

# QStrain 4.2

## Quick Start Manual

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# Getting Started

## 1 Workflow Overview

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														
<table border="1"> <tr><td>QStrain</td></tr> <tr><td>Select Series</td></tr> <tr><td>Select Analysis Type</td></tr> <tr><td></td></tr> <tr><td></td></tr> <tr><td></td></tr> <tr><td>Complete strain analysis</td></tr> </table>	QStrain	Select Series	Select Analysis Type				Complete strain analysis	<table border="1"> <tr><td>QStrain</td></tr> <tr><td>Select Series</td></tr> <tr><td>Select Analysis Type</td></tr> <tr><td><b>Manually</b> draw contours</td></tr> <tr><td>Review Contours</td></tr> <tr><td>Verify ED &amp; ES phase</td></tr> <tr><td>Complete strain analysis</td></tr> </table>	QStrain	Select Series	Select Analysis Type	<b>Manually</b> draw contours	Review Contours	Verify ED & ES phase	Complete strain analysis
QStrain															
Select Series															
Select Analysis Type															
Complete strain analysis															
QStrain															
Select Series															
Select Analysis Type															
<b>Manually</b> draw contours															
Review Contours															
Verify ED & ES phase															
Complete strain analysis															

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

## 2 Workflow: Performing a QStrain Analysis

QStrain application supports the following strain related analyses.

- LV long axis (Apical)
- LV short axis (SAX)
- Atrial images (Atrium)
- RV images (Right Ventricle)

To navigate through the analysis steps.

- Click  in the vertical toolbar to continue to the next stage of an analysis.
- Click  in the vertical toolbar to go to the previous stage of an analysis.
- Click  in the vertical toolbar to go to the Loading a Series & Analysis stage.
- In the ED/ES Review viewport, click  to accept and click  to reject contour changes.
- In the Sequence M-Mode Selection window click  to return to the analysis.
- In the Time to Peak Segmental Analysis window click  to return to the analysis.

### 2.1 QStrain Analysis General Steps

QStrain analyses share the same steps.

- Loading Series
- Analysis Selection
- Creating Contours
- Completing Global Strain Analysis.
  - Optional: SAX Analysis: Add a reference point, for each slice.
  - ED ES Phase Review: Sequence M-Mode
  - Complete detailed Regional analysis, in the Time to Peak Analysis.

