Medis
MEDICAL IMAGING

QStrain 4.4

User Manual

Table of Contents

1   Overview

The QStrain generic workflows and the workspace are described in this section.

1.1 Workflows

A QStrain analysis can be started either from QMass, or as a standalone application.

The following table describes the steps in the workflow of a QStrain analysis started directly from QMass, or QStrain as a standalone application.

For further details refer to the section, Workflow: Performing a QStrain Analysis.

Table 1 : QMass + QStrain workflow / QStrain standalone workflow

QMass + QStrain	QStrain standalone
Load Series	
Automatic Contour Detection Review Contours	
Start QStrain Analysis: Automatic load series data & contours	Start QStrain Analysis
QStrain	**QStrain**
Select Series	Select Series
Select Analysis Type	Select Analysis Type
	Manually draw contours
	Review Contours
	Verify ED & ES phase
Complete strain analysis	Complete strain analysis

ⓘ The preferred workflow is to start QStrain from QMass, utilizing the automatically detected contours.

1.2 The QStrain Workspace

QStrain is launched from the Medis Suite app toolbar, or the app context menu, or from the app

pane by selecting the QStrain app icon [icon]. Detailed information on how to start an application and how to load series into the application, is described in the Medis Suite user manual. QStrain can also be started from QMass.

This chapter covers the following topics:

- Workflows

- Overview

- Toolbars

- Windows layouts

- Mouse controls

- Frame selection

1.2.1 Overview

QStrain application consists of six primary windows each representing a step in the analysis workflow. A vertical toolbar to the right-hand side of the application, shows the buttons required to complete each step in the analysis process.
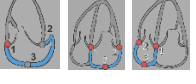
The following list describes the basic steps to complete a generic QStrain analysis.

- Series Loading & Analysis selection
- Contour Editing
- ED-ES contour review
- ED-ES phase review (Sequence/M-Mode selection).
- Global Strain Analysis
- Time to Peak detailed regional analysis

1.2.2 Toolbars

A vertical toolbar on the right-hand side of the application allows one to navigate through the different steps of an analysis. In each step of the analysis process, different icons are shown in the toolbar.

The list below describes the purpose of each icon.

Icon	Function
Series & Analysis Selection Toolbar	
	Forward button
	Back button
	Remove series
Contour Editing Toolbar	
	Phase indicator ES
	Phase indicator ED
	Guide contours LV SAX
	Guide contour LV LAX (2CH, 3CH, 4CH)
	Guide contours Left Atrium | Right Atrium
	Guide Contours RV
Analysis Toolbar	
	About Box.
	Go back to Series & Analysis selection Window
	Send Movie, Snapshot to Medis Suite
	Window Width, Window Level
	Decrease, Increase or go back to initial arrow size

Icon	Function
	Go to ES or ED phase
	Mirror the image
	Switch parametric over B-mode
	Change the visualization method for the contour tracing
	Apply the reference point
	Switch from 2D to 3Dview
	Go to sequence / M-mode selection
	Enable/Disable M / M-mode overlay in the volume graphs.
	Make a new tracing contours from scratch. Modifying the contour for the ED or ES phase.
	Segmental and detailed strain results!
Time to Peak toolbar	
	View results based on Endo contours
	View results based on Endo and Epi contours
	View results based on Epi contours

You cannot move toolbars to another part of the main application window.

You cannot hide toolbars.

The following list describes the icons that are not in the vertical toolbar.

Icon	Function
Viewport Tools	
	Play or stop cine movie
	Go to next or previous phase
	View viewport in Full screen
	View viewport in Normal screen

1.2.3   Windows Layout

QStrain application analysis consists of a sequence of steps to complete an analysis. The following list describes each window or dialog in correspondence with the sequential steps of a QStrain analysis.

- Series & Analysis Selection Window
- Contour Creation Window
- LV SAX Reference Point Placement Dialog
- Sequence / M-Mode Selection Window
- Analysis Window
- Time to Peak Segmental Analysis Window

1.2.3.1   Series & Analysis Selection Window

The initial series & analysis selection window workspace consists of four sections. The series list overview, CINE viewport, Analysis selection pane and a wizard step vertical toolbar.
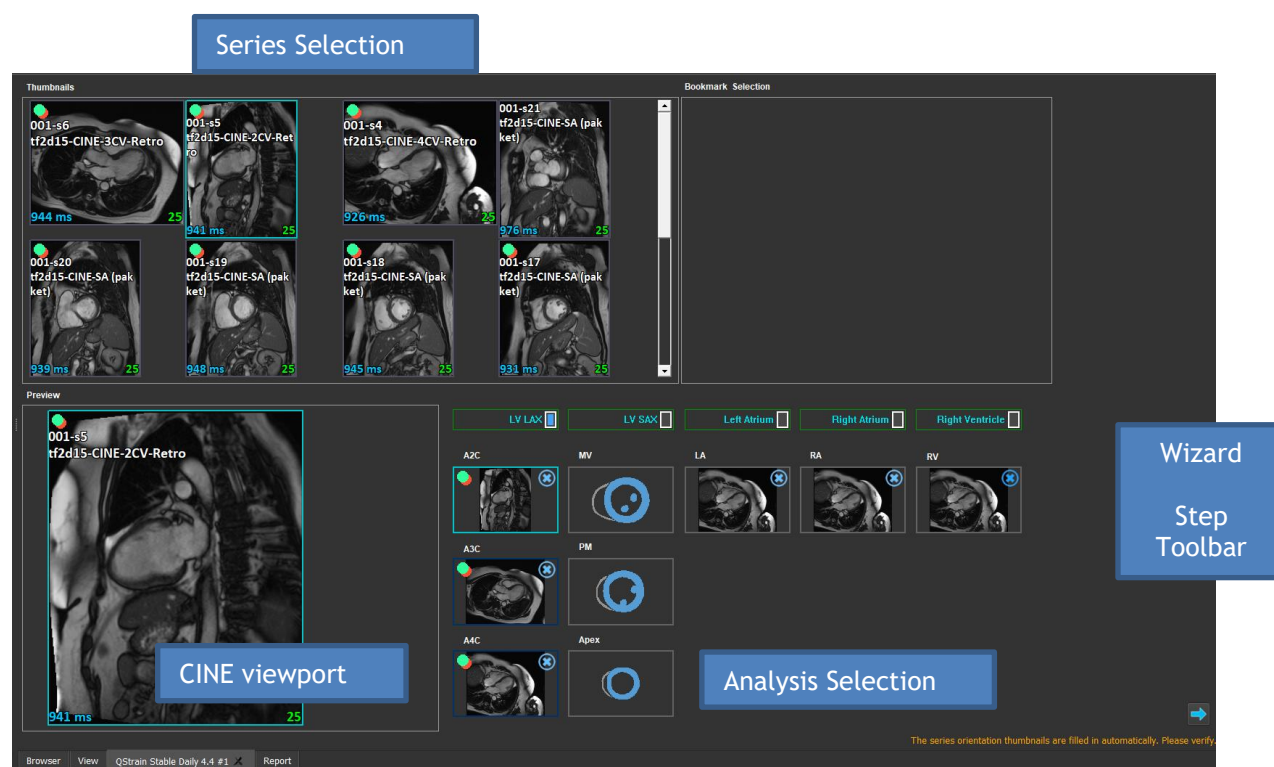
Figure 1 : Series & Analysis Selection Step

1.2.3.2   Contour Creation Window

After selecting a series, contours need to be drawn in the selected series before progressing to the analysis. This window consists of two sections, the Viewport and the Toolbars.
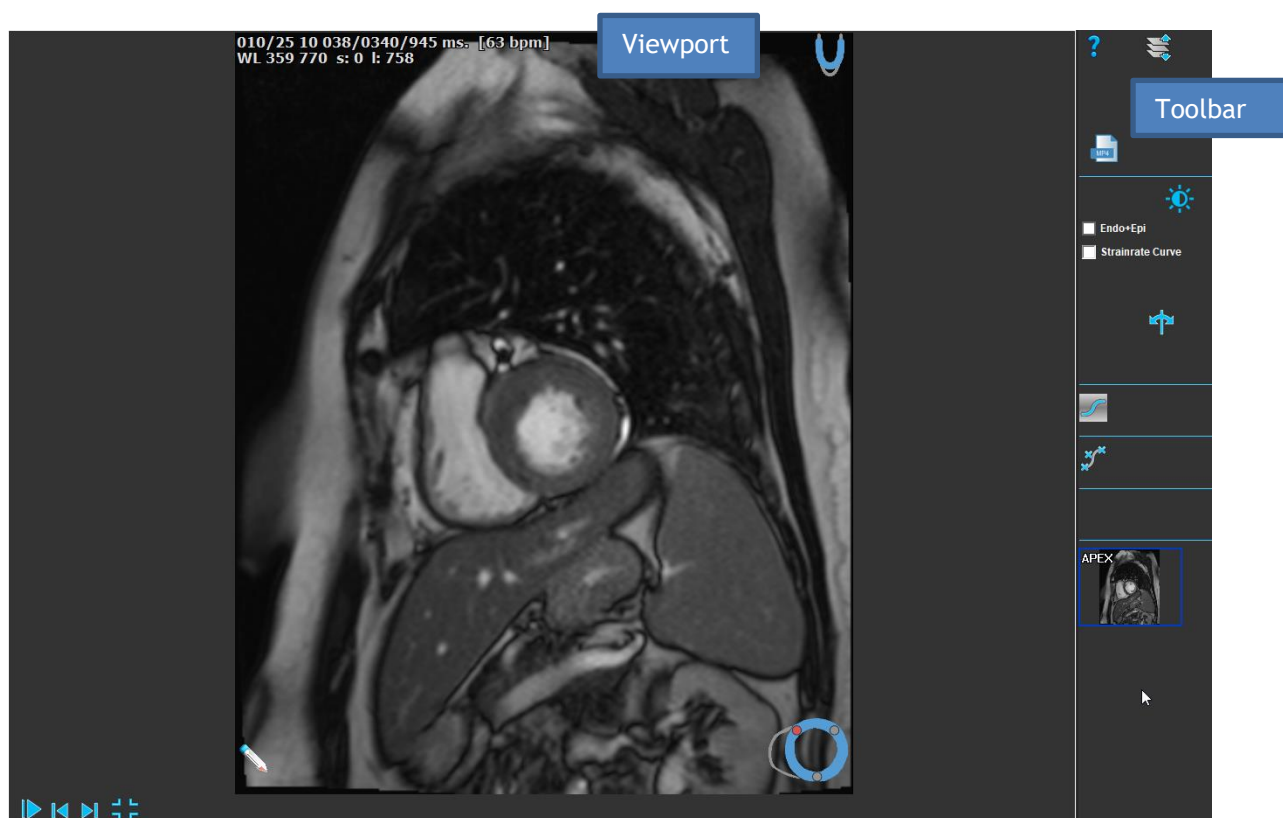
Figure 2 : Contour Editing Step

1.2.3.3   ES Contour Review & Modification Window

Once the contours have been created or imported, the ED and ES phases are set.

The ES contours modification window facilitates editing the ES contour edit points. For further details refer to the section, ED ES Management.

