10 Cardiac MR Analysis

MR Cardiac in the IntelliSpace Portal is a suite of applications, which contains the MR Cardiac Viewer and the following analysis applications: Functional Long Axis, Functional Left Ventricle & Right Ventricle, Temporal Enhancement, Spatial Enhancement, Mapping and Whole Heart.

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.

Overview

MR Cardiac on the IntelliSpace Portal enables protocol and ExamCard-based organization of a Cardiac MR study, enabling a seamless connection between acquisition, review, and analysis. Bookmarks are available to frame the preparation by a technical assistant or to save work for a later time.

With a single-click selection you can select different types of viewing protocols. Automatic cine mode for functional series is available as well as pan and zoom links between different orientations to allow quick visual analysis in different layouts.

Qualitative scoring can be done using the AHA (American Heart Association) segment scoring panel for different types of analysis.

Valid imaging series

The series type that is suitable for each analysis method is indicated at the start of the analysis description in the following sections.

Estimation of calculated volumes

The default volume computation method is the common sum of discs method. In This method summarizes the areas of the contours drawn in each slice, multiplied by the sum of the slice thickness and the inter-slice gap.

To estimate calculated volumes correctly, acquisition should cover the complete LV from apex to base. If there is insufficient coverage, the volume calculation will be underestimated. If too much is included in the analysis, volume calculation will be overestimated.

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 slice level.

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References

Dulce, M. C., Mostbeck, G. H., Friese, K. K., Caputo, G. R., Higgins, C. B. "Quantification of the Left Ventricular Volumes and Function with Cine MR Imaging: Comparison of Geometric Models with Three-dimensional Data". *Cardiac Radiology*, No. 188: 371-376, 1993.

Schulz-Menger J, Bluemke DA, Bremerich J, Flamm SD, Fogel MA, Friedrich MG, et al. “Standardized image interpretation and post processing in cardiovascular magnetic resonance 2020 update. Society for Cardiovascular Magnetic Resonance (SCMR) Board of Trustees Task Force on Standardized Post Processing”. *J Cardiovasc Magn Reson*, 22:19, 2020.

User Interface

Screen layout

The Cardiac MR package consists of the following main workflow steps:

- Labeling
- Viewing
- Analysis

The screen that is displayed when you start the Cardiac MR depends on the labeling status of the series selected for analysis.

Labeling

The **Labeling** screen of the Cardiac MR package lists all series selected for analysis, with labeling options in the upper-right corner. Task guidance is provided on the left.

Viewing

The Cardiac MR package opens in the **Viewing** screen.

The **Viewing** screen of the Cardiac MR package displays series selected for analysis in the main viewport. Viewing protocols, analysis tools, and task guidance are provided on the left.

You can switch between the **Labeling** screen and the **Viewing** screen using the step selector in the upper-left corner.

Analysis

Cardiac analysis packages are launched from the **Viewing** screen. The following analysis packages are available:

- Functional LA analysis
- Functional LV & RV analysis
- Spatial Enhancement SA LV analysis
- Temporal Enhancement SA LV analysis
- Whole Heart analysis

3000063387 91_A/881 * 2021-06-30

- Mapping analysis

Slice numbering

NOTICE

Slice numbering is provided for two directions (Head/Feet and Feet/Head) to guarantee the communication of correct slices for referral. In some situations, the acquisitions can be scanned from apex to valve slice instead of the default valve to apex direction. As DICOM does not have a clear indication for slice direction in valve or apex, the software indicates Head direction as valve slice direction and Feet direction as apex direction.

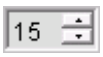
Task Guidance

Similar to all packages on the IntelliSpace portal, also the Cardiac MR package provides a task guidance panel in the left part of the screen.

NOTICE

Follow the steps of the Task Guidance to make optimal use of the Cardiac MR function.

Toolbar



Speed (frames per second)

To change the playback speed of the slices in movie mode, click the up or down arrow in the **Speed** box.

Movie Mode

Use the Movie Mode tool to play or pause review of the slices:

-  **Play backward**
-  **Pause**
-  **Play forward**

Keyboard Shortcuts

While working with the Cardiac MR packages, you can show or hide all annotations by pressing F12.

More Functions within the Cardiac MR package

In IntelliSpace Portal MR packages, the most important functions can be performed via the Task Guidance and the toolbar. However there are more functions which you can access via the right mouse menus.

For more information, see section “Right mouse menus” on page 12.

Launch the Cardiac MR package

▷ In the 'Directory' tab of the activity bar:

1. Select the study that you want to analyze, or select a subset of series within a study.
2. Click 'Cardiac MR Analysis' or 'Cardiac MR Viewer'.

⇨ The Cardiac MR package opens.

NOTICE

If the Cardiac MR Analysis package is opened from a viewer other than Cardiac MR, the current viewer is closed and Cardiac MR is opened instead.

- The MR Cardiac package opens with **Viewing** and displays images depending on labeling.
- If one or more of the series are not yet labeled (not known to the system), or the labeling is incorrect, navigate to the **Labeling** screen to apply or update labels.

Both step are described in the following workflow.

Labeling workflow

The **Labeling** screen displays a list of the series selected in the study. Thumbnail images of each series are displayed for reference. Each series should be labeled with its scan type and orientation. If applicable, a stress level label can also be applied. Details of currently applied labels are displayed on the right side of the series list.

Accurate labeling is required to display series correctly in viewing protocols, and to select the correct analysis application for quantitative analysis. If any series are unlabeled, you can use the **Labeling** screen to apply labels.

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.

3000063387 91_A/881 * 2021-06-30

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Additionally, some series from multi-vendor sources might be joined automatically. You can use the **Split** function to split these series.

1. To split a series, select the series in the series list and then click **Split** in the task guidance panel.
2. In case you want to merge a series that has been previously split, select one of the split series and then click **Merge** in the task guidance panel.

Label the Series

1. Select an unlabeled series in the series list.
2. In the labeling panel in the upper-right corner, select a **Scan Type** label and an **Orientation** label.

NOTICE

To be able to load series in viewing protocols, these labels are a minimum requirement.

⇨ Series with the same name as the selected series are automatically labeled in the same way. For best results, we recommend that the series orientation is noted in the series name.

⇨ When you apply an orientation label, all other series with the same orientation are labeled in the same way.

NOTICE

To apply the same label to several unlabeled series, press CTRL and click each series, or drag with the left mouse button.

3. If stress is a key factor for a series in the list, also select a **Stress Level** label.

⇨ This label allows the series to be loaded in comparative stress/rest viewing protocols. For functional stress protocols, it is important to also label the non-functional series as 'rest' in order to compare to stress series.

4. When all series are correctly labeled, click the right arrow in the Cardiac MR title panel to switch to the **Viewing** screen.

NOTICE

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", "contrast", "native" or "enhanced". This ensures that the correct analysis tools are available when viewing and analyzing the series.

Viewing workflow

When the Viewing screen is displayed, by default "Favorite Protocol" 2x2 layout, which shows available priority series are displayed in viewports in the main display area.

The Viewing screen provides the following tasks:

- Filter the displayed series using viewing protocols.
- Apply visual scoring (optional step).
- Select an analysis type and start analysis.

Select Protocol

1. Select a viewing protocol from the protocol list in the **Select Protocol** step of the task guidance panel.

⇨ Only series that match the selected viewing protocol are displayed in the main display area. This allows quick review of a case before performing analysis. If multiple series with the same orientation are present, they are displayed as tabs in the viewport.

2. The first selected protocol shown by default "Favorite Protocol" 2x2 layout shows available priority series.

⇨ You can configure preferred series by **Add** or replace series using the series browser in the image view port header and selecting Save as a new protocol to update favorite protocol default priorities.

3. You can switch to all series viewing protocol as a default by deselecting Favorite protocol using the right click option on the select protocol panel in the task guidance.
4. To maximize a viewport, double-click the title bar of the viewport (blue header). Double-click the title bar again to return to the previous view.

5. When a viewport contains multiple tabs, you can display the next series, by clicking **Next Series** in the toolbar.
   - You can also display the next series by pressing N on the keyboard.
   - To display the previous series, press ALT+N on the keyboard, or click the arrow next to **Next Series** in the toolbar and select **Previous Series**.

⇨ This function is most helpful when reviewing all series in full screen mode (maximized viewport).

6. You can also open series in a viewport using the series browser in the image viewport header.

3000063879l_A/881 * 2021-06-30

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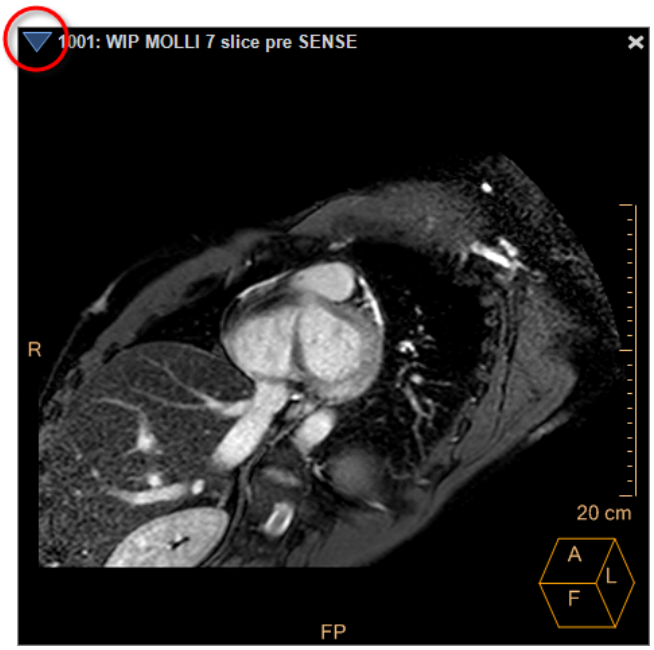

Fig. 45: Series browser

⇨ The series browser indicates the current loaded series with a checkmark. Series currently loaded in other viewports are indicated in bold, italic type. Series that are not yet loaded are indicated in normal type. You can select a series in the series browser to open it in the viewport. If the viewport already contains a series, you are prompted to choose between replacing the existing series, or adding the new series as a tabbed view.

7. If a series contains multiple slices, double-click the image to tile the slices in the viewport.

⇨ This allows you to review multiple slices at once. Double-click an image to return to the previous view.

8. Scroll through the images of the displayed series to view the area of interest.

   You can use the following interactions to review the series:

   - Adjust the movie playback.
   - Display reference lines.
   - Zoom and pan lock.

9. To adjust the movie playback, do one of the following:

   - Click **Play backward** or **Play forward** in the toolbar to set the playback direction.
   - Increase or decrease the playback speed using the up and down arrows in the **Speed (fps)** box in the toolbar.
   - While movie playback is enabled, drag with the right mouse button to adjust the playback speed.
   - Click **Pause** in the toolbar to stop playback.

⇨ If you start movie playback and then select another series, movie playback is automatically started for the newly selected series.

10. To display reference lines in series viewports, select **Show reference lines** in the toolbar.

⇨ When this function is enabled, reference lines are displayed in series viewports, indicating the position of the slice displayed in the selected viewport.

11. To lock zoom and pan interactions, click **Lock Zoom/Pan link** in the toolbar.

NOTICE

Lock Zoom/Pan link is enabled by default when you select a viewing protocol other than "All series".

⇨ When zoom and pan interactions are locked, all series are zoomed or panned simultaneously. Zoom and pan lock assists you with comparing areas of interest in all displayed series.

12. To correct misalignments when using zoom and pan lock, do the following:
    - Deactivate **Lock Zoom/Pan link** in the toolbar.
    - Adjust the zoom or pan factor on individual series.
    - Enable **Lock Zoom/Pan link** again.

Filtering the protocol list (optional step)

If there are viewing protocols that you do not use, you can hide these protocols in the protocol list. Hidden viewing protocols are not deleted, and can be enabled again at any time. The full protocol list can be reviewed by right-clicking when the pointer is over the protocol list.

NOTICE

During normal use, the viewing protocol list in the task guidance panel displays only viewing protocols that are enabled and for which a corresponding series has been loaded.

1. Right-click anywhere in the viewing protocol list.

⇨ The full viewing protocol list is displayed with check marks next to protocols that are enabled.

2. Click a protocol to hide or enable it.
3. To close the list without making changes, press ESC on the keyboard.

Creating a New Protocol

You can create a custom screen layout using series that you have selected in the **Viewing** screen and save it as a new protocol.

► Press and hold Ctrl and then select multiple series.

300006338791_A/881 * 2021-06-30

- Click **Create new viewing protocol** in the task guidance panel and select an appropriate layout from the list.

⇨ The selected series are loaded in the new protocol.

- When the layout is configured as desired, click **Save as new viewing protocol** in the task guidance panel and enter a name to identify the new protocol for future use.

NOTICE

For best use and maximum benefit of both system viewing protocols and custom viewing protocols, series descriptions should be entered consistently at the time of acquisition, including an indication of series orientation. Series descriptions are used by the system for the identification of series.

Position Point Linking

You can mark a point of interest in a slice and display an indicator on the matching location on other series and orientations.

1. Click **Position Link Point** in the toolbar of the task guidance panel.
2. Click on a point of interest in a slice.

⇨ An eight-point marker is displayed at the point of interest.

⇨ Four-point markers are displayed in other series at the matching location. These markers indicate relative point locations, and may not indicate the exact matching location. Markers that indicate a good matching location display a larger marker, while markers indicating a more approximate matching location are smaller.

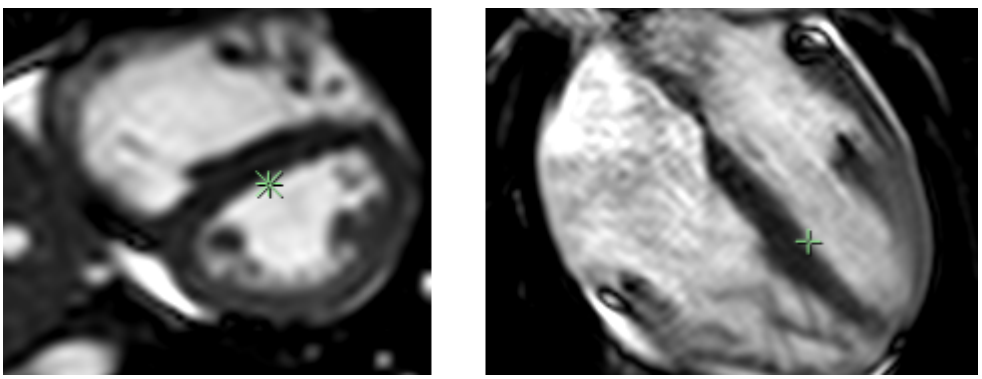

Fig. 46: Eight-point marker (left) and four-point marker (right)

Visual AHA - Scoring

If desired, you can score your findings from visual analysis using AHA methodology (American Heart Association). Various templates are provided for you to add color-coded findings according to anatomical regions.

1. Click **Start Visual Analysis** in the task guidance panel.

⇨ The **Visual AHA Scoring** panel is displayed.

2. Select a visual analysis method in the **New Visual Analysis** list.

⇨ A segment chart and scoring categories are displayed in the **Visual AHA Scoring** panel.

3. To score segments, select a scoring category and then click any segments that you want to score with that category.

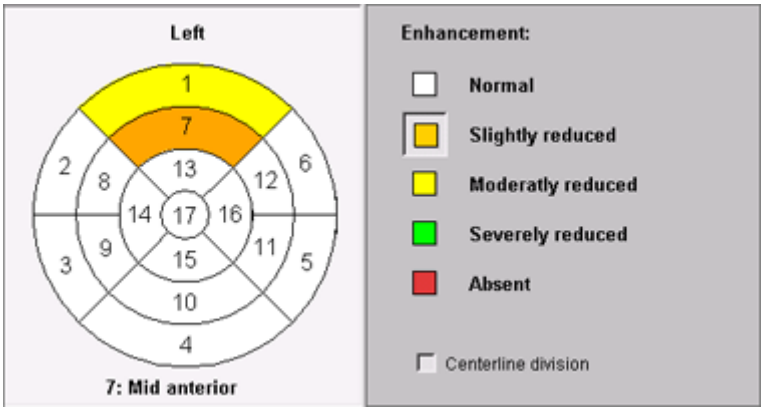

Fig. 47: Visual scoring

4. If available with the selected visual analysis method, you can divide segments along the centerline by selecting **Centerline division** below the scoring categories.

⇨ Dividing segments in this way allows you to score segments differently either side of the centerline.

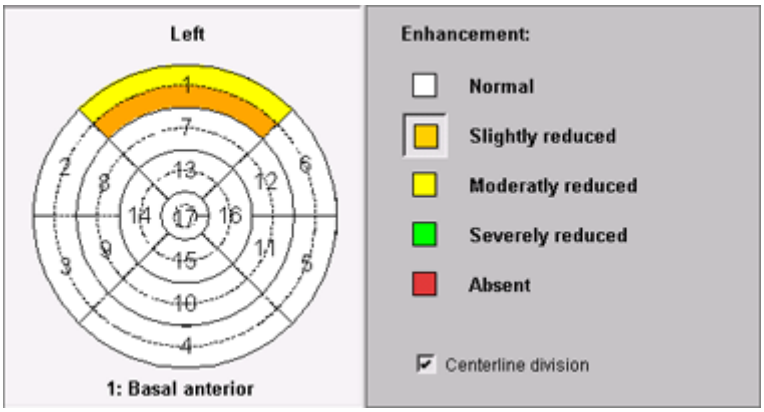

Fig. 48: Visual scoring with centerline division enabled

5. If desired, you can select another visual analysis method from the **New Visual Analysis** list and perform another visual analysis.

⇨ Each analysis that you perform is listed in the **Select Visual Analysis** box below the **New Visual Analysis** list. Select an analysis from the **Select Visual Analysis** box to display the visual analysis scoring.

6. To send the selected visual scoring analysis to the Report application, click **Report current visual analysis**.

300006338791_A/881 * 2021-06-30

⇨ Images that are sent to the Report application are automatically saved in the 'Summary Images' series, available in the Directory.

7. To delete the selected visual scoring analysis, click **Delete current visual analysis**.
8. To close the **Visual AHA Scoring** panel, click **Close**.

Start Quantitative Analysis

1. Select the series that you want to analyze.

   To select more than one series (for example, for biplane LA functional analysis), select the first series, then press CTRL and select the second series.

⇨ When you select a series, suitable analysis types are listed in the task guidance panel.

2. To start the analysis, select an analysis type and click **Start Analysis Application** in the task guidance panel.

NOTICE

You can also select QFlow from the MR Cardiac Viewer. This starts QFlow analysis within MR Cardiac analysis, providing the option for improved comparison and integration of results with function analysis.

MR Analysis types

NOTICE

The results of analysis depend on the quality of the acquisition. Analysis results should always be confirmed by visual assessment of the original images.

NOTICE

Phase number and trigger delay may not be a reliable indicator for ED and ES images, due to e.g. trigger problems. Always visually inspect all phases to verify which images are used for ED and ES phases.

Help guidance

Detailed help guidance for each step of the following analysis types is available at any time from the task guidance panel.

To view the help guidance panel, click **Help** in the task guidance panel. To close the help guidance panel, click **Help** again, or click **Close** in the upper-right corner of the help guidance panel.

Saving results

You can save the results of any analysis that you perform. The procedure for saving results is the same for each analysis type, and it is summarized here for reference.

1. To save the contours/segmentation only, use the **Save Results** tool in the common tools panel.

⇨ The **Save results** dialog box is displayed allowing you to select a file name, file format, and destination. The contours/segmentation are saved as a new series in the selected location.

2. To create a derived series from the current series, including the segmentation, use the **Generate Series** tool in the common tools panel.

⇨ A dialog box is displayed allowing you to select a file name, file format, and destination. You can save the series in DICOM format, or in non-DICOM format. If you select a non-DICOM format, you should additionally select a filesystem destination to export the series to.

NOTICE

The **Generate Series** tool can currently only be used with series analyzed in the Functional analysis tool.

3. To export the analysis results in CSV format, right-click one of the upper viewports (displaying the slice) and click **Export results and segmentation**.

⇨ The **Export results and segmentation** dialog box is displayed allowing you to select a destination for the CSV file. You can save the file to a repository, or export the file to a directory on your workstation.

4. To send the analysis results to a report, use the following reporting options in the common tools panel:

   -  Click **Send selected image(s) to report** to send images from the analysis results to a report. The images are available in the **Summary Images** panel in the Report application.
   -  Click **Report display** to send a snapshot of the current display layout to a report. The image is available in the **Summary Images** panel in the Report application.
   -  Click **Report Clinical Results** to send the numerical data from the analysis results to a report. The first time that you select this option during an analysis procedure, a dialog box is displayed allowing you to add details of risk factors, clinical history, and patient parameters and information. These details are included in the report.

⇨ The first time that you select one of these reporting options during an analysis procedure, a dialog box is displayed allowing you to select an existing report or create a new report. Subsequently, during the analysis procedure, images and results are sent to the same report when you select a reporting option.

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5. To save numerical results, use the **Save All Tables** tool in the common tools panel.

