Simplicit^{90}Y 2.4.0 Help Guide

MIRADA
The Imaging Software People

Simplicit^{90}Y 2.4.0 Help Guide

Mirada Medical's Simplicit^{90}Y 2.4.0 is a software application designed for accelerating dosimetry planning and improving ^{90}Y workflows.

Topics in this Help Guide:

Notices

Summary: Find here important notices about the use of Simplicit^{90}Y.

Within this section you can find information about the product that is of importance for safety or regulatory reasons.

Revision history

Issue	Date	Reason for release	Revision	Necessary for safety reasons
Help Guide	30th October 2020	First release	R0	N/A
Help Guide	18th January 2021	Added Authorized European Representative	R1	No

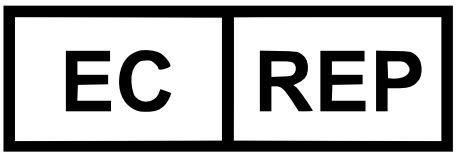
Note on SUV calculations

When using SUV calculation during PET assessment certain assumptions are made with regard to the reference time for the acquisition of the data series. Variability in interpretation of requirements outlined in the DICOM Standard with regard to determination of the start reference time during acquisition and the time of tracer injection may result in variability in the SUV values calculated by different vendors.

It is important to note that due to inconsistency of approach throughout the industry, the acquisition time used in SUV calculation may be any of the acquisition times presented in the DICOM data. It is equally important to note that SUV is affected by a number of physiological factors which cause variability. Taking these two factors into account, SUV can be thought of as a simplified measure of radiopharmaceutical uptake which has a complementary rather than directive role in the assessment, treatment and staging of disease.

CE

In compliance with Council Directive 93/42/EEC.



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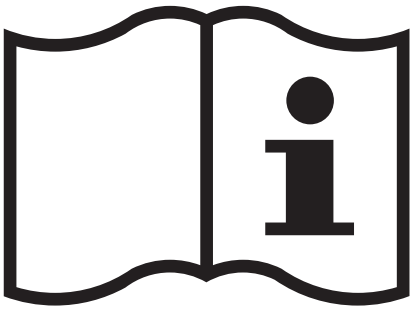


https://mirada-medical.com/eifu-Simplicit90Y-2-4-0-row/

Alternative formats

An online version of the Simplicit^{90}Y 2.4.0 instructions for use (including this help guide) is available at https://mirada-medical.com/eifu-Simplicit90Y-2-4-0-row/ and may contain updates that were made in the time since you were delivered your copy of Simplicit^{90}Y 2.4.0.

A physical copy of the Simplicit^{90}Y 2.4.0 instructions for use (including this help guide) is also available upon request from support@mirada-medical.com.

Topics in this section:

- Regulatory statement
  Important notices about the use of Simplicit^{90}Y 2.4.0.
- Warnings
  The warnings listed here relate to specific functions and modes of use for the software. These are also listed in applicable topics elsewhere in the user guide.
- Data supported
  Simplicit^{90}Y supports a range of data types.

Regulatory statement

Summary: Important notices about the use of Simplicit^{90}Y 2.4.0.

Intended use

Simplicit^{90}Y 2.4.0 is a standalone software device intended for use by Nuclear Medicine (NM) or Radiology practitioners. The intended use of the system is to provide digital processing, review and reporting of medical images, including data display, quality control, image manipulation and quantification analysis capabilities.

Software components provide functions for performing operations related to image display; manipulation, analysis and quantification and can operate on computer workstations.

Indications for use

Simplicit^{90}Y 2.4.0 can run on a dedicated workstation and is intended for use by Nuclear Medicine (NM) or Radiology practitioners for display, processing and reporting of NMI data, including planar scans (Static, Whole Body) and tomographic scans acquired by gamma cameras or PET scanners.

The NM or PET data can be coupled with registered anatomical scans from other modalities including fused CT scans, and with physiological signals in order to depict, localize, and/or quantify the distribution of radionuclide tracers and anatomical structures in scanned body tissue for clinical diagnostic purposes.

The system is intended to be used by physicians for viewing and assessing image data for general clinical diagnostic purposes with additional features and optimized workflow for Yttrium-90 (^{90}Y) dosimetry.

Contraindications for use

None known.

Cautions

The device presents medical image information, acquired from scanner systems, which can be used as part of a clinical diagnostic process (diagnosis, staging, treatment assessments and follow up of disease) and to provide dosimetry information to support ^{90}Y radioembolization treatment planning. The clinical diagnostic process uses many other sources of information to form the assessment of the condition of the patient, including blood tests, clinical examination, case history and genetic profiles. The information that medical imaging provides, as presented by Simplicit^{90}Y 2.4.0, is a complement to these standard methods. Simplicit^{90}Y 2.4.0 should not therefore be solely used to directly drive a clinical decision making process.

Data compression

Simplicit^{90}Y 2.4.0 does not apply any data compression techniques. Lossy compressed data can be loaded into Simplicit^{90}Y 2.4.0 at the discretion of users. It is important to understand that the use of lossy compressed data may result in lower quality images that can affect the accuracy of image display and quantification. Where lossy compressed data has been loaded into Simplicit^{90}Y 2.4.0, the data will be labeled as such in the application.

Computational performance

Unless explicitly agreed to by Mirada Medical, no responsibility is taken for the duration required to perform functions within the software environment. Specific performance requirements can only be agreed to if the product is delivered on Mirada Medical specified hardware.

Accuracy

The actions of the user may directly affect the accuracy of functions within the software environment. Therefore, it is the responsibility of the user to determine if the results of image visualization are satisfactory.

Reporting

While the device is a quality product, manufactured under a rigorous quality control program, it is not a secure repository for clinical reports. Any comments, images or annotations compiled into any form of report and provisionally stored by the software environment are at the user's risk. No responsibility is taken by Mirada Medical for damaged reports, incomplete record manipulation, storage/retrieval problems or network-based security issues unless specifically agreed.

Security

The software tool may, by virtue of its usage, contain confidential patient information. The security and configuration of the computing hardware used to execute the software is the responsibility of the end-user. This includes secure imaging local area networks (LANs), appropriate firewall provision, network directory permissions, etc.

Cyber security

Simplicit^{90}Y is designed to use data sent to it in DICOM format only from sources within a hospital network as configured by users. Simplicit^{90}Y does not include any firewall or anti-virus protection and is not specifically designed to protect against malicious attack. Users are strongly advised to ensure that appropriate measures are in place in the infrastructure around Simplicit^{90}Y to protect against malicious attack as well as to comply with data protection regulations. Such measures may include, but are not limited to, secure local area networks (LANs), appropriate firewall provision, network directory permissions and anti-virus protection.

User credentials

Simplicit^{90}Y uses Windows credentials for some functions. System administrators should ensure that Simplicit^{90}Y is secured for use by clinicians only, and users should not share their account details.

Coexistence with other software

While there are currently no known safety issues or performance limitations with regard to Simplicit^{90}Y coexisting on the same workstation as other software applications, it is recommended that Simplicit^{90}Y is not used on a workstation with other software applications installed.

Printing

Mirada Medical takes no responsibility for the faithfulness or quality of a generated hard-copy result of a printing device not supplied by Mirada Medical and/or installed/configured by Mirada Medical.

User installation/operation

User-performed installation and configuration of the software is entirely at the user's risk unless otherwise agreed by Mirada Medical (on the basis of an extended EULA/service contract). This includes any disruption to existing installations, software (or software licenses) or data loss.

Diagnostic and therapeutic restrictions

Use of the software as a primary viewing or diagnostic device

The software is designed as an aid to diagnosis, enabling information to be used as an input into a diagnostic process. Other methods and procedures should be in place to enable a diagnosis to be reached without the aid of this software. The software should not be used as the sole basis for forming a diagnosis, to do so would constitute a misuse of the software.

Warnings

Summary: The warnings listed here relate to specific functions and modes of use for the software. These are also listed in applicable topics elsewhere in the user guide.

Warning: Unsupported modalities, data or image types may cause the software to function incorrectly, to return invalid results or to reject the data if an attempt is made to load them into the software. Attempt to load invalid data along with valid data may cause both sets of data to be rejected by the software.

Warning: If data has been compressed prior to use in the application and the data contains the appropriate compression information – this will be displayed on screen.

Warning: Care should be taken to ensure that data selected is for the intended patient.

Warning: You should ensure that a correct lung shunt fraction value is specified or that the lung shunt calculated is reasonable.

Warning: When using the Lung Shunt Fraction workflow step, you should review any manually entered values.

Warning: When calculating the lung shunt fraction from regions, ensure that the regions are labelled correctly.

Warning: The degree of mis-registration between datasets can affect the performance of registration. The Registration QC step should be used to check for registration quality issues resulting from such data. It is the user's responsibility to ensure that the registrations used by the application are of sufficient quality and, if not, to correct the registration.

Warning: If VOIs are drawn wholly outside, or partially outside the bounds of a whole liver segmentation, quantification results might include unintended tissue. A warning will be presented where created VOIs assigned to a dosimetric type, in whole or part, fall outside a whole liver segmentation.

Warning: If viable tumor VOIs are drawn partially outside the bounds of a tumor segmentation, quantification results might include unintended tissue. A warning will be presented where created VOIs labelled as viable tumor, extend partially outside a tumor VOI (though not when drawn independently of a tumor VOI).

Warning: If multiple drawn VOIs overlap, the subsequent summed ratio might be calculated at more than 100%. The system will present a warning when overlapping VOIs are created.

Warning: When specifying your quantification method, care should be taken to ensure that the intended unit of quantification is selected. The quantification method applied is displayed as active text within the image pane.

Warning: If changes are made in previous workflow steps, the results of dosimetry calculations will update. However, the specified levels of activity and absorbed dose for perfused volumes will not be altered. You must check that the specified level of activity and absorbed dose are appropriate and correct them if necessary.

Warning: Care should be taken to not confuse VOIs/ROIs and Isodose lines. The system enables you to toggle VOIs and ROIs to hide and show them to enable viewing of Isodose lines in isolation or alongside VOIs and ROIs.

Warning: The dose-volume histogram produced by the application is not a reliable source for quantitative evaluation and should only be used as a qualitative measure.

Warning: When using PET, SPECT or NM images, the partial volume effect can result in a lower apparent activity concentration (or number of counts) than should be present in the image, due to limited resolution of the image relative to the size of a region. To reduce the impact of the partial volume effect, dosimetry assessment should be performed in regions at least two to three times greater than the spatial resolution of the imaging system used to acquire the images. If performing voxel-wise quantification, particularly for small structures, you should be conscious of this potential source of error. For more information on this topic, see the Imaging Protocols topic available from the sidebar.

Warning: When using planar NM images, verify the orientation and, if using a geometric mean, that the application is correctly identifying the image orientation.

Warning: Simplicit^{90}Y 2.4.0 does not apply any data compression techniques. Lossy compressed data can be loaded into Simplicit^{90}Y 2.4.0 at the discretion of users. It is important to understand that the use of lossy compressed data may result in lower quality images that can affect the accuracy of image display and quantification. Where lossy compressed data has been loaded into Simplicit^{90}Y 2.4.0, the data will be labelled as such in the application.