The window consists of:

- Viewport
- Cine movie control
- Myocardium expansion and reduction tool.
- Toolbar

There are minor differences between the ED and the ES review and modifications windows.
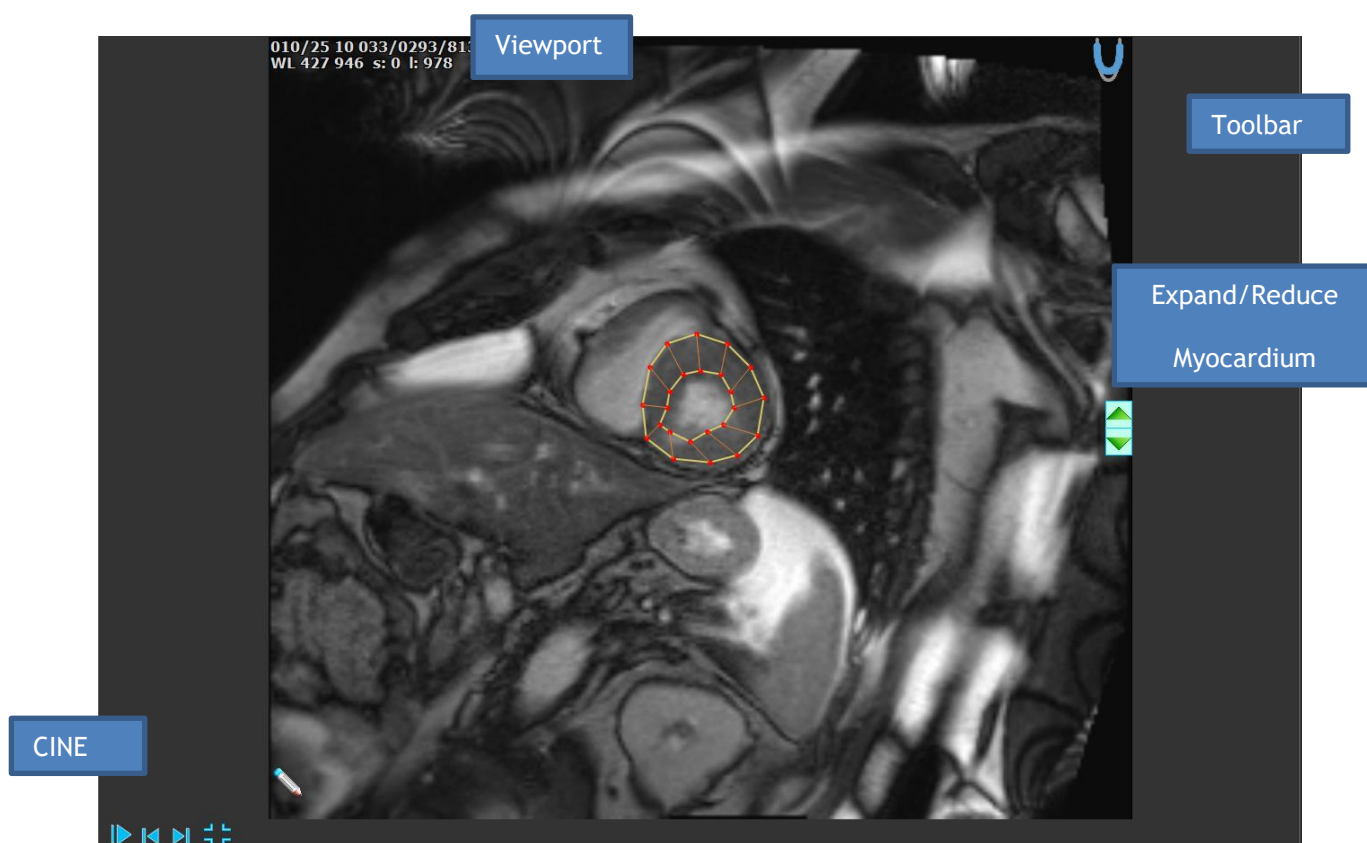
Figure 3 : ES Review & Modification Window

1.2.3.4   ED Contour Review & Modification Window

Once the contours have been created or imported, the ED and ES phases are set.

The ED contours modification window facilitates editing the ED contour edit points. The ED & ES review and modification window displays the ED and ES phase position in a volume graph. For further details refer to the section, ED ES Management. The window consists of:

- Viewport
- Volume graphs indication the ED and ES phase position
- Cine control: To scroll through the images.
- Toolbar
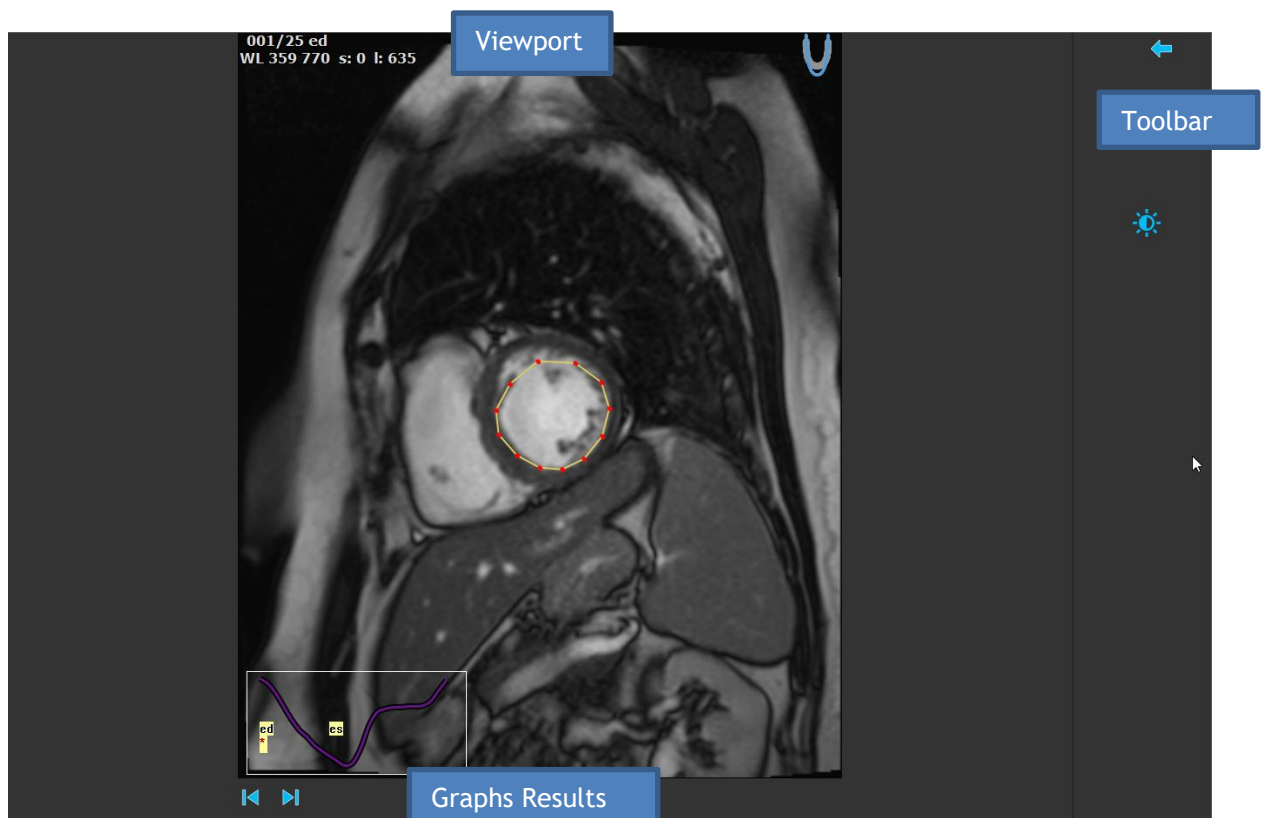
Figure 4 : ED Review Window

1.2.4   Analysis Window

The analysis window is shown after the data has been selected and the contours have been created or imported.

The analysis window consists of a vertical toolbar and a central viewport which comprises of four sections: The Viewport, graphic result, numeric results, and the 17 segment model results.
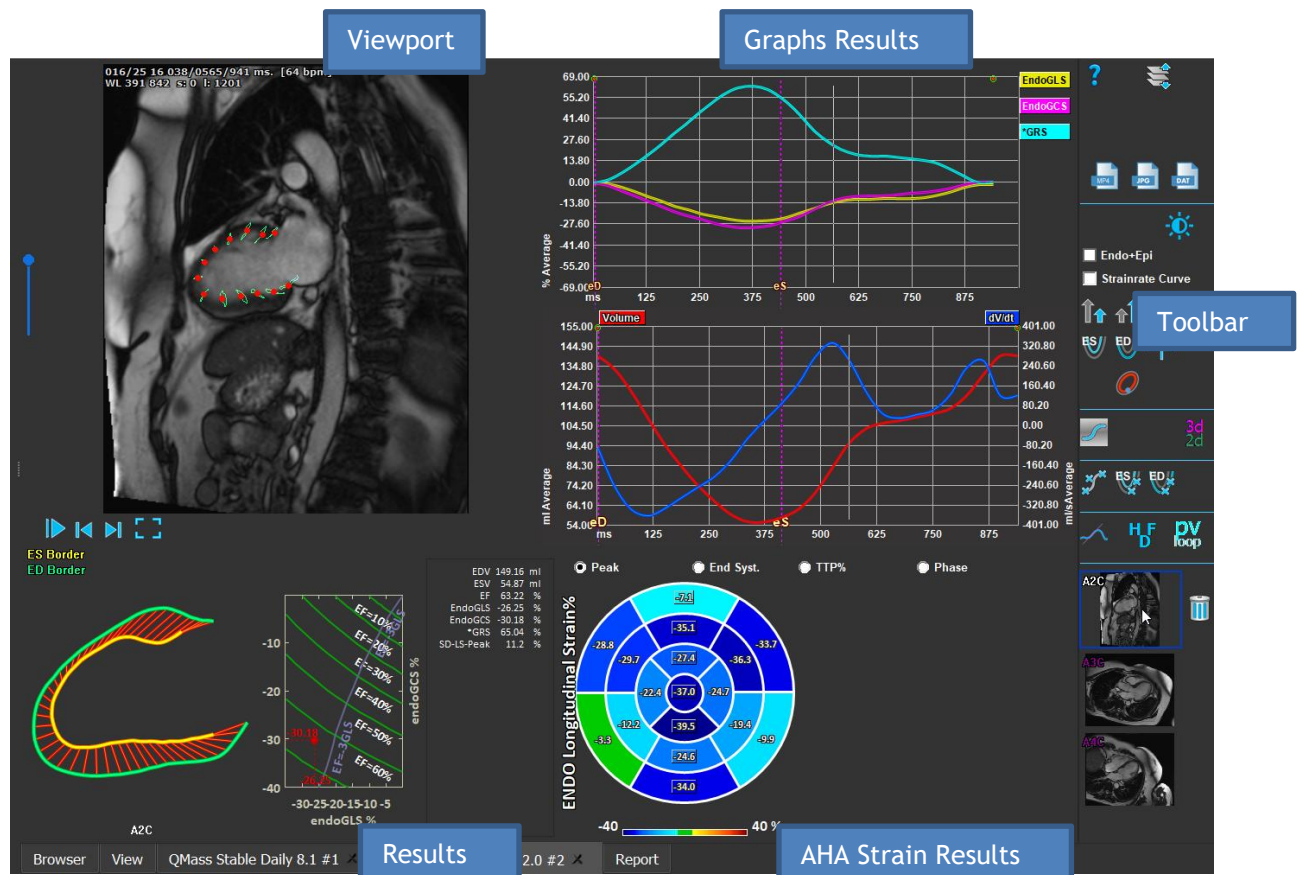
Figure 5 : Analysis window overview

From the Analysis window you can access the following windows:
- ES/ED modification window
- Reference point
- Sequence/M-Mode
- Time to Peak

1.2.4.1   LV SAX Reference Point Placement Dialog Box

The LV SAX analysis requires a reference point placement on all slices. The following window facilitates setting the reference point in the correct position.
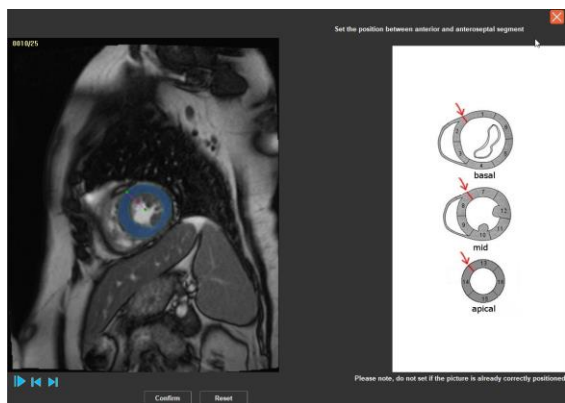
Figure 6 : LV SAX Reference Point Placement Window

To start the LV SAX Reference Point dialog box:

- In the vertical toolbar, press to start the LV SAX Reference Point dialog box.

