DLT is a sophisticated deep neural network trained on hundreds of images created with a variety of different reconstruction techniques, including LBS, ToF, PSF and BSREM. DLT plus ultra-high sensitivity providing the benefits most associated with hardware-based Time-of-Flight, better signal-to-noise ratio and contrast recovery.

[redacted] Q.Prep

7.1

Q.Prep is designed to facilitate the patient exam preparation:

- o Ability to view parameters of prior exams
- o Compare prior parameters to current exams
- o Ability to pre-enter study information

[redacted] 2m PET/CT Scan Length

A full 2 meter scan range is achieved through the use of a cradle extender and special acquisition protocols.

[redacted] - MotionMatch & MotionVUE

7.1

Motion Management tools allow the reduction of motion artifacts caused by patient breathing and cardiac movement by acquiring motion information during the scan and incorporating it into motion related PET/CT applications

MotionMatch has been design to optimize the workflow for PET and CT respiratory gating, simplify data acquisition and enhance the clinical effectiveness of 4D phase-matched reconstruction. MotionMatch also provides improved visualization capabilities and provides better integration of the respiratory gating device by allowing direct transfer of the respiratory waveform file to the operator console.

MotionVUE allows the user to review the images processed with MotionCorrect, Advantage 4D and Retro Phase Matched Reconstruction. The user is able to view and save the binned images, including fused review of binned PET and binned CT.

MotionVUE's flexibility allows the user to load any combination of PET and/or CT series:

- Binned CT or binned PET only
- Binned CT with static PET or gated PET
- Binned CT with static and gated PET

[redacted] PET Cardiac Omni Package

7.1

The PET Cardiac Package enables the user to acquire cardiac PET exams.

This package contains the following items necessary for PET cardiac studies:

- PET Cardiac Gating capability (P5051LH)
- Cardiac PET ACQC (P5051LE)
- Cardiac VUE (P5051LV)
- Automatic, multi-directional ACQC PET/CT Correction (P5051AR)

ECG monitor is not provided with this package.

Attenuation Correction Quality Control ensures proper cardiac registration in PET and CT, particularly useful for Cardiac stress PET/CT exams. Mis-registered PET and CT attenuation correction data due to motion may automatically be corrected using flexible geometrical transforms. Automatic ACQC is fully integrated in the patient scan workflow, saving technologist time, enabling reproducibility, reduces manual errors, and inter and intra user variability. Automatic ACQC reduces overall procedure time and improves IQ.

[redacted] Dynamic VUE Software Option 7.1

Dynamic VUE. Quantitative review of dynamic PET datasets with time activity curves.

PET's ability to noninvasively measure the metabolic activity of cells in the human body provides valuable information of the biochemical and biological activity of a living subject. Using this diagnostic tool, clinicians are able to obtain early information on the state of cardiac disease, neurological disorders, and cancer. A program that lets you view a graphic representation of this molecular activity over time would give you key information about the early onset and progression of various disease states.

Overview:

Dynamic VUE lets you make optimum use of the information PET and PET/CT scanners provide from dynamic PET scans. With it, you have to ability to quantitatively review Dynamic PET datasets and generate time activity cures and summing images over time.

Features:

- Exclude frames with motion artifacts and sum selected frames to review a single high-count images series.
- Application of ROIs for cardiac perfusion analysis.
- Ability to chart time activity curves between ROIs in each brain hemisphere for comparison.
- Sum an entire series over time or one location with a single click.
- Reframe a dynamic series to create a new series by summing different time frames.
- Draw a freehand ROI on an image and edit its properties.
- Create location activity curves for multiple ROIs.
- Export curve statistics to a portable format.
- Cine images can be displayed at 40 fps.

[redacted] Co Registration Phantom for NEMA2018 3.13.1 7.6

Pet-CT co -registration phantom enables us to test co-registration error between PET and CT data per requirements of NEMA 2018.

Data is acquired with objects visible by both PET and CT (markers) at 6 locations within the PET and CT FOV, with mass distributed on the bed.

Co-registration error is determined by calculating the distance between the centroids of the PET and CT images of the markers.

Markers need to be placed at following points in space: positions (x,y) at (0,1), (0,20), and (20,0), near the bed edge and 100cm from the bed edge.

[redacted] 0.35 Sec Rotation Option

Provides the capability of a 360-degree rotation in 0.35 seconds. This additional rotation time will enhance the user's ability to reduce exam times and potentially lower patient breath-holds, allowing up to 175 mm/sec acquisition speeds.

[redacted] Advantage 4D for AW 7.1

Advantage 4D is a non-invasive software option that can be used to provide and display CT CT images of all phases of a breathing cycle for the evaluation of respiration-induced motion. The software will allow the user to retrospectively define the optimal respiratory phase from an image quality standpoint, and group images by the phase selected.

It performs the following functions:

- Examines the motion profile generated by the vendor devices
- Sorts images by the phase of the respiratory cycle. Generates multiple phase series for 2D, 3D and 4D viewing
- Automatic (Auto4D mode) or manual processing
- Measurement of motion extent

Requires VolumeShare7 or higher, and Advantage 4D hardware.

All software packages are Non-Transferable to other hardware and are Non-Returnable.

[redacted] Cardiac PKG 7.1

Cardiac package is innovative cardiac options package and gives customers access to cardiac acquisition and productive post-processing workflow. This package is including SmartScore Pro, ECG trace, Cardiac enhance filter, CardIQ SnapShot and ECG Wave on Gantry.

CardIQ SnapShot is an integrated cardiovascular helical image acquisition option. The CardIQ SnapShot Software can be used to Acquire ECG Gated CT images of Cardiovascular anatomy with Improved temporal resolution to reduce heart motion effects and artifacts. More specifically, with CardIQ SnapShot option, users can acquire cardiac images of patients using the following cardiac imaging techniques: (1) Retrospectively EKG-gated helical scanning method - SnapShot: primarily used for cardiac morphology imaging, with this technique, cardiac images of single or multiple cardiac phases at any given Z-axis location can be acquired and generated. (2) EKG-gated Multi-slice CINE Scan mode: used primarily for coronary artery calcification scoring (CACS) studies or for cardiac morphology Imaging. Once a specific imaging model is selected, helical pitch and/or gantry rotation speed will be automatically selected for optimal scan coverage and image quality.

SmartScore Pro is CT Operator Console Acquisition Software for Prospective Gating.

The ECG trace provided by the Ivy monitor (option) will be displayed on the CT operator's console with this option. Allowing the user to display the live trace of the patient's heart rate and display the actual location of the window of time when the image is being acquired. It will provide easy access to patient cardiac output status and assist in providing visual feedback for optimum acquisition start.

Cardiac Image Filters provides users the capability to reconstruct filtered images using three steps of noise (pixel noise standard deviation) reduction for helical and axial cardiac imaging, which may allow a reduction of mA while maintaining an acceptable level of image performance.

ECG trace provides users the capability to display the heart rate and ECG waveform based on the data from the ECG equipment on the Xtream tablet to review the patient heart rate during cardiac scanning.

[redacted] SSF enabler option 7.1

SSF enabler option allows to use SnapShot Freeze function without SnapShot Pulse and Snapshot Assist.

SnapShot Freeze is an intelligent motion correction algorithm designed to reduce blurring of coronary arteries due to motion artifacts. SnapShot Freeze reduces motion artifacts up to 6X, equivalent to a 0.058s Equivalent Gantry Rotation Speed with Effective Temporal Resolution of 29msec*. This benefit is delivered by characterizing the vessel motion (path and velocity) to derive the optimal vessel position at the target phase.

[redacted] SnapShot Assist Temporal Enhance 7.1

Helps users optimize ECG-gated CT acquisitions based on patient heart rate characteristics.

SnapShot Assist uses the patient's recorded heart rate information to display scan parameters (including scan mode, cardiac phases, padding and pitch) that could be used during the cardiac CT scan.

SnapShot Assist generates a cardiac scan parameter recommendation using the patient's ECG analysis and user defined protocol selection algorithm. It uses the patient's recorded heart rate information to predict the heart rate behavior during a CCTA scan to assist the user with optimization of the parameters on a per-patient basis.

Acquisition parameters displayed include scan mode (Cine SnapShot Pulse, Helical SnapShot Segment, etc.), cardiac phases, padding, and pitch. User Profiles define scan parameters within the heart rate and variability categories for a specific patient group and cardiac scan mode.

[redacted] AWE Connection 7.1

The AW Server client on the CT console is a software option that provides access to applications hosted on an AW Server, at the CT console.

It offers customers the use of applications on the CT console for improved workflow and productivity.

[redacted] Coronal Head Holder 7.5

Coronal head holder to support the patient, allowing the acquisition of direct coronal images.

[redacted] Strap Auto Tration 7.5

Usage: Traction patient

Length, width, height: 60inch(length); 2inch(width)

[redacted] TG-66 Adjustable Kit for Flat Table Tops as part of Radio therapy Planning Procedures

Enables accurate patient positioning in the trans-axial plane that may help improve the accuracy of radiotherapy planning.

The kit consists of mechanical elements that are permanently installed on the cradle by means of a dedicated calibration tool.

Once installed, GE-supported flat table tops can be easily mounted and removed based on the clinical protocol.

[redacted] Omni Rear Gantry Lasers

Rear Laser Landmark for Omni PET/CT scanner

[redacted] IVY Monitor Set

IVY Monitor 7800 with cardiac cable kit

The Model 7800 is Ivy Biomedical's fifth generation of cardiac trigger monitors intended primarily for use on patients in applications requiring precision R-wave synchronization. Incorporating a simple, easy-to-use touchscreen interface, the 7800 displays two simultaneous ECG vectors along with the patient's heart rate. The Trigger ECG vector (top waveform) can be selected from Leads I, II, III, or Auto Lead Select. The Second ECG vector (bottom waveform) can be selected from Leads I, II, III. If required, High and Low heart rate alarm limits can be adjusted to bracket the patient's heart rate so that a violation of these limits produces an audible and visual indication of the alarm.

- Impedance Measurement: Measures Impedance between the patient's skin and each individual ECG electrode
- Automatic operation: After patient cables are connected and the monitor is receiving an ECG signal, the monitor finds the peak of the R-wave and generates synchronization pulses
- Bright TFT active matrix 8.4 in. color touch screen LCD with a wide viewing angle and large heart rate characters enhance visibility of patient data
- Polarity lock helps reduce the number of false triggers when tall T waves or deep S waves occur
- Color trigger mark indicates timing of each trigger pulse with respect to the ECG
- System interlock function indicates proper connection with the imaging device
- Integrated USB Drive - allows user to store and retrieve ECG events for retrospective analysis
- Auto-notch selects the correct ECG notch filter. This reduces interference on the ECG signal

The Kit includes:

Cardiac Trigger Monitor; set of 4 RT lead wires - 30 in, low noise patient cable - lead, Ethernet Internet cables, ECG adult electrode (box of 40), cord-set hospital grade (12ft), NuPrep Gel, USB Memory Stick, Recorder Paper, Roll Stand for 7000 series and IPC cable. Also includes Cardiac Cable kit E8007TB.