Warning: If using data that is not labelled using the DICOM tag for ^{90}Y, you should verify that the data is indeed correct.

Warning: If using planar NM data to calculate a geometric mean and the data is from different image series, ensure that the two orientations can be appropriately used together.

Warning: When using the summation mode, you should ensure the specified dose and activity is appropriate for all perfused volumes.

Warning: When performing dosimetry, ensure that the correct image is assigned to the anchor role, as this will be used to calculate volumes.

Data supported

Summary: Simplicit^{90}Y supports a range of data types.

Supported image modalities

The following data types are supported:

- CT
- MR
- NM
- SPECT
- PET

Supported image types

The following image types are supported:

- Multiphase CT
- Cone beam CT
- Multiphase MR
- Planar NM
- ^{99m}Tc-MAA SPECT/CT
- FDG PET/CT
- ^{90}Y PET/CT (post-treatment only)
- ^{90}Y SPECT/CT (post-treatment only)

> ⚠ **Warning:** If using data that is not labelled using the DICOM tag for ^{90}Y, you should verify that the data is indeed correct.

> ⚠ **Warning:** When using PET, SPECT or NM images, the partial volume effect can result in a lower apparent activity concentration (or number of counts) than should be present in the image, due to limited resolution of the image relative to the size of a region. To reduce the impact of the partial volume effect, dosimetry assessment should be performed in regions at least two to three times greater than the spatial resolution of the imaging system used to acquire the images. If performing voxel-wise quantification, particularly for small structures, you should be conscious of this potential source of error. For more information on this topic, see the Imaging Protocols topic available from the sidebar.

Supported data types

The following data types are supported:

- Implicit Little Endian
- Explicit Little Endian

> ⚠ **Warning:** If data has been compressed prior to use in the application and the data contains the appropriate compression information – this will be displayed on screen.

> ⚠ **Warning:** Unsupported modalities, data or image types may cause the software to function incorrectly, to return invalid results or to reject the data if an attempt is made to load them into the software. Attempt to load invalid data along with valid data may cause both sets of data to be rejected by the software.

Supported data objects

The following DICOM objects are supported:

- Secondary capture
- RTSS
- Simplicit^{90}Y saved sessions

Launching and overview

Summary: This section describes how to launch the application and general usage of tools within the application.

About

When launching Simplicit^{90}Y, you select the data you want to load and then which data roles you want to assign it to. For information about how to load data, see Launching the application and assigning data.

The first workflow step in Simplicit^{90}Y is the *Overview* step. In this step, you can review the data you have loaded with standard image tools that are available throughout the application. For information about how to use these tools, see Manipulating images.

Topics in this section:

Launching the application and assigning data

Summary: Load data into Simplicit^{90}Y and assign images to appropriate roles.

About

Simplicit^{90}Y is launched from DBx, where initial data selection takes place. You can then assign data to roles that determine how they will be displayed and what they are used for in the main workflow of the application.

Procedure

To launch Simplicit^{90}Y, complete the following steps:

1. In DBx, select the data that you want to load into Simplicit^{90}Y and click the Simplicit^{90}Y icon.

   > ⚠ **Warning:** Care should be taken to ensure that data selected is for the intended patient.

2. The application will automatically assign data when enough information is available. Review these assignments and then, if necessary correct them:

   - Click and drag data into the correct data roles. Valid roles are highlighted with a green border.
   - Right-click data and select any of the valid roles to which it can be assigned.
   - Click **Clear** at the bottom of the window to un-assign all data.
   - Click **Auto-populate** at the bottom of the window to return to the automatic data assignments.
   - To preview data, click the data to select it and then use the image tools in the right pane of the window. For more information about using image tools, see Manipulating images.

3. To confirm your assignments and launch the application, click **OK** in the bottom-right corner of the window.

Data roles

The following data roles are available:

- **Planning**
  This role must be filled. It can be filled with a CT or MR image volume.
- **CBCT**
  This role can be filled with a cone-beam CT. It is used to provide additional information and is not used for quantification.
- **Planar**
  This role can be filled with a planar NM image.
- **SPECT CT**
  This role can be filled with a CT image. It is expected to have the same frame of reference as the SPECT role.
- **SPECT**
  This role can be filled with a SPECT image. It is expected to have the same frame of reference as the SPECT CT role.

- **PET CT**
  This role can be filled with a CT image. It is expected to have the same frame of reference as the PET role.
- **PET**
  This role can be filled with a PET image. It is expected to have the same frame of reference as the PET CT role.

The most recent, appropriate image series will be automatically assigned to each role.

> **Note:** A **PET** or **SPECT** image is required for multi-compartment dosimetry while a **Planar** image is required for a lung shunt fraction derived from regions of interest.

> **Note:** Data roles other than **Planar** cannot be occupied by multiple image volumes that have different frames of reference.

Next steps

When you have loaded data into the application, review your images using the tools described in Manipulating images, or provide a lung shunt fraction, as described in Lung shunt fraction.

Configuring the language displayed by Simplicit^{90}Y

Summary: This section describes how to configure the language displayed by the application.

About

You can select from the following languages within Simplicit^{90}Y 2.4.0:

- English (United States)
- French (France)
- Italian (Italy)
- German (Germany)
- Spanish (Spain)
- Portuguese (Portugal)
- Dutch (Netherlands)

> **Note:** The decimal separator is determined by the language selected. All languages other than English will apply a decimal comma, as opposed to a decimal point, as the decimal separator.

Procedure

To select the language displayed by Simplicit^{90}Y 2.4.0, complete the following steps:

1. Click **Tools** and select *Options*. The *Options* window is displayed.
2. Click the **Language** tab.
3. Select your desired language using the drop-down menu displayed.
4. Restart Simplicit^{90}Y to apply these changes.

Manipulating images

Summary: Information about how to use image manipulation tools to effectively view your images.

About

Simplicit^{90}Y provides a range of tools for viewing your images. This topic covers the use of the following tools:

- Zoom
- Pan
- Scroll through slices
- Window and level settings

Procedure

To manipulate the manner in which your images are displayed, use the following methods:

- To select an image to view, click it in the image selector bar at the top of the window.

  If the image is three-dimensional, axial, coronal and sagittal views will be displayed. If the image is planar, the single slice is displayed.

- To zoom the image to your desired scale, use one of the following methods:
  - Hold the **Ctrl** key and use your scroll wheel to zoom in and out. Scroll up to zoom in and scroll down to zoom out.
  - Click the **Zoom into the image** icon and then click the image and drag in the vertical direction to zoom. Drag upwards to zoom out and drag downwards to zoom in.

- To locate the views in other image panes to a position in your current image pane, drag the crosshairs to where you want the views to intersect.

  > **Tip:** At any time, you can toggle between an image pane being maximized or part of a layout by double clicking the image pane. You can also toggle between the two settings by clicking the **Toggle whether the view is maximized** icon .

- To pan an image, use one of the following methods:
  - Click and drag with the middle mouse button.

- Click and drag while holding the **Ctrl** key.
- Click the **Pan image** icon and then drag the image with your cursor.

> **Tip:** To stop using a tool, press the **Esc** key.

- To scroll through slices of a plane, use one of the following methods:
  - Use your scroll wheel to scroll through slices. The direction in which you scroll depends upon the orientation of the image.
  - Click the **Navigate through the volume slices** icon and then click and drag the image in the vertical direction.

- To adjust the window and level settings, use one of the following methods:
  - Use the sliders in the toolbox to adjust the level, by dragging the horizontal bar, and the window, by dragging the end markers. The slider displays intensity in grayscale (or any specified colormap) and an intensity histogram in blue.

  - Click the **Adjust window and level** icon and then click the image and drag in the vertical direction to adjust the window and in the horizontal direction to adjust the level.
  - To reset the window and level settings, click the **Reset Window/Level** icon .
  - To choose a preset Window/Level setting, click the **Image** menu and then select **Visualization**. In the Visualization window, you can select and specify preset Window/Level settings and change your colormap.

- To reset the zoom and pan of an image in all image panes, click the **Reset zoom, pan and orientation of all views** icon .

> **Note:** All views will be reset even when viewing a single, maximized view.

Features of image panes

Summary: Every image pane contains important information about the data it is displaying.

About

Information useful for identifying an image and information about how the image is being viewed are displayed in all four corners of an image pane. Some of this information is active text and can be edited to change how the image is displayed.

The following table describes the information displayed:

Information	Location
Patient name	Top-left
Patient gender, patient age, and patient date of birth (Year-Month-Day)	Top-left
Institution name	Top-left
Image compression (only present if image is lossy compressed)	Top-left
Display scale (active text)	Top-right
Field of view	Top-right
Window and level (active text, per layer in fused views)	Top-right
Data role and pixel intensity at crosshairs (active text)	Bottom-left
Anatomical plan	Bottom-right
Slice index and Z-coordinate (active text)	Bottom-right
Acquisition date	Bottom-right
Series description and acquisition orientation	Bottom-right

Active text

Active text is information in an image pane that you can interact with. By clicking the active text, additional options are provided:

- **Scale**
  Change the zoom of the image using the slider, or click **Zoom to fit** to scale the window to show the full image with a minimum of empty space.
- **Window and Level**
  Choose a colormap for display and select pre-defined window and level settings. You can also create custom window and level settings and save them for later use.
- **Slice Index**
  Specify a slice to view.
- **Pixel Intensity at Crosshairs**
  Choose the units that you want to display intensity in.

Modifying anchor roles

Summary: Change which image volume is used as the anchor volume.

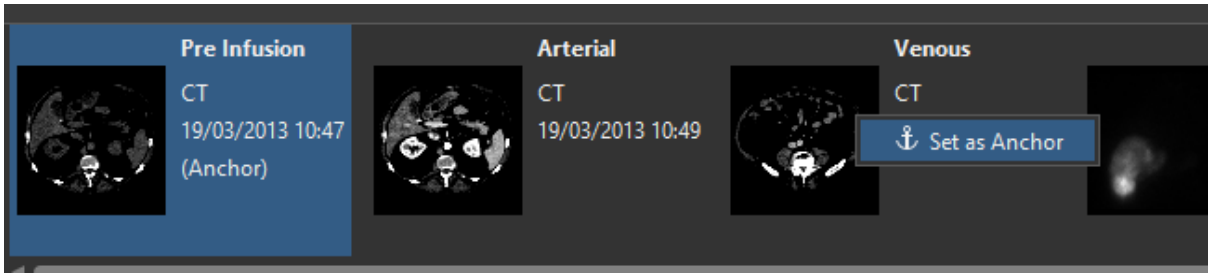
About

The anchor volume is the image volume to which other image volumes are registered. It is helpful to set your most useful or highest quality image volume as the anchor.

The anchor volume is also used for the calculation of statistics during the *Dosimetry* workflow step.

Procedure

To change the anchor volume, in the *Overview* or *Segmentation* workflow step, in the data browser at the top of the window, right-click the image volume that you want to set as the anchor volume and select **Set as anchor**.



You can only set image volumes from the **Planning** role to be the anchor volume. These can be CT or MR images. For more information about data roles, see Launching the application and assigning data.