1.2.4.2   Sequence / M-Mode Selection Window

The sequence / M-Mode selection window is used to verify and modify the ED and ES phase.
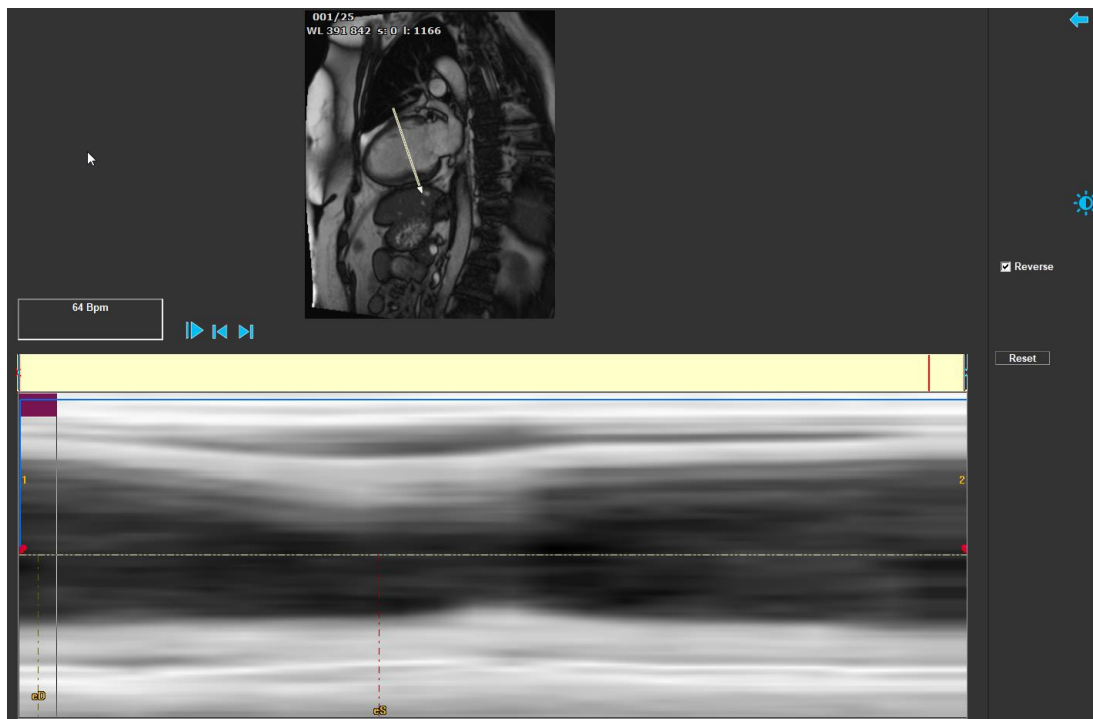
Figure 7 : Sequence M-Mode Window
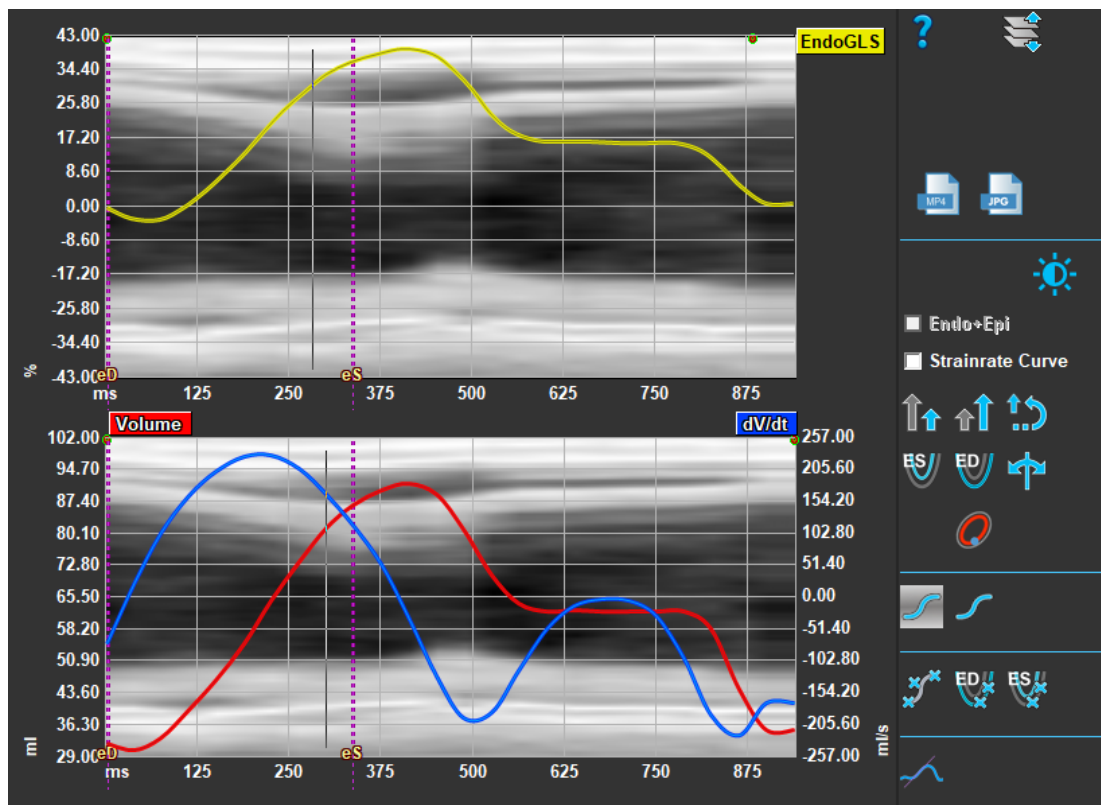
Figure 8 : Sequence M-Mode in Global Strain Graphs

1.2.4.3   Time to Peak Segmental Analysis Window

The Time to Peak Segmental Analysis Window shows either LAX or SAX orientational analysis results. The window consists of a vertical toolbar and central viewport with the following sections:

- Image viewing
- Graphic results
- Numerical results
- 17 Segment Model results
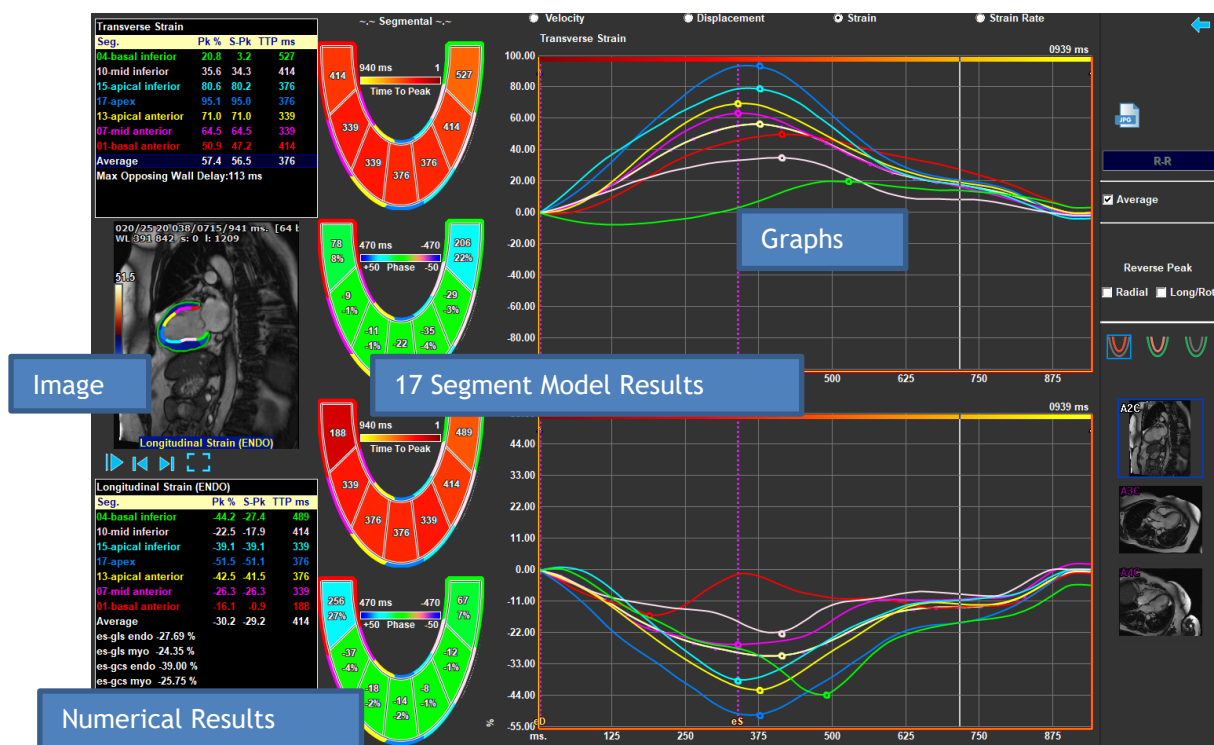
Figure 9 : Time To Peak Analysis Window (LAX)

Figure 10 : Time To Peak Analysis (SAX)

The regional results are distinguishable by color. The 17 segmental model is also interactive, highlighting the numerical region results as well as enabling or disabling the graphs.

1.3 Mouse Controls

1.3.1 Zooming

You can zoom in and out of the viewport using **Zooming**.

To activate the zooming mouse control:

- Hover over the image

To zoom in and out:

- Point to the location you want to zoom in on and use your scroll wheel to zoom in and out.

1.3.2 Pan

You can pan an image in the viewport.

To activate the panning mouse control:

- Hover over the image

- Press the left mouse button.

To pan an image:

- Activate the panning mouse control.

- Drag the mouse to pan the image.

1.3.3   Contrast & Brightness & Gamma

You can adjust the contrast, brightness, and gamma.

To modify the image Contrast

- Press   in the vertical toolbar.

- Click and drag the ruler below the   symbol.

To modify the image Brightness

- Press   in the vertical toolbar.

- Click and drag the ruler below the   symbol.

To modify the image Gamma

- Press   in the vertical toolbar.

- Click and drag the ruler below the   symbol.

To reset the default contrast, brightness, and gamma setting

- Press   in the vertical toolbar.

- Click the symbol   .

1.4 Frame Selection

You can move forward or backward through the frames in the image in several ways.

To move through the frames using buttons:

- Press ◄| or |► below the viewport to move to the previous or next frame.

Or,

- Press �❘▶ below the viewport to play a cine through the frames in forward direction.

  Click again on ▶| to stop the cine.

To move through the frames using keys:

- Press the left or right arrow key to move to the previous or next frame.