[redacted] Patient arm support for nuclear PET/CT, MRI 7.5

Features/Benefits

- Ergonomically designed positioning product developed to prevent arm and shoulder pain and to also reduce related motion artifact that commonly occurs during supine imaging
- This safe, clinically proven Patient Arm Support combines total arm support and passive restraint, thereby increasing patient comfort during extended procedures

- Designed to accommodate virtually all patients, this product not only enhances patient comfort it improves patient throughput

Specifications

- Velcro-mounted; easily cleaned
- Sold per Each

Compatibility

- Compatible with most Nuclear Imaging systems and can also be used in MRI, CT and PET applications

[redacted] Contoured patient leg rest for nuclear, PET/CT, MRI 7.5

Features/Benefits

- The Contoured Leg Rest is a unique support product created to prevent the cycle of low back stress and pain that commonly occurs during supine imaging and treatment
- Positioned under the knees, the Contoured Leg Rest produces mild lumbar spine extension and hip flexion, causing the pelvis to rotate forward creating greater low back support and torso stability. The unique leg recesses create additional lateral support thereby minimizing both rotational and translational body motion

Specifications

- Constructed of full support polyfoam with a seamless coated finish
- Velcro-mounted; easily cleaned
- 18 cm tall from table surface to top of support
- Sold per Each

Compatibility

- Compatible with most Nuclear Imaging systems and can also be used in MRI, CT and PET applications

[redacted] PET-CT VQC Phantom for Volumetric Registration- 25 cm, 20 cm, 15 cm systems

3.13.1 7.6

Overview

- Make sure you're getting the most from your GE system by checking it with our custom designed imaging phantoms
- Recommended for accurate calibration of your PET or CT detector and easier quality control
- Designed to be held in place during use by standard source holders provided with scanning equipment
- No mechanical maintenance is required

Compatibility

For use with Discovery MI/MI DR and Discovery IQ PET system 3, 4, 5 Gen2 6 ring (15 cm, 20 cm, 25 cm, 30 cm) detectors, and Discovery 710, 690, 610, 600 and Optima 560

3.13.1 7.6

[redacted] PET Annulus DQA (Daily Quality Assurance) Imaging Phantom

Overview

Designed exclusively for the Discovery™ MI, Discovery IQ PET and SIGNA™ PET/MR systems

- Make sure you're getting the most from your GE system by checking it with our custom designed imaging phantoms
- Recommended for accurate calibration of your PET detector and easier quality control
- Designed to be held in place during use by standard source holders provided with scanning equipment
- No mechanical maintenance is required

Compatibility

For use with MI system Gen2 6 ring (30 cm)

3.13.1 7.6

[redacted] DQA Phantom Shield Container - non-mobile use only (use with catalog# [redacted]

Overview

DQA Phantom Shield Container for Discovery MI 30 cm, non-mobile use.

Specifications

- Wheels feature swivel castors for easy mobility and wheel locks for added stability
- Lid features a handle for easier opening
- Spring loaded covered hinge assists when lifting the lid
- Container latch seals the phantom inside to ensure radiation gaps are eliminated
- Latch includes option to use a padlock to secure the phantom in the container
- The container's interior walls feature a soft plastic for easier with a chain or cable
- Gusset holes allow the facility to secure the shield to the site with a chain or cable
- Weight – approximately 300 lb/136 kg
- Lead shielding thickness to maintain and not exceed 2.0 mRem/hr. radiation dose on any external surface using maximum source activity of 66 MBq.

WARNING: The PET Annulus Phantom Shield should not be taken into an MRI environment

Compatibility

System compatibility: Discovery MI system Gen2 6-ring (30 cm) - catalog# E8008PV

[redacted] NEMA IEC Body Phantom Set™ 3.13.2 7.6

Overview

Main Applications

- Simulation of whole-body imaging especially using PET and camera-based coincidence imaging techniques
- Evaluation of reconstructed image quality in whole body PET and camera-based coincidence imaging
- Determination of the coincidence count rate characteristics in brain and cardiac imaging
- Evaluation of the relationship between true coincidence count rate and radioactivity
- Determination of the address errors caused by address pile up
- Evaluation of the count loss correction scheme

Research Specifications

- Interior length of phantom: 180 mm 3.13.2
- Externally fillable spheres (6) inner diameter: 10 mm, 13 mm, 17 mm, 22 mm, 28 mm, and 37 mm.
- Distance from sphere plane to inside wall: 70 mm
- Volume of empty cylinder: 9.7 liters
- Cylindrical insert dimension:
- Outside diameter: 51 mm
- Length: 180 mm

5.5

[redacted]- Eaton 14.4 KVA 3-Phase Partial System UPS, including GEH INTERFACE KIT [redacted], for GE CT and PET/CT Scanners

Overview:

Eaton's 14.4 KVA 3-Phase partial system UPS (Uninterruptible Power Supply) has been specifically configured to coordinate with compatible GE CT and PET/CT scanners.

The partial system UPS provides clean, reliable, constant voltage power to the scanner electronics. It helps protect the system's sensitive electronic components from damaging power anomalies such as high frequency noise transients and over voltage and under voltage conditions.

Specifications:

- Rating: 14.4 KVA
- Input voltage range: three phases; 102-132V/phase
- Input frequency range: 45-65 Hertz
- Input power factor: >95% typical
- Output frequency: 50 or 60 Hertz, autosensing
- Output regulation: Voltage distortion: Overload capacity: 110% for 10 minutes; 125% for 1 minute; 149% for 5 seconds
- Efficiency: >90% typical
- Battery backup time: >10 minutes typical 5.5
- Battery recharge time: < 3 hours to 80% capacity typical
- Operating temperature: 50°F - 104°F (10°C - 40°C)
- Floor heat dissipation: 5122 BTU/hour typical @11.5 KVA

- Humidity: 20-80% relative humidity, non-condensing
- Audible noise (norm mode): Dimensions (H x W x D): 49 inches x 12 inches x 32 inches (1245 mm x 305 mm x 813 mm)
- Weight: 620 lbs (277 kg)

[redacted] CT MDP CE 160A 400V 50Hz 3 phases

Overview:

The CE MDP (Main Disconnect Panel) and UPS Control Panel serve as the main power disconnect between the GE CT, PET or PET/CT system and the facility power source. On systems where the optional partial system UPS is included in the system, the panel provides UPS emergency power-off control function via a UPS control cable included with the UPS. An integrated 30mA Residual Current Device is included to protect equipment and personnel. The optimally designed MDP saves time, installation labour, and valuable mounting space by consolidating the main circuit breaker, the feeder overcurrent devices, surge protectors, magnetic contactors, and UPS emergency power off into a compact factory manufactured panel. 7.4

Remote Emergency Power Off

- Includes two normally closed contact blocks attached to the back of the emergency off push button
- This emergency off push button must be mounted in an extra deep switch box with mud ring. The contact block on the back of the EPO extends 35 mm into the switch box and terminates from the side

Physical Characteristics

- Dimensions (Height x Width x Depth): 929.4 x 423.8 x 207 mm
- Handle depth: 71.9 mm
- Weight: approx. 32.7 kg
- Semi-flush mounting: 152.4 mm of the enclosure can be recessed in the wall
- Mounting holes are 10 mm diameter for up to 8 mm bolts

Note: Structural engineer shall define the proper fixing/anchoring hardware

Components supplied with each panel

- The Main Disconnect and UPS Control Panel
- An Installation, Operations & Service Manual
- (2) sets of Emergency Power Off pushbuttons with 2NC on each EPO
- Drawings and Electrical Schematics

[redacted] Welcome pack – 16 Credits

Customised Training:

Get the best out of your GE HealthCare equipment with LEVEL UP! A 3-step education programme tailored to your team needs.

1. Get Ready: Together we define your site application requirements, advise on pre-training via Digital Academy (LMS) and plan your Get Started sessions.

2. Get Started: Training and handover of your system by a member of our expert Clinical Education team.

3. Equipment Lifecycle: We provide you with privileged access to WeConnect, our user community and central hub for educational resources. We also offer opportunities to access our long-term learning solutions via LEVEL UP! Credits.

Continuous Education:

LEVEL UP! Credits may be used to access any of our educational solutions. These include (but are not limited to):

- On-site training at Your facility (1 day = 8 credits)
- Remote training sessions (1 hour = 1 credit)
- Classroom Session at a GE HealthCare Academy (1 day/1 attendee = 4 credits)
- Immersion training at a Partner Site (1 day/1 attendee – 4-8 credits)
- 12 months access to Digital Academy (10 learners + 1 manager = 8 credits)

Credits are valid for 12 months from the Product warranty start date when associated with a product purchase; or the effective date of the signed Agreement if purchased as standalone. Unused credits within this timeframe will expire without refund.

[redacted] 16-Training Credits Education Package for PET

At GE HealthCare, we believe that continuous professional development is essential for all healthcare workers. Demands on staff time is continually increasing and the GEHC Clinical Education team are focused on providing flexible educational solutions. Our goal is to offer opportunities to gain the knowledge and skills needed to optimize equipment performance, clinical practice, and patient care.

The LEVEL UP! Credit packages are designed to provide flexible training options, to be used to support efficient and effective staff development needs.

LEVEL UP! Credits may be use for Clinical Education linked to GEHC Imaging products located at your facility. The Credits may be used to access any of our educational solutions. These include (but are not limited to):

- On-site training at Your facility (1 day = 8 credits)
- Remote training sessions (1 hour = 1 credit)
- Classroom Session at a GE HealthCare Academy (1 day/1 attendee = 4 credits)
- Immersion training at a Partner Site (1 day/1 attendee – 4-8 credits)
- 12 months access to Digital Academy (10 learners + 1 manager = 8 credits)

This Package is valid for 12months from the Product warranty start date when associated with a product purchase; or the effective date of signed Agreement if purchased as standalone. Unused credits within this timeframe will expire without refund.

Additional credits may be purchased separately.

GEHC will provide the Customer with the Education Services described in the General Terms & Conditions attached hereto, based on the LEVEL UP! credits package chosen by the customer in this quotation. By signing the quotation, including this long description, the Customer declares having fully read and understood the General Terms & Conditions of Education Services as well as this quotation and fully agrees with and accepts such terms.