You can also specify text that is used to identify the anchor volume from an image volume's series description. For more information, see User preferences.

Lung shunt fraction

Summary: Before calculating dosimetry statistics, provide a lung shunt fraction.

About

The lung shunt fraction represents the proportion of activity absorbed by the patient's lungs. It can be set manually or calculated from image data.

> ⚠ **Warning:** You should ensure that a correct lung shunt fraction value is specified or that the lung shunt calculated is reasonable. Guidance for upper limits on the received dose for lungs and shunted activity can be found in the TheraSphere® and TheraSphere® iDoc® labels.

> ⚠ **Warning:** You should ensure that a correct lung shunt fraction value is specified or that the lung shunt calculated is reasonable.

For information about calculating the lung shunt fraction from image data, see Calculating a lung shunt fraction from a planar image.

Procedure

To set a lung shunt fraction manually, complete the following steps:

1. In the **Workflow** section of the sidebar, click **Lung Shunt Fraction** or click **Workflow** and select *Lung Shunt Fraction*.
2. In the **Lung Shunt Fraction** section of the sidebar, select **Use value** if it is not already selected.
3. In the **Use value** field, enter the percentage of activity you have determined will be lost to the lungs.

> ⚠ **Warning:** When using the Lung Shunt Fraction workflow step, you should review any manually entered values.

Next steps

When you have defined a lung shunt fraction, you should ensure that registrations between your images are of adequate quality. For more information, see Registration QC.

Topics in this section:

- Calculating a lung shunt fraction from a planar image
  Draw regions from which Simplicit^{90}Y will calculate a lung shunt fraction.

Calculating a lung shunt fraction from a planar image

Summary: Draw regions from which Simplicit^{90}Y will calculate a lung shunt fraction.

About

In the *Lung Shunt Fraction* workflow step, draw structures on a planar image for the lung and liver and use these to calculate a value for the lung shunt fraction.

> ⚠ **Warning:** When calculating the lung shunt fraction from regions, ensure that the regions are labelled correctly.

The equation with which the lung shunt fraction is calculated can be found in Lung shunt fraction.

Procedure

To draw regions and calculate a lung shunt fraction from those regions, complete the following steps:

1. In the *Lung Shunt Fraction* workflow step, select the planar image you want to use from the data browser at the top of the window.
2. Use the **Image** tools in the toolbox to adjust the image to best display the activity in the lungs and liver. The **Window/Level** tool is particularly useful for this. For more information about viewing images, see Manipulating images.
3. Use any of the segmentation tools, found in the **Segmentation Tools** section of the toolbox, to draw structures:

    a. In the **Structures** section of the toolbox, select the structure that you want to draw. To calculate a lung shunt fraction, you need both **Liver** and **Lungs** structures, while **Background** is only necessary if you want to apply background correction.

    b. Click and use any of the segmentation tools:

    - **Ellipse Region** and **Rectangle Region**

      Click and drag to create an ellipse or rectangle region. Once placed, you can adjust the size of the region by clicking it and then dragging the anchor points.

    - **Freehand tool to draw regions**

      Click and drag to draw the outline of a region. When you release, the region will connect the start and end points with a straight line.

    - **Click points to draw a polygon region**

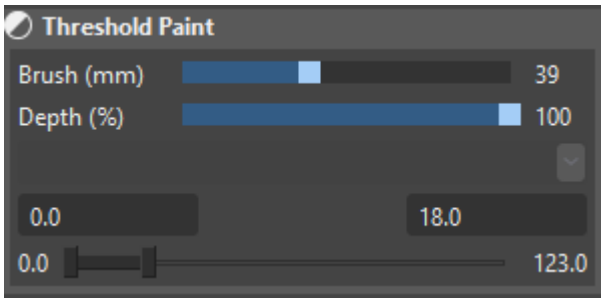
      Click to place points and create a polygonal region. Double-click the last point to close the region with a straight line to the first point.

    - **Paint brush tool for manual editing of regions** and **Erase tool for manual editing of regions**

      Click and drag to paint a region or erase it, respectively. Hold the **Shift** key and use the scroll wheel to adjust the size of the paintbrush or eraser.

    - **Paint brush tool for manual editing of regions by threshold** and **Erase tool for manual editing of regions by threshold**

Click and drag to paint a region or erase it, respectively. The change is only applied to voxels that fall within a specified range of intensity. To specify the range, use the slider at the bottom of the **Threshold Paint** section of the toolbox, or specify values in the associated fields. Hold the **Shift** key and use the scroll wheel to adjust the size of the paintbrush or eraser.



- **Nudge tool to paint or erase depending on brush position** and **Nudge tool to paint or erase based on a threshold**

> **Note:** By default, the **Liver**, **Lungs** and **Background** structures are provided, empty. If you delete one of these and need to add a new one, click the **Create a new structure that is initially empty** tool in the **Segmentation Tools** section of the toolbox and then provide a name and type for the region.

4. In the **Lung Shunt Fraction** section of the toolbox, click the **Use regions** radio button. The Select ROIs window is displayed.
5. If you have drawn a background region, click **Background correction**.
6. If you have dual-headed data loaded and want to use a geometric mean, click **Geometric mean**. If the link between the dual-headed data is not clear to the application, this option is disabled. To provide information about the orientation of the data, see Modifying the orientation of planar images.
7. Click **OK**.

More on this topic:

- Modifying the orientation of planar images
  If the orientation information of loaded planar images is insufficient or incorrect, you can correct it.

Modifying the orientation of planar images

Summary: If the orientation information of loaded planar images is insufficient or incorrect, you can correct it.

About

When calculating a lung shunt fraction using the application, you can apply a geometric mean. If the orientation of images used to calculate the geometric mean is incorrect, you can correct it. If the information is not sufficient for the application to identify linked data, you can provide it.

> ⚠ **Warning:** If using planar NM data to calculate a geometric mean and the data is from different image series, ensure that the two orientations can be appropriately used together.

Procedure

To correct or supply planar orientation, complete the following steps:

1. Click **Modify Planar Orientation** in the Select ROIs window. If you need to open this window, click the **Select value** icon in the **Lung Shunt Fraction** section of the toolbox.
2. In the Modify Planar Orientation window, use the drop-down menus in the right column to specify the orientation of images shown in the left column. You must set Anterior and Posterior orientations for a single image each.

> **Tip:** To check you have the correct image, use the image pane and associated image manipulation tools.

> ⚠ **Warning:** When using planar NM images, verify the orientation and, if using a geometric mean, that the application is correctly identifying the image orientation.

Registration QC

Summary: Ensure that the registrations between your images are of sufficient quality.

About

The *Registration QC* workflow step provides tools for verifying the quality of registrations between images that you have loaded into Simplicit^{90}Y and for correcting registrations when they are inadequate.

Simplicit^{90}Y supports manual, semi-automatic and automatic registration. By default, automatic rigid registrations are applied when image volumes do not share a frame of reference.

> **Note:** Planar images are never registered to other images and registration tools are disabled when viewing them.

> ⚠ **Warning:** The degree of mis-registration between datasets can affect the performance of registration. The Registration QC step should be used to check for registration quality issues resulting from such data. It is the user's responsibility to ensure that the registrations used by the application are of sufficient quality and, if not, to correct the registration.

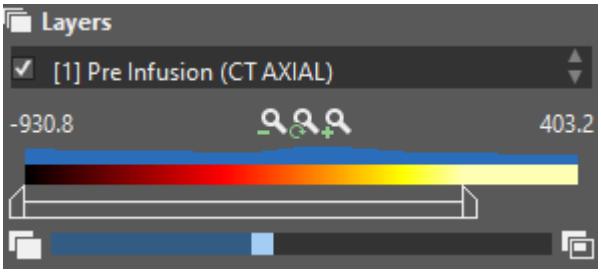
Viewing registrations

To view registrations and assess their quality, complete the following steps:

1. When you first open the *Registration QC* workflow step, the relationships between data roles are shown in the **Registration Overview**. To display the relationships between images within data roles as well, click **Dosimetry**. To return to viewing only the relationships between data roles, click **Back**.
2. To view the registration between two image volumes, click the line linking the two image volumes in the **Registration Overview**. Alternatively, right-click one of the image volumes in the **Registration Overview** and select the registration that you want to view.

   > **Note:** Green lines indicate that a deformable registration has been applied. Red lines indicate all other registration types.

3. Fused views of the two image volumes are displayed, showing axial, coronal and sagittal views. The anchor image will be displayed in grayscale by default, and the other image volume will be displayed in a yellow-to-red colormap by default. To alter the transparency of the overlaid image, use the **Transparency** slider in the **Layers** section of the toolbox.



> **Tip:** You can change the colormap of a layer by clicking the Window/Level active text. For more information, see Features of image panes

4. To pan the images, click and drag with the middle mouse button.

Performing an automatic registration

To perform automatic registrations, complete the following steps:

1. Select the registration you want to modify, as described in the previous section.
2. If the registration is locked, due to the images sharing a frame of reference, right-click one of the images and unlock the appropriate registration.
3. If you want to perform a local registration, where the algorithm considers only a section of the image, select the region that you want to base the registration on, from the list of structures in the **Local Registration** section of the toolbox. Then click the **Enable local registration** icon  .
4. Use the **Automatic Registration** tools:
    - Use **Reset Registration** to revert the registration to an identity transformation.
    - Use **Automatic Rigid** to run a rigid registration that applies the same translation, rotation and scaling to the whole of the image volume. Use the additional options button to set the speed and granularity of the registration.
    - Use **Multi-Modal Deformable** to run a deformable registration that is optimized to work well with differing modalities. Translation, rotation and scaling is not uniform across the image volume. Use the additional options button to select an algorithm optimized to different modality combinations.
    - Use **CT Deformable** to run a deformable registration that is optimized to work well between two CT scans. Translation, rotation and scaling is not uniform across the image volume. Use the additional options button to set the speed and granularity of the registration.
    - Use **Smooth Deformation** to reduce sharp changes in registration between different parts of the image volume. This is only useful for a deformable registration.

Performing a manual registration

To perform manual registration and semi-automated registration, complete the following steps:

1. Select the registration you want to modify, as described in the previous section.
2. If the registration is locked, due to the images sharing a frame of reference, right-click one of the images and unlock the appropriate registration.
3. Use the **Manual Registration** tools:
    - Use the **Fused** and **Landmarks** buttons to toggle between fused views and rows of fused and single views.
    - Click **Manual Rigid** to enable a tool to translate and rotate the top layer of the fused view relative to the base layer. Click and drag to translate or click and drag the displayed circle to rotate.
    - If using the **Landmarks** option, use **Place Landmarks** to place landmarks on the top layer of the fused view and on the base layer in the single views. These landmarks should indicate the same anatomical

location in each image. Place several landmarks for an effective registration.

- To perform a registration that minimizes the differences between corresponding markers, click **Landmark Rigid**.
- To delete a marker that you have already placed, select it from the **Marker** list and click **Delete**.
- To center the views on the marker, click **Go To Source** or **Go To Target**.
- To prevent rotation, select **Translation only**.

Using loaded registrations

If you have loaded a DICOM registration into Simplicit^{90}Y, you can apply this registration by selecting it in the **Loaded Registrations** section of the toolbox.