To modify the speed of the cine:

- Click and drag the ruler 🔵 to the left of the viewport.

1.4.1 Full Screen Selection

The image viewport can be full screen.

To switch to a full screen view.

- Press ⌐ ¬ below the viewport.

To disable the full screen view.

Press ⌐ ¬ below the viewport.

<div align="right"># Workflow</div>

2 Workflow: Performing a QStrain Analysis

QStrain application supports the following strain related analyses.

- LV long axis   (LV LAX)
- LV short axis   (LV SAX)
- Atrial images   (Left Atrium or Right Atrium)
- RV images   (Right Ventricle)

To navigate through the analysis steps.

- Click [image] in the vertical toolbar to continue to the next stage of an analysis.

- Click [image] in the vertical toolbar to go to the previous stage of an analysis.

- Click [image] in the vertical toolbar to go to the Loading a Series & Analysis stage.

- In the ED/ES Review viewport, click [image] to accept and click [image] to reject contour changes.

- In the Sequence / M-Mode Selection Window click [image] to return to the analysis.

- In the Time to Peak Segmental Analysis Window the button [image] means return to the analysis window.

2.1 QStrain Analysis General Steps

QStrain analyses share the same steps.

- Loading Series
- Analysis Selection

2.1.1 Loading contours

QStrain accepts contours from AutoQ generation and from QMass (when QStrain is started from QMass). In the data selection dialog, you can see if contours are available for a series by the Red/Green dot in the top left of a series.

QMass can provide contours for Left Ventricle Endo and Epi contours for both SAX and LAX series.

AutoQ can provide contours for Left Ventricle Endo and Epi contours for both SAX and LAX series, Right Ventricle Endo and Epi contours for LAX series and can provide Left and Right atrium Endo contours.

When contours are loaded a warning message is presented in the status bar.

Automatically created contours are loaded. Please verify.

Figure 11 Message when contours are loaded.

ⓘ Contours are only used when applicable for the selected analysis.

ⓘ Contours are used as input for the tracking. Therefor the contours after tracking can be slightly different because of the tracking.

- Creating Contours
- Completing Global Strain Analysis.
  - o Optional: LV SAX Analysis: Add a reference point, for each slice.
  - o ED ES Phase Review: Sequence M-Mode
  - o Complete detailed Regional analysis, in the Time to Peak Analysis.
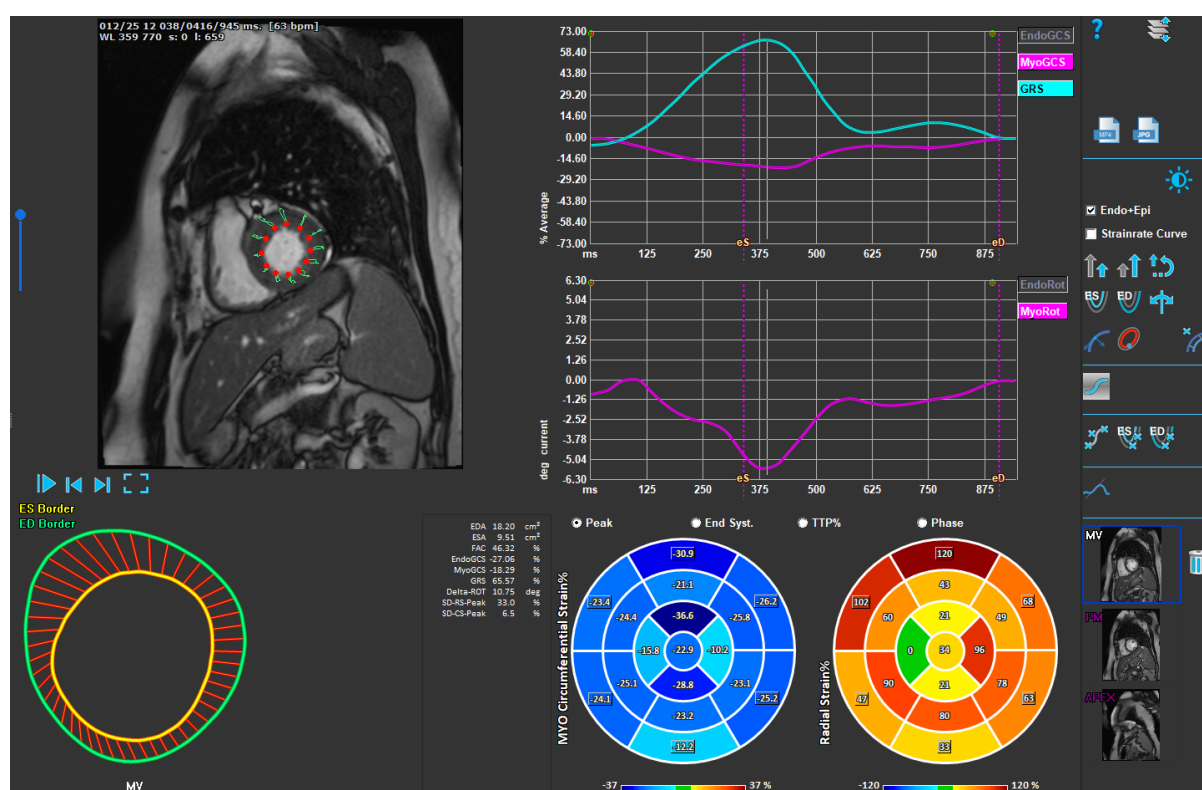
Figure 12 : LV SAX Analysis
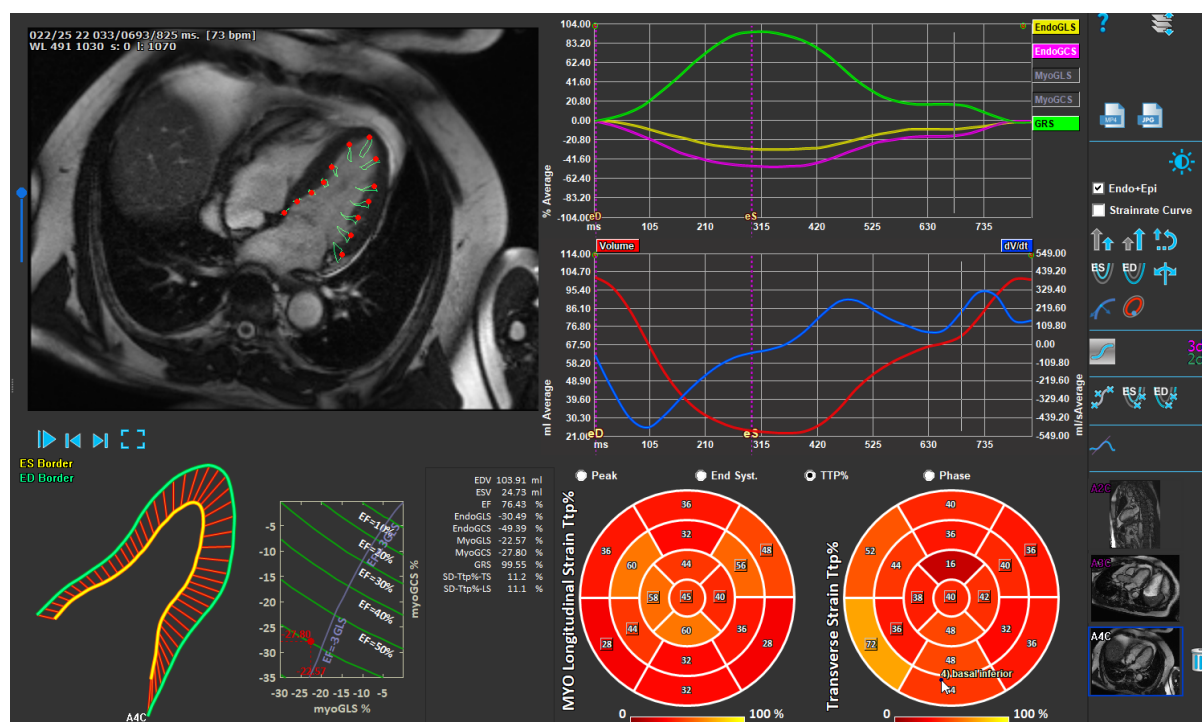
Figure 13 : LV LAX Analysis

2.2 **Loading Series**

The first step of a strain analysis is loading the series. A series, or multiple series can be loaded into QStrain from the **Series Browser** of Medis Suite. Refer to the Medis Suite user manual for detailed instructions.

QStrain supports MR and CT series.

To load series from the Series Browser of Medis Suite

1. Select the set of strain series in the image or text view of the Medis Suite **Series Browser**.

2. Click and drag the selected items onto the QStrain application icon.

Or,

1. Select all series in the image or text view of the Medis Suite **Series Browser**.

2. Right-click above the selected series to open a context menu.

    Choose QStrain.

This will load the series into the series analysis selection viewport.

To load series from QMass

- Select the icon in the **General** toolbar in QMass.

🛈 All the series data loaded in QMass and their related contours that have been created in QMass, will be loaded into QStrain.

🛈 QStrain only loads MR and CT DICOM series.

2.3 Analysis Selection

QStrain application supports the following strain related analyses.

- LV long axis   (LV LAX)
- LV short axis   (LV SAX)
- Left Atrial   (Left Atrium)
- Right Atrial   (Right Atrium)
- RV   (Right Ventricle)

Figure 14: Series & Analysis Selection

2.3.1 Automatic series coupling

The loaded series are automatically coupled at start to long axis chamber orientation views if they contain sufficient positional data and if they fit. If multiple series are suitable for a specific image localization, the most recent is coupled. Automatic localization of series can be overridden by manual selection.

If series are automatically coupled a warning is given. The user should always check if the coupled series is the correct series.

Figure 15 Message when series are automatically coupled to views.

ⓘ For Left Atrium both a 2ch or 4ch can be suitable. A 2ch will be coupled if both are available.

ⓘ In case multiple series for a series type are available the latest acquisitioned series will be used.

2.3.2   Manual selection and coupling

Series selection.

- Select a series from the left viewport.

Couple a series with an image orientation.
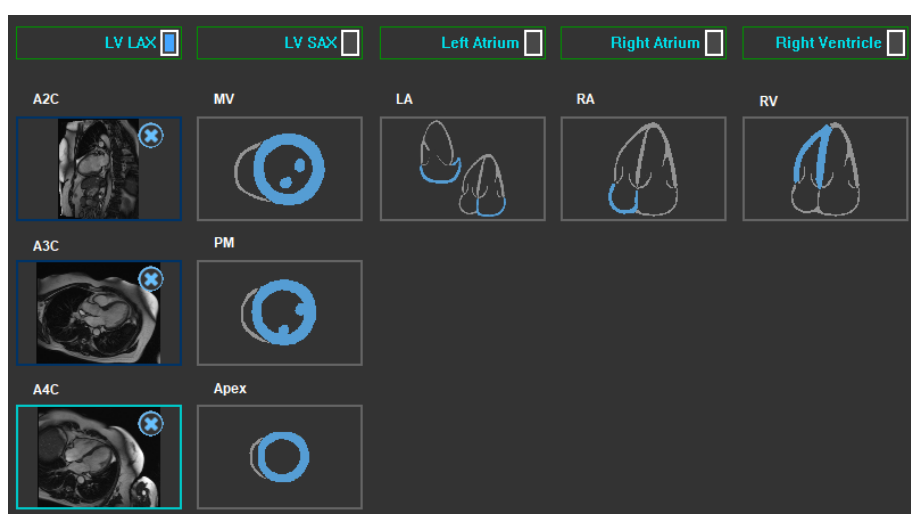
Figure 16 : Couple a series with an orientation.

