10 MR Cardiac Suite

MR Cardiac is a suite of applications that contains the MR Cardiac Viewer and a number of analysis applications.

Overview

MR Cardiac is a suite of applications in Advanced Visualization Workspace focused on MR Cardiac reading and diagnosis. The suite includes an advanced viewer and six applications:

- MR Cardiac Viewer
- Functional LV/RV (Left Ventricle/Right Ventricle) analysis
- Functional Long Axis analysis
- Spatial enhancement
- QFlow
- Quantitative Mapping
- Temporal enhancement

MR Cardiac Suite can also launch external applications, triggered by the type of data inside the suite.

Indications for Use

The MR Cardiac Viewer is indicated for side-by-side review of single, multiple or all available cardiac series in a default or in a user-defined viewing protocol. The MR Cardiac Viewer supports the user in review of cardiac anatomy and motion.

Intended Users

The MR Cardiac Suite is intended to be used by adequately trained and qualified medical professionals, including but not limited to physicians and medical technicians. The main clinicians or medical and para-medical professionals who use the MR Cardiac Suite application are listed below:

- Radiologists in the radiology department/clinic
- 3D technologists in the radiology department

Other clinicians/roles using the MR Cardiac Suite are listed below:

- Cardiologists and Cardiology technologists
- Referring Physicians

Intended Patient Population

The MR Cardiac Suite is indicated to support the diagnosis, management, and follow-up of patients with suspected or diagnosed cardiovascular disease (e.g. heart failure, myocardial disorders, valvular diseases, cardiac masses, pericardial disease, and ischemic heart disease).

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Benefits

When used as specified in the Intended Use, under the circumstances and conditions as specified in the Indications for Use, the MR Cardiac Suite assists the user to interpret clinical cardiac MR image data according to the clinical context and on par with the state of the art, thus realizing a positive impact on diagnosis or patient management.

Specifically, with the resulting radiological conclusions obtained from quantitative and qualitative information of the heart and adjacent roots of large vessels via the MR Cardiac Suite and noninvasive medical imaging techniques, in combination with other clinical investigations and patient history, the referring physician can advise the patient on his or her current condition, determine whether additional investigations are warranted, present the patient with treatment options to prevent reoccurrence or worsening of the presenting symptoms, and optionally (if diagnosed) control the evolution of the cardiac disease by taking action in controlling risk factors with heart-healthy lifestyle changes and/or medication and/or interventional therapy.

Contraindications

None.

Calculation of cardiac volumes

The default volume computation method is the common sum-of-discs method. This method computes a volume as the sum of the products of areas (of the contours drawn in each slice) and slice separations (sum of the slice thickness and the inter-slice gap). Alternatively, volume computation according to Simpson’s rule can be selected.

For accurate volume computation, acquisition should cover the complete chamber (LV/RV) from apex to base. If there is insufficient coverage, the volume will be underestimated.

The accuracy of volumetric measurements is mainly determined by accurate identification of the most basal slice level and accurate definition of the endo/epi contours at this level.

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MR Cardiac Suite workspace

Screen layout

Application workspace

Upon launch, the MR Cardiac Suite opens in the **Viewer**. The **Viewer** displays series that you selected for analysis in the main viewport.

You can launch all MR Cardiac Suite integrated analysis applications, including additional analysis applications for the same patient, on the **Analysis** tabs. The application workspace shows the active application.

Suite title bar

The suite title bar is located at the top of the suite. It contains the following:

- **Workflow** and workflow steps - define and select a sequence of steps you repeat as part of a reading protocol.
- 

Studies - open the timeline.
- **Label Data** - open a dialog box to modify any attribute. Use when automatic labeling fails to recognize a critical attribute like orientation or scan type.

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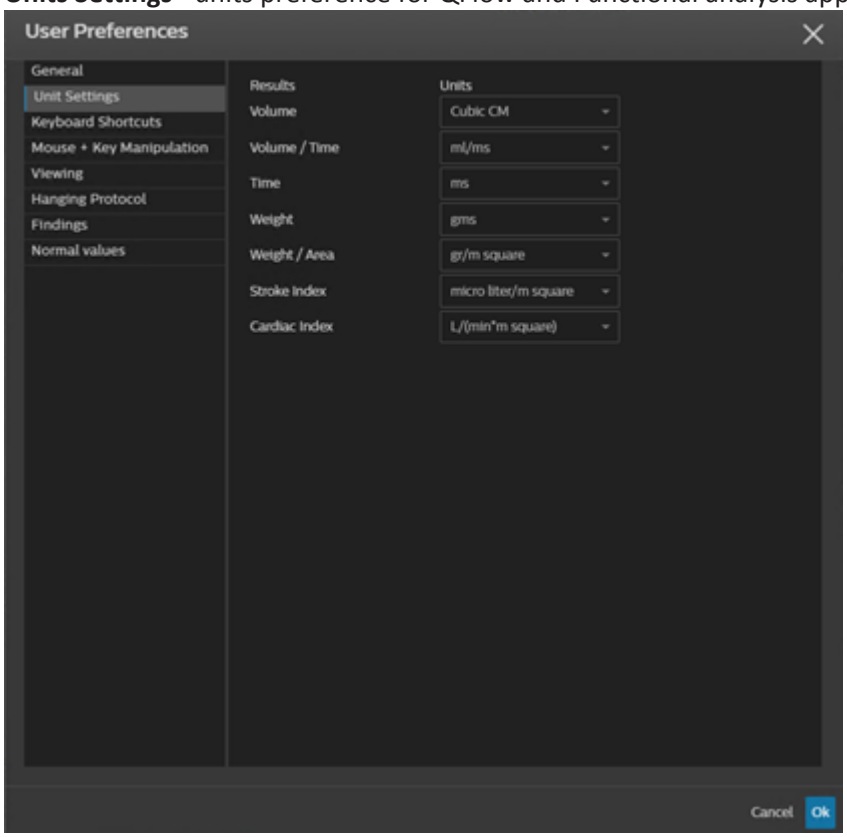
- **Split display** - launch several applications on the same display.

- **User Preferences** - open a dialog box that contains:
  - **General** - select a checkbox to avoid notifications on launching applications.
  - **Units Settings** - units preference for QFlow and Functional analysis applications.



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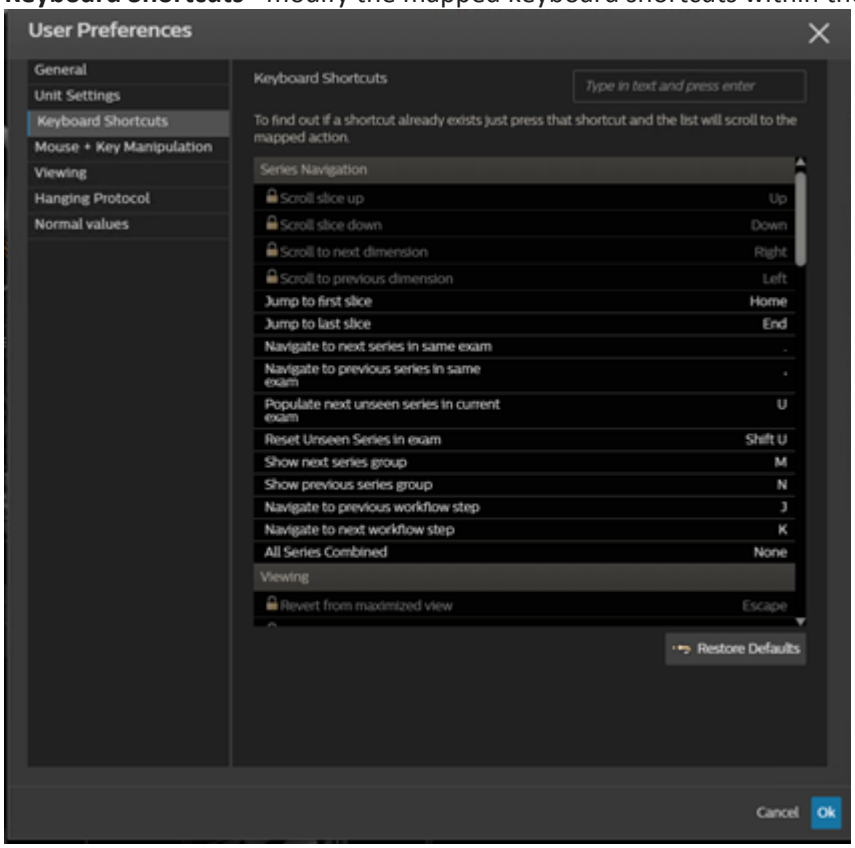
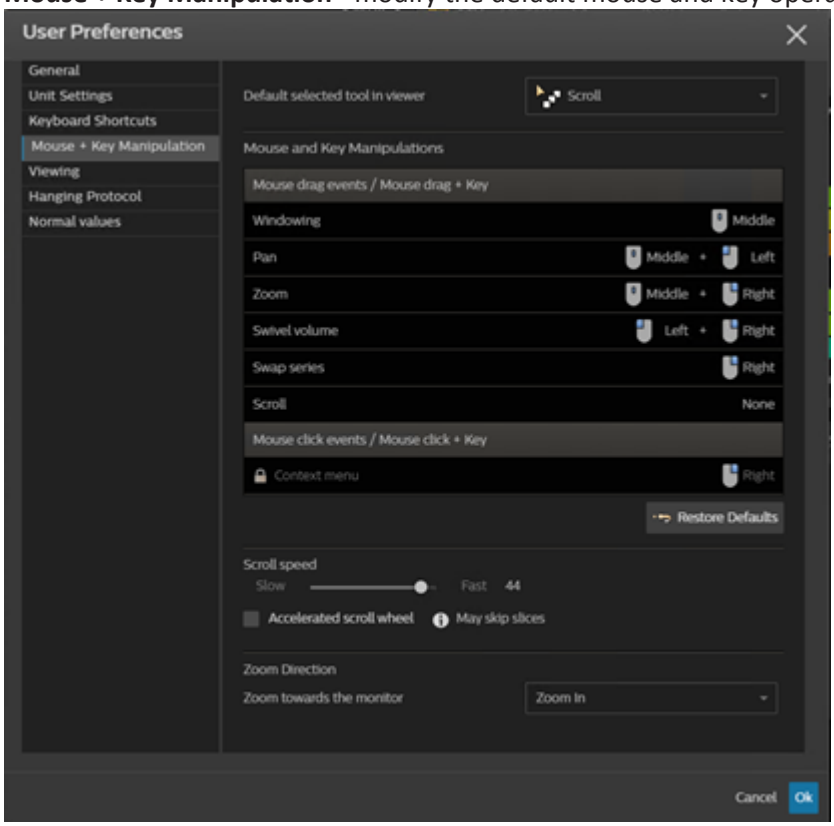
– **Keyboard Shortcuts** - modify the mapped keyboard shortcuts within the suite.



– **Mouse + Key Manipulation** - modify the default mouse and key operations.



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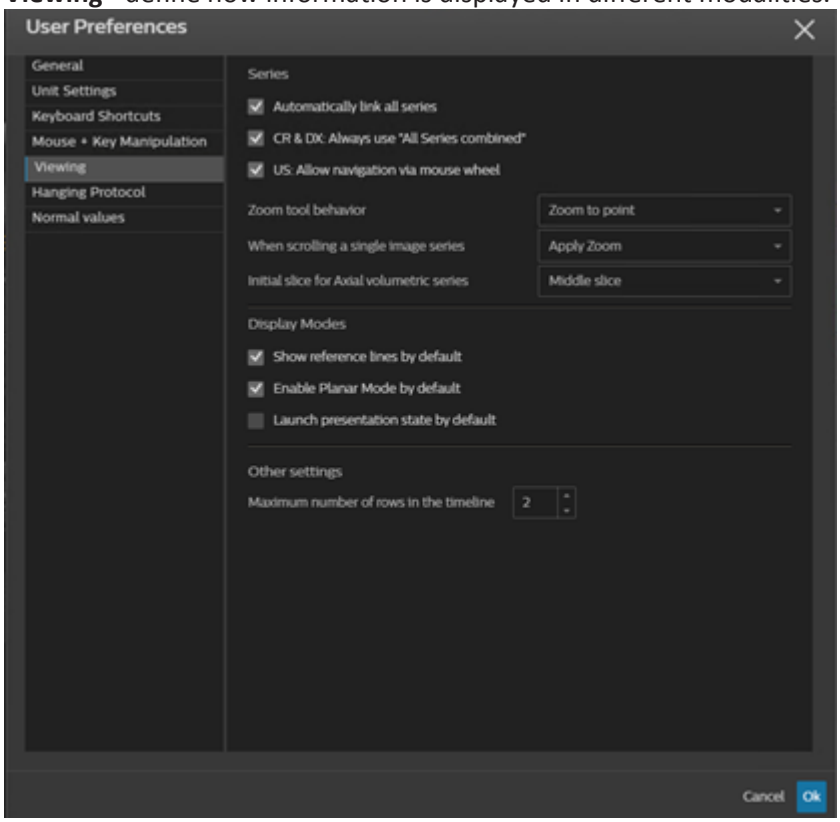
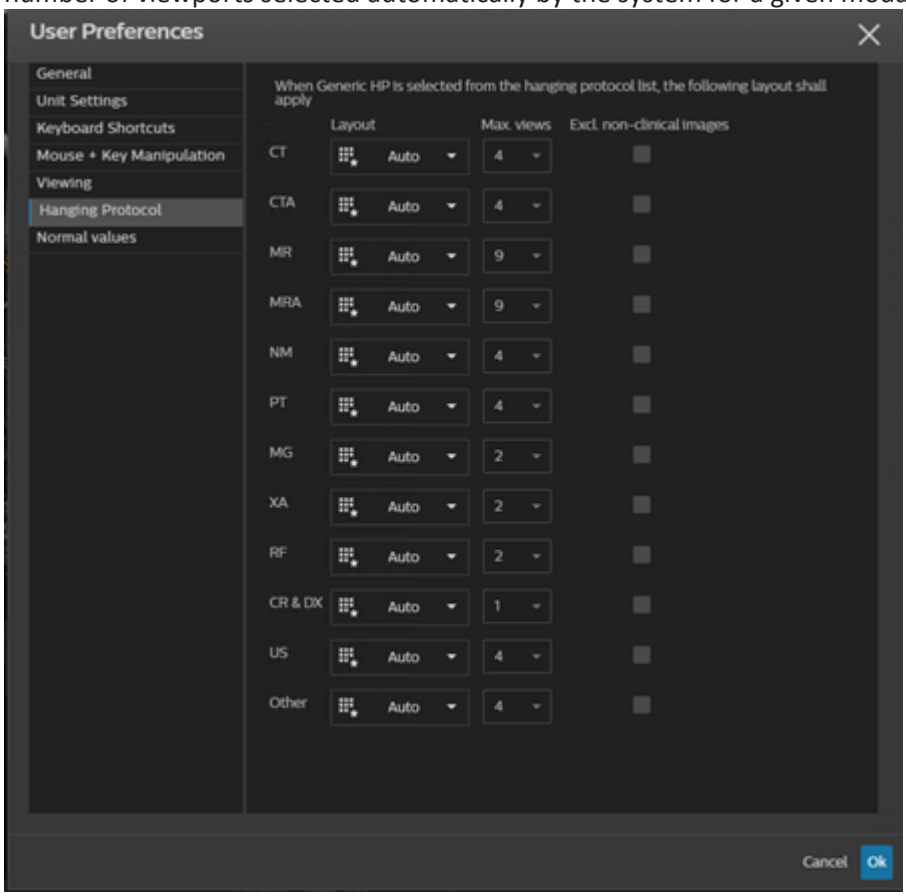
– **Viewing** - define how information is displayed in different modalities.



– **Hanging Protocol** - define **Viewer** layout per modality. **Max views** defines the maximum number of viewports selected automatically by the system for a given modality.



– **Normal values** - Configure normal values for the Functional LV/RV and Mapping applications for all users of the same server. Select an application from the upper list menu. The databases of normal values appear. You can replicate and then edit to create your own. Optionally, select a favorite for the application to utilize. Please note that for

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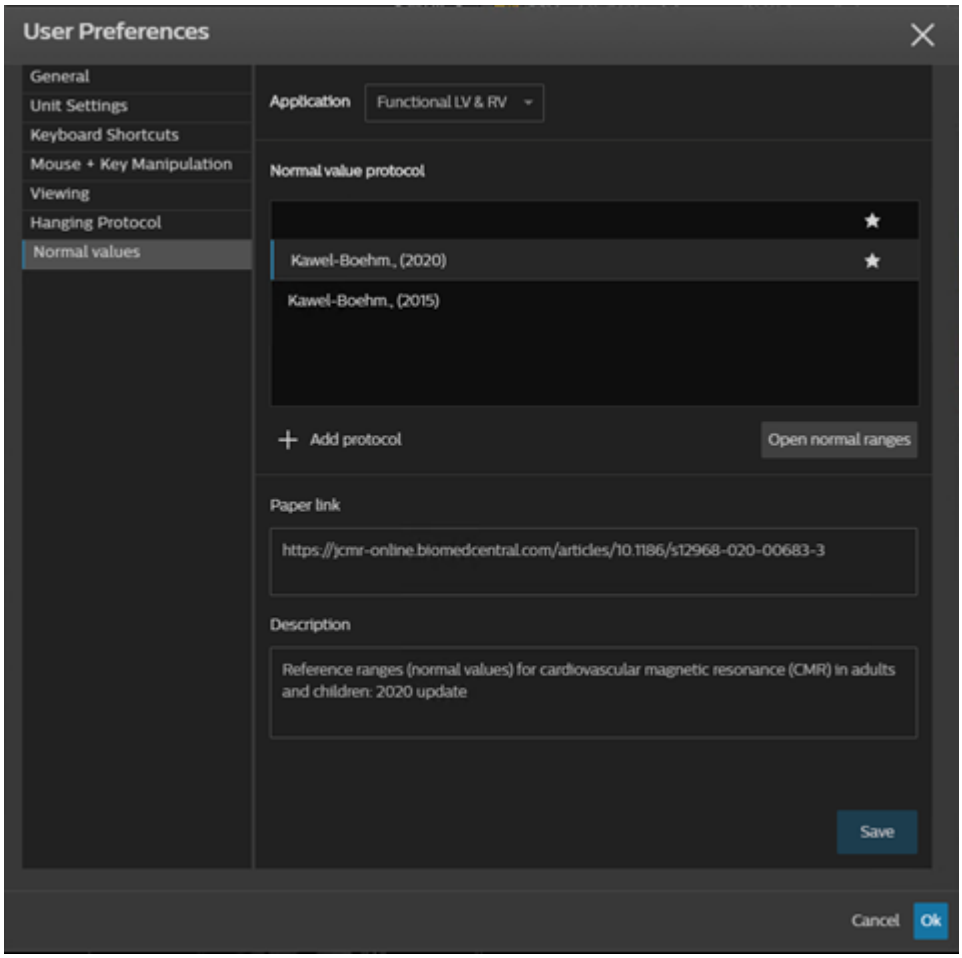
Mapping there are no predefined normal values, and you can define the normal values based on the site standards.

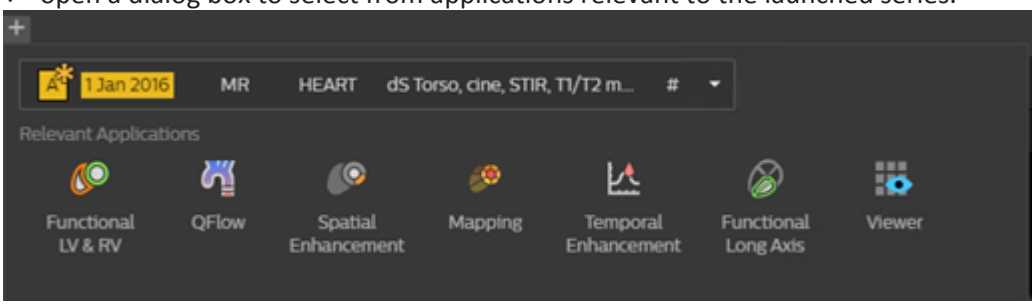


- Exit - close the suite.

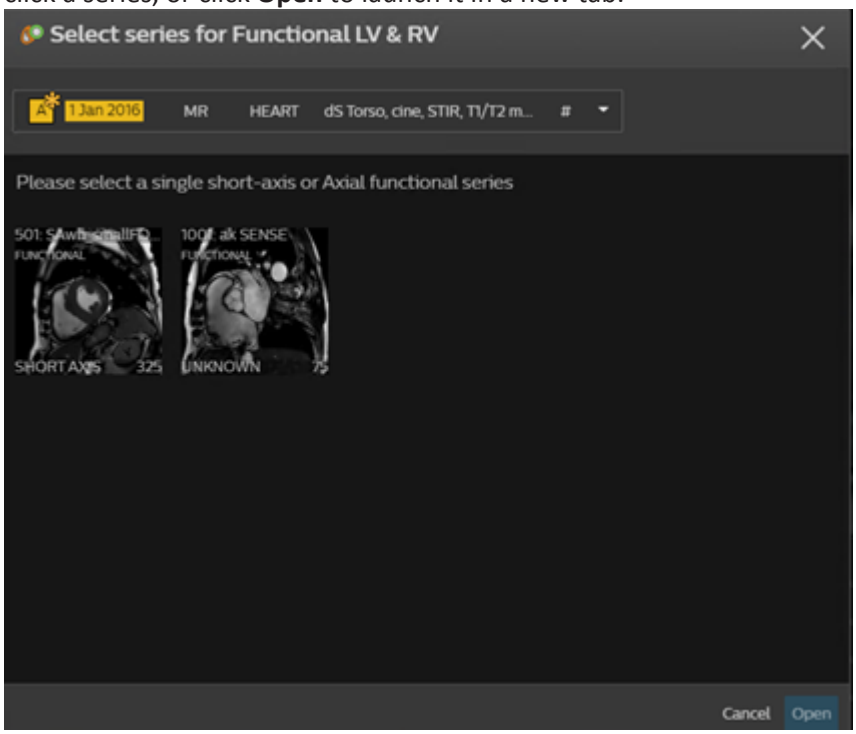
Application launch and navigation bar

Located under the suite title bar, this tab-based bar lets you launch, and navigate between, applications. To navigate to active applications, click the application icon. When you split the display, this bar appears twice.

- **+** - open a dialog box to select from applications relevant to the launched series.



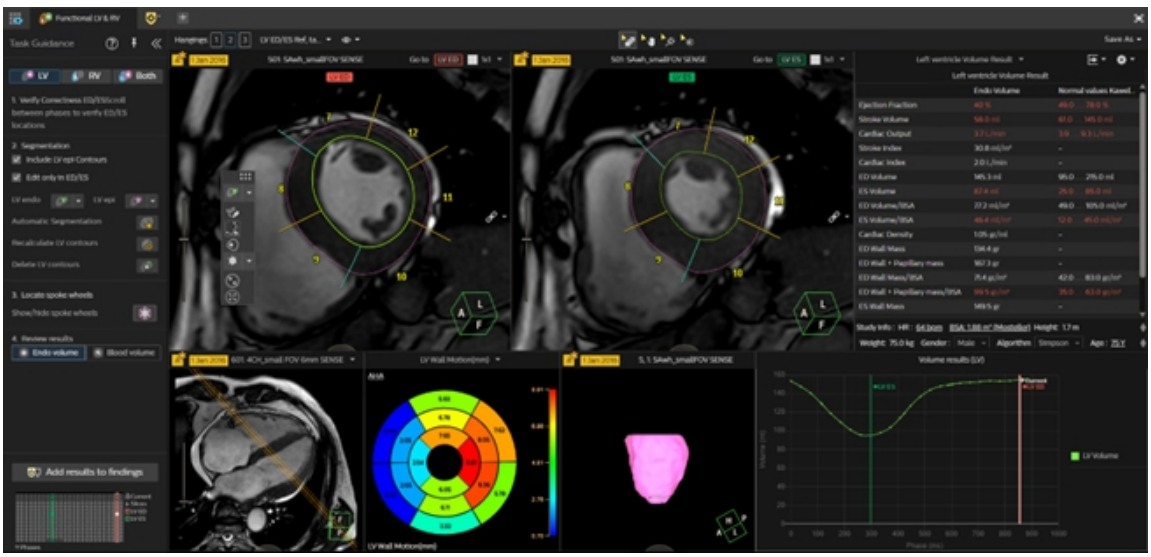
– If more than one series fit the selected application, another dialog appears where you select the relevant series, including prior studies for the patient, if available. Double-click a series, or click **Open** to launch it in a new tab.



– Some applications allow you to select multiple series, including 2CH and 4CH in Functional LA, Native and Enhanced in Mapping, and Rest Stress in Temporal.

-  Navigate to findings dashboard.

Application workspace



Each MR Cardiac Suite application contains the following workspace features:

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- An upper toolbar that contains:
  - **Hanging Protocol**
  - Viewing options
  - Mouse options
  - **Save as**
- Main display: includes the relevant images and additional viewports, such as tables and graphs, according the application.
- Application help button

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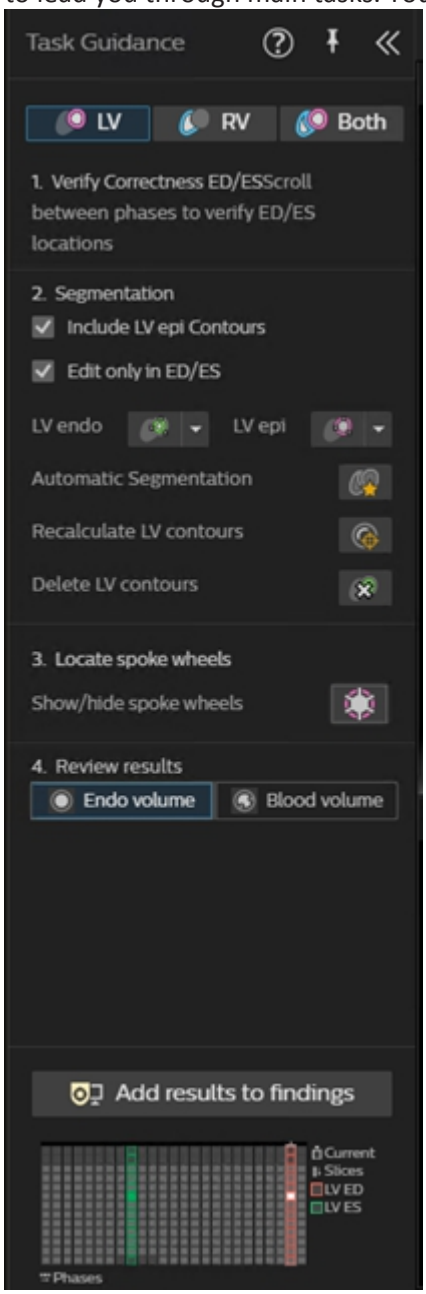
- **Task guidance**. A panel on the left side of the screen that shows optional, guided workflows to lead you through main tasks. You can collapse or expand it as needed.



- **Add results to findings**: located below Task Guidance. Click this once you complete your work.

Studies timeline

In MR Cardiac Suite, access the patient's imaging history from the timeline. The timeline contains the following components:

- Timebar – a chronological summary of the patient’s imaging history.
- Exam rack – all of the patient's exams in chronological order.
- Series rack(s) – all series that belong to the exams selected in the exam rack.

In order to see all series in a study, including priors, click **Studies** on the top-right of the suite title bar. This opens a timeline of all of the patient's studies in the AVW database. Select a study to see all series of that study.

Populate the Viewer

Access images to populate the Viewer:

1. Click the timebar to access the timeline.
2. On the exam rack, click an exam to open it. It is automatically assigned an identification icon, and the series rack opens below. If you click on an open exam, clicking it displays the relevant series rack.
3. To populate a series from the timeline, do either of the following:

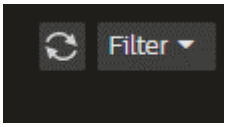
- Drag and drop the relevant series thumbnail into the required arrangement in the viewing area.
- Click the series thumbnail to populate the series to an empty viewport.

Populate an exam

Populate a full exam to the Viewer without going through the series one-by-one:

1. Click the timebar to access the timeline.
2. Drag and drop the relevant exam thumbnail into the viewing area.

Filter the timeline



You can filter timeline content based on Modality, Body Part, and Anatomical focus. There are several indicators that the timeline is filtered:

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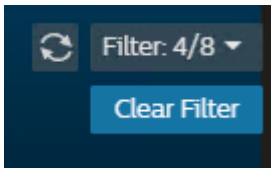
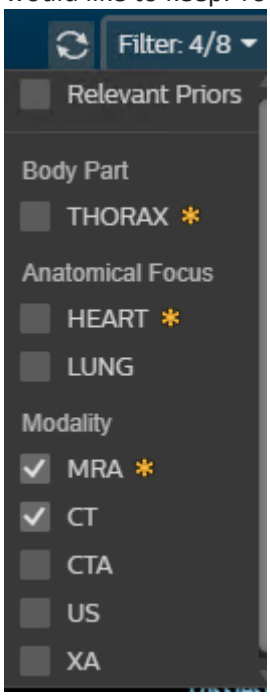
- The timeline background color changes.
- 

The **Clear Filter** button appears under the **Filter** button.
- The **Set Filter** button shows the number of visible exams out of the total.
- The exam rack lists the number of visible exams out of the total.

To apply filtering, do either of the following:

- Click **Set Filter** on the right side of the timebar. In the filtering panel, select the items you would like to keep. To exit the filtered view, click the **Clear Filter** button.



- In the timeline, right-click the exam you want to keep. Select either **Modality**, **Body Part**, or **Modality + Body Part** .

Exam information

When hovering over the exam card, a tool tip appears with exam details, including the first lines on the exam report's impression section. You can show the full report on the tool tip by adjusting your user preferences.

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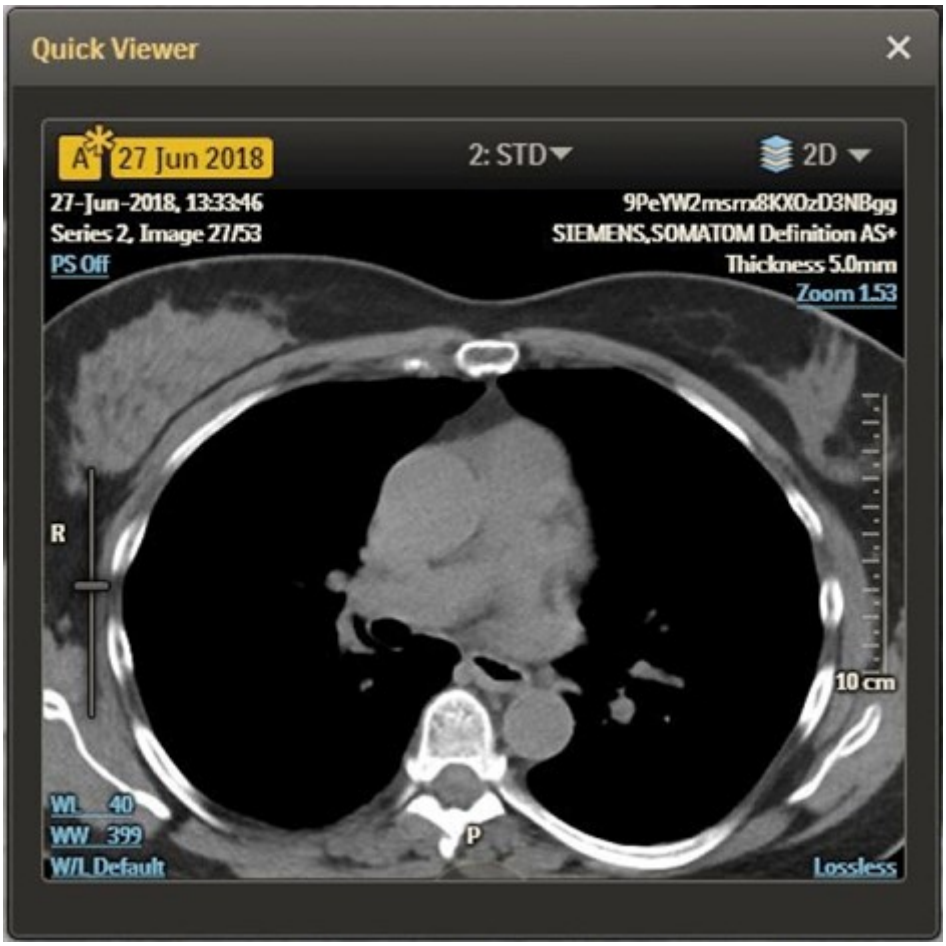
Quick Viewer



Double-clicking any series on the timeline opens a Quick Viewer. You can drag the Quick Viewer to any location in the Viewer, as well as resize it.

Label Data

When automatic labeling fails to recognize a series attribute critical to MR Cardiac Suite applications, on the suite title bar, click **Label Data** to open the **Labeling** dialog box. Here, you can modify any series attribute in the table, including **Scan Type**, **Orientation**, and **Rest/Stress**. The table also shows the number of phases, slices, and dynamics as identified by the application.

In the **Labeling** dialog box, you can filter series using the **Select** list menus, where you can also make multiple selections by pressing Control + Click.

Merge Series & **Split Series**

- Any change you make within a multiple selection is applied to all the selected entries.
- Any changes in labeling impact all users, so use caution.
- **Advanced Labeling** – a detailed review and modification of the entry fields.