Next steps

When you have confirmed that your registrations are adequate, you can begin segmenting your images. For more information, see Segmentation.

Segmentation

Summary: Create structures to identify anatomy relevant to treatment.

About

In the *Segmentation* workflow step, create the **Whole Liver** and **Perfused Volume** structures.

If you are a performing multi-compartment dosimetry, you can also create structures for the **Tumor**, **Viable Tumor** and **Normal Tissue** types.

Procedure

To create your essential structures, complete the following steps:

1. Create a **Whole Liver** structure. To generate an initial structure, it can be convenient to use the **Segment liver on selected series** or **Segment on selected series** tools  in the **Segmentation Tools** section of the toolbox. How this tool is used depends on your image modality:

   - For a CT image, clicking the tool will create a **Whole Liver** structure and assign it the correct structure type. This tool is most effective using a contrast-enhanced CT.
   - For an MR image, clicking the tool runs an initialization algorithm. When the initialization is complete, click and drag from the center of the liver to grow a region that roughly describes the liver. You can add to the region by clicking and dragging multiple times, or remove the last addition by pressing **Ctrl** + **Z**. When satisfied with the initial structure, click **Auto segmentation** in the **MR Segmentation Tool** section of the toolbox. A second algorithm runs to refine the structure.

     Tip: When growing your initial region with the **MR Segmentation Tool**, be careful not to capture any nearby structures, such as the kidneys. It is better to capture less of the liver than to capture another structure.

   - For a CBCT image, clicking the tool runs an initialization algorithm. When the initialization is complete, click and drag to draw rough estimates of contours on individual slices in the axial view, which are then used to run an adaptive algorithm to snap the contours to structure boundaries in the image. Draw the contours on several slices, ensuring you include the top and bottom slices of the structure. When satisfied, click **Auto segmentation** in the **CBCT Segmentation Tool** section of the toolbox. Another algorithm runs to linearly interpolate between the slices you have drawn.

     Tip: You might want to use a different image volume for your segmentation. You can select these from the top of the application window.

   It is possible that the automatically segmented structure will need some correction. The **Nudge** tool  can be useful for this. To use the **Nudge** tool, click and drag from within the structure to push the boundary outwards, or from outside the structure to push the boundary inwards. To adjust the diameter of the tool, hold the **Shift** key and use the scroll wheel. To adjust the depth, use the slider in the **Region Editing Tools** section of the toolbox to specify the depth of the tool proportional to its diameter.

> **Note:** When using the **Nudge** tool, multiple slices are affected. You should check other slices for unintended changes before continuing.

A complete list of tools can be found in: Segmentation tools.

If you do not want to use the automatic segmentation, or if it fails to run correctly, you will need to draw the liver manually. Before you start using any tools, select the **Whole liver** structure in the **Structures** section of the toolbox.

2. Create the **Perfused Volume** structure. To divide the **Whole Liver** structure, it can be convenient to use the **Split a region along a line** tool  . Click in two places to create a line between the two points and bisect your **Whole Liver** structure. Click a third time to create a region on the side that you clicked, or regions on both sides if you clicked close to the bisecting line. The created region or regions will have the correct structure type.

> **Tip:** Before clicking the third time to confirm the structure or structures, you can draw additional lines on other slices of the image volume. When the region is split, the lines are interpolated linearly to form the splitting plane.

If you do not want to use the split tool, you will need to draw the perfused volume manually. You can also use the **Perform a Boolean action between two structures** tool  to perform a Union, Minus or Intersection operation to ensure that the **Perfused Volume** structure is contained entirely within the **Whole Liver** structure.

> **Note:** You must have a structure with the **Perfused Volume** type assigned to it. If you need to assign this manually, double-click the structure in the **Structures** section of the toolbox and then select **Perfused Volume** from the **Type** drop-down menu.

3. If performing multi-compartment dosimetry, use the various segmentation tools described in Segmentation tools to create additional structures and assign these the appropriate type.

> ⚠ **Warning:** If VOIs are drawn wholly outside, or partially outside the bounds of a whole liver segmentation, quantification results might include unintended tissue. A warning will be presented where created VOIs assigned to a dosimetric type, in whole or part, fall outside a whole liver segmentation.

> ⚠ **Warning:** If viable tumor VOIs are drawn partially outside the bounds of a tumor segmentation, quantification results might include unintended tissue. A warning will be presented where created VOIs labelled as viable tumor, extend partially outside a tumor VOI (though not when drawn independently of a tumor VOI).

> ⚠ **Warning:** If multiple drawn VOIs overlap, the subsequent summed ratio might be calculated at more than 100%. The system will present a warning when overlapping VOIs are created.

Next steps

When you have created the structures that you need, you can proceed to the *Dosimetry* step. For more information, see Dosimetry.

Topics in this section:

- Segmentation tools
  A list of segmentation tools available in Simplicit^{90}Y.
- Exporting an RTSS
  Export a radiotherapy structure set (RTSS).

Segmentation tools

Summary: A list of segmentation tools available in Simplicit^{90}Y.

About

When creating structures to use for dosimetry calculations, local registrations, or calculating a lung shunt fraction, you can use the tools listed in this topic.

> **Tip:** You can choose which tools are displayed by the application by right-clicking in the **Segmentation Tools** section of the toolbox and selecting **Configure Tools**. Use the check boxes to hide or show the tools.

Tools

Tool	Icon	Usage
Fill internal holes that are not connected to the outside in 2D		With a structure selected, click to fill any holes in in 2D on the current slice. **Note:** You can select whether to fill holes in 2D on the current slice, or all slices of a region, if you are operating within the Segmentation section of the sidebar. You can fill holes in 2D on the current slice only if you are operating within the Lung Shunt Fraction section of the sidebar
Create a new structure that is initially empty		Click to create an empty structure and specify its type, name and color.
Ellipse Region		Click and drag to create an ellipsoid region in 2D.
Rectangle Region		Click and drag to create an rectangular region in 2D.
Freehand tool to draw regions		Click and drag to draw the outline of a region in 2D.
Click points to draw a polygon region		Click to create points and draw a polygon region in 2D.

Tool	Icon	Usage
Filled Region		Click and drag to create a 3D cuboid region. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Region with Absolute Threshold		Click and drag to create a cuboid area from which a region is created, using voxels whose intensity falls within a range of absolute values. By selecting the region, you can adjust the upper and lower thresholds in the **Threshold Settings** section of the toolbox. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Region with % of Max Threshold		Click and drag to create a cuboid area from which a region is created, using voxels whose intensity falls within a range of absolute values. By selecting the region, you can adjust the upper and lower thresholds in the **Threshold Settings** section of the toolbox. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Paint brush tool for manual editing of regions		Click and drag to create or add to a region. Hold the **Shift** key and use your scrollwheel to adjust the diameter of the brush or use the **Region Editing Tools** section of the toolbox to adjust the depth of the brush relative to its diameter.

Tool	Icon	Usage
Paint brush tool for manual editing of regions by threshold		Use the **Threshold Paint** section of the toolbox to specify the upper and lower thresholds used by the tool. Click and drag to create or add to a region according to whether voxels fall within the specified range. Hold the **Shift** key and use your scrollwheel to adjust the diameter of the brush and use the **Region Editing Tools** section of the toolbox to adjust the depth of the brush relative to its diameter.
Nudge tool to paint or erase depending on cursor position		Click and drag from inside a selected structure to add to it, or from outside a selected structure to remove from it. If no structure is selected or if the structure is empty, clicking and dragging will create the structure. Hold the **Shift** key and use your scrollwheel to adjust the diameter of the tool and use the **Region Editing Tools** section of the toolbox to adjust the depth of the tool relative to its diameter.
Nudge tool to paint or erase using a threshold		Use the **Threshold Paint** section of the toolbox to specify the upper and lower thresholds used by the tool. Click and drag from inside a selected structure to add to it voxels falling within a threshold, or from outside a selected structure to remove from it voxels falling outside of the threshold. If no structure is selected or if the structure is empty, clicking and dragging will create the structure. Hold the **Shift** key and use your scrollwheel to adjust the diameter of the tool and use the **Region Editing Tools** section of the toolbox to adjust the depth of the tool relative to its diameter.
Eraser tool for manual editing of regions		Click and drag to erase from a structure.

Tool	Icon	Usage
Eraser tool for manual editing of regions by threshold		Use the **Threshold Paint** section of the toolbox to specify the upper and lower thresholds used by the tool. Click and drag to erase from a structure any voxels that fall outside of the specified threshold.
Painting tool to adaptively segment regions		Click and draw a rough outline containing the area you want to segment. On the slice it was drawn, the outline of the region is segmented using information in the image. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Delete contours from the selected structure		With a structure selected, click a region to delete the contiguous area in that slice from the structure without deleting any separated regions. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Copies the content of the selected structure from the closest slice onto the current slice		With a structure selected, click to replace the contents of the current slice with a copy of the nearest slice with part of the current structure drawn on it. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.

Tool	Icon	Usage
Split a region along a line		With a structure selected, click in two points to form a line bisecting the region. Click a third time to create either a region on the side that you click, or two regions on either side if you click near to the line. Alternatively, before clicking the third time, create additional bisecting lines in other slices to create a curved plane along which to perform the split. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Generate a margin for a structure		With a structure selected, click to open a window for generating margins. Select the structure to which you want to apply margins and select the structure that you want to save the margins as. If you want to save as a new structure, click **Generate New Structure**. Use the numeric fields to specify margins to apply in each anatomical direction. If you want to apply different margins for different directions, deselect **Link all**. Use the individual **Link/Unlink the values** icons to specify whether opposite directions should be linked. Use the **Margin Type** drop-down menu to specify the type of structure to create. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.

Tool	Icon	Usage
Interpolate missing slices using linear interpolation		With a structure selected, click to fill all slices between the first and last, using linear interpolation between any available slices. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Fill internal holes that are not connected to the outside in 3D		With a structure selected, click to fill any holes in the 3D structure. Specify whether to fill all holes or holes smaller than a given volume. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Remove free-floating disconnected portions		With a structure selected, click to remove disconnected structures in 3D. Specify whether to remove all but the largest region or regions smaller than a given volume. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.

Tool	Icon	Usage
Smooth a structure by blurring the outline		With a structure selected, click to smooth the outline of the structure. Specify the intensity of the smoothing (the value specified is the standard deviation used to create a Gaussian filter). **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Perform a Boolean operation between two structures		Click to open the Boolean Operation window. Select the first structure, the type of Boolean operation, the second structure, and the output structure. If you want to use a new structure for the output, click **Create Empty Structure**. If using an existing structure, the contents of that structure will be overwritten.
Segment liver on selected series (CT only)		Click to run an automatic liver segmentation. This will take some time to run. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Segment on selected series (MR only)		Click to initialize. Click and drag multiple times from the center of the liver to create an initial region. Click **Auto segmentation** to make automated improvements to the segmentation. **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.