⇨ The Save all tables dialog box is displayed allowing you to select a file name, file format, and destination. You can save the tables as DICOM, or as HTML, text, or comma-separated values.

6. To save the contents of a numerical results table, right-click the table and click **Copy**. You can then paste the data to a desktop application, such as a text editor, a spreadsheet, or presentation software.

7. To save the complete layout in the main display area, including segmentation and annotations, use the **Save Bookmark** tool in the common tools panel.

NOTICE

Before saving a bookmark, you should save any key images that you have created.

⇨ Segmentations and analysis results are always saved in a bookmark. However, some viewing aspects such as display layout and bull's eye plot selection might be need to set manually when a bookmark is opened later.

8. To save an image as a key image, press the spacebar when the image is displayed.

⇨ You can view saved images by clicking **Key Images** in the task menu of the task guidance panel.

⇨ After performing analysis on a study, you can access the key image viewer in the Directory. Using the key image viewer, you can provide a title and a comment for each image.

Saving a Series as a Movie

1. Click the  **Save Selected Images As** icon in the Common Tools panel.
2. If desired, change the description in the **Description** box.
3. Select **Movie** in the **Format** box.
4. Adjust the quality of the saved movie; drag the **Quality** slider between **Low** or **High**. The higher the quality, the larger the size of the saved movie file.
5. To de-identify the images, select **De-identify** (this function removes patient information before saving the images).
6. Select the location where you want to save the images in the **Destination** box.
7. Click **OK**.

3000063879l_A/881 * 2021-06-30

Findings Navigator

The Findings Navigator is located at the bottom of the screen and provides an area where you can collect manual measurements, selected quantitative analysis parameters, and KIN images (key note images). You can then export these findings in one step.

1. Click the blue Findings Navigator bar at the bottom of the screen to display the findings panel.

⇨ The Findings Navigator automatically hides when your pointer focus moves away from the panel. To keep the panel open, click the pin icon on the left side of the Findings Navigator bar.

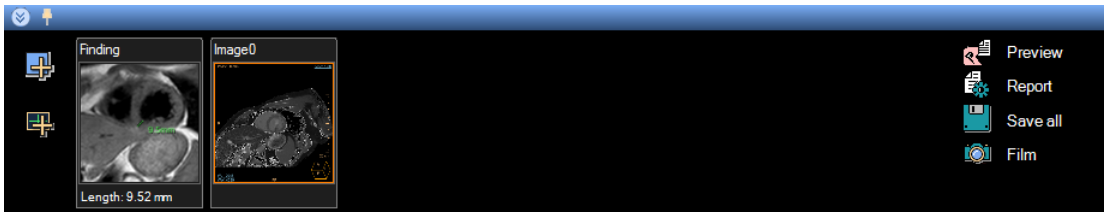

Fig. 49: Findings Navigator

2. To save a finding, click **Add Image** on the left side of the Findings Navigator panel.
3. If there is more than one manual measurement in the view, select whether to capture one of the findings or all of the findings.

⇨ If you want to capture just one finding, click **Select Finding** in the pop-up dialog box and then click on the finding.

⇨ Findings are stored in the Findings Navigator panel.

4. To save the contents of the entire display as a KIN image, do one of the following:
   - Click **Add Display** on the left side of the Findings Navigator panel.
   - Press SPACE.

⇨ A key image note is stored in the Findings Navigator.

5. To view a finding in more detail, click the finding in the Findings Navigator.
6. To review your findings before saving, click **Preview** on the right side of the Findings Navigator.

⇨ An overview of all findings is displayed, together with basic patient details and a box where you can enter comments. You can use the preview function to ensure your findings are complete before saving them or sending them to a report.

7. To delete a finding, if desired, right click the finding and click **Delete**.
8. To switch the preview off, click **Overview On/Off** at the bottom of the preview.
9. To save the findings, click one of the available export options on the right side of the Findings Navigator:
   - **Report**
   - **Save all**
   - **Film**

3000063879l_A/881 * 2021-06-30

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⇨ These options are also available at the bottom of the preview screen.

Configuration Options for Table Results

For each analysis application, you can configure which parts of numerical table results are captured when you create a finding from a table.

1. Click **Table Settings** in the task guidance toolbar.
2. For each available table type, select which parameters are to be included in the analysis tables within the application, and in the tables that are captured in the Findings Navigator.
3. Click **OK** to confirm your settings.

Framingham Heart Study

The methodologies used in the results summaries of the following analysis types are based on the findings of the Framingham Heart Study, which identifies the common factors or characteristics that contribute to cardiovascular disease. For more details of this study, please see the following web page:

www.framinghamheartstudy.org

Bull's-Eye Results Plots

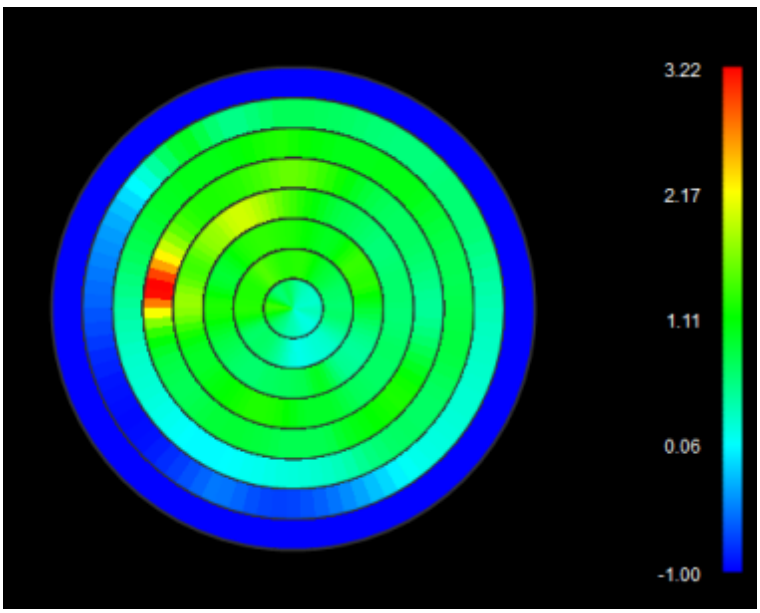

Fig. 50: Bull's-Eye Results Plot

Bull's-eye results plots are displayed in the results screen after analysis. They provide a quick reference of the results pertaining to segments and slices. The following interactions are available with bull's-eye plots.

300006338791_A/881 * 2021-06-30

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Window Level And Window Width

You can change the color scale threshold for a bull's-eye plot, a color-coded segment display, or a temporal enhancement diagram, by adjusting the window level or window width.

To adjust the **window width**, move the pointer over the plot, hold the middle mouse button, and do one of the following:

- Drag left to decrease window width.
- Drag right to increase window width.

To adjust the **window level** move the pointer over the plot, hold the middle mouse button, and do one of the following:

- Drag down to decrease the window level.
- Drag up to increase the window level.

Slice Selection

When you click a slice in the bull's-eye plot, the corresponding slice and analysis results are displayed.

Tooltips

When you pause the pointer over a segment, a tooltip is displayed indicating the segment and slice number, and the relevant results values.

Functional Long Axis Analysis

Overview

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

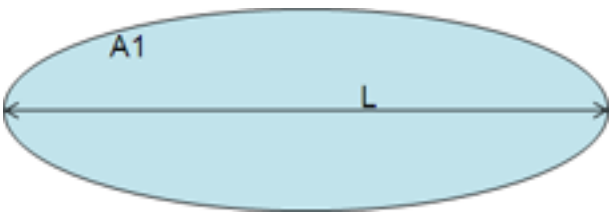

Fig. 51: ALEF method, single-plane ellipsoid model

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

V = Volume, A = Area, L = Length

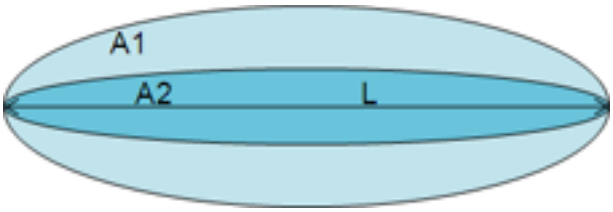

Fig. 52: ALEF method, biplane ellipsoid model

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

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 package is provided in the task guidance panel.

Starting the analysis package

▷ 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.

▷ In the Cardiac MR **Viewing** screen, select one of the following:

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

▷ Select **Functional LA LV** in the analysis type list in the task guidance panel.

1. Click **Start Analysis Application** in the task guidance panel.

⇨ The Functional LA package opens in the **Segment** screen and displays LA views 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.

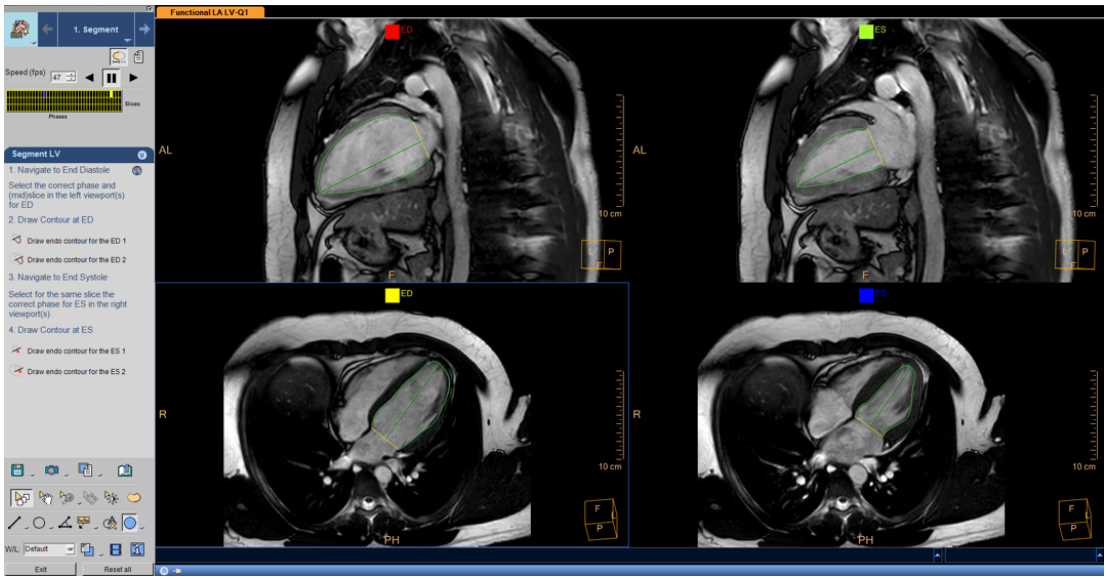

Fig. 53: Functional LA package - Segment screen

2. Select the optimal mid slice in the ventricle and the optimal phase/dynamic for ED and ES definitions. You can navigate through the slices and phases/dynamics using the following keyboard shortcuts:
   - PAGE UP: Go to the first slice.
   - PAGE DOWN: Go to the last slice.
   - HOME: Go to the first phase/dynamic.
   - END: Go to the last phase/dynamic.
   - UP ARROW / DOWN ARROW: Step through the slices.
   - LEFT ARROW / RIGHT ARROW: Step through the phases/dynamics.

Indications for Use

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

Segment LV step

1. Scroll to the ED image to verify that it is correct or select an alternative image.
2. Scroll to the ES image to verify that it is correct or select an alternative image.

⇨ The image navigator in the toolbar displays the currently selected phases in the image views (the selected phases are color-coded with the images).

3000063387 91_A/881 * 2021-06-30

Fig. 54: Image navigator

⇨ The **Segment LV** task guidance panel provides tools for drawing contours in the images.

3. Use the following tools to draw contours:
   -  Draw endo contour at ED in 2CH
   -  Draw endo contour at ED in 4CH
   -  Draw endo contour at ES in 2CH
   -  Draw endo contour at ES in 4CH
4. Draw contours on each image for the ED and ES phase.
   - 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.
   - Optional step: reposition the midline to the apex to fine-tune the contour for optimal results.

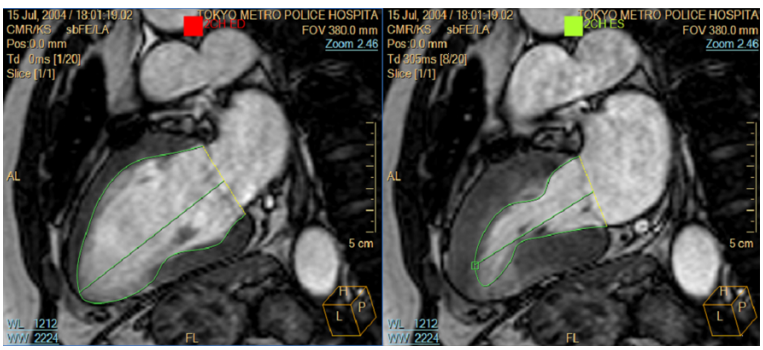

Fig. 55: Contours drawn on the ED and ES images

View Results step

1. When you have drawn contours on all images, click the right arrow in the title panel to display the **View Results** screen.

⇨ In the **View Results** screen, the results of the analysis are displayed in a results summary panel. The following steps describe how to fine-tune the results summary.

2. The patient's heart rate is entered automatically from the acquisition information. However, if you need to correct the heart rate, enter a number in the **Heart rate** box in the **View Results** task guidance panel.
3. If desired, select a different results protocol from the **Select Result Protocols** list in the task guidance panel.
4. To change the layout of the results summary, right-click the results summary table and select an option.
5. To display the results adjusted for the patient's BSA do the following:
   - Right-click the results summary table.
   - Click **BSA Calculation**.
   - If patient's weight and height are not available from the acquisition information, enter the weight and height in the **BSA Calculation** dialog box.
   - 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 summary table, click **BSA Formula Type**, and 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.

300006338791_A/881 * 2021-06-30

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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

NOTICE

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

References

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3000063879l_A/881 * 2021-06-30

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Functional LV & RV Analysis

Overview

The Functional LV & RV analysis package provides short-axis functional volumetric analysis of both the left and right ventricles (LV and RV). When performing RV analysis, images with other orientations can be loaded, such as axial images. To perform segmentation correctly, the analysis package requires multi-slice, multi-phase images.

NOTICE

Series that have a different slice distance to the series being analyzed cannot be loaded.

The package enables fast, automatic segmentation of the left and right ventricles, with optional manual editing tools. Extensive heart wall analysis (motion, thickness, and thickening) and optional papillary muscle extraction are included. If only the volumetric parameters are of interest, you can choose to do just a quicker endo volume analysis.

Auto Preprocessing

Processing preferences allow you to manage the settings for LV and RV segmentation of cardiac MR data. For more information, see the **Processing** section of the **Preferences** dialog box in the **Directory** screen.

When processing is enabled, LV and RV segmentation is performed automatically when a series is imported to IntelliSpace Portal from a scanner or PACS. The results are saved in the **Patient Directory**.

The automatic LV and RV segmentation process segments all volumes of short-axis multi-slice multiphase series, and then saves the registered series with the study. Processing can be enabled or disabled in the **Processing** section of the **Preferences** dialog box.

Manual Processing

To process a cardiac MR series manually before loading it in the application, right-click the series, point to **Run Processing** and then select **LV/RV Segmentation**.

Task Guidance

Guidance for this analysis package is provided in the task guidance panel.

3000063387 91_A/881 * 2021-06-30

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▷ In the Cardiac MR **Viewing** screen, select a select a functional, multi-slice, multi-phase series.

▷ Different orientations may be loaded:

- For LV analysis, SA orientations may be used.
- For RV analysis, axial or 4CH series may be used.

▷ For correct analysis, select a series in which the whole LV and/or RV is scanned from valve to apex.

▷ Select **Functional LV & RV** in the analysis type list in the task guidance panel.

1. Click **Start Analysis Application** in the task guidance panel.

⇨ The Functional LV & RV package opens in the **Segment** screen.

⇨ When you perform LV analysis with a series in SA orientation, the layout of the main viewport is configurable. By default, a single view is displayed, but additional layouts are available, displaying ED and ES in side-by-side viewports, or displaying all slices of the SA series in one viewport. For details, see section “Selecting a layout” on page 170.

⇨ 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 the endo and epi contours for LV and the endo countour for RV.

⇨ If functional views with different orientations are available, they are displayed in reference views.

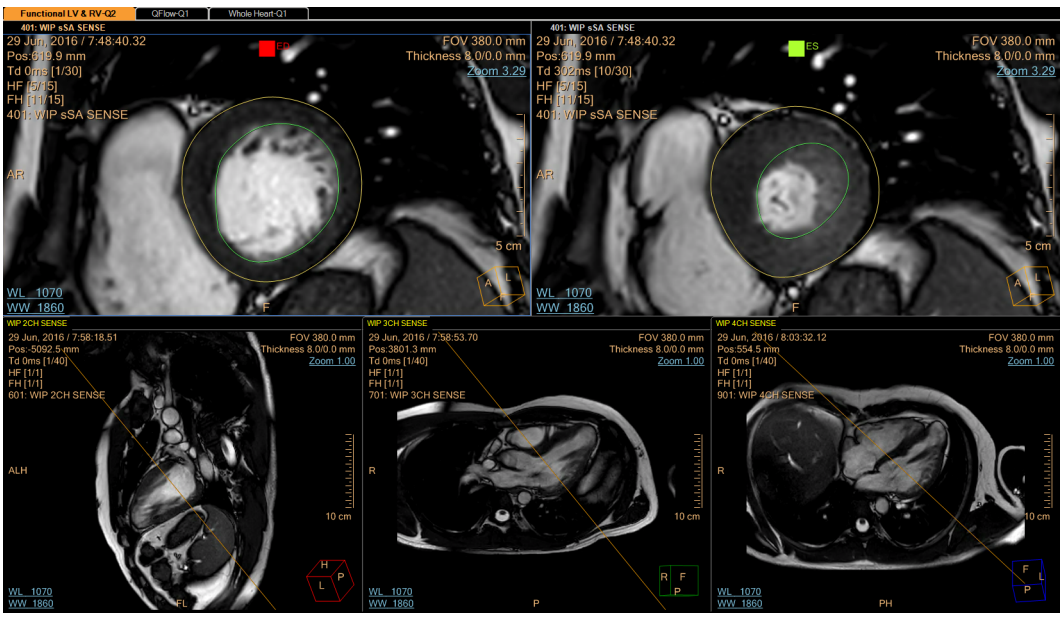

Fig. 56: Segment screen, with LV ED/ES Layout

2. You can navigate through the slices and phases using the following keyboard shortcuts:
   - PAGE UP: Go to the first slice.
   - PAGE DOWN: Go to the last slice.
   - HOME: Go to the first phase.

- END: Go to the last phase.
- UP ARROW / DOWN ARROW: Step through the slices.
- LEFT ARROW / RIGHT ARROW: Step through the phases.

⇨ Workflows for LV analysis and RV analysis are available independently; you can choose to perform both analysis workflows, or perform only LV analysis or only RV analysis. Procedures for both workflows are described in the following sections.

Settings

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

- Select different units to be used for analysis.

Indications for Use

The MR Cardiac 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.

Selecting a layout

When you perform LV analysis with a series in SA orientation, several layout options are available.

1. To select a layout, click the layout selector in the toolbar, and then select a layout from the layout list.
   - Single SA view.
   - Side-by-side SA views displaying ED and ES.

⇨ Selecting a layout sets a preference on the system; the next time that you start a session, the selected layout will be displayed.

NOTICE

The Layout Manager cannot be used to create new layouts in this application.

Viewport interaction

All slices of the SA series are displayed in one viewport (this provides a quick overview of the segmentation for ED and ES phases on all slices, without needing to navigate through each slice).

- To navigate to a single slice, double-click the preferred slice.
- To move back to the multi-slice view, double-click again in the image.

3000063387 91_A/881 * 2021-06-30

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Segment LV step

The task guidance panel provides tools for defining ED and ES, defining the segmentation range (valve plane to apex plane), drawing contours, and adding spoke wheels.

1. Define the **ED** and **ES**.

⇨ You define these settings by entering the time for ED and ES in the task guidance panel. Alternatively, select **LV ED/ES Layout** using the layout selector in the toolbar, then scroll to ED in the left viewport and scroll to ES in the right viewport.

NOTICE

For accurate analysis, it is important that you define the ED and ES in this step, or at least verify the input.

⇨ These settings are used to calculate the contours: the ED setting is used to detect contours by the automatic contour detection method in the following step.

2. If segmentation has not been done, select **Apply segmentation** and then select one of the following options:

-  **Automatic segmentation**
-  **Semi-automatic segmentation**

NOTICE

Automatic segmentation is enabled only if the application is launched without automatically preprocessed results.

⇨ The automatic segmentation tool allows you to segment the LV epi and endo contours and the RV endo contour automatically. Calculation of the segmentation begins automatically when you select the action. Automatic segmentation displays contours in SA view.

NOTICE

Automatic segmentation may take some time (approximately 90 seconds) to segment the LV epi and endo contours and the RV endo contour. During this time, further interactions with the currently active tab are blocked.

NOTICE

Automatic segmentation cannot be interrupted or stopped while it is in progress.