[redacted] 60-Training Credits Education Package for PET

At GE HealthCare, we believe that continuous professional development is essential for all healthcare workers. Demands on staff time is continually increasing and the GEHC Clinical Education team are focused on providing flexible educational solutions. Our goal is to offer opportunities to gain the knowledge and skills needed to optimize equipment performance, clinical practice, and patient care.

The LEVEL UP! Credit packages are designed to provide flexible training options, to be used to support efficient and effective staff development needs.

LEVEL UP! Credits may be use for Clinical Education linked to GEHC Imaging products located at your facility. The Credits may be used to access any of our educational solutions. These include (but are not limited to):

- On-site training at Your facility (1 day = 8 credits)
- Remote training sessions (1 hour = 1 credit)
- Classroom Session at a GE HealthCare Academy (1 day/1 attendee = 4 credits)
- Immersion training at a Partner Site (1 day/1 attendee – 4-8 credits)
- 12 months access to Digital Academy (10 learners + 1 manager = 8 credits)

This Package is valid for 10 years from the Product warranty start date when associated with a product purchase; or the effective date of signed Agreement if purchased as standalone. Unused credits within this timeframe will expire without refund.

Additional credits may be purchased separately.

GEHC will provide the Customer with the Education Services described in the General Terms & Conditions attached hereto, based on the LEVEL UP! credits package chosen by the customer in this quotation. By signing the quotation, including this long description, the Customer declares having fully read and understood the General Terms & Conditions of Education Services as well as this quotation and fully agrees with and accepts such terms.

[redacted] MIM Software - Cardio - Single User, Perpetual License (MIM-CAR-CC) - For ROW only

6.1.10

Supports vendor neutral multi-modality image fusion and analysis. Provides Quantitative Analysis for Cardiac PET and SPECT. Analysis for Cardiac SPECT/PET including perfusion, function, viability for PET and SPECT, automated perfusion and viability difference imaging, robust deformable image segmentation, accurate template-based alignment to the left ventricle. Available separately or as part of the Nuclear Medicine Solution. On-Premise software for a perpetual license term, which includes the software and upgrades and support, as described at MIM Software's Support Page for one-year from the Go-Live Date. Thereafter a separate support and maintenance contract will have to be purchased to continue to receive upgrades and support. Customer's use of the Software is subject to MIM Software's clickwrap End User License Agreement.

NI_PET_PURC_SERVER EXTENSION - Purchased Services and HW

Purchased services and hardware to extend the AWS L server for MIM software installation. 6.2.1

[redacted] AW SERVER STANDALONE L - E-Delivery

AW Server

The AW Server delivers distributed 3D visualization capabilities throughout the enterprise and at any remote reading location. It utilizes state-of-the-art thin client technology to convert virtually any PC to a high-end 3D post processing station. In addition to this, it serves as a workflow engine enabling optimal collaboration among physicians and allowing 3D visualization to be leveraged easily to diagnose diseases quickly and make sound decisions. The AW Server also enables faster turnaround of post-processed results to referring physicians by allowing them to access the data instantly, while maintaining security and privacy of patient data.

The AW Server offers a vendor neutral OpenAPI PACS integration interface that enables launching the AW Server client from a variety of PACS software, both GE Healthcare provided and 3rd party. This capability supports passing the patient context to the client and even the application desired to be launched, so that time is saved and applications can be launched directly into the most relevant layout. This functionality may require work on the part of the PACS workstation or third party software provider.

The following capabilities are included in this catalog:

- AW Server client software which may be deployed to an unlimited number of systems by simply downloading the client application from the AW Server's web interface.
- Support for 10 concurrent log–in sessions
- Up to 16,000 concurrent images (equivalent to 512x512 CT slices) per active 3D user
- Concurrent Volume Viewer licenses
- Support for additional VolumeShare 7 based advanced applications which require purchasable concurrent license(s)
- Support for a single instance of GSI Viewer (requires optional license purchase).
- Virtualization supported.

Key features:

- Access to 3D visualization capabilities including MIP/MPR/VR, segmentation, fly-through and PET/CT
- "Smart Compression" technology automatically displays full fidelity static images even when compression is turned on for increased interactivity. This allows for diagnostic reads on full fidelity static images even at low bandwidth.
- On-image visual indicators notify user when compression is in effect.
- Intuitive work list interface with custom work lists, easy access to priors and exam states.
- Programmable ability to automatically push saved results to one or more DICOM hosts such as PACS when closing a session.
- Optional pre-processing capability to automatically process exams in background based on preset rules, minimizing wait time and keeping exams ready to read.

- Ability to open up to 3 simultaneous application sessions per active user and instantly switch between these sessions.
- Ability to save the state of post processing any time and restore it from any client, allowing multiple radiologists or technologists to contribute to post processing results.
- Ability to float application licenses between AW workstations (requires VolumeShare 2 or later) and one or more AW Server(s)
- Enterprise directory integration for single sign on user authentication with audit trails.
- Open API for PACS integration

Performance and intended uses:

Performance and interactivity on client PC's depend on the network bandwidth, latency and client PC configuration. To attain optimal performance, minimum bandwidth required is 40Mbps (LAN) with a latency of 20ms or lower. The server may be used over WAN/Internet as well although performance will heavily depend on round trip latency between client PC and server. A minimum of 3Mbps bandwidth is required.

HW Configuration: 6.2.1

7.7.2

- Intel Xeon CPU with SSE 4.1 (45 nm or newer)
- OS GE HELiOS 6
- 8 core vCPU
- 256 GB vRAM
- 2 NICs
- 300 GB OS vHDD
- 7.2 TB image storage vHDD
- Fully redundant hot plug power and cooling 6.2.2.1

Server hardware specifications listed here are minimum server hardware capabilities. Specific server hardware is subject to change without prior notice.

Concurrent licenses for supported advanced applications are optionally purchasable.

The server supports various compression levels selectable by user. The "Smart Compression" technology applies selected compression level only when user is interacting with the images to optimize performance. The images are automatically displayed at full fidelity once interaction stops. Clear visual indication on the images indicates any time compression is being applied to the images.

[redacted] AW Server UPS 6.2.3.1

HPE line interactive, single phase Uninterruptible Power System (UPS) solutions can protect up to 10 servers and other devices in both rackmount and desktop IT environments. Standard features include intuitive front panel displays for local management, and HPE Enhanced Battery Management (EBM) that helps to extend the service-life of your batteries. Protects more devices by providing up to 14% more wattage compared to traditional Uninterrupted Power Supplies. • HPE Enhanced Battery Management (EBM) technology delivers up to 50% longer battery life. • Industry leading efficiency of up to 99% helps to ensure minimal power loss and lower power costs. • Battery backup time up to 40 min for AWS L version• Batteries can be hot-swapped safely without every shutting down IT equipment.

6.2.3.1

[redacted] Q.Freeze 2 - eDelivery

Q.Freeze is the first ever imaging technique to combine the quantitative benefits of 4D PET/CT imaging into a single static image that uses 100% of the counts collected in the acquisition. The resulting incredible image quality has the dual benefit of frozen patient motion and reduced image noise from utilizing all available data.

Q.Freeze generates the Q.Freeze series, a respiratory motion-corrected PET volume, statistically similar to conventional static PET with significantly reduced or eliminated blurring effects due to patient respiration.

Q.Freeze shows an average motion correction down to 1mm with 80% lesion volume and 70% lesion maximum activity concentration recovery on Q.Freeze Series as compared to conventional static PET volume

Q.Freeze is leveraging the “MotionFreeZE” technology:

- Optical flow-based registration. A non-rigid registration technology that leverages the estimated motion between different gates of a gated PET for every voxel using optical flow equations with the following additional constraints:
- Multi-resolution approach takes into consideration the low SNR level of the PET imaging and provides robust accurate registration
- Models tissue viscosity and elasticity by taking into consideration the anatomical environment of the lesion
- Statistical median algorithm is used to generate the optimal summation of gates into a single Q.Freeze series by analyzing the quality of the registration in each part of the image. Q.Freeze is used to generate an all count gated series where counts are summed back to each respiratory phase.

[redacted] MIM Software - Encore - Single User, Perpetual License (MIM-EN-CC) - For ROW only

6.1.5, 6.1.6

Provides a diverse set of radiology and nuclear medicine diagnostic viewing and processing tools. Supports vendor neutral multi-modality image fusion and analysis. Provides automatic and semi-automatic NM processing functionality through the use of MIM Workflows and built-in algorithms of RECIST1.1. and RECIST1.0. On-Premise software for a perpetual license term, which includes the software and upgrades and support, as described at MIM Software's Support Page for one-year from the Go-Live Date. Thereafter a separate support and maintenance contract will have to be purchased to continue to receive upgrades and support. Customer's use of the Software is subject to MIM Software's clickwrap End User License Agreement.

[redacted] MIM Software - MIM Neuro Add-On- Single User, Perpetual License (MIM-NP-AD)

6.1.8

PET and SPECT quantitative analysis solution capable of image subtractions and co-registration with anatomical (CT, MR) images; includes FDG, Amyvid, NeuraCeq, Vizamyl, HMPAO, and DaTscan Neuro Normals. On-Premise software for a perpetual license term, which includes the software and upgrades and support, as described at MIM Software's Support Page for one-year from the Go-Live Date. Thereafter a separate support and maintenance contract will have to be purchased to continue to receive upgrades and support. Customer's use of the Software is subject to MIM Software's clickwrap End User License Agreement .

[redacted] MIM Software - SurePlan MRT - Single User, Perpetual License (MIM-SM-CC)

6.1.12

Provides a comprehensive platform for targeted therapy planning, including AI based segmentation, multi-modality fusion and dose calculation and review tools. Includes functionality for SPECT quantification for a single camera. On-Premise software for a perpetual license term, which includes the software and upgrades and support, as described at MIM Software's Support Page for one-year from the Go-Live Date. Thereafter a separate support and maintenance contract will have to be purchased to continue to receive upgrades and support. Customer's use of the Software is subject to MIM Software's clickwrap End User License Agreement.

[redacted] MIM Software - Lesion ID Pro - Single User, Perpetual License (MIM-LI-CC)

Powered by Contour ProtégéAI®, supports PSMA PET and PSMA SPECT. Must be used with a MIM Encore or MIM SurePlan MRT Concurrent License. On-Premise software for a perpetual license term, which includes the software and upgrades and support, as described at MIM Software's Support Page for one-year from the Go-Live Date. Thereafter a separate support and maintenance contract will have to be purchased to continue to receive upgrades and support. Customer's use of the Software is subject to MIM Software's clickwrap End User License Agreement.