- **Merge Series** and **Split Series** – you can split series that contain multiple orientations, such as multi-frame series.
  - For example, a temporal enhancement series might contain SA and 2CH planes. Splitting such a series allows you to label the image series of each plane individually. Additionally, some series from multi-vendor sources might be joined automatically. You can use the Split function to split these series.
  - To split a series, select the series in the series list, then click **Split** in the **Task Guidance** panel.
  - If you want to merge a series that has been previously split, select one of the split series, then click **Merge** in the **Task Guidance** panel.

Workflows

Create a new workflow

A workflow step can include either viewing hanging protocol, or an application with predefined preferences.

1. Launch relevant data. In the **Viewer**, prepare the first step, such as a hanging protocol, then open the **Workflow** list and click **+ Create new workflow**.
2. The **Save new Workflow** dialog box opens. Type the workflow name, for example, "Myocarditis", then click **Save**.
3. Launch the next application you want to use, for example, Functional LV/RV. Then configure that application according to your needs, for example, "Include in Analysis to show only LV Endo".
4. To the right of the **Workflow list**, open the steps list, then click **+ Add Step**. The **Save new Step** dialog box opens. Type the step name, then click **Save**.
5. Launch other applications to add them as steps.

Optionally, split the screen into two, and navigate each of them to another application. Go to the result stage, and save this as a step.

Edit a workflow

Right-click on a workflow in the **Workflow** list to:

- Rename
- Delete
- Mark it as public.

Right-click on a step in the steps list to:

- Rename
- Delete
- Overwrite it with the current launched state.
- Move that step up or down in the list.

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Use a workflow

Launch a study, then select a workflow from the **Workflow** list. Use the arrows to activate the steps. When a specific step does not fit the launched study, it appears grayed out and will be skipped.

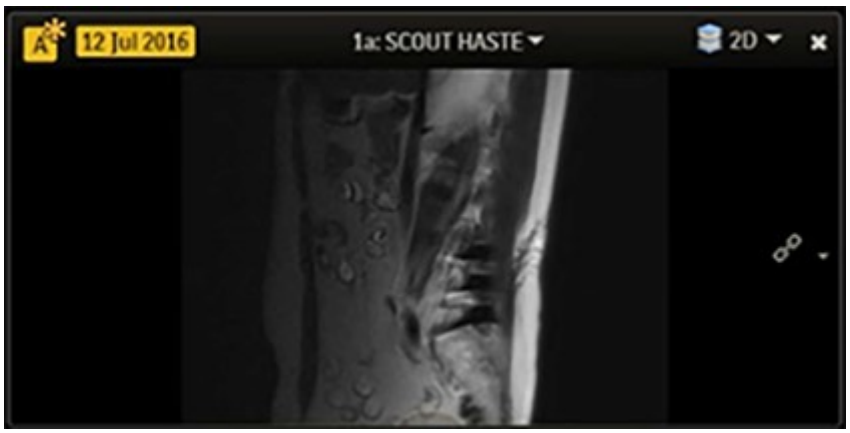
Viewer

In the MR Cardiac Suite **Viewer**, you can perform general viewing operations on all studies that you launch. You can select a grid layout or Hanging Protocols, and populate each viewport by either dragging a series, or by using the Quick Series Selector. You can also populate a layout with a full study.

Quick Series Selector

After you populate a series of a specific exam, you can access all series of that same exam, without using the timeline:

1. Click the series name in the center of the header.



2. Scroll through the list menu and select which series to view.

All Series Combined

In the Quick Series Selector, you can opt to view all series as a single arrangement. This allows you to scroll through all images of that exam, without populating each series separately.

1. From the header, activate the Quick Series Selector.

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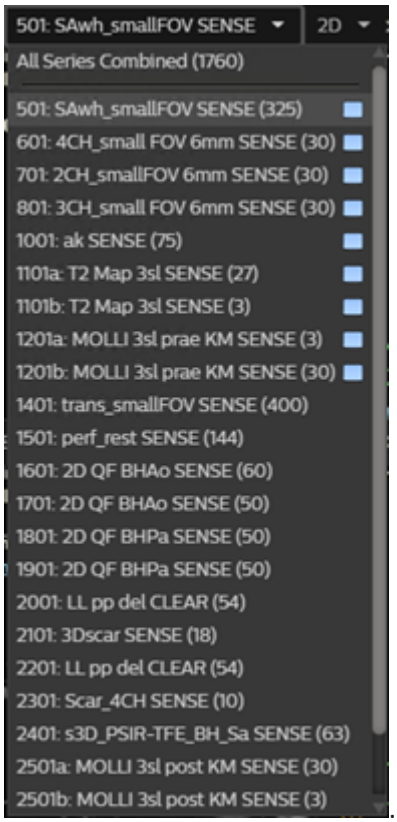


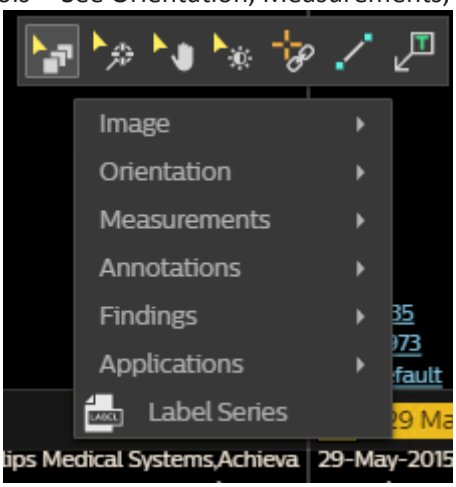
2. Select **All Series Combined**.

You can configure how CR/DX series are displayed in the **Viewer**. The default is a single series population from the timeline, where the Quick Series menu displays only that specific series.

Viewer context menu

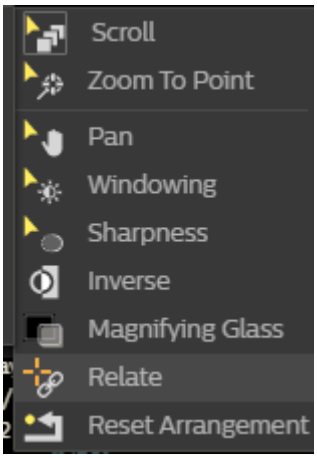
If you right-click a selected viewport, a context menu opens that contains:

- Viewing tools -- See Orientation, Measurements, Annotations, Findings, and Applications for details.



- Imaging tools -- Appear in a toolbar above the context menu, as listed in the table below.

Image

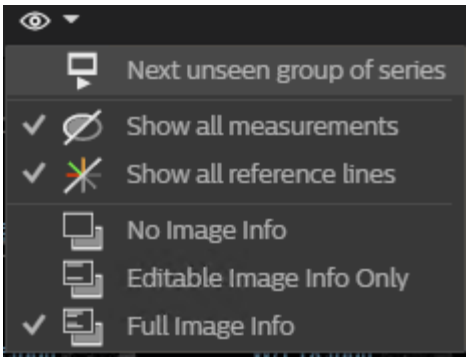


Icon	Tool	Description
	**Scroll**	Navigate between series images. • Vertical scroll enables navigation between slices. • For multi-dimensional data like CT or MR (e.g., perfusion, diffusion, etc.), vertical scroll navigates through the Z axis, while horizontal scroll navigates through dimensions. On the upper-left side of the image, you see a functional annotation of the phase you are in. You can manually change the phase to move to a different dimension.
	**Zoom To Point**	Zoom in and out of an image.
	**Pan**	Move the image within the display area.
	**Windowing**	Refine the image for viewing purposes. Functional Image overlays -- Depending on the modality, there is an annotation in the bottom left corner of the image. Click that annotation to either type in values or, for CT images, select from predefined values in the list menu. 
	**Sharpness**	Select the tool, then use your left mouse button to manipulate it on a selected image.
	**Inverse**	Invert colors on an image.

Icon	Tool	Description
	**Magnifying Glass**	Magnify regions of an image by moving over them. Resize for zooming and windowing.
	**Relate**	Align the volume in different orientations. Rotates the image 90 degrees to the right. 1. Select the tool. 2. Click on a point on the image to align. All relevant images align to the relevant location, and the **Relate** tool icon appears on the image to indicate the relate point. You can also toggle the **Relate** tool on and off by pressing **R**.
	**Reset Arrangement**	Revert zoom, pan, and windowing changes made to images.

You can also use the mouse and the arrow keys to manipulate images. For further information refer to section “Shortcuts” on page 198.

View Menu



The **View Menu** controls the display of the entire viewing area, including:

- Toggling the display of: reference lines, image information, and previously created measurements. This is useful when measurements are obscuring underlying anatomy, or if you want to interpret images without seeing previously created measurements.
  - **Show all measurements** - deselect to hide all existing measurements in the **Viewer**, but newly created measurements are displayed. Select to show all measurements in the **Viewer**.
  - **Editable Image Info Only** displays only adjustable information, such as zoom factor and windowing level. All nonfunctional information is hidden.

- Viewing the next or previous group of an unseen series
  - To display the next set of series belonging to the currently displayed exam, use the **Navigate to next group of series** keyboard shortcut (default: **M**).

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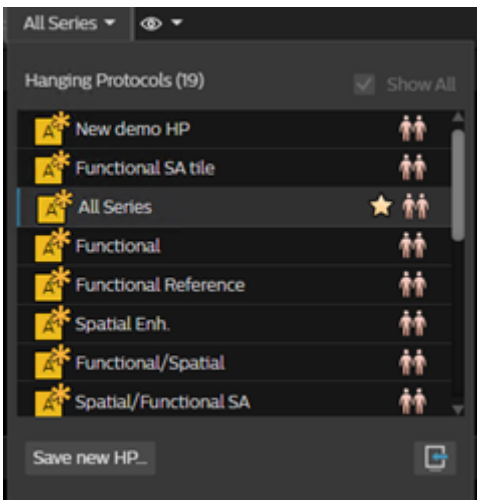
– To display the previous group of the series, use **Navigate to previous group of series** (default: **N**).

Scroll bar and Findings

A scroll bar appears on the left side of every arrangement that contains more than one image. Move the scroll bar up to move slices up, and move it down to move slices down. You can also use your mouse to scroll.

- You can navigate to **Findings** locations created for the patient, which appear as circles on the scroll bar. **Findings** created on the same series are marked with a full circle; **Findings** created on another series or another exam are marked with a dashed circle. A **Findings** hint displays all **Findings** that can be accessed by scrolling through the images, including those created on a prior exam.
- When multiple **Findings** appear next to each other, they appear as a single circle. Click on the circle to display the first finding. To navigate to a specific finding within grouped **Findings**, hover your cursor over the circle to display finding cards for all grouped **Findings**, then click the relevant card to display that finding.
- To populate a finding in any viewport, drag the finding card to a viewport.

Hanging Protocols



A Hanging Protocol enables you to hang exams according to your own specifications, so you can create efficient, individual reading workflows. For example, you can select a Hanging Protocol as the default for when you select similar exams to display in the **Viewer**. Only the user who

creates the Hanging Protocol can use the context menu to view, edit, rename, make public, inspect, and delete that protocol. In the **Hanging Protocols** tab, there are pre-existing protocols to choose from, but you can also create your own. The **Hanging Protocols** list displays the Hanging Protocols most suited to the current loaded exam, and any other exam displayed on the screen. Additionally, the application automatically generates hanging protocols based on data types, such as ”All functional”, “All spatial”, etc.

Create a new Hanging Protocol (HP):

1. Select a series to display.
2. Set a layout, viewing mode, and tiling mode for each viewport.
3. Click the **Hanging Protocols** tab to open the **Hanging Protocols** window.
4. Click **Save new HP....**. The **Save new Hanging Protocol** dialog box opens.
5. Type a name for the Hanging Protocol.
6. Select applicable check boxes.
7. Click **Save**.

Generic Hanging Protocol

An “All series” Hanging Protocol (HP) is a protocol that automatically displays series from the exam according to their order in the timeline. "All series" HP limit the number of viewports per modality, so that images are not too small. If the last viewport is populated, there may be series in the exam that are not displayed.

You can select the default "All series" HP layout, and maximum number of viewports, in **User Preferences**, where you can also select whether:

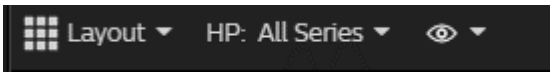
- The "All series" HP loads relevant priors by default (per modality).
- The relevant prior is loaded in Compare mode.
- To exclude non-clinical images, such as Scouts and Reference images, from "All series" HP.

When you activate an "All series" HP, the default layout for the loaded modality is applied. Alternatively, you can automate the layout according to the number of series in the exam if you select **Auto layout** in **User Preferences**.

Activate a Hanging Protocol:

1. Click the **Hanging Protocols** tab. The **Hanging Protocols** window opens.
2. Optionally, hover your mouse over a Hanging Protocol to display a preview.
3. Click a Hanging Protocol to activate it.

Layouts



Select a grid that divides the **Viewer**. On the top-left bar, click **Layout**.

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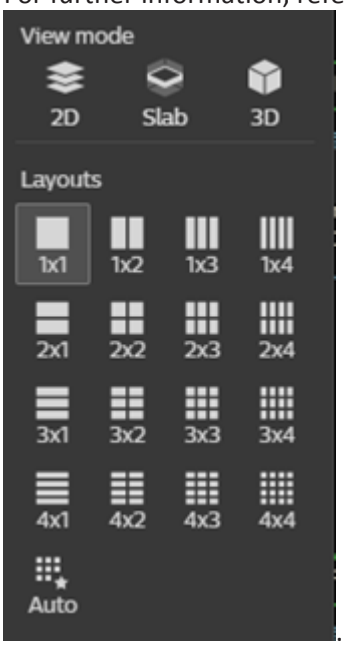
For arrangements that include a series with multiple images, you can select the internal layout on the right side of the **Viewer** title bar. In this panel, you can also switch to either **Slab** or **3D** (volumetric) mode. On multi-dimension series' tile view, you can select which dimension to tile. For further information, refer to **Viewing modes**



Linking

You can link between series to scroll, zoom, and pan series together while showing the same anatomy in both images. The series may be from the same exam, where the link shows a slice from the same spatial position, or from different exams, where the link is based on registration algorithm results.

WARNING

The correctness of a link between series should be reviewed.

When layout is in **Slab** or **3D** viewing modes, the link also maintains the same orientation in all series. When populated, the displayed series are divided into link groups according to whether they are on the same spatial space, or are registered. The chain icon appears on the viewport of each series that belongs to the link group of the current, active series:

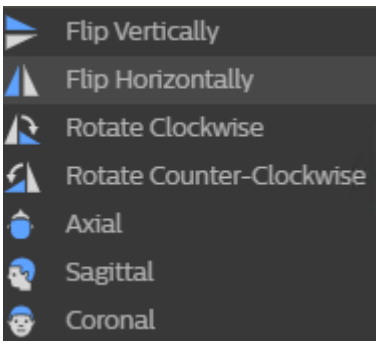
-  The series participates in a link group with the currently-active series.
-  The series participates in a link group with the currently active series, but all links were broken.

Scroll, zoom, and pan manipulations are not synced to another series within the link group.

For further information, refer to **Link menu**.

Orientation

In the **Viewer** context menu, click **Orientation** to manipulate image orientation with the following tools:



Icon	Tool	Description
	Flip Vertically	Flip the image 180 degrees vertically.
	Flip Horizontally	Mirror- flip the image left to right.
	Rotate Clockwise	Rotates the image 90 degrees to the right.
	Rotate Counter-Clockwise	Rotates the image 90 degrees to the left.
	Axial	Change the main image to axial orientation.
	Sagittal	Change the main image to sagittal orientation.
	Coronal	Change the main image to coronal orientation.

Use the **Axial**, **Sagittal**, and **Coronal** tools to change the image orientation of the main image in volume viewing, **Slab** and **3D**, modes.

NOTICE

When activating these tools in 2D viewing mode, the arrangement will switch to Slab viewing mode and apply the selected orientation.

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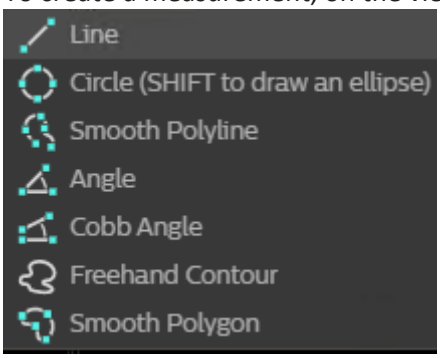
Measurements

Measurement tools enable you to quantify distance, angle, area, and volume.

To create a measurement, on the viewport's context menu, click **Measurements**.



Then select a tool to draw a measurement on the image.

Measurements appear on the images and can be edited and deleted at all times after creation.

Line

Measure the distance between two points. To create a measured line:

1. Click the image to create a start point.
2. Click the image again to create an end point.
3. A line is created. Optionally:
   - Display grab points by hovering over the line. Click a grab point to drag it to another location.
   - Move the line by hovering your cursor over it, then moving your cursor towards the middle of the line. The cursor changes to the  Move icon. Click the icon and move the line.

Smooth Polyline

Measure the distance of a curved line:

1. Click on the image to create a start point for the line.
2. Click on the image again to add a connection point.
3. Double-click on the image to create the end point.
4. A smooth polyline line is created. Optionally:
   - Display grab points by hovering over the line. Click a grab point to drag it to another location.

– Move the line by hovering your cursor over it, then moving your cursor towards the middle of the line. The cursor changes to the  Move icon. Click the icon and move the line.

Circle/Ellipse

Measure a region with a circle by default, which you can change to an ellipse via keyboard shortcut.

Create a circle measurement:

1. Click on the image to create a start point.
2. Click on the image again to create an end point.

Create an ellipse measurement:

1. Select the  Circle tool.
2. Hold SHIFT while you click the image to create a start point.
3. Click the image again to create an end point.

Edit the circle/ellipse:

Hover over the circle/ellipse to display grab points. Click a grab point to drag it.

Move the Circle/Ellipse Measurement

Move the circle/ellipse by hovering over it with your cursor, then moving towards the middle of the line. The cursor changes to the  Move icon. Click the icon to move the measurement.

Angle

Measure an angle between two connecting lines:

1. Click the image to create a start point for the first line.
2. Click the image again to create an end point for the first line.
3. Click the image on the start point to create a second line.
4. Click the image again to create the end point for the second line.
5. An angle measurement is created. Optionally:
   – Display grab points by hovering over the line. Click a grab point to drag it to another location.

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- Move the line by hovering your cursor over it, then moving your cursor towards the middle of the line. The cursor changes to the  Move icon. Click the icon and move the line.

Cobb Angle

Measure an angle between two non-connecting lines:

1. Click the image to create a start point for the first line.
2. Click the image again to create an end point for the first line.
3. Click the image on the start point to create a second line.
4. Click the image again to create the end point for the second line.
5. An open angle measurement is created. Optionally:
   - Display grab points by hovering over the line. Click a grab point to drag it to another location.
   - Move the line by hovering your cursor over it, then moving your cursor towards the middle of the line. The cursor changes to the  Move icon. Click the icon and move the line.

Freehand Contour

Measure an area by drawing closed contours:

1. Click and drag the mouse to create a freehand contour.

Smooth Polygon

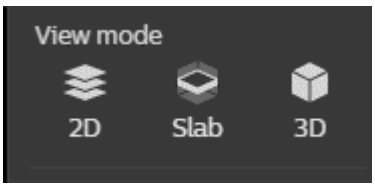
Measure an area by creating closed contours using control points:

1. Click the image to create a start point for the line.
2. Click the image again to add a connection point.
3. Double-click the image to close the polygon.

3D Segmentation

Segment an area on CT/MR images to measure the volume and main diameters.

3D Segmentation can be used only on volumetric CT/MR datasets and is performed in **Slab** mode. When **3D Segmentation** is activated in 2D mode, the viewport automatically changes to **Slab** mode.



Create 3D Segmentation in Slab view:

1. Position the center of the contour in the center of the lesion.
2. Hold the Shift key while using your mouse wheel to modify the contour size, until it matches the boundaries of the lesion.
3. Click the left mouse button to create a 3D Segmentation.

CAUTION

Verify correctness of the contour on all three views (Axial, Coronal, and Sagittal) before creating the 3D Segmentation.

To create **3D Segmentation** using only your mouse:

1. Position the center of the contour in the center of the lesion.
2. Hold down the left mouse button while you drag your cursor to the boundaries of the lesion.
3. Release the left mouse button.

Tips for successful segmentation

1. 3D Segmentation is best performed when there is a contrast between the lesion and its surrounding tissue. In order to improve the accuracy of 3D Segmentation, modify windowing levels so that there is maximum contrast between the lesion and its surroundings.
2. 3D Segmentation accuracy is optimal when slice thickness is small (2mm or lower) and the distance between slices is small (2mm or lower).
3. It is possible to create 3D Segmentation using any orientation. Use the orientation where the lesion is largest, for optimal results.

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4. During segmentation, all orientations are centered around the anatomy that is selected by the mouse cursor. Use scroll and mouse movements to focus on the center of the lesion before changing size and creating the segmentation. After you complete segmentation, the system will calculate the following:

   – Volume (cm3)
   – Long axis – the longest diameter of the segmented lesion, in the orientation of the original slices. Appears on the slice where the longest diameter is detected.
   – Short axis – the longest diameter of the segmented lesion, which is perpendicular to the long axis. Appears on the slice where the longest diameter is detected.

Edit an existing 3D Segmentation:

1. Switch viewport to **Slab** rendering mode.
2. Click on the 3D Segmentation color tissue.
3. Use the left mouse button to hold and move the contour of the 3D Segmentation. Release the mouse button when the contour is on the edge of the lesion.

CAUTION

To ensure correct volumetric measurement, verify the correctness of segmentation in all images of the lesion. Scroll up/down to verify the segmentation is accurate and edit as needed.

Delete an existing 3D Segmentation in 2D/Slab view:

1. Click the 3D segmentation label (Volume: XXX cm3).
2. In the **Findings** panel, click **Delete Finding**.

Delete an existing 3D Segmentation in Slab view only:

1. Click the 3D segmentation color tissue to enter Edit mode.
2. On your keyboard, press **Delete**.

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Annotations

Icon	Tool	Description
	Pixel Value	Measure the value of a specific pixel: 1. Select the tool. 2. Click a point on the image to measure the pixel value. 3. A measurement is created. 4. Hover over the angle measurement to highlight it and display grab points. 5. Click on a grab point to drag it.
	Arrow and Text	Enable an arrow annotation for marking and free text: 1. Select the tool. 2. Click a point on the image to create the arrow head. 3. Click the image again to create an end point for the arrow line. 4. Optionally, add text to the arrow: – Double-click the new arrow annotation. A text box opens. – Enter text, then click outside the box to save the text. 5. Click outside the box to close it. Move an arrow annotation: 1. Hover over the arrow to highlight it and display grab points. 2. Click a grab point to drag it. To edit text, click the text box. To add text, highlight the arrow and double-click. Move the arrow and text box: 1. Hovering over the arrow and text box while moving your cursor towards the middle of the line. 2. The cursor changes to the  Move icon. Click to move the arrow and text box.

Findings

Icon	Tool	Description
	Add to Findings Dashboard	Save the selected image to the exam's **Findings** list. For further information, refer to the **Scroll bar** section of **Viewer**.
	Export Image	Export an image to save locally.

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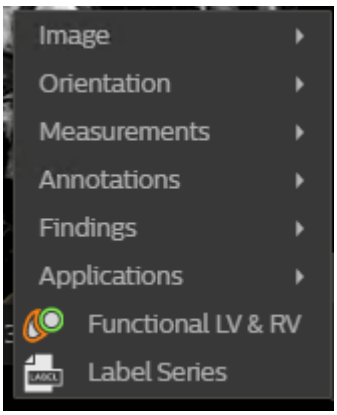
Applications



In the **Viewer** context menu:

- Any MR Cardiac Suite applications relevant to that series are displayed, for example **Functional LV/RV**.

  It is also possible to launch CCA when the context menu is on a valid CTA series. CCA then launches as an Analysis application inside AVW.
- From the **Applications** submenu, you can launch small applications, called Inspection modes, on top of the Viewer. The following inspection modes are only available when relevant to the data type on either an image- or pixel- level:

NOTICE

Tools appear only when relevant.

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Icon	Tool	Description
	**Analysis local vessel**	A simplified local visualization for evaluating blood vessels on CT & MR. A quick analysis of a vessel. Basic measurements are available. Opens the **Quantification Inspector** window, which contains: • Coronal view -- appears on the left side, and shows the location of the point of interest. Reposition the lesion point by grabbing it and placing it on any other area of that vessel, or a different vessel. All other viewports will adjust to the new location and update accordingly. • Cross-sectional view -- appears in the top right panel, and shows the cross-sectional image of the point of interest, together with some basic measurements. Scroll this view to move the measurements along the vessel to analyze the area of interest and its surroundings. • Longitudinal view -- appears in the lower right panel, and shows the longitudinal view with reference to the cross-sectional point. • **Add as Finding** button -- appears in the lower area of the **Quantification inspector**. Saves this instance of the view to the **Findings** list of this exam. You can activate this finding to get back to the same state as when you marked it as a finding.
	Prior Comparison	Available only if there is a matching series in relevant priors for this patient, as calculated from the series and pixel area. Quickly view a specific anatomical location in relevant prior exams. Opens the **Comparison inspector** that displays suggested relevant priors. To select a different series to compare with, use the **Quick Series Selector** from the top of the relevant prior and select a series. Drag-and-drop a series from the timeline to the arrangement in the **Comparison inspector** view.
	Compare series	Available only if there is another relevant series in the same exam, as calculated from the series and pixel area. Quickly view a specific anatomical location in multiple series of the same exam. Opens the **Comparison inspector** that displays suggested series. When there are other relevant series, click **Next** or **Previous** to invoke the different sets and compare within the exam. To select a different series to compare with, use the **Quick Series Selector** from the top of the relevant arrangement and select a series. Drag-and-drop a series from the timeline to the arrangement in the **Comparison inspector** view.

Tab. 11: Inspection modes you can activate from the **Applications** submenu:

Shortcuts

Mouse operations

You can access basic viewing tools using the mouse buttons:

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Tool	Mouse Shortcut
Fast scroll	Left mouse button
Slow scroll	Mouse wheel
Viewer context menu	Right mouse button
Windowing	Middle mouse button
Pan	Middle mouse button + left mouse button
Zoom	Middle mouse button + right mouse button
Swap arrangements	Right mouse button + drag and drop to the desired arrangement
Context Menu	Right mouse button

NOTICE

Mouse manipulations can be customized to any combination of mouse keys.

Additional User Preferences

Fast scroll speed bar determines the responsiveness of fast scroll, and allows reduced skipping of slices.

Accelerated wheel scroll bar determines the responsiveness of the mouse wheel; if the rate is increased, slices may be skipped.

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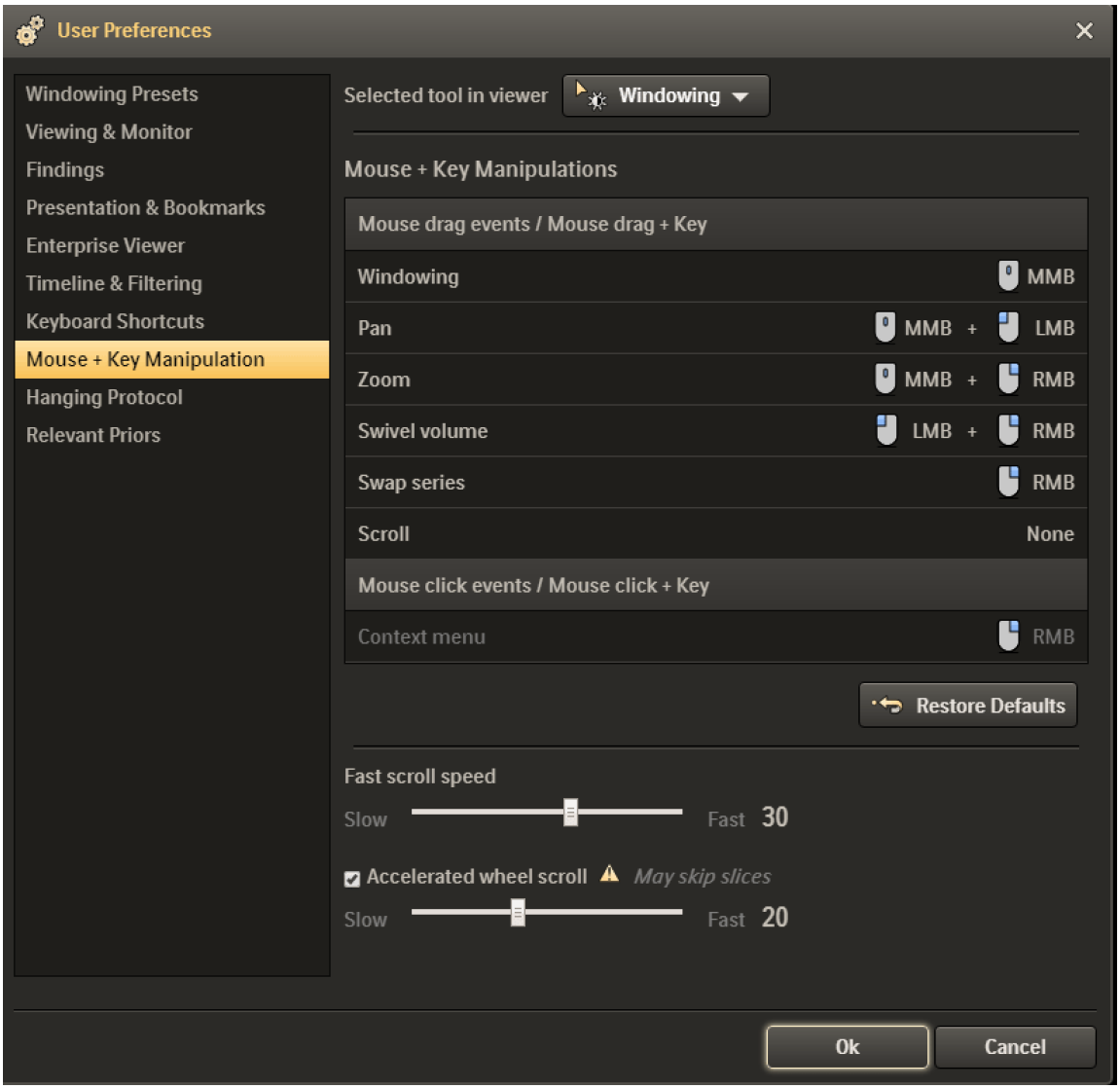

Keyboard shortcuts

Keyboard shortcuts that appear with **None** in the list below do not have a predefined shortcut, but can be configured.

Personal keyboard shortcuts can be configured in the **User Preferences** panel.

Functionality	Tool	Keyboard shortcut

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Series Navigation	Scroll slice up/down	Up/Down arrows
	Scroll to different dimensions	Left/Right arrows
	Jump to first slice	Home
	Jump to last slice	End
	Navigate to next series in same exam	**.** (period)
	Navigate to previous series in same exam	**,** (comma)
	Populate next unseen series in current exam	U
	Reset Unseen Series in exam	Shift + U
	Navigate to next group of series	M
	Navigate to previous group of series	N
	Navigate to previous workflow step	
	Navigate to next workflow step	
	All Series Combined	None

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Viewing	Revert from maximized view	Esc
	Volume rendering - Average	Shift + D 1-5, 7 where 1=Average, 2=MIP, 3=VIP, 4=MinIP, 5, 7=SurfaceMIP
	Move to Slab view	Shift + M
	Move to 3D view	Shift + V
	Zoom in/out	+/- (Add/Subtract)
	Hide/Show measurements	Shift + H
	Hide/Show grid	G
	Toggle Relate mode	R
	Play/Pause Cine	Pause-Break
	Move to 2D view	Shift + S
	Monitor Setup	Shift + F10
	Spine Labeling	Alt + S
	Enable CLAHE	Alt + C
	Link All	L
	Link Exams	E
	Maximize/Minimize	None
	Show/Hide reference lines	None
	Restore Default Link	None
	Link/Unlink Me	None
	Scroll	None
	Zoom	None
	Zoom to Point	None
	Pan	None
	Windowing	None
	Magnifying Glass	None
	Reset Arrangement	None
	Full Image Information	None
	Editable Image Info Only	None
	No Image Information	None
	Invert Gray Scale	None
	Sharpness	None
	Rotate Counter-Clockwise	None
	Rotate Clockwise	None
	Flip Horizontally	None

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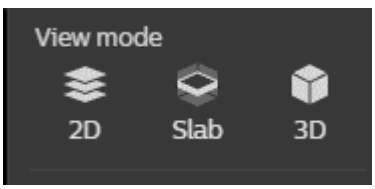
Viewing Slab/3D	Windowing (CT only)	1, 2, 3, 4, 5, 6, 7, 8, 9, 0
	Volume image background color (CT only)	B
	Flip volume image	D
	Rotate volume image	Left/Right arrows
	Move to Axial view	A
	Move to Coronal view	C
	Move to Sagittal view	S
	Target Volume	None
	Bounding Cube	None
Findings	Add as finding	Space
	Navigate between findings	Shift + Z
	Export Image	None
Reports	View Report	None
Measurements	Calibration mode	None
	Arrow + Text Annotation	None
	Pixel Value	None
	Line	None
	Line (Persistent)	None
	Smooth Polyline	None
	Circle	None
	Ellipse	None
	Angle	None
	Cobb Angle	None
	3D Segmentation	None

Viewing modes

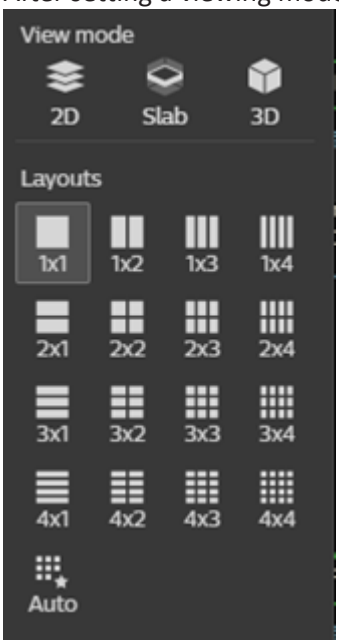


You can view volumetric images in three different viewing modes:

- 2D

- Slab
- 3D

After setting a viewing mode, you can change the inner tiling of the arrangement.