CAUTION

Automatic segmentation was neither designed nor validated for use in pediatric cases. Manual segmentation is recommended.

3. Define the range for segmentation by indicating the valve plane and apex plane.

   To define the segmentation range, do the following:

   - Optional step: Use the reference lines in the reference views to set the valve slice and the apex slice.
   -  Scroll to the valve slice, click **Set center of blood pool for valve slice** in the guidance panel, and then click on the center of the LV blood pool in the slice.
   -  Scroll to the apex slice, click **Set center of blood pool for apex slice** in the guidance panel, and then click on the center of the LV blood pool in the slice.

⇨ Calculation of the segmentation begins automatically when at least two points are identified.

⇨ Automatic segmentation displays contours in the SA view.

NOTICE

Avoid having the outflow tract in your segmentation. It is quicker to add additional contours after the segmentation around the valve slices for ED and ES for more accurate LV volume calculation.

NOTICE

If you are only interested in volume results, clear the check box for epi contours in the task guidance panel.

This provides faster results, as time is not spent verifying and correcting the epi contours and only the endo volume results are displayed. Blood volume with papillary correction is not displayed.

300006338791_A/881 * 2021-06-30

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NOTICE

For the results summary table only the ED and ES contours are needed for calculation of the results. It is very important that these phases are correctly segmented.

If you only want to draw ED and ES manually, you can use the contour tools in the task "3 - Verify/Draw Contours" in the task guidance panel.

NOTICE

The contour tools include a **Drop Seed** tool  that allows you to click in the blood pool to detect the contour. If the detected contour is not complete, click again in another part of the blood pool.

4. We recommend the following process as the simplest way to verify contours:
   - Verify and propagate edits on the first phase of all slices.
     - Use the arrow keys on the keyboard to step through the phases.
     - Click **Propagate edits over phases**  in the task guidance panel to propagate edits.
   - Verify and propagate edits on ES phases.
   - When using the single viewport layout, click **Play forward**  in the toolbar to start movie playback; this is an effective way to rapidly verify all contours.
   - When using the side-by-side viewport layout, do not scroll through the slices as this changes the ED and ES values that you have already set in the first step of this task. If desired, you can verify the contours in the results screen later in the workflow of this package.
   - Optional step: Add only contours for ED and ES phases for apex and valve slices.
5. To edit a contour, do the following:
   - Select any of the interactor tools.
   - Pause the pointer over the edge of the contour to display the contour nodes.
   - Drag an existing node to a new position, or click and drag on the edge of the contour to create and reposition a new node.
   - To delete one or more nodes, drag a node to another node; this action combines the nodes and deletes any nodes in between them.

NOTICE

You can start over by redrawing the contour using the **New epi contour** tool  or the **New endo contour** tool  in the task guidance panel. You can also use manual contour tools such as the freehand, spline or drop seed tools.

Clicking one of these tools automatically removes the existing contour. The contour tools remain selected until you select a different interaction tool. This allows you to rapidly draw several contours.

6. Navigate to the apical slice at ED and draw contours.

⇨ These contours improve the accuracy of the myocardial mass calculation.

7. Use the image navigator in the toolbar to identify any slices with invalid contours and correct them.

⇨ Slices with invalid contours are indicated with a cross in the image navigator.

8. To view RV contours in the LV view, select **Show RV Contours** in the task guidance panel.

NOTICE

The **Show RV Contours** option is not available if RV contours are not present.

9. After drawing contours on all slices, create a spoke wheel on all slices using the following tools in the task guidance panel:
   - Use the up and down arrows in the **No. seg** box to define the number of segments.
   - Click **New spoke**  . Spoke wheels are propagated automatically over phases and slices.
   - Verify the spoke wheel. Spoke wheels can be moved or rotated; click **Help**  in the task guidance panel for details.
   - Verify the spoke wheel in each slice to ensure correct analysis results.
10. Do one of the following:
    - Select **Navigate to RV Segmentation** in the task guidance panel to review or segment the RV.
    - Select the right arrow at the top of task guidance panel to navigate to the results view for the LV.

Segment RV step

1. To segment or review the RV, click the task selector and then click **Segment RV**.

300006338791_A/881 * 2021-06-30

⇨ The **Segment RV** task guidance panel is displayed.

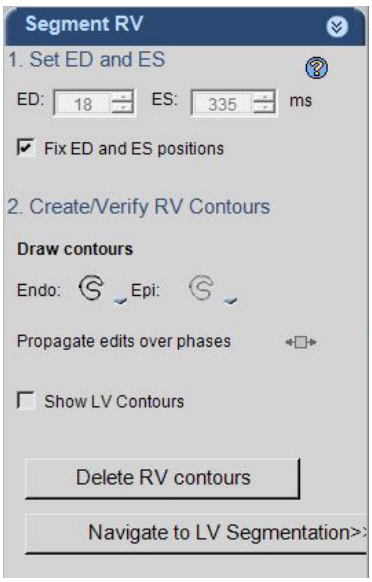

Fig. 57: Segment RV task guidance panel

⇨ The **Segment RV** layout displays the ED and ES tile views in the upper-left and upper-right corners with the available reference views arranged below.

NOTICE

The RV segment layout displays RV endo contours if you launched the application from the **Patient Directory** with preprocessed LV and RV results or if you selected the automatic segmentation option in the **Segment LV** step.

3000063879l_A/881 * 2021-06-30

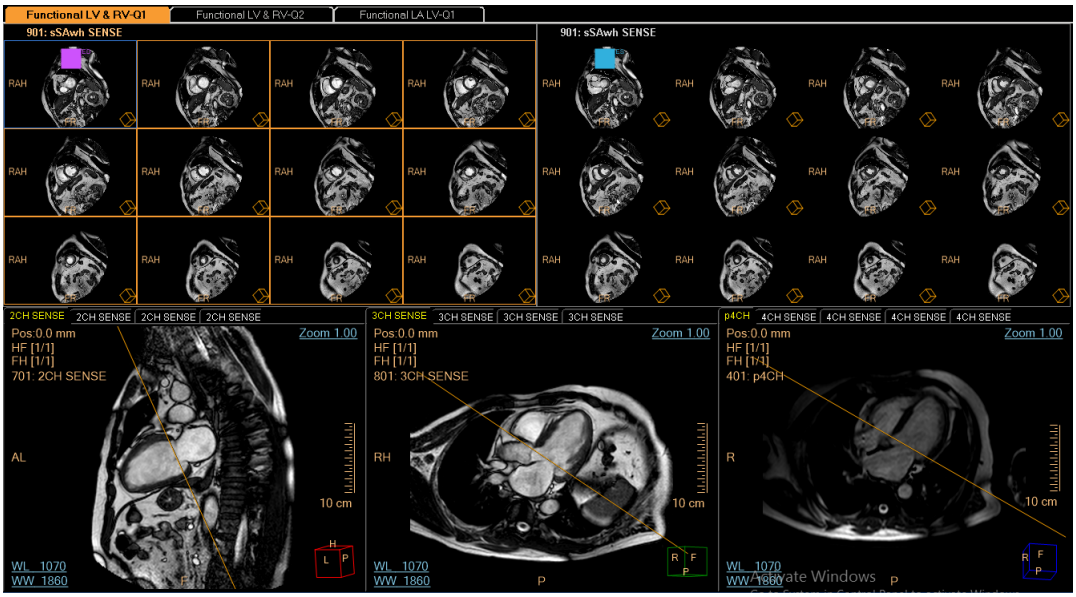

Fig. 58: Segment RV layout

2. Play the movie of the series or scroll through the phases to verify that the end systole (ES) and end diastole (ED) phases are correctly identified by the application.
3. If the ES and ED phases are not correctly identified, select **Fix ED and ES positions** in step 1 of the task guidance panel.
4. If the application was launched with results, review the RV endo contours and edit them as needed using the tools described in the following steps.
5. Click **New endo contour** in step 2 of the task guidance panel and draw closed endo contours on the ED and ES phases.

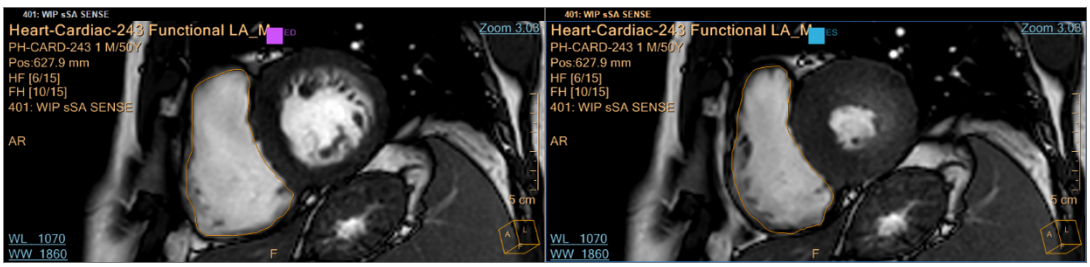

Fig. 59: Drawing the endo contours on ED and ES

6. If relevant, draw multiple RV endo contours on phases where RV structures are split as islands.

3000063387 91_A/881 * 2021-06-30

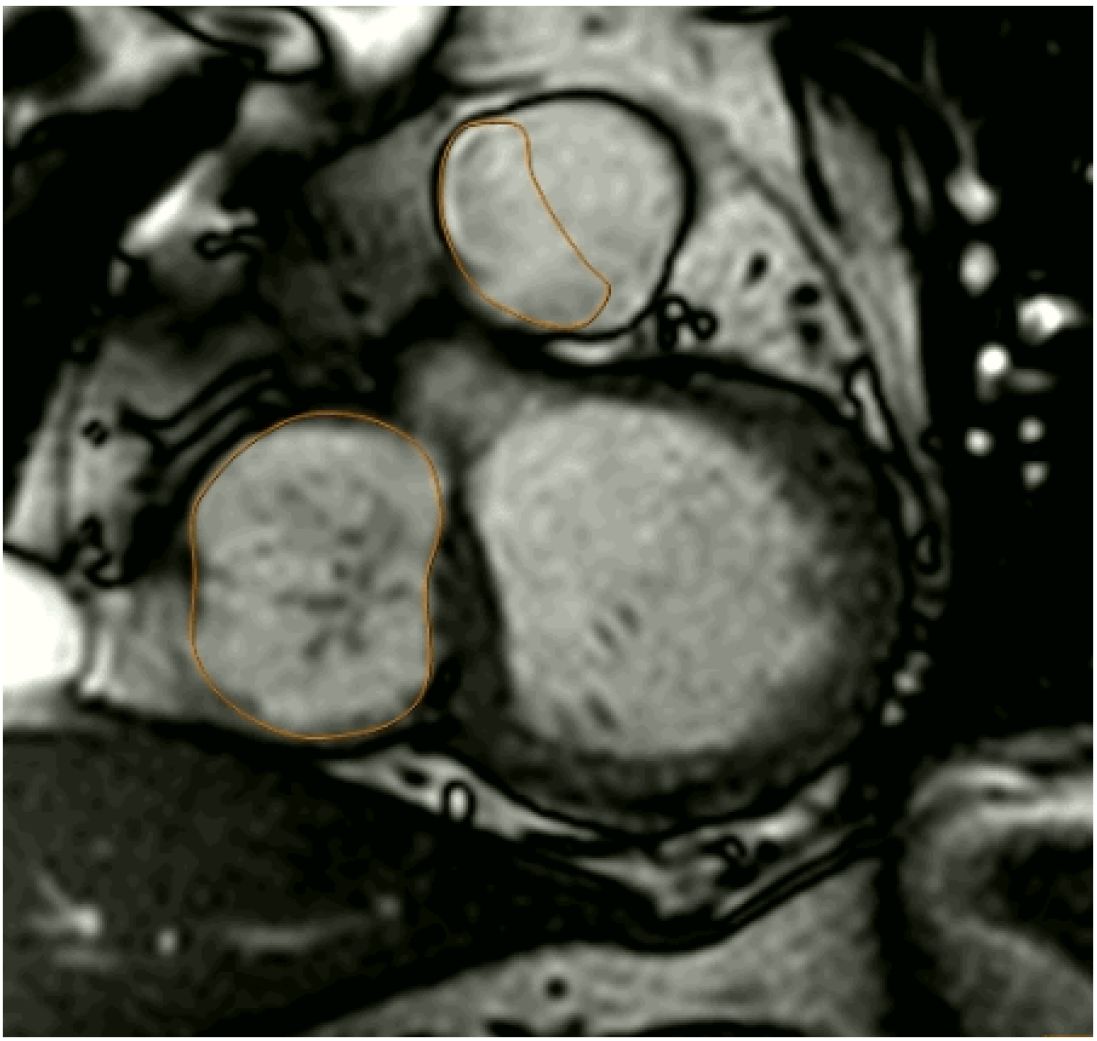

Fig. 60: Drawing multiple RV endo contours

NOTICE

RV epi contours are not allowed on phases with multiple RV endo contours.

Propagation over phases is not possible for the slices with multiple RV endo contours in any of the phase.

7. After drawing or editing the contours, click **Propagate edits over phases**.

8. Click **New epi contour** in step 2 of the task guidance panel and draw open epi contours on the ED and ES phases.
9. To view LV contours in the RV view, select **Show LV Contours** in the task guidance panel.

NOTICE

Endo contours must be drawn before you can draw epi contours.

⇨ The application automatically closes the contours.

NOTICE

RV epi contours are not available with automatic segmentation and must be drawn manually. Propagation is not available for epi contours.

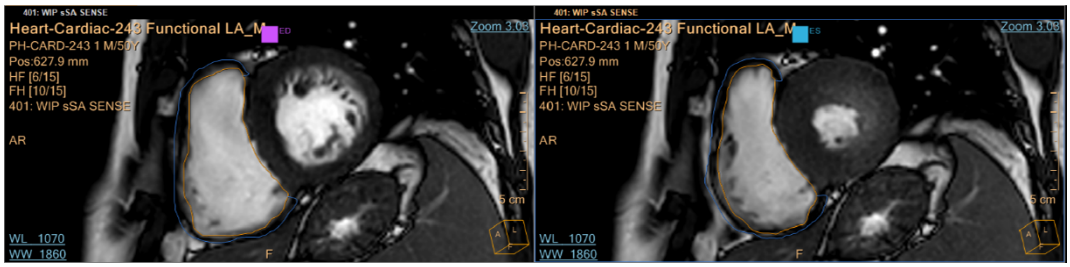

Fig. 61: Drawing the epi contours on ED and ES

10. Play the movie of the series or scroll through the phases to verify that the contours have been propagated correctly in all phases.
11. If the automatic segmentation of the RV is not satisfactory and you want to continue with manual segmentation, select **Delete RV Contours** in the task guidance panel.

⇨ The RV contours are removed from all slices and phases.

NOTICE

Contours should be drawn on all slices containing the RV.

12. Do one of the following:
    - Select **Navigate to LV Segmentation** to go back to the **Segment LV** step.
    - Select the right arrow at the top of the task guidance panel to go to the **View Results** step.

View Results step

1. When you have drawn contours and spoke wheels, click the right arrow in the title panel to display the **View Results** screen.

3000063387 91_A/881 * 2021-06-30

NOTICE

To display results correctly, you need to have at least defined endo contours for ED and ES phases. To have regional results plots, a spoke wheel should be defined. To have AHA bull's eye results, at-least three slices shall be defined with both endo, epi contours and spoke wheel in all phases. There should not be any crossing endo or epi contours. RV results are not available if RV contours were not reviewed or segmented in the **Segment RV** step.

⇨ In the **View Results** screen, the results of the analysis are displayed. The following steps describe how to fine-tune the results summary.

2. In the task guidance panel of the **View Results** screen, you can change the following options, if desired:
   - In the **Verify ED/ES** section, you can change the calculated ED and ES.
   - In the **Set Patient Heart Rate** section, you can correct the patient's heart rate.
3. In the **Choose Result Method** section, select the display method for the results:
   - **Blood Volume** (correction for papillary muscle and visualization of papillary extraction).
   - **Endo Volume** (no correction for papillary muscle).

⇨ An automatic algorithm extracts papillary muscle based on a calculation of percentage of blood per voxel. A blue mask shows the amount of calculated blood per voxel, and visualizes this with a gradient change in blue overlay. Light blue is higher percentage of blood, darker blue is higher percentage of papillary muscle.

NOTICE

LV blood volume results are displayed only if both endo and epi contours are defined for the LV. RV blood volume results are displayed only if both endo and epi contours are defined for the RV.

3000063879l_A/881 * 2021-06-30

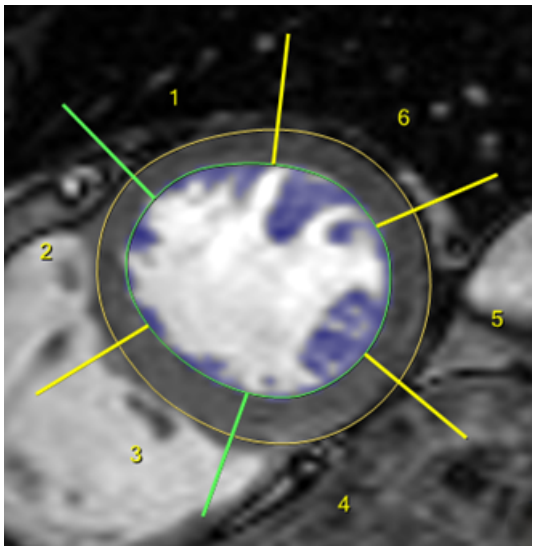

Fig. 62: Visualization of Papilliary Extraction

4. In the **Select Result Protocols** section, select the results layout that you want to view.

⇨ Each layout displays a results graph of volume over time, results summary table, slice view with contours and spoke wheels, and bull's-eye plots, as appropriate for the selected protocol and type of results: **Detailed** (94 angles), **Regional** (spoke definition), or **AHA**.

⇨ You can double-click any viewport in the Results screen to display the viewport maximized. Double-click the viewport again to return to the default results layout.

⇨ A global layout is also available that additionally displays a results summary. If the RV has been segmented, you can choose to view each layout for the LV only, for the RV only, or for both the LV and RV.

5. You can right-click the results summary table and choose to display the results as a summary table or diastolic function table.

6. To display the results adjusted for the patient's BSA do the following:
   - Right-click the results summary table.
   - Click **BSA Calculation**.
   - Enter the patient's weight and height in the **BSA Calculation** dialog box.
   - Click **OK**.

NOTICE

Patient weight and height information entered for the BSA calculation is retained for other applications (Functional LV/RV, Functional LA/LV) in the same session.

3000063387 91_A/881 * 2021-06-30

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 summary table, click **BSA Formula Type**, and then select a calculation formula.

7. To display the results adjusted for the patient's age and gender do the following:
   - Right-click the results summary table.
   - Click **Patient Details**.
   - Enter the patient's age and gender in the **Patient Details** dialog box.
   - Click **OK**.
8. To edit the values used for calculating results normalized for age and gender, click **Edit Normal Values** and then edit the values in the **Edit Normal Values** dialog box. For details of the default values used for normalization, see section “Normal Values” on page 189.

⇨ Alternatively, you can disable the use of normal values altogether. This prevents adjustments for normal values from appearing in reports.

9. When viewing a bull's-eye results plot, you can right-click the plot and configure the following items:
   - Select a results parameter.
   - Select a results layout: **Detailed**, **Regional**, or **AHA**.

NOTICE

The AHA bull's-eye plots are calculated automatically if you have defined contours and spoke wheels on at least the apex, mid, and base slice. At least 4 spokes should be defined on the apex slice and 6 spokes on the mid and base slices.

NOTICE

The accuracy of the results is dependent on the input for acquisition (perpendicular to the LV), and the accuracy of the verification and edits. The accuracy of the contour algorithm is dependent on the image quality of the acquisition. Low image quality, signal, or artifacts may have a negative influence on the calculated contours.