Choose the analysis type.

- Check the checkbox of the analysis to perform.
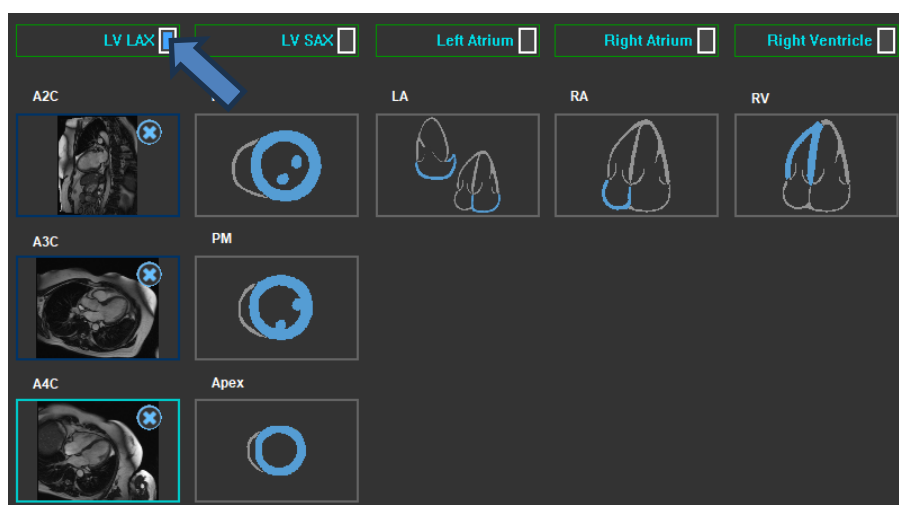
Figure 17 : Select QStrain Analysis Type.

ⓘ Only one analysis type can be selected.

ⓘ A green or red circle in the upper left corner of the viewport indicates epi or endo contours are imported with the selected series.

The selected series are coupled with a given QStrain analysis. LV LAX and LV SAX analyses facilitate up to three series, each representing one slice. Left|Right Atrium and RV analyses are limited to one series.

To couple a series with a LV SAX Analysis.

- Select a series in from the series list.

- Click and drag viewport image onto the corresponding level, Mitral Valve , Papillary Muscle or Apex icons.

To couple a series with a LV LAX Analysis.

- Select a series in from the series list.

- Click and drag viewport image onto the corresponding A2C , A3C or A4C chamber view icons.

To couple a series with a Left Atrium Analysis.

- Select a series in from the series list.

- Click and drag viewport image onto the Atrium icon.

To couple a series with a Right Atrium Analysis.

- Select a series in from the series list.

- Click and drag viewport image onto the Atrium icon.

To couple a series with a RV Analysis.

- Select a series in from the series list.

- Click and drag viewport image onto the RV icon.

To remove a series from an Analysis

- Click on the icon next to the series you want to remove

To select the series in the viewport already selected in an Analysis orientation.

- Click on the Analysis orientation view icon to select the corresponding series in the viewport

2.3.3   Automatic series mirroring

Series selected for an analysis are checked if mirroring is needed and will be mirrored when the analysis is started.

When one or more series are mirrored a warning message is presented in the status bar.

Figure 18 Message when series are automatically mirrored.

2.4   Contours Management

Contours are a prerequisite of a strain analysis. The following section explains the contour management related aspects of QStrain.

ⓘ When contours are loaded from QMass or AutoQ, the Contour Editing workflow of the analysis is automatically surpassed.

2.4.1   Loading contours

QStrain accepts contours from AutoQ generation and from QMass (when QStrain is started from QMass). In the data selection dialog, you can see if contours are available for a series by the Red/Green dot in the top left of a series.

QMass can provide contours for Left Ventricle Endo and Epi contours for both SAX and LAX series.

AutoQ can provide contours for Left Ventricle Endo and Epi contours for both SAX and LAX series, Right Ventricle Endo and Epi contours for LAX series and can provide Left and Right atrium Endo contours.

When contours are loaded a warning message is presented in the status bar.

Automatically created contours are loaded. Please verify.

Figure 19 Message when contours are loaded.

ⓘ Contours are only used when applicable for the selected analysis.

ⓘ Contours are used as input for the tracking. Therefor the contours after tracking can be slightly different because of the tracking.

2.4.2   Creating Contours

The first step of the QStrain analysis is to define the Endocardium and optionally the Epicardium contours. QStrain contours may be added via the 'Contour Creation Window' viewport or imported with the selected series.

2.4.2.1   Enable the Contour Creation window.

- After completing the series selection and analysis in the 'Series & Analysis Selection Window', click in the vertical toolbar.

Or,

- In the analysis viewport, click or , or in the vertical toolbar.

Or,

- In the analysis viewport, select the checkbox Endo+Epi in the vertical toolbar.

2.4.2.2   To create a contour.

When the contour editing window is open, edit the contours as follows:

1. Click to set the first edit point on the image, in the recommended position displayed by the contour point indicator.

2. Click to set the second edit point on the image, in the recommended position displayed by the contour point indicator.

3. Right-click to set the last edit point on the image, in the recommended position displayed by the contour point indicator. A contour will be generated.

ⓘ Select the check box Endo + Epi to generate both Endo and Epi contours.

ⓘ Clear the check box Endo + Epi to generate the Endo contour only.

2.4.3   Creating Contours by Indicators

In the bottom right corner of the Contour Editing viewport, a contour position indicator recommends the ideal position placement of the progressive contour points.

LV SAX
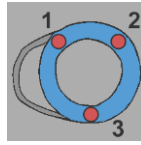
LV SAX placement indicators as follows .

LV LAX
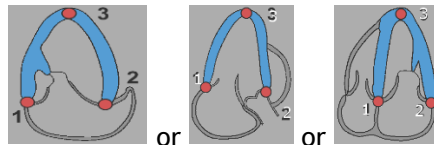
LV LAX placement indicators are as follows or or .
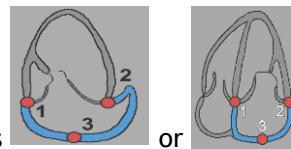
Left Atrium

Left Atrium placement indicators are as follows or .

Right Atrium

Right Atrium placement indicators are as follows .

RV
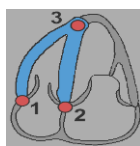
RV placement indicators are as follows .

2.4.4   Editing Contours

2.4.4.1   Modify contours

To modify an existing contour

Moving Edit-points:

- Hover the mouse cursor over the Edit-point. The cursor changes to double-sided arrow cursor.
- Click and drag the mouse to move the edit-point. If the contour is already created (Three edit points present), new contour will be displayed based on the new position of edit-points.
- Release the mouse to end editing and the contour shown while dragging becomes final.

Rubber-banding edit contours:

- Hover the mouse cursor over the contour. The cursor changes to rubber-banding cursor.
- Click the left mouse button and drag the mouse to edit the contour. A section of contour will be edited with mouse motion.
- Release the mouse to end editing and the contour shown while dragging becomes final.

Moving contours (Ctrl + LMB Click and drag):

- Press the Ctrl key and click left mouse button on viewport area and drag the mouse to move the contour. If both Epi and Endo contours are present the contour near to the mouse click point will be selected for move.
- The contour will move the same distance and direction as the mouse moves.
- Release the mouse button to end the move.
- Press Ctrl + Shift + LMB Click and drag to move both Epi and Endo contours simultaneously.

Smoothening contours (Shift + S):

- Press the Shift + S keys to smoothen the selected contour, i.e either ES or ED contour.
- The last contour manually edited, using rubber-band or move edits, will be the selected contour.

2.4.4.2   Remove all contour points.

- Click on the edit point in the vertical toolbar.

2.4.4.3   Undo/Redo edits.

- Press Ctrl + Z to undo the edits done on contour, i.e. moving, rubber-banding, smoothening contour OR moving edit-points.
- Press Ctrl + Y to redo the undo action, provided no new editing is performed after undo.
- Undo/Redo can only be done as long as editing is not finished, or additionally in ED edit page, if frame is not changed.

2.4.5 Finish Contour Editing

After contours have been defined, the analysis can be continued.

To continue from the Contour Editing window to the Analysis window.

- Select the in the vertical toolbar.

Or,

- Right-click in the Viewport

2.5 Analysis Accessories

The vertical toolbar in the analysis window, contains utilities that assist in the strain analysis workflow.

2.5.1 Creating a Reference Point for LV SAX Analysis

Reference points enhance the accuracy of the results.

To set a reference point in a LV SAX analysis.

- Choose the LV SAX a slice from the vertical toolbar.
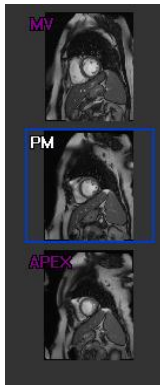
- Select the in the vertical toolbar.

- Click on the Anterior Septum as indicated in LV SAX Reference Point Placement Dialog.

- Click Confirm.

🛑 LV SAX strain analysis requires a reference point placement on the anterior septum of each slice.

2.5.2   ED ES Management

2.5.2.1   ED ES Contour Review & Modification

The 'ES Contour Review & Modification Window' facilitates one to update the ED and ES contours.

To enable the ES Contour Review & Modification Window.

- In the analysis window click in the vertical toolbar.

To enable the ED Contour Review & Modification Window

- In the analysis window click in the vertical toolbar.

2.5.2.2   ED ES Phase Review: Sequence M-Mode

The Sequence M-Mode is a utility that assists in managing the position of the ED and ES phase. A Sequence M-Mode line is used to create an M-Mode image. Typically, the M-Mode line is drawn from the outer ventricular walls across the diameter of the ventricle. The ED and ES phase positions can then be adjusted on the M-Mode image.

Sequence M-Mode editing consists of three steps.

- Define a line across a ventricle.
- Evaluate the M-Mode image.
- Review/Modify the ED and ES position.
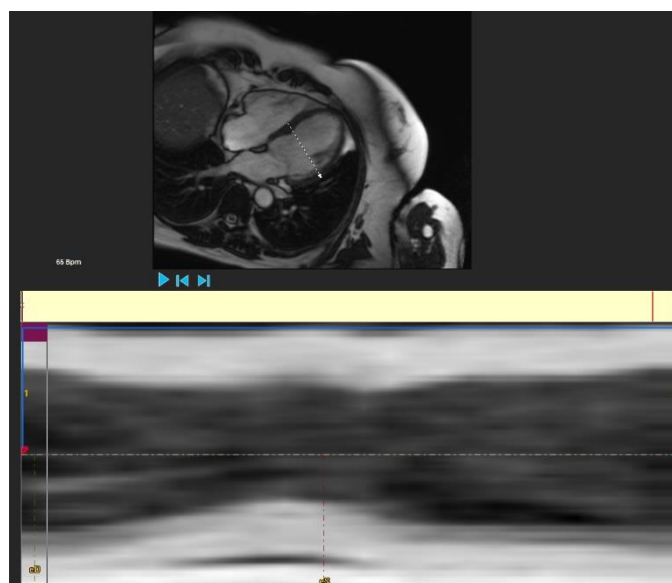
Figure 20: Sequence M-Mode ED ES Phase Review