Tool	Icon	Usage
Segment on selected series (CBCT only)		Click to initialize. Click and drag to draw rough contours on individual slices that are then adaptively segmented according to image data. Draw contours on several slices, ensuring the top and bottom slices are contoured. Click **Auto segmentation** to run adaptive interpolation **Note:** This tool is not available if you are operating within the Lung Shunt Fraction section of the sidebar.
Draw Temporary Rulers		Click and drag, but do not release, to create a 1D ruler. When you release the cursor, the ruler will disappear.

Note: When using the Nudge, Paint and Erase tools (and their threshold variants), multiple slices are affected. You should check other slices for unintended changes before continuing.

Exporting an RTSS

Summary: Export a radiotherapy structure set (RTSS).

Prerequisites

To complete this task, you must have created at least one structure or region. For more information on this topic, see Segmentation.

About

Having created a structure or a region on an image, you can export a radiotherapy structure set for use outside of Simplicit^{90}Y in a treatment planning system (TPS).

Procedure

To export an RTSS, complete the following steps:

1. Click **File**, hover your mouse over **Export** and select *Export RTSS*. The *Export* window is displayed.
2. Use the **Export structures for** drop-down menu to select the datasets from which you want to export an RTSS.
3. From the **Regions to export** list, select the regions that you would like to export.
4. Within the **Structure Set Label** field, enter a label for the RTSS to be associated with the DICOM tag (3006,0002).
5. (Optional) Within the **Series Description** text field, enter a description to be associated with the DICOM tag (0008,103E).
6. (Optional) Within the **Structure Set Name** field, enter a name for the RTSS to be associated with the DICOM tag (3006,0004).
7. (Optional) Within the **Operator name** field, enter a name for the operator to be associated with the DICOM tag (0008,1070).
8. Click **Next**.
9. Use the **Associate with** drop-down menu to select the data series with which you would like to associate your exported RTSS.
10. Click **Export**.

Dosimetry

Summary: In the Dosimetry workflow step, calculate the activity and dose that will be received by different regions.

About

If you are performing standard compartment dosimetry, with a structure for only the perfused volumes and whole liver, see Performing standard dosimetry.

If you are performing multi-compartment dosimetry, with additional structures as well as the perfused volumes and whole liver, see Performing multi-compartment dosimetry.

Next steps

When you have completed your dosimetry, generate a report. For more information, see Report.

Topics in this section:

- Performing standard dosimetry
  Perform dosimetry, considering only whole liver and perfused volume structures.
- Performing multi-compartment dosimetry
  Perform dosimetry with structures for the whole liver, perfused volume, and various tumor volumes.

Performing standard dosimetry

Summary: Perform dosimetry, considering only whole liver and perfused volume structures.

About

When performing dosimetry, you will select one or more perfused volumes to consider and set a dose to be received, using various statistics to choose the appropriate dose.

> ⚠ **Warning:** If changes are made in previous workflow steps, the results of dosimetry calculations will update. However, the specified levels of activity and absorbed dose for perfused volumes will not be altered. You must check that the specified level of activity and absorbed dose are appropriate and correct them if necessary.

> ⚠ **Warning:** When performing dosimetry, ensure that the correct image is assigned to the anchor role, as this will be used to calculate volumes.

For details about how different statistics are calculated or relate to each other, see Statistics and properties.

Procedure

To perform standard dosimetry, complete the following steps:

1. If it is not already selected, click **Standard Dosimetry** in the **Dosimetry type** section of the toolbox.
2. In the upper-right corner of the application window, review the **Whole liver volume** and **Lung Shunt Fraction**. If these are incorrect, return to previous workflow steps to correct them.
3. Provide a **Residual Fraction** value.

   > ⚠ **Warning:** When specifying a residual fraction, you should ensure that the values are calculated in accordance with the guidance provided in the TheraSphere® help guide.

4. If any volume overlaps or inconsistencies are detected by the application, a warning is displayed in the right column of the application window. Click the **Additional information** icon for details and to choose whether to fix or accept the issue.

   > **Tip:** If you choose to fix the issue, the **Perform a Boolean operation between two structures** tool can be useful to perform intersections and ensure that there is complete overlap or no overlap, as appropriate.

5. In the right column of the application window, use the check boxes for each perfused volume to specify whether the region was or is to be perfused with microspheres. If you want to perfuse multiple volumes, select **Summation mode**.

   > ⚠ **Warning:** When using the summation mode, you should ensure the specified dose and activity is appropriate for all perfused volumes.

6. You can use any of the three following methods to specify an activity or dose:

   - Use the slider to adjust the activity.
   - Use the **Activity, GBq** field to specify an activity directly.
   - Use the **Perfused tissue absorbed dose, Gy** field to specify a dose directly.

   > ⚠ **Warning:** When specifying the activity and absorbed dose that you want to achieve, you should ensure that the values are in accordance with the guidance provided in the TheraSphere® label.

   There is a maximum activity of 15 GBq, which is also enforced upon the perfused tissue absorbed dose value.

   As you set or adjust the activity and dose, the statistics in the **Totals** section are updated. Ensure that the values of these statistics are appropriate for treatment.

Next steps

When you have completed your dosimetry, generate a report. For more information, see Report.

> **Tip:** To save a session and so that you can return to it later, click **File** and select **Save session**. Provide a series description and specify which DICOM series the session is associated with.

Performing multi-compartment dosimetry

Summary: Perform dosimetry with structures for the whole liver, perfused volume, and various tumor volumes.

About

When performing dosimetry, you will select one or more perfused volumes to consider and set a dose to be received, using various statistics to choose the appropriate dose.

> **Warning:** If changes are made in previous workflow steps, the results of dosimetry calculations will update. However, the specified levels of activity and absorbed dose for perfused volumes will not be altered. You must check that the specified level of activity and absorbed dose are appropriate and correct them if necessary.

> **Warning:** When performing dosimetry, ensure that the correct image is assigned to the anchor role, as this will be used to calculate volumes.

For details about how different statistics are calculated or relate to each other, see Statistics and properties.

Procedure

To perform multi-compartment dosimetry, complete the following steps:

1. Click **Multi-compartment Dosimetry** in the **Dosimetry type** section of the toolbox.
2. Use the data selector at the top of the window to select the dosimetry volume that you want to use as a record of ^{90}Y activity or as a prediction of how the activity will be distributed.
3. Click **Confirm** in the right column of the application window.
4. In the upper-right corner of the application window, check the **Whole liver volume** and **Lung Shunt Fraction**. If these are incorrect, return to previous workflow steps to correct them.
5. Provide a **Residual Fraction** value.

   > **Warning:** When specifying a residual fraction, you should ensure that the values are calculated in accordance with the guidance provided in the TheraSphere® help guide.

6. If any volume overlaps or inconsistencies are detected by the application, a warning is displayed in the right column of the application window. Click the **Additional information** icon for details and to choose whether to fix or accept the issue.

   > **Tip:** If you choose to fix the issue, the **Perform a Boolean operation between two structures** tool can be useful to perform intersections and ensure that there is complete or no overlap, as appropriate.

7. In the right column of the application window, use the check boxes for each perfused volume to specify whether to calculate activity and dose for that volume. If you want to consider multiple perfused volumes, select **Summation mode**.

> ⚠ **Warning:** When using the summation mode, you should ensure the specified dose and activity is appropriate for all perfused volumes.

8. You can use any of the three following methods to specify an activity or dose:

   - Use the slider to adjust the activity.
   - Use the **Activity, GBq** field to specify an activity directly.
   - Use the **Perfused tissue absorbed dose, Gy** field to specify a dose directly.

   There is a maximum activity of 15 GBq, which is also enforced upon the Perfused tissue absorbed dose value.

> **Tip:** Click **Display isodose lines** in the toolbox for a more detailed display of dose distribution.

> ⚠ **Warning:** Care should be taken to not confuse VOIs/ROIs and Isodose lines. The system enables you to toggle VOIs and ROIs to hide and show them to enable viewing of Isodose lines in isolation or alongside VOIs and ROIs.

As you set or adjust the activity and dose, the statistics in the **Totals** section are updated. Ensure that the values of these statistics are appropriate for treatment.

> **Tip:** When you have selected a **Calculate** checkbox, you can access the dose-volume histogram window, which provides additional methods for assessing the dose received by structures. For more information, see Viewing a dose-volume histogram.

Next steps

When you have completed your dosimetry, generate a report. For more information, see Report.

> **Tip:** To save a session and so that you can return to it later, click **File** and select **Save session**. Provide a series description and specify which DICOM series the session is associated with.

More on this topic:

- Viewing a dose-volume histogram
  In multi-compartment dosimetry, view a DVH to assess dose coverage.

Viewing a dose-volume histogram

Summary: In multi-compartment dosimetry, view a DVH to assess dose coverage.

About

The dose-volume histogram is available when performing multi-compartment dosimetry. It allows you to review how much dose is received by a given fraction of a volume, or what fraction of a volume receives a given dose.

> ⚠ **Warning:** The dose-volume histogram produced by the application is not a reliable source for quantitative evaluation and should only be used as a qualitative measure.

Procedure

To view a dose-volume histogram, complete the following steps:

1. When you have clicked **Calculate** for one of your perfused volumes, click the **Tools** menu and select **Show Dose-Volume Histogram**.

   The histogram is displayed. The x-axis displays the dose and the y-axis the volume receiving that dose.

   Each region is displayed on the histogram using a different color. If a region has been hidden in the **Structures** section of the toolbox, it will not be displayed in the histogram.

   - To change the scale of the x-axis, use the scroll wheel.
   - To change the units of volume, click **Volume** on the y-axis and then use the radio buttons to select the units that you want to use. Click **OK** to apply changes and close the dialog box, **Cancel** to discard changes and close the dialog box, or **Apply** to apply the changes but keep the dialog box open.
   - The table on the right of the window displays D and V values for the region selected in the top-right of the Dose-Volume Histogram window. A D value, such as D95, shows the minimum dose received by that percentage of the region (in this case, 95% of the region receives at least the displayed dose). The final D value can be edited so that you can view the received dose for any proportion of the region. V values can be calculated for any dose entered in the **V** field and calculates the volume within the region that receives at least the specified dose.

     > **Tip:** While you have the Dose-Volume Histogram window open, you can still make changes to the main *dosimetry* workflow step. These changes are reflected in the dose-volume histogram and the D and V values.

   - To save the graph to the image gallery, click the **Save Graph to Image Gallery** icon  in the top-left of the window.
   - To export a .csv file containing the data from the histogram, click the **Export Histogram to CSV file** icon  or click **File**, hover your mouse over **Export** and select *Export CSV*.

Report

Summary: Create a report to present outside of the Simplicit^{90}Y application.

About

When you need to present data to patients or other practitioners, you can create and customize a report. For more information on this topic, see User preferences. This report can then be exported as a PDF file, or as several images.

Procedure

To create and export a report, complete the following steps:

1. Click the **Report** workflow step or click **Workflow** and select *Report*.

   In the Reports view, different pages of the report are displayed as tabs at the top of the window and the report itself is previewed in the main pane. In the toolbox, various tools are available for customizing your report.

2. To edit entire pages, perform one or more of the following actions:

   - Click **Add Page** to add a new page to your report.
   - Click **Remove Page** to remove the current page from your report.
   - Click **Flip Page** to switch a page between portrait and landscape orientations.