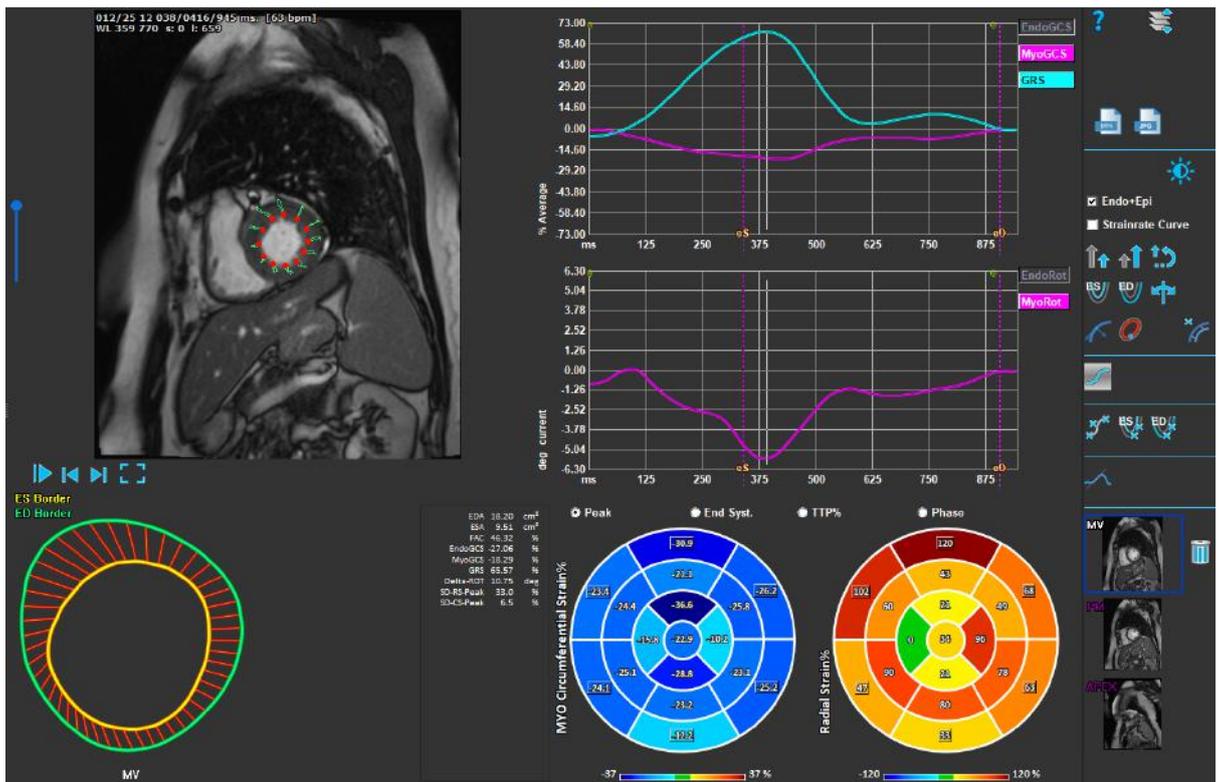


Figure 1 : SAX Analysis

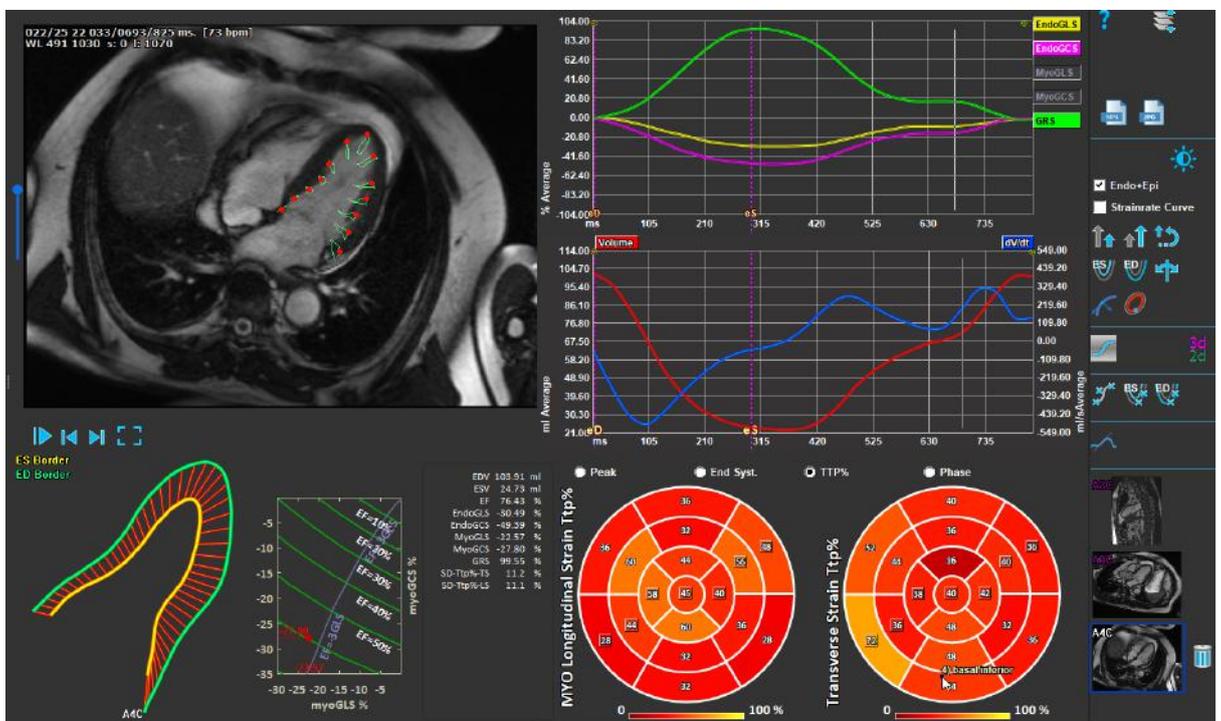


Figure 2 : LAX Analysis

## 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** (Apical)
- **LV short axis** (SAX)
- **Atrial** (Atrium)
- **RV** (Right Ventricle)