Changing viewing modes

To change the viewing mode:

1. Click on the **Viewing mode** button on the left side of the arrangement header. A menu opens.
2. Select a viewing mode: **2D**, **Slab** (Standard or Planar), or **3D**.

2D viewing mode

You can view the original, acquired images.

Changing inner tiling

The **View mode** you select affects the available inner tiling **Layouts**.

To change the inner tiling of the arrangement:

1. Click **View mode** on the left side of the arrangement header. A menu opens.
2. In the menu, select the inner tiling.

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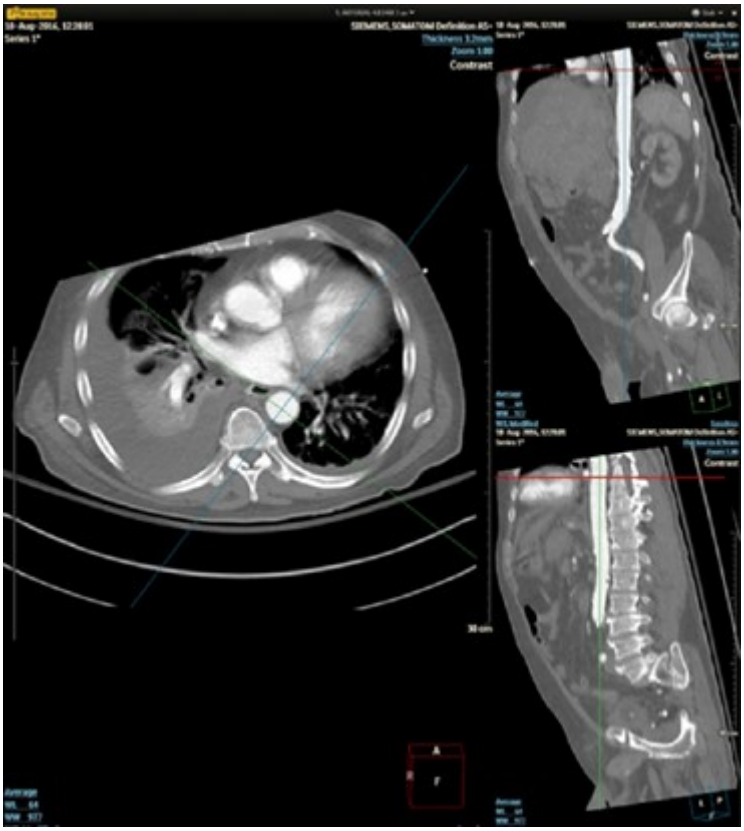
Slab viewing mode



- **Slab Standard**: Vew and manipulate slab images. The two reference images show orthogonal axis orientations (regardless of slab rotation in the main image). Color-coded crosshairs in the reference images indicate that the orthogonal axes: axial (red), coronal (green), and sagittal (blue). Only the axial (red) crosshair can be rotated.

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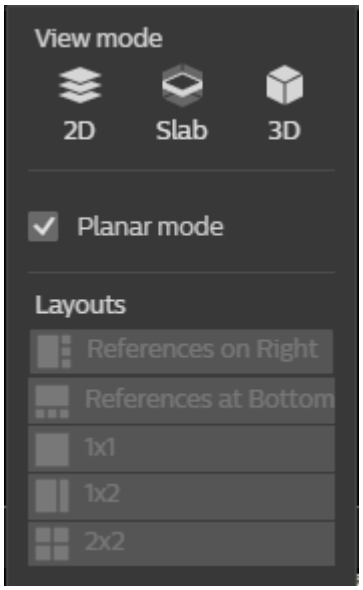
- **Slab Planar**:



An alternative mode of displaying the three orthogonal views in three viewports. There is no “main” or Slab image. Each image can be manipulated independently, while the axes remain oriented at 90 degrees to each other. Crosshairs appear on all three planar viewports, and can be moved and rotated. The crosshairs mark the rotational center in Planar mode, around which views can be rotated. Changing the rendering and thickness in one Planar viewport affects all viewports.

Planar Mode

Activate **Planar mode** by selecting the checkbox:

You can manipulate each image independently, while the axes remain oriented at 90 degrees to each other. Crosshairs appear on all three planar viewports. They can be moved and rotated. The crosshairs mark the rotational center in **Planar mode**, around which the views can be rotated. Changing the rendering and thickness in one Planar viewport affects all viewports.

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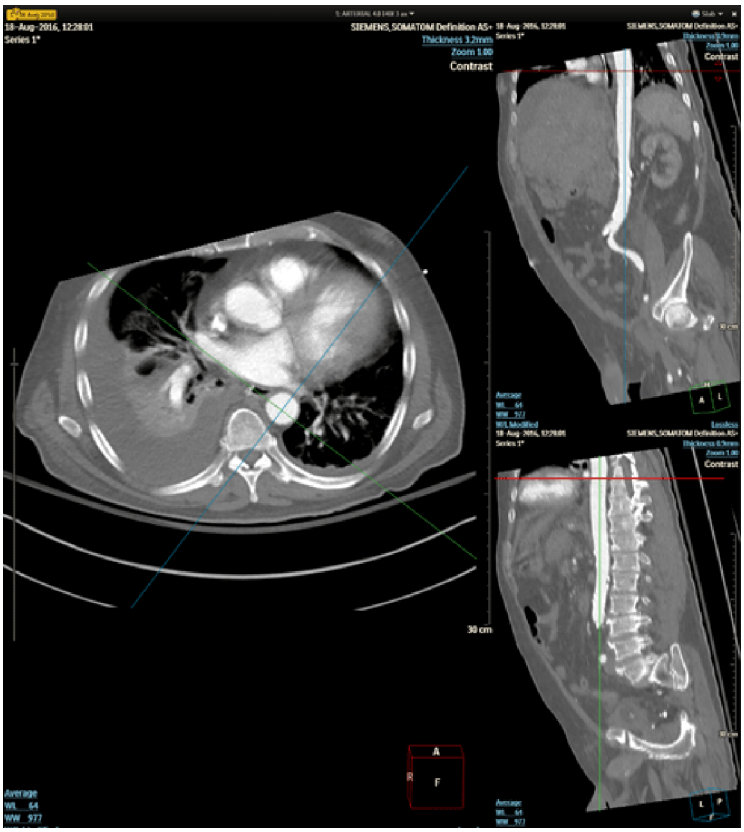
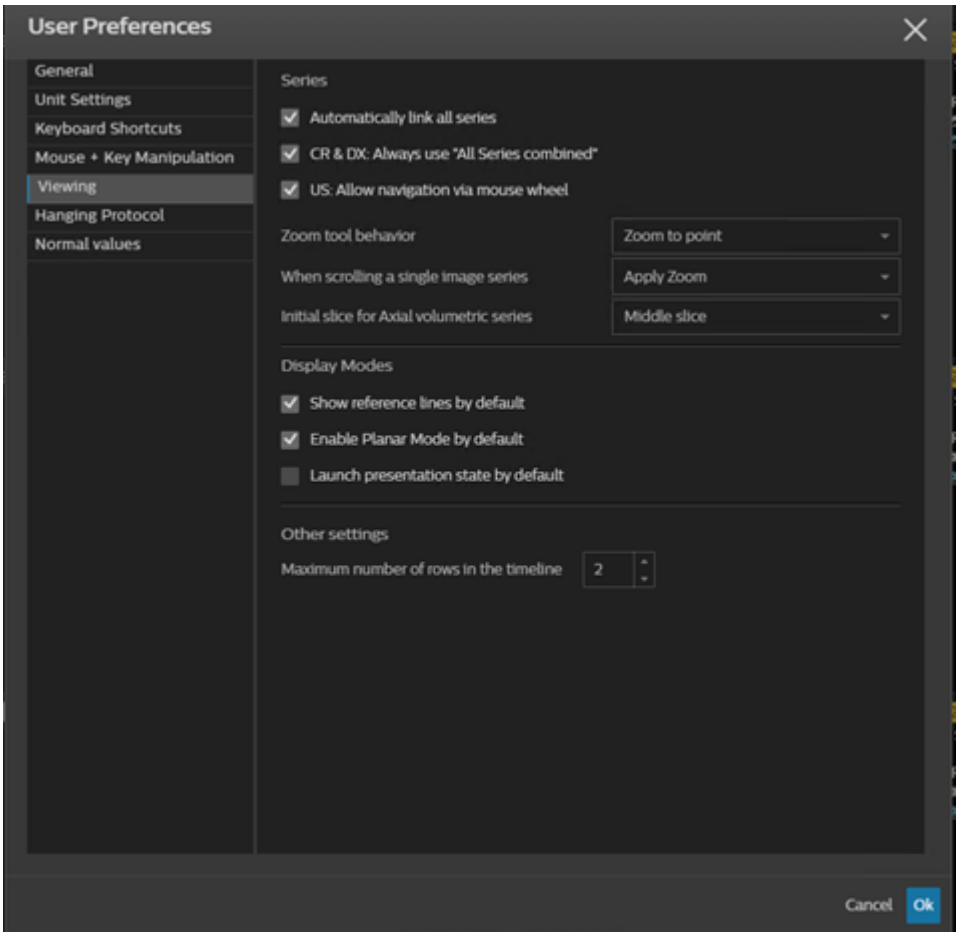


To set **Planar mode** as the default **Slab** mode, go to **User Preferences** > **Viewing**. In the **Planar Mode** area, select the **Enable Planar Mode by default** checkbox.



3D viewing mode

View a 3D volume-rendered image, with three reference images.

There are dedicated clipping functions, such as:

- **Target Volume**: segment large, complex volumes (such as the heart and aorta).
- **Bounding cube**: analyze small objects (such as neuro vessels). This resembles **Target Volume** and is a quick method for focusing on an object.

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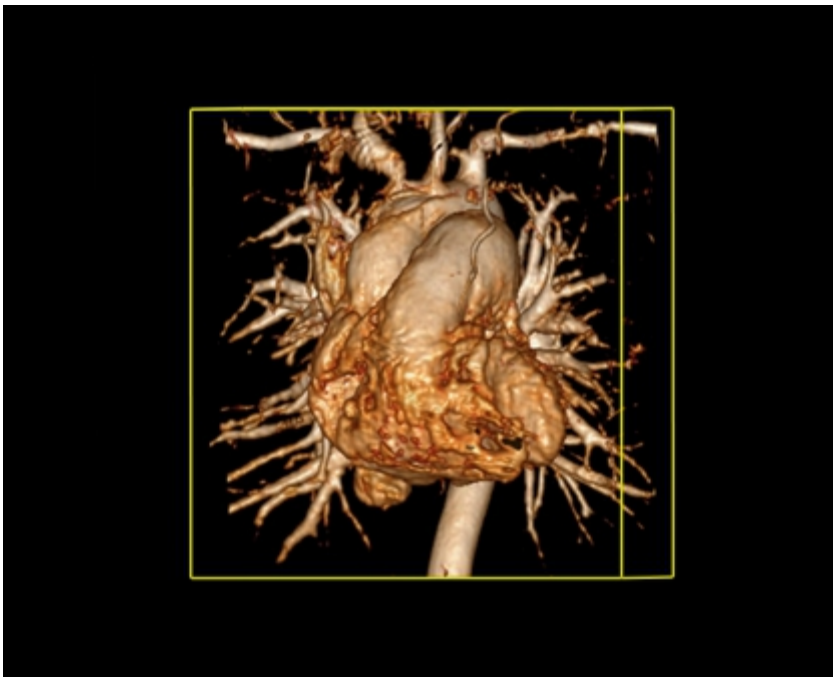
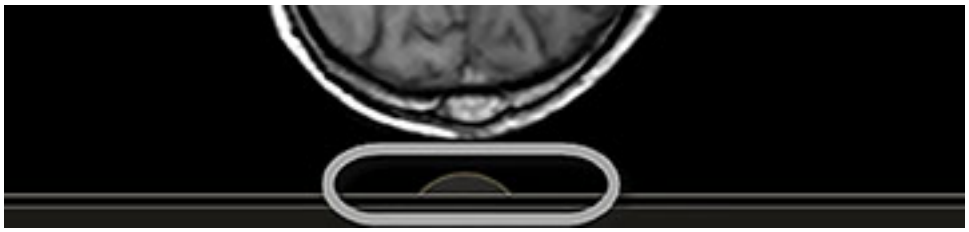


Cine/Movie bar

The Cine tool allows easy navigation through exam and series images without the need to go to the timeline. For single frame data, the Cine is hidden by default, whereas for multi-frame data, the Cine tool is applied automatically and images play to show an easy view of the acquisition. The Cine tool is available in the lower area of every arrangement and applies only to that arrangement.

To run the Cine tool:

1. Hover over the Cine tool hint in the lower central area of the arrangement to display the Cine tool.



2. 

Click **Play** to start scrolling slices.

3. 

Click **Pause** to pause scrolling slices.

4. 

Click **Next** or **Previous** to move only one slice at a time in the required direction.

5. 

Click **Nex**t or **Previous** series to move through the series of the same exam.

6. 

Click **Frame per Second** to adjust the scrolling rate, and adjust the speed bar to the required speed rate.

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7. 
   Pin the Cine bar so it remains visible in this arrangement without reverting to being hidden.

NOTICE

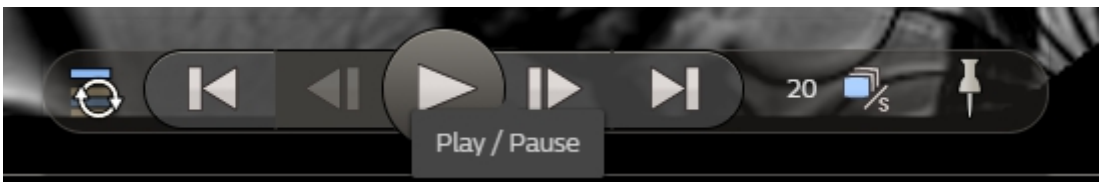
When loading multi-frame data, the Cine tool is pinned automatically.

Scrolling

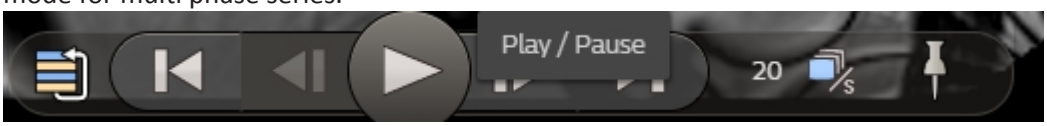
The Cine widget supports multidimensional sequences by allowing continuous scroll of multi-dimensional series (such as Cardiac MR multi-phase).

For multidimensional sequences, a dedicated icon is available to the left of the Cine widget, where there are two modes available:

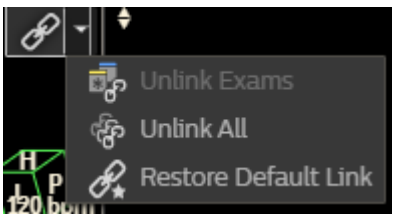
- **Play phases for this location only.**



- **Play phases for all locations.** This allows continuous Cine within phases of a certain location, and then automatically moves to the next in a sequential order. This is the default mode for multi phase series.



Link menu



The Link menu contains:

1. **Unlink Exams** – breaks the link in order to fix a bad registration between exams, or in order to scroll each exam series without also scrolling the other exam simultaneously. Available only when multiple exams are shown on a layout. When only a single exam is shown, or if you previously selected **Unlink All** , this option is not available.
2. **Link Me** – when the default state is **Unlink All** and you want to link only specific series.

3. **Unlink All** – break all link groups in order to scroll a series independently within an exam, or fix the alignment of a series within the same exam. This option breaks the link between exams as well as within each exam, so each series will scroll on its own.
4. **Restore Default Link** – reset link groups to system default as if loading the exam again. Link groups are reset, and the shown location is reset to correlate with the currently active viewport.

Breaking and editing links

It may be necessary to break a link if:

- You are dissatisfied with the registration results, and suspect that scrolling one series results in wrong slices on the other series.
- You want to pause an image on a specific anatomical location, such that it does not scroll away by changing the location of other displayed series.

To break a link, and then optionally align slices to more correct anatomical locations:

1. Click the **Link** icon to break links between exams, or from the **Link** list menu, select **Unlink All**.
2. Optionally, scroll, zoom, or pan images until they show the same anatomical location and the images are aligned.

   Then click the **Link** icon again to link this specific location. It is saved as the current link, and any scroll to either viewport will maintain the relative difference, in order to keep showing matched anatomical locations on all viewports.

Restoring default links

After breaking or editing a link, it may be necessary to return to the application's default links to show images as when the exams were first loaded. To restore default links:

1. Display the list menu by hovering your cursor over the **Link** icon.
2. To restore all links, select **Restore Default Link** from the menu. Links are now on their anatomical matching location, according to registration results.

Functional LV & RV Analysis

Indications for Use

The MR Cardiac Suite Functional Left Ventricle & Right Ventricle (LV&RV) application is indicated to support users with assessment of LV and RV function using multi-slice short axis and axial cardiac MR cine data.

Overview

MR Cardiac Suite application Functional Left Ventricle & Right Ventricle (Functional LV & RV) allows volumetric analysis of both the left and right ventricles.

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The application calculates cardiac functional parameters such as volumetric parameters, wall motion, wall thickness, and thickening. You can configure the result tables, and the values indexed by Body Surface Area (BSA). You can report each parameter based on a normal range that you define, and report wall characteristics based on a 16-segment AHA model. You can collect, save, and export both manually- and automatically-calculated results in a Findings Navigator. For short axis, the application launches with contours, spokes, and polar maps positioned and initiated using the AHA model by default.

NOTICE

To perform segmentation correctly, the analysis package requires multi-slice, multi-phase images.

Auto Preprocessing

LV and RV segmentation:

- is performed automatically when a series is imported to Advanced Visualization Workspace from either a scanner or PACS. The results are saved in the **Patient Directory**.
- segments all volumes of short-axis, multi-slice multi-phase series, and saves the registered series with the study.

When you launch the application from the **Patient Directory** for a patient with preprocessed LV and RV segmentations, the application displays LV RV analysis with both endo and epi contours for LV, and the endo contour for RV.

Manual Processing

To process a cardiac MR series manually before loading it in the application, right-click the series, click **Run Processing**, then select **fCMR Preprocessing**.

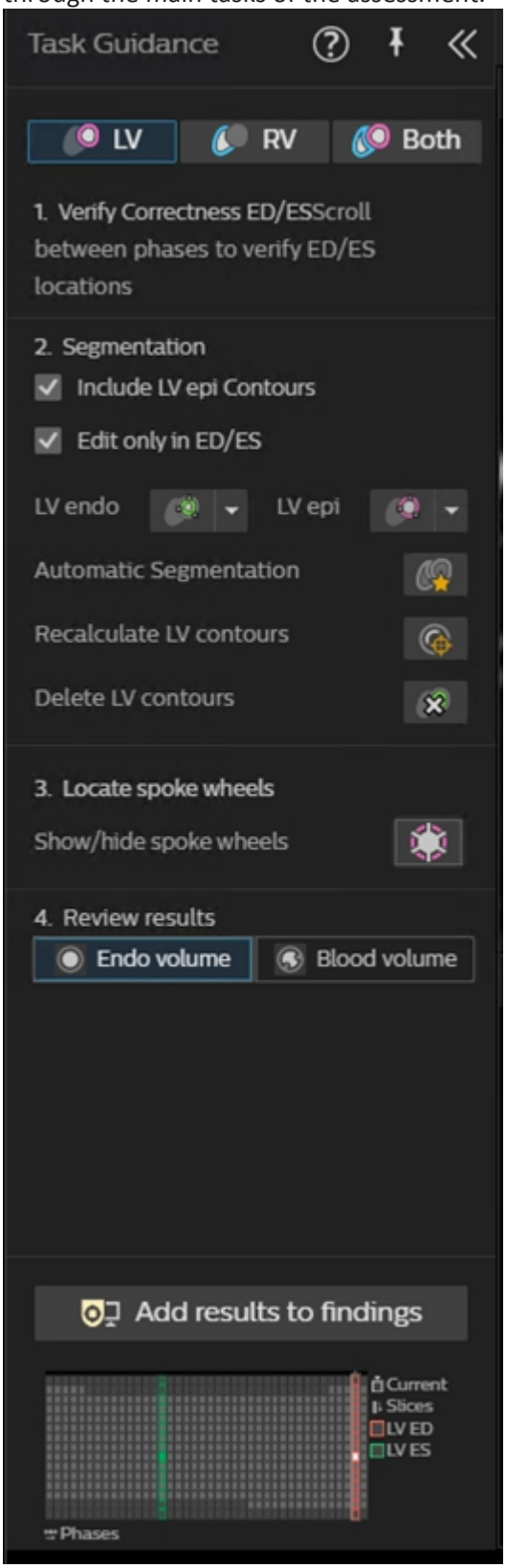
Application modes

In Functional LV & RV, you can select from the following working modes:

1. Focus on LV
2. Focus on RV
3. Both (LV & RV)

The application displays only the contours and tools relevant to the mode you select. For example, in **Focus on LV**, only LV contours are displayed on the image, only LV contour creation tools are provided, and only LV results are displayed in the tables and graph.

In each of the working modes, the left **Task Guidance** panel shows a workflow that leads you through the main tasks of the assessment.

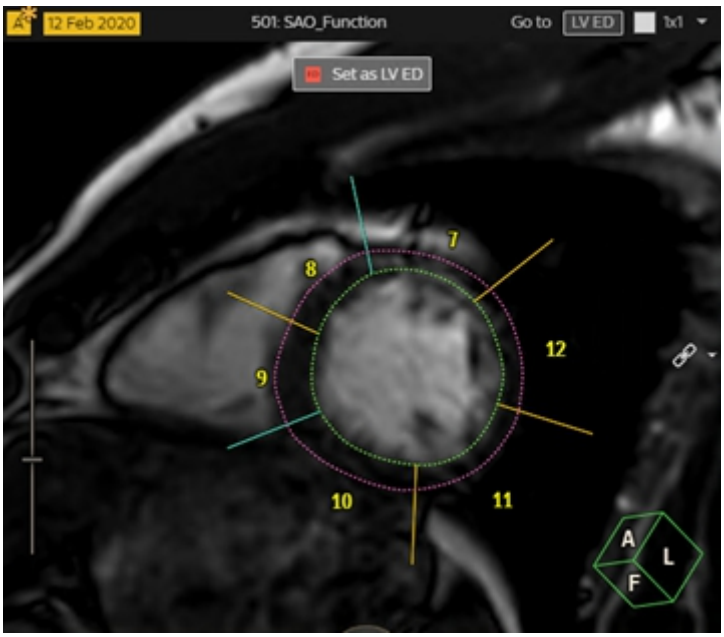


There is no mandatory order, though it is recommended to go step-by-step. Results are displayed and updated following any edit operations.

Application hanging protocols

In each working mode, the application provides several hanging protocols that fit the selected ventricle. The hanging protocols vary by the type of viewports (polar maps, number of reference series, etc.). For optimal workflow, mark both your Favorite and Default hangings. The application will launch the selected default, and show Favorites as shortcut buttons on the navigation bar:

Modify ED/ES

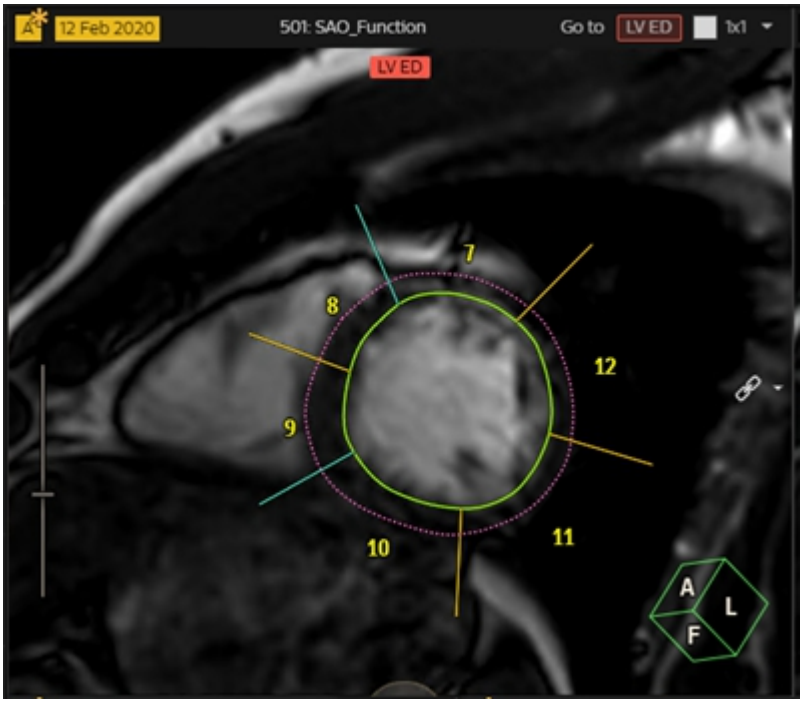


When you launch **Functional LV & RV**, ED and ES phases are automatically calculated according the volume curve, when it exists. As these results are based on an automatic segmentation, you are still expected to review, and modify these phases if needed. Each viewport is related to a specific phase, for example LV ED.

To modify ED/ES:

- Scroll between phases using the left and right arrow keys, or your mouse. Scrolling does not modify the selected phase unless you click, for example, **Set as LV ED** on the image.
- If you want to navigate back to the original phase, on the **Go to** toolbar at the top right-hand side of the screen, select **LV ED**, or any other option displayed according to the viewport.

Edit contours



When you launch a series for the first time, LV and RV contours are generated. Ventricle volume in each phase is calculated from these contours. When you edit the contours, volume is recalculated and displayed in the volume graph.

When you launch the application from a patient's **Patient Directory**, the application displays LV RV analysis with the endo and epi contours for LV, and the endo contour for RV.

You can review, edit, and redraw contours of the phases using the hanging protocols, and the full set of drawing and editing tools on the **Create/edit contours** toolbar.

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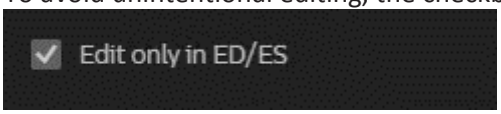
To avoid unintentional editing, the checkbox **Edit only in ED/ES** is selected by default.



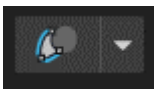
This prevents you from unintentionally working on other phases. When you select **Edit only in ED/ES**, you cannot edit any phase that is not ED/ES, and are only able to edit contours on phases that are defined as ED or ES. If you do want to edit in all phases, clear this checkbox.

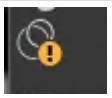
There is always a default editing tool selected. This selected tool becomes active as soon as you select a contour. The mouse indicates that the tool is active on a specific contour.

Select a contour by clicking it. The selected contour is shown as a solid line, while the other contour is displayed as a dotted line.

Editing tools

The **Editing contours** floating toolbar contains drawing and editing tools.

Icon	Function	Instructions
Drawing tools	Draw the...	Click to add a point while the contour connects between points.
	LV Endo contour using a spline.	
	LV Epi contour using a spline.	
	RV Endo contour using a spline.	
	RV Epi contour using a spline.	

Icon	Function	Instructions
	LV Endo contour freehand.	Click and draw the shape by dragging the mouse along the ventricle contour. Double-click to end the drawing. Edit the contour using the other editing tools.
	LV Epi contour freehand.	
	RV Endo contour freehand.	
	RV Epi contour freehand using a spline.	
Editing tools		
	Edit a contour freehand.	Edit the contour by dragging the mouse, and redrawing the section.
	Edit a contour using a spline.	Click a point or the contour itself to create a new point, then drag the point.
	Edit using a nudge tool.	Push the selected contour inside or outside. Resize the circle using CTRL + mouse wheel.
	Expand a contour.	Every click expands the contour by one pixel.
	Contract a contour.	Every click contracts the contour by one pixel.
	Undo	Undo the most recent edit operations.
	Resolve intersections.	When endo and epi contour intersect, push the other contour away from the one that was last edited.

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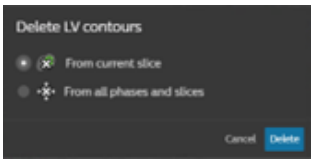
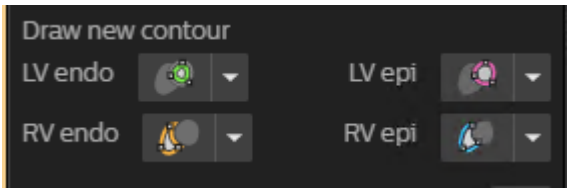
Icon	Function	Instructions
	Delete contours.	1. Select the contours to delete.  2. A dialog box opens. Select either **All contours on current slice**, or **All contours on all phases and slices**. Alternatively, right-click the image to **Delete current contour** or **Delete contour from all phases**.
	Show/Hide spokes wheel.	To see polar maps displayed by regions or AHA model, show the spokes and set their location. For correct analysis results, verify that spokes are well-positioned on all slices. • To trigger recalculation of RV EPI contours, drag a blue spoke individually by hovering over its edge until a yellow sphere appears. This also automatically triggers recalculation of the yellow spokes. • You can rotate the whole wheel. Hovering over the middle of a spoke until a small wheel appears. Changes in spokes are: • propagated to the other phases, but not to the other slices. • reflected in the polar map results.
	Propagate	Once a contour is edited, propagate these edits to other phases.

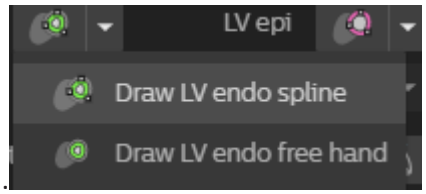
Drawing contours

You can draw a new contour instead of editing an existing contour.

1. Either select the contour you want to draw from the **Task Guidance** toolbar,



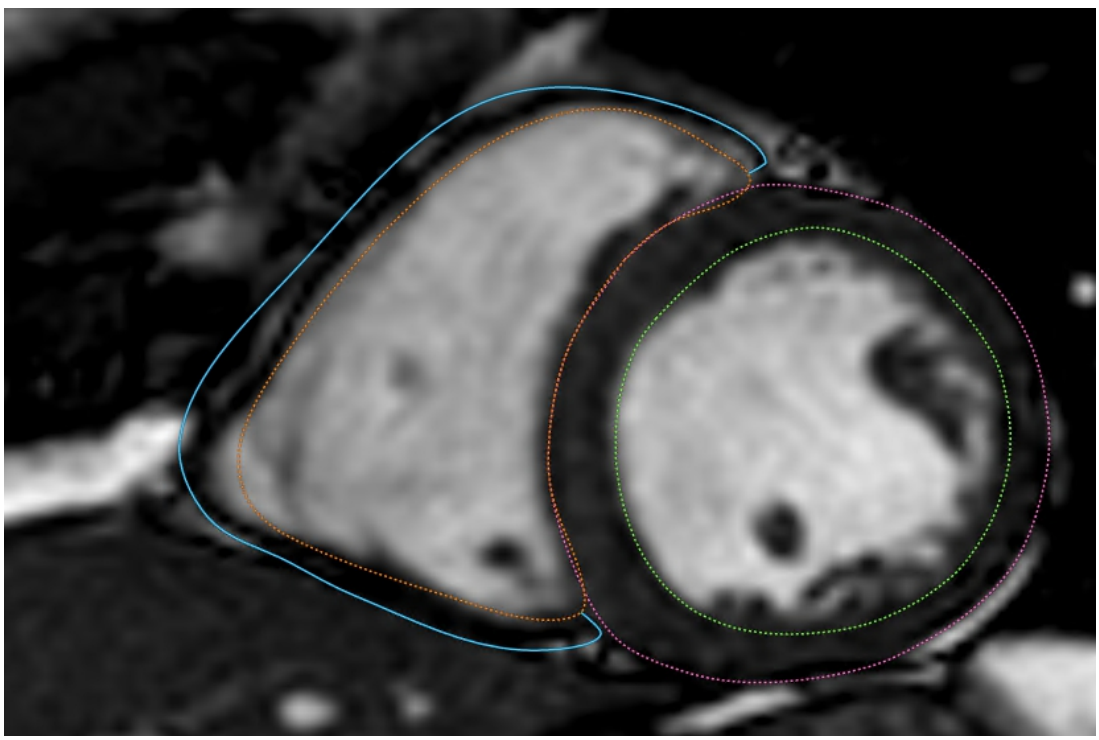
or select the Redraw tool on the **Editing contours** tool bar from the last selected contour.

2.  Select spline or free hand. 

3. The cursor changes to indicate a drawing tool is active.

   Different colors indicate different contours. As you start to draw a new contour, the previous contour disappears.
4. Draw the LV contours.
   - Click to start drawing the contour.
   - All drawing tools, except for the RV Epi Contour tool, allow you to create closed ROIs.
   - Double-click to end the drawing.
5. Draw the RV Epi contours.

   The RV EPI contour expects you to draw an opened ROI around the RV Endo. The application closes them automatically on double-click toward the RV Endo, as shown in the following image:



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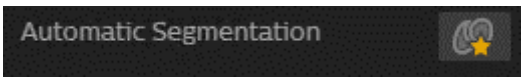
6. Drawing RV Endo contours.