3. To add elements, click one of the following in the toolbox:

   - **Add items - Text**
     A simple text field. Double-click the text field on the page to modify the text that will be displayed.
   - **Add items - Patient info**
     A summary of patient information.
   - **Standard dosimetry - Summary**
     A table displaying the perfused volumes' statistics from standard dosimetry.
   - **Standard dosimetry - Totals**
     A table displaying the totals of the perfused volumes' statistics from standard dosimetry.
   - **Multi-compartment dosimetry - Summary**
     A table displaying the perfused volumes' statistics from multi-compartment dosimetry.
   - **Multi-compartment dosimetry - Totals**
     A table displaying the totals of the perfused volume's statistics from multi-compartment dosimetry.

   > **Note:** If you return to previous steps in the workflow and make changes, the report will not automatically update. To initiate an update, click **Refresh**.

4. With the exception of headers and footers, you can edit elements on a report page. To do so, perform one or more of the following actions:

   - Move an element by clicking and dragging it.

- Resize an element by clicking it and then using the anchor points to resize it.
- Change the layering of elements by right clicking the element and selecting **Bring to front**, **Send to back**, **Bring forward**, or **Send backward** to move the element to the top layer, bottom layer, next layer up, or next layer down respectively.
- Delete an element by right clicking the element and selecting **Delete**.

5. To customize your header, use the **Report** tab of the Options window, accessed through the **Tools** menu. For more information, see User preferences.

6. To export your report, complete one of the following set of steps:

   - To export your report as a set of images, complete the following steps:

     i. Click **Export**.

     ii. (Optional) In the **Series description** field, provide a description of the report.

     iii. (Optional) In the **Performing physician** field, provide the name of the performing physician.

     iv. (Optional) In the **Operator name** field, provide the name of the current operator.

     v. (Optional) In the **Modality** field, provide the imaging modality used.

     vi. From the **Associate with Series** drop down menu, select the dataset with which you would like the report to be associated.

     vii. Click **OK**.

   - To export your report as a PDF file, complete the following steps:

     i. Click **Create PDF**.

     ii. Browse for the location to which you would like to save your report.

     > **Note:** When a PDF is generated, heights and widths are based on your current display. As such, it is recommended that you maximize the application window before generating a PDF.

Secondary captures

Summary: Capture image panes for later reference or for use outside of Simplicit^{90}Y.

About

You can capture secondary images within Simplicit^{90}Y that you can refer to later, after making other changes to the dataset, or that you can use outside of the application.

Secondary captures are accessible within the **Image Gallery** section of the toolbox. Alternatively, you can click **Workflow** and select *Secondary Capture*.

Procedure

To take secondary captures, select from the following options:

- To capture a single image pane, complete the following steps:

  1. Click the image pane that you want to capture.
  2. Click the **Add current view to Image Gallery** icon or click **Edit** and select *Capture view*. The viewport is captured, including all active text.

  > **Tip:** You can also press **Ctrl** + **E** to perform this action.

  > **Note:** You can copy this view to your clipboard by clicking **Edit** and selecting *Copy View to Clipboard* or pressing **Ctrl** + **K**.

- To capture the entire window, click the **Add window to Image Gallery** icon or click **Edit** and select *Capture Screenshot*.

  > **Tip:** You can also press **Ctrl** + **Shift** + **E** to perform this action.

  > **Note:** You can copy this screenshot to your clipboard by clicking **Edit** and selecting *Copy Screenshot to Clipboard* or pressing **Ctrl** + **Shift** + **K**.

To view secondary captures, select from the following options:

- To view the secondary capture screen, click the **Switch to the Secondary Capture screen** icon .
- Double-click the capture that you want to view. This capture is displayed within the **Secondary Capture** screen.

To delete one or more captures, select the capture, or captures, within the **Image Gallery** section of the toolbox and click the **Remove selected images from the gallery** icon .

Tip: You can select multiple captures by holding the **Shift** or **Ctrl** keys.

Topics in this section:

- Exporting secondary captures
  Export secondary captures as different image types or a DICOM object.

Exporting secondary captures

Summary: Export secondary captures as different image types or a DICOM object.

About

To complete this task, you must first have created at least one secondary capture. For more information, see Secondary captures.

Procedure

To export one or more secondary captures from the image gallery, complete the following steps:

1. Within the **Image Gallery** section of toolbox, select the secondary captures that you want to export.

   > **Note:** You should ensure that the slice number is displayed within your secondary captures as there will be no other way of identifying the location of the image upon export.

2. Click the **Export selected image** icon  . The *Export* window is displayed.
3. (Optional) Within the **Series Description** text field, enter a description to be associated with the DICOM tag (0008,103E).
4. (Optional) Within the **Performing physician** text field, enter the name of the performing physician to be associated with the DICOM tag (0008,1050).
5. (Optional) Within the **Operator name** text field, enter the name of the operator to be associated with the DICOM tag (0008,1070).
6. If enabled, use the **Associate with Series** drop-down menu to select the image set with which you want to associate your exported secondary capture(s). When you launch Simplicit^{90}Y using that image set as part of your selection, the associated secondary captures are available.
7. Click **Export**.

Statistics and properties

Summary: A list of statistics found in Simplicit^{90}Y.

About

The following calculated statistics and properties to enter are found in the *Dosimetry* step of the application, for either standard dosimetry or multi-compartment dosimetry:

Statistic	Definition
Whole liver volume	The volume of the structure with the Whole Liver type.
Lung Shunt Fraction	The percentage of activity recorded from the lungs. If this was manually entered, a label is shown. No label is shown for fractions calculated by the application. For the equations used by the application to calculate this value, see Lung shunt fraction.
Residual Fraction	The fraction of activity from the ordered vial that was not or will not be injected. This accounts for imperfect delivery from a vial.
Volume (of a Perfused volume)	The volume of the structure.
Perfused Fraction (of a Perfused volume)	The proportion of the whole liver that the perfused volume constitutes, as a percentage.
Activity (of a Perfused volume)	The activity that was, or is to be, absorbed by the perfused volume. For the equations used to calculate this value, see Perfused tissue absorbed dose and activity.
Perfused tissue absorbed dose (of a Perfused volume)	The dose that was, or is to be, absorbed by the perfused volume. For the equations used to calculate this value, see Perfused tissue absorbed dose and activity.
Num. Perfused Volumes	Displays the number of Perfused volume structures selected for treatment.
Required activity	The activity required to be administered to achieve the specified Activity and Perfused tissue absorbed dose.
Perfused fraction	The total fraction of the Whole liver structure that is selected for treatment.
Whole liver absorbed dose	The total dose that was, or is to be, absorbed by the Whole liver structure. For the equations used to calculate this value, see Whole liver normal tissue absorbed dose.
Whole liver normal tissue absorbed dose	The total dose that was, or is to be, absorbed by the Whole liver normal tissue. For the equations used to calculate this value, see Whole liver absorbed dose.

Statistic	Definition
Lung absorbed dose	The dose that was, or is to be, absorbed by the lungs. For the equations used to calculate this value, see Lung absorbed dose.
Perfused tumor absorbed dose (in a Perfused volume)	The dose that was, or is to be, absorbed by the tumor structures in this perfused volume. For the equations used to calculate this value, see Perfused tumor absorbed dose.
Perfused viable tumor absorbed dose (in a Perfused volume)	The dose that was, or is to be, absorbed by the viable tumor structures in this perfused volume. For the equations used to calculate this value, see Perfused viable tumor absorbed dose.
Perfused normal tissue absorbed dose (in a Perfused volume)	The dose that was, or is to be, absorbed by the normal tissue structures in this perfused volume. For the equations used to calculate this value, see Perfused normal tissue absorbed dose.
Total perfused tissue absorbed dose	The total dose that was, or is to be, absorbed by the perfused volume structures. For the equations used to calculate this value, see Total perfused tissue absorbed dose.
Perfused tumor absorbed dose	The total dose that was, or is to be, absorbed by the tumor structures in all perfused volumes. For the equations used to calculate this value, see Perfused tumor absorbed dose.
Perfused viable tumor absorbed dose	The total dose that was, or is to be, absorbed by the viable tumor structures in all perfused volumes. For the equations used to calculate this value, see Perfused viable tumor absorbed dose.
Perfused normal tissue absorbed dose	The total dose that was, or is to be, absorbed by the normal tissue structures in all perfused volumes. For the equations used to calculate this value, see Perfused normal tissue absorbed dose.

Topics in this section:

- Imaging protocols
  Details of appropriate imaging protocols for post-radioembolization imaging.
- Lung shunt fraction
  The equations used to calculate a lung shunt fraction from regions on a planar image.
- Perfused tissue absorbed dose and activity
  The relationship between the Perfused tissue absorbed dose and Activity for a perfused volume.
- Total perfused tissue absorbed dose
  A definition of the total perfused tissue absorbed dose statistic.
- Whole liver absorbed dose

The definition of the Whole liver absorbed dose statistic.

- Whole liver normal tissue absorbed dose
  A definition of the whole liver normal tissue absorbed dose statistic.
- Lung absorbed dose
  The definition of the Lung absorbed dose statistic.
- Perfused tumor absorbed dose
  The definition of the perfused tumor absorbed dose statistic.
- Perfused viable tumor absorbed dose
  The definition of the perfused viable tumor absorbed dose statistic.
- Perfused normal tissue absorbed dose
  The definition of the Perfused normal tissue absorbed dose statistic.

Imaging protocols

Summary: Details of appropriate imaging protocols for post-radioembolization imaging.

Protocols

When coupled with appropriate imaging protocols for reconstruction of ^{90}Y activity concentrations, PET and SPECT scanners from the current generation can be used for quantitative analysis of post-radioembolization imaging.

When available, time-of-flight and resolution recovery methods are recommended.

The following tables list examples of imaging protocols that have been shown to result in images that can be better quantitively analyzed, provide a greater accuracy of counts and therefore facilitate a greater accuracy of ^{90}Y dosimetry.

PET

Vendor	Scanner	Reconstruction Method
Philips	Gemini TF	3D BLOB OSEM, 4i 8s, ToF, with no filter.
Siemens	Biograph (various)	3D OSEM, 2i 21s, Resolution Recovery (PROMPTS + RANDOMS acquisition), with all pass filter.
Siemens	Biograph mCT	3D OSEM, 2i 21s, Resolution Recovery, ToF, with all-pass filter.
GE	Discovery 600, Discovery STE, Discovery RX	3D OSEM, 2i 24s with all-pass filter.
GE	Discovery 690, Discovery 710	3D OSEM, 2i 24s, Resolution Recovery, ToF, with all-pass filter.