The ED and ES phases can be verified and modified if necessary, using the M-Mode image. The resulting M-Mode overlay image will automatically be displayed in the volume graph of in the analysis window. The overlay can be toggled off and on.
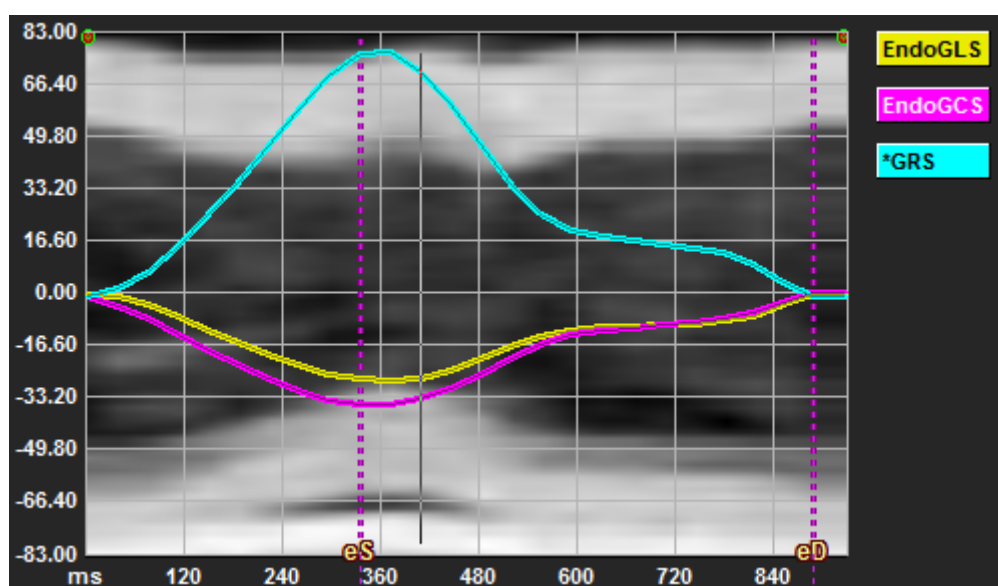
Figure 21: M-Mode Overlay in Analysis Window Volume Graph

To draw the M-Mode line.

- In the analysis viewport, click in the vertical toolbar.

- In the image, click to begin the M-Mode line.

- Right-click to end the M-Mode line.

To update the ED or ES phase.

- Click and drag the ED or ES vertical gridlines in the M-Mode image.

- Click in the vertical toolbar to return to the analysis window.

To enable / disable M-Mode overlay in volume graphs.

In the analysis window.

- Click to enable or disable the M-Mode in the strain graph.

2.5.3   Time to Peak Analysis

The Time to Peak analysis provides detailed 17 segment AHA model regional strain results. The regional results are distinguishable by color. The segment model and the corresponding graphs are interactive and facilitate enabling and disabling of the regional results.

The following color scheme is used to distinguish the different segment model regions and their corresponding results.

Basal		Mid		Apical	
Basal	Anterior	Mid	Anterior	Apical	Anterior
Basal	Anterorlateral	Mid	Anterorlateral	Apical	Inferior
Basal	Inferiorlateral	Mid	Inferiorlateral	Apical	Septal
Basal	Inferior	Mid	Inferior		Lateral
Basal	Inferorseptal	Mid	Inferorseptal		
Basal	Anterorseptal	Mid	Anterorseptal		

To start a Time to Peak analysis.

- Click in the vertical toolbar to return to the analysis window.

To select a region.

In the Time to Peak Segmental Analysis Window:

- Hover over the Segment model.

Or,

- Hover over the graphs.

To enable / disable a region.
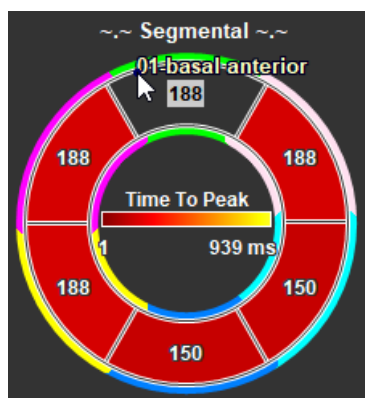
Figure 22 : Enable/Disable SAX TTP Region *Figure 20 : Enable / Disable LAX TTP Region*

In the Time to Peak Segmental Analysis Window.

- Click the segment to enable or disable.

To enable / disable all regions.

In the Time to Peak Segmental Analysis Window.

- Click the center of the segment model to enable or disable all segments.

To switch regional analysis type.
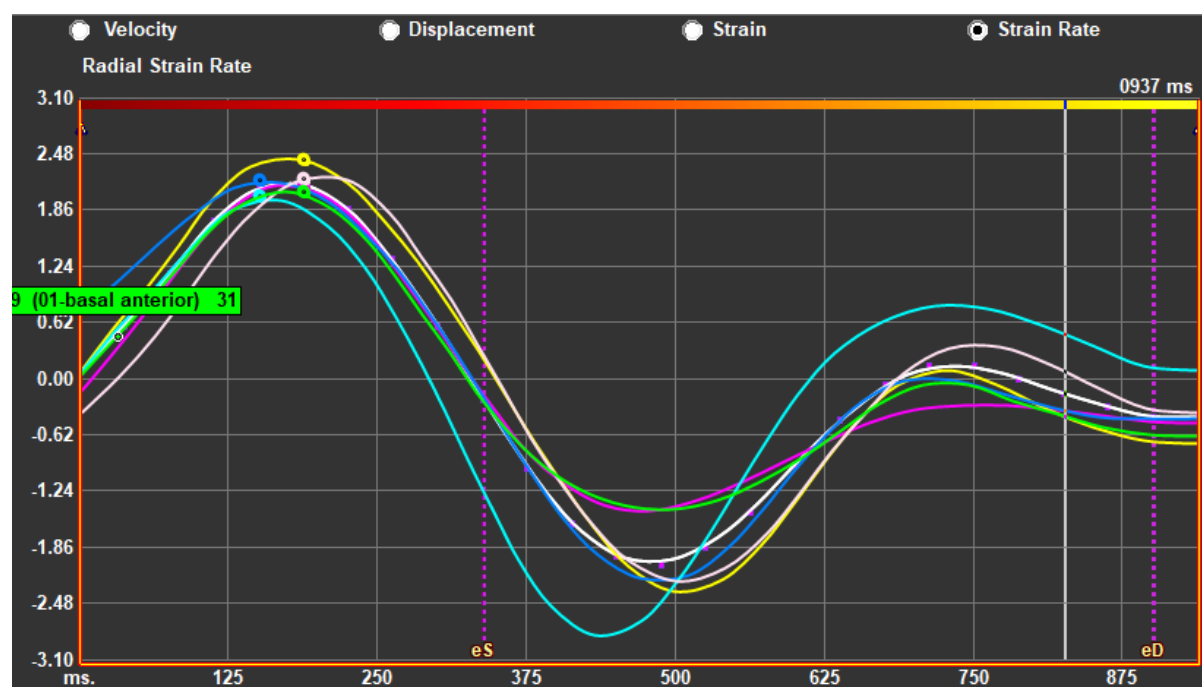
Figure 21: Select Strain Results Type

In the Time to Peak Segmental Analysis Window

- Select either 'Velocity', 'Displacement', 'Strain' or 'Strain Rate'.

To switch between Endocardium, Epicardium or Myocardium regional results.

In the Time to Peak Segmental Analysis Window

- Click ![icon] in the vertical toolbar for the Endocardial regional results.

- Click ![icon] in the vertical toolbar for the Epicardial regional results.

- Click ![icon] in the vertical toolbar for the Myocardial regional results.

2.5.4   3D Movie

QStrain has a 2D/3D view to assist in the visualization of strain whilst performing a strain analysis.
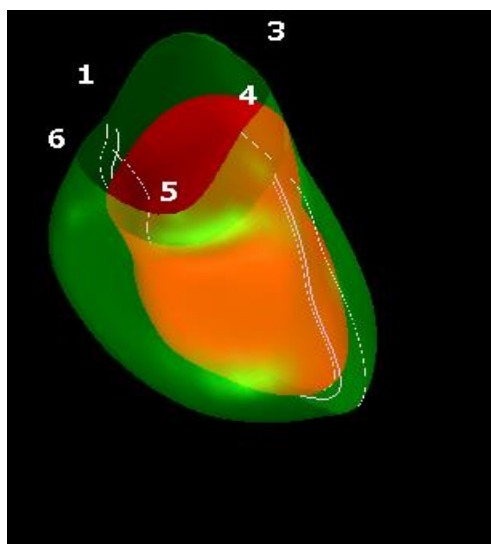
Figure 232: 3D View of Strain

To enable 3D view

- Load and complete an analysis of at least 2 LAX series.

- In the analysis viewport, click ![3d/2d icon] in the vertical toolbar.

2.5.5   Inward Displacement

Inward Displacement is a value defined for each point of the endocardial border, which represents the component of the displacement vector that is directed toward the "center of contraction". Such center is defined as a point on the LV axis whose position ranges from one half and two-third

of the base-apex distance, for the basal to the apical regions, respectively. Inward Displacement computation is carried out only for LAX data.

Inward Displacement is measured starting from the end-diastolic frame, assumed as the rest position. It, therefore, normally increases during systole to reach a positive peak value at end-systole and decrease during diastole to eventually return to zero at end-diastole.

Normalized Inward Displacement (ID %)

Inward Displacement is measured in mm. Moreover, it is normalized with the initial (end-diastolic), local distance to the LV center and expressed in %, where 0% means no contraction and 100% corresponds to a theoretical limit of a regional end-systolic size that shrinks to zero.

Inward Index (II %)

Inward Index (II) is an index that shows the relation between the inward displacement (ID) and a standard reference value (IIsv). Inward Index is computed as ID/IDsv*100 and is expressed in percentage.

Inward Displacement display in Analysis Page

The Inward Displacement measurements are done for each segment individually and are shown in 17-segment AHA model in Analysis window.

The standard deviation calculated on the segmental inward displacement (SD-ID) and inward index (SD-II) are shown as Results section.

In addition, Inward Displacement peak %, Time to peak % and Phase % can be viewed by making selection in vertical toolbar.
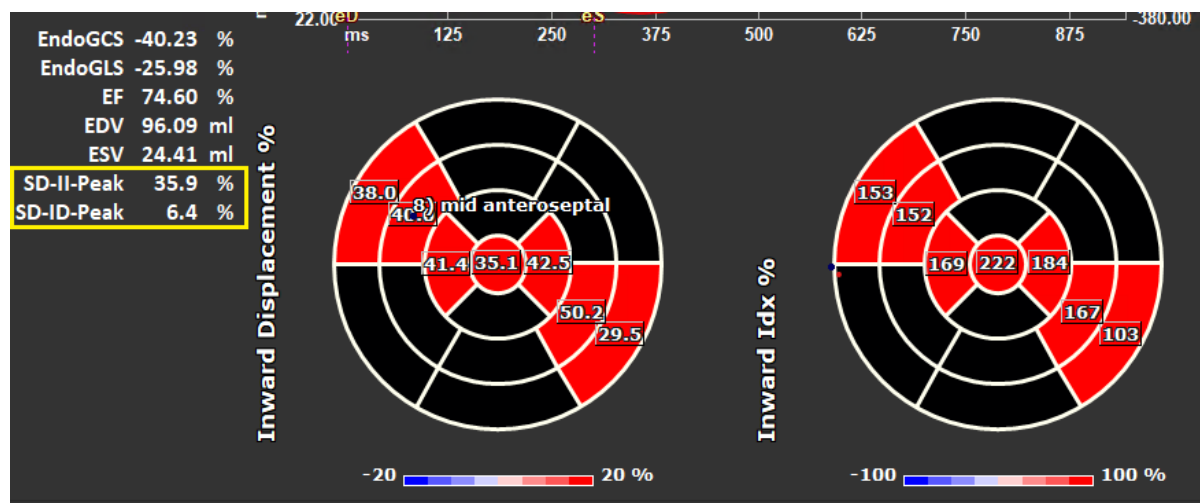
Figure 243: Inward Displacement results

To view the Inward Displacement 17 segment AHA model and results

- In the analysis viewport, select the "Inward Displacement" ☑ Inward Displacement checkbox in the vertical toolbar.
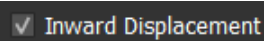
On selecting InwD checkbox, the strain results in 17 segment AHA model are replaced by InwD results. To view the strain results again, select "Strain" ☑ Strain checkbox.