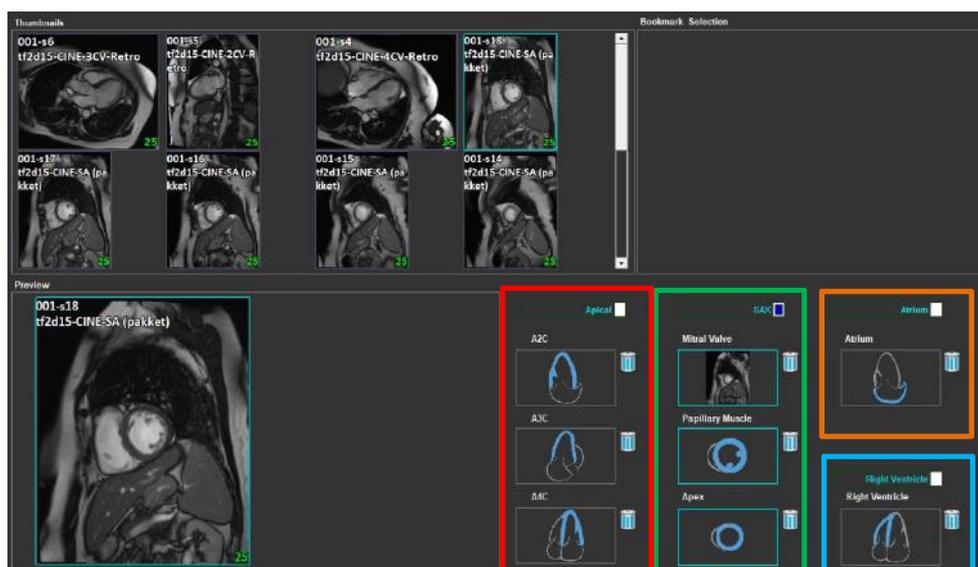


Figure 3 : Series & Analysis Selection

Series selection.

- Select a series from the left viewport.

**Couple a series with an image orientation.**

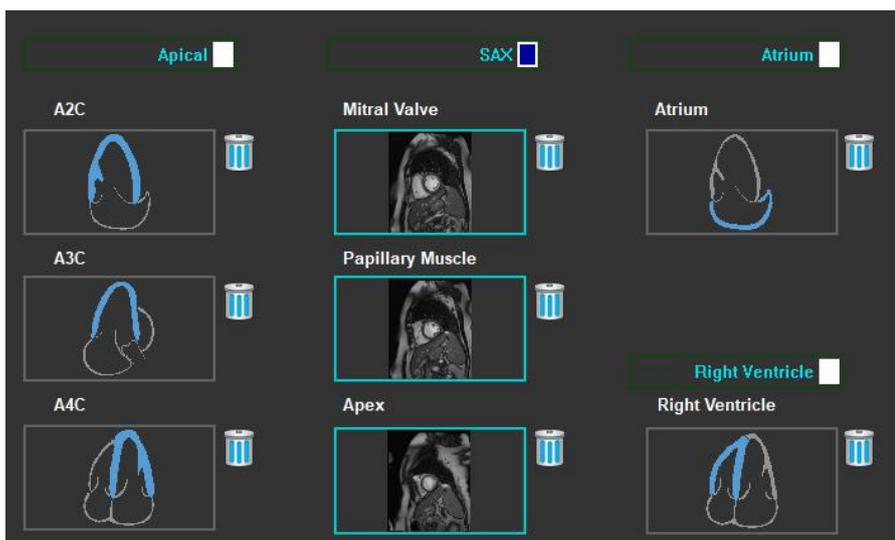


Figure 4 : Couple a series with an orientation

**Choose the analysis type.**

- Check the checkbox of the analysis to perform.