[redacted] MIM Software - 3rd party- Cedars: Deluxe Perfusion SPECT; QGS + QPS, PlusPack (CED-DLXS-CC)

6.1.10

Cedars Deluxe SPECT

A comprehensive set of nuclear cardiology protocols for automated advanced cardiac analysis, including:

- Cedars Sinai Quantitative Perfusion SPECT- - Automatic 3-Dimensional software approach to quantitative Perfusion SPECT.
- Cedars Sinai Quantitative Gated SPECT- - An application calculating the ejection fraction of the left ventricle and a 3D surface display is generated.
- Cedars Sinai Quantitative Perfusion SPECT with Tl-201 and Tc-99m tracers provide an objective and quantifiable assessment of myocardial viability, which can help predict the likelihood of myocardial function recovery following coronary revascularization.
- Cedars Sinai Companion- - QGS and QPS applications features:
    - 17 segment scores and templates in QPS
    - Diastolic filling parameters in QGS
    - Eccentricity ratio in QGS
    - PlusPack Package:
    - Prone/Supine
    - Stress/Rest registration and serial change
    - Shape Index
    - Kinetic (CFR/Dynamic SPECT)
    - Motion correction (MoCo) for Dynamic SPECT. Pattern matching and segmentation algorithms are used in conjunction to minimize motion error metrics over the set of acquired projections; the resulting motion corrected projections are then presented to the operator for validation or modification.

[redacted] MIM Software - 3rd party- Cedars: Deluxe Perfusion PET; QPET, PlusPack, Fusion/CT (CED-DLXP-CC)

Cedars Deluxe PET

A comprehensive set of PET cardiology protocols for automated advanced cardiac analysis, including:

- Quantitative PET (QPET™) automatic segmentation, quantification and analysis of static and gated myocardial perfusion PET, with support for both short axis and transverse datasets.
  Including the following features for PET:
  - Automatic 3-Dimensional software approach to quantitative Perfusion PET
  - PET perfusion databases based on quantification of Rb-82 and N-13-ammonia perfusion PET images.
  - Calculating the ejection fraction of the left ventricle and a 3D surface display is generated based on PET gated data.
- FDG Viability
  Optional module for QGS and QPS applications features
  - Viability quantification
  - Scar and mismatch percentage
  - Extent and severity polar maps of scar and mismatch 6.1.11
- Pluspack Package:
  - Prone/Supine
  - Stress/Rest registration and serial change 6.1.10
  - Shape Index
  - Kinetic (CFR/Dynamic PET)
  - Motion correction for Dynamic PET

[redacted] MIM Software - 3rd party - Cedars Fusion/CT for SPECT Add-On (for CaSc) - 1 user

Cedars Fusion/CT module adds features related to coronary CT angiography (CTA) and multi-modality registration including 3D LV surfaces with mapped perfusion or viability information.

Fused image display to assess or correct image registration (for CTA and attenuation CT data)

- Calcium scoring
- CT MIPS
- Automatic Registration
- Fusion (SPECT/PET - CT/CTA)

Date: **September 04, 2025**

Refers to the Public Tender for „No. 3925785 – Positron Emission Tomograph with Accessories"

Hospital of Lithuanian University of Health Sciences, Kaunas Clinics, Eiveniu str. 2, Kaunas, Lithuania

We, GE Medical Systems Société en Commandite Simple, a company duly existing under the laws of France and having a registered seat at 283 Rue de la Minière, 78530 Buc, France, with commercial name GE HealthCare, in its capacity as European MDR Authorized Representative of **GE Medical Systems, LLC**, 3000 North Grandview Blvd, Waukesha, WI 53188, USA, the manufacturer of PET/CT Omni Legend 32 do hereby confirm the following:

1. The attenuation corrections for PET using CT images obtained during another, previous examination taken on the same patient is performed on the operator console of the offered PET/CT scanner Omni Legend 32. 6.1.4
2. EARL 2 criteria based protocol[1]

Marking	Description	Numerical value	Unit of measure
PAT	The required 18F (fluorine-18) radioisotope activity specified per 1 kg of patient body weight for the proposed digital positron emission tomography (PET) system, Omni Legend 32 (prior to its upgrade to a long axial field of view (LAFOV) PET-CT system) for a scanning protocol that meets EARL 2 criteria and is adapted for oncological applications using 18F-FDG which is provided below. The protocol refers to a patient weighing 75 kg and 175 cm in height, with scanning performed from the patient's eyebrows to the mid-thighs.	0.88 PAT	MBq/kg
S	The scanning time with the proposed digital positron emission tomography (PET) system, Omni Legend 32 (prior to its upgrade to a LAFOV PET-CT system), following the scanning conditions specified in the protocol with the declared FDG activity.	5 S	minutes
P	Patient preparation time for examination with the proposed digital positron emission tomography system, Omni Legend 32.	1,5 P	minutes

3. Typical patient preparation time P for examination on Omni Legend 32 using AI based Auto Positioning 3D camera and standard acquisition protocol is 90 second. P
4. The scanning protocol meeting EARL 2 criteria and adapted for oncological applications using 18F-FDG for Omni Legend 32 is as follows: PAT S
   1 min/bed position, 5 bed positions, overlap 45%, scanning range for 175 cm patient from the eyebrows to the mid-thighs.

On behalf and for GE Medical Systems SCS

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Authorized Signatory

Date of signature: September 04, 2025

[1][18F]FDG administered activity reduction capabilities of a 32-cm axial field-of-view solid-state digital bismuth germanium oxide PET/CT system while maintaining EARL compliance, Alina van de Burgt et al., Physica Medica 131 (2025) 104935

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[^{18}F]FDG administered activity reduction capabilities of a 32-cm axial field-of-view solid-state digital bismuth germanium oxide PET/CT system while maintaining EARL compliance

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ABSTRACT

Purpose: To assess the lower [^{18}F]FDG limit in administered activity and/or scan time reduction capabilities of a digital-BGO 32-cm axial field-of-view PET system while being compliant with current and updated EANM Research Ltd Fluorine-18 accreditation specifications ($EARL_1$ and $EARL_2$).

Methods: $EARL_1$ and $EARL_2$ compliance of the digital-BGO system (Omni Legend 32 cm) was tested for several reconstructions, including those that apply precision deep learning-based image enhancement (PDL) as post-processing, using the calibration QC and NEMA IEC phantom measurements. The image quality QC scan was repeated every hour for 7 h, with each subsequent hour representing a lower administered activity, and reconstructed for various times per bed position, i.e. 30, 60, 120, 180, and 300 s. For each of the image quality QC images, coefficient of variation (COV) of the background compartment, and mean, maximum and peak activity concentration recovery coefficients (RC_{mean}, RC_{max} and RC_{peak}) of differently-sized spheres were calculated and compared to current and updated EARL accreditation specifications.

Results: When we apply 1 min per bed position for PET acquisition, [^{18}F]FDG administration can be reduced by a factor of ~ 4 for $EARL_1$, by a factor of ~ 8 for $EARL_2$ (2 mm voxels) and by a factor of ~ 4 for $EARL_2$ (4 mm voxels) using both standard reconstructions and PDL post-processing compared to current EANM recommendations for [^{18}F]FDG administration (7 MBq·min·bed^{-1}·kg^{-1}).

Conclusions: Reduction in [^{18}F]FDG administered activity is possible by at least a factor 4 for 1 min/bed with the Omni Legend 32 cm PET/CT while maintaining $EARL_1$ and $EARL_2$ compliance.

1. Introduction

Positron emission tomography/computed tomography (PET/CT) imaging is a powerful tool that enables whole body non-invasive visualization and quantification of biological processes at the molecular level [1]. Continuous advancements in PET/CT technology have led to improved image quality and increased sensitivity, thereby potentially enhancing diagnostic accuracy which may lead to better patient outcomes [2]. Recently, a digital PET/CT with bismuth germanium oxide scintillating crystals coupled to silicon photomultipliers (SiPM) over an extended 32 cm axial field-of-view (FOV) was introduced (Omni Legend; GE HealthCare, Milwaukee, USA). This novel non-time-of-flight PET/CT system demonstrates high count rates (peak noise-equivalent count rates: ~500 kcps) and a superior sensitivity (45–49 cps/kBq) according to the National Electric Manufacturer's Association (NEMA) NU2-2018 standard [3], while maintaining a spatial resolution comparable to other current SiPM-based time-of-flight PET/CT systems [4–6]. Moreover, it incorporates precision deep learning-based image enhancement (PDL) that aims to provide improved feature sharpness and convergence comparable to hardware-based time-of-flight reconstruction [7]. The enhanced sensitivity of the system provides possibilities to reduce both scan duration and/or the administered activity of radiopharmaceuticals. Shorter scan durations may enhance patient comfort, increase patient throughput and decrease the risk of patient motion. Lowering the

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administered activity offers opportunities for cost savings and reduces the risks associated with radiation exposure for both staff and patients [5]. Kennedy et al. briefly highlighted the potential to reduce administered activity and scan time of the Omni legend PET/CT system for various radiotracers and injected activities [5], but a thorough investigation into the administered activity and/or scan time reduction capabilities of this new system has not yet been conducted. This study aims to assess the lower limit in administered activity of 2-deoxy-2-[^{18}F]fluoro-D-glucose ([^{18}F]FDG) and/or scan time reduction capabilities for the Omni Legend PET/CT while being compliant with current and updated European Association of Nuclear Medicine (EANM) Research Ltd Fluorine-18 accreditation specifications ($EARL_1$ and $EARL_2$).

2. Material and methods

$EARL_1$ and $EARL_2$ compliance of the Omni Legend system was tested using calibration QC and NEMA IEC phantom measurements [8–11].

2.1. Phantom studies

All PET acquisitions covered two bed positions with a 47 % bed overlap and were performed on an EARL ^{18}F standards 1 and 2 accredited PET/CT system (Omni Legend 32 cm, GE Healthcare, Milwaukee, USA) [8,9]. Prior to each PET scan, a low-dose CT scan (120 kVp, 52 mAs, with dose modulation) was acquired for attenuation correction purposes.

For the calibration QC scan, a cylindrical uniformity phantom with a diameter of 20 cm and a length of 30 cm was filled with distilled water and 82.2 MBq of [^{18}F]FDG, and placed in the centre of the FOV. A PET scan was acquired in list-mode for 5 min per bed position.