2.5.6   Image position

The spatial positioning of an image can be automatically or manually flipped.

To start automatic image position correction

- After completing the series selection and analysis in the 'Series & Analysis Selection Window', click ➡ in the vertical toolbar.
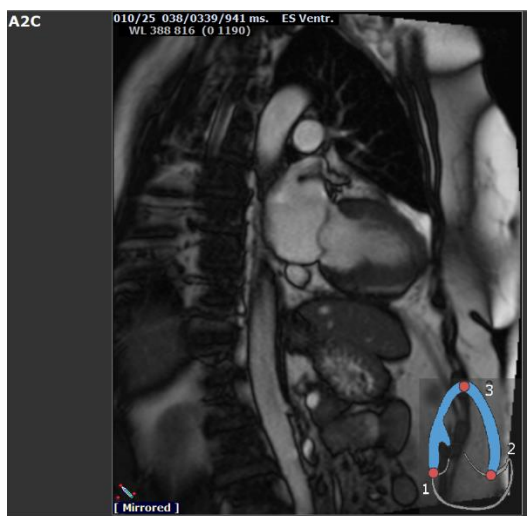
Figure 25 : Before Image Position Flip
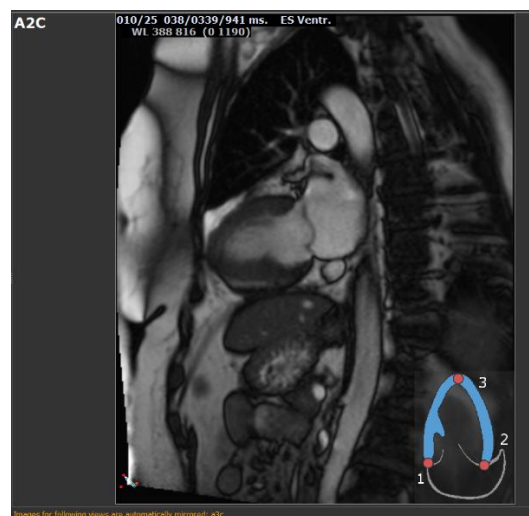
Figure 26 : After Image Position Flip

To manually flip a series

- In the analysis viewport, click 🔀 .

Or,

- In the 'ES Contour Review & Modification Window', click 🔀 .

Or,

- In the Sequence / M-Mode Selection Window, click 🔀 .

🛑 The user must ensure that spatial position is accurate. Flipping can modify the results. Make sure to review the spatial position is accurate and correct it if necessary.

🛑 A warning message will indicate that the image has been flipped manually or automatically. Make sure to review results and correct if necessary.

<div style="text-align: right">

Results

</div>

3   QStrain Results

The QStrain results are visible in QStrain, in the Medis Suite Findings and the Medis Suite Report. SnapShots and movies may also be added to the results. QStrain analysis provides the following sets of strain results.

- Global
- Standard Regional
- Detailed Regional (Time to Peak Analysis)

The primary strain results are as follows.

- Global Radial Strain   (GRS)
- Global Circumference Strain   (GCS)
- Global longitudinal Strain   (GLS)

⊙   Refer to

Results Overview for further details on the Results
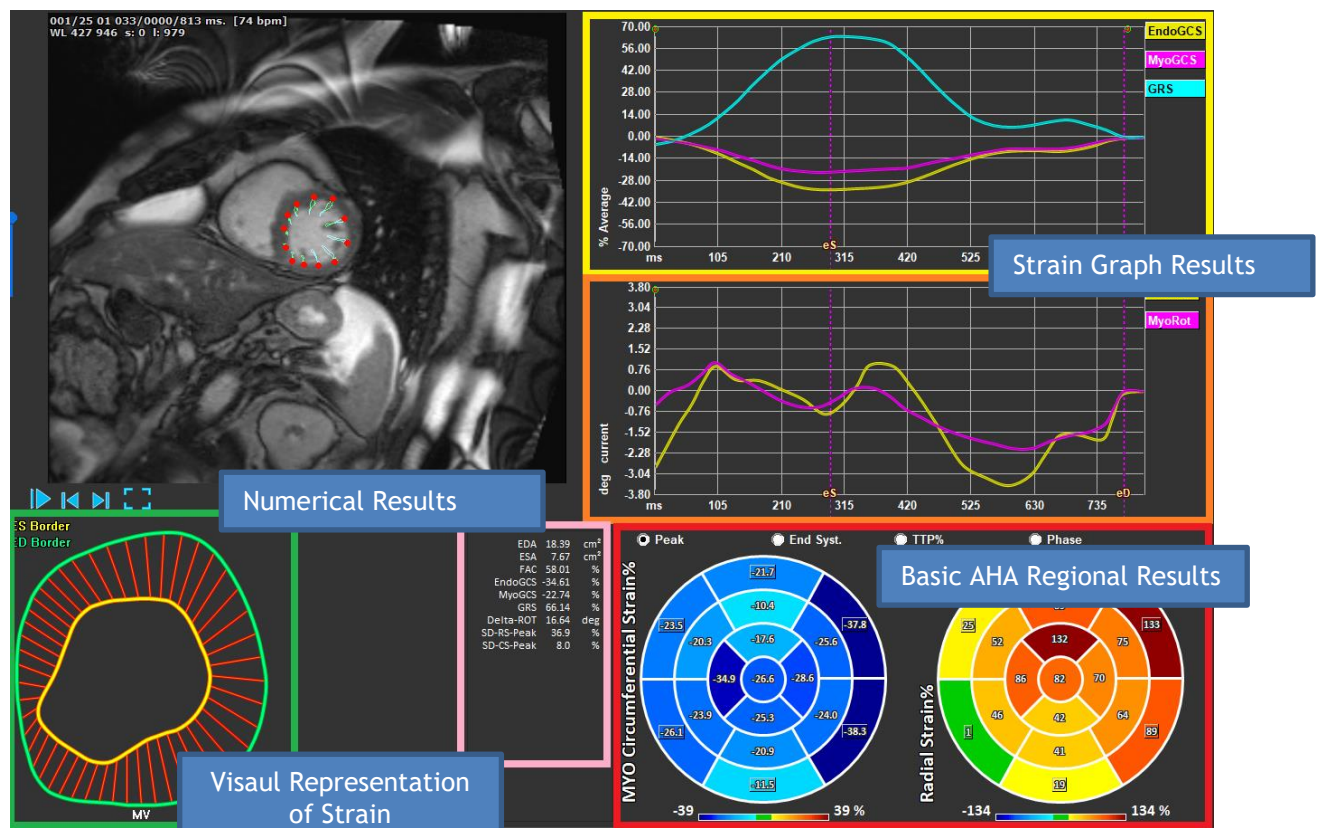
Figure 27: Results Sections Overview

3.1 Global Strain Results Graphs

The global results are accessible from the analysis window. There are two graphical results graphs. The upper graph shows Global Strain curves, while the lowers shows Rotational Strain curves in LV SAX analysis and Area Curves in the LV LAX, Left Atrium, Right Atrium and RV analysis.
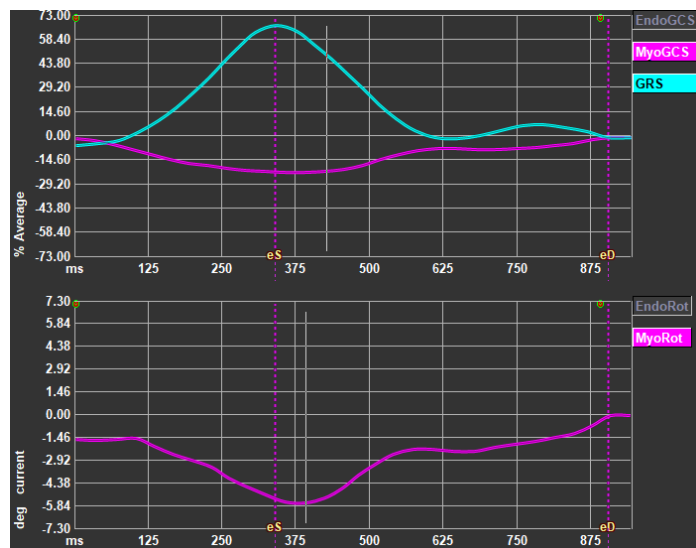
Figure 28: Analysis Strain Graphs

To enable Strain Rate curve

In the analysis viewport, select the checkbox Strainrate Curve in the vertical toolbar.

To set ES and ED phases after processing

When the processing of the global results is produced, ES and ED phases are set according to the average volume or area curves. However, the ES and ED phases can be moved manually acting on these graphs: the time position of these phases can be shifted by pressing the mouse on the ES and ED vertical cursors and releasing them at the desired position.

ⓘ Myocardial Strain results are available when both Endo and Epi contours are available.

ⓘ The rotation strain is slice dependent and therefore reflects the strain of the selected slice.

3.2 Global Strain Numerical Results

The numerical global results are accessible from the analysis window.
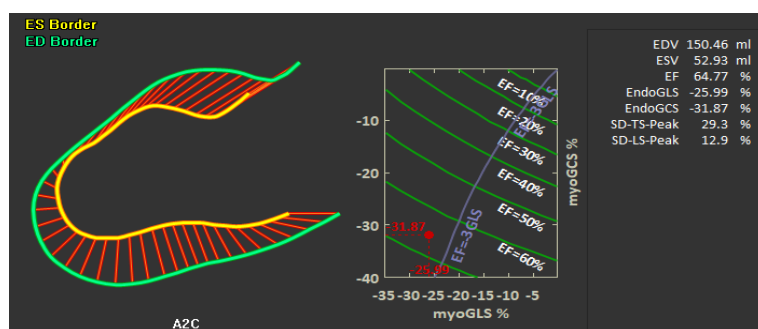
Figure 29: LAX Numerical Results
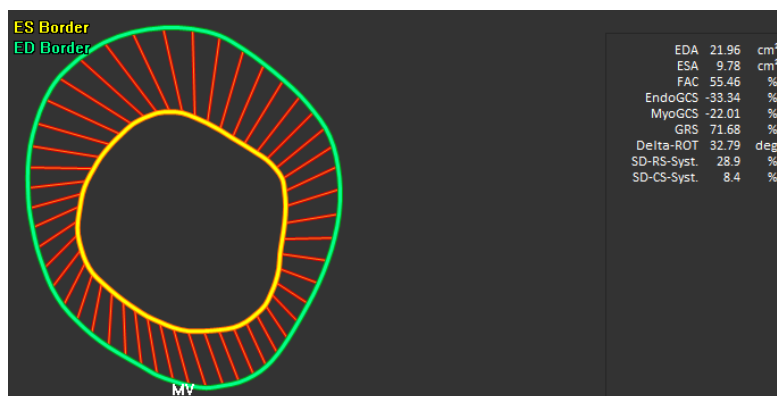
Figure 30: SAX Numerical Results

3.3 Standard Regional Strain Results

The standard regional results are accessible from the analysis window.
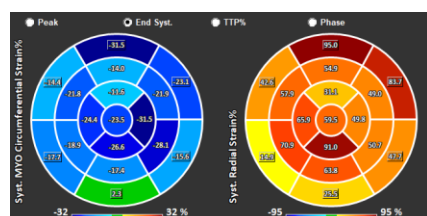
Figure 31: Standard Regional Results

3.4 Detailed Regional Results (Time To Peak)

Detailed regional results are accessible from the Time to Peak Segmental Analysis Window.