   When you draw RV Endo contours, it will not remove or replace the current contours. This allows you to segment up to four ROIs on a slice, usually when close to the valve. You must manually remove a ROI to replace it.

Automatic segmentation



If the preprocessing was not triggered, the segmentation algorithm can be triggered manually from the application by clicking **Automatic Segmentation**.

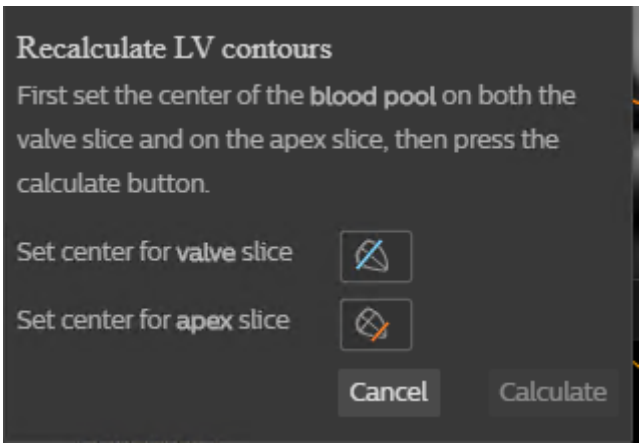
Recalculating LV contours

You can re-segment LV contours by providing the base and apex locations.

1. On the **Task guidance** panel, click **Recalculate LV contours**.

2. Scroll to the valval (base) slice location, then click **Set center for valve slice**.

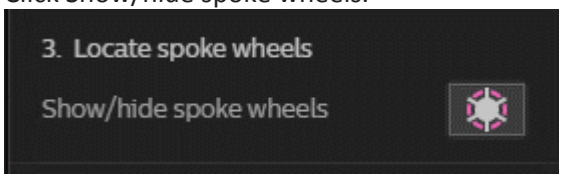


3. Scroll to the apex slice location, then click **Set center for apex slice**.
4. Click **Calculate**. The LV contours are recalculated and displayed.

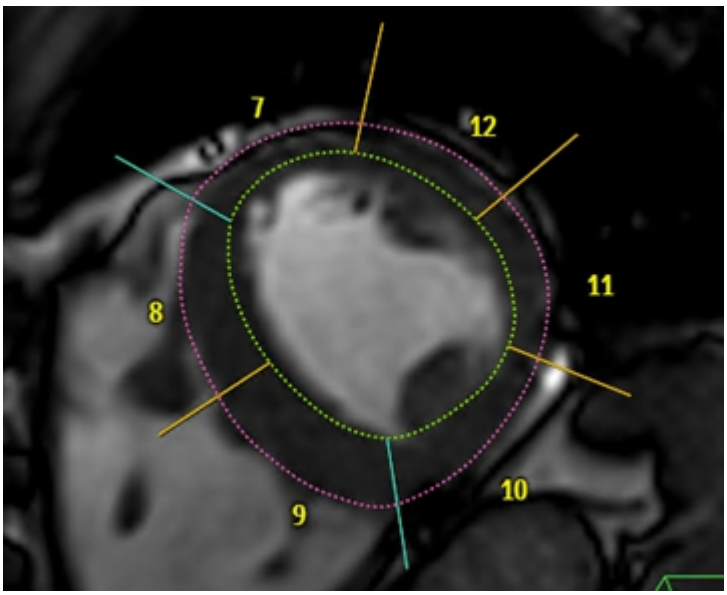
Setting spoke wheels

The application determines the spokes' location based on the LV & RV contours intersection. The default number of spokes in each slice is calculated based on the AHA model, meaning that in apical slices there are only 4 spokes. As the polar maps are calculated based on the spokes' location, it is important to verify their location.

1. Click Show/hide spoke wheels.



2. The spoke wheels display on the image.



3. Adjust the spokes to ensure correct analysis results:
   - Blue spokes can be relocated independently and trigger recalculation of the RV EPI contours.
   - Hover over the center of any spoke until the cursor changes to a small wheel, and then rotate the whole wheel.
   - Hover over the end of a spoke to select and move a single spoke.

The adjustments made to the spoke wheel are reflected in the polar map results.

NOTICE

Changes made to the spoke wheel are propagated to other phases, but not to the other slices.

Calculation mode

Endo volume vs. Blood volume.

Results

- Volume graph
- Table

- Polar map (bullseye)

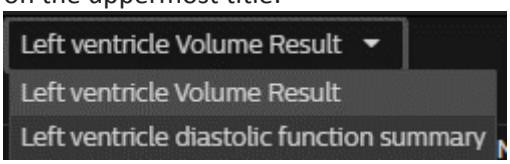
You can still edit the contours and change the ED/ES on the graph at this stage.

Results summary table

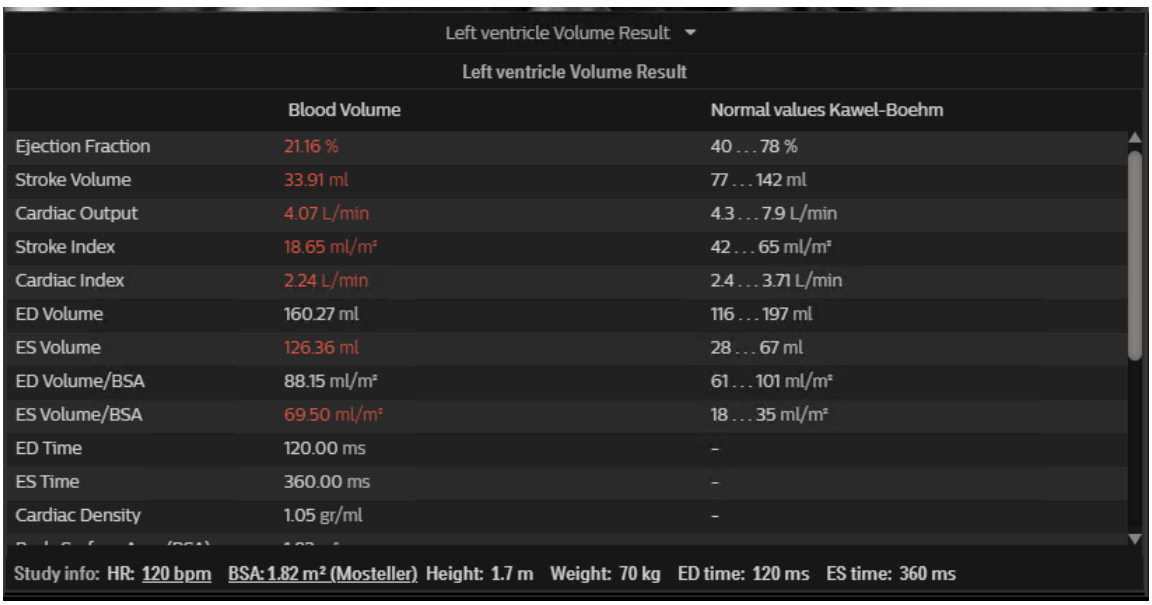
NOTICE

Double-click the **Results** table to maximize it in the viewport.

The results table includes several pages. You can switch between the pages using the list menu on the uppermost title:



Each page includes the study results alongside **Normal values**:



For information on the normal values, refer to the upcoming section "Normal values".

You can choose to display the following results for Endo Volume (if available) or Blood Volume. For definitions of these terms, see the upcoming section “Terminology”.

- Ejection fraction (%)
- Stroke volume (ml)
- Cardiac output (L/min)
- Stroke index (ml/m2)
- Cardiac index (L/(min*m2))

- ED volume (ml)
- ES volume (ml)
- ED volume/BSA (ml/m2)
- ES volume/BSA (ml/m2)
- ED time (ms)
- ES time (ms)
- Cardiac density (gr/ml)
- ED wall mass (gr)
- ED wall + papillary mass (gr)
- ED wall mass/BSA (gr/m2)
- ED wall + papillary mass/BSA (gr/m2)
- BSA (m2)
- Heart rate (bpm)

Diastolic function table

You can choose to display the following results for Endo Volume (if available) or Blood Volume. For definitions of these terms, see the upcoming section “Terminology”.

- Peak ejection rate (ml/ms)
- Time to peak ejection rate (ms)
- First peak filling rate (ml/ms)
- Time to first peak filling rate (ms)
- First filling volume (ml)
- Second peak filling rate (ml/ms)
- Time to second peak filling rate (ms)
- Second filling volume (ml)
- Minimum filling rate (ml/ms)
- Time to minimum filling rate (ms)
- First over second filling volume (ml)
- Peak ejection rate/BSA (ml/(ms*m2)
- First peak filling rate/BSA (ml/(ms*m2)
- First filling volume/BSA (ml/m2)
- Second peak filling rate/BSA (ml/(ms*m2)
- Second filling volume/BSA (ml/m2)
- Minimum filling rate/BSA (ml/(ms*m2)
- First over second filling volume/BSA (ml/m2)

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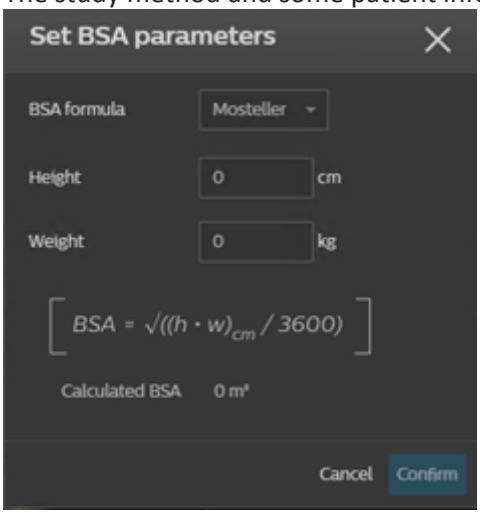
The study method and some patient information displays at the bottom of the table:



You can modify these values.

- Click **Set BSA parameters** to change:
  - BSA method
  - Heart rate (HR)
  - Height
  - Weight
- Click **Configure table** to configure the table contents.
  - Select the type of **Table** from the list menu.
  - Select the required parameters for the table.

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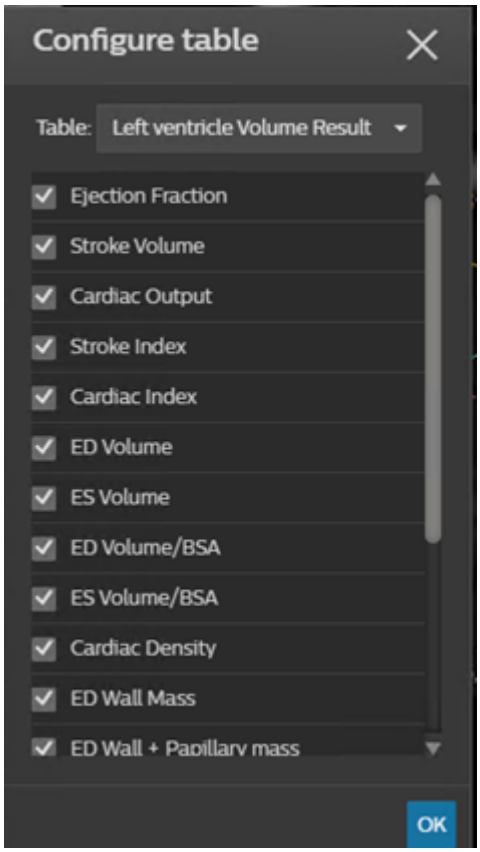
– Click **OK**.



Normal values

Background

Diagnosis is summary of visual assessment, anamnesis and parameters calculated by analysis. A normal range displayed in analysis results does not have effect on the analysis calculation itself and is not part of the "diagnosis chain".

Normal ranges can differ depending on age, gender, ethnic origin, and applied CMR scan techniques such as scan protocols on site, vendor, analysis software (algorithms), with or without papillary muscle extraction.

Recommendations

It is recommended to verify if the normal range used in this software (factory settings) may apply to the population group and scan techniques used. In order to set your own normal ranges, use the **Edit Normal Values** panel from the right mouse menu in the table view. If you do not need an overview of normal values, select **Hide** from the right mouse menu.

The methods and input data used to display the normal range values (factory settings) in this software are described in detail in the following references:

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Kawel-Boehm et al., 2020
Kawel-Boehm N, Hetzel SJ, Ambale-Venkatesh B, Captur G, Francois CJ, Jerosch-Herold M, et al. Reference ranges (“normal values”) for cardiovascular magnetic resonance (CMR) in adults and children: 2020 update. Journal of Cardiovascular Magnetic Resonance 2020;22:87. https://doi.org/10.1186/s12968-020-00683-3

Petersen et al., 2019
(EACVI) Petersen SE, Khanji MY, Plein S, Lancellotti P, Bucciarelli-Ducci C. European Association of Cardiovascular Imaging expert consensus paper: a comprehensive review of cardiovascular magnetic resonance normal values of cardiac chamber size and aortic root in adults and recommendations for grading severity. Eur Heart J Cardiovasc Imaging 2019;20:1321–31. https://doi.org/10.1093/ehjci/jez232

Chuang et al., 2014
Chuang ML, Gona P, Hautvast GLTF, Salton CJ, Breeuwer M, O’Donnell CJ, et al. CMR reference values for left ventricular volumes, mass, and ejection fraction using computer-aided analysis: The Framingham Heart Study. J Magn Reson Imaging 2014;39:895–900. https://doi.org/10.1002/jmri.24239

Chuang et al., 2012
Chuang ML, Gona P, Hautvast GLTF, Salton CJ, Blease SJ, Yeon SB, et al. Correlation of Trabeculae and Papillary Muscles With Clinical and Cardiac Characteristics and Impact on CMR Measures of LV Anatomy and Function. JACC: Cardiovascular Imaging 2012;5:1115–23. https://doi.org/10.1016/j.jcmg.2012.05.015

The following tables indicate the values used as factory setting for normal range. The results are normalized for age and gender.

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NOTICE

For RV normal values a low amount of studies are available providing normal values in younger adults. We use a generic template offered by the RSNA committee. The application offers the freedom to adjust these settings from your own experience or study using the application. Be aware that RV calculation is highly dependent on the accuracy of your segmentation.

Normal Values: Female

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	61.0%	78.0%	61.0%	78.0%	66.6%	89.0%	66.6%	89.0%
Stroke volume	63.0 ml	115.0 ml	37.0 ml/m^2	57.0 ml/m^2	51.0 ml	87.0 ml	28.0 ml/m^2	46.0 ml/m^2
ED volume	94.0 ml	136.0 ml	56.0 ml/m^2	80.0 ml/m^2	69.0 ml	124.0 ml	39.0 ml/m^2	61.0 ml/m^2

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
ES volume	24.0 ml	61.0 ml	14.0 ml/m²	30.0 ml/m²	10.0 ml	39.0 ml	5.0 ml/m²	18.0 ml/m²
ED wall mass	48.0 gr	101.0 gr	28.0 gr/m²	49.0 gr/m²	88.0 gr	146.0 gr	54.0 gr/m²	75.0 gr/m²

Tab. 12: Female, Age Group < 18

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	61.0%	78.0%	61.0%	78.0%	66.6%	89.0%	66.6%	89.0%
Stroke volume	63.0 ml	115.0 ml	37.0 ml/m²	57.0 ml/m²	51.0 ml	87.0 ml	28.0 ml/m²	46.0 ml/m²
ED volume	94.0 ml	136.0 ml	56.0 ml/m²	80.0 ml/m²	69.0 ml	124.0 ml	39.0 ml/m²	61.0 ml/m²
ES volume	24.0 ml	61.0 ml	14.0 ml/m²	30.0 ml/m²	10.0 ml	39.0 ml	5.0 ml/m²	18.0 ml/m²
ED wall mass	48.0 gr	101.0 gr	28.0 gr/m²	49.0 gr/m²	88.0 gr	146.0 gr	54.0 gr/m²	75.0 gr/m²

Tab. 13: Female, Age Group 18 - 29

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	61.0%	78.0%	61.0%	78.0%	66.6%	89.0%	66.6%	89.0%
Stroke volume	63.0 ml	115.0 ml	37.0 ml/m²	57.0 ml/m²	51.0 ml	87.0 ml	28.0 ml/m²	46.0 ml/m²
ED volume	94.0 ml	136.0 ml	56.0 ml/m²	80.0 ml/m²	69.0 ml	124.0 ml	39.0 ml/m²	61.0 ml/m²
ES volume	24.0 ml	61.0 ml	14.0 ml/m²	30.0 ml/m²	10.0 ml	39.0 ml	5.0 ml/m²	18.0 ml/m²
ED wall mass	48.0 gr	101.0 gr	28.0 gr/m²	49.0 gr/m²	88.0 gr	146.0 gr	54.0 gr/m²	75.0 gr/m²

Tab. 14: Female, Age Group 30 - 39

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Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	61.0%	78.0%	61.0%	78.0%	66.6%	89.0%	66.6%	89.0%
Stroke volume	63.0 ml	115.0 ml	37.0 ml/m²	57.0 ml/m²	51.0 ml	87.0 ml	28.0 ml/m²	46.0 ml/m²
ED volume	94.0 ml	136.0 ml	56.0 ml/m²	80.0 ml/m²	69.0 ml	124.0 ml	39.0 ml/m²	61.0 ml/m²
ES volume	24.0 ml	61.0 ml	14.0 ml/m²	30.0 ml/m²	10.0 ml	39.0 ml	5.0 ml/m²	18.0 ml/m²
ED wall mass	48.0 gr	101.0 gr	28.0 gr/m²	49.0 gr/m²	88.0 gr	146.0 gr	54.0 gr/m²	75.0 gr/m²

Tab. 15: Female, Age Group 40 - 49

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	60.0%	80.0%	60.0%	80.0%	66.4%	83.5%	66.4%	83.5%
Stroke volume	59.0 ml	112.0 ml	36.0 ml/m²	60.0 ml/m²	51.0 ml	87.0 ml	28.0 ml/m²	46.0 ml/m²
ED volume	90.0 ml	162.0 ml	50.0 ml/m²	82.0 ml/m²	63.0 ml	112.0 ml	36.0 ml/m²	60.0 ml/m²
ES volume	20.0 ml	48.0 ml	11.0 ml/m²	27.0 ml/m²	12.0 ml	33.0 ml	7.0 ml/m²	19.0 ml/m²
ED wall mass	41.0 gr	83.0 gr	25.0 gr/m²	44.0 gr/m²	81.0 gr	149.0 gr	50.0 gr/m²	77.0 gr/m²

Tab. 16: Female, Age Group 50 - 59

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	63.0%	82.0%	63.0%	82.0%	64.7%	86.0%	64.7%	86.0%
Stroke volume	59.0 ml	101.0 ml	35.0 ml/m²	58.0 ml/m²	47.0 ml	78.0 ml	27.0 ml/m²	44.0 ml/m²
ED volume	82.0 ml	139.0 ml	48.0 ml/m²	79.0 ml/m²	61.0 ml	105.0 ml	36.0 ml/m²	59.0 ml/m²
ES volume	17.0 ml	46.0 ml	10.0 ml/m²	26.0 ml/m²	9.0 ml	33.0 ml	5.0 ml/m²	19.0 ml/m²

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
ED wall mass	70.0 gr	77.0 gr	26.0 gr/m^2	42.0 gr/m^2	81.0 gr	136.0 gr	48.0 gr/m^2	73.0 gr/m^2

Tab. 17: Female, Age Group 60 - 69

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	69.0%	85.0%	69.0%	85.0%	68.1%	85.7%	68.1%	85.7%
Stroke volume	59.0 ml	96.0 ml	36.0 ml/m^2	57.0 ml/m^2	45.0 ml	72.0 ml	28.0 ml/m^2	41.0 ml/m^2
ED volume	74.0 ml	129.0 ml	47.0 ml/m^2	75.0 ml/m^2	58.0 ml	93.0 ml	36.0 ml/m^2	55.0 ml/m^2
ES volume	15.0 ml	37.0 ml	9.0 ml/m^2	21.0 ml/m^2	9.0 ml	29.0 ml	5.0 ml/m^2	17.0 ml/m^2
ED wall mass	42.0 gr	76.0 gr	26.0 gr/m^2	45.0 gr/m^2	77.0 gr	127.0 gr	49.0 gr/m^2	75.0 gr/m^2

Tab. 18: Female, Age Group > 70

Normal Values: Male

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	59.0%	76.0%	59.0%	76.0%	64.4%	83.9%	64.4%	83.9%
Stroke volume	76.0 ml	139.0 ml	42.0 ml/m^2	65.0 ml/m^2	59.0 ml	93.0 ml	30.0 ml/m^2	48.0 ml/m^2
ED volume	120.0 ml	214.0 ml	61.0 ml/m^2	101.0 ml/m^2	89.0 ml	138.0 ml	40.0 ml/m^2	69.0 ml/m^2
ES volume	37.0 ml	75.0 ml	18.0 ml/m^2	35.0 ml/m^2	16.0 ml	49.0 ml	8.0 ml/m^2	23.0 ml/m^2
ED wall mass	74.0 gr	110.0 gr	41.0 gr/m^2	54.0 gr/m^2	121.0 gr	204.0 gr	68.0 gr/m^2	97.0 gr/m^2

Tab. 19: Male, Age Group < 18

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	59.0%	76.0%	59.0%	76.0%	64.4%	83.9%	64.4%	83.9%
Stroke volume	76.0 ml	139.0 ml	42.0 ml/m^2	65.0 ml/m^2	59.0 ml	93.0 ml	30.0 ml/m^2	48.0 ml/m^2
ED volume	120.0 ml	214.0 ml	61.0 ml/m^2	101.0 ml/ m^2	89.0 ml	138.0 ml	40.0 ml/m^2	69.0 ml/m^2
ES volume	37.0 ml	75.0 ml	18.0 ml/m^2	35.0 ml/m^2	16.0 ml	49.0 ml	8.0 ml/m^2	23.0 ml/m^2
ED wall mass	74.0 gr	110.0 gr	41.0 gr/m^2	54.0 gr/m^2	121.0 gr	204.0 gr	68.0 gr/m^2	97.0 gr/m^2

Tab. 20: Male, Age Group 18 - 29

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	59.0%	76.0%	59.0%	76.0%	64.4%	83.9%	64.4%	83.9%
Stroke volume	76.0 ml	139.0 ml	42.0 ml/m^2	65.0 ml/m^2	59.0 ml	93.0 ml	30.0 ml/m^2	48.0 ml/m^2
ED volume	120.0 ml	214.0 ml	61.0 ml/m^2	101.0 ml/ m^2	89.0 ml	138.0 ml	40.0 ml/m^2	69.0 ml/m^2
ES volume	37.0 ml	75.0 ml	18.0 ml/m^2	35.0 ml/m^2	16.0 ml	49.0 ml	8.0 ml/m^2	23.0 ml/m^2
ED wall mass	74.0 gr	110.0 gr	41.0 gr/m^2	54.0 gr/m^2	121.0 gr	204.0 gr	68.0 gr/m^2	97.0 gr/m^2

Tab. 21: Male, Age Group 30 - 39

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	59.0%	76.0%	59.0%	76.0%	64.4%	83.9%	64.4%	83.9%
Stroke volume	76.0 ml	139.0 ml	42.0 ml/m^2	65.0 ml/m^2	59.0 ml	93.0 ml	30.0 ml/m^2	48.0 ml/m^2

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
ED volume	120.0 ml	214.0 ml	61.0 ml/m^2	101.0 ml/m^2	89.0 ml	138.0 ml	40.0 ml/m^2	69.0 ml/m^2
ES volume	37.0 ml	75.0 ml	18.0 ml/m^2	35.0 ml/m^2	16.0 ml	49.0 ml	8.0 ml/m^2	23.0 ml/m^2
ED wall mass	74.0 gr	110.0 gr	41.0 gr/m^2	54.0 gr/m^2	121.0 gr	204.0 gr	68.0 gr/m^2	97.0 gr/m^2

Tab. 22: Male, Age Group 40 - 49

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	60.0%	78.0%	60.0%	78.0%	65.4%	82.3%	65.4%	82.3%
Stroke volume	77.0 ml	142.0 ml	40.0 ml/m^2	68.0 ml/m^2	65.0 ml	105.0 ml	32.0 ml/m^2	52.0 ml/m^2
ED volume	116.0 ml	197.0 ml	57.0 ml/m^2	100.0 ml/m^2	90.0 ml	148.0 ml	44.0 ml/m^2	70.0 ml/m^2
ES volume	28.0 ml	67.0 ml	14.0 ml/m^2	34.0 ml/m^2	18.0 ml	46.0 ml	9.0 ml/m^2	21.0 ml/m^2
ED wall mass	76.0 gr	139.0 gr	38.0 gr/m^2	67.0 gr/m^2	131.0 gr	206.0 gr	65.0 gr/m^2	97.0 gr/m^2

Tab. 23: Male, Age Group 50 - 59

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	60.0%	81.0%	60.0%	81.0%	61.1%	83.8%	61.1 %	83.8%
Stroke volume	74.0 ml	135.0 ml	38.0 ml/m^2	67.0 ml/m^2	50.0 ml	101.0 ml	27.0 ml/m^2	51.0 ml/m^2
ED volume	103.0 ml	192.0 ml	49.0 ml/m^2	97.0 ml/m^2	75.0 ml	151.0 ml	39.0 ml/m^2	71.0 ml/m^2
ES volume	23.0 ml	70.0 ml	11.0 ml/m^2	34.0 ml/m^2	12.0 ml	51.0 ml	6.0 ml/m^2	24.0 ml/m^2

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Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
ED wall mass	67.0 gr	133.0 gr	35.0 gr/m^2	63.0 gr/m^2	108.0 gr	202.0 gr	57.0 gr/m^2	95.0 gr/m^2

Tab. 24: Male, Age Group 60 - 69

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
Ejection fraction	65.0%	83.0%	65.0%	83.0%	64.5%	89.8%	64.5%	89.8%
Stroke volume	65.0 ml	136.0 ml	33.0 ml/m^2	67.0 ml/m^2	53.0 ml	100.0 ml	27.0 ml/m^2	48.0 ml/m^2
ED volume	94.0 ml	182.0 ml	48.0 ml/m^2	90.0 ml/m^2	75.0 ml	129.0 ml	40.0 ml/m^2	69.0 ml/m^2
ES volume	19.0 ml	52.0 ml	10.0 ml/m^2	28.0 ml/m^2	8.0 ml	45.0 ml	3.0 ml/m^2	25.0 ml/m^2
ED wall mass	72.0 gr	127.0 gr	39.0 gr/m^2	65.0 gr/m^2	109.0 gr	209.0 gr	58.0 gr/m^2	99.0 gr/m^2

Tab. 25: Male, Age Group > 70

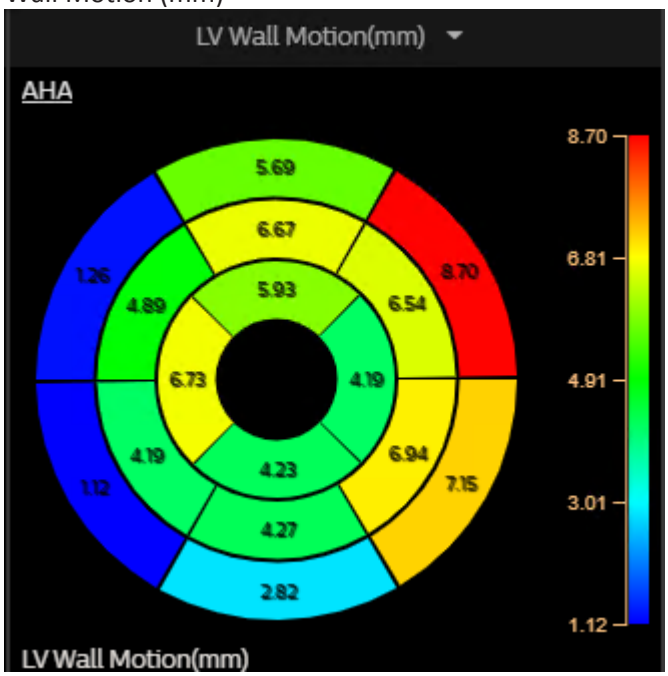
Polar maps

Polar maps, also referred to as bull's eye plots, display according to the spoke wheel settings.

Use the right mouse menu to configure the Polar map to display the following results. For definitions of these terms, see the upcoming section “Terminology”.

- Wall Thickness (mm)
- Wall Thickening Absolute (mm)
- Wall Thickening Relative (%)
- Time of Maximum Thickness (s)

- Wall Motion (mm)



You can display each set of results as detailed, regional, or AHA, where regional results display average results per segment.

Polar maps represent the numeric results in colored concentric rings for one heart phase. Each ring represents a slice. The slice at the apex is in the center. The direction is looking from atrium to apex. The colors represent values of results according to vertical bar coloring. Move the pointer over the segments in the Polar map to get numerical information about the presented result values.

Double-click a Polar map to maximize it in the viewport.

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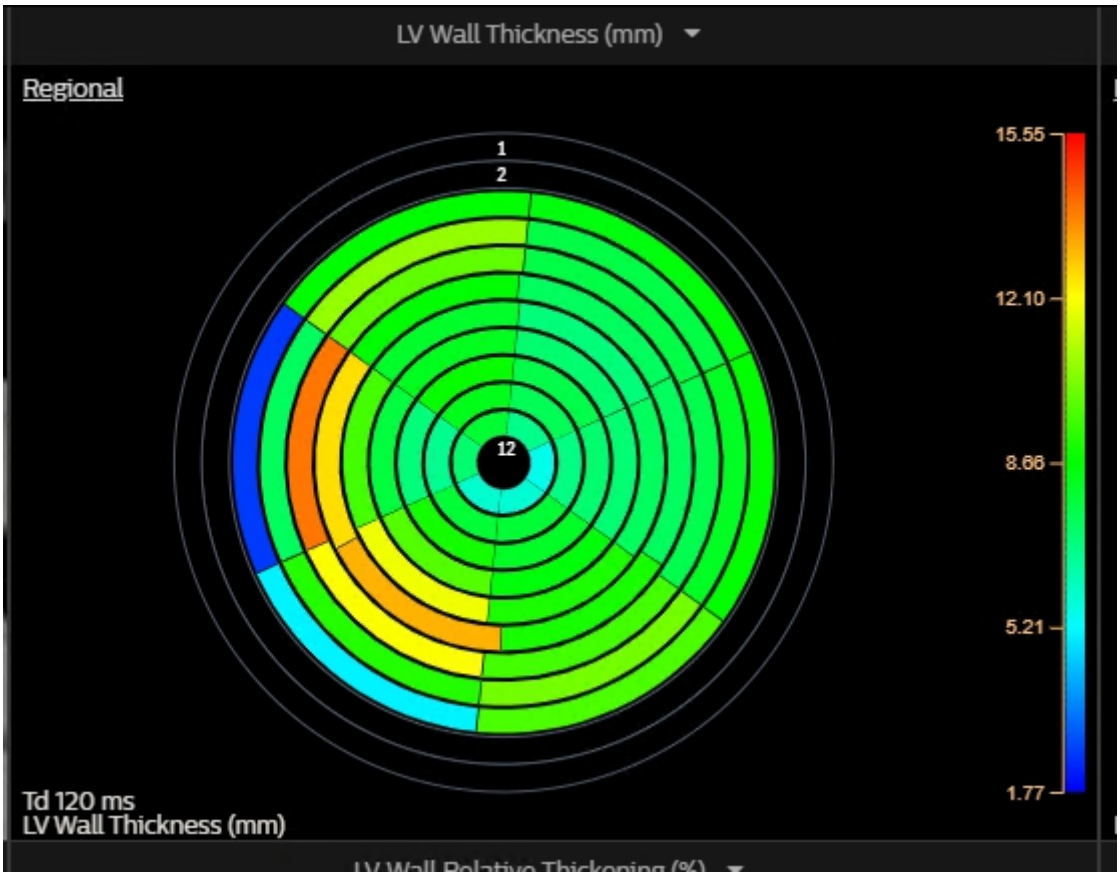
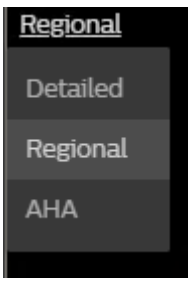


- Click on the upper left annotation to switch between polar map options:
  - Detailed
  - Regional
  - AHA



NOTE

Polar map default mode is AHA.

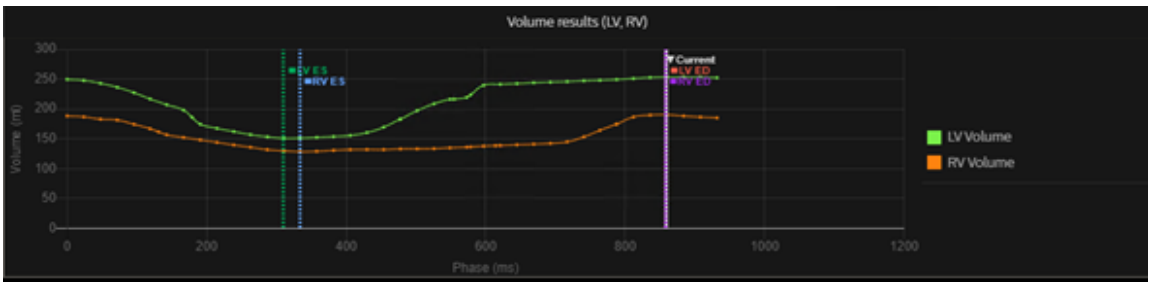
- Click on a ring to move the image to the same slice.
- Hover over any location to display a tooltip with the location and values.

- Click the map's title to open a list menu and select a different option.