Volume over Time Graph and Manual Contours

After automatic contour detection, the slope of the volume over time graph is smooth:

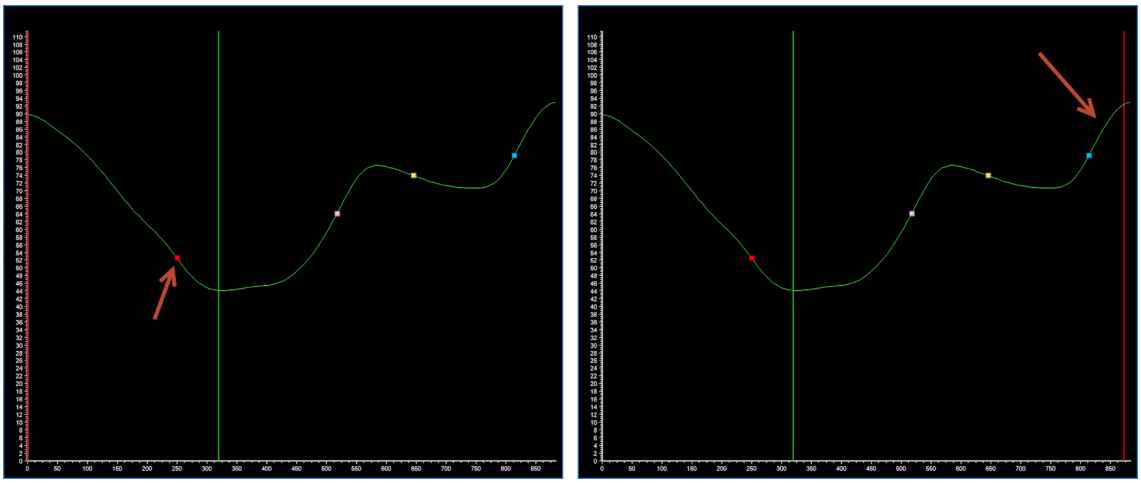

Fig. 63: Volume over time graph after automatic contour detection (displaying ED at first phase (left) and last phase (right))

However, if manual contours are added to the valve slice, or if the ejection fraction is very low, the **Peak ejection** marker (red), may appear in the wrong temporal position. This causes the slope of the volume over time graph to appear unsmooth, as indicated here:

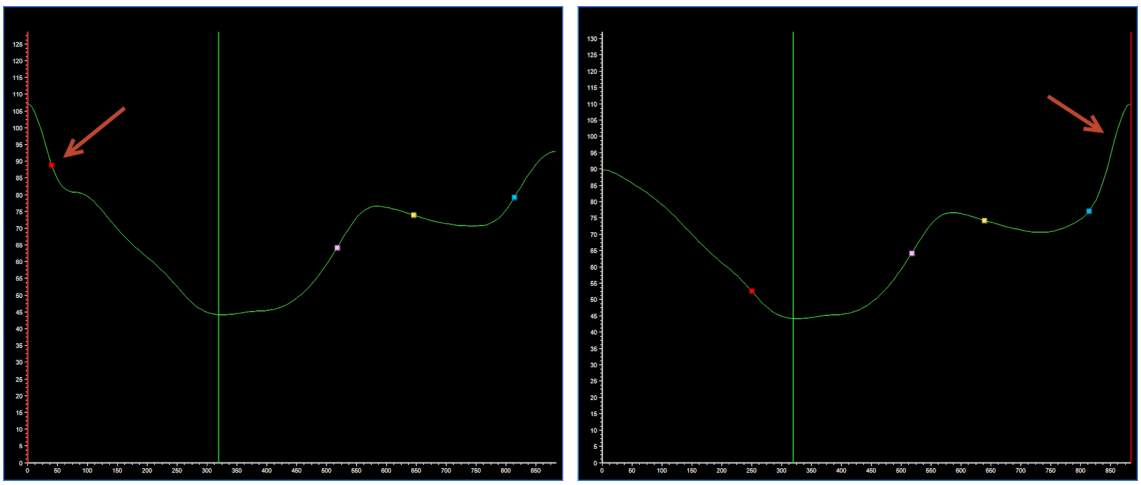

Fig. 64: Volume over time graph after manual contours have been added, or if the ejection fraction is low (displaying ED at first phase (left) and last phase (right))

In this situation, please note that the function parameters displayed in the results summary table (global layout) are correct.

Results summary tables

Results summary tables display analysis results indexed to BSA where applicable. Results are displayed next to normal ranges for comparison. Results that fall outside the normal range are displayed in red. Use the right-mouse menu to configure the results summary table for LV and RV to display the following sets of results. (For definitions of these terms, see section “LV and RV analysis terminology” on page 185.)

3000063387 91_A/881 * 2021-06-30

Results summary table

You can choose to display the following results for Endo Volume (if available) or Blood Volume.

- Ejection fraction (%)
- Stroke volume (ml)
- Cardiac output (L/min)
- Stroke index (ml/m^2)
- Cardiac index (L/(min*m^2))
- ED volume (ml)
- ES volume (ml)
- ED volume/BSA (ml/m^2)
- ES volume/BSA (ml/m^2)
- ED time (ms)
- ES time (ms)
- Cardiac density (gr/ml)
- ED wall mass (gr)
- ED wall + papillary mass (gr)
- ED wall mass/BSA (gr/m^2)
- ED wall + papillary mass/BSA (gr/m^2)
- BSA (m^2)
- Heart rate (bpm)

	Left ventricle - results summary	
	Endo Volume	Normal Values
Ejection fraction	51 %	65 . . . 83 %
Stroke volume	45.6 ml	65.0 . . . 136.0 ml
Cardiac output	3.0 L/min	4.2 . . . 8.8 L/min
Stroke index	23.5 ml/m²	33.0 . . . 67.0 ml/m²
Cardiac index	1.5 L/(min*m²)	2.1 . . . 4.4 L/(min*m²)
ED volume	89.8 ml	94.0 . . . 182.0 ml
ES volume	44.2 ml	19.0 . . . 52.0 ml
ED volume/BSA	46.2 ml/m²	48.0 . . . 90.0 ml/m²
ES volume/BSA	22.7 ml/m²	10.0 . . . 28.0 ml/m²
ED time	0.0 ms	N/A
ES time	320.0 ms	N/A
Cardiac density	1.05 gr/ml	N/A
ED wall mass	90.9 gr	72.0 . . . 127.0 gr
ED wall + papillary mass	110.3 gr	N/A
ED wall mass/BSA	46.8 gr/m²	39.0 . . . 65.0 gr/m²
ED wall + papillary mass/BSA	56.7 gr/m²	N/A
BSA	1.94 m²	
Heart Rate	65 bpm	

Fig. 65: Example of results summary table

NOTICE

Double-click the results table to maximize it in the viewport.

Diastolic function table

You can choose to display the following results for Endo Volume (if available) or Blood Volume.

- 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*m^2)
- First peak filling rate/BSA (ml/(ms*m^2)
- First filling volume/BSA (ml/m^2)
- Second peak filling rate/BSA (ml/(ms*m^2)
- Second filling volume/BSA (ml/m^2)
- Minimum filling rate/BSA (ml/(ms*m^2)
- First over second filling volume/BSA (ml/m^2)

	Left ventricle - diastolic function summary	
	Endo Volume	Normal Values
Peak ejection rate	0.21 ml/ms	N/A
Time to peak ejection rate	250 ms	N/A
First peak filling rate	0.30 ml/ms	N/A
Time to first peak filling rate	518 ms	N/A
First filling volume	29.8 ml	N/A
Second peak filling rate	0.29 ml/ms	N/A
Time to second peak filling rate	814 ms	N/A
Second filling volume	15.8 ml	N/A
Minimum filling rate	N/A	N/A
Time to minimum filling rate	646 ms	N/A
First over second filling volume	1.9	N/A
Peak ejection rate/BSA	0.11 ml/(ms*m²)	N/A
First peak filling rate/BSA	0.15 ml/(ms*m²)	N/A
First filling volume/BSA	15.3 ml/m²	N/A
Second peak filling rate/BSA	0.15 ml/(ms*m²)	N/A
Second filling volume/BSA	8.1 ml/m²	N/A
Minimum filling rate/BSA	N/A	N/A
First over second filling volume/BSA	1.0	N/A

Fig. 66: Example of diastolic function results summary table

NOTICE

Double-click the results table to maximize it in the viewport.

Bull's-eye plots

Using the right mouse menu, you can configure the bull's-eye plots for LV and RV to display the following results. For definitions of these terms, see section “LV and RV analysis terminology” on page 185.

- 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 (regional results display average results per segment).

The bull's-eye plots 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 Bull’s eye to get numerical information about the presented result values.

Double-click a bull's-eye plot to maximize it in the viewport.

LV and RV analysis terminology

LV and 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 (V_{ED})**: 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.

  $V_{ED} = V_{EDF} + V_{LDF}$
- **Early diastolic filling volume (V_{EDF})**: 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 (V_{LDF})**: 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.

300006338791_A/881 * 2021-06-30

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- **Time of end diastolic volume (T_{ED})**: Moment when the volume of the left ventricle has reached V_{ED}; in ms.
- **Time of first peak filling rate T_{PFR1}**; in ms.
- **Time of second peak filling rate (T_{PFR2})**; in ms.
- **Time of minimum filling rate (T_{MF})**: 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 (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 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 (T_{PER})**: The time when the peak ejection rate occurs; in ms.
- **Time of end systolic volume (T_{ES})**: 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).

  $SV = V_{ED} – V_{ES}$
- **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
- **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
- **The fraction of the early and late filling volumes**:

  V_{EDF} / V_{LDF}

300006338791_A/881 * 2021-06-30

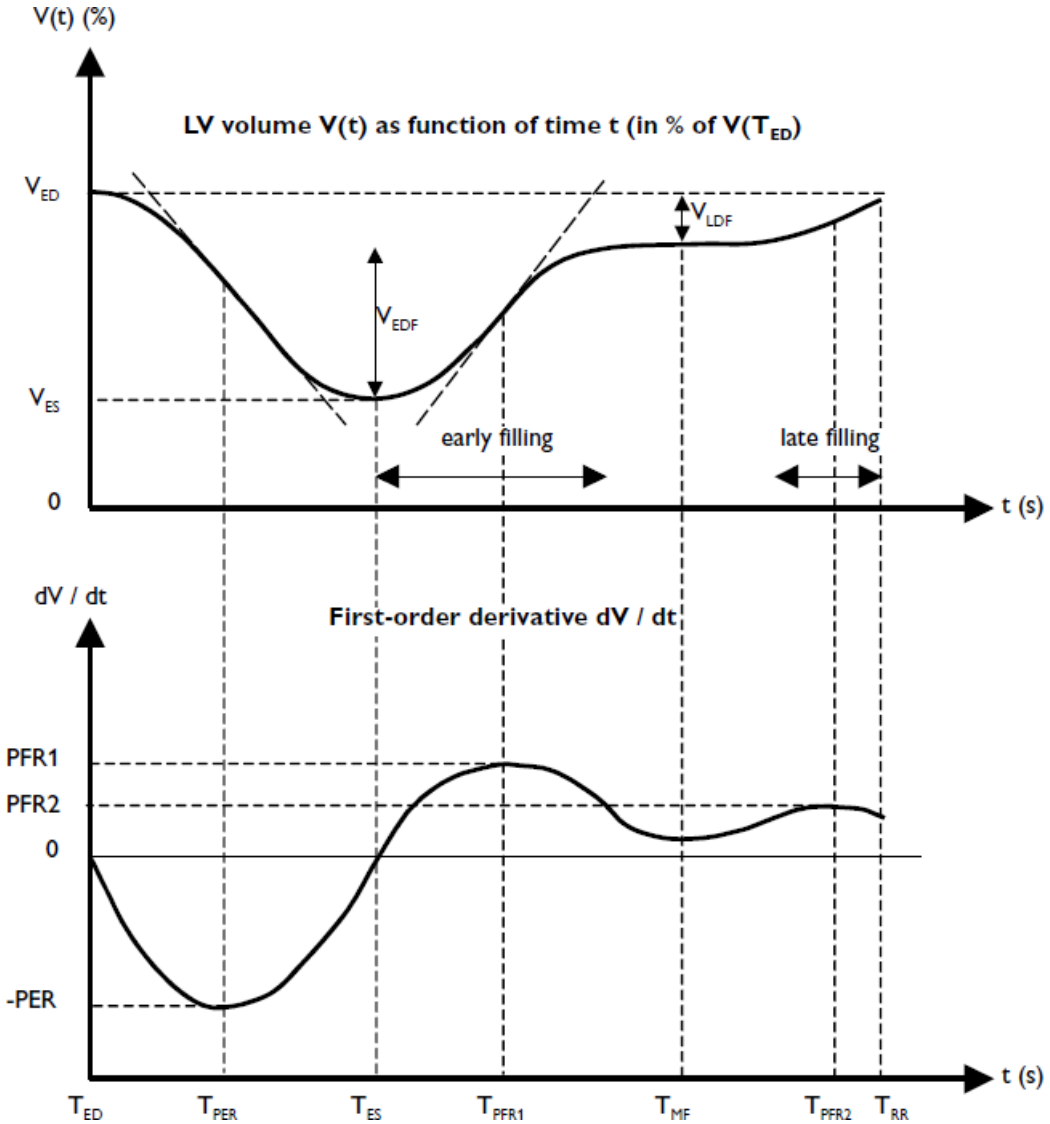

Fig. 67: Volume curve V(t) and its first-order derivative dV/dt, with various systolic and diastolic functional parameters

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. 68: 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.

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:

Chuang et al.; CMR Reference Values for Left Ventricular Volumes, Mass, and Ejection Fraction Using Computer-Aided Analysis: The Framingham Study; Journal of Magnetic Resonance Imaging 2014; 39: 895-900

Chuang et al.; Correlation of trabeculae and papillary muscles With Clinical and Cardiac Characters and Impact on CMR Measures of LV Anatomy and Function ; JACC: Cardiovascular Imaging 2012;5: 1115-23

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

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.

3000063879l_A/881 * 2021-06-30

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
ES volume	24.0 ml	61.0 ml	14.0 ml/m^2	30.0 ml/m^2	10.0 ml	39.0 ml	5.0 ml/m^2	18.0 ml/m^2
ED wall mass	48.0 gr	101.0 gr	28.0 gr/m^2	49.0 gr/m^2	88.0 gr	146.0 gr	54.0 gr/m^2	75.0 gr/m^2

Tab. 11: 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/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
ES volume	24.0 ml	61.0 ml	14.0 ml/m^2	30.0 ml/m^2	10.0 ml	39.0 ml	5.0 ml/m^2	18.0 ml/m^2
ED wall mass	48.0 gr	101.0 gr	28.0 gr/m^2	49.0 gr/m^2	88.0 gr	146.0 gr	54.0 gr/m^2	75.0 gr/m^2

Tab. 12: 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/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/m^2	30.0 ml/m^2	10.0 ml	39.0 ml	5.0 ml/m^2	18.0 ml/m^2
ED wall mass	48.0 gr	101.0 gr	28.0 gr/m^2	49.0 gr/m^2	88.0 gr	146.0 gr	54.0 gr/m^2	75.0 gr/m^2

Tab. 13: Female, Age Group 30 - 39

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
ES volume	24.0 ml	61.0 ml	14.0 ml/m^2	30.0 ml/m^2	10.0 ml	39.0 ml	5.0 ml/m^2	18.0 ml/m^2
ED wall mass	48.0 gr	101.0 gr	28.0 gr/m^2	49.0 gr/m^2	88.0 gr	146.0 gr	54.0 gr/m^2	75.0 gr/m^2

Tab. 14: 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/m^2	60.0 ml/m^2	51.0 ml	87.0 ml	28.0 ml/m^2	46.0 ml/m^2
ED volume	90.0 ml	162.0 ml	50.0 ml/m^2	82.0 ml/m^2	63.0 ml	112.0 ml	36.0 ml/m^2	60.0 ml/m^2
ES volume	20.0 ml	48.0 ml	11.0 ml/m^2	27.0 ml/m^2	12.0 ml	33.0 ml	7.0 ml/m^2	19.0 ml/m^2
ED wall mass	41.0 gr	83.0 gr	25.0 gr/m^2	44.0 gr/m^2	81.0 gr	149.0 gr	50.0 gr/m^2	77.0 gr/m^2

Tab. 15: 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/m^2	58.0 ml/m^2	47.0 ml	78.0 ml	27.0 ml/m^2	44.0 ml/m^2
ED volume	82.0 ml	139.0 ml	48.0 ml/m^2	79.0 ml/m^2	61.0 ml	105.0 ml	36.0 ml/m^2	59.0 ml/m^2
ES volume	17.0 ml	46.0 ml	10.0 ml/m^2	26.0 ml/m^2	9.0 ml	33.0 ml	5.0 ml/m^2	19.0 ml/m^2
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. 16: 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. 17: 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

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. 18: 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. 19: 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

Parameter	Endo Volume				Blood Volume			
	Min	Max	Min	Max	Min	Max	Min	Max
			BSA Normalized				BSA Normalized	
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 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
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 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. 22: 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
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. 23: 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. 24: Male, Age Group > 70

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Spatial Enhancement SA LV Analysis

Overview

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

If segmentation from a Functional LV & RV analysis is available, automatic registration provides automatic contours. Spatial enhancement differences can be analyzed using different methods: freehand threshold, reference segment, or reference area with adjustable standard deviation. The results summary allows you to compare enhanced areas with non-enhanced areas.

Guidance for this analysis package is provided in the task guidance panel.

▷ In the Cardiac MR **Viewing** screen, select a suitable Spatial Enhancement SA series.

▷ The **Scan Type** label should be "Spatial enhancement" and the **Orientation** label should be "SA".

▷ The series should be based on an Inversion Recovery technique.

▷ Select **Spat. Enh. SA** in the analysis type list in the task guidance panel.

1. Click **Start Analysis Application** in the task guidance panel.

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

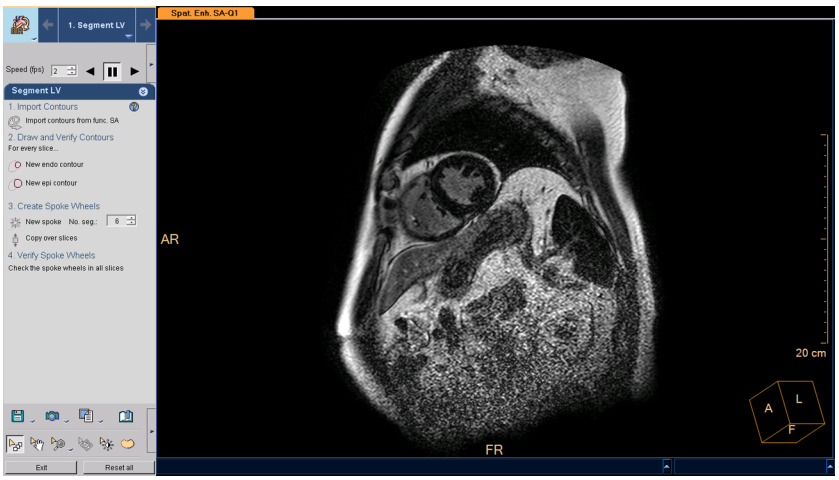

Fig. 69: Segment LV screen

⇨ If contours are available from a previously performed Functional LV & RV analysis, the 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.

Indications for Use

The MR Cardiac 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.

Segment LV step

Tools for drawing contours and spoke wheels are available in the task guidance panel.

1. If a functional SA series with contours is available in the study, you can import contours clicking **Import Contours** in the task guidance panel.
2. If contours have been imported, verify the contours on each slice and correct them if necessary.
3. 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 (in case of enhanced area in the slice showing the aorta, start with this slice).
4. To draw contours manually, use the following tools in the task guidance panel.
   -  **New endo contour**.
   -  **New epi contour**.
5. Click along the path of the contour at regular intervals.
6. To close a contour, double-click on the path of the contour.
7. To edit a contour, do the following:
   - Select any of the interactor tools.
   - Pause the pointer over the edge of the contour to display the contour nodes.

3000063387791_A/881 * 2021-06-30

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- Drag an existing node to a new position, or click and drag on the edge of the contour to create and reposition a new node.
- To delete one or more nodes, drag a node to another node; this action combines the nodes and deletes any nodes in between them.

8. Repeat this process to draw contours on all slices.
9. After drawing contours, create a spoke wheel on all slices to assist with the analysis.
   - Use the up and down arrows in the **No. seg** box to define the number of segments.
   -  Click **New spoke**.

10. Click **Copy Over Slices** in the task guidance panel to copy the spoke wheel to all slices that contain contours.
11. Verify the spoke wheel in all slices.

    Spoke wheels can be moved or rotated; click **Help** in the task guidance panel for details.

Define Threshold step

1. When the segmentation is configured correctly, click the right arrow in the title panel to display the **Define Threshold** screen.

⇨ The **Define Threshold** screen allows you to define the threshold for higher spatial intensity using tools in the task guidance panel. The following steps describe the options available.

2. In the task guidance panel, select the image type to use for the analysis.
3. In the task guidance panel, select the method for setting the initial signal intensity threshold.

⇨ You can select between the following methods:

- Full Width at Half Maximum (FWHM), based on setting the threshold using enhanced voxels in the segmentation (this is the default method)
- Manual
- Automatic, based on a reference segment
- Automatic, based on a reference area

⇨ Thresholding methods are described in the following steps.

4. To set the threshold using FWHM, select **FWHM** in the task guidance panel.

⇨ 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.