Figure 32: Detailed Regional Results. TTP

4   Results Overview

The following lists define the results that are available from each QStrain analysis.

4.1 LV long axis (LV LAX) results

QStrain provides the following list of results:

- EDV
- ESV
- EF
- Endo GLS
- Endo GCS
- Myo GLS (Only if EPI contour is segmented)
- Myo GCS (Only if EPI contour is segmented)
- GRS (Only if EPI contour is segmented)
- SD-LS-Peak (Only when Peak AHA view is selected)
- SD-TS-Peak (Only when Peak AHA view is selected, and EPI contour is segmented)
- SD-LS-Syst. (Only when End Syst. AHA view is selected)
- SD-TS-Syst. (Only when End Sys. AHA view is selected, and EPI contour is segmented)
- SD-Ttp%-LS (Only when TTP% AHA view is selected)
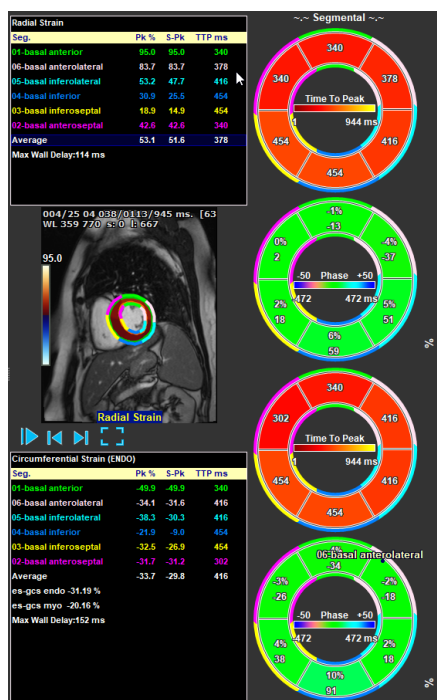- SD-Ttp%-TS (Only when TTP% AHA view is selected, and EPI contour is segmented)
- SD-Ph%-LS (Only when Phase AHA view is selected)
- SD-Ph%-TS (Only when Phase AHA view is selected, and EPI contour is segmented)
- SD-II-Peak - % (only when Peak AHA view and Inward Displacement is selected)
- SD-ID-Peak - % (only when Peak AHA view and Inward Displacement is selected)
- SD-II-Syst. - % (only when End Syst. AHA view and Inward Displacement is selected)
- SD-ID-Syst. - % (only when End Sys. AHA view and Inward Displacement is selected)
- SD-Ttp%-ID - % (only when TTP% AHA view and Inward Displacement is selected)
- SD-Ph%-ID – % (only when Phase AHA view and Inward Displacement is selected)

4.2 LV Short axis (LV SAX) results

QStrain provides the following list of results:

- EDA
- ESA
- FAC
- Endo Rot
- Endo GCS
- Myo Rot (Only if EPI contour is segmented)
- Myo GCS (Only if EPI contour is segmented)
- GRS (Only if EPI contour is segmented)
- Delta Rot (Only when all slices in LV-SAX are present)
- SD-CS-Peak (Only when Peak AHA view is selected)
- SD-RS-Peak (Only when Peak AHA view is selected, and EPI contour is segmented)
- SD-CS-Syst. (Only when End Syst. AHA view is selected)
- SD-RS-Syst. (Only when End Syst. AHA view is selected, and EPI contour is segmented)
- SD-Ttp%-CS (Only when TTP% AHA view is selected)
- SD-Ttp%-RS (Only when TTP% AHA view is selected, and EPI contour is segmented)

- SD-Ph%-CS (Only when Phase AHA view is selected)
- SD-Ph%-RS (Only when Phase AHA view is selected, and EPI contour is segmented)

4.3 Left Atrium or Right Atrium results

QStrain provides the following list of results:

- EDV
- ESV
- EF
- Endo GLS
- Endo GCS
- FAC

4.4 RV long axis (Right Ventricle)

QStrain provides the following list of results:

- EDA
- ESA
- FAC
- Endo GLS
- Myo GLS (Only when EPI contour is segmented)
- GRS (Only when EPI contour is segmented)

5   Reporting

QStrain results are made available in the Medis Suite Results pane and in the Medis Suite report.

Figure 33 : Medis Suite Report with QStrain Results

The Reporting functionality of Medis Suite is described in the Medis Suite user manual. The Medis Suite documentation is available from the User documents tab, which can be opened as follows;

- Press F1.

- Pushing the ![help] help button.

- Select the Medis Suite main menu button in the upper right corner ![menu] > **Help** > **User Documents**

6 Sessions

The QStrain state can be saved in a Medis Suite session. The session can be reloaded to continue or review the analyses.

The session functionality in Medis Suite is described in the Medis Suite user manual. The Medis Suite documentation is available from the User documents tab, which can be opened as follows;

- Press F1.

- Pushing the help button.

- Select the Medis Suite main menu button in the upper right corner > **Help** > **User Documents**

Shortcut Keys

When you are working with QStrain, you can use several combinations of keys on your keyboard and mouse actions to quickly perform the following tasks.

Press	To
Layout	
F11	Show or hide the workspace windowpanes
Image control	
Scroll wheel	Zoom
Procedures	
Navigation Controls	
Arrow left	Display the previous time point
Arrow right	Display the next time point

7   Parameters / Measurements

7.1 Strain Parameters

GLS   Global Longitudinal Strain

GRS   Global Radial Strain

GCS   Global Circumferential Strain

MyoRot   Myocardial Rotation

Delta-ROT   Delta Rotation, difference between basal and apical rotation

Pk%   Peak strain value as a percentage

S-Pk   Strain value at ES as a percentage

TTP ms   Time to peak in milliseconds

7.2 Velocity Parameters

Pk   Peak velocity

S-Pk   Velocity at ES

TTP ms   Time to the peak velocity in milliseconds

7.3 Displacement Parameters

Pk   Maximum displacement

S-Pk   Displacement at ES

TTP ms   Time to the maximum displacement in milliseconds

7.4 Strain Rate Parameters

Pk 1/s   Strain rate peak in 1/s

S-Pk   Strain rate at ES in 1/s

TTP ms   Time to the strain rate peak in milliseconds

7.5 General Parameters

ED	End diastolic phase
ES	End systolic phase
EDA	ED Area
ESA	ES Area
FAC	Fraction Area Change
EDV	ED Volume
ESV	ES Volume
EF	Ejection Fraction
TTP	Time to Peak
Max Wall Delay	Difference between lowest and highest TTP

Appendix I. Main Cardiac Mechanics Variables Derived from Tracking Technology

For further reading, see the following articles:

Tissue Tracking Technology for Assessing Cardiac Mechanics
Piet Claus, PHD, Alaa Mabrouk Salem Omar, MD, PHD, Gianni Pedrizzetti, PHD, Partho P. Sengupta, MD, DM, Eike Nagel, MD, PHD

Table 2 Main Cardiac Mechanics Variables Derived From Tracking Technology

Main Cardiac Mechanics Variables Derived From Tracking Technology		
	Definition	Parameters
Displacement, cm	Distance between instantaneous and initial (often end-diastolic) position of a myocardial segment	Longitudinal displacement Radial displacement Circumferential displacement
Velocity, cm/s	Velocity of displacement (displacement/time) accuracy is highly frame-rate dependent	Longitudinal velocity Radial velocity Circumferential velocity
Strain, %	Change in length of an object within a certain direction relative to its initial (often enddiastolic) length	Global/segmental longitudinal strain (GLS/LS) Global/segmental radial strain (GRS/RS) Global/segmental circumferential strain (GCS/CS)
Strain rate, 1/s	The speed of deformation accuracy is highly frame-rate dependent	Peak systolic global longitudinal strain rate (GLSR-S) Early diastolic global longitudinal strain rate (GLSR-E) Late diastolic global longitudinal strain rate (GLSR-A) Peak systolic global radial strain rate (GRSR-S) Early diastolic global radial strain rate (GRSR-E) Late diastolic global radial strain rate (GRSR-A) Peak systolic global circumferential strain rate (GCSR-S) Early diastolic global circumferential strain rate (GCSR-E) Late diastolic global circumferential strain rate (GCSR-A)
Rotation	Results from shortening and lengthening of helically oriented myocardial fibers causing counterclockwise rotation of the apex and clockwise rotation of the base as viewed from the apex	Peak systolic apical rotation (apical-R) Peak systolic basal rotation (basal-R) LV twist (LVT) LV torsion (LV-tor) Percentage of LV untwist at mitral valve opening (%LV-UT-MVO) LV untwist rate (LV-UTR) Time to peak untwist (TTP-UT)
LV ¼ left ventricular		

Appendix II. Accuracy of Measurements

Analysis on long axis data

		Unit	Expected accuracy	Precision QStrain	Precision Medis Suite report	Accuracy source
EDV	ED Volume	ml	2 %	0.01	0.1	AMID Accuracy document
ESV	ES Volume	ml	3 %	0.01	0.1	AMID Accuracy document
EF	Ejection Fraction	%	2	0.01	0.1	From EDV/ESV volume accuracy
EndoGLS	Global Longitudinal Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
EndoGCS	Global Circumferential Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
MyoGLS	Global Longitudinal Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
MyoGCS	Global Circumferential Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
GRS	Global Radial Strain	%	± 4.5	0.01	0.1	AMID Accuracy document
SD-TS-Peak	SD Transversal Strain Peak	%	± 1.5	0.1	0.1	Based on Strain accuracy
SD-LS-Peak	SD Longitudinal Strain Peak	%	± 1.5	0.1	0.1	Based on Strain accuracy
SD-TS-Syst	SD Transversal Strain End Systoly	%	± 1.5	0.1	0.1	Based on Strain accuracy
SD-LS-Syst	SD Longitudinal Strain End Systoly	%	± 1.5	0.1	0.1	Based on Strain accuracy

Analysis on short axis data

		Unit	Expected accuracy	Precision QStrain	Precision Medis Suite report	Accuracy source
EDA	ED Area	cm^2	1.5 %	0.01	0.1	AMID Accuracy document
ESA	ES Area	cm^2	4 %	0.01	0.1	AMID Accuracy document
FAC	Fraction Area Change	%	1	0.01	0.1	From EDA/ESA area accuracy
MyoGCS	Global Circumferential Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
EndoGCS	Global Circumferential Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
GRS	Global Rotational Strain	%	± 4.5	0.01	0.1	AMID Accuracy document
Delta-rot	Delta Rotation	°	1°	0.01	0.1	AMID Accuracy document
SD-RS-Peak	SD Rotational Strain Peak	%	± 4.5	0.1	0.1	Based on Strain accuracy

SD-CS-Peak	SD Circumferential Strain Peak	%	± 1.5	0.1	0.1	Based on Strain accuracy
SD-RS-Syst	SD Rotational Strain End Systoly	%	± 4.5	0.1	0.1	Based on Strain accuracy
SD-CS-Syst	SD Circumferential Strain End Systoly	%	± 1.5	0.1	0.1	Based on Strain accuracy

If the expected accuracy is a percentage, it is relative to the value. If no percentage is mentioned, it is an absolute error. In case the unit is %, interpret the error as percent-point.