Volume graph

Volume graphs show the volume curve of LV and RV during all phases. The X axis represents the phases, and the Y axis represents the volume in milliliters (ml).

The ventricles' volume in each phase is calculated from the contours. When the contours are changed, volume is recalculated and represented on the graph.

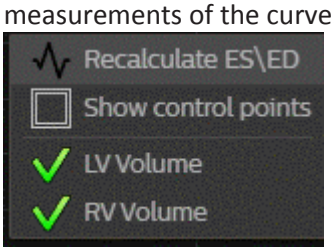


All information displayed on the curves is color-coded and described in the graph legend. The graph legend also includes information regarding time to peak.

Trackers on the graph show the ED and ES locations:

- **LV ED** location
- **LV ES** location
- **RV ES** location
- **RV ED** location
- **Current** shows the location of the currently selected viewport.

- Hover on the curve line to display a tooltip displaying the location phase and volume.
- Drag trackers to change their phase location.
- When two locations merge, the trackers are merged and can be dragged from the title.
- Hide or display each of the curves by clicking on the legend or context menu on the curve.
- Use the context menu to recalculate the ED/ES based on the minimum and maximum measurements of the curve.



Showing control points displays the following time points on the graph:

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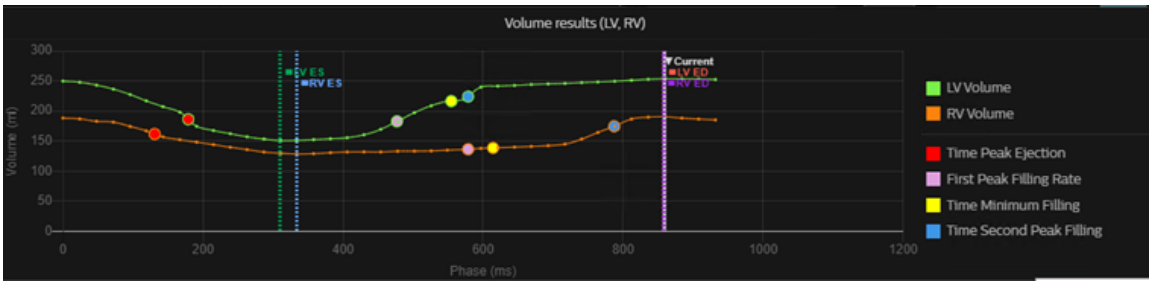

Terminology

Functional LV & RV Analysis uses the following terminology:

- **End diastolic phase (ED)**: The phase at the beginning of a heartbeat where the heart is at rest', i.e. where the blood volume is at a maximum.
- **ED volume (VED)**: The amount of blood that is in the heart at the end diastolic phase; expressed in milliliters (ml). The volume is calculated by adding up the blood volumes per slice in the end diastolic phase. The blood volume of one slice is calculated by multiplying the area of the endo contour at that slice with half of the distance between the slice above and beneath that slice. VED = VEDF + VLDF
- **Early diastolic filling volume (VEDF)**: The amount of blood that is in the left ventricle after the early diastolic filling; in ml. The early diastolic filling is the filling of the left ventricle due to the relaxation of the myocardium.
- **Late diastolic filling volume (VLDF)**: The amount of blood that is in the heart after the late diastolic filling, also called atrial filling volume; in ml. The late diastolic filling is the filling of the left ventricle due to the contraction of the left atrium (the so-called "atrial kick").
- **Minimum filling rate**: The minimum filling rate in the diastolic filling of the ventricle; in ml/ms.
- **Peak filling rate 1 (PFR1)**: The maximum filling rate in the early diastolic filling of the ventricle; in ml/ms.
- **Peak filling rate 2 (PFR2)**: The maximum filling rate in the late or atrial diastolic filling; in ml/ms.
- **Time of end diastolic volume (TED)**: Moment when the volume of the left ventricle has reached VED; in ms.
- **Time of first peak filling rate TPFR1**; in ms.
- **Time of second peak filling rate (TPFR2)**; in ms.
- **Time of minimum filling rate (TMF)**: Time when the filling rate is minimum at the transition from the early diastolic filling phase to the late diastolic filling phase; in ms.
- **End systolic phase (ES)**: The phase where the heart is fully contracted, i.e. where the blood volume is at a minimum.
- **ES volume (VES)**: The amount of blood that is in the heart at the end systolic phase; in ml. VES is calculated in a similar way as VED with the difference that the slices are taken from the end systolic phase.

- **Peak ejection rate (PER)**: The maximum ejection rate in the systolic phase; in ml/ms.
- **Time of peak ejection rate (TPER)**: The time when the peak ejection rate occurs; in ms.
- **Time of end systolic volume (TES)**: Time of maximum contraction; in ms.
- **Stroke volume (SV)**: The amount of blood that is pumped out per heartbeat, i.e. the difference between the blood volume at the end diastolic phase and the end systolic phase; in (ml). SV = VED – VES
- **Stroke index (SI)**: The stroke volume relative to the body surface area; in (ml/beat/m2). SI = SV / BSA
- **Body Surface Area (BSA)**: The estimated (not measured) area of the patient's body surface; in m2. For adults, the approximate value of BSA can be calculated using Mosteller's formula: BSA = √ (Height [cm] x Weight [kg]) / 3600
- **Cardiac output (CO)**: The amount of blood that is pumped out per minute; in liter (l). The heart rate is in beats per minute (bpm). CO = (SV × HeartRate) / 1000
- **Cardiac Index (CI)**: The cardiac output relative to the body surface area; in l/min/m2. CI = CO / BSA
- **The fraction of the early and late filling volumes**: VEDF / VLDF

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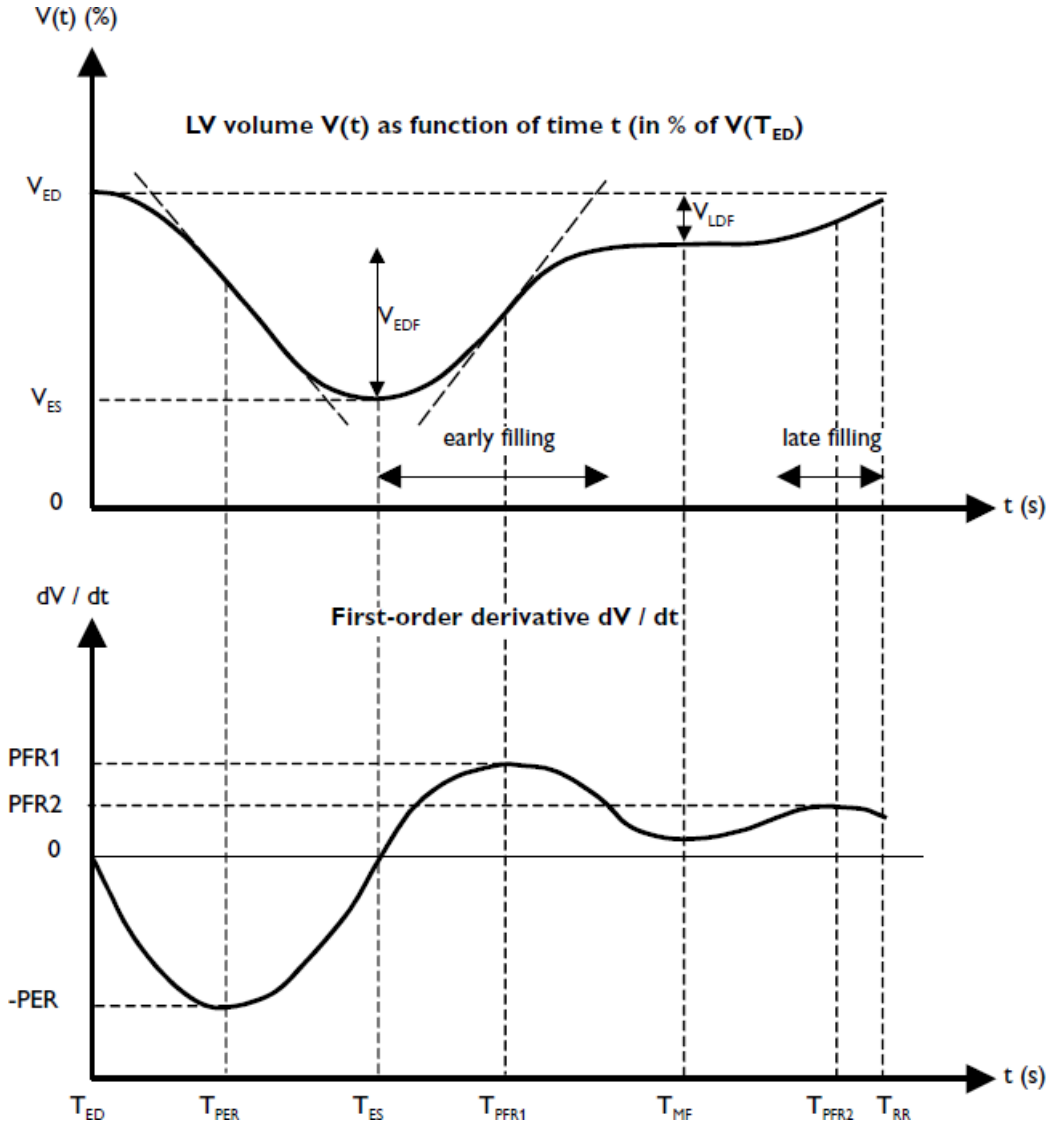


Fig. 43: Volume curve V(t) and its first-order derivative dV/dt, with various systolic and diastolic functional parameters

Terminology used in heart wall results

- **Detailed wall thickness**: The thickness of the heart wall (in millimeters) at a given slice and phase for a number of sample points (every four degrees). The thickness is computed by generating a centerline contour between the endo and epi contour drawn at that slice and phase.
- **Regional wall thickness**: The average thickness of the heart wall (in millimeters) per segment defined by the spoke wheel drawn at the same slice and phase as the endo and epi contour.
- **Detailed wall thickening**: The thickening of the heart wall over time at a given slice for a number of sample points. The thickening is computed by taking the difference of the thickness in the end diastolic phase and end systolic phase and divide that by the thickness in the end diastolic phase for each sample point.

- **Regional wall thickening**: The average thickening of the heart wall over time at a given slice per segment, defined by the spoke wheels drawn at the ED and ES phase of that slice. The thickening is computed by taking the difference of the average thickness in the end diastolic phase and end systolic phase and divide that by the average thickness in the end diastolic phase for segment of the spoke wheel.
- **Global wall thickening**: The average thickening of the complete heart wall over time at a given slice.
- **Detailed wall motion**: The motion of the heart wall (in millimeters) over time at a given slice for a number of sample points (every four degrees). The wall motion is computed by generating a centerline contour between the endo contours at the ED and ES phase at that slice.
- **Regional wall motion**: The average motion of the heart wall (in millimeters) over time at a given slice per segment, defined by the spoke wheel drawn at the ES phase of that slice.

The following coordinate system is used in the presentation of the wall thickness, wall thickening and wall motion results when there are no spoke wheels drawn.

Fig. 44: Coordinate system for heart wall results

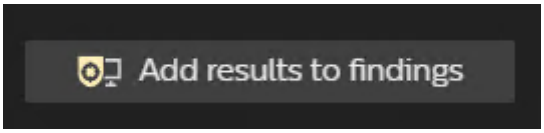
When spoke wheels are drawn, zero degrees is defined at the first spoke.

- **Wall mass**: The mass of the heart wall in grams at a given phase. The wall mass which is computed by taking the (corrected) blood volume (cm^3) at that phase and multiplying it with a cardiac density factor of 1.05 g/cm^3.
- **Time of detailed maximum thickness**: For 90 sample points (every 4 degrees) the moment of maximum wall thickness is computed during one heart cycle. The phase number with the maximum wall thickness is indicated in the graph and Bull's eye.
- **Time of regional maximum thickness**: For one segment the moment of maximum wall thickness is computed during one heart cycle. The phase number with the maximum wall thickness is indicated in the graph and bull's eye.

NOTICE

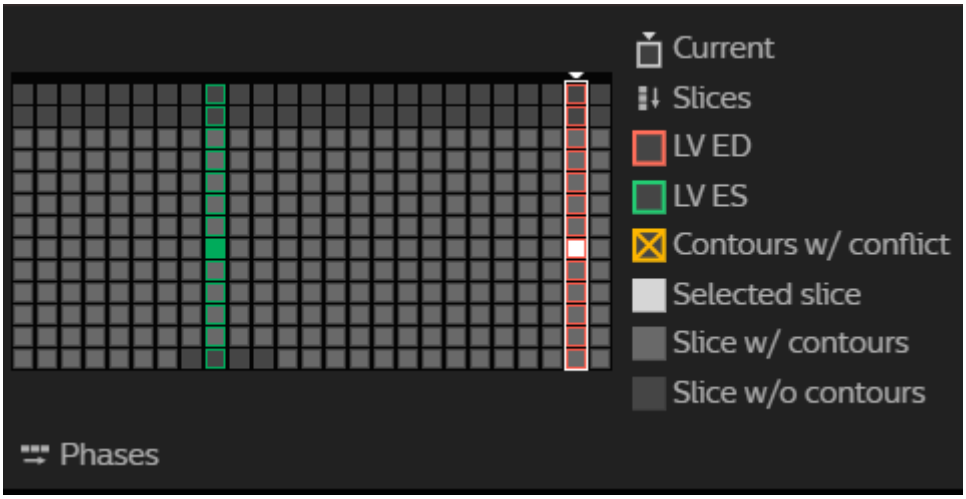
When results cannot be calculated, the text 'n/a' (= not available) is displayed.

Add results to findings



This saves the results (edited contours, etc.) as a bookmark in the findings dashboard.

Slice phase matrix



This shows a matrix of all the slices and phases, with indications of:

- Where contours exist.
- The location of ED/ES.
- The current location, etc.

Navigate to any slice by clicking on a square in the matrix.

Accuracy of Measurements

- Cardiac volume computation is available through two algorithms:
  - Riemann integration
  - Simpson integration
- For cardiac shapes, the Simpson algorithm is more accurate and gives a difference of 10-12% over the Riemann algorithm for adult hearts. However, the Simpson algorithm can only be used when there are a minimum of three contours and if there are no gaps in the contour stack (all slices from the first contour to the last contour have valid contours in them).
- Note that for correct volume calculation of a ventricle, the complete ventricle should be present in the acquired MR images, and the endocardial contour should be available on each individual image slice.

- When these conditions are not satisfied, the computation defaults to the Riemann algorithm.
- For both algorithms, it is assumed that the slices are equidistant and all slices are present.

QFlow Analysis

Indications for Use

The QFlow application supports the visualization and quantification of blood flow dynamics by assisting in the review of MR phase-contrast data.

Intended Users

The QFlow application is intended to be used by adequately trained and qualified medical professionals, including but not limited to physicians and medical technicians. The main clinicians or medical and para-medical professionals who use the QFlow application are listed below:

- Radiologists in the radiology department/clinic
- 3D technologists in the radiology department

Other clinicians/roles using the Philips Advanced Visualization Workspace are listed below:

- Cardiologists and Cardiology technologists
- Neurologists
- Referring Physicians

Intended Patient Population

The intended patient population covers all patients with phase contrast MRI as part of their imaging examinations.

Benefits

If the device is used as specified in the Indications for Use, under the circumstances and conditions as specified in the Indications for Use, the QFlow application assists you in viewing and interpreting anatomy and flow-related MR (phase-contrast) data sets. This application assists in excluding or confirming the presence of ambiguity in flow-through vessels, valves, or the spinal cord/aqueduct.

The expected patient benefits are that with the use of the application, the investigating radiologist or cardiologist can specify flow-related conditions, and can use QFlow results solely or in conjunction with other cardiac-related qualitative and quantitative application results to define a report for the referring physician. Based on the results of the requested flow conditions, the referring physician can define and/or advise a diagnosis and treatment path to the patient, or propose actions to control risk factors with healthy lifestyle changes and/or medicines, or further investigations.

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Overview

This postprocessing application calculates quantitative information as flow velocity or flow rate, and then visualizes it as 2D color flow maps overlaid on anatomical references. You can use these flow maps to view stroke volumes, or to analyze CSF flow.

To perform 2D flow analysis correctly, QFlow requires images with multiple acquisitions over a single cardiac cycle, resulting in multiple phases. Images typically contain phase images and magnitude images.

Results from QFlow Analysis include stroke volume, forward and backward flow volumes, flux, stroke distance, mean velocity, maximum velocity, minimum velocity, peak velocity, and vessel area.

Valid imaging series

Scans suitable for QFlow are triggered PCA scans containing at least PCA/Phase images and FFE/Modulus, and optionally PCA/Modulus images.

Reliable results are achieved when the scan is acquired perpendicular to the vessels of interest, although scans in the same plane as the vessels can also be loaded for viewing.

Phase wrapping

Phase wrapping causes incorrect value of the velocity in QFlow analysis. Phase wrapping may occur if the VENC value, the (maximum) velocity encoding value, used during acquisition is too low compared to the actual maximum blood flow velocity in the vessel or structure.

Directly after acquisition, you should inspect the MRI data for phase wraps. If phase wraps are present, you should repeat the acquisition using a higher VENC value.

Contraindications

None.

User Interface

Screen layout

QFlow Analysis has a default layout of two image viewports, a graph viewer, a table viewer, a toolbar, and panels.

Viewports

The slice you select for viewing appears in both viewports, in the upper part of the main display area. The first viewport displays the source image's first slice in imaging volume (FFE/M image). The second viewport displays a PCA/P image. You can change the image type of each viewport by using the control in the lower-left corner of that viewport. You can also add a color overlay indicating flow to the second viewport, using the context menu.

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Task Guidance

Similar to all MR Cardiac Suite applications, QFlow Analysis provides a **Task Guidance** panel on the left side of the workspace. This panel displays the following workflow steps:

1. Segment vessel/valve
2. Results

The Workflow section in the following pages of these Instructions for Use is based on this **Task Guidance**. For details, see section “Workflow” on page 244.

NOTICE

Follow the steps of the Task Guidance to make optimal use of the QFlow Analysis application.

Scroll images and phases

You can browse through images and phases using your mouse wheel, or by dragging the scroll icon up and down, or horizontally.

You can also use the **Cine/Movie bar** to view images in a movie format, in order to play and pause review of slices. For more information, see the section "Cine/Movie bar" in the "MR Cardiac Suite workspace" chapter of these Instructions for Use.

Settings

To change the application settings, click **Show settings dialog**. You can configure the following settings:

- Select different units to use for analysis.
- Display forward flow analysis as always positive in the analysis graph and numerical results.

Workflow

Launch QFlow

1. Optionally, select a suitable QFlow (triggered PCA) scan. If there are several QFlow series, it is possible to select all of the in the application launcher – each will be opened in another tab If you do not select a scan, MR Cardiac Suite finds appropriate QFlow series, based on DICOM information, when you launch QFlow.
2. In the navigation bar, click **+**, then click **QFlow**. A new window opens with relevant series thumbnails. If there are several QFlow series, you can select all of them; each open in their own tab.

   Alternatively, right-click phase images and select **QFlow**.

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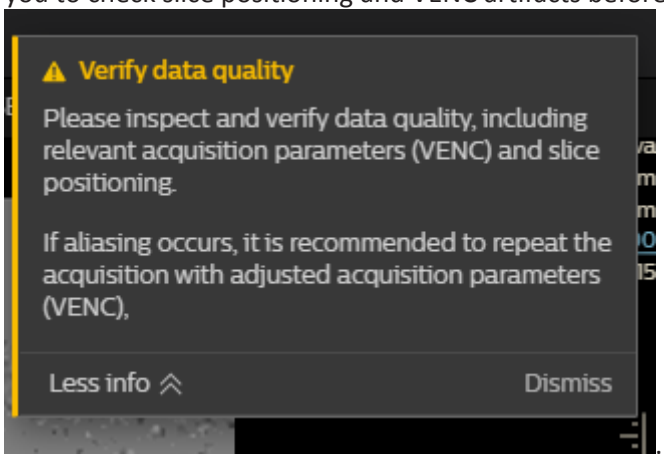
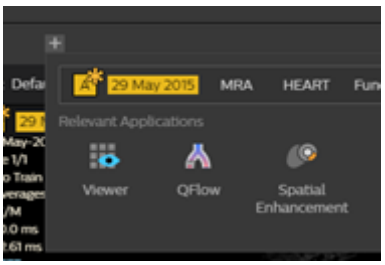
3. A **Verify data quality** notification appears on the right side of the workspace, prompting you to check slice positioning and VENC artifacts before beginning analysis



4. The QFlow application opens.

If there are several QFlow series, you can select all of them in the application launcher. Each opens in another tab

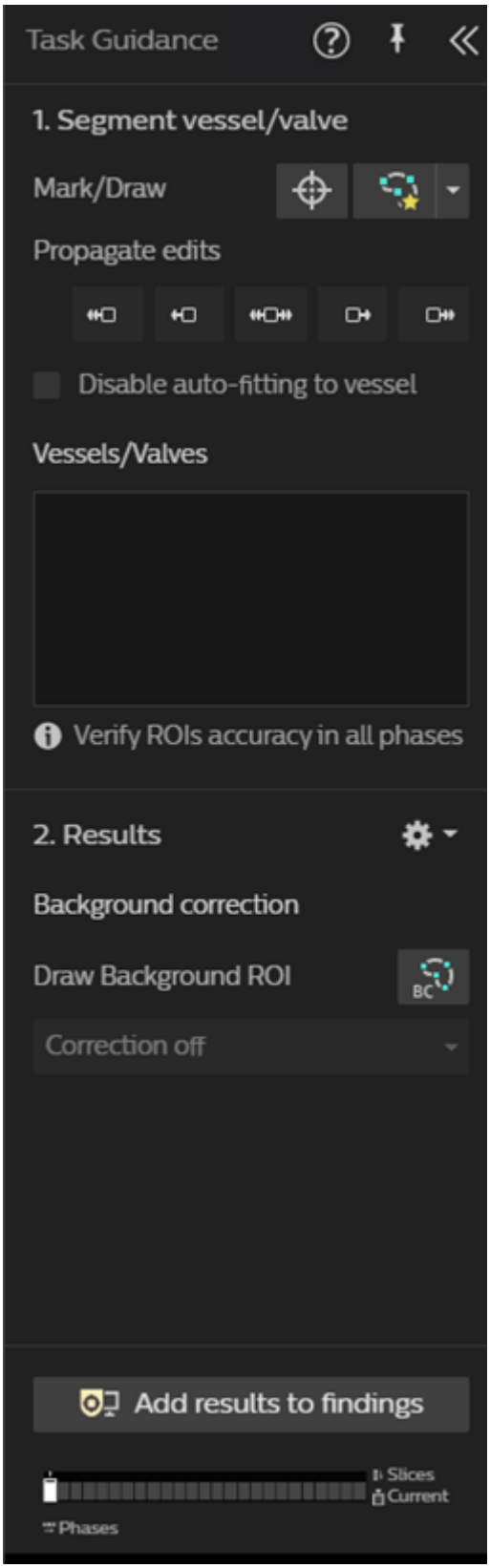


Application steps

The application has two steps:

1. Segment vessel/valve
2. Results

These steps are displayed in the **Task Guidance** panel, where each step includes the relevant tools.



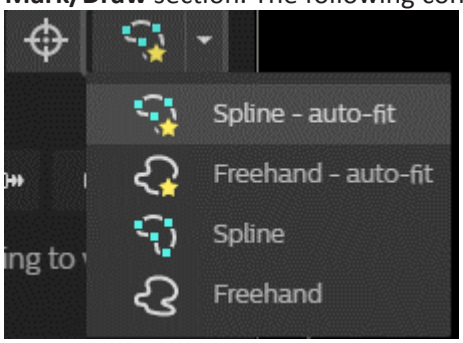
The recommended workflow is to go step by step. You can collapse the **Task Guidance** panel to show only buttons.

1. Segment vessel/valve

In this first step of the application, draw, label, and edit contours that define a vessel or valve in the scan.

Mark/Draw

1. Scroll through phases to select a phase that clearly displays the vessel or valve you want to analyze, and where the area of interest contains the highest velocity.
2. The selected phase is displayed in the main display area. Optionally, you can change the type of image using the viewport control **image type**. You can set the image type independently in each image viewport. The following image types are available:
   - FFE/M (anatomical)
   - PCA/M (model)
   - PCA/P (phase, showing velocity with colored areas of high and low intensity, this type of image is typically used as an overlay). You can use the **Change window level** tool to reduce image noise by dragging up and down, or to change the upper limit of the velocity scale on the right side of the viewport by dragging right and left.
3. Select a contour tool from the floating toolbar or from the **Task Guidance** panel, in the **Mark/Draw** section. The following contour tools are available in the list menu:



   -  **Seed point**: select the target sign to drop a seed point at center of the vessel of interest. This encircles the vessel with an editable spline contour.
   -  **Spline**: draw a contour by clicking the edges of the vessel to encircle it. The contour takes the curved shape of the vessel. To complete the curve, double-click.
   -  **Freehand**: use a pencil to draw the curve path of the vessel, then double-click to complete it.
   -  **Spline - auto-fit**: create a close spline contour. Start with one point at the edge of the vessel, then increase the number of points by clicking at the periphery of the vessel. Double-click to complete the segmentation.
   -  **Freehand - auto-fit**: create a closed, freehand contour. Press the mouse button to start drawing, and do not release the button until you finish drawing. The segemnted vessel, or ROI, takes the shape of the vessel once you release the mouse button.

NOTICE

If anatomical structures cover only a few pixels (e.g., small vessels), contours should be verified carefully in order to avoid inaccurate results.

NOTICE

The Seed point is suitable for large vessels. For smaller vessels, better results can be obtained using the Spline or Freehand methods.

Name and delete contours

After you create a contour, the **Choose vessel name** dialog box opens automatically, where you can either select a label or write a custom name. The list of names appears on the **Task Guidance** panel.

Right-click a selected contour to access **Delete** and **Rename** options from the context menu. You can also delete contours by pressing DELETE on your keyboard.

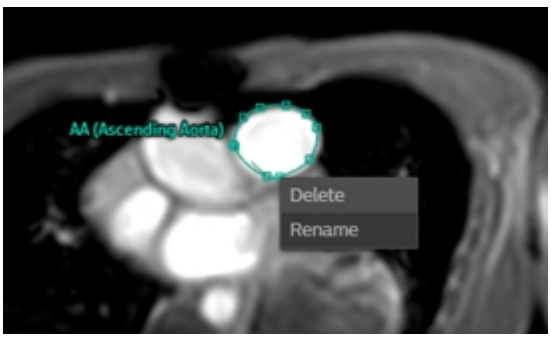


Fig. 45: Labeled contour

Verify and edit contours

1. Verify that the contours accurately define the vessel or valve in every phase of the slice. You can use the **Cine/Movie bar** to view images in a movie format, in order to play and pause review of slices. For more information, see the section "Cine/Movie bar" in the "MR Cardiac Suite workspace" chapter of these Instructions for Use.
2. Verify the accuracy of the contour and make corrections if needed.

   To edit a **Spline** contour, hover over the ROI seeds. The ROI points get highlighted, then you can drag these points.

   – If one point touches an adjacent point, the points merge with one another.
   – To add a new point, hover over the line and a **+** icon appears. Click it to create new point.

   To edit a **Freehand** contour, hover just outside the ROI line. A **+** icon appears. Draw by pressing your mouse button. Once you finish, the old ROI merges with the new added segment.

Pan: To shift an entire ROI, move the cursor over the edge of the contour. A **move** icon appears. Drag the contour to a new position.

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Additional editing tools provided in the toolbar:

- Expand
- Erode
- Nudge

To draw new ROI, click again on any drawing tools, and start drawing on the vessels.

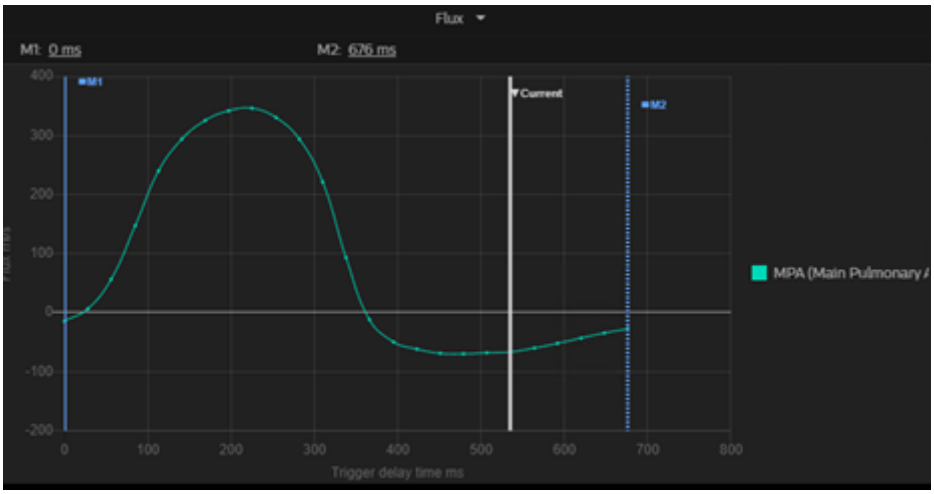
Propagate edits

Once you complete editing the contour, you can propagate the ROI to various directions. Edited ROI is propagated to match anatomy, where the default is an auto-fit to the vessel. In the **Task Guidance** panel you can select the checkbox **Disable auto-fitting to vessel**.

Vessels/Valves table

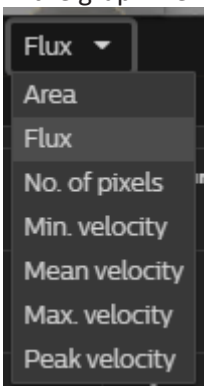
All segmented vessels (ROI) are listed in the **Task Guidance** panel in the **Vessels/Valves** table. Use this list to navigate between ROIs when they are in different slices, and to **Show** / **Hide** each of them.

Results graph



Once you complete a ROI, the resultant graph and table contents appear in the lower two viewports. If you draw additional ROIs, all are shown together on the graph and the image.

By default, the graph viewer shows the flow graph of **Flux** over all phases of heart cycle. To select different graphs like **Mean velocity**, **Max. velocity**, or **Area** under the curve, click the title in the graph viewport to open a list menu.



Results table

The lower right viewport shows the table of content averaged over phases, and contains vital information useful for different pathological findings, including:

- Stroke volume
- Forward flow volume
- Backward flow volume
- Regurgitant fraction
- Absolute stroke volume
- Mean flux
- Stroke distance
- Mean velocity
- Peak velocity
- Peak pressure gradient
- Forward flow volume / BSA

- Backward flow volume / BSA

ROI-based results are shown for comparison side-by-side in the table. You can:

- Show or hide table content using the **Configure table** option in the context menu of the table viewport.
- Switch between total **Analysis results** or **Current phase results** in the list menu on the table.
- Update the values of **Volume Inside**, **Volume Outside**, **Max Velocity**, and **Min Velocity** in the table by dragging the **M1** and **M2** lines on the graph.
- Change the BSA method of calculation by right-clicking on the table, and selecting **Change BSA calculation method**. The **Set BSA parameters** dialog box opens. The Mosteller formula is used by default.
- Change the heart rate manually by clicking on the heart rate in the table.

Copy the table contents by right-clicking and selecting **Copy to clipboard** or **Copy all table to clipboard** and pasting in a document such as Excel, Word, etc.

Background correction

NOTICE

Series acquired with a Philips scanner are automatically corrected for bias or eddy current.

Background correction gives more accuracy when calculating the graph, as it accounts for a baseline correction to the existing velocity graph. Toggle background correction on in order to draw ROI:

- Either on a magnitude image or phase image.
- At a place where there is no/barely any flow noticed.

There are two types of background correction methods:

- **On each phase**: baseline correction done on values calculated from each phase.
- **Mean over all phase**: baseline correction done on mean value of all phases.

NOTICE

The correction should be done in the slice of interest because the background correction ROI can only be used in one slice.

Save results

To save results, click **Add results to finding**.

Understanding the results

General Parameters

Heart Rate	As derived from acquisition.
Velocity Encoding	As derived from acquisition.
Velocity Direction	As derived from acquisition.

Right-click the results summary table and click **Analysis results**. These results are only generated for multiphase scans.

Stroke volume

- The net amount of blood that passes the contour (1 RR-interval).

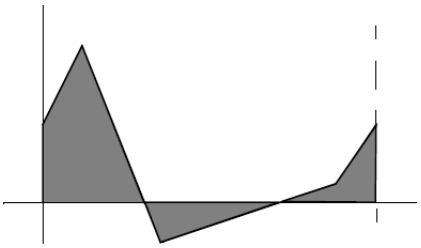


Fig. 46: Stroke volume (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

Forward flow volume [ml]

- The amount of the blood that passes the contour in the positive flow direction (1 RR-interval).

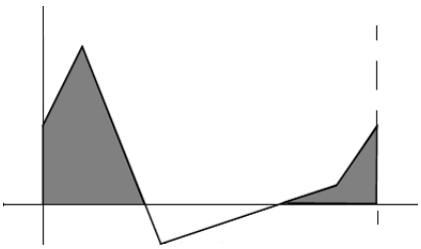


Fig. 47: Forward flow volume (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

Backward flow volume [ml]

- The amount of blood that passes the contour in the negative flow direction (1 RR-interval).

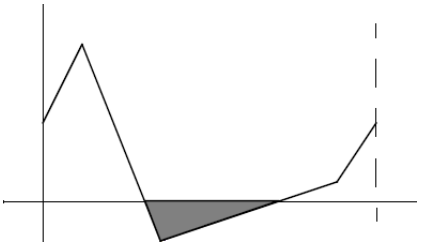


Fig. 48: Backward flow volume (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

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Regurgitant fraction

- Fraction of backward to forward flow.