For assessing the system-specific patient [^{18}F]FDG activity using image quality QC scans, a NEMA IEC body phantom, equipped with six fillable spheres varying in diameter (10, 13, 17, 22, 28, and 37 mm) and a lung insert, was filled with distilled water, and 2.39 kBq/mL (uniform background compartment) and 22.6 kBq/mL (spheres) of [^{18}F]FDG, simulating a sphere to background ratio of ~ 10:1. The spheres of the phantom were positioned in the centre of the FOV. A PET scan was acquired in list-mode for 10 min per bed position (T0), and repeated every hour for 7 h (T0 + 1 h to T0 + 7 h), with each subsequent hour representing a lower activity. Boellaard et al described the entire procedure for assessing system-specific patient [^{18}F]FDG activity preparations for quantitative [^{18}F]FDG PET/CT studies [10].

More details for preparation and acquisition requirements of EARL fluor-18 accreditation can be found in the EARL standard operating procedures [11].

2.2. PET reconstructions

The list-mode data of the PET scan of the calibration QC were histogrammed into sinograms of 300 s per bed position, while the list-mode data of each PET scan (T0 till T0 + 7 h) of the image quality QC were histogrammed into sinograms of 30, 60, 120, 180, and 300 s per bed position. The 300 s per bed position of T0 was used to validate the image quality of the reconstructions to be $EARL_1$ or $EARL_2$ compliant. The following five reconstructions were performed:

- $EARL_1$ images were reconstructed using a 3D maximum likelihood ordered subset expectation maximization reconstruction (3D OSEM) (VUEPointHD (VPHD)) with 4 iterations and 12 subsets, followed by a 7 mm full-width-at-half-maximum (FWHM) Gaussian filter and a 192x192 matrix, resulting in a voxel size of 3.65 x 3.65 x 2.07 mm^3 (1).
- $EARL_2$ 2 mm images were reconstructed using a Bayesian penalised likelihood reconstruction (BPL; Q.Clear) with a β parameter of 1500 and a 384x384 matrix, resulting in 1.82 x 1.82 x 2.07 mm^3 voxels (2), and repeated with PDL post-processing using a 'low' level of contrast-enhancement (3).
- $EARL_2$ 4 mm images were reconstructed using BPL with a β parameter of 1200 and a 192 x 192 matrix, resulting in 3.65 x 3.65 x 2.07 mm^3 voxels (4), and repeated with the 'low' level of PDL post-processing (5).

All reconstructions were performed with corrections for attenuation, scatter, normalization, decay, and dead time. For each of the image quality QC images, coefficient of variation (COV) of the background compartment, and mean, maximum and peak activity concentration recovery coefficients (RC_{mean}, RC_{max} and RC_{peak}) of differently-sized spheres were calculated and compared to current and updated EARL accreditation specifications [8,10,12].

2.3. Data analysis

For each PET image of the calibration QC, the average volumetric standardized uptake value (SUV) bias, which cannot exceed 10 %, is calculated by:

$$SUV_{bias}(\%) = \left(\frac{C_{measured}}{C_{calculated}} - 1\right) \times 100\% \quad (1)$$

In this equation $C_{measured}$ represents the activity concentration measured from images and $C_{calculated}$ is the true activity concentration calculated from injection data. The SUV_{bias} was generated using the manual tool implemented in IDL (version 8.4; Harris Geospatial Solutions, Bloomfield, USA) by Boellaard et al [8,12]. Maximum, peak and mean SUV recovery coefficients (RC_{max}, RC_{mean} and RC_{peak}) were computed for all spheres on each reconstructed PET image quality QC images using an in-house-developed algorithm in MATLAB (version 2018b; MathWorks, Massachusetts, USA), cross-validated with the aforementioned manual tool implemented in IDL by Boellaard et al [8,12], with a deviation of < 1 %. In short, this in-house-developed algorithm in MATLAB, using the known geometry of the NEMA IEC body phantom, locates the centroids of the spheres from the PET image and draws volumes of interest (VOIs) on the six spheres together with 3 cm rectangular VOIs (n = 9) at predetermined locations (relative to the sphere location and depending on the sphere orientation and position) in the background compartment of the phantom (Fig. 1), onto each

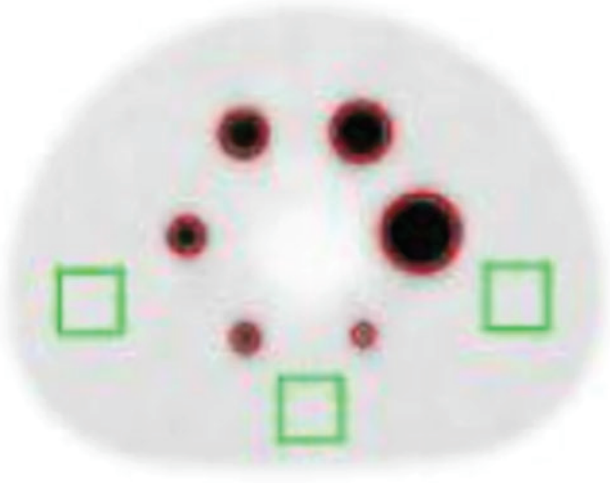

Fig. 1. Visualization of the template of the NEMA IEC body phantom geometry used by the in-house-developed algorithm, showing the volumes-of-interest (VOIs) of the six spheres identified on the PET image (red circles) and the rectangular background VOIs (3 cm, n = 9, green squares) in axial view. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

reconstructed PET image. To limit the effects of partial voxels, using the known sphere diameter, a raster of sample points is created every 0.1 mm and the values are interpolate in these 0.1 locations, thereby creating a finer sampling than the original voxels. For each sphere, the max and peak values are obtained (for the calculation of RC_{max} and RC_{peak}) from the original PET images, and a VOI is created by a 50 % background-corrected isocontour method to derive the mean value for the calculation of RC_{mean}. The RC values are calculated by:

$$RC = \frac{S_{measured}}{S_{calculated}} \quad (2)$$

In this equation $S_{measured}$ represents the max, peak or mean activity concentration measured from the VOIs of each sphere and $S_{calculated}$ is the true activity concentration calculated from injection data for the spheres. The obtained RC values should comply to the $EARL_1$ (RC_{max} and RC_{mean}) and $EARL_2$ (also includes RC_{peak}) accreditation specifications [11]. In addition, the coefficient of variation (COV), determined by dividing the standard deviation by the mean of the pixel values within a VOI, was initially computed for each individual 3 cm rectangular VOIs placed in the background compartment (n = 9). Subsequently, the final COV parameter was obtained by averaging these 9 COV values. It was essential that the resulting average COV remained below 15 % [10].

3. Results

3.1. $EARL_1$ and $EARL_2$ compliance

The calibration QC revealed a median SUV bias of 1.16 % (range: 0.40—1.55 %). RC_{max}, RC_{mean} and (when applicable) RC_{peak} of all tested reconstructions were $EARL_1$ or $EARL_2$ compliant (Fig. 2 and **Supplemental file S1**).

3.2. Administered activity and/or scan time reduction capabilities

When we apply 1 min per bed position for PET acquisition, [^{18}F]FDG administration can be reduced by a factor of ~ 4 for $EARL_1$, by a factor of ~ 8 for $EARL_2$ (2 mm) and by a factor of ~ 4 for $EARL_2$ (4 mm) using both standard reconstructions (Fig. 3A) and PDL post-processing (Fig. 3B) compared to current EANM recommendations for FDG administration (7 MBq·min·bed^{-1}·kg^{-1} of [^{18}F]FDG for a 75 kg patient [9]). This indicates a decrease in MBq/kg for the used reconstructions to 1.75 MBq/kg, 0.88 MBq/kg and 1.75 MBq/kg, respectively. $EARL_2$ reconstructions (2 mm and 4 mm voxels) both with and without PDL allowed similar reductions in administered activity, with lower COV values for with PDL (maximum COV difference: 5.2 % for 2 mm and 16.5 % for 4 mm). Due to the higher beta value applied for $EARL_2$ 2 mm, $EARL_2$ 4 mm voxel size has generally higher COVs than 2 mm, contrary to the expectation of smaller voxels exhibiting higher noise and COV (maximum COV difference: 32.4 % with PDL and 45.5 % without PDL).

4. Discussion

This phantom study provides an initial insight into the applicable lower limit in [^{18}F]FDG administered activity and/or scan time reduction while being $EARL_1$ and $EARL_2$ Fluorine-18 compliant for the Omni Legend PET/CT system. Despite the larger voxel size, $EARL_2$ (4 mm) COV data were higher overall than $EARL_2$ (2 mm), which may be attributed to the higher beta value used in the 2 mm BPL reconstruction. Moreover, using the same method to assess reduction in administered activity, van Sluis et al. reported factors of reductions in administered activity at 1 min/bed of ~ 8 ($EARL_1$), ~4 ($EARL_2$, 4 mm) and 1 ($EARL_2$, 2 mm), where our results gave factors ~ 4, ~8 and ~ 4, respectively [13]. This difference can be explained by their use of a different scanner and reconstruction algorithms. Furthermore, our data show comparable findings for $EARL_2$ 2 mm on the Omni Legend system compared to Kennedy et al. (0.88 for our study compared to 1 MBq·min·bed^{-1}·kg^{-1} for Kennedy et al), yet scan times and reduction in administered activity are less thoroughly covered in their study [5]. Note that each institution is advised to explore different reconstruction parameters of their scanner to ensure EARL compliance with our indicated reductions in administered activity.