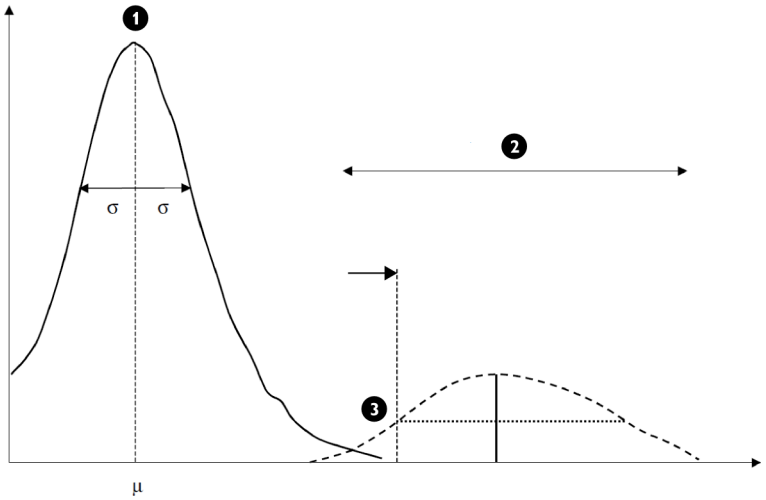


Fig. 70: Histogram of Intensity Using FWHM, x-axis: intensity, y-axis: probability, 1: normal area, 2: enhanced area intensity range, 3: threshold T halfway between minimum and maximum

NOTICE

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

5. To set the threshold manually using the threshold slider, select **Manual** in the task guidance panel and do the following:
   - Scroll to the slice closest to the valve plane that displays enhanced myocardial areas (visible as transparent orange overlay in the image).
   - Drag the slider until the orange overlay matches the enhanced area accurately.
   - Alternatively, use the up and down arrows in the **Intensity** box to use a specific setting.
   - Inspect all slices and verify that the threshold setting is correct.

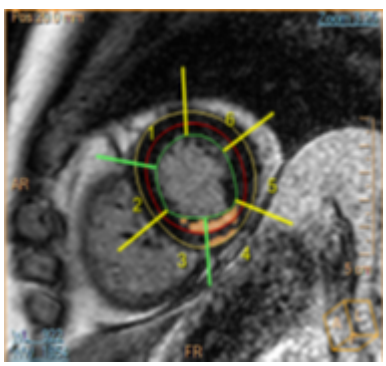


Fig. 71: Enhanced myocardial areas (red overlay)

6. To set the threshold using a normal segment, select **Reference Segment** in the task guidance panel and do the following:
   - Navigate to the slice containing a normal segment to use as a reference.

- Click the segment.
- If desired, make small adjustments using the following functions in the task guidance panel:
  - Drag the slider.
  - Change the setting in the **Intensity** box.
  - Change the setting in the **Nr of standard deviations** box.

7. To set the threshold by defining a normal area, select **Reference Area** in the task guidance panel and do the following:
   - Navigate to the slice containing a normal area to use as a reference.
   - Draw an ROI around the reference area (double-click to complete the ROI).
   - If desired, make small adjustments using the following functions in the task guidance panel:
     - Drag the slider.
     - Change the setting in the **Intensity** box.
     - Change the setting in the **Nr of standard deviations** box.

⇨ In case of automatic thresholding using a normal segment or area, the threshold is derived from the normal segment or area (this implies that a normal segment or area 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.

NOTICE

With c = 3 you may assume (99.9% probability) that everything above the threshold T can be seen as enhanced area.

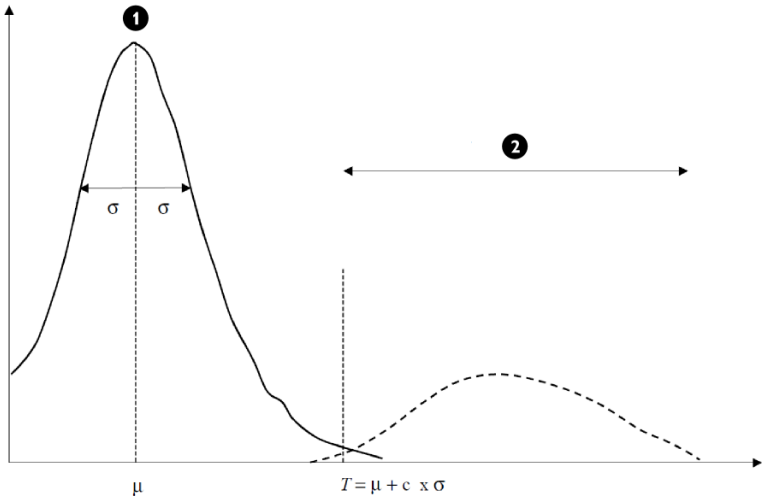


Fig. 72: Histogram of Intensity, x-axis: intensity, y-axis: probability, 1: normal area, 2: enhanced area intensity range

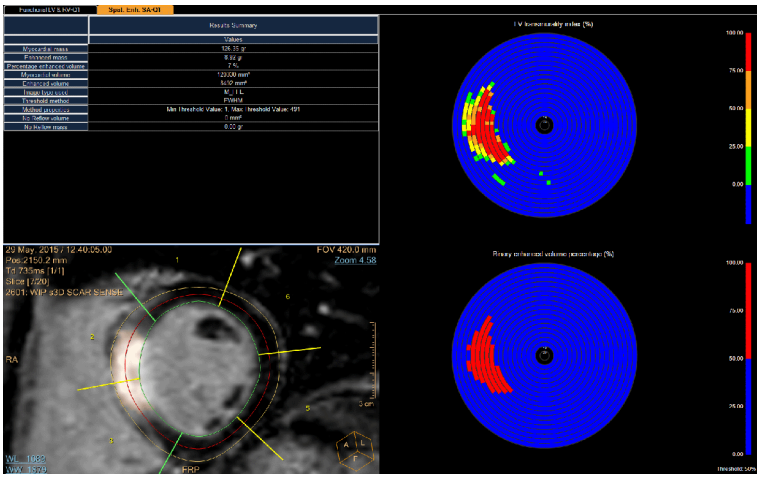
8. If the results of the threshold procedure are not completely satisfactory, you can edit the enhanced area manually using the following tools:

   -  MicroVascular 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 a simple paint 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 be added to the **Enhanced volume** and **Enhanced mass** parameters in the Results table. You can adjust the brush width by clicking the down arrow next to the **Paint enhanced area** tool.
   -  To remove areas displayed as "scar" (due to incorrect contours or partial volume effects), click **Erase enhanced area** and remove the affected areas. You can adjust the eraser width by clicking the down arrow next to the **Erase enhanced area** tool.

View Results step

1. Click the right arrow in the title panel to display the **View Results** screen.

⇨ The Results screen, displays a summary results table, bull's-eye plots, and the source image with contours and spoke wheels. When you click on a slice in a bull's-eye plot, the corresponding source slice image is displayed.



⇨ The upper bull's-eye plot displays the **LV transmurality index**, which is aligned with the visual scoring panel (see below), and indicates the percentage of enhanced area.

⇨ The lower bull's-eye plot displays the **Binary enhanced volume percentage**, with the threshold set at 50%. Using the right-mouse menu, you can view the endo segment or the epi segment in this plot.

⇨ Using the right-mouse menu, you can also display an **LV enhanced volume percentage** plot, which you can view using **Detailed** (94 angles), **Regional** (spoke definition), or **AHA** results. Using the right-mouse menu, you can view the endo segment or the epi segment in this plot.

⇨ When viewing the Binary enhanced or LV enhanced protocols, you can adjust the threshold of the color scale by dragging up or down with the middle mouse button.

2. You can display bull'seye-plots as desired using the right-mouse menu, or you can choose a layout protocol from the task guidance panel to display are specific layout. The following layout protocols are available:
   - **Detailed Spat. Enh.** (default layout).
   - **Enhanced % and Transmurality index %**
   - **Endo/Epi Enhanced %**

Red	76-100%
Orange	51-75%
Yellow	26-50%
Green	1-25%
Blue	0%

Tab. 25: Visual Scoring

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300006338791_A/881 * 2021-06-30

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Temporal Enhancement SA LV Analysis

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.

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Overview

Temporal enhancement analysis indicates how well the blood flows from the coronary arteries into the myocardium. The Temporal Enhancement SA LV analysis package 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 package 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. User-defined contours and spokes wheels are available to segment anatomically relevant areas. Furthermore, this package allows for a convenient bull’s-eye plot so that the end result can be easily viewed from the base to the apex of the heart, as it was defined by the user. Rest and stress studies can be directly compared to detect the presence of a coronary-artery stenosis.

Guidance for this analysis package is provided in the task guidance panel.

- ▷ In the Cardiac MR **Viewing** screen, select a suitable Temporal Enhancement SA series.
- ▷ The **Scan Type** label should be "Temporal Enhancement" and the **Orientation** label should be "SA".
- ▷ It is preferable that the series contains at least 20 dynamics, with a minimum of 5 dynamics as a baseline. Baseline dynamics are the first dynamics to be acquired in a series, and which do not yet contain enhancement. The first dynamics can be used to enable baseline correction and reset the calculated graphs to the baseline. This is especially useful if rest and stress exams need to be compared.

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▷ Analysis can be done on a single stress or rest series, or you can select both for analysis for a direct comparison. Additionally, to compare series, the stress series should be labeled as "stress" and the rest series should be labeled as "rest".

▷ Select **Temp. Enh.** in the analysis type list in the task guidance panel.

NOTICE

If you start analysis of a Temporal Enhancement series without a second Temporal Enhancement series available in the MR Cardiac Viewer, you can add the additional series using **Add to running application** in the right-mouse menu in the **Directory**. You can now select both Temporal Enhancement series from the MR Cardiac Viewer and start a comparison analysis.

1. Click **Start Analysis Application** in the task guidance panel.

⇨ The Temporal Enhancement SA LV package opens in the **Preparation** screen.

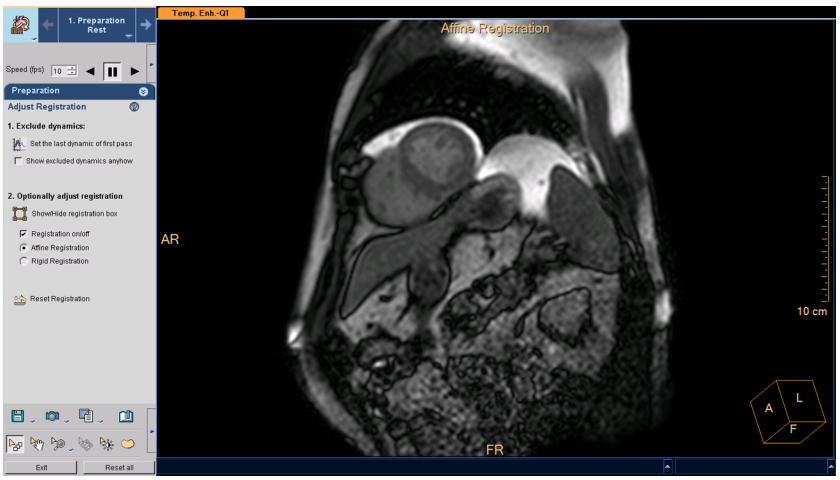

Fig. 73: Temporal Enhancement package - Preparation screen

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.

Preparation step

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.

During the Preparation step, registration is automatically calculated for each slice. Two automatic registration methods are available:

- **Affine Registration** compensates for breathing motion and skewing movements.

3000063879l_A/881 * 2021-06-30

- **Rigid Registration** compensates for in-plane translation and rotation movements.

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.

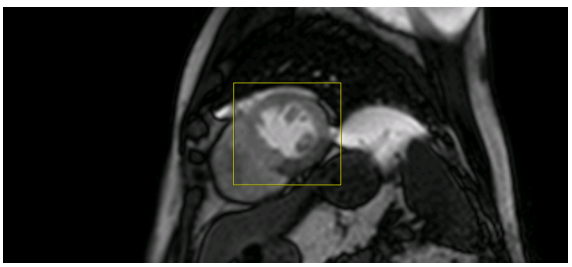

Fig. 74: Registration box

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

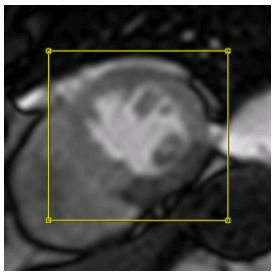

Fig. 75: Adjust the registration box by dragging the corner points

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.

Segment step

1. When the registration is configured correctly, click the right arrow in the title panel to display the **Segment** screen.

⇨ Tools are available in the task guidance panel of the **Segment** screen for drawing contours.

2. Use the following tools in the task guidance panel to draw contours on each slice:
   -  **New endo contour**
   -  **New epi contour**

⇨ If there is a contour already defined on the slice, it is removed when you select one of these tools.

3. Click along the path of the contour at regular intervals.
4. To close a contour, double-click on the path of the contour.
5. To edit a contour, do the following:
   - Select any of the interactor tools.
   - Pause the pointer over the edge of the contour to display the contour nodes.
   - Drag an existing node to a new position, or click and drag on the edge of the contour to create and reposition a new node.

3000063387 91_A/881 * 2021-06-30

- To delete one or more nodes, drag a node to another node; this action combines the nodes and deletes any nodes in between them.

6. Repeat this process to draw contours on all slices.

⇨ It is not necessary to draw contours on all slices. Analysis results are evaluated slice by slice.

NOTICE

Be very constrictive when drawing contours on the borders of the LV, as there might still be some movement on a slice between the dynamics, or there might be ‘dark rim artifacts’.

7. Create a spoke wheel on all slices that contain contours (spoke wheels assist with the analysis).
   - Use the up and down arrows in the **No. seg** box to define the number of segments.
   - Click **New spoke**  .
   - Verify the spoke wheel. Spoke wheels can be moved or rotated; click **Help** in the task guidance panel for details.
   - Repeat for all slices with contours.

View Results step

1. When the segmentation is configured correctly, click the right arrow in the title panel to display the **View Results** screen.

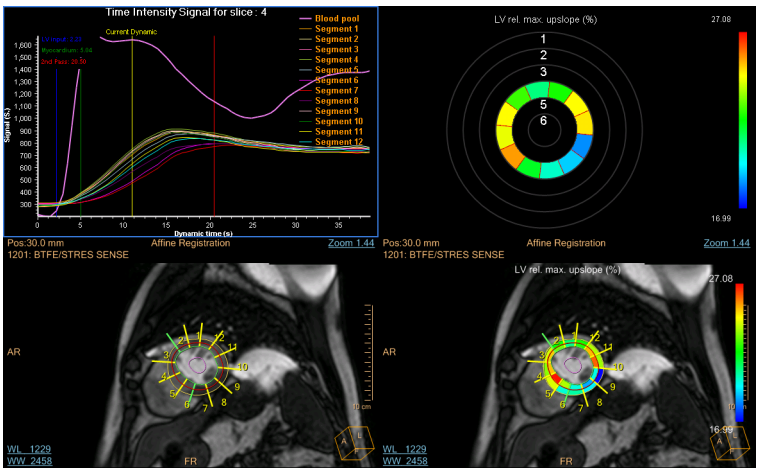

Fig. 76: View Results screen

⇨ 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.

2. 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.

3. 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.

3000063387 91_A/881 * 2021-06-30

- 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.)

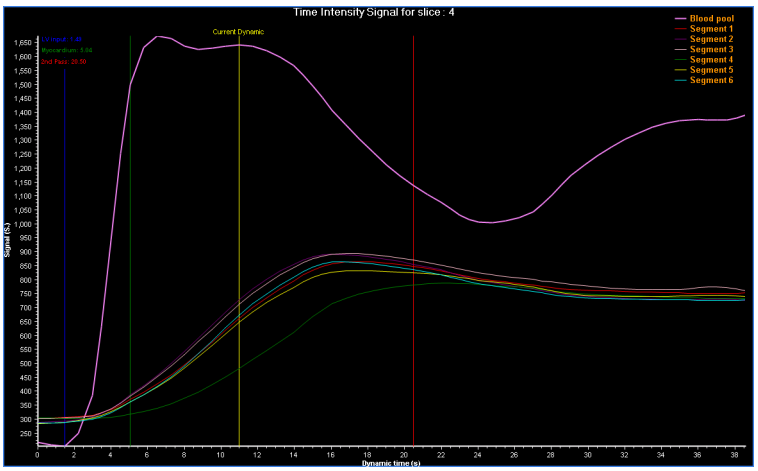

Fig. 77: Time Intensity Signal graph

⇨ 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.

4. 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 and choose which segments to show or hide (the graph is rescaled accordingly).
5. 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.
6. 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.

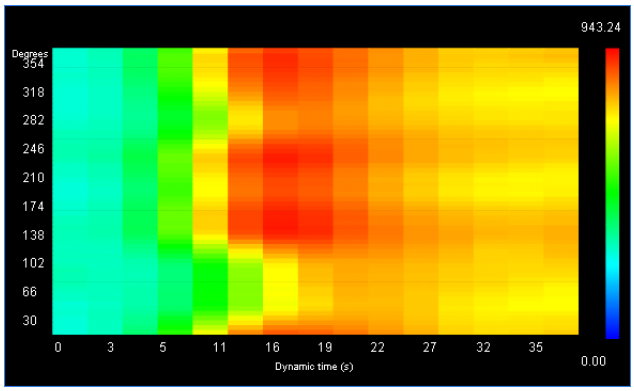

Fig. 78: Temporal enhancement diagram

⇨ 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.

7. Right-click the TED and select a display type:
   - Detailed
   - Transmural
   - Endo Cardial
   - Epi Cardial
8. 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 213.

9. If you select the Mean Signal Intensity parameter, you can view this parameter for each dynamic separately in the bull's-eye plot and color-coded segment display.

⇨ You can also view this parameter replayed as a movie:

- Right-click the color-coded segment display and select **Mean Signal Intensity**.
-  Click **Play Forward** in the toolbar.
-  To stop movie playback, click **Pause**.

10. 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**.
11. 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:

3000063387 91_A/881 * 2021-06-30

- 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.

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.

3000063879l_A/881 * 2021-06-30

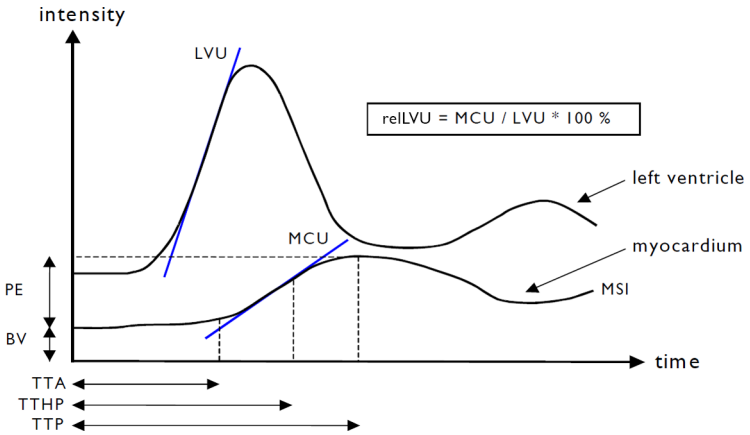

Fig. 79: Slope-related analysis parameters

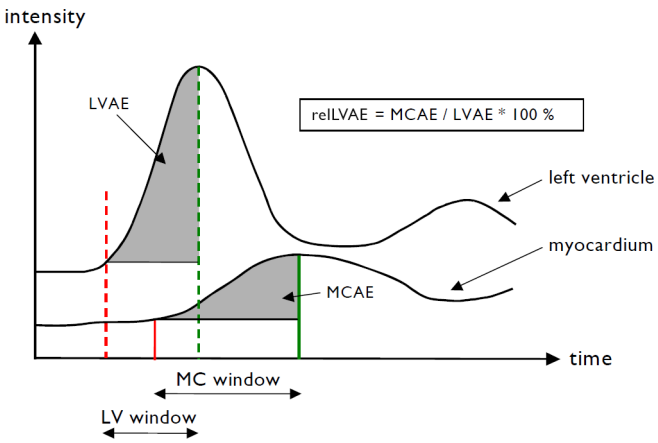

Fig. 80: Area-related analysis parameters

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3000063387791_A/881 * 2021-06-30

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Whole Heart Analysis

The Whole Heart analysis application allows you to review any 3D or MRA scanned data and segment the entire heart and vascular structures around or outside the heart (but not limited to this area), to create a high-quality surface-rendered 3D model. The 3D model can be used to communicate anatomical structures, such as complex structures and connections in congenital disease or the shape of the left atrium and pulmonary veins to prepare for ablation procedures.

The main features of this application are as follows:

- Review of 3D or MRA data in orthogonal slab viewers to support the segmentation of 3D models.
- 3D viewer to support the review of the 3D models in volume rendering, surface rendering, or MIP mode.
- Segmentation and editing tools such as seeding, masking, injection, 3D smart ROI.

- Automatic and semi-automatic whole heart segmentation algorithm to segment individual tissues.
- Tissue management list to manage all created 3D models (tissues).
- Combine 3D models from different dynamics and series into one view.
- Batch tool to generate and save rotational or linear overview of the 3D models or volume rendering as a presentation to be saved in other locations such as PACS and RIS.
- Advanced 3D model export module to prepare 3D models for 3D printing (STL), or to be exported to navigation system software used in intervention procedures (VTK).
- 3D models can be exported in separate or combined files, and a 3D PDF report can be created as a supporting report for the 3D models created.

Rendering Methods

This application can be used to accommodate the visualization and communication of 3D structures, specifically from 3D acquisitions such as **Whole Heart** and **3D Angio (MRA)**. This application can create both volume-rendered and surface-rendered models. Each rendering method provides different benefits.

Volume Rendering

Volume Rendering (VR) is a protocol that displays 3D content based only on the windowing of signal intensity and opacity. Multiple protocols are available by default and can be edited.