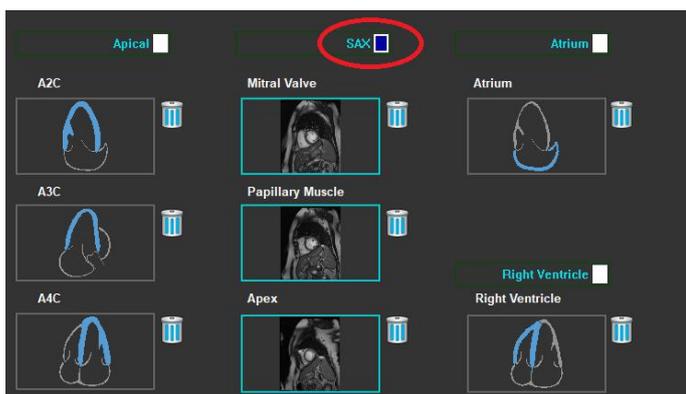


Figure 5 : Select QStrain Analysis Type

- ⚠ 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. LAX and SAX analyses facilitate up to three series, each representing one slice. Atrium and RV analyses are limited to one series.

**To couple a series with a 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 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 an 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

## 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 imported from QMass, the Contour Editing workflow of the analysis is automatically surpassed.

### 2.4.1 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 ES or ED contour editing and review windows or the contours may be imported with the selected series.

#### 2.4.1.1 Enable the Contour Creation window.

- After completing the series selection and analysis in the Series 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.

#### 2.4.1.2 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.

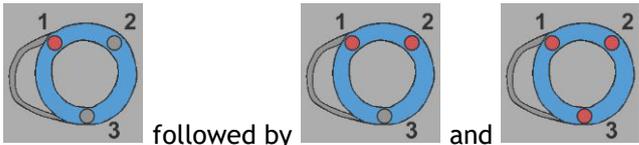
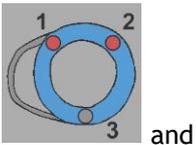
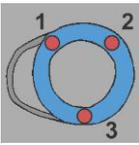
! Clear the check box Endo + Epi to generate the Endo contour only.

## 2.4.2 Creating Contours by Indicators

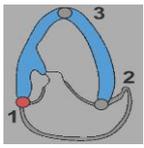
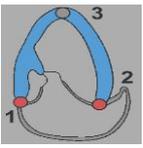
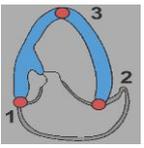
In the bottom right corner of the Contour Editing viewport, a contour position indicator recommends the ideal position placement of the progressive contour points.

### 2.4.2.1 Contour Point Indicators (SAX)

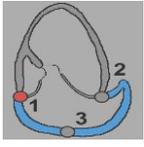
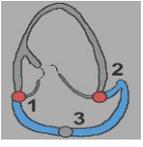
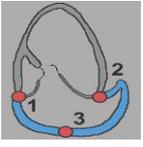
SAX

SAX placement indicators as follows,  followed by  and .

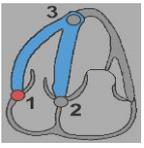
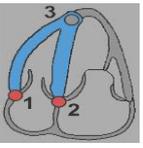
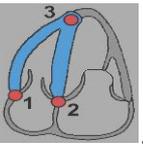
LAX

LAX placement indicators are as follows,  followed by  and .

Atrium

Atrium placement indicators are as follows,  followed by  and .

RV

RV placement indicators are as follows,  followed by  and .

## 2.4.3 Editing Contours

### 2.4.3.1 To modify contours

To modify an existing contour.

1. Hover the mouse cursor over the contour edit point to be modified.

2. Click and drag the mouse to move the contour edit point.
3. Release the mouse to set the edit point.

### 2.4.3.2 To remove all contour points.

1. Click on the edit point  in the vertical toolbar.

### 2.4.3.3 To remove a contour point.

1. Hoover the mouse cursor over the contour edit point to be removed.

Right-click to the contour edit point.