Our study has limitations. First, the NEMA IEC body phantom only simulates a 75 kg patient. Preferably, the validation should be replicated using phantoms simulating various patient sizes [14]. Second, we used one strategy to assess the reduction in administered activity, however, alternative methods are available to assess reduction in administered activity [15–18]. Third, this phantom does not reflect real-world conditions. Ideally, for future work we recommend that a clinical study should be performed to validate the image quality, the potential role of deep learning-enhanced post-processing and quantitative accuracy

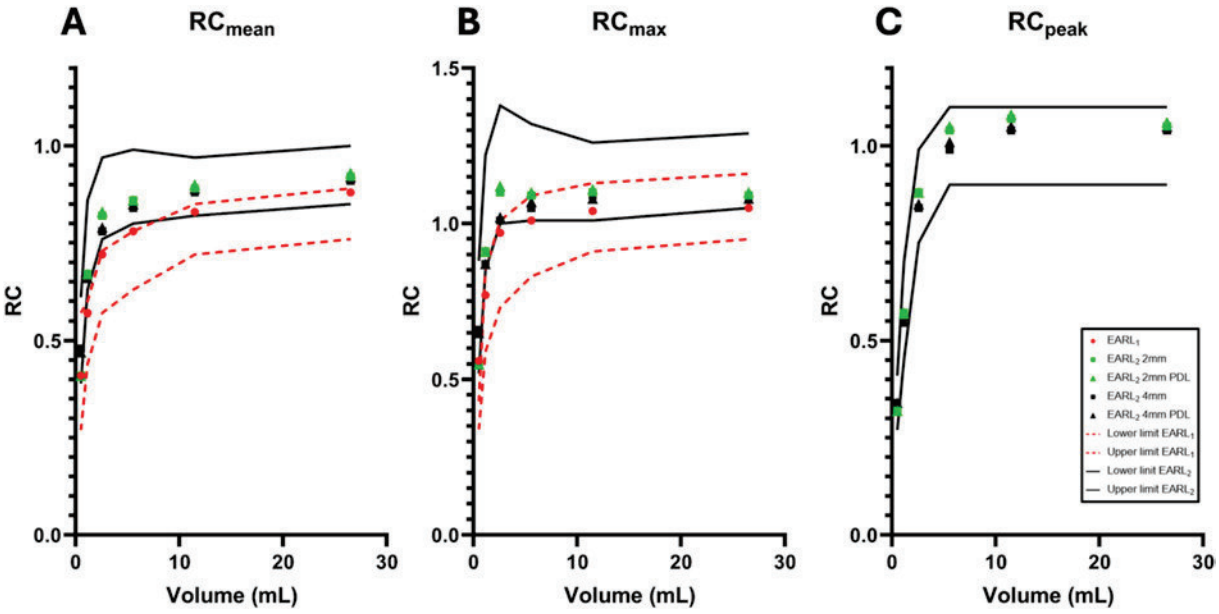

Fig. 2. Max (A), mean (B) and peak (C; only $EARL_2$) recovery coefficients (RC) as a function of volume (mL), derived from the image quality QC scan acquired at T0, using 300 s per bed position. PDL: precision deep learning image enhancement.

A

No PDL	Activity (MBq/kg)	Time per bed position (s)														
		$EARL_1$					$EARL_2$ 2mm					$EARL_2$ 4mm				
		30	60	120	180	300	30	60	120	180	300	30	60	120	180	300
T0	4	12.6	9.7	7.9	6.2	3.9	9.6	6.7	4.9	3.6	2.6	11.3	8.5	5.9	4.1	3.2
T0 + 1h	2.73	17.1	12.4	8.6	6.8	4.1	10.2	7.7	4.4	3.6	2.7	13.4	8.6	5.7	4.3	3.5
T0 + 2h	1.87	19.2	13.6	11.1	7.6	5.7	10.6	8.9	6.2	5.3	3.8	15.4	11.0	7.7	5.9	4.3
T0 + 3h	1.29	24.1	17.4	12.6	9.9	8.0	17.6	10.3	7.1	5.8	5.1	24.2	13.9	9.2	6.9	5.7
T0 + 4h	0.88	25.3	18.2	12.7	11.0	8.8	18.3	12.6	8.0	6.5	5.0	30.5	16.8	9.6	7.9	5.7
T0 + 5h	0.56	30.2	20.3	19.2	16.3	10.9	25.0	15.4	12.8	10.0	7.0	44.4	21.3	16.7	12.6	8.9
T0 + 6h	0.41	32.7	27.3	20.7	16.5	13.1	28.8	21.7	11.6	9.8	8.2	58.3	37.9	18.8	12.8	10.0
T0 + 7h	0.28	36.5	30.5	20.5	16.8	15.1	40.7	24.3	15.1	11.7	9.9	86.2	52.9	23.3	15.7	12.3

B

PDL	Activity (MBq/kg)	Time per bed position (s)									
		$EARL_2$ 2mm					$EARL_2$ 4mm				
		30	60	120	180	300	30	60	120	180	300
T0	4	8.7	6.2	4.0	2.9	2.2	7.8	6.3	4.5	3.2	2.4
T0 + 1h	2.73	8.3	7.0	3.4	2.9	2.5	12.4	5.9	4.1	3.0	2.5
T0 + 2h	1.87	8.3	7.5	5.6	4.6	3.0	13.6	7.7	5.6	4.5	3.0
T0 + 3h	1.29	14.4	8.5	6.0	5.0	4.4	18.0	10.1	6.1	4.8	4.2
T0 + 4h	0.88	14.3	10.2	6.8	5.6	4.2	22.8	13.4	6.5	5.2	4.1
T0 + 5h	0.56	20.5	12.2	10.9	8.6	6.2	34.0	15.2	12.8	9.3	6.4
T0 +6h	0.41	23.5	17.8	9.0	9.1	7.3	49.9	29.5	13.2	10.0	7.4
T0 + 7h	0.28	37.3	19.1	11.9	11.2	8.5	69.7	40.0	16.3	10.6	8.5

COV ≤ 15 All recovery coefficients comply to accreditation specifications

COV ≤ 15 One or more spheres fall outside the accreditation specifications for SUV mean, maximum and/or peak activity concentration recovery coefficients

COV > 15

Fig. 3. $EARL_1$ and $EARL_2$ (2 mm and 4 mm) compliance illustrating coefficient of variation (COV) at various [^{18} F]FDG activity dosages and scan durations for reconstructions without (A) and with (B) precision deep learning image enhancement (PDL). SUV: standardized uptake value.

using [^{18}F]FDG PET data of patients scanned at the chosen lower regime in administered activity and/or reduced scan times. Note that the identified lower limits of [^{18}F]FDG administered activity only apply to the Omni Legend 32 cm PET/CT and that new studies should be performed to investigate the lower limits of [^{18}F]FDG administered activity for other PET systems.

In conclusion, we demonstrate in this phantom study that a reduction in [^{18}F]FDG administered activity is possible by at least a factor 4 for 1 min/bed with the Omni Legend 32 cm PET/CT while maintaining $EARL_1$ and $EARL_2$ compliance. A clinical study should be performed to validate these findings.

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Declaration of competing interest

FK is an employee of GE HealthCare. PD and FV have received a speaker honorarium from GE Healthcare (fees received by institution).

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Appendix A. Supplementary material

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ejmp.2025.104935.

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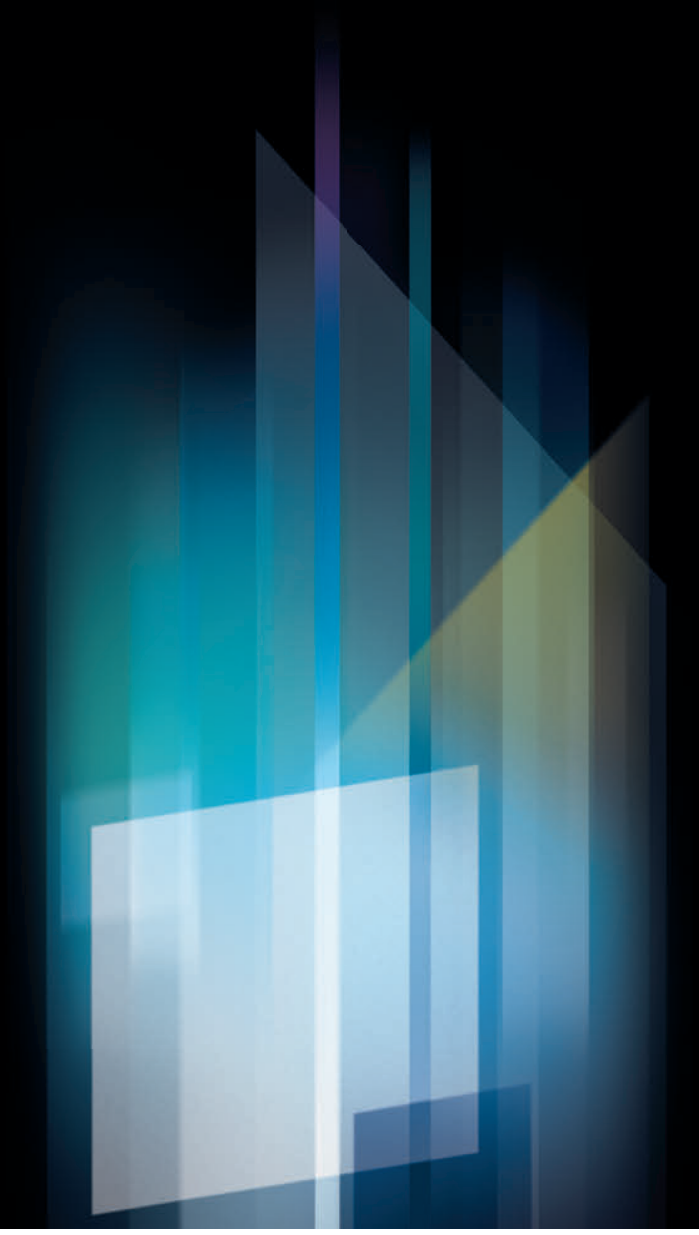
mim cardiac™

Quantitative Analysis for Cardiac PET and SPECT



mim cardiac™

Quantitative Analysis for Cardiac PET and SPECT

MIMcardiac® is a quantitative analysis solution for both PET and SPECT. The software also features multi-modality image registration for anatomical correlation with CCTA and MR and for improved comparisons of stress and rest images.

Robust Edge Detection

Generating quantitative information for cardiac analysis begins with accurate left ventricular segmentation. MIMcardiac provides a robust deformable image segmentation method that generates reliableLV volumes and functional parameters such as ejection fraction. 6.1.10

MIMcardiac's edge detection utilizes deformable template-based alignment for image segmentation, overcoming limitations of traditional threshold-based cardiac segmentation methods, which can have difficulty with large perfusion defects or segmenting low activity areas of the heart such as the base.

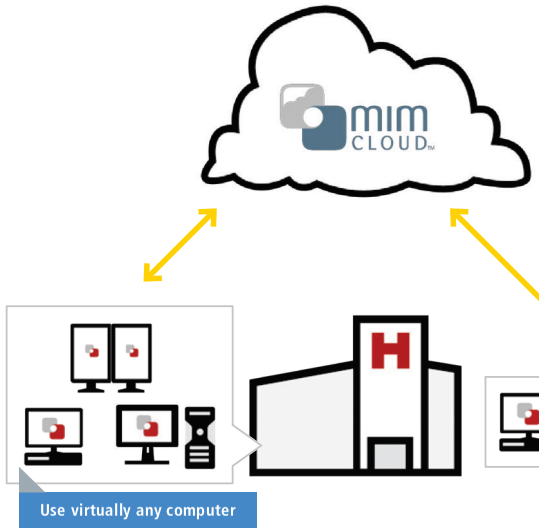
Transient ischemic dilatation (TID) statistics are also provided.