Benefit of VR: VR approaches a realistic view of the anatomy and is specifically helpful for creating a movie or batch for communication in PACS.

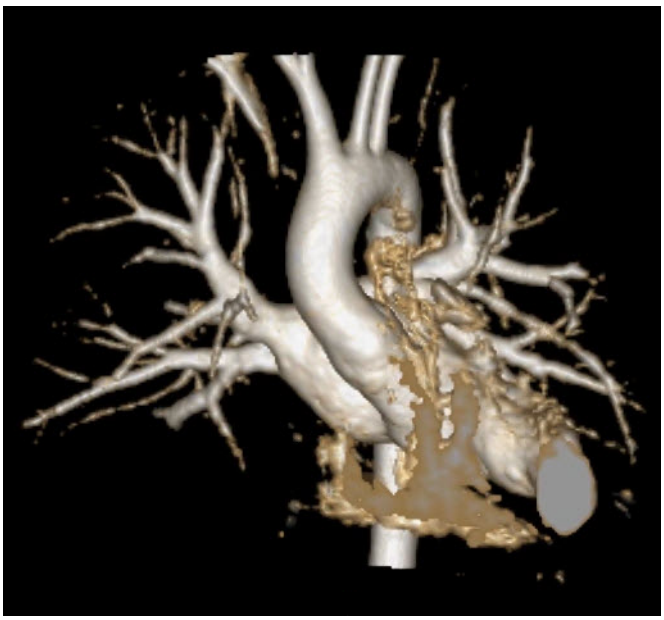

Fig. 81: Volume-rendered 3D heart model

3000063387791_A/881 * 2021-06-30

Surface Rendering

Surface Rendering (SR) is a 3D representation of segmented pixels from a 3D volume. It only shows pixels that are segmented or included.

Benefit of SR: SR assists with identifying multiple 3D structures using colors can be defined by the user. This is very useful for visualizing connections of complex vasculature or for preparing structures for 3D printing or procedure planning.

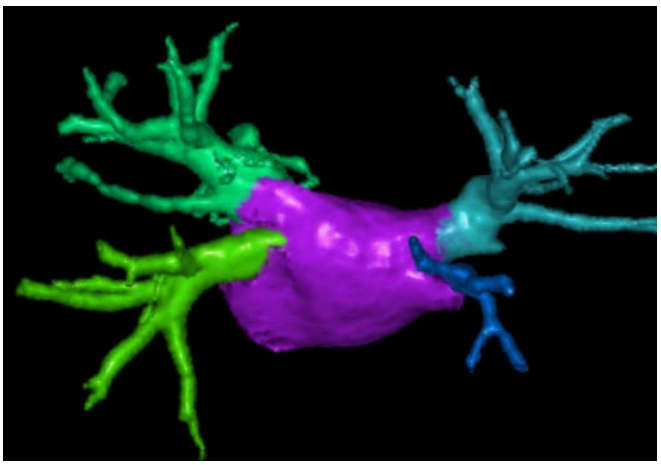

Fig. 82: Surface-rendered 3D heart model

Overview of the modeling process

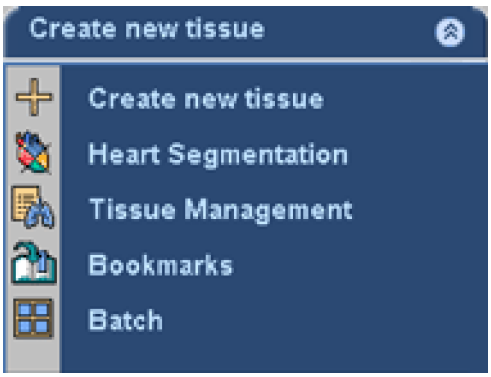

Fig. 83: Whole heart modeling process

The modeling process comprises the following options:

- **Create new tissue**: You can creates tissues using masking and seed-based segmentation or general segmentation tools.
- **Heart Segmentation**: Alternatively, you can start automatic segmentation to create an initial heart model that includes all the heart chambers and the aortic root, and then continue adding detail by creating further tissues manually in the **Create new tissue** step.
- **Tissue Management**: Review and verification of each tissue in preparation for batch creation or 3D model export. From this step, segmentation tools are also available for making corrections to tissues. If needed, you can also return to the first step and continue creating new tissues.

When the heart model is correctly defined, you can export the 3D model in your preferred format.

Guidance for each step of the process is provided in the task guidance panel.

Indications for Use

The MR Cardiac Whole Heart application allows users to review cardiac anatomy on 3D or MRA images and segment the entire heart and surrounding vasculature to create a surface-rendered 3D model that can be exported for 3D printing. The application is indicated to assist users with demonstration of anatomical structures for multiple purposes such as communication with patients, support in planning of ablation procedures or educational purposes.

Opening a series

1. In the Cardiac MR **Viewing** screen, select a suitable 3D whole heart or MRA series.

   For the **Whole Heart** application to function correctly, the series should be scanned in 3D (isotropic voxels).

   The **Orientation** label may be set as any of the following:

   - Axial
   - Coronal
   - Sagittal
   - Other

2. In case of a dynamic series, select the dynamic that displays the area of interest that you want to use to create the model.

NOTICE

Ensure that you select a suitable dynamic as only one dynamic can be loaded in the **Whole Heart** application. Multiple dynamics cannot be loaded. However, you can create and export separate tissue models from different dynamics of the same or different series, and then combine these models in the **Whole heart** application (after saving the tissues with the **Save Results As** function) or the **3D Modeling** application. For more information, refer to the **3D Modeling** Instructions for Use after creating tissue models in the **Whole Heart** application.

3. Select **Whole Heart** in the analysis type list in the task guidance panel of the **Viewing** screen.

4. Click **Start Analysis Application** in the task guidance panel.

⇨ The Whole Heart package opens in the **Create new tissue** screen, displaying the 3D visualization of the series and 2D reference views in separate viewports.

5. You can now start creating tissues for the 3D model.

300006338791_A/881 * 2021-06-30

Philips

Creating a new tissue

The **Create new tissue** screen allows you to use smart segmentation tools to isolating the required part of the heart and save it as a tissue. This option is useful when the automatic heart segmentation fails to separate heart components due to an abnormality of the heart or in pediatric cases. The workflow starts with defining a mask that includes the areas that display only the anatomy of interest, sculpt the area of interest, and then drop seeds (inclusion and exclusion) to define a tissue in detail. You can use this option to define different tissues in the heart, and name and save them with different colors. The resulting model can be exported as STL, if needed, and saved as a batch.

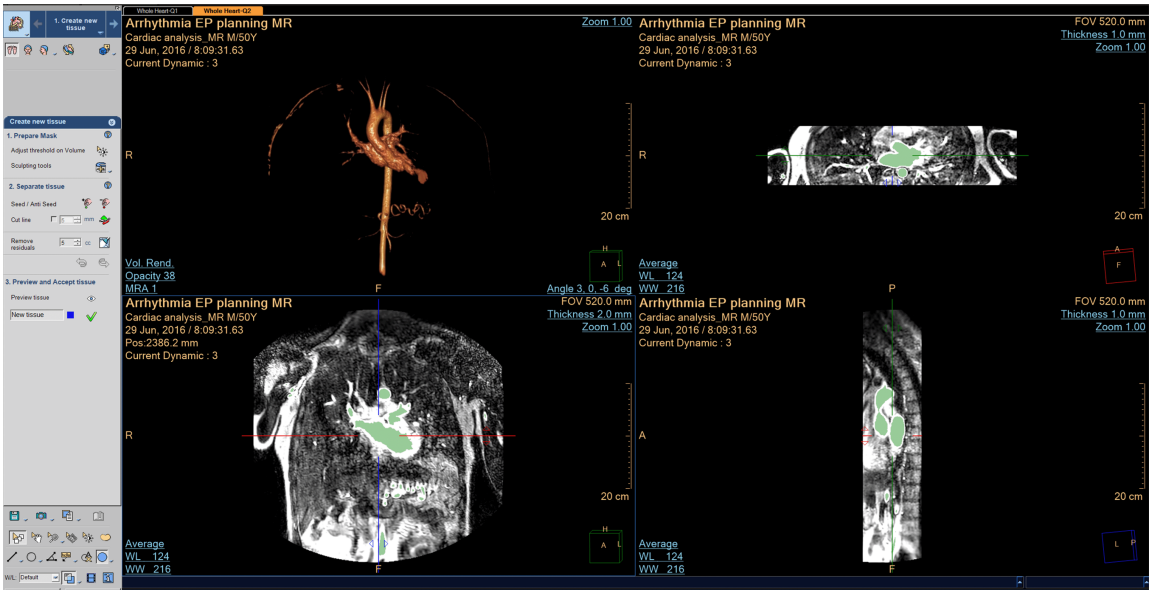

Fig. 84: Create new tissue screen

The **Create new tissue** task guidance panel provides the tools needed for this task.

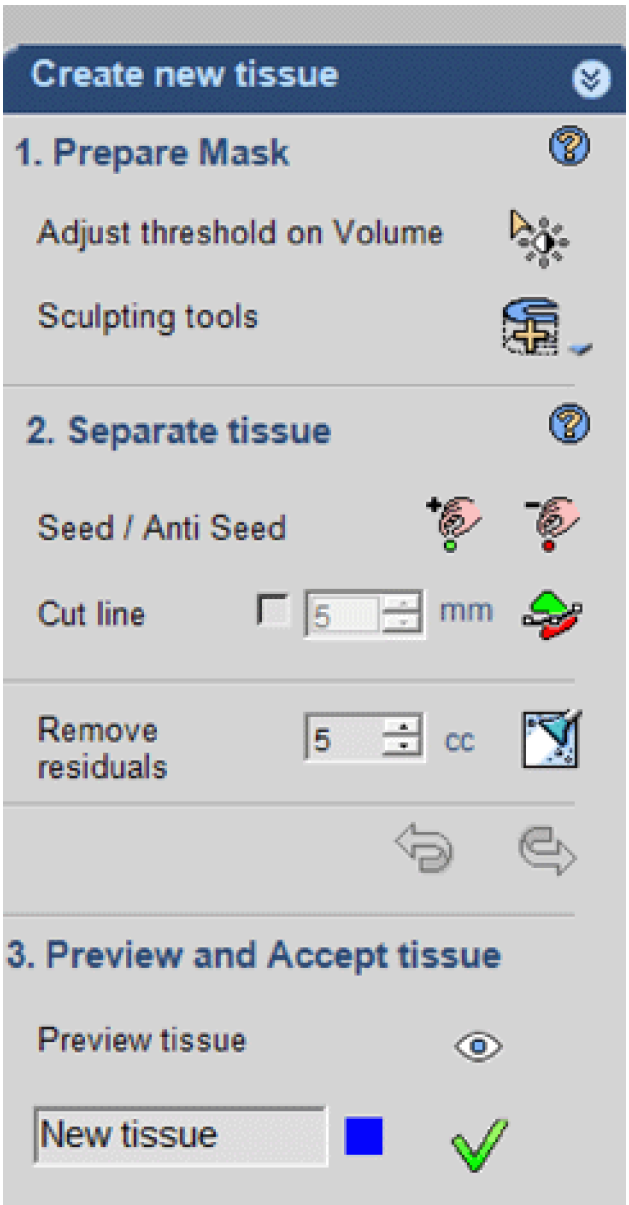

Fig. 85: Create new tissue task guidance panel

NOTICE

The following procedure provides the most efficient workflow for segmenting tissues.

Step 1 - Prepare Mask

1. Adjust the threshold on the Volume image using the windowing tool to display a clear view of the region of interest.

   The mask that defines the region of interest is displayed in the MPR viewports and should cover the parts that should be included in the final tissues.

3000063387 91_A/881 * 2021-06-30

To use the windowing tool, hold the middle mouse button and do the following:

- Drag upward to increase the window level.
- Drag downward to decrease the window level.
- Drag to the right to increase the window width.
- Drag to the left to decrease the window width.

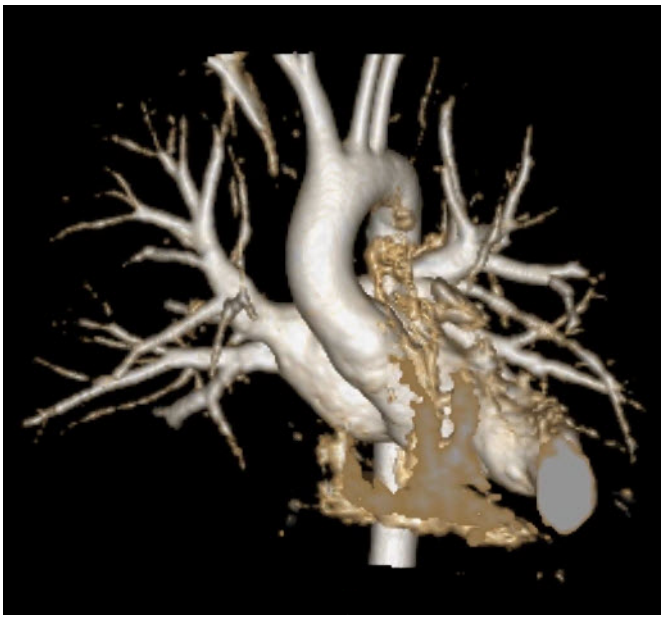

Fig. 86: Displaying a view of the heart

2. Use the **Sculpt** tool in the task guidance panel to focus on the area of interest in the view, by including or excluding areas from the view. Areas of interest should be fully included, while areas not of interest should be excluded. The sculpting tools can be used on the volume or MPR.
3. When the region is suitably defined, navigate to the region of interest using the **Pan** and **Zoom** tools in the common tools panel, or use the **Relate Point** tool on the 3D model to update all 2D slab viewers to the area of interest.

NOTICE

Be sure to adjust the windowing optimally before continuing to the next step (seed planting). Once you start to plant seeds, the windowing cannot be adjusted.

Step 2 - Separate Tissue

This tool allows you to isolate a region of interest, and create tissue using seeds, anti seeds, and cut line. The tool interactively calculates the region by including the regions with green seeds and excluding the regions with red seeds. The border between the included and excluded regions is calculated automatically based on the pixel intensity. The cut line can be used when borders between the regions cannot be identified by intensity.

1. Click **Seed** in the task guidance panel and click the areas that you want to include in the tissue. Clicking results in green seeds. The seeds can be located on the volume or MPR image.

   There is no limit to the number of seeds that you can place.

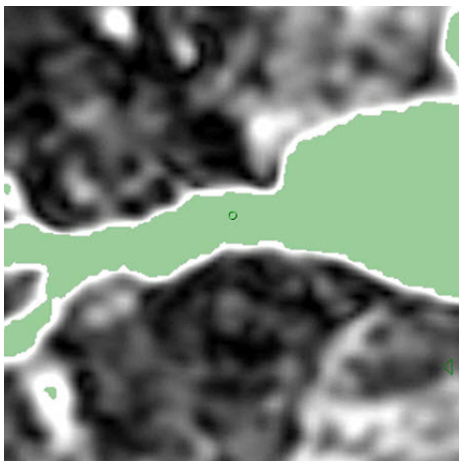

Fig. 87: Adding a seed

2. To exclude areas from the tissue, click **Anti Seed** in the task guidance panel and click the areas that you want to exclude.

Fig. 88: Adding an anti-seed

3. If the boundary between an included area and an excluded area is not correctly defined by the seed tools, click **Cut line** in the task guidance panel and drag or click along the path of the correct boundary. Using this feature allows you to cut specific parts that cannot be removed via seeds.

   You can specify the depth of the cut in the defined plane by selecting the **Cut line** check box in the task guidance panel and entering a depth value. If you do not select the **Cut line** check box, the **Cut line** tool cuts through the entire stack.

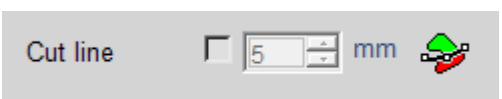

Fig. 89: Cut line functions

300006338791_A/881 * 2021-06-30

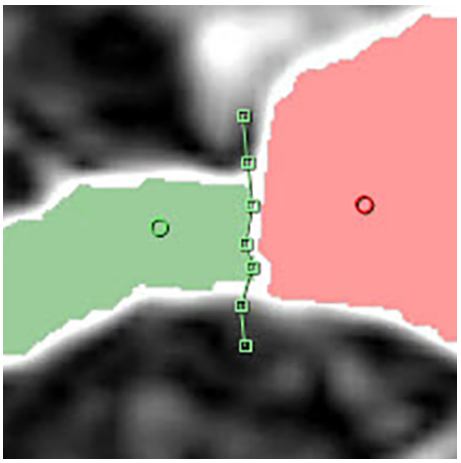

Fig. 90: Defining a cut line

4. Click **Remove Residuals** to remove smaller areas that remain but that are not needed. This can be performed at any time.

   You can specify a maximum volume for residuals in the task guidance panel. Any areas less than this volume are removed when you click **Remove Residuals**.

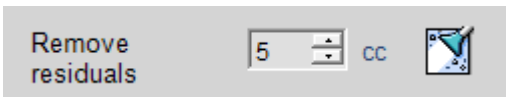

Fig. 91: Remove residuals functions

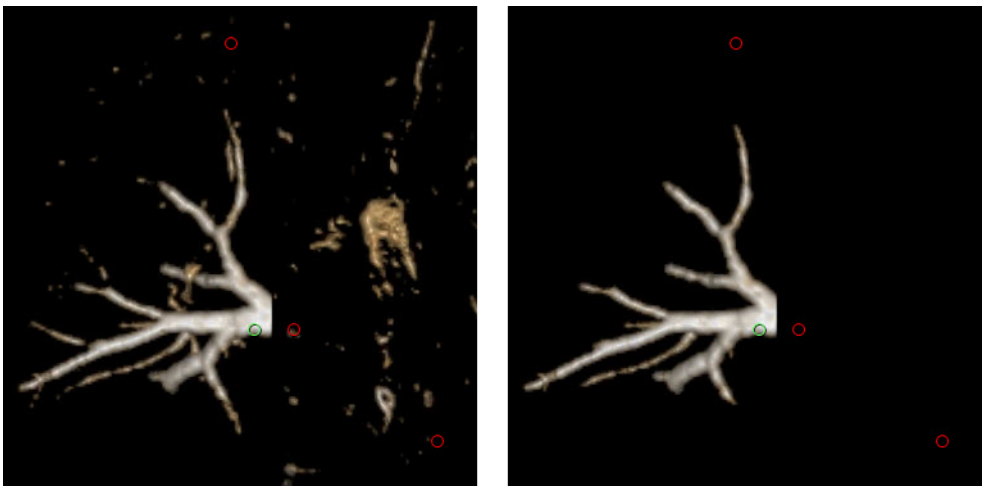

Fig. 92: Removing residuals (before and after)

Once a tissue is accepted, the application automatically switches to the Tissue Management stage and displays the created tissue. It is still possible to edit any created tissue using the editing tools in the Tissue Management stage.

Step 3 - Preview and Accept Tissues

1. Click preview to see the tissue with surface rendering (mainly recommended if the tissue is exported as STL).

2. When the tissue is completed, type the tissue name, select tissue color, and accept the tissue.

When the tissue is accepted, the application changes automatically to the **Tissue Management** task. In this task, you can select and edit the created tissue using standard editing tools. If you want to create another tissue, go to the **Create new tissue** step again, and give the tissue a different name before accepting it.

Tissue Management

When you have created all the tissues needed for the model, you should review the tissues in the **Tissue management** screen to verify that they are correctly segmented in preparation for export.

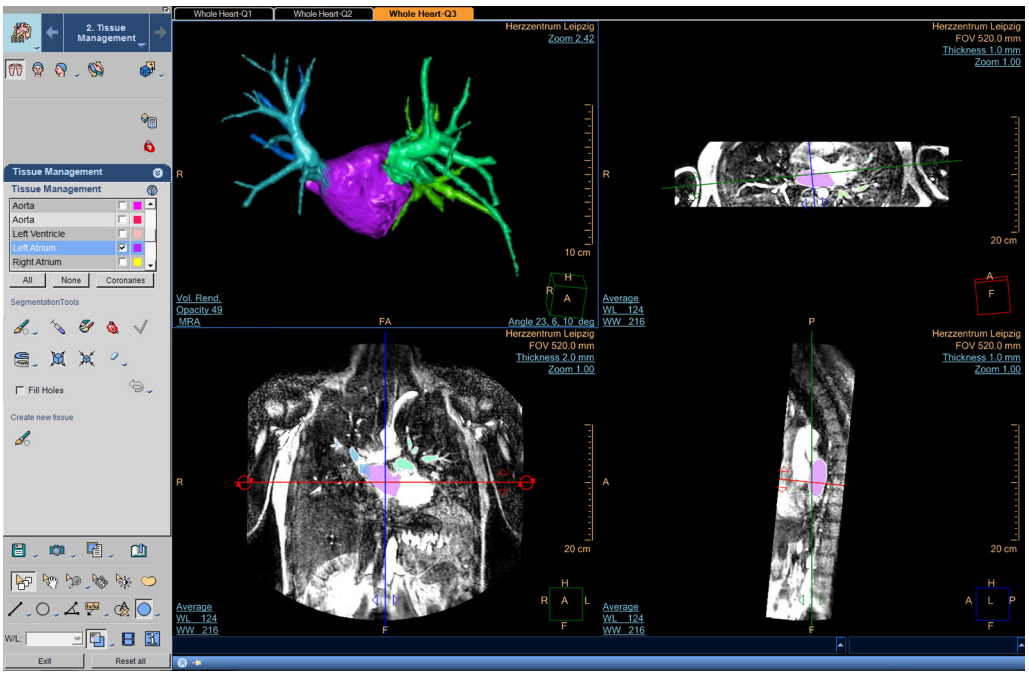

Fig. 93: Tissue management screen

The **Tissue Management** task guidance panel provides a list of tissues that have been created, with tools to show or hide individual tissues and to change the color of each tissue. Editing tools are also available to refine tissues if needed.