Absolute stroke volume

- Absolute value of forward flow PLUS absolute value of backward flow (1 RR-interval).

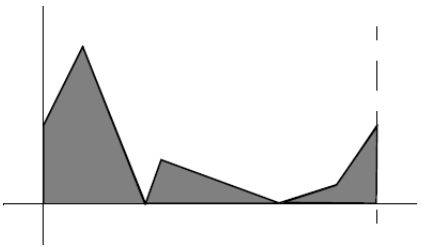

Fig. 49: Absolute stroke volume (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

Mean flux [ml/s]

- Stroke volume x heartbeat / 60 (1 RR-interval).

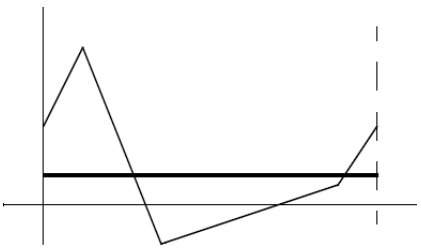

Fig. 50: Mean flux, indicated by the horizontal line in the graph (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

Stroke distance

- Net distance the blood proceeds in the vessel in 1 RR-interval.

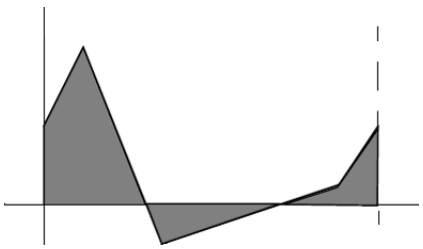

Fig. 51: Stroke distance (x-axis = trigger delay time (ms), y-axis = mean velocity (cm/s))

Mean velocity

- Stroke distance x heartbeat / 60 (1 RR-interval).

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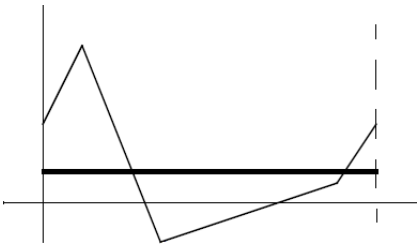

Fig. 52: Mean velocity, indicated by the horizontal line in the graph (x-axis = trigger delay time (ms), y-axis = mean velocity (cm/s))

Peak velocity

- Peak blood flow velocity

Current Phase Results for each ROI (vessel contour)

Right-click the results summary table and click **Current phase results**. The results are available per slice, per phase and per vessel.

- Positive flow is flow into the plane (maximum positive: displayed white), e.g. in Feet-to-Head direction and in Right-to-Left direction.
- Negative flow is flow out of the plane (maximum negative: displayed black), e.g. in Head-to-Feet direction and in Left-to-Right direction.

Trigger delay [ms]	• Time between R-peak and acquisition of the specific slice.
Flux [ml/s]	• Blood volume that passes the contour per second. This is the same as 'mean velocity * area'. Note that this value is only calculated if the flow direction is perpendicular to the image.
Area [cm2]	• Area of the pixels that are partially or fully included in the contour. To visualize this area, right-click in an image viewport and select 'Filled graphics'.
Nr. of pixels	• Pixels that are partially or fully included in the contour.
Mean velocity [cm/s]	• Mean blood flow velocity.
Maximum velocity [cm/s]	• Highest measured positive flow in the contour.
Minimum velocity [cm/s]	• Highest measured negative flow in the contour.
Peak velocity [cm/s]	• Either maximum velocity or minimum velocity, whichever has the highest absolute value.
Velocity Standard Deviation [cm/s]	• Standard deviation of the mean velocity.

NOTICE

To show Cardiac Output, change the unit for Flux to L/min in the settings dialog (see below). In the mean analysis results the Cardiac Output can be read from the parameter Mean Flux.

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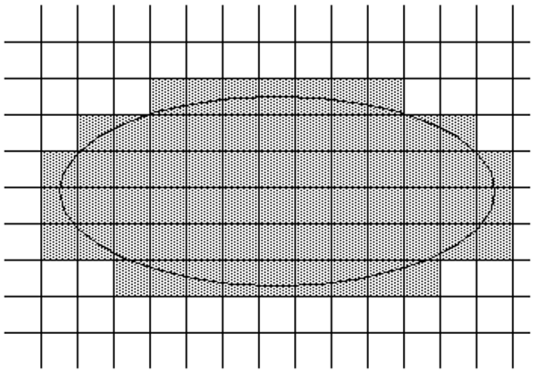


Fig. 53: The pixels that are taken into account for quantitative flow calculations.

Note that the units for each result type can be chosen by the user. Available units are:

Result	Available units	Default unit
Area	mm^2, cm^2	cm^2
Distance	cm, mm, m	cm
Dynamic Time	ms, s	depends on length of series
Flux	mm^3/s, ml/s, ml/min, L/min	ml/s
Trigger Delay Time	ms, s	ms
Velocity	mm/s, cm/s, m/s	cm/s
Volume	mm^3, ml, cc, cm^3	ml

Procedure for analyzing E/A ratio for Mitral Valve

To analyze E/A ratio, we recommend that you use the following procedure.

1. Plan a QFlow series for the mitral valve when it is nearly at the end of the diastolic stage (opening stage).

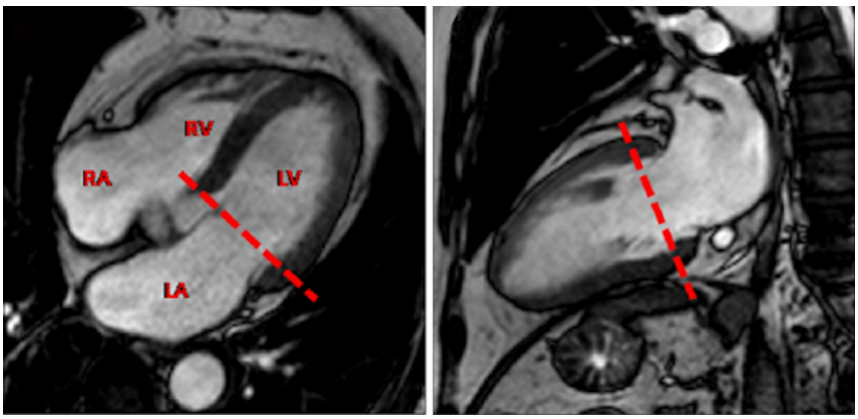


Fig. 54: Example of the recommended planned situation for the series (these images are provided by courtesy of Ricardo Duarte and Gabriel Fernandez "Assessment of LV DF by MRI")

⇨ Avoid being too close to the cardiac base as this may cause distortion or include LA inflow tract or aortic outflow tract. This position includes both LV inflow and LV outflow.

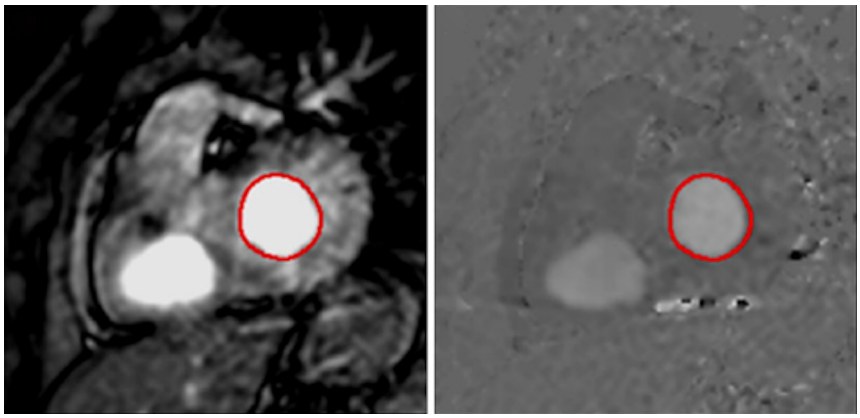
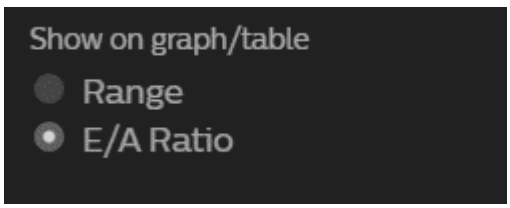


Fig. 55: Example of an optimal result (these images are provided by courtesy of Ricardo Duarte and Gabriel Fernandez "Assessment of LV DF by MRI")

2. To create the contour, use the following steps. (These steps minimize the need for editing as the entire LV inflow and outflow is included.)
   - Select the **Spline** contour tool.
   - Display the **LV ED** phase.
   - Create the contour.
   - Select **Mitral Valve** in the vessel name list.



⇨ After you define the contour, the analysis results are displayed.

NOTICE

When you label a contour as Mitral Valve, you can assess diastolic function by investigating the ratio between early diastolic filling peak and the atrial kick. This tool also allows you to measure the deceleration time.

3. In the **Results** step in the **Task Guidance** panel, select **E/A ratio for Mitral Valve**.
4. Set the position of the rulers correctly in the analysis graph.

⇨ Rulers are added to the analysis graph allowing you to indicate the following positions:

- Early peak (Emax)
- Deceleration time (Emin)
- Atrial peak (Amax)

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⇨ A yellow line is displayed between Emax and Emin. This line provides assistance with positioning Emin; the line reflects the deceleration slope of the flow when Emin is positioned correctly.

⇨ Emin should be set such that the deceleration line has a similar downslope to the graph between Emax and Amax.

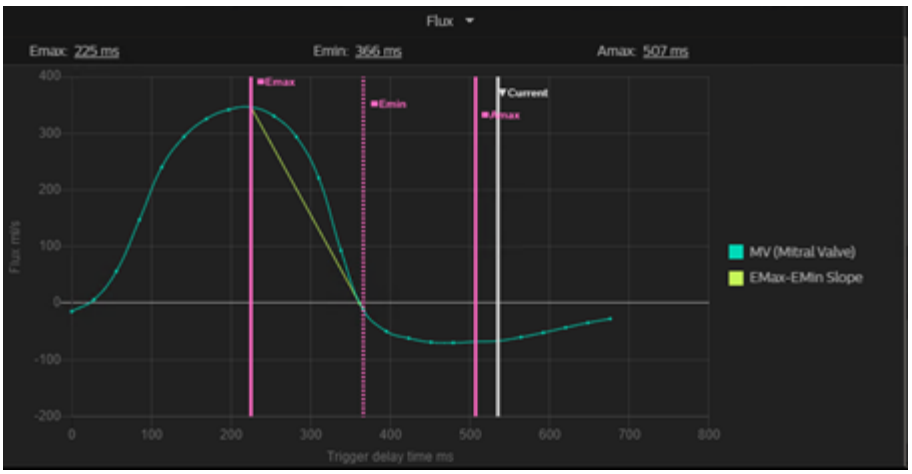


Fig. 56: Setting the position of the E/A ratio rulers in the analysis graph

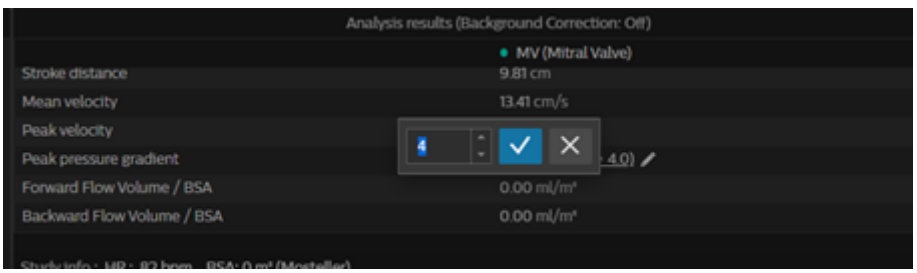
⇨ The deceleration time is calculated as the time between Emax and the point where the slope intersects the baseline (indicated by the arrow in the figure above). The normal range for the deceleration time is 140-220 ms.

⇨ The deceleration rate represents the measured upslope from the deceleration line.

5. Verify the position of the rulers.

⇨ Numerical values of the ruler positions are displayed in the task guidance panel. You can adjust these values directly in the task guidance panel, if desired.

⇨ A section is added to the numerical results table indicating the **E/A Ratio**, the **Deceleration Time**, and **Deceleration Rate**.



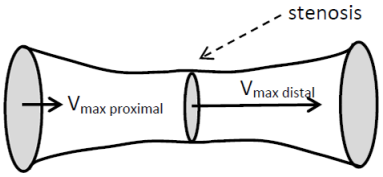
Peak pressure gradient

The pressure gradient over, for example, stenotic cardiac valves or aortic stenosis is considered to be a measure of severity of the disease. It is important to measure the maximum flow velocity (Vmax) distal from the expected stenosis, which can be performed with QFlow MRI.

The peak pressure gradient is available in QFlow by using the simplified Bernoulli equation as defined in literature (see references below).

In reference [1], it is explained that the decrease in pressure (the pressure gradient) ΔP over a stenosis can be calculated using the modified Bernoulli equation:

$$(P_{\text{distal}} - P_{\text{proximal}}) = K \times (V_{\text{max distal}} - V_{\text{max proximal}})^2,$$



P_{distal} and P_{proximal} are the pressures distally and proximally of the stenosis, respectively, $V_{\text{max distal}}$ and $V_{\text{max proximal}}$ the maximum velocities distally and proximally of the stenosis, and K a constant.

Under the assumption that $V_{\text{max proximal}}$ is small compared with $V_{\text{max distal}}$ this can be further simplified to:

$(P_{\text{distal}} - P_{\text{proximal}}) = 4 \times V_{\text{max distal}}^2$ or $\Delta P = 4V_{\text{max}}^2$

In reference [2], a method is proposed to measure V_{max}, namely: “the peak velocity was calculated as the average of the top 10% velocities from contiguous pixels within the vessels. The final peak velocity was calculated as the maximum of the peak velocities at systole”.

Using a user-defined Pressure Gradient

Using a series of anatomically accurate models of aortic coarctation, the laboratory portion of a study (reference [3]) found that the loss coefficient (K), commonly taken to be 4.0 in the simplified Bernoulli equation P =KV2, was a function of stenosis severity. The values of the loss coefficient ranged from 2.8 for a 50% stenosis to 4.9 for a 90% stenosis.

For this reason the user is able to change the loss coefficient (K) in the results table.

NOTICE

This function and option should only be used by certified MR Cardiac Suite users.

References

[1] M.B. Srichai et al., "Cardiovascular applications of phase-contrast MRI”, AJR 2009; 192:662–675.

[2] C.D. Lew et al., “Peak velocity and flow quantification validation for sensitivity-encoded phase-contrast MR imaging”, Ac. Rad 2007;14(3):258-269.

[3] JonN. Oshinski, et al., “Improved Measurement of pressure Gradients in Aortic Coarctation by Magnetic Resonance Imaging’; J am Coll Cardiol.1996;28(7):1818-1826

Additional tools and options

Color overlays

In the toolbar above the applications, there are three color overlay icons. Selecting the icons overlays the magnitude and phase image with (red and blue) color spectrum showing two opposing velocities.

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Viewing and editing any phase without scrolling

The layout option per viewport can be changed to 1X1 tiling, and you can then zoom in on images and contours edited on any phase, without scrolling through slices.

Pixel values

To see the intensity value of any pixel:

1. From the context menu select **Annotation**, then **Pixel value**.
2. Place a marker on any point of the image to see the value of that pixel intensity at that phase.

Velocity probe

A velocity probe is available in the toolbar, which you can use to hover over the image to see the velocity of any point.

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Lotz, J., Meier, C., Leppert, A., Galanski, M. "Cardiovascular Flow Measurement with Phase-Contrast MR Imaging: Basic Facts and Implementation". *RadioGraphics*, No. 22: 651-671, 2002.

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Zile, M. R., Brutsaert, D. L. "New Concepts in Diastolic Dysfunction and Diastolic Heart Failure: Part I (Diagnosis, Prognosis, and Measurements of Diastolic Function)". *Circulation*, No. 105: 1387-1393, 2002.

Background Correction

Lan, T., Erdogmus, D., Hayflick, S. J., Szumowski, J. U. "Phase Unwrapping and Background Correction in MRI". IEEE Workshop on Machine Learning for Signal Processing, 239-243, 2008.

Rigsby, C. K., Hilpipre, N., McNeal, G. R., et al. "Analysis of an automated background correction method for cardiovascular MR phase contrast imaging in children and young adults". *Pediatr Radiol*, No. 44: 265-273, 2014.

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Functional LA (Long Axis) Analysis

Indications for Use

The MR Cardiac Suite Functional LA (Long Axis) application is indicated to assist the user with assessment of LV function from single and multi-slice long axis cardiac cine data.

Overview

The Functional LA application provides rapid long-axis functional analysis for LV, based on an ALEF method (Area Length Ejection Fraction). The application allows for both single and multi-slice acquisition.

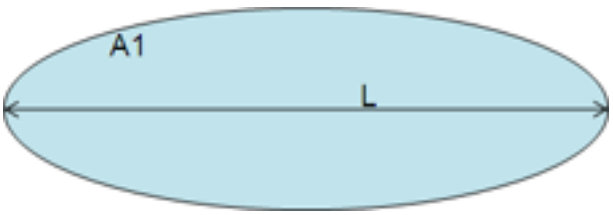

Fig. 57: ALEF method, single-plane ellipsoid model

$V = 8 \times A1^2 / 3 \times \pi \times L$

V = Volume, A = Area, L = Length

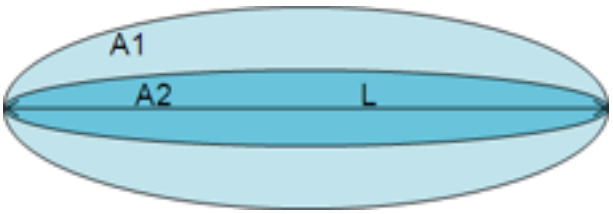

Fig. 58: ALEF method, biplane ellipsoid model

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$V = 8 \times A1 \times A2 / 3 \times \pi \times L$

V = Volume, A = Area, L = Length

You can perform this analysis on a single 2CH or 4CH series, or you can use biplane series for a more accurate result.

NOTICE

To calculate the most accurate ALEF results, it is critical in both the acquisition and the analysis stages to plan and select the most representative slice for a mid-ventricle measurement.

NOTICE

The accuracy of this analysis method depends on the acquired series displaying the maximum volume for LV. The acquisition should be made perpendicular to the SA plane.

NOTICE

To use the biplane method, select two series that have been scanned perpendicular to each other.

Guidance for this analysis application is provided in the **Task Guidance** panel.

Starting the application

▷ On the application launch and navigation bar, click **+** to open the application launcher, then select the **Functional LA** icon.

▷ You can load series with phases or real-time (RT) acquired data with dynamics. Using dynamics provides improved quantification of arrhythmic patients using the ALEF method. The **Select series for Functional LA** dialog box opens, where you can press CTRL to select more than one series:

- A suitable functional LA view 2CH or 4CH series
- A dynamic RT 2CH, 3CH, or 4CH series

▷ The application opens.

1. The LA views appear in two columns, showing the mid-slice of the stack. The first column displays the first phase, which is typically the End Diastolic (ED) phase. The second column displays the End Systolic (ES) phase as calculated by the system.
2. Once you draw contours, the results automatically appear in the table on the right.

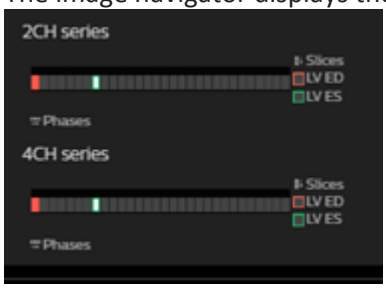
3. **Set ED and ES**The initial ED and ES are located in default pashes. Scroll to the correct ED and correct ES, then select the optimal mid-slice in the ventricle and the optimal phase/ dynamic for ED and ES definitions.

If there are two series, you can unlink them in order to select different ED and ES phases for the series. In the **Task Guidance** panel, clear the **Link Phases** checkbox.

Draw contours

1. Scroll to the ED image, then click **Set ED** on the image, unless it is already the selected ED.
2. Scroll to the ES image, then click **Set ES** on top the image, unless it is already the selected ES.

⇨ The image navigator displays the currently selected phases, color-coded with the images:



⇨ The drawing tool is available either from the floating toolbar or the **Task Guidance** panel. Select the drawing tool and draw the contour on ED and ES of participating series:

3. Draw a contour starting at one side of the valve plane, following the endocardium to the other side of the valve plane. Double-click to complete the contour. The valve plane and the long axis are drawn automatically.

   Optionally, reposition the midline to the apex in order to fine-tune the contour for optimal results.

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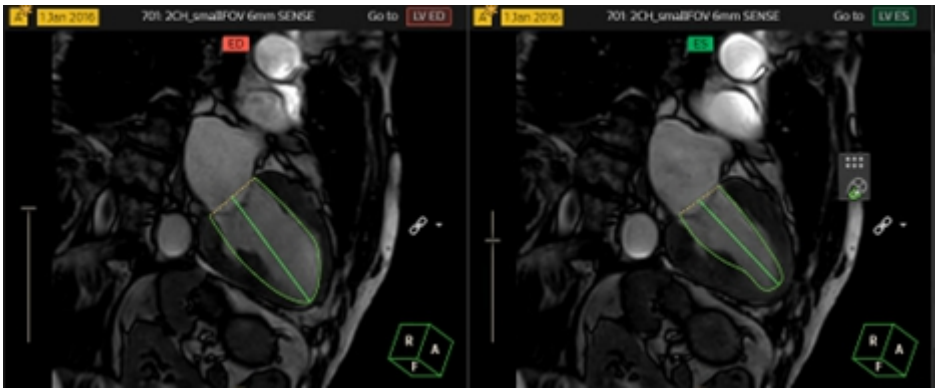
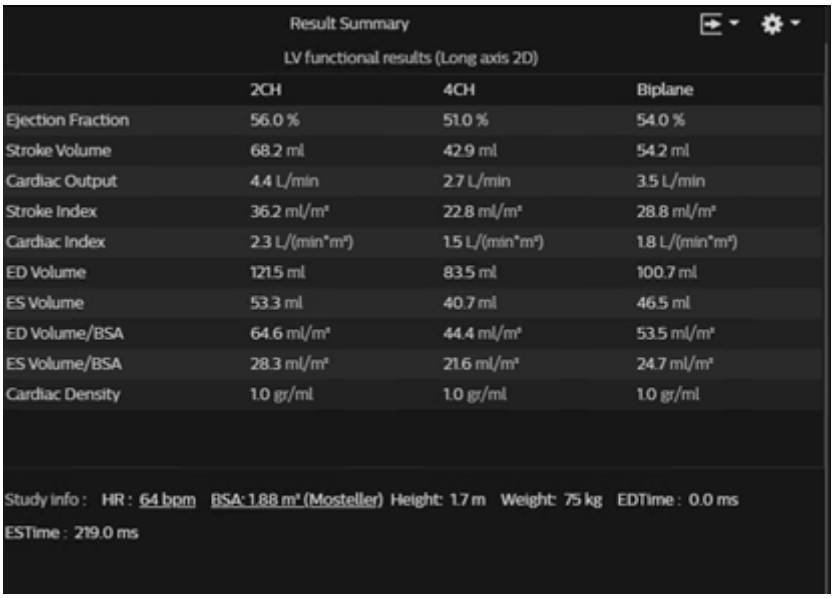


Results are displayed when contours are present.

View results



Result Summary

LV functional results (Long axis 2D)

	2CH	4CH	Biplane
Ejection Fraction	56.0 %	51.0 %	54.0 %
Stroke Volume	68.2 ml	42.9 ml	54.2 ml
Cardiac Output	4.4 L/min	2.7 L/min	3.5 L/min
Stroke Index	36.2 ml/m²	22.8 ml/m²	28.8 ml/m²
Cardiac Index	2.3 L/(min*m²)	1.5 L/(min*m²)	1.8 L/(min*m²)
ED Volume	121.5 ml	83.5 ml	100.7 ml
ES Volume	53.3 ml	40.7 ml	46.5 ml
ED Volume/BSA	64.6 ml/m²	44.4 ml/m²	53.5 ml/m²
ES Volume/BSA	28.3 ml/m²	21.6 ml/m²	24.7 ml/m²
Cardiac Density	1.0 gr/ml	1.0 gr/ml	1.0 gr/ml

Study info : HR : 64 bpm BSA: 1.88 m² (Mosteller) Height: 1.7 m Weight: 75 kg EDTime : 0.0 ms

ESTime : 219.0 ms

The **Result Summary** panel displays the results of the analysis. The following steps describe how to fine-tune the results summary.

- The patient's heart rate, and other information, is entered automatically from the acquisition information. You can edit heart rate, patient width, and height directly at the bottom of the **Result Summary** table.
- To change the layout of the results summary, right-click the and select an option.
- To display results adjusted for the patient's BSA, right-click the **Result Summary** table. Click **BSA Calculation**. If the patient's weight and height are not available from the acquisition information, enter the weight and height in the **BSA Calculation** dialog box, then click **OK**.

NOTICE

The BSA calculation uses Mosteller's formula by default: √ Height (cm) x Weight (kg) / 3600. To use an alternative calculation (for example, for pediatrics), right-click the Result Summary table, click **BSA Formula Type**, then select a calculation formula.

Calculating the results

Blood volumes (V) are calculated as follows in the Functional LA analysis package:

- **End diastolic phase (ED)**: The phase at the beginning of a heartbeat where the heart is 'at rest', i.e. where the blood volume is at a maximum.
- **End systolic phase (ES)**: The phase where the heart is fully contracted, i.e. where the blood volume is at a minimum.
- **ED volume (V_{ED})**: The amount of blood that is in the heart at the end diastolic phase; expressed in milliliters (ml).

  $V_{ED} = 8 / 3\pi \times A^2/1$

  Where A is the area of the endo contour (cm^2) and l the length of the long axis line (cm) between the intersections with the short axis line and the endo contour at the ED image.
- **ES volume (V_{ES}): The amount of blood that is in the heart at the end systolic phase; in ml. V_{ES} is calculated in a similar way as V_{ED} with the difference that A and l are taken from the ES image.**
- **Stroke volume (SV)**: The amount of blood that is pumped out per heartbeat, i.e. the difference between the blood volume at the end diastolic phase and the end systolic phase; in ml.

  $SV = V_{ED} - V_{ES}$
- **Stroke index (SI)**: The stroke volume relative to the body surface area; in ml/beat/m^2.

  SI = SV/BSA
- **Body Surface Area (BSA)**: The estimated (not measured) area of the patient's body surface; in m^2. For adults, the approximate value of BSA can be calculated using Mosteller's formula:

  BSA = √ (Height [cm] x Weight [kg]) / 3600
- **Ejection fraction (EF)**: The amount of blood that is pumped out per heartbeat relative to the blood volume at the end diastolic phase in percentages.

  $EF = (SV / V_{ED}) \times 100$
- **Cardiac output (CO)**: The amount of blood that is pumped out per minute; in liter (l). The heart rate is in beats per minute (bpm).

  CO = (SV × HeartRate) / 1000
- **Cardiac Index (CI)**: The cardiac output relative to the body surface area; in l/min/m^2.

  CI = CO / BSA

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NOTICE

When results cannot be calculated, the text ‘n/a’ (= not available) is displayed.

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Spatial Enhancement

Indications for Use

The Spatial Enhancement application allows review, segmentation and quantification of T1w and T2w multi-slice, single-phase short axis MR images. The application is indicated to support the user with assessment of myocardial tissue characteristics that may point to pathologies on the tissue level, such as fibrotic tissue.

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Overview

Late gadolinium enhancement is a technique used in cardiac MRI for cardiac tissue characterization, for the assessment of myocardial scar formation and regional myocardial fibrosis. Late gadolinium enhancement is also known by the terms "late enhancement" or "delayed enhancement". Late gadolinium enhancement is based on the shortening of T1 and different regional distribution patterns of gadolinium-based contrast agents within the extracellular space of the myocardium. It also depends on varying uptake and washout patterns within the normal myocardium and different disease processes. This is depicted by applying an inversion pulse to null the inherent signal of the myocardium after a certain amount of time.

The Spatial Enhancement application provides analysis and identification of spatial enhancement, based on time intensity signal changes.

If segmentation from the Functional LV & RV Analysis application is available, automatic registration provides automatic contours. You can analyze spatial enhancement differences using different methods: freehand threshold, reference segment, or reference area with adjustable standard deviation. You can compare enhanced areas with non-enhanced areas using the **Results summary** table.

Guidance for this application is provided in the **Task Guidance** panel.

Image acquisition

Late gadolinium enhancement is usually conducted with an inversion-recovery prepared T1 weighted gradient echo, and either manually adapted inversion time or as a PSIR sequence with a phase-sensitive inversion-recovery-based reconstruction algorithm. Typically, late gadolinium enhancement is measured around 10-20 min after administration of a gadolinium-based contrast agent.

Interpretation

Late gadolinium enhancement is a result of regional differences in myocardial extracellular volume and different uptake and washout patterns within the extracellular space, and is seen in myocardial injury, e.g., myocyte necrosis, myocardial edema, myocardial scar tissue, and focal areas of fibrosis, and can be related to different cardiac diseases regarding its distribution and other tissue properties and clinical parameters.

Clinical applications

Late gadolinium enhancement is applied in these various clinical scenarios, and can help to detect and characterize various myocardial diseases:

- **Myocardial infarction**
  - Detection and quantification of regional myocardial fibrosis and myocardial scar tissue.
  - LGE is considered a surrogate for infarct size.
  - Detection of microvascular obstruction (MVO).
  - LGE is a strong predictor of outcome (superior to ventricular volumes and function).

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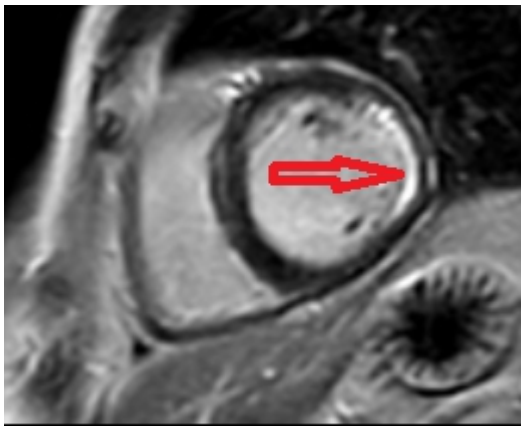
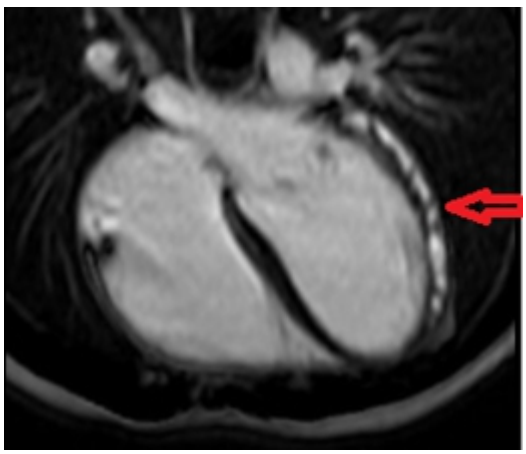
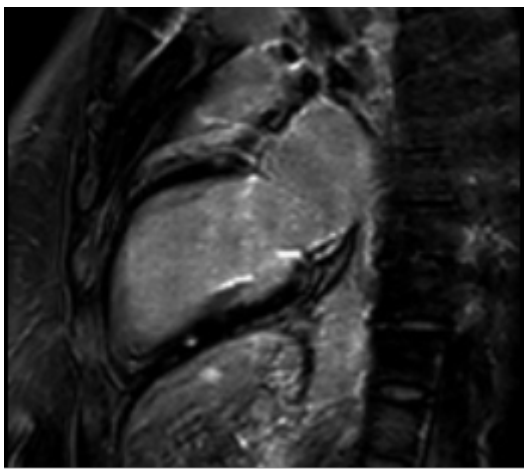


- **Myocarditis**
  - Patchy mid myocardial and/or focal subepicardial enhancement as an expression of potentially irreversible injury (myocyte necrosis, fibrosis, edema).
  - Can represent one of two main criteria in the diagnosis of acute myocarditis.



- **Cardiac Sarcoidosis**



  - Patchy mid myocardial and/or focal sub-epicardial enhancement as an expression of potentially irreversible injury.

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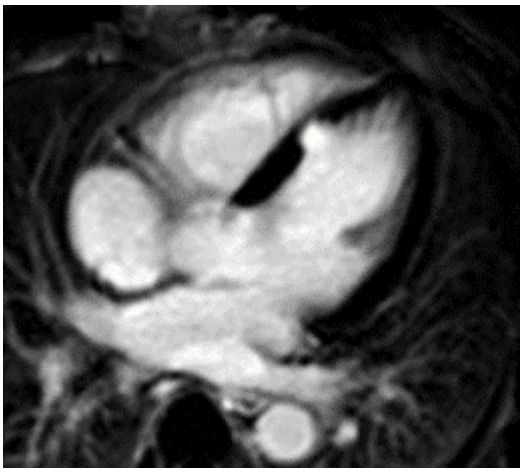
  - Linked to cardiac arrhythmia even with preserved left ventricular function.