Perfusion Analysis 6.1.11

Polar mapping of perfusion activity utilizes template-based deformable registration to align the patient's image to a standard template for improved mapping to the polar plots.

Polar plot features include: 17, 19, and 20 segment models; blackout maps, reversibility maps, and z-score maps; segmental scores with summed stress scores (SSS) summed rest scores (SRS), and summed difference scores (SDS), and choice of auto-normalization or max voxel normalization.

A non-attenuated corrected Tc99m sestamibi SPECT normal database is provided. Users can also create their own normal databases. 6.1.11



Remote Access and Storage

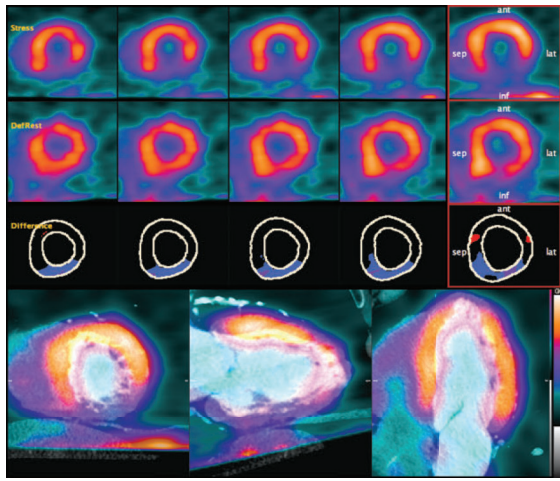
You can access images from anywhere in the world using MIM's thin-client licensing solution via MIMcloud™. Additionally, MIM's cloud-based storage solution provides a method for off-site storage and backup of data.

Stress & Rest Alignment and Serial Change 6.1.11

MIMcardiac's fusion technology is also utilized for aligning stress-to-rest images or serial exams making it easier to compare the same area of myocardium between scans.

Perfusion differences are highlighted using a color-coded display overlaid on the patient's image. Difference images allow the patient's own scan to serve as the control for comparison. 6.1.10

Difference images can also be created for viability studies highlighting differences in perfusion and metabolism.



HeartAlign

HeartAlign™ is a landmark-based deformable registration method that is used to match a patient's scan to a template or to another image for the same patient. An affine registration is performed for the initial alignment correcting for orientation and size differences. The landmark-based deformable registration is performed next to correct for shape differences between the images. Using this same deformation, contours are transformed back to the original patient image. This method of matching can also be used for stress and rest images or serial exams to help highlight changes.

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CE 1639

Date: **September 05, 2025**

Refers to the Public Tender for „No. 3925785 – Positron Emission Tomograph with Accessories”

Hospital of Lithuanian University of Health Sciences, Kaunas Clinics, Eiveniu str. 2, Kaunas, Lithuania

We, GE Medical Systems Société en Commandite Simple, a company duly existing under the laws of France and having a registered seat at 283 Rue de la Minière, 78530 Buc, France, with commercial name GE HealthCare, in its capacity as European MDR Authorized Representative of **GE Medical Systems, LLC**, 3000 North Grandview Blvd, Waukesha, WI 53188, USA, the manufacturer of PET/CT Omni Legend do hereby confirm the following:

1. MIMneuro software is supporting static and dynamic brain perfusion studies. There is no Normal Database for ^{15}O included. The tool can be used for studies with other tracers/isotopes including ^{15}O.

6.1.9

On behalf and for GE Medical Systems SCS

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Jennifer Thery - EMEA Contract Specialist
Authorized Signatory

Date of signature: September 05, 2025

Cedars-Sinai
Cardiac Suite

User's Manual

CSI, QGS + QPS / QPET, QBS, ARG, MoCo, and AutoRecon

Version 2017 Rev. I (2024-09)

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CE Marking
Cedars-Sinai Cardiac Suite is CE Marked to the Medical Device Directive 93/42/EEC.

MD	Medical Device
US	Manufactured in the United States of America
Basic UDI-DI	08646870002473P
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User Assistance Information

For service or support questions, please contact your vendor's customer support line.

If you purchased your software directly from Cedars-Sinai Medical Center, please email:

support@thecardiacsuite.com

or call:

+1-844-CSMC-AIM (+1-844-276-2246)

Online documentation

You may view and download this user manual, in English and other supported languages, from the following location:

https://thecardiacsuite.com/ifu

Printed Copy

You may request a printed copy of this document by sending an email to the support address above. Please include your complete mailing address as well as this document reference:

USRMAN-2017-I-EN

WARNING

Do not install software applications not approved directly by your workstation vendor. The system is only warranted and supported as configured and delivered. Refer to the vendor documentation for detailed system requirements.

Installation of Cedars-Sinai Cardiac Suite on vendor workstations is only to be performed by an authorized service engineer or applications specialist.

Table of Contents

1 Introduction

1.1 Indication for Use

The Cedars-Sinai Medical Center (CSMC) Cardiac Suite of applications is intended to enable an automated display, review, and quantification of Nuclear Medicine Cardiology medical images and datasets obtained from patients who have undergone a compatible medical scan1. CSMC Cardiac Suite may be used in multiple settings including the hospital, clinic, or office environments. The results provided should be reviewed by qualified healthcare professionals (e.g., radiologists, cardiologists, or general nuclear medicine physicians) trained in the use of medical imaging devices.

1.2 Description of Device

The Cedars-Sinai Cardiac Suite is a stand-alone software solution for Cardiac SPECT and PET imaging processing and review. Cedars-Sinai Cardiac Suite (non-viewer) minimum system requirements include a computer with at least 4GB RAM, 2GB hard disk space for software installation, a display resolution at least 1280x1024 with 16-bit color, a network adapter, a mouse (or other pointer device; trackpad, trackball, etc.) and one of the supported operating systems. CSMC Cardiac Suite operates on camera independent reconstructed SPECT and/or PET image files and Cardiac CT image files.

CSMC Cardiac Suite will be marketed as a comprehensive application suite that includes QGS+QPS (Quantitative Gated SPECT + Quantitative Perfusion SPECT) in a single application (aka AutoQUANT) and CSImport applications. This allows automatic processing and review of quantitative and qualitative information generated by nuclear medicine studies. Purchasable options consist of Quantitative Blood Pool SPECT (QBS), QARG (for reporting purposes), Fusion (SPECT/CT/CTA and/or PET/CT/CTA), AutoRecon, Motion Correction (MOCO) and QPET. QPET also includes viability quantification and two additional databases (rubidium and ammonia) for processing PET studies.

QGS+QPS is an application which combines both Quantitative Perfusion SPECT (QPS) and Quantitative Gate SPECT (QGS) into a common application. Quantitative Perfusion SPECT (QPS) is an application designed for LV (Left Ventricle) and RV (Right Ventricle) extraction and analysis. QPS provides a tool to review and quantify perfusion Cardiac SPECT and PET data sets to determine the location, orientation, and anatomical extent of the left ventricle of the heart, to construct 3D contour maps of the heart, and to calculate the heart volume. Physicians use this information to assess the anatomical and physiological functionality of the heart and analyze the presence of myocardial defects through comprehensive imaging modalities. Stress-

[1] See “1.2. Description of Device”

Rest Registration is a direct method for detecting changes between stress and rest images. It is a practical and fully automatic algorithm for quantification of stress-induced changed from paired stress and rest scans and does not use protocol-specific databases. Prone-supine quantification allows quantification of perfusion on prone images as well as combined quantification of prone/supine datasets by applying heuristic rules, which allow automatic elimination of image artifacts based on the relative defect locations on prone and supine images. The shape index parameter defines 3D left ventricular (LV) geometry derived from LV contours in end systolic and end diastolic phases. QPS includes an algorithm for the quantification of myocardial perfusion, using normal limits created from studies of low-likelihood normal patients only. The algorithm has been validated in a large group of patients demonstrating equivalent diagnostic performance despite the use of simplified normal limits. The following databases are being provided (for male and female): Prone Stress MIBI, Rest MIBI, Rest MIBI AC (Attenuation Corrected), Rest Thallium, Stress MIBI, Stress MIBI AC, Stress Thallium. Optional normal limits databases offered are Rubidium for PET, Ammonia for PET. QPS provides the ability for user generated normal limits files using the simplified method. QPS also includes a variable, Total Perfusion Deficit (TPD), which combines defect extent and severity values. The new quality control (QC) automatically detects quantitative segmentation failures. In the event of a failure a different algorithm is applied. Quantitative Gated SPECT (QGS) is an application designed for LV (Left Ventricle) and RV (Right ventricle) extraction and analysis. QGS provides a tool to review and quantify function Cardiac SPECT and PET data sets to determine the location, orientation, and anatomical extent of the left ventricle of the heart, to construct 3D contour maps of the heart, and to calculate the heart volume (for the left ventricular wall). Physicians use this information to assess the anatomical and physiological functionality of the heart and analyze the presence of myocardial defects through comprehensive imaging modalities. A new Phase page included in QGS page gives access to phase information for gated datasets. A new technique to create cardiac "motion-frozen" perfusion or viability images, by warping ECG-gated images to the end-diastolic position has been added. Such "motion-frozen" perfusion and viability images have improved resolution and contrast by removing blurring effect caused by cardiac motion. The new quality control (QC) automatically detects quantitative segmentation failures. In the event of a failure a different algorithm is applied. QGS+QPS can also generate and display TID (Transient Ischemic Dilation) and LHR (Lung Heart Ratio or Lung Heart Counts). A new group processing algorithm has been added which allows for simultaneously solving left ventricular geometry for all of the available datasets. It allows the algorithms, in regions where structure cannot be definitively determined for one or more of the datasets, to make decisions that exploit all the available information and that do not introduce arbitrary inter-study inconsistencies.