## 2.4.4 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

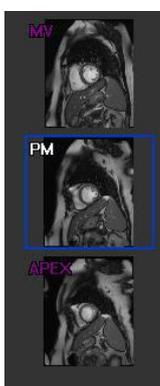
The vertical toolbar in the analysis window, contains utilities that assist in the strain analysis workflow.

### 2.5.1 Creating a Reference Point for SAX Analysis

Reference points enhance the accuracy of the results.

To set a reference point in a SAX analysis.

- Choose the SAX a slice from the vertical toolbar.



- Select the  in the vertical toolbar.
- Click on the Anterior Septum.
- Click Confirm.

 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 window facilitates updating 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.

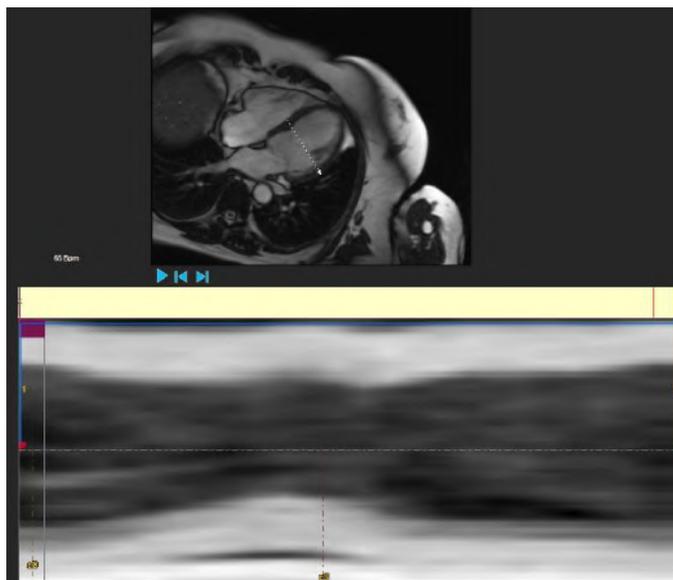


Figure 6 : Sequence M-Mode ED ES Phase Review

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.

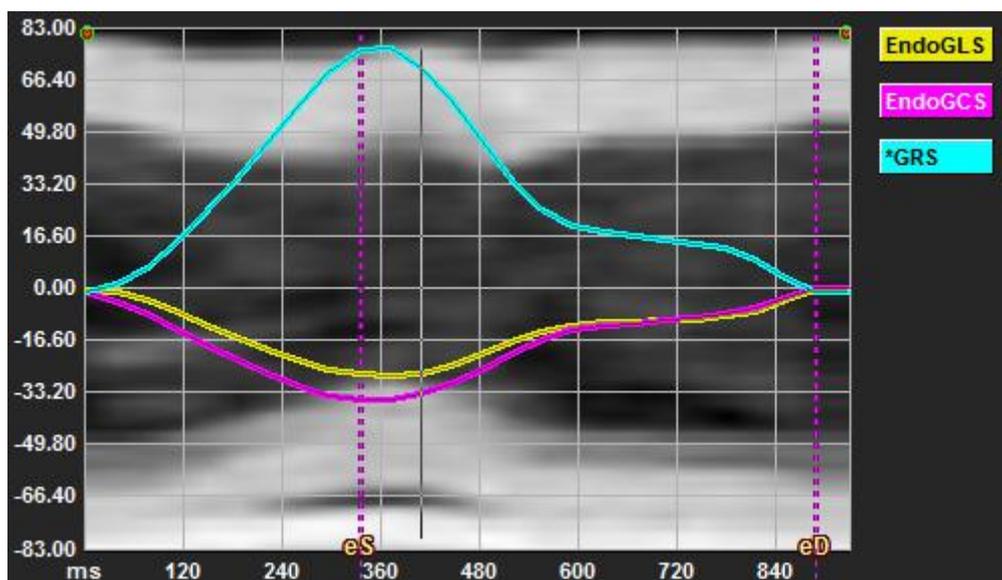


Figure 7 : M-Mode Overlay in Analysis Window Volume Graph

**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	Anterolateral	Mid	Anterolateral	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 analysis window:

- Hover over the Segment model.

Or,

- Hover over the graphs.

To enable / disable a region.