For further information, these protocols were confirmed in the papers by Willowson et al[2] and Pasciak et al.[12]

Bremsstrahlung SPECT

Paper	Scanner	Energy window (keV)	Collimators	Matrix size/voxel size	Projections	Reconstruction	Recommendation
[Elschot b][8]	Symbia T16 SPECT/CT (SIEMENS)	50-250	High Energy	128 x 128 (4.8mm voxel)	• 360° • 120 s/step	OSEM 60 iterations with 8 subsets + MC	CDR modelling
[Fabbri][7]	Symbia-T2 SPECT/CT (SIEMENS)	36-204	Medium-energy general purpose (MEGP)	128 x 128 (4.8mm voxel)	• 64 views • 40 s/step	OSEM 3D fast	
[Siman][9]	Symbia TruePoint SPECT/CT (SIEMENS)	90–125 (most appropriate)	Medium-energy low penetration (MELP)	128 x 128 (4.8mm voxel)	• 2 x 64 views • 360° • 28 s/step	• OSEM (8i, 16s) • No post-reconstruction filter	Background Compensation (BC)
[Mikell a][10]	Symbia T16 SPECT/CT (SIEMENS)	90-125 primary, 312-413 scatter	MELP	4.8mm voxel size	• 128 views • 360° • 28 s/step	• 3D OSEM (Flash3D) (4i, 8s) • 9.6mm FWHM Gaussian post-reconstruction filter	

Paper	Scanner	Energy window (keV)	Collimators	Matrix size/voxel size	Projections	Reconstruction	Recommendation
[Porter][11]	Discovery 670 dual-headed SPECT/CT camera (GE)	50-150	MEGP	128 x 128	• 90 views • 360° • 20 s/view	OSEM (5i, 15s - recommended)	MC collimator modelling

Minimum activity concentration - PET and SPECT

If the activity concentration in a volume of interest is lower than the reported range/minimum activity for the specific object size, the accuracy of the counts in the region will be reduced and will affect the accuracy of post-treatment dosimetry.

The following tables list examples of imaging protocols that deliver a minimum activity concentration for the given structure sizes.

PET

Region	Paper	Relationship between ^{90}Y Activity concentration images and size	Recommendations and remarks
Background (modelling healthy liver)	[Willowson a][1]	37 kBq/mL (minimum studied).	
Background (modelling healthy liver)	[Willowson a][2]	50 – 300 kBq /mL (range studied). 10% error across range 5% error at 300 kBq/mL with TOF.	
Background (modelling healthy liver)	[D'Arienzo][3]	257 kBq/mL (uniform cylindrical phantom). 310 - 890 kBq/mL (anthropomorphic phantom)	No correction needed for PVEs as they are not significant in background.

Region	Paper	Relationship between ^{90}Y Activity concentration images and size	Recommendations and remarks
Hot spheres (modelling lesions)	[D'Arienzo][3]	minimum studied: 310 kBq/mL (12.4% deviation, non-TOF PET, PVE corrected). maximum studied: 5,500 kBq/mL (3.6% deviation, non-TOF PET, PVE corrected)	PVEs dominate in NEMA spheres < 28mm diameter (11.5 ml) Longer scan time for non ToF PET PVEs in the liver assumed to be negligible.
Hot spheres (modelling lesions)	[Werner][4]	detectability: ≥ 17mm NEMA sphere diameter (non-TOF, @ 3,600 kBq/mL).	1MBq/mL minimum recommended activity concentration. Non ToF leads to reliable detectability.
Hot spheres (modelling lesions)	[Willowson a][1]	detectability: ≥ 13mm NEMA sphere diameter (TOF) for ≥ 650kBq/mL.	PVEs dominate in spheres ≤ 28mm, TOF is recommended.
Hot spheres (modelling lesions)	[Willowson b][2]	maximum studied: 2,500kBq/mL (15% deviation, TOF + RR PET in 37mm sphere). NEMA spheres ≤ 20mm dominated by PVEs	40 min acquisition in a 2-bed setting.
Hot spheres (modelling lesions)	[Carlier][5]	detectability: ≥ 17mm NEMA sphere diameter (TOF, ≥ 490 kBq/mL). ≥ 22mm NEMA sphere diameter (non-TOF, ≥ 490 kBq/mL) ≥ 10mm NEMA sphere diameter (TOF, ≥ 1MBq/mL) ≥ 10mm NEMA sphere diameter (non-TOF, ≥ 3MBq/mL)	Non ToF leads to reliable detectability.

Bremsstrahlung SPECT

Region	Paper	Relationship between ^{90}Y Activity concentration images and size	Recommendations and remarks
Background	[Dewaraja b][6]	1168 ml for 0.92 MBq/ml	
Tumor	[Fabbri][7]	8 ml with minimum of 31 MBq/ml	
Tumor	[Dewaraja b][6]	14 ml sphere with 4.5 MBq/ml	Scatter correction based on Calibration factors (MDA group) or partial MC correction to be clinically applicable.
Tumor	[Elschot b][8]	25mm diameter tumors with 2.4 MBq/ml	Improve optimization of detection windows. Use pre-defined CDR kernels.

References

[1]Willowson et al (2012) Quantitative 90Y image reconstruction in PET. *Med Phys*. 39 (11): 7153-7159. doi: 10.1118/1.4762403.

[2]Willowson et al (2015) A multicentre comparison of quantitative 90Y PET/CT for dosimetric purposes after radioembolization with resin microspheres. *EJNMMI*. 42:1202-1222. doi: 10.1007/s00259-015-3059-9.

[3]D'Arienzo et al. (2017) Phantom validation of quantitative Y-90 PET/CT-based dosimetry in liver radioembolization. *EJNMMI Research*. 7:94. doi:10.1186/s13550-017-0341-9.

[4]Werner et al (2010) PET/CT for the assessment and quantification of 90Y biodistribution after selective internal radiotherapy (SIRT) of liver metastases. *EJNMMI*. 37:407-408. doi: 10.1007/s00259-009-1317-4.

[5]Carlier et al. (2013) Assessment of acquisition protocols for routine imaging of Y-90 using PET/CT. *EJNMMI Research*. 3:11. doi:10.1186/2191-219X-3-11

[6]Dewaraja et al. (2017) Improved quantitative 90Y bremsstrahlung SPECT/CT reconstruction with Monte Carlo scatter modelling. *Med Phys*. 44(12): 6364 - 6376. doi:10.1002/mp.12597.

[7]Fabbri et al. (2009) Quantitative Analysis of 90Y Bremsstrahlung SPECT-CT Images for Application to 3D Patient-Specific Dosimetry. *Cancer Biotherapy & Radiopharmaceuticals*. 24(1): 145-153. doi:10.1089/cbr.2008.0543.

[8]Elschot et al. (2013) Quantitative Monte Carlo–Based 90Y SPECT Reconstruction. *J Nucl Med*. 54:1557–1563. doi: 10.2967/jnumed.112.119131.

[9]Siman et al. (2016) Practical reconstruction protocol for quantitative 90Y bremsstrahlung SPECT/CT. *Med Phys*. 43:9: 5093-5103. doi:10.1118/1.4960629

[10]Mikell et al. (2015) Comparing voxel-based absorbed dosimetry methods in tumors, liver, lung, and at the liver-lung interface for 90Y microsphere selective internal radiation therapy. *EJNMMI Physics*. 2:16. doi: 0.1186/s40658-015-0119-y.

[11]Porter et al. (2018) Phantom and clinical evaluation of the effect of full Monte Carlo collimator modelling in post-SIRT yttrium-90 Bremsstrahlung SPECT imaging. *EJNMMI Research*. 8:7. doi: 10.1186/s13550-018-0361-0.

[12]Pasciak et al. (2014) Radioembolization and the dynamic role of 90Y PET/CT. *Frontiers in Oncology*. 4:38. doi:10.3389/fonc.2014.00038.

Lung shunt fraction

Summary: The equations used to calculate a lung shunt fraction from regions on a planar image.

About

In the *Lung Shunt Fraction* workflow step, you can specify that a lung shunt fraction is calculated from a planar NM image or a SPECT image. You can also specify whether to apply background correction and whether to use a geometric mean of two planar images with opposite orientations.

Definition

The lung shunt fraction is calculated as the following:

$$F = \frac{C_{lung}}{C_{lung} + C_{liver}} \times 100$$

where:

- F is the lung shunt fraction as a percentage
- C_{lung} is the activity, in counts, of the lung region
- C_{liver} is the activity, in counts, of the liver region

Additionally, background correction can be applied as follows:

$$C'_X = C_X - (C_{BG} \times \frac{N_X}{N_{BG}})$$

where:

- C'_X is the background-corrected activity of region X
- C_X is the uncorrected activity of region X
- C_{BG} is the uncorrected activity in the background region
- N_X is the number of voxels in region X
- N_{BG} is the number of voxels in the background region

You can also use a geometric mean of the counts:

$$C_{GM} = \sqrt{C_A \times C_P}$$

where:

- C_{GM} is the geometric mean of the activity for the region, in counts.
- C_A is the activity for the region in the anterior image, in counts.
- C_P is the activity for the region in the posterior image, in counts.

Note: Background correction is applied before the geometric mean is calculated.

Perfused tissue absorbed dose and activity

Summary: The relationship between the Perfused tissue absorbed dose and Activity for a perfused volume.

About

In the *Dosimetry* workflow step, the perfused tissue absorbed dose statistic is either specified, calculated from a specified activity, or set using the dose slider. These set the estimated dose or activity that was or is to be delivered to the perfused tissue structure.

Definition

The relationship between the activity in the perfused volume, Apv and the perfused tissue absorbed dose, Dpv is given by:

$$A_{pv} = \frac{M_{pv} \times D_{pv}}{50 \times (1 - F) \times (1 - R)}$$

Alternatively, it can be rearranged as:

$$D_{pv} = \frac{50 \times A_{pv} \times (1 - F) \times (1 - R)}{M_{pv}}$$

Where:

- A_{pv} is the activity for the perfused volume selected for calculation, in GBq.
- D_{pv} is the dose for the perfused volume, in Gy.
- F is the lung shunt fraction.
- R is the residual fraction.
- The constant 50 is the dose in Gy delivered to 1 kg of mass by 1 GBq of ^{90}Y.
- M_{pv} is the mass of the perfused volume in kg.

The mass of the perfused volume, M_{pv}, is calculated as:

$$M_{pv} = \frac{V_{pv} \times \rho_{liver}}{1000}$$

Where:

- M_{pv} is the mass of the union of perfused volume in kg.
- V_{pv} is the volume of the union of perfused volumes in cm^3.
- ρ_{liver} is the liver tissue density in kg/cm^3.

Total perfused tissue absorbed dose

Summary: A definition of the total perfused tissue absorbed dose statistic.

About

As part of multi-compartment dosimetry in the *Dosimetry* workflow step, the total perfused tissue absorbed dose statistic is calculated.

Definition

The Total perfused tissue absorbed dose is calculated as the following:

$$D_{pv} = \frac{50 \times A_{pv} \times (1 - F) \times (1 - R)}{M_{pv}}$$

Where:

- D_{pv} is the total perfused volume dose in Gy.
- A_{pv} is the sum of activities for each perfused volume selected for calculation, in GBq.
- F is the lung shunt fraction.
- R is the residual fraction.
- The constant 50 is the dose in Gy delivered to 1 kg of mass by 1 GBq of ^{90}Y.
- M_{pv} is the mass of a union of the perfused volume VOIs selected for calculation, in kg.

The mass of the union of the perfused volume VOIs, M_{pv}, is calculated as:

$$M_{pv} = \frac{V_{pv} \times \rho_{liver}}{1000}$$

Where:

- M_{pv} is the mass of the union of perfused volume in kg.
- V_{pv} is the volume of the union of perfused volumes in cm^3.
- ρ_{liver} is the liver tissue density in kg/cm^3.