Quantitative Blood Pool SPECT (QBS) is an optional application. QBS is an interactive standalone software application for the automatic segmentation and quantification of gated short axis

blood pool (red blood cells, RBC) SPECT. The application can be used for automatic generation of left and right ventricular endocardial surfaces and valve planes from three-dimensional (3D) gated short axis blood pool images; automatic calculation of left and right ventricular volumes and ejection fractions; calculation and display of polar maps representing wall motion and parametric values (FFH amplitude and phase); two-dimensional (2D) image display using standard American College of Cardiology (ACC) cardiac SPECT conventions; and 3D image display. It also provides the following functionalities: ability to combine isosurfaces extracted from the data with the calculated endocardial surfaces in various ways (endocardial borders displayed as wireframes, shaded surfaces, both, or parametric); ability to map parametric values (First Fourier Harmonic (FFH) amplitude and phase) on the surfaces; ability to display parametric images (FFH amplitude and phase) for gated planar, gated raw projections and gated short axis images; ability to display cine loops of the original images; ability to generate count-based quantitative values using the automatically- and semi automatically-computed surfaces as ROIs and user-selectable thresholds; ability to generate and display phase histograms for FFH phase images and to display the mean and standard deviation of the peaks corresponding to atrial and ventricular voxels. After ventricular segmentation, a phase histogram for each ventricle is also computed and displayed; and ability to display normalized images for all gated images (i.e., images that do not exhibit count drop-off caused by arrhythmia). In addition, QBS supports manual identification of the left-ventricular (LV) region, to separate it from the right ventricle (RV) in cases where the automatic algorithm fails or returns unsatisfactory results; ability to generate filling rates from interpolated time-volume curves; and the ability to rotate, zoom, and cine surfaces.

A nuclear image fusion package is available as an option to QGS+QPS for both SPECT/CT and PET/CT hybrid applications. The fusion option includes a page that allows for display of segmented and labeled coronary vessels with PET 3D data. Functionality includes orthogonal planes using alpha blending, roving window and synchronized cursor. It allows users to perform quality control of SPECT/CT/CTA or PET/CT/CTA alignment and has generic multimodality fusion capabilities. This feature provides display of fused images in a visual format. Additionally, included for PET analysis is the Hibernating Myocardium Assessment (mismatch and viability); this module allows quantitative assessment of "hibernating myocardium" by quantification of changes between PET perfusion and viability images in hypo-perfused area. Scar and Mismatch parameters are reported as a percentage of the Left Ventricle and are displayed in polar coordinates or a 3D surface display. A new registration algorithm has been added which automatically registers SPECT/PET with CTA/CT datasets.

Quantitative PET (QPET) is an optional module which adds automatic segmentation, quantification and analysis of static and gated myocardial perfusion PET, with support for both

short axis and transverse datasets. The QPET module includes dynamic PET capabilities, such as calculation of absolute blood flow within the myocardium.

CSImport is an application designed to import datasets from a variety of sources, store them in a local image database, and launch any number of applications that use this data for their processing purposes. CSI also provides a variety of data management tools, and includes a DICOM Store Service Class Provider (SCP) service that allows DICOM-compliant systems to push images to your PC for processing and review.

AutoRecon is a one-step application for automatic reconstruction and reorientation of raw tomographic data (raw projections), with an emphasis on cardiac images. The application offers a choice of filtering and reconstruction options (including iterative reconstruction) and automatic reorientation (>95%). AutoRecon offers several automatic processing modules for single-photon emission computed tomography (SPECT) studies. Although it is mainly designed for cardiac data, many of its functionalities can be applied to other types of SPECT studies. AutoRecon provides automatic reorientation of three-dimensional, transaxial myocardial perfusion SPECT images. AutoRecon is comprised of four modules: reconstruct, reorient, motion and filter. Each module has associated pages that present data and the controls necessary to perform the specific task for which the page has been designed. The program can be used interactively on one or more datasets or in batch mode to process data without further intervention from the user. If matching rest and stress datasets are provided, AutoRecon will automatically operate in dual mode.

MoCo (Motion Correction) is an optional application for the automatic and manual correction of SPECT acquisition motion artifacts. Pattern matching and segmentation algorithms are used in conjunction to minimize motion error metrics over the set of acquired projections; the resulting motion corrected projections are then presented to the operator for validation or modification.

ARG/QARG (Cedars-Sinai Reporting) is a tool that produces comprehensive nuclear cardiac reports. QARG includes data collection utilities, data consistency checks, report generation, search utilities and several administrative tools. During the data collection process users are automatically prompted to resolve potential inconsistencies. Once the data acquisition is complete, the reports are generated. Reports not only contain derived values, but output clear sentences designed to send to the referring physician. QARG merges data from all3 sources to produce a single comprehensive report.

CSView (Cedars-Sinai Viewer) is an application designed as a generic medical image viewer, with an emphasis on planar Nuclear Medicine (NM) studies. CSView includes customizable display layouts, image manipulation controls; brightness/contrast adjustments, color scales, zooming

panning, rotation and flipping. CSView also includes a tool for conducting flood uniformity analysis.

The results provided should be reviewed by qualified healthcare professionals (e.g., radiologists, cardiologists, or general nuclear medicine physicians) trained in the use of medical imaging devices.

1.3 Contraindications

There are no absolute contraindications for the use of the Cedars-Sinai Cardiac Suite.

1.4 Clinical benefits

The Cedars-Sinai Cardiac Suite achieves its intended performance under normal conditions of use. The Cedars-Sinai Cardiac Suite has a positive impact on the health of an individual by its use as an aid in detecting, localizing, and diagnosing lesions and organ function for the evaluation of heart diseases and disorders. The Cedars-Sinai Cardiac Suite has a positive influence on the health of an individual when used as an aid in managing cardiology and other diseases.

1.5 Intended patient population

The Cedars-Sinai Cardiac Suite may be used to display, review, and quantify images from all patients who have undergone a compatible medical scan (see section 1.2, description of device). There are no exclusions to the intended patient population.

1.6 Serious Incident Reporting

If a serious incident occurs with this medical device, report it to the manufacturer and to the competent medical authority for the user/patient's country.

1.7 Interference risk

There is no known risk of interference with other equipment when used within its intended purpose.

1.8 New features

There are many new features in this version of the Cedars-Sinai Cardiac Suite. These are some of the most important.

1.8.1 Version 2017

- QGS+QPS, QPET, QBS

- **Coronary Calcium Score** quantification.
- **SPECT CFR/MBF** quantification, including residual activity correction.
- **Motion correction for dynamic PET/SPECT datasets** used for CFR/MBF quantification.
- **Planar Blood Pool (MUGA)** scan quantification.
- **3D Iterative algorithm** for processing reduced count images.
- **Raw projections (MIPS)** for PET.
- **LV count** computed from contoured myocardium.
- **Updated Splash** page.

1.8.2 Version 2015

- QGS+QPS, QPET, QBS
  - **Right Ventricle (RV)** quantification for gated datasets is now available in QGS+QPS.
  - The new **'Quality' page** for QGS+QPS and QBS allows users to easily review raw dataset integrity and easily spot any acquisition errors.
  - The new **Smart Defect Editor** for QGS+QPS gives users the ability to edit defects on perfusion polar maps.
  - The new **Fast Dataset Selector** feature for QGS+QPS allows users to easily toggle between different dataset combinations and layouts.
  - The new **Color Scale Manager** for QGS+QPS, QPET and QBS gives users the ability to import/export color scale palette files.
  - **Phase Analysis** algorithm was modified for QGS+QPS in order to exclude basal count variations that do not correspond to actual myocardial thickening but instead are caused by valve plane motion between diastole and systole.
  - **Group processing / Reproducibility** option for QGS+QPS and QPET, which allows for simultaneously solving left ventricular geometry for all of the available datasets.

- QARG
  - **HL7 support** for structured reports generated using the Automated Report Generator (ARG).
  - **Advanced Distribution Server** provides multiple options for distributing finalized reports.
  - **MIBG** reporting is now supported.

1.8.3 Version 2013

- CSImport has been completely overhauled with improved user interface and performance. Some of the new features include:
    - Support for SQL database backend.
    - User and site centric access control, similar to QARG.
    - User specific options for storing data privately or publically.
    - Enhanced task management system.
    - Deleted items management utility for recovering deleted items.
    - Enhanced logging for operations such as importing, replacing, deleting, etc.
    - Options for reconciling or linking studies.
    - Advanced filtering options that include options such as patient position (prone/supine/…), gating (static/gated/dynamic), patient state (rest/stress/…), etc.
- QARG contains a significant number of enhancements and new features. Some of the new features include:
    - Support for blood pool studies (includes integrated support for QBS), pyrophosphate studies and CTA studies.
    - Advanced appropriate use criteria engine based on ASNC guidelines.
    - Automated options for generating detailed administrative reports.
    - Advanced report distribution engine.
    - Simplified user interface and report templates.
    - Standard, IAC (formerly ICANL) compliant, 1 page report templates.
    - Support for opening multiple studies or reports.
- Multi-monitor (unlimited) display mode for QGS+QPS and QBS.

1.9 Maintenance

The Cedars-Sinai Cardiac Suite version 2017 may be updated from time to time with minor new features and non-critical bug fixes. Users will be notified of update availability.

1.10 Statement of Accuracy

The Cedars-Sinai Cardiac Suite of applications is not intended to provide diagnoses or therapeutic recommendations but is intended to enable an automated display, review, and quantification of nuclear Medicine Cardiology medical images and datasets. Cedars-Sinai Cardiac Suite may be used in multiple settings including the hospital, clinic, doctor's office, or remotely. The results provided should be reviewed by qualified healthcare professionals (e.g.,

radiologists, cardiologists, or general nuclear medicine physicians) trained in the use of medical imaging devices.

Cedars-Sinai Cardiac Suite applications have been in continuous, worldwide use for over 20 years. Their algorithms and methodologies have been validated through numerous, widely published and cited studies, including this representative selection:

Category ↳ Metric	Description	References
LV segmentation		
Volume	LV chamber volume, gated or ungated	Germano G, Kiat H, Kavanagh PB, Moriel M, Mazzanti M, Su HT, Van Train KF, Berman DS. Automatic quantification of ejection fraction from gated myocardial perfusion SPECT. J Nucl Med. 1995 Nov;36(11):2138-47. PMID: 7472611. Germano G, Erel J, Kiat H, Kavanagh PB, Berman DS. Quantitative LVEF and qualitative regional function from gated thallium-201 perfusion SPECT. J Nucl Med. 1997 May;38(5):749-54. PMID: 9170440. Germano G, Kavanagh PB, Waechter P, Areeda J, Van Kriekinge S, Sharir T, Lewin HC, Berman DS. A new algorithm for the quantitation of myocardial perfusion SPECT. I: technical principles and reproducibility. J Nucl Med. 2000 Apr;41(4):712-9. PMID: 10768574. Sharir T, Germano G, Waechter PB, Kavanagh PB, Areeda JS, Gerlach J, Kang X, Lewin HC, Berman DS. A new algorithm for the quantitation of myocardial perfusion SPECT. II: validation and diagnostic yield. J Nucl Med. 2000 Apr;41(4):720-7. PMID: 10768575.
EDV	LV chamber volume at end-diastole	
ESV	LV chamber volume at end-systole	
SV	LV stroke volume	
EF	LV ejection fraction	
Perfusion analysis		