- **Cardiac Amyloidosis**

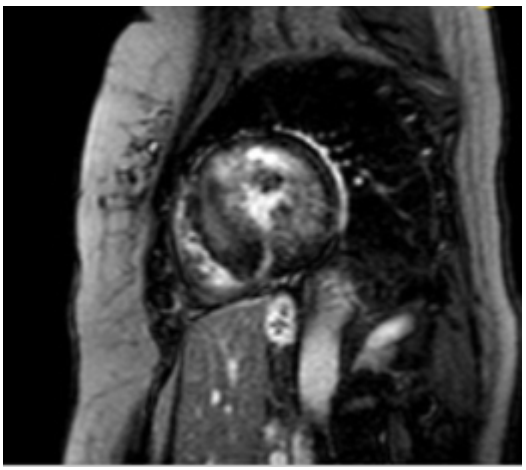
  Subendocardial enhancement in a non-coronary distribution and poor contrast difference between blood and myocardium due to abnormal blood-pool/tissue gadolinium kinetics.

- **Dilated Cardiomyopathy**



  - Detection of intramyocardial mid-wall fibrosis.
  - Predictor of ventricular arrhythmia and sudden cardiac death (SCD).

- **Hypertrophic Cardiomyopathy**



  - Patchy/streaky intramyocardial patterns at the right ventricular insertion sites within the hypertrophied myocardium suggest fibrosis.
  - Prognostic value: increased risk of sudden cardiac death especially if extensive or diffuse (>15% wall mass).

MRI data types supported

The Spatial Enhancement application supports single-phase short-axis data for analysis with the following data types:

- IRGE (Inversion recovery gradient echo) or M/IR

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- PSIR (Phase-sensitive inversion recovery) or CR/IR and M/IR together in a single series.

Launch application

You can launch the Spatial Enhancement application by:

- Right-clicking a viewport containing a valid data type, and then selecting the application.

  A valid data type has a **Scan Type** label of **Spatial enhancement** and an **Orientation** label of **SA**. The series should be based on an Inversion Recovery technique.
- Clicking **+** on the application launcher, and then selecting **Spatial Enhancement**. A dialog box opens containing all valid data for the application, where you can select a series to analyze.

The Spatial Enhancement SA LV package opens in the **Segment LV** screen and displays the LV view.

If contours are available from a previously performed Functional LV & RV analysis, these contours are automatically loaded in the application. If multiple contours are available, they are displayed in a dialog box; select which contours to use for the analysis. The contours are registered and fitted to the loaded series.

NOTICE

It is also possible to open and analyze a series displaying RV, atria, or other anatomy, if you set the labeling for these series as 'Spatial Enhancement' and 'SA' in the Labeling screen. For correct estimations, the tissue must also be fully segmented. In this case, contours have to be drawn manually.

If you do set labels in this way, please note that such series will automatically be labeled in the same way the next time that you use the application.

NOTICE

If you used the Endo Only option in the Functional LV & RV analysis, epicardial contours are not available.

Workflow

Tools for editing contours and segments are available in the **Task Guidance** panel. If the data you selected has multiple image types, CR_IR is the default. Otherwise, the M_IR image type is chosen for analysis.

Hanging layouts

You can hang layouts in this stage. There are 3 Hanging Protocols (HP):

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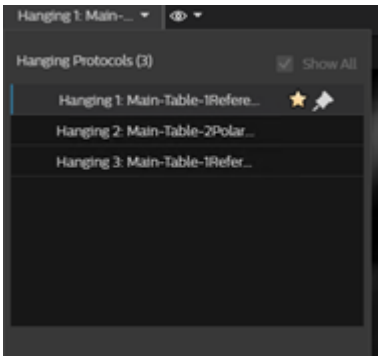
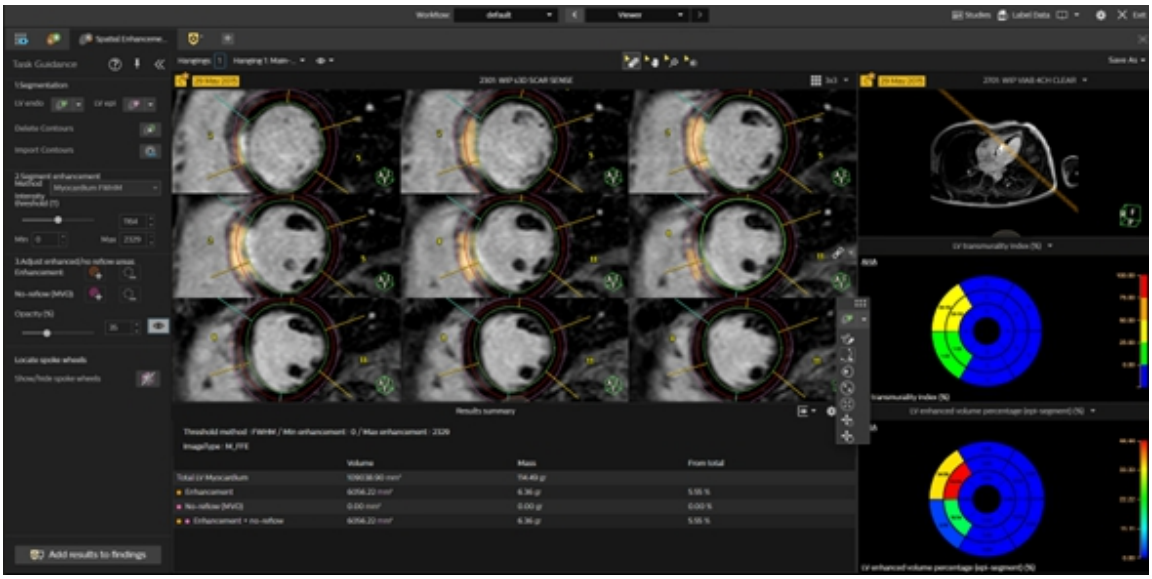


- All slice + reference view (2ch/3ch/4ch) + polar maps
- Image + table and two polar maps
- Image + one ref viewport + one polar map

1. Segmentation

This is the first workflow step in the **Task Guidance** panel.

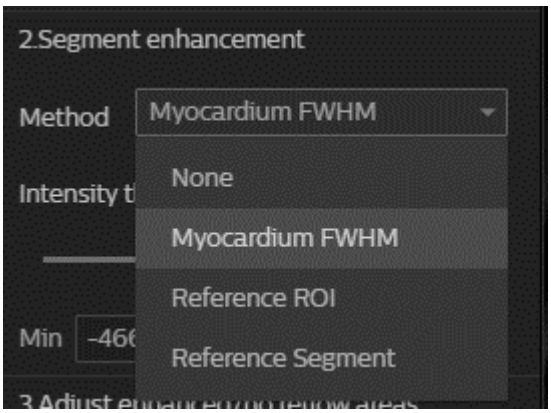


- If the data has functional fCMR results created by auto-preprocessing, epi and endo contours are segmented and shown automatically. This is achieved by selecting the closest phase on functional data with regards to the data in Spatial Enhancement. The application uses Td (Trigger delay) time. Register these two datasets, and then propagate the epi and endo contours.
- If contours are available, verify the contours on each slice and correct them if necessary.
- If contours are not available to import, draw the contours manually. Before drawing the contours, inspect all slices in the direction from valves to apex. Choose the slice where the aorta is not visible anymore. However, in case of an enhanced area in the slice showing the aorta, start with this slice.

2. Segment enhancement

This is the second workflow step in the **Task Guidance** panel.

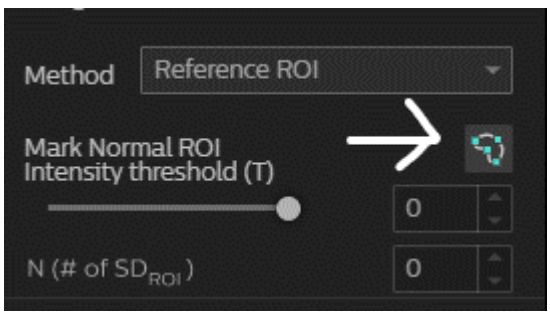
The following methods for semi-automatic, or manual, segmentation of enhanced tissue inside myocardium are available in the **Method** list menu of the **Task Guidance** panel.



NOTICE

As the Myocardium FWHM method is focused on enhanced pixels, it should only be used when a clear enhanced area is available in the series.

- None
- **Myocardium FWHM**:
  - By default, when contours are available, segment enhancement is applied using the **Myocardium FWHM** method by default.
  - The FWHM method is derived from the enhanced voxels within the LV segmentation. It is focused on the higher pixel values from a histogram, and the threshold is set by defining the middle of this Gaussian peak at half maximum.
- **Reference ROI** - Set the threshold by defining a normal area:
  - Navigate to a slice containing a normal area to use as reference.
  - On the **Task Guidance** panel, click the icon to draw a ROI, double-clicking to complete the ROI.



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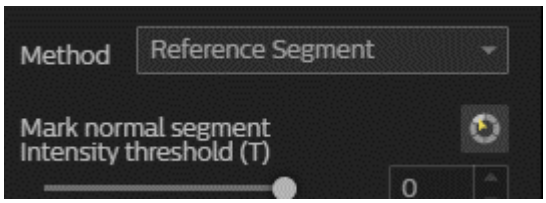
  - Optionally, make small adjustments in the **Task Guidance** panel by dragging the slider or using the list box near **Mark Normal ROI Intensity threshold (T)**, and by using the list box to the right of **N** (# of Standard Deviations).

- **Reference Segment** - Make sure spokes are added before selecting this method, or a dialogue box opens to add spokes.
  - Navigate to a slice containing a normal segment to use as a reference.
  - Select **Mark normal segment** from the **Task Guidance** panel, then click on the healthy segment.



  - Optionally, make small adjustments in the **Task Guidance** panel by dragging the slider or using the list box near **Mark Normal ROI Intensity threshold (T)**, and by using the list box to the right of **N** (# of Standard Deviations).
  - In case of automatic thresholding using a normal segment or ROI, the threshold is derived from the normal segment or ROI (this implies that a normal segment or ROI must be present).
  - A histogram of the intensity (the pixel values) in the myocardium is shown in the figure below. The first peak in the histogram corresponds to the normal segment or area. The pixel value μ at this peak is the mean value of the normal segment or area. The standard deviation σ determines the variation in the normal segment or area. A threshold T is calculated based on a user-selectable constant c:
    $T = \mu + c \times \sigma$
    The default value for constant c is 3. With c = 3 you may assume (99.9% probability) that everything above the threshold T can be seen as enhanced area.

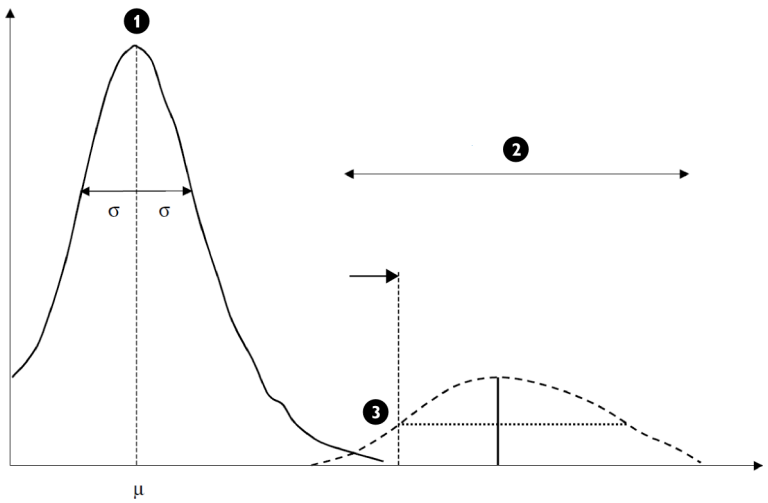


Fig. 59: Histogram of Intensity Using FWHM, x-axis: intensity, y-axis: probability, 1: normal area, 2: enhanced area intensity range, 3: threshold T halfway between minimum and maximum

3. Adjust enhanced / no reflow areas

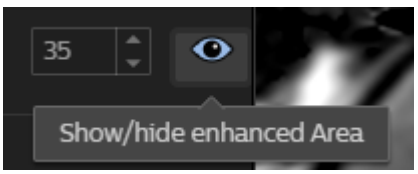
This is the third workflow step in the **Task Guidance** panel.

If the results of the threshold procedure are not completely satisfactory, you can edit the enhanced area manually using the following tools:

- Add and remove **Enhancement**.
- Add and remove **No-reflow (MVO)**.
- Change the size of the painted pixels using manual editing tools: CTRL + mouse wheel, then clicking inside the myocardium.

Micro-Vascular Obstruction areas (MVO) are not automatically detected, and seen as "normal tissue" due to the "normal" signal intensity of the image pixels. For this reason, the product contains add/remove tool to manually add pixels for MVO. Click **Paint enhanced area** and add threshold volume by painting in the affected area. The amount of manually added pixels for MVO is designated as **No Reflow volume** and **No Reflow mass** in the **Results summary** table. These additional pixels are also added to the **Enhanced volume** and **Enhanced mass** parameters in the Results table.

The eye button can be toggled on and off to show and hide color overlays.



Results table

The **Results summary** table, polar map, and the source image with contours and spoke wheels are visible in the application. When you click a slice in a polar map, the corresponding source slice image is displayed.

The polar maps shown by default are **LV transmurality index (%)** and **LV enhanced volume percentage (%)**. You can select the following types of polar maps from the list menu in the map's title:

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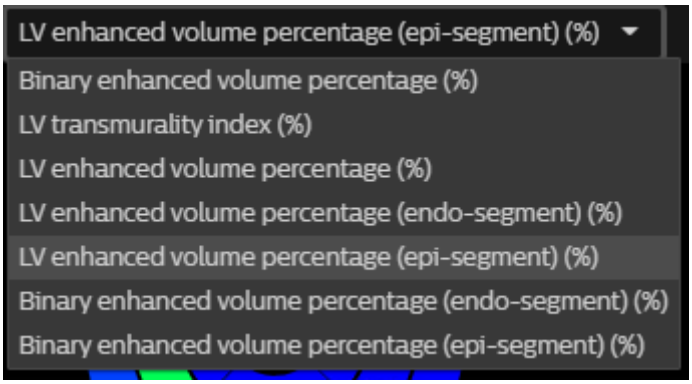
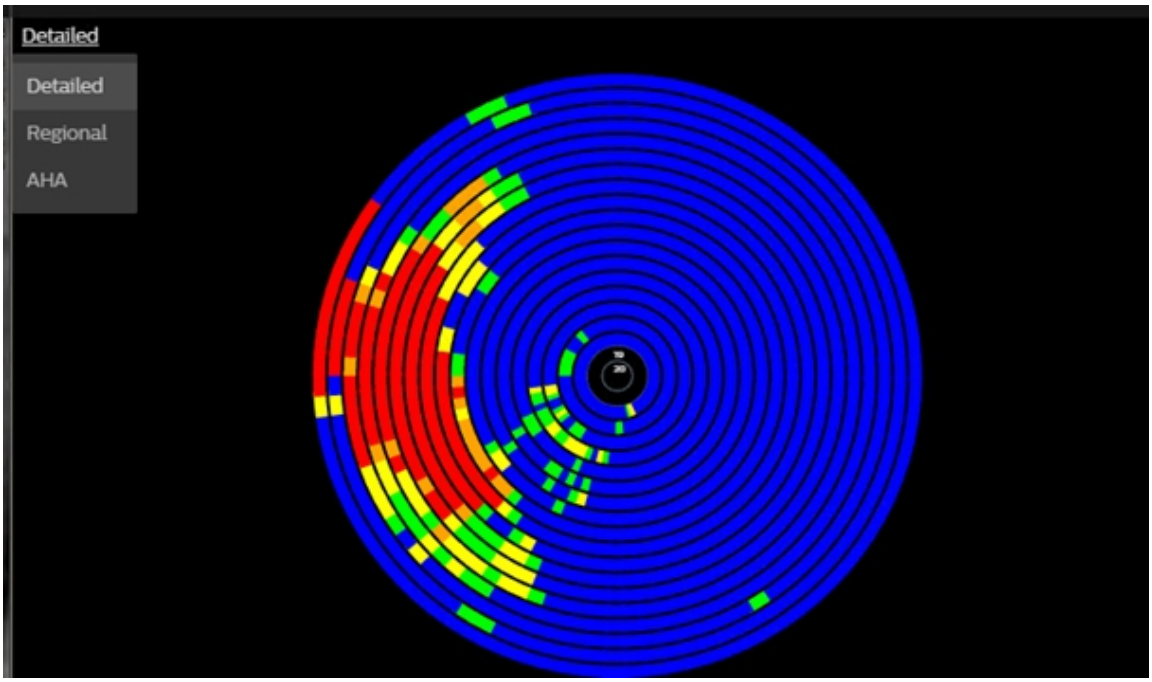


- **LV enhanced volume percentage (endo-segment) (%)**
- **LV enhanced volume percentage (epi-segment) (%)**
- **Binary enhanced volume percentage (%)**
- **Binary enhanced volume percentage (endo-segment) (%)**
- **Binary enhanced volume percentage (epi-segment) (%)**

Switch to **Detailed**, **Regional**, or **AHA** formats for the polar map using the context menu, or from the drop-down menu on the lefthand side of the map.

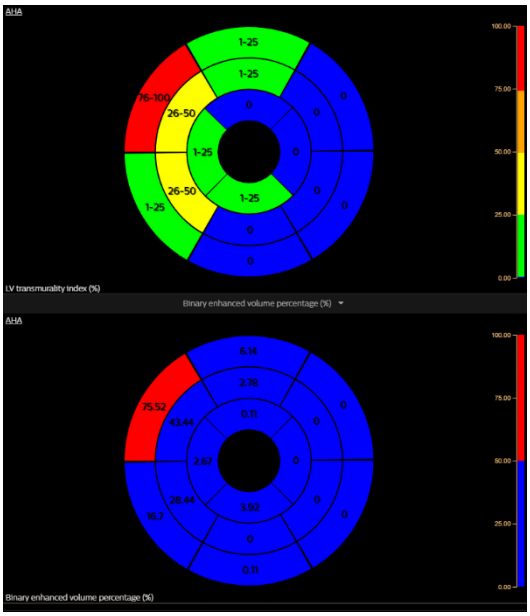


- When viewing the **Binary enhanced** or **LV enhanced** protocols, you can adjust the threshold of the color scale by dragging the middle mouse button up or down.
- The table shows the results summary of the:
  - Enhancement volume, Mass and % from total
  - No-reflow (MVO) volume, Mass and % from total

  - Addition of both these segmentations for total transmural segmentation quantifications.
- The **Binary enhanced volume percentage**, with the threshold set at 50%.

NOTICE

You want to ensure that in any segment the overall enhanced tissue + MVO do not exceed 75%. Anything above this is usually considered a non-viable segment. This is the diagnostic capability of this application.



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Breeuwer, M., Paetsch, I., Nagel, E., et al. "The detection of normal, ischemic and infarcted myocardial tissue using MRI". *Proceedings of CARS - International Congress Series*, No. 1256: 1153-1158, 2003.

Bruder, O., Schneider, S., Nothnagel, D., et al. "Acute Adverse Reactions to Gadolinium-Based Contrast Agents in CMR". *JACC: Cardiovascular Imaging*, Vol. 4, No. 11: 1171-1176, November 2011.

Breeuwer, M., Paetsch, I., Nagel, E., et al. "The detection of normal, ischemic and infarcted myocardial tissue using MRI". *International Congress Series*, No. 1256: 1153-1158, 2003.

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Ordovas, K. G., Higgins, C. B. "Delayed Contrast Enhancement on MR Images of Myocardium: Past, Present, Future". *Radiology*, Vol. 261, No. 2: 358-374, November 2011.

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Vermes, E., Childs, H., Carbone, I., Barckow, P., Friedrich, M. G. "Auto-Threshold Quantification of Late Gadolinium Enhancement in Patients With Acute Heart Disease". *Journal of Magnetic Resonance Imaging*, No. 37: 382-390, 2013.

Mapping

Indications for Use

The MR Cardiac Mapping application allows to load, review and quantify MR T1 native, T1 Enhanced, T2 and T2* MR data and to generate parametric maps. The application is designed to visualize and quantify signal differences for regions of interest within or between acquisitions. It is indicated to support users with detecting abnormalities that affect the myocardium in a diffuse fashion, such as edema, fat buildup or storage diseases.

Overview

The Mapping analysis application allows you to verify and quantify parametric maps. You can work with data from the following sources:

- Raw data from the scanner (without maps): If you use raw data, Mapping allows you to generate the parametric map and perform motion correction or exclude a sub-optimal time point.
- Parametric maps delivered directly by the scanner. If you use maps directly from the scanner, you may still re-calculate improved parametric maps and apply motion correction or exclude a sub-optimal time point.

Local and regional segmentation options provide tools to investigate user-defined regions.

Labeling for Mapping analysis

If you plan to open T1, T2, or T2* series in the Mapping analysis application, the series must be labeled correctly for "orientation", "native" or "enhanced". This ensures that the correct analysis tools are available when viewing and analyzing the series.

NOTICE

Before starting the Mapping application, you should check that the series have correct labels. This is most important if you want to compare regions from native T1 and enhanced T1 series. When the series description contains the same name, the system cannot recognize the difference between the two, and so it will provide the series with the same label, and a "hematocrit corrected" value cannot be calculated. For example, in the following figure, series have been scanned with different T1 but have the same name (hence the series in the upper-right corner displays a sub-optimal pixel range).

Which data to use for map creation

In order to generate map, there are a minimum number of required time points, according to the following terminology:

- T1 MOLLI & shMOLII – “Inversion times”
- T1 SASHA - “Saturation times"
- T2/T2*- “Echo times”

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T1 MOLLI	≥3
T1 SASHA	≥3 Saturation time = 0 mandatory
T1 shMolli	=7 Nothing less, nothing more.
T2	≥3
T2*	≥3

Hanging Protocols

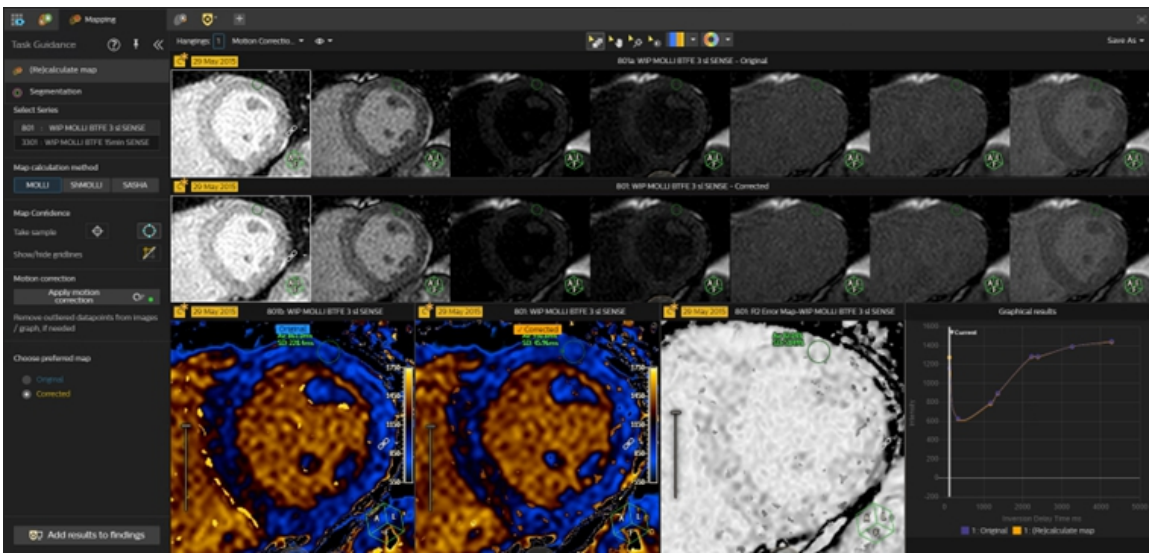
There are several **Hanging Protocols** designed to fit the different use cases of this application, including hangings that include polar maps or tables. Review the **Hanging Protocols**, and select your favorite per data type (T1, T2 , T2*).

Application stages

This application includes two stages:

1. (Re)calculation - verify the quantify of the parametric maps, and apply motion correction as needed.
2. Segmentation - segment the myocardium and ROI, and view results.

Screen layout



Upper toolbar

There are two buttons in the upper toolbar:

From left to right:

1. Select the color map.

2. Show color only inside the Myocardium (between the rings).

The display includes the following elements:

- First row - Time points of the source data. Scroll up and down for other slices.
- Second row - Corrected time points, after applying motion correction. If motion correction has not been applied, a duplication of the original series is shown. Scroll up and down for other slices.
- Original map. The original parametric map provided by the scanner.
- Generated and recalculated map:
  - Generated map - This map is generated by the application, and does not include corrections.
  - Recalculated map - This map includes corrections.
- Error map to review the confidence. The grayscale represents a ratio from 0 to 1, where 0% (bad) fit = black, and 100% (good) fit = white.
- Graph displaying the signal intensity of a selected voxel.

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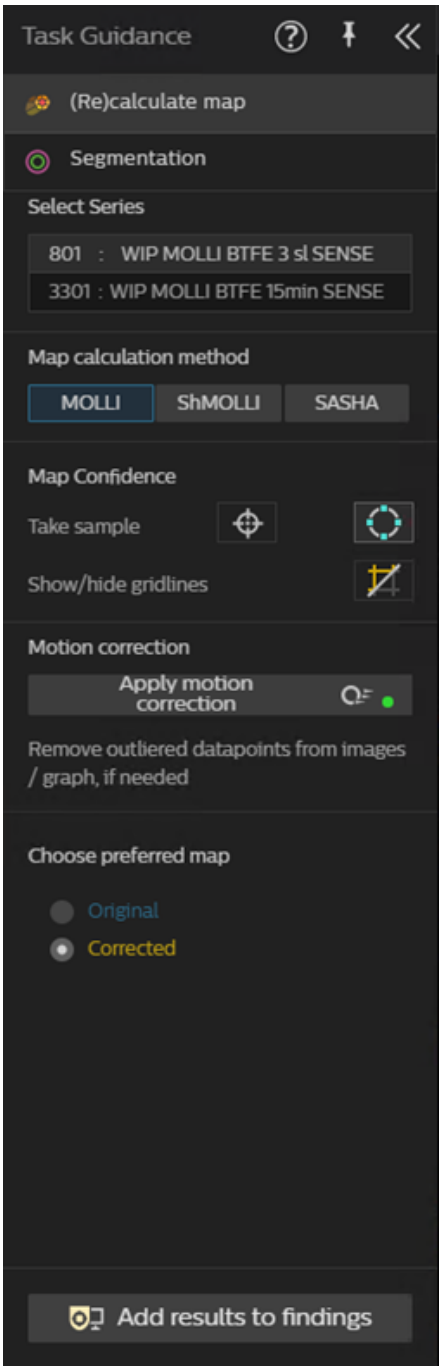
Task Guidance



In the **Task Guidance** panel, under:

(Re)calculate map:

- When you load raw (source) data in the Mapping application, the first step is to verify the source data and calculate improved parametric maps. **Select Series** to choose series to review or correct.

- Before you **Apply motion correction**, check that the **Map calculation method** you select matches the scanning protocol, to ensure a more accurate calculation.

Map Confidence:

- **Take sample** using either a seed or circle. Drop on the source map to review the signal intensity and identify outlier time points. Data with no expected motion appears on the graph in a checkmark-type shape.
- **Show/hide grid** displayed on the time points. You can modify the size and location of the grid box. Use zoom and pan to locate the image inside the box as needed.

NOTICE

This box is used for detecting motion between time points, and does not have any effect on the Motion Correction.

Apply motion correction

Click **Apply motion correction** to correct the and recalculate the entire map. Exclude an outlier time point by right-clicking either a point on the graph, or a time point image.

Choose preferred map

Select which map to use for the analysis. Please note that once correction is applied, the **Corrected** map is selected by default.

(Re)Calculate map

When you load raw (source) data in the Cardiac Mapping application, the first step is to verify the source data and calculate improved parametric maps.

Segmentation

NOTICE

Inspect and verify the accuracy of all automatic contours before reviewing their results. Make sure to exclude non-myocardial voxels.
Measurements from the myocardium should been taken with care to include only intramural regions and avoid myocardial borders. To get good T1, T2, or T2* measurements, pixels that may include blood pool or epicardium should be avoided to prevent inclusion of partial volume effects in the calculations.

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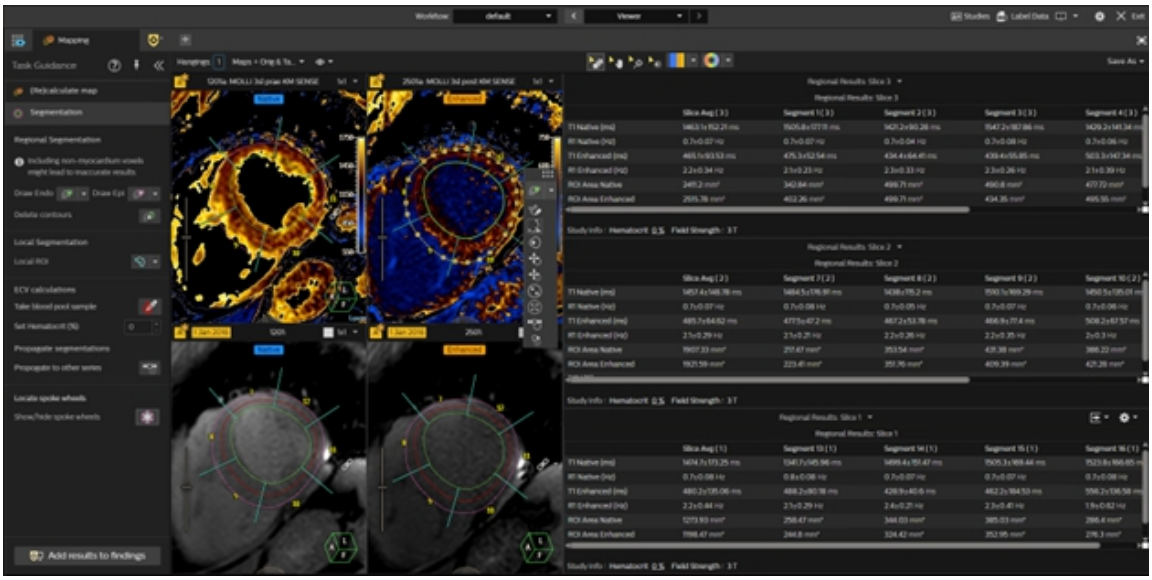

In the **Task Guidance** panel, under:

Regional Segmentation, the following drawing tools are available. Use ESC to exit the tool or change back to the default cursor.

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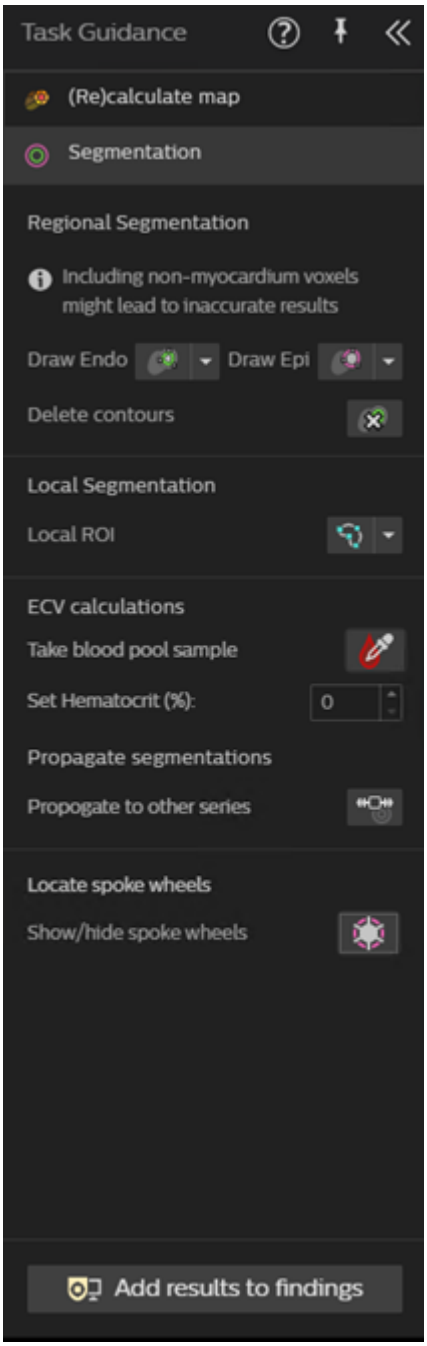
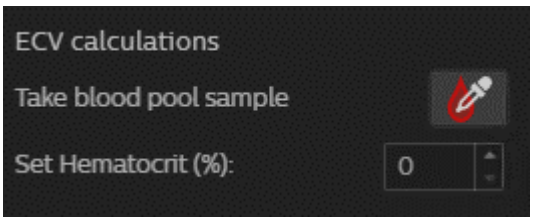


Icon	Title	Usage
	Draw Endo contour with a spline tool.	Every mouse click adds a point, the contour connects between the points.
	Draw Epi contour with a spline tool.	

	Draw Endo contour with a freehand tool.	Click the mouse anywhere on the contour, and drag it along the expected contour.
	Draw Epi contour with a freehand tool.	
	Local segmentation tool	Draw ROI on the relevant organ to get the parametric map average value in the ROI.
	Edit contour freehand.	Edit the contour by dragging the mouse, and then redrawing the section.
	Edit contour using spline.	Click a point, or the contour itself, to create a new point, then drag that point.
	Edit using nudge tool.	Push the selected contour inside or outside using the circle tool. Resize the circle using CTRL + mouse wheel.
	Expand contour.	Every click expands the contour by one pixel
	Contract contour.	Every click contracts the contour by one pixel
	Undo	Undo your last edit operations.
	Resolve intersections.	When endo and epi contour intersect, push the other contour away from the one that was last edited.
	Pan active slice selected contour	Click and hold the contour you wish to pan over, then move to the desired location. Release to lock position.
	Pan all contours (on the selected slice)	Click and hold the contours, then move to the desired location. Release to lock position.
	Propagate selected contour	Select the contour to propagate, then click this tool.
	Propagate active slice contours	Click to propagate all contours to the other series.