Whole liver absorbed dose

Summary: The definition of the Whole liver absorbed dose statistic.

About

In the *Dosimetry* workflow step, the whole liver absorbed dose is displayed. This is the dose that was or is to be delivered to the whole liver structure by the specified target activity or target dose for all perfused volumes.

Definition

The whole liver absorbed dose, D_{liver}, is given by:

$$D_{liver} = \frac{50 \times A \times (1-F) \times (1-R)}{M_{liver}}$$

where:

- D_{liver} is the dose that was or is to be delivered to the whole liver structure in Gy.
- A is the summed target activities of all perfused volumes in GBq.
- F is the lung shunt fraction.
- R is the residual fraction.
- M_{liver} is the whole liver mass in kg.
- the constant 50 is the dose in Gy delivered to 1 kg of mass by 1 GBq of ^{90}Y.

The mass of the whole liver, M_{liver} , is calculated as:

$$M_{liver} = \frac{V_{liver} \times \rho_{liver}}{1000}$$

Where:

- M_{liver} is the whole liver mass in kg.
- V_{liver} is the volume of the liver in cm^3.
- ρ_{liver} is the liver tissue density in g/cm^3, assumed to be 1.03 g/cm^3.

Whole liver normal tissue absorbed dose

Summary: A definition of the whole liver normal tissue absorbed dose statistic.

About

As part of multi-compartment dosimetry in the *Dosimetry* workflow step, the Whole liver normal tissue absorbed dose statistic is calculated.

Definition

The whole liver normal tissue absorbed dose is calculated as the following:

$$D_{wlnt} = \frac{\left[\left(\frac{A_{pv1}}{C_{pv1}}\right) C_{pv1-t} + \left(\frac{A_{pv2}}{C_{pv2}}\right) C_{pv2-t} + \cdots + \left(\frac{A_{pvN}}{C_{pvN}}\right) C_{pvN-t}\right] \times 50 \times (1-F) \times (1-R)}{\rho V_{Whole\ liver\ normal\ tissue}}$$

Where:

- D_{wlnt} is the whole liver normal tissue absorbed dose, in Gy.
- A_{pvi} is the injected activity, in GBq, of perfused volume i.
- C_{pvi} is the number of counts in perfused volume i.
- $C_{pvi\text{-}t}$ is the number of counts in perfused volume i minus the counts in tumors and viable tumors (inside perfused volume i).
- F is the lung shunt fraction.
- R is the residual fraction.
- ρ is the liver tissue density in kg/cm^3, assumed to be 1.03x10^{-3} kg/cm^3.
- $V_{Whole\ liver\ normal\ tissue}$ is the total volume of the normal whole liver (i.e. excluding any tumors and viable tumors), in cm^3.

Lung absorbed dose

Summary: The definition of the Lung absorbed dose statistic.

About

In the *Dosimetry* workflow step, the lung absorbed dose statistic is calculated. This is the amount of dose absorbed by the lungs, estimated through the lung shunt fraction.

Definition

The Lung absorbed dose, D_{lung}, is given by:

$$D_{lung} = \frac{50 \times A \times F \times (1 - R)}{M_{lung}}$$

Where:

- D_{lung} is the dose delivered to the lungs in Gy.
- A is the total target activity in GBq.
- F is the lung shunt fraction.
- R is the residual fraction.
- 50 is the dose in Gy delivered to 1 kg of mass by 1 GBq of ^{90}Y.
- M_{lung} is the lung mass in kg, assumed to be 1 kg.

Perfused tumor absorbed dose

Summary: The definition of the perfused tumor absorbed dose statistic.

About

As part of multi-compartment dosimetry in the *Dosimetry* workflow step, the perfused tumor absorbed dose statistic is specified or calculated.

Definition

The perfused tumor absorbed dose is calculated as the following:

$$D_t = \frac{\left[\left(\frac{A_{pv1}}{C_{pv1}}\right) C_{t \cap pv1} + \left(\frac{A_{pv2}}{C_{pv2}}\right) C_{t \cap pv2} + \cdots + \left(\frac{A_{pvN}}{C_{pvN}}\right) C_{t \cap pvN}\right] \times 50 \times (1 - F) \times (1 - R)}{\rho V_t}$$

where:

- D_t is the tumor absorbed dose, in Gy.
- A_{pvi} is the injected activity, in GBq, of perfused volume *i*.
- F is the lung shunt fraction.
- R is the residual fraction.
- $C_{t \cap pvi}$ is the number of counts in the volume formed by the intersection of the tumor VOI and perfused volume *i*, on the functional dataset.
- C_{pvi} is the number of counts in perfused volume *i* on the functional dataset.
- ρ is the tumor tissue density in kg/cm^3, assumed to be 1.03x10^{-3} kg/cm^3.
- V_t is the volume of the tumor, in cm^3.

Perfused viable tumor absorbed dose

Summary: The definition of the perfused viable tumor absorbed dose statistic.

About

As part of multi-compartment dosimetry in the *Dosimetry* workflow step, the perfused viable tumor absorbed dose statistic is specified or calculated.

Definition

The perfused viable tumor absorbed dose is calculated as the following:

$$D_{vt} = \frac{\left[\left(\frac{A_{pv1}}{C_{pv1}}\right) C_{vt \cap pv1} + \left(\frac{A_{pv2}}{C_{pv2}}\right) C_{vt \cap pv2} + \cdots + \left(\frac{A_{pvN}}{C_{pvN}}\right) C_{vt \cap pvN}\right] \times 50 \times (1 - F) \times (1 - R)}{\rho V_{vt}}$$

Where:

- D_{vt} is the viable tumor absorbed dose, in Gy.
- A_{pvi} is the injected activity, in GBq, of perfused volume *i*.
- F is the lung shunt fraction.
- R is the residual fraction.
- $C_{vt \cap pvi}$ is the number of counts in the volume formed by the intersection of the viable tumor VOI and perfused volume *i*, on the functional dataset.
- C_{pvi} is the number of counts in perfused volume *i* on the functional dataset.
- ρ is the tumor tissue density in kg/cm^3, assumed to be 1.03x10^{-3} kg/cm^3.
- V_{vt} is the volume of the viable tumor, in cm^3.

Perfused normal tissue absorbed dose

Summary: The definition of the Perfused normal tissue absorbed dose statistic.

About

As part of multi-compartment dosimetry in the *Dosimetry* workflow step, the perfused normal tissue absorbed dose statistic is specified or calculated.

Definition

The perfused normal tissue absorbed dose is calculated as the following:

$$D_{nt} = \frac{\left[\left(\frac{A_{pv1}}{C_{pv1}}\right) C_{nt \cap pv1} + \left(\frac{A_{pv2}}{C_{pv2}}\right) C_{nt \cap pv2} + \cdots + \left(\frac{A_{pvN}}{C_{pvN}}\right) C_{nt \cap pvN}\right] \times 50 \times (1 - F) \times (1 - R)}{\rho V_{nt}}$$

Where:

- D_{nt} is the normal tissue absorbed dose, in Gy.
- A_{pvi} is the injected activity, in GBq, of perfused volume *i*.
- F is the lung shunt fraction.
- R is the residual fraction.
- $C_{nt \cap pvi}$ is the number of counts in the volume formed by the intersection of the normal tissue VOI and perfused volume *i*, on the functional dataset.
- C_{pvi} is the number of counts in perfused volume *i* on the functional dataset.
- ρ is the liver tissue density in kg/cm^3, assumed to be 1.03x10^{-3} kg/cm^3.
- V_{nt} is the volume of the normal tissue, in cm^3.

User preferences

Summary: A list of configurable options in Simplicit^{90}Y.

About

Simplicit^{90}Y provides a wide range of customization, much of it accessed through the Options window. These settings are managed on a per-user basis, unless otherwise stated.

To open the Options window, click the **Tools** menu and select **Options**.

Click **Apply** to apply changes and keep the Options window open, **OK** to apply changes and close the Options window, or **Cancel** to discard changes and close the Options window.

User preferences

The following user preferences are available through the Options window:

Preference	Tab	Description
Default anchor	Default series	Specify a series description that, if found, prioritizes that image volume to be the anchor series.
Default series for liver auto-segmentation	Default series	Specify a series description that, if found, prioritizes that image volume to be used for the automatic CT liver segmentation. The algorithm is designed for use with contrast-enhanced CT scans and the venous phase often gives the best results.
Iso-dose line thickness	Dose	The thickness of iso-dose lines in pixels.
Iso-dose color look up table	Dose	Select which table to use for dose ranges and colors in the *Dosimetry* workflow step. To edit this list, add, delete and copy in the left column of the Options window. To edit a table, add, edit and delete iso-dose values in the right column.
Viewer options	Quantification	For the selected modality, specify which statistics are displayed in region labels.
Units	Quantification	Specify the units of length and volume.
Institution name	Report	Specify the institution name, to be displayed in the header of the *Report* workflow step.

Preference	Tab	Description
Export settings	Report	Specify the refresh behavior when exporting a report, whether to automatically open exported PDF files, and the paper size used in the PDF files.
Header logo	Report	Browse your file system for a logo to use in the *Report* workflow step.
Save and export	Save and export	Specify whether to prompt to save the session when closing the application.
Segmentation tools	Segmentation	Specify which tools you want to be available in the Segmentation Tools section of the toolbox, for the listed workflow step.

Warning: When specifying your quantification method, care should be taken to ensure that the intended unit of quantification is selected. The quantification method applied is displayed as active text within the image pane.

Keyboard shortcuts

Summary: The keyboard shortcuts and mouse gestures available in Simplicit^{90}Y.

Hotkeys

The following table lists the keyboard shortcuts and gestures available in Simplicit^{90}Y:

Shortcut	Action
Esc	Clears your current tool selection.
F1	Open the Help Guide.
Ctrl + Z	Undo the previous action.
Crtl + Y	Redo an undone action (not available after a new action has been performed).
Ctrl + C (Report workflow step only)	Copy selected text.
Ctrl + V (Report workflow step only)	Paste selected text (must be into a text box).
Ctrl + X (Report workflow step only)	Cut selected text and add it to the system clipboard.
Ctrl + E	Capture the selected view and save it to the image gallery.
Ctrl + Shift + E	Capture the entire application window and save it to the image gallery.
Ctrl + K	Capture the selected view and copy it to the system clipboard.
Ctrl + Shift + K	Capture the entire application window and copy it to the system clipboard.
Ctrl + L	Select the Ellipse Region tool.
Ctrl + R	Select the Rectangle Region tool.
Delete	Delete the selected structure or structures.
Ctrl + Delete	Delete all structures.
Up arrow (axial view selected only)	Move up one slice.
Down arrow (axial view selected only)	Move down one slice.
Page Up (axial view selected only)	Move up ten slices.
Page Down (axial view selected only)	Move down ten slices.
Scroll-wheel	Scroll through slices.
Ctrl + Scroll-wheel	Zoom in and out.

Shortcut	Action
Shift + Scroll-wheel (with paint, erase or nudge tool selected)	Change diameter of tool.
Middle-click and drag	Pan image.