3000063879l_A/881 * 2021-06-30

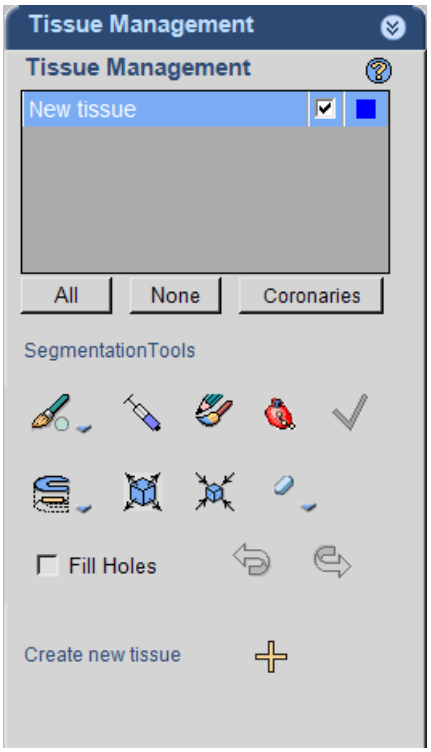

Fig. 94: Tissue Management task guidance panel

1. To open the **Tissue Management** task, click the right arrow in the title panel of the **Create new tissue** tab.

2. To calculate the volume of the displayed segments, click **Calculate volume** in the tools panel above the task guidance panel.

NOTICE

The volume is calculated from the included voxels. Be aware that hollow structures within the selected tissue are not taken in account for the volume calculation. Alternatively, select the Fill Holes check box in the task guidance panel to include hollow structures in the selected tissue.

3. To show or hide a tissue, select or clear the corresponding check box in the **Tissue Management** panel.

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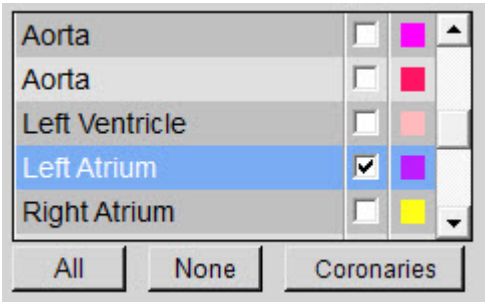

Fig. 95: Tissue Management panel

4. You can also show tissues using the filter button below the **Tissue Management** panel:
   - **All**
   - **None**
   - **Coronaries**
5. To change the color of a tissue, click the corresponding color chip and select a color.
6. To refine a tissue, use the **Segmentation tools** below the **Tissue Management** panel.

   For details of using these tools, see section “Using the segmentation tools” on page 226.

7. To go back to the **Create new tissue** screen and add a tissue to the heart model, click **Create new tissue** in the **Tissue Management** task guidance panel.

⇨ When you have verified all tissues, you can export the heart model in your preferred format.

Using the segmentation tools

Segmentation tools are provided in the task guidance panel for refining the tissue.

1. To add or extend vessels to the heart model, do the following:
   - Click **Draw Center Line**  in the task guidance panel.
   - Click in the MPR image along the path of the vessel. The centerline is displayed in the 3D view.
   - Click **Accept**  to create or extend the vessel.

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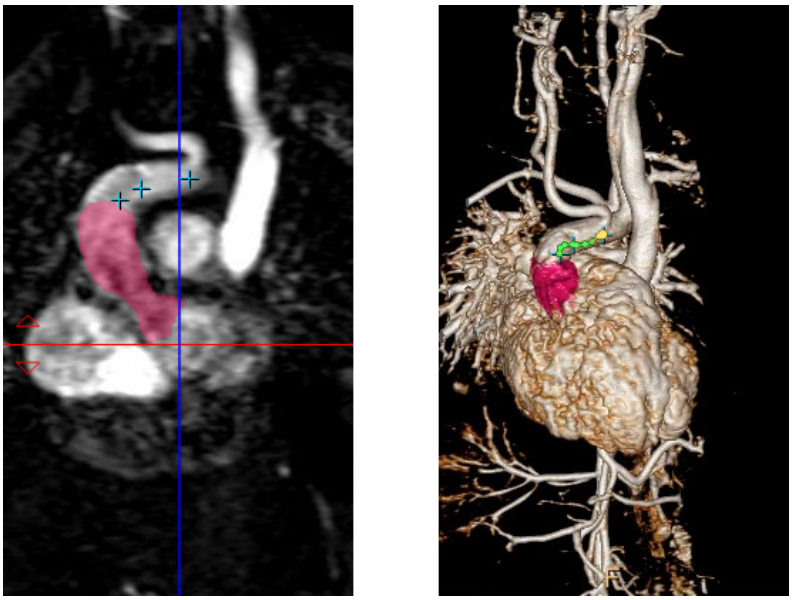

Fig. 96: Creating a centerline

2. To edit the tissue using the smart segmentation tool, click **Smart segmentation** in the task guidance panel to open the **Edit** panel.

⇨ The **Edit** panel follows the active viewport and provides tools to edit the tissue in the 2D reference views.

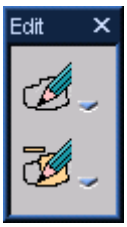

Fig. 97: Smart segmentation - Edit panel

⇨ To add areas to the tissue, the following semi-automatic 3D segmentation tools are available (click the arrow next to the upper tool in the **Edit** panel to access these tools):

-  **Add smart ROI to tissue**. Click and drag to create a contour. When you release the mouse button, the segmentation is created.
-  **Add brush to tissue**. Click to display a contour that adapts to the boundaries of the tissue. Press CTRL and rotate the scroll wheel on the mouse to increase or decrease the size of the contour. Move the mouse to change the position of the contour. Click again to define the contour and create the segmentation. Alternatively, you can click and drag with this tool to add to the segmentation.

-  **Add auto-centered brush to tissue**. This tool works in a similar way to the brush tool. Additionally, when you drag with this tool, the segmentation is based on the center of the current tissue and scrolls through the data set. This is useful for segmenting tubular structures.

⇨ To subtract areas from the tissue, the following tools are available (click the arrow next to the lower tool in the **Edit** panel to access these tools). The tools function in the same way as their counterparts above, but they remove areas from the segmentation instead of adding to it:

-  **Subtract smart ROI from tissue**.
-  **Subtract brush from tissue**
-  **Subtract auto-centered brush from tissue**

⇨ When using these tools, the **Parameters** panel is also displayed to allow you to adjust the adaptiveness and smoothness of the segmentation.

- **Adaptiveness**: Controls how closely the segmentation adapts to curved edges and borders of the tissue.
- **Smoothness**: Adjusts the smoothness of the segmented borders. Increasing the smoothness reduces noise in the segmentation, but makes it harder to segment irregular borders.

3. To edit the tissue, use the following tools in the task guidance panel:

   - Click **Inject**  and then click and hold in an area to fill the area. This tool fills additional unsegmented areas with color and adds them to the active tissue.
   - Click **Erase**  and then click an area to remove it. You can adjust the eraser width by clicking the down arrow next to the tool.
   - Click **Brush**  and then paint an area. You can adjust the brush width by clicking the down arrow next to the tool.
   - Click **Expand**  to increase the edges of the selected segment. Each click expands the edge by one voxel.
   - Click **Erose**  to reduce edges of the selected segment. Each click reduces the edge by one voxel.

4. To fill gaps in the areas that you have added, select **Fill Holes** in the task guidance panel.

5. To include or exclude defined areas in the segmentation, click the down arrow next to the **Include/Exclude** tool in the task guidance panel, select a tool and then draw an area.

⇨ The following tools are available:

-  Exclude Freehand
-  Include Freehand
-  Exclude circle
-  Include circle
-  Exclude rectangle
-  Include rectangle

Performing automatic segmentation

As an alternative workflow, you can run the automatic segmentation process from the **Heart Segmentation** task guidance panel to create an initial segmentation that includes all the heart chambers and the aortic root, and then continue the process with verifying and editing the tissues of interest in the **Tissue Management** step.

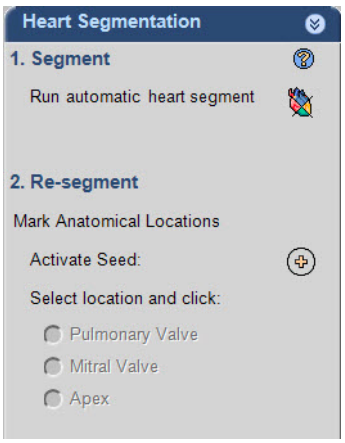

Fig. 98: Heart Segmentation task guidance panel

1. Click the task selector and select the **Heart Segmentation** task to display the **Heart Segmentation** task guidance panel.

2. Click **Run Segmentation**.

NOTICE

The results of the automatic segmentation may depend on the image quality of the acquisition. Be aware that the coronaries are also included in the segmentation based on the input algorithm, but the application does not contain dedicated coronary tracking tools. These tools may not give the expected results for editing coronaries.

Re-segment

1. If automatic segmentation did not produce expected results, you can indicate known tissues to guide the segmentation process and re-segment the data: Click **Activate Seed**, select a landmark in the task guidance panel, and then click the corresponding landmark in one of the 2D reference views (you can adjust the position of the seed crosshair by dragging).

⇨ You may need to scroll the image to locate the landmark.

2. Complete this step for all three anatomical locations.

⇨ After automatic segmentation, use the task selector to switch to the **Tissue Management** screen and verify that the segments are correct. Alternatively, continue creating tissues in the **Create new tissue** screen.

Creating a 3D Model

You can create a 3D model either using the standard batch tool or by exporting a 3D model. Exporting a 3D model allows you to save the model as a 3D PDF or in formats that are suitable for 3D printing (such as STL, VTK, and OBJ). The export option also allows you to save the tissues as a whole 3D model or as separate tissues.

Creating a 3D Model Using the Batch Tool

You can create a 3D visualization of the heart using the **Batch** step.

1. Select the **Batch** step in the task guidance panel.

300006338791_A/881 * 2021-06-30

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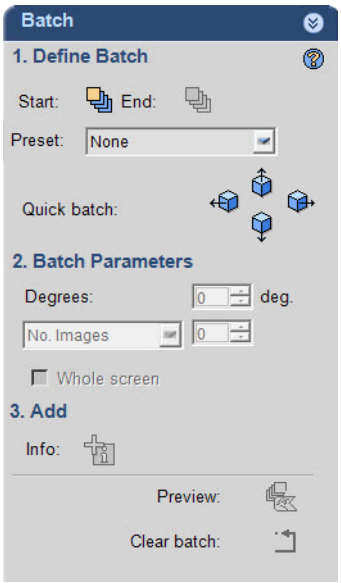

Fig. 99: Batch step

2. Define the range for the batch:
   - Select the first slice that you want to include in the batch and click **Start**.
   - Select the last slice and click **End**.
   - Alternatively, you can create a quick batch to create a left-right or head-feet rotational batch by selecting an option in one of the 4 directions shown in the task guidance panel.
3. Define the parameters for the batch:
   - The degrees of rotation for the model.
   - The number of images to create.
   - To include the whole screen in the visualization, select **Whole screen**.
4. If desired, click **Add** to add patient/image information to the visualization.
5. To preview the batch before exporting the visualization, click **Preview**.
6. If you want to clear your settings and start again, click **Clear batch**.
7. When the batch settings are configured as desired, right-click the 3D view and then click **Save volume as 3D volume**.

Creating a 3D Model Using the Export Tool

1. To create and export a 3D model, right-click the 3D viewer and select **Export to 3D Model** from the context menu.

⇨ The **Export to 3D model** dialog box is displayed, allowing you to define the format, quality, and destination for the volume.

3000063879l_A/881 * 2021-06-30

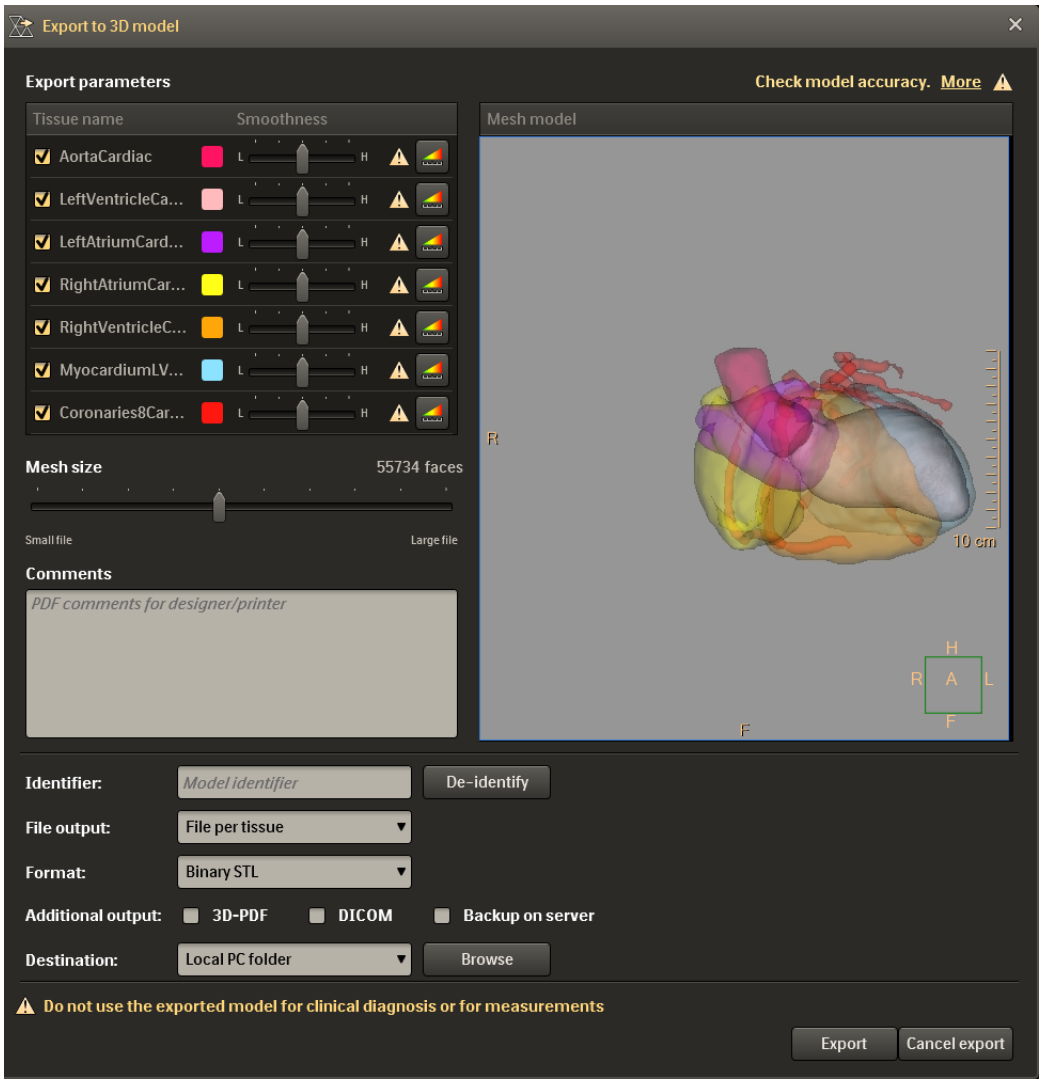

Fig. 100: Export to 3D model dialog box

2. Select the tissues in the **Tissue List** that you want to include in the exported model.
3. Use the sliders to define the smoothness of the mesh output.
4. Enter an identifier for the model (it will be used as the folder name for the exported model).
5. Select a format for the volume. You can choose between STL, VTK, or OBJ format.
6. If desired, select additional outputs, such as 3D PDF.
7. Select an export option to export the tissues:
   - **Export separated**: The selected tissues are exported as separate models (separate files).
   - **Export combined**: The selected tissues are exported as a single model (one file).
   - **3D PDF Only**: Only export the 3D PDF.
8. Select an export destination.

⇨ The tissues are exported to the export location in the selected format.

3000063879l_A/881 * 2021-06-30

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Mapping Analysis

Cardiac Mapping analysis 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, Cardiac Mapping allows you to perform motion correction or exclude a sub-optimal time point. You may then calculate improved parametric maps based on higher quality source data, before moving on to the **Segmentation** step.
- Parametric maps delivered directly by the scanner. If you use maps directly from the scanner, Cardiac Mapping analysis begins with the **Segmentation** step. You also have the option to perform a quality check on the maps, and recalculate them, if desired.

Local and regional segmentation options provide tools to investigate user-defined regions and create color-coded maps based on customizable look-up tables (color bars). This allows you to focus on a user-defined normal range in the color maps.

You can load a maximum of four series of the same contrast but acquired at different time or orientation. To select multiple series in the **Viewing** step before starting the analysis, hold the CTRL key while selecting 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).

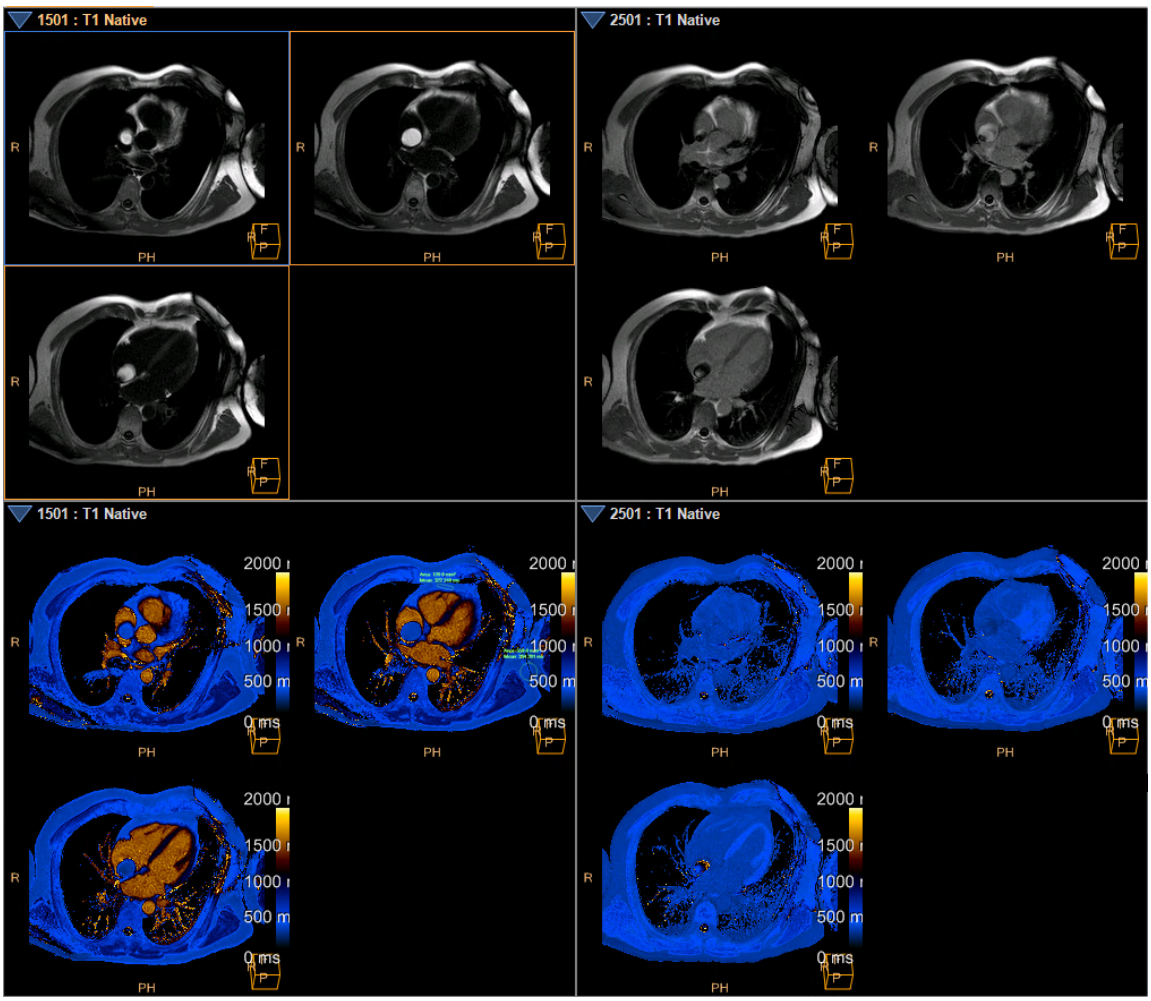


Fig. 101: Selecting series for Mapping analysis in the Viewing step

Source data and pixel maps are considered as one series, and both are loaded in one column for review and analysis.