	Delete contours	Open a dialog box to select which contours to delete: 1. All contours on current slice. 2. All contours on all phases and slices.
	Show/Hide spokes wheel	Once applied, verify that spokes are well positioned on all the slices. The blue spokes' location can be adjusted individually. The whole wheel can be rotated from the middle of a spoke.

ECV calculations



NOTICE

ECV calculations are valid only when Native and Enhanced series are launched to the application.

To receive ECV results, use the following tools:

- Take a blood pool sample on one slice from a native series to propagate to the enhanced series.
- Input hematocrit value: Fill the patient Hematocrit value.

Result table

Numerical results tables

The results in the table display the actual average calculated value from the segmented area on the parameter MAP, expressed in milliseconds (ms) and including the Standard Deviation (±SD). For each T1 or T2 (*) time, the R1 or R2 (*) value is calculated and expressed in Hz.

The table displays general parameters like ROI area and the used field strength, which are saved together with the results. Parameters are displayed as follows for the different result protocols:

- Local results: The table displays results for all local ROIs. Each column displays results for a drawn ROI. The column can be identified by the name and slice displayed.

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- Regional results: Each column displays the results for each segment of the myocardial segmentation for the currently selected slice in the view. The table header displays the selected slice.

T1 mapping and hematocrit normalized value

For T1 mapping, the table combines results for native and enhanced T1 in a single column to provide a comparison. The "Hematocrit normalized relative change in longitudinal relaxation rate" (Ɛ) is calculated automatically when the value for ‘Hematocrit’ is provided in the task guidance panel. Myocard and blood ROI’s should be available for each native and enhanced series of same orientation.

ECV is calculated with the following formula:

- ECV = (1-heamatocrit) (delta $R1_{myocardium}$/delta $R1_{blood}$)

NOTICE

To proceed, the correct "Hematocrit" should be entered as determined from a blood sample taken around the time of acquisition. Once this value is entered, it can be saved with the study and the segmentations using the option **Save results as** in the common tools. When saved, this hematocrit value is available when the study is reloaded in the application.

Configure results table

Use the gear icon to:

- **Configure table setting**: Select the results to include in each table.
  Normal values: Shows the selected database of normal values. You can modify the normal value selection in the suite **User Preferences** dialog.

Add results to findings

This saves the results (edited contours, etc.) as a bookmark in the findings dashboard.

T1 Mapping References

Moon et al.: Myocardial T1 mapping and extracellular volume quantification: a Society for Cardiovascular Magnetic Resonance (SCMR) and CMR Working Group of the European Society of Cardiology consensus statement. Journal of Cardiovascular Magnetic Resonance 2013 15:92.

Kellman et al.: Extracellular volume fraction mapping in the myocardium, part 1: evaluation of an automated method. Journal of Cardiovascular Magnetic Resonance 2012 14:63.

Kellman et al.: Extracellular volume fraction mapping in the myocardium, part 2: initial clinical experience. Journal of Cardiovascular Magnetic Resonance 2012 14:64.

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T2 Mapping References

Wassmuth et al.: Variability and homogeneity of cardiovascular magnetic resonance myocardial T2-mapping in volunteers compared to patients with edema. Journal of Cardiovascular Magnetic Resonance 2013 15:27.

Ubachs et all.: Myocardium at risk by magnetic resonance imaging: head-to-head comparison of T2-weighted imaging and contrast-enhanced steady-state free precession. European Heart Journal- Cardiovascular Imaging (2012) 13; 1008-1015.

T2* Mapping References

Pennell et all.: From the American Heart Association Cardiovascular Function and Treatment in b-Thalassemia Major: A consensus Statement From the American Heart Association. Circulation 2013;128:281-308.

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Temporal Enhancement

The MR Cardiac Suite Temporal Enhancement application is indicated to assist users with review and analysis of individual rest or stress acquisitions and/or rest-stress comparison of multi-slice dynamic cardiac MR acquisitions in one application.

Indications for Use

The MR Cardiac Temporal Enhancement application is indicated to assist users with review and analysis of individual rest or stress acquisitions and/or rest-stress comparison of multi-slice dynamic cardiac MR acquisitions in one application.

Overview

Temporal enhancement analysis indicates how well the blood flows from the coronary arteries into the myocardium. The Temporal Enhancement application provides temporal enhancement analysis of dynamically resolved cardiac data (multi-dynamic, multi-slice). Analysis results are derived from changes over dynamic phases and include all relevant clinical parameters.

The application allows automatic registration (image alignment) of the time series of images to correct for patient and breathing motion. Manual tools are also available to correct the alignment. You can also define contours and spoke wheels to segment anatomically relevant areas. Furthermore, this application allows for a convenient bull’s eye plot where you can easily view the end result from the base to the apex of the heart, as you defined them. Rest and stress studies can be directly compared to detect the presence of a coronary-artery stenosis.

Myocardial perfusion and viability assessment is important for many reasons, mainly to:

- Diagnose, locate and grade the severity of coronary artery disease
- Identify candidates who would benefit from revascularization

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- To evaluate response to revascularization

Also known as first-pass images, these are T1 weighted, gradient-echo sequences. Image acquisition is performed 3 minutes after gadolinium contrast administration. If there is a hypo-enhanced area, this implies a zone of myocardial infarction that is non-viable

Guidance for this analysis package is provided in the **Task Guidance** panel.

Image acquisition

- Short axis images are acquired, which are perpendicular to the left ventricular long axis.
- Generally systole phase of slices are chosen(where myocardium is the thickest).
- The same phase is imaged continuously to see the inflow and uptake of GD contrast in mayocard.
- A sufficient number of images should be acquired 50-60 heartbeats to ensure contrast has passed through the left ventricle.
- Depending on experience and institutional policy rest perfusion imaging might be omitted

Interpretation

- **Stunned myocardium**: Stunned myocardium refers to a state in which there is wall dysfunction, but the perfusion (resting and stress) is normal.
- **Dilated cardiomyopathy**: In idiopathic dilated cardiomyopathy, the left heart is markedly dilated and thinned, and mid-wall enhancement, especially in the septum, is present in more than 50% of patients.
- **Hibernating myocardium**: With hibernating myocardium, the myocardium shows decreased perfusion on both stress and resting phase (seen as a fixed defect), but the myocytes are viable and will benefit from revascularization.
- **Myocardial ischemia**: Myocardial ischemia refers to a state in which there is decreased perfusion of the myocardium when stressed (such as during exertion) but normal perfusion during rest (seen as reversible perfusion defect). These patients will significantly benefit from treatment.
- **Myocardial infarction**: In myocardial infarction, there is absent perfusion both when the heart is stressed and at rest (a fixed defect) and the myocytes are not viable. Perfusion MRI at rest and during a vasodilator stress administration using a ‘first-pass' technique shows a signal increase in normal myocardium. Enhancement is limited in the ischemic myocardium. There will be no benefit from revascularization.
- **Myocarditis**: Early perfusion from gadolinium enhancement in regional vasodilatation and increased blood volume due to the inflammation in myocarditis causes early postcontrast enhancement
- **Dilated cardiomyopathy**: In idiopathic dilated cardiomyopathy, the left heart is markedly dilated and thinned, and mid-wall enhancement, especially in the septum, is present in more than 50% of patients

Screen layout

Application launch

You can launch the Temporal Enhancement application by either:

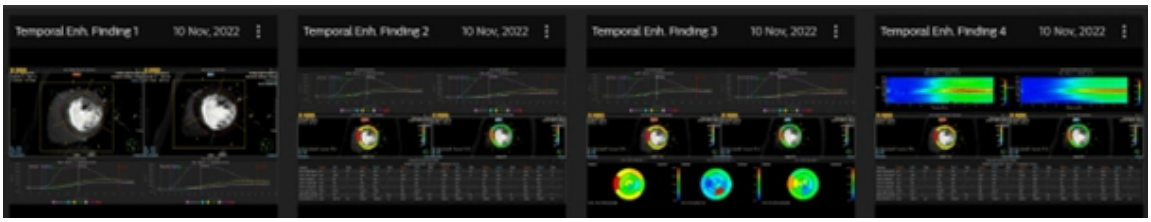
- Right-clicking the viewport of a valid data type.
- Selecting **+** from the application launcher, then selecting **Temporal Enhancement**. A dialog box opens containing valid data, where you can select a series to analyze.

You can manually label data as **stress** or **rest** from the **label data** option.

Inside the application

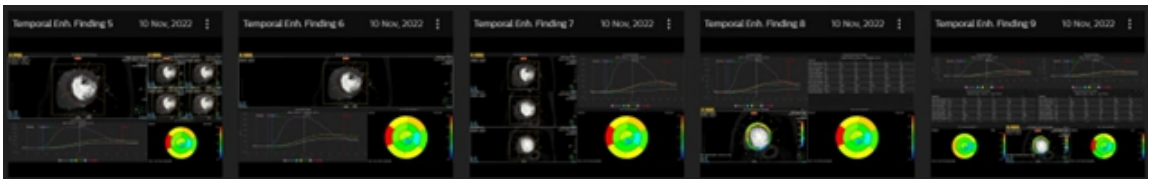
You can use the application for comparing both stress and rest scans, or only stress, or only rest. There are a total of 14 **Hanging Protocol** (HP) including stress rest comparison. A maximum of 3 HPs can be saved as Favorite. Hovering over each HP shows a pictographic representation of the results and view format of that particular HP. The listed HPs can be divided into the following three modes.

Comparison modes:



- Stress-rest-Graph (default favorite)
- Stress-rest-Graph-Table
- Stress-rest-Graph-Polarmap
- Stress-rest perfusogram-table

Stress / Rest only modes:



- Stress / Rest-enlarged stress-graph-polar map
- Stress / Rest-Graph-Polarmap
- Slice Stress / Rest,Graph,Polarmap
- Graph,Table polarmap,Stress-Fusion
- Stress / Rest endo and epi compare results

The context menu, floating toolbar, and **Task Guidance** panel contain the following tools, where the images below show how to reach these tools from the context menu:

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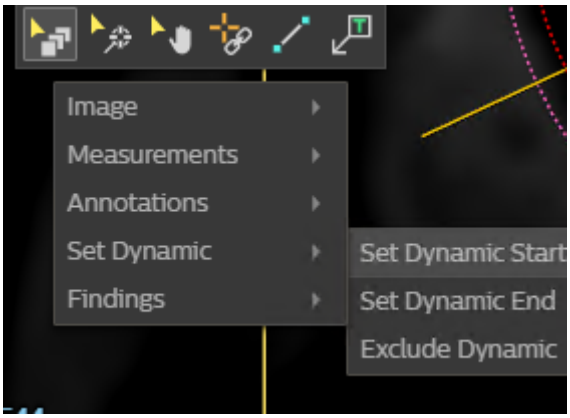

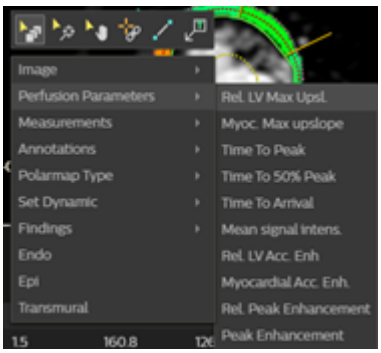

Tool	Function
Set Dynamic Start	Set start of dynamic for calculation.
Set Dynamic End	Mark end of dynamic for calculation.
Exclude Dynamic	Exclude a certain dynamic from the calculation.
Tool	**Function**
	Draw contour options
	Edit contour with freehand drawing
	Edit contour in spline mode
	Increase and decrease contours by nudging them from the inside or outside.
	Change diameter of the selected contour by eroding and expanding.
	Include supporting GIFs when hovering over icons.
Tool	**Function**

	Draw endo contour.
	Draw epi contour.
	Choose registration type. **Affine** compensates for breathing motion and skewing movements. **Rigid** compensates for in-plane translation and rotation movements.
	Show / hide registration box.
	Reset registration box to its original position in selected type of registration.
	Show / hide spokes.
	Turn on Baseline Correction for calculating parameters with regards to baseline.

Tab. 26: Context menu inside the viewport

Application components

- Images:
  - Are displayed as dynamic in tiled view. Double-click to enlarge, or click on the viewport header to maximize.
  - You can scroll horizontally for dynamics, and vertically for slices.
  - In specific HP, three slices of the same scan are split and displayed.
  - Use a toggle button to hide or show the spoke wheel, contours, and color overlays.
  - Delete certain dynamics if the image quality is bad.
- The graph:
  - Shows six segments and blood pool intensity over the dynamics
  - Updates when you edit contours, the registration box, or baseline correction.
  - Can be smoothed when you apply spatial and temporal filters.
  - Can be zoomed and panned.
- Table:

  The table shows different parameters calculated from the slope of LV and Myocardium, and areas under the curve:
  - Slope-based: Rel. LV max upslope, Myo. Max upslope, TTP, TTA, TT50%P, Rel. Peak enhancement, Peak enhancement.
  - Area-based: Mean Sig. Intensity, Rel. LV accu., Myo. Acc.

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In comparison mode, the ratio of parameters are displayed except Mean signal intensity, TTP, TT50%P, and TTA.
When you change the registration box, contours, or graph markers, the table updates.

- Polar maps are:
  - Displayed according to
    Endo, epi, transmural for determining ischemic distribution; and
    Regional or detailed according spoke segmentation or entire pixel intensity distribution, respectively.
  - Windowing can be performed on the polar map to play with the color scale, but that will not change table values.

Workflow

The position of the heart in images may vary during acquisition because of breathing or patient motion. Registration (image alignment) is used to compensate for these movements.

Typical workflow with auto contours:

1. Upon launch, the application automatically identifies:
   - The dynamic series with stress and/or rest data.
   - The start and end dynamic for selecting first pass dynamic range for analysis.
   - The dynamic, and contours are imported.
   - The registration box, using the epi contour. Affine registration is applied between dynamics to minimize motion artifacts.

     Affine registration compensates for breathing motion and skewing movements.
2. You can verify contours. Use tools from the floating toolbar and **Task Guidance** panel to edit registration and contours on dynamics and slices.
3. A spoke wheel is automatically placed by the application, and results are created.
4. You can:
   - Apply **Baseline Correction** and verify rulers on the graph.
   - Use different hanging protocols to review results and export findings.
   - Compare layouts to check between endo and epi regions, or between stress and rest perfusion scans.

Typical workflow without auto contours:

1. Upon launch, the application automatically identifies the dynamic series with stress and/or rest data.
2. Identify the start and end dynamic for selecting first pass dynamic range for analysis.
3. Draw endo and epi contours on a good dynamic where the myocardium is fully visible.
4. The application uses the epi contour to define the registration box. Affine registration is applied between dynamics to minimize motion artifacts.

Affine registration compensates for breathing motion and skewing movements.

5. You can verify contours. Use tools from the floating toolbar and **Task Guidance** panel to edit registration and contours on dynamics and slices.
6. A spoke wheel is automatically placed by the application, and results are created.
7. **Baseline Correction** is applied by default. You can verify the rulers on the graph.
8. You can:
   - Use different hanging protocols to review results and export findings.
   - Compare layouts to check between endo and epi regions, or between stress and rest perfusion scans.

The task guidance panel provides the following steps:

- **Exclude dynamics**

  By default, all images are included in the analysis. However, in many cases, not all images can be used for quantifying the results. Therefore to focus only on the area of interest, you may exclude dynamics at the start and at the end of the acquisition.

  Excluding dynamics allows you to improve the quality of your analysis by focussing on the bolus that you would like to measure.

- **Optionally adjust registration**

  If automatic registration is not satisfactory, you can adjust it manually using tools in the task guidance panel.

1. To exclude dynamics at the start of the acquisition, scroll horizontally to the dynamic where you want to start the analysis, and then click **Set the first dynamic for analysis** in the task guidance panel.
2. To exclude dynamics at the end of the acquisition, scroll horizontally to the last dynamic that you want to use for analysis, and then click **Set the last dynamic for analysis** in the task guidance panel.

NOTICE

A minimum of 15 dynamics is required for analysis.

⇨ Excluded dynamics are colored red in the image navigator in the toolbar, and they are not displayed in the viewport when you scroll.

3. If you prefer to see excluded dynamics while scrolling, select **Show excluded dynamics anyhow** in the task guidance panel.

4. To view the registration box displayed on the current slice, click **Show/Hide registration box** in the task guidance panel.

⇨ For correct results, the registration box should completely contain the left ventricle.

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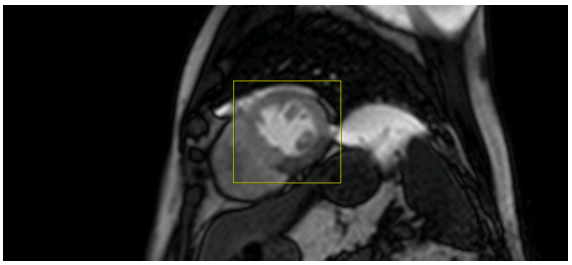

Fig. 60: Registration box

5. To adjust the registration box manually, move the pointer over a corner of the box and drag the corner point to reposition it.

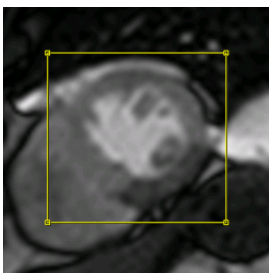

Fig. 61: Adjust the registration box by dragging the corner points

6. Review the other slices and repeat this step if the automatic registration is not satisfactory.
7. Alternatively, select **Rigid Registration** in the task guidance panel to try to improve the registration.

NOTICE

The registration method currently in use is displayed at the top of the viewport.

8. To reset the registration and start again, click **Reset Registration** in the task guidance panel.

Hanging Protocol (HP)

Stress-rest-Graph

This HP is set as default when both stress and rest scans are opened. If the **Baseline Correction** is turned on for one, it is on for both. This HP allows viewing all dynamics of both stress and rest, where you can verify start and end dynamic from images and the graph.
Common functionalities:

- The contours and registration box can be edited, and will be automatically propagated for all dynamics.
- Zoom and pan is also available for the graphs.
- There are 3 filters for spatial and temporal smoothing of the graph (low, medium & high).

- By default, the graph is shown for Transmural calculation, which you can change to endo or epi by right-clicking to open the context menu in the graph.
- The displayed markers and segments of the graph came be turned on and off for visualization.

Stress-rest-Graph-Table

This HP provides comparison of table and graph, with color overlay on images for stress and rest scans.

- The number of graphs is equal to the number of slices.
- You can scroll up and down on the image, and horizontally for the dynamics.
- Changing from Transmural to Endo and Epi updates the graph and table for both stress and rest.
- The table also displays the ratio of the following parameters.
- Select overlays for different parameters by opening the context menu inside the viewport. All parameters are listed inside **perfusion parameters** subgroup
- The color overlay can also be switched to regional (based on spoke wheel segmentation) or detailed (entire range of colors displayed depending on calculated values of each pixel over ranged dynamic), or as an AHA model.
  These colors are displayed based on endo, epi or transmural segmentation.

Stress-rest-Graph-Polarmap

This HP provides comparison of two graphs, two separate polar maps, and an additional polar map with slice-wise ratio of the following parameters.
These polar maps can be selected from the lower-middle list menu on the viewport.

- All other functionality is similar to the other Stress-rest **Hanging Protocol**.
- Spoke wheels can be switched to 4, 6, or 12. That slice then updates in all polar maps.

Stress-rest perfusogram-table

This HP provides an image with perfusion color overlay and TID graph for both stress and rest.

- The perfusogram can also be switched to endo, epi or transmural (segment-based) from detailed, which is the default.
- The X-axis shows the time dynamics included in the calculation, and the Y-axis shows the degree (In detailed view) and segments in (Epi, endo, and transmural).
- The 0° starts at +ve X-axis and rotates clockwise.

Stress-enlarged stress-graph-polar map

When a single perfusion study is present, and it marked as stress or rest, this HP is launched by default.

- You can also navigate to this HP to see only a large stress image and polar map graph, or a tiled view of the dynamics together.
- All other functionalities are the same as other the previous **Hanging Protocol** in this list.

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Stress-Graph-Polarmap

A tiled view, a polar map, and a graph are displayed for the stress scan. All common functionalities are the same as previous graphs in this list.

SliceStress,Graph,Polarmap

There are two columns: the right column contains the graph and polar maps, the left column has three slices of the same scan separated. The graph updates with the respective slice of the selected viewport.

Graph,Table polarmap,Stress-Fusion

This HP provides a graph, a table values polar map, and a fused color overlay on the image.

Stress endo and epi compare results

This HP:

- Provides the ability to compare between an endo and epi segment of the same slice over the ranged dynamics.
- Contains two graphs, two tables, and two polar maps, with an image viewport displaying color overlays.
- Can be used to differentiate the position of exact damage, and determine if tissue is viable or salvaged.

HPs available for rest scan

- Rest-enlarged rest-graph-polar map
- rest-Graph-Polarmap
- SliceRest,Graph,Polarmap
- Graph,Table polarmap,Rest-Fusion
- Rest endo and epi compare results

Add results to findings

Click Add results to findings in order to add results from different HP to the finding dashboard.

Results

The Results screen displays viewports containing the Time Intensity Signal graph, a table results view, the source image with contours and spoke wheel, and the source image with color-coded segment display (including centerline division). To view a bull's-eye results plot instead of the table results view, right click the table results view and select the bull's-eye results plot.

NOTICE

Results are displayed per slice. However, the bull's-eye results plot provides a representation of results over multiple slices.

NOTICE

If you are analyzing rest and stress series for comparison, the Preparation step and the Segment step must be performed for each series before you can view the results summary.

Options for configuring the displayed results are available in the task guidance panel.

1. Select whether to turn **Baseline Correction** on or off by selecting the appropriate check box in the task guidance panel.

NOTICE

The **Baseline Correction** function corrects for intensity inhomogeneity in the myocardium. Inhomogeneity in dynamically retrieved data sets could have a negative influence on the Temporal Enhancement analysis results. To perform Temporal Enhancement analysis correctly, the data set should be corrected for inhomogeneity. When using a Philips scanner, use the CLEAR function during scanning to correct for inhomogeneity. When using a scanner from another vendor, you can turn baseline correction on in the task guidance panel to apply this correction.

⇨ If rest and stress comparison is available, you should configure the **Baseline Correction** setting for both **Rest** and **Stress**.

NOTICE

Rulers are not applied to the Time Intensity Signal graph (and therefore results are not displayed) until you configure the **Baseline Correction** setting in the task guidance panel.

2. Verify, and if necessary adjust, the vertical rulers in the Time Intensity Signal graph. These rulers represent the timing parameters, as follows:
   - Dashed ruler (**Base Start** and **Base End**): These rulers are only displayed if **Baseline Correction** is turned on. Verify that these are the correct baseline dynamics. If dynamics are not used for the baseline, move the lines all the way to the left, or turn **Baseline Correction** off in the task guidance panel.
   - Blue ruler (**LV input**): Verify that this position is the start of the blood pool enhancement.
   - Green ruler (**Myocardium**): Verify that this position is the start of myocardial enhancement (higher intensity).
   - Red ruler (**2nd Pass**): Verify that this position is the start of second pass; typically this is the dip in the blood pool curve. (Refer to the image below.)

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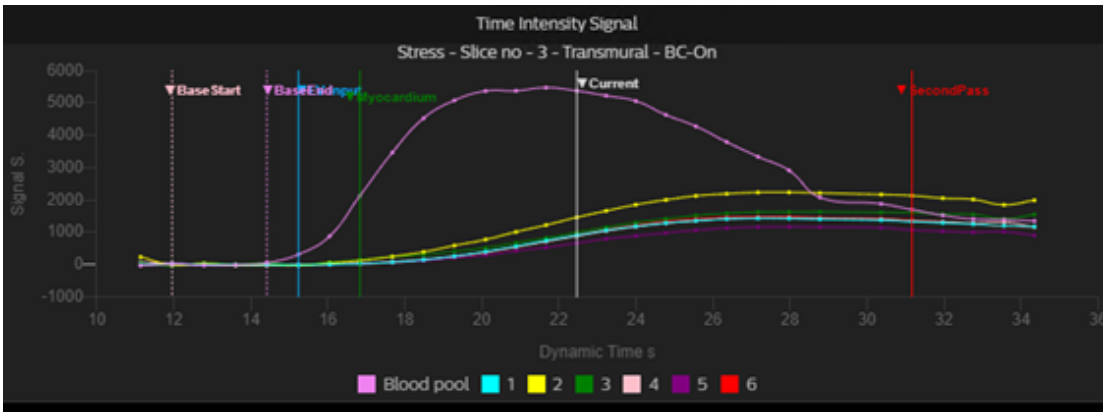

⇨ The x-axis of the Time Intensity Signal graph represents the total dynamic time of the selected image matrix, while the y-axis represents the range of MR signals.

3. The following functions are also available with the Time Intensity Signal graph:
   - Select **Optionally hide rulers** in the task guidance panel to hide the rulers in the graph. You can hide the rulers if all timing parameters are set correctly.
   - Right-click the graph and choose to show or hide the rulers' legend.
   - Right-click the graph, or use the legends below the graph, to choose which segments to show or hide (the graph is rescaled accordingly).
4. Further options for fine-tuning the calculations in the Time Intensity Signal graph are available from the right mouse menu:
   - Change the strength of the spatial filter, or turn it off altogether. This filter applies smoothing for spatial anomalies.
   - Change the strength of the temporal filter, or turn it off altogether. This filter applies smoothing for anomalies over time.
   - Choose to show or hide segments, endo, and epi results.
5. To view results using a different protocol layout, select a result protocol in the task guidance panel.

⇨ If you select the **Detailed** result protocol in the task guidance panel, the Mean Signal Intensity is displayed as a temporal enhancement diagram (TED). This diagram is a color representation of the intensities of individual segments in the myocardium as a function of time.

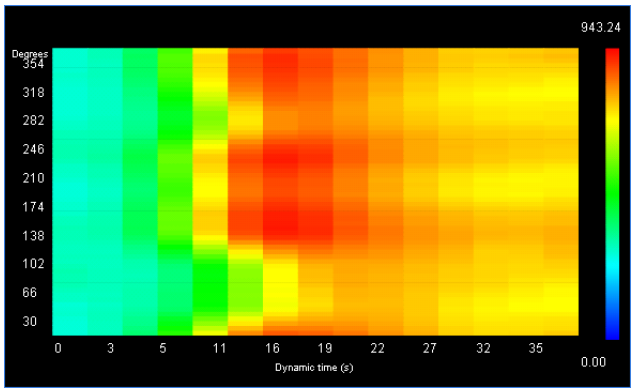

Fig. 62: Temporal enhancement diagram

⇨ The diagram provides a quick overview of the differences in enhancement of the myocardium.

⇨ The number of rows in a TED is equal to the number of segments (epi, endo, spoke wheel segmentation). Each row contains a color representation of the MSI value for each dynamic of one segment. Each row starts with the MSI value of a segment at the first dynamic while each row ends with the MSI value of a segment at the last dynamic.

6. Right-click the TED and select a display type:
   - Detailed
   - Transmural
   - Endo Cardial
   - Epi Cardial
7. Several analysis parameters are available for the bull's-eye plot and color-coded segment display. The current analysis parameter is displayed above each viewport. To select a different analysis parameter, right-click the bull's-eye plot or color-coded segment display and select a parameter.

⇨ For details of the available parameters, see section “Analysis parameters” on page 301.

8. You can also select the results display type for the bull's-eye plot and color-coded segment display in the right-mouse menu. Select **Detailed** (94 angles), **Regional** (spoke definition), or **AHA**.
9. To change the color scale threshold for the bull's-eye plot, color-coded segment display, and temporal enhancement diagram, move the pointer over the plot or diagram and do the following:
   - Drag left to decrease window width.
   - Drag right to increase window width.
   - Drag down to decrease the window level.
   - Drag up to increase the window level.

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Analysis parameters

You can analyze the results in the **Results** screen using the following parameters. To select a parameter, click the right mouse button and select the parameter in the shortcut menu.

relative LV Accumulated Enhancement (relLVAE): The ratio (in percentage) of the Myocardial Accumulated Enhancement (MCAE) and the LV Accumulated Enhancement (LVAE).

relLVAE = MCAE / LVAE × 100%

Myocardial Accumulated Enhancement (MCAE): The area under the curve from Time To Arrival (TTA) to Time To Peak (TTP). Measured in MR signal units x seconds.

relative LV maximum Upslope (relLVU): The ratio (in percentage) of the Myocardial maximum Upslope (MCU) and the LV maximum Upslope (LVU).

relLVU = MCU / LVU × 100%

Myocardial maximum Upslope (MCU): The maximum upslope of the myocardial signal, measured in MR signal units per second.

relative Peak Enhancement (relPE): The ratio (in percentage) of peak enhancement and baseline value.

relPE = PE / BV × 100%

Peak Enhancement (PE): The peak height (the difference between maximum myocardial signal and baseline value), measured in MR signal units.

Time To Peak (TTP): Time to reach the maximum in the myocardial enhancement, measured in seconds.

Time To 50% Peak (TTHP): Time to reach half of the maximum myocardial enhancement, measured in seconds.

Time To Arrival (TTA): Time to the start of the myocardial enhancement, measured in seconds.

Mean Signal Intensity (MSI): The average enhancement in a myocardial segment (selected time by the user), measured in MR signal units.

Baseline Value (BV): Baseline signal, measured in MR signal units.

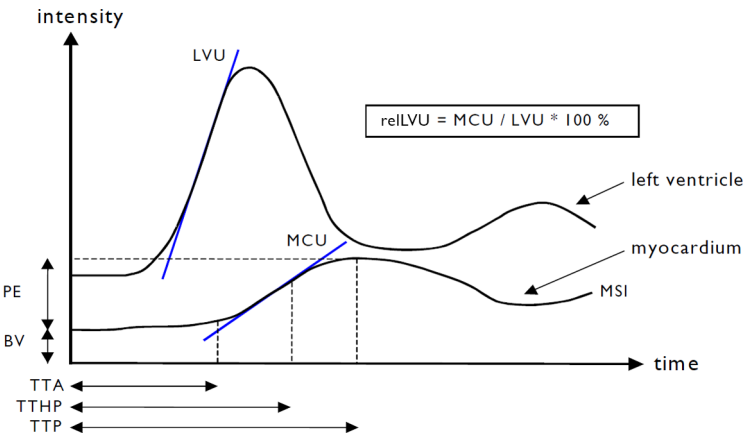

Fig. 63: Slope-related analysis parameters

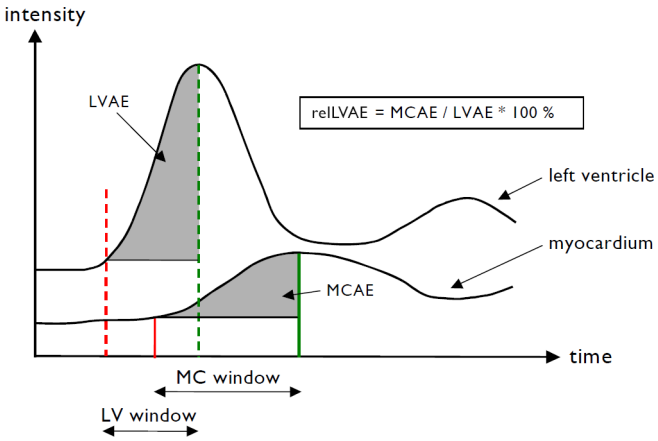

Fig. 64: Area-related analysis parameters

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Glossary

Term	Description
AHA	American Heart Association
AIP	Average Intensity Projection. See also MIP, VIP
AVW	Advanced Visualization Workspace
CT	Computed Tomography
CR	Computed Radiography. See also DR.
csv	comma-separated values
DICOM	Digital Imaging and Communications in Medicine
DR	Digital Radiography
DX	Digital X-Ray
ED	End Diastolic
EMR	Electronic Medical Records
ES	End Systolic
fps	Frames per second
FN	Findings Navigator
FWHM	Full Width at Half Maximum

Term	Description
HIS	Hospital Information System
IBE	IntelliBridge Enterprise
ICB	Image Control Bar
ICMT	Image Curve Manipulation Tool
LSF	Line spread function. See also PSF.
LA	Left Atrium
LV	Left Ventricle
MVO	MicroVascular Obstruction
MIP	Medical Imaging Platform
MIP	Maximum Intensity Projection. See also AIP, VIP
MRI	Magnetic Resonance Imaging
MUGA	Multiple-gated acquisition
NCCT	Non-Contrast CT
PACS	Picture Archiving and Communication System
PD	Patient Directory
PET	Positron Emission Tomography
PSF	Point Spread Function. See also LSF.
RGBA	Red Green Blue Alpha color model
ROI	Region of Interest
QA	Quality Assurance
RA	Right Atrium
RV	Right Ventricle
SC	Screen Capture
Std	Standard Deviation
SR	Surface Rendering
SUVbw	Standardized Uptake Value based on body weight
Third party	Any person or entity (including, without limitation, private and public organizations and government authorities) outside Philips.
TAVI	Transcatheter aortic valve implantation
US	Ultrasound
VIP	Volumetric Intensity Projection. See also AIP, MIP

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Term	Description
VR	Volume Rendering
XA	Angiography
XCT	X-Ray Computed Tomography

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