If a motion-corrected series (MOCO) is available, the MOCO series is loaded instead.

If multiple series are selected the series will be displayed in separate columns allowing for easy comparison and contour copying. If a multi-slice series is loaded, all slices are shown in individual tiles in the view.

The Mapping analysis workflow consists of the following steps:

- **(Re)Calculate Maps**
  - The application opens in this step if you load raw (source) data without parametric maps.
- **Segmentation**
  - The application opens in this step if you load series with parametric maps created by the scanner. You can choose to go back to the first step and recalculate the maps, if desired.
- **Results**

You can also customize the color maps that are displayed during Mapping analysis. For details, see section “Customizing the Color Map” on page 242.

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.

(Re)Calculate Maps step

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.

NOTICE

You can also return to this step from the **Segmentation** step and recalculate parametric maps if you are not satisfied with the quality of maps provided by the scanner.

The task guidance panel provides tools for applying selecting the map that you want to use for analysis. Optional tools for improving the quality of the map are also available.

3000063879l_A/881 * 2021-06-30

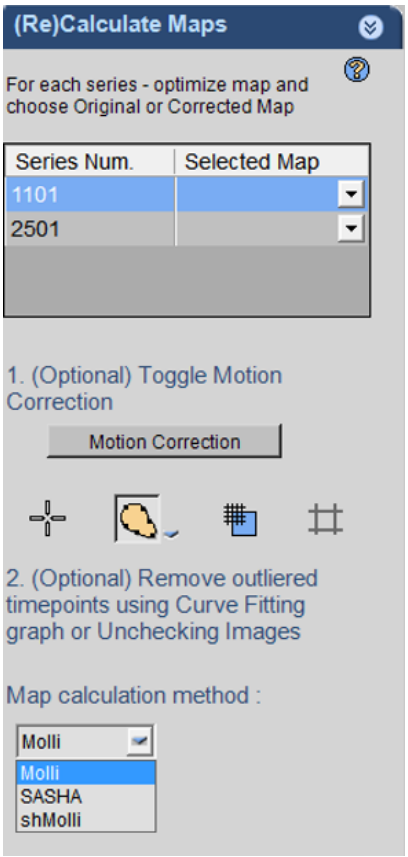


Fig. 102: (Re)Calculate Maps task guidance panel

When you load a series in the **(Re)Calculate Maps** step, the newly calculated parametric map is displayed in the lower-right view. If an original map from the scanner is also available, it is displayed in the lower-left view for comparison.

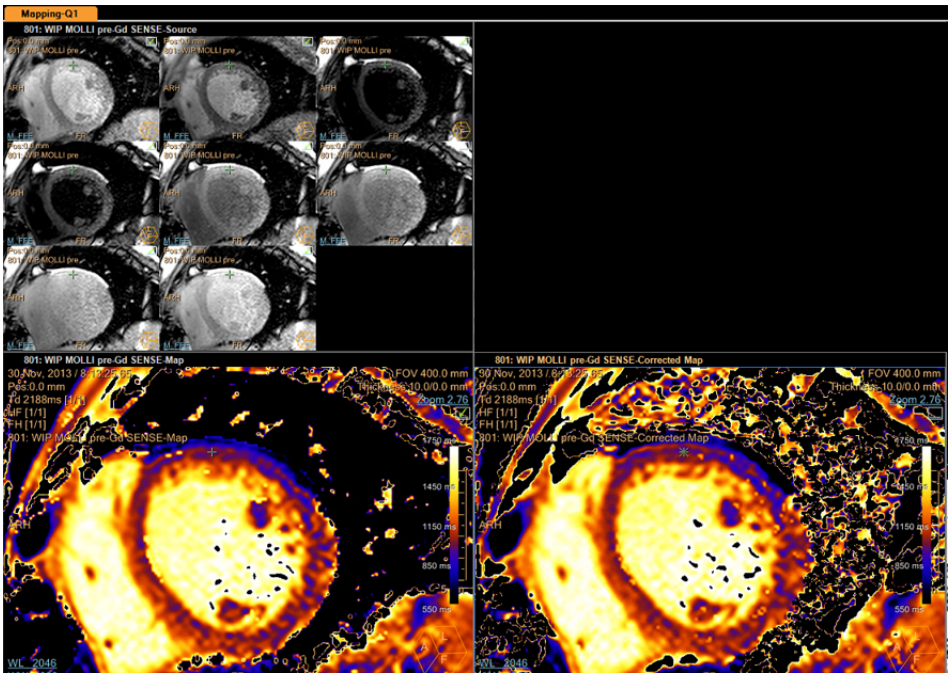


Fig. 103: (Re)Calculate Maps step

R^2 Error Map

You can view an error map as a quality check for the newly calculated map.

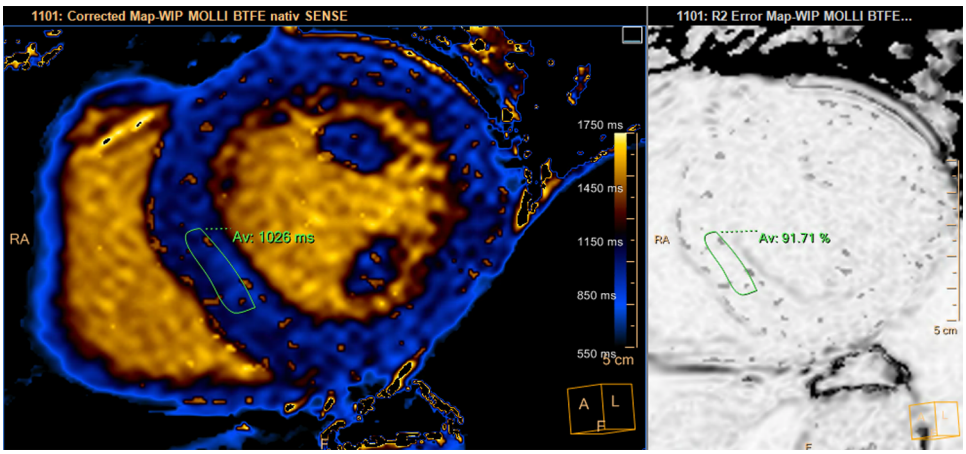


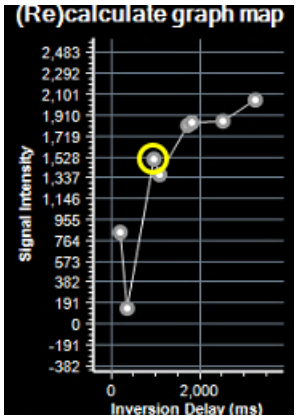
Fig. 104: R^2 error map

The grayscale represents a ratio from 0 to 1: 0% (bad) fit = black 100% (good) fit = white. You can also draw an ROI to review the confidence level of the fit for a specific region.

Detecting Outlying Time Points

1. You can use the **Point** and **ROI** tools available in the task guidance panel to detect motion in the raw data images.

   ⇨ After you set a point or define an ROI in a source image, a graph is displayed, which you can use to identify outlying time points that reduce the quality of the map. You can exclude these outliers from the analysis and improve the quality of the resulting parametric map.

⇨ 

2. Right-click an outlier point in the graph and deselect it. You can also deselect an outlier by clearing the check box in the source image.

3. You can also use the **Grid** tool available in the task guidance panel to place a box around the ventricle, which provides visual feedback of motion in the series.

4. To adjust the spacing of the grid, click **Grid Size** in the task guidance panel.

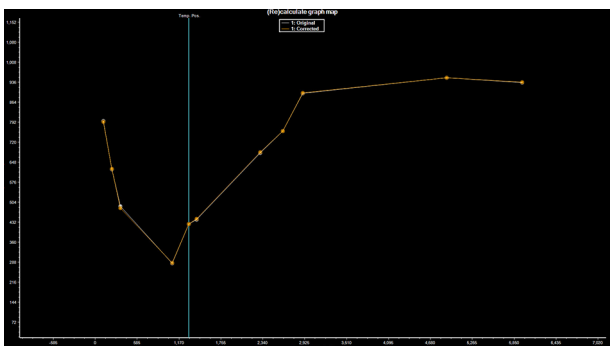
Using Motion Correction

For various clinical applications, motion estimation or motion compensation is a key functionality. Motion can be caused by patient motion, by breathing motion or, in the context of follow-up imaging, by different positioning or status of the patient. In addition, motion-similar effects can be caused by imaging-induced distortion.

Image registration/motion correction has the purpose to relate the information contained in one image to information given in another image. To this end, a transformation (or mapping function) is searched such that each position in the one image is mapped onto a corresponding and meaningful position in the other image. The software is named FEIR (Fast Elastic Image Registration) since its methodology is based on a (simplified) physical model of material elasticity and since its computational runtime is much lower compared to other state-of-the-art approaches.

1. To use motion correction, click **Motion Correction** in the task guidance panel.

⇨ Motion correction is applied using a FEIR (2D) algorithm. A graph is displayed showing the extent of the adjustments that motion correction has provided.

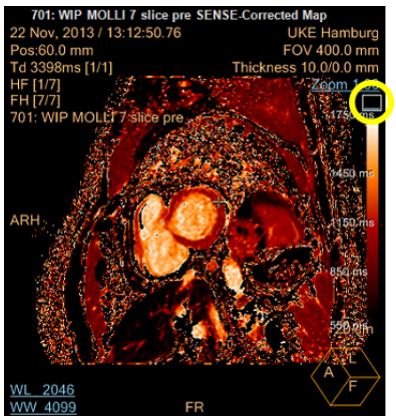
⇨ 

⇨ The default mapping uses the **Molli** fit for T1 mapping.

2. To change the mapping, click the **Map calculation method** list in the task guidance panel and select a different fit method (depending on the acquisition method used).
3. Right-click the graph to select viewing options for the graph. You can configure the visibility of the following items:
   - Data for the original source
   - Date for the corrected source
   - Grid overlay

Selecting a Parametric Map

1. For each series loaded, review the maps and select the map that you want to use. You can select the map using one of the following methods:
   - Select the map in the task guidance panel.
   - Select the check box in the map that you want to use.



⇨ After selecting a map, you can proceed to the **Segmentation** step.

Segmentation step

The following workflows are available in the **Segmentation** step:

- Check the quality of the parametric maps.
- **Local**: Draw single ROIs for comparison.
- **Regional**: Draw myocardial contours to investigate the entire myocardium. Using this workflow you can also segment user-defined regions or segment according to the AHA model (optional).

The task guidance panel provides tools for segmentation.

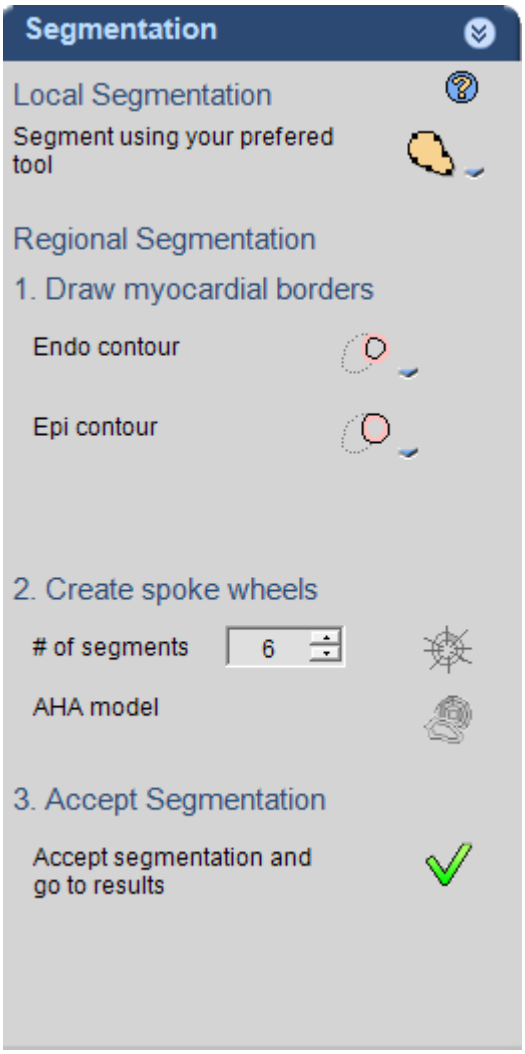


Fig. 105: Segmentation step task guidance panel

In each workflow, the following contour tools are available:

- **Spline contour**: Click along the edge of the contour and then double click to complete the contour.
- **Freehand contour**: Drag along the edge of the contour. The contour is created as you drag. To complete the contour, release the mouse button.

You can edit a contour by moving the pointer to the edge of the contour and dragging a control point.

NOTICE

Calculations after segmentation are taken from the color map, therefore we recommend drawing and verifying the contours on the color map. However, contours that you draw on the color map are also displayed on the source images, allowing you to scroll through all inversion delays (T1) or echos (T2 and T2*) and check for motion.

1. Before starting segmentation, check the quality of the parametric maps.
   - If the quality of the maps is acceptable, click  in the task guidance panel and continue with this procedure.
   - If the quality of the maps can be improved, click  in the task guidance panel to return to the **(Re)Calculate Maps** step. For details, see section "(Re)Calculate Maps step" on page 235.
2. To perform local segmentation, do the following:
   - Select a contour tool in the **Local Segmentation** section of the task guidance panel and draw a contour.
   - Select a contour name in the pop-up list or add a new label in the field at the bottom of the list.
3. To perform regional segmentation, do the following on one slice:
   - Select an **Endo contour** tool in the **Regional Segmentation** section of the task guidance panel, draw the endo contour and select or add a contour label in the pop-up list.
   - Select an **Epi contour** tool in the **Regional Segmentation** section of the task guidance panel, draw the epi contour and select or add a contour label in the pop-up list.
   - Optional step in the T1 workflow: Select a **Blood contour** tool in the **Regional Segmentation** section of the task guidance panel, draw the blood contour and select or add a contour label in the pop-up list.

NOTICE

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.

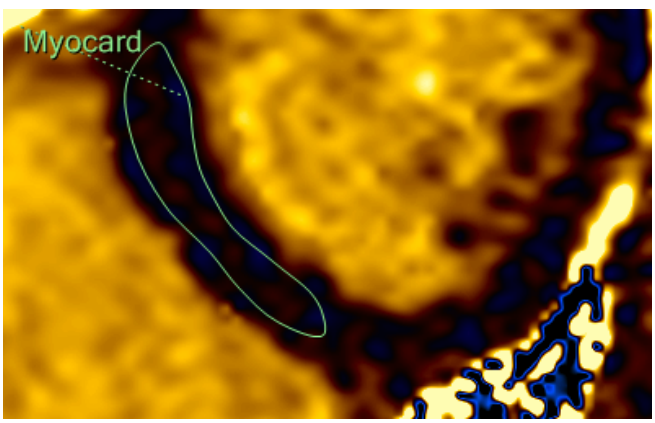


Fig. 106: Take care to avoid myocardial border when creating a contour

4. To compare measurements between two different loaded series, the exact ROI can be copied to the same image location in another series with the same orientation. To copy a contour, right click the contour and select one of the following copy functions:
   - **Copy all ROIs from this series to series of same orientation**
   - **Copy all ROIs from this slice to slice of same orientation**
   - **Copy this ROI to series of same orientation**
5. To adjust the position of a ROI, right click the ROI, then click **Pan ROI** and move the ROI to the correct position.

⇨ This is useful when series are acquired with a different breath hold or cardiac trigger.

⇨ You can also pan a ROI by dragging it while holding the SHIFT key.

⇨ To pan all ROIs at once, right click a ROI, select **Pan All ROIs**, and then move a ROI to the correct position (all ROIs are moved). Alternatively, you can pan all ROIs by dragging a ROI while holding the CTRL key.

6. To apply a spoke wheel to the contours, select the number or segments and click **Create spoke wheels** in the task guidance panel.

7. When the segmentation is correctly configured, click **Accept Segmentation** in the task guidance panel.

Customizing the Color Map

You can customize the color map in the following ways:

- Restrict color information to the inside of the ROI
- Change the color map type
- Change the color range

Color Inside ROI

► To show color information inside the ROI only, click **Show Color Inside of ROI** in the task guidance panel toolbar.

⇨ This tool allows you to draw an ROI on a grayscale map, while still visualizing color information in the defined color range inside the ROI (see **Color Map Type** and **Color Range** below).

Color Map Type

1. To change the color map type, click **Color map** in the task guidance panel toolbar.
2. Select a preset color map from the list.

NOTICE

If you experience difficulties drawing contours on the color map, you can select a grayscale map using the **Color map** function.

300006338791_A/881 * 2021-06-30

Color Range

1. To adjust the display of color maps according to field strength, click **Color range** in the task guidance panel toolbar.
2. In the **Colormap Settings** dialog box, select a **Field Strength**, and then adjust the **High** and **Low** values for map types as desired.

⇨ To revert your changes, if desired, click **Restore Default**.

3. Click **Apply**.

NOTICE

T1, T2, and T2* times are different for each field strength. If multiple types of scanner data are used, it is recommended to set the expected ranges for each type of scanner.

Results step

1. Select a **Result Protocol** from the task guidance panel.

⇨ **Local**: Displays all results from all single ROI measurements in the selected series.

⇨ **Regional**: Displays only the results from myocardial contours with regional segmentation. Results are shown for each separate slice from the selected series and they are displayed in a table and graph. You can switch between graph view or bulls-eye view.

Graph View

The graph displays the actual measured signal intensity for each time point (x-axis) of the source data for each ROI. Therefore a connecting curve is not displayed as it does not represent the actual fitted curve of the pixel map.

The graph allows you to assess the accuracy of the measured points. It displays the average signal intensities in the user-defined ROIs of the different echoes or inversion delays from the selected series and slice.

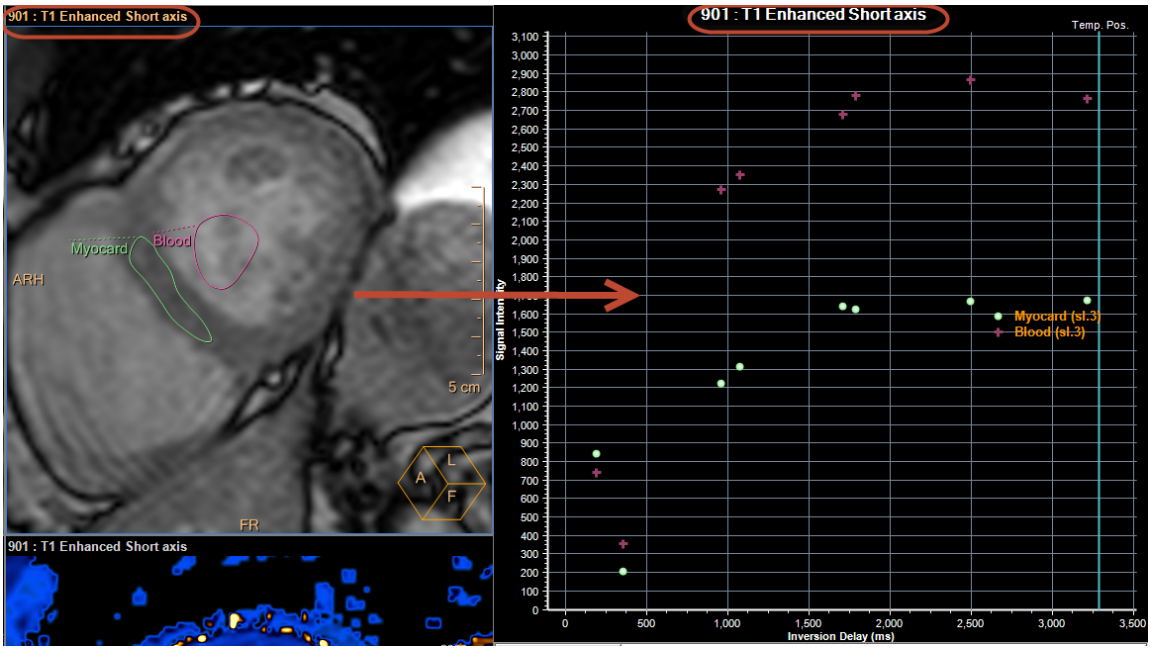


Fig. 107: Graph view in the Mapping analysis application

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.
- 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.

Ɛ is calculated with the following formula:

- $Ɛ = (1\text{-heamatocrit}) (\text{delta } R1_{myocardium}/\text{delta } R1_{blood})$

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.

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.

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.

Carpenter et all.: On T2* Magnetic Resonance and Cardiac IronClinical Perspective. Circulation. 2011;123:1519-1528.

3000063879l_A/881 * 2021-06-30

300006338791_A/881 * 2021-06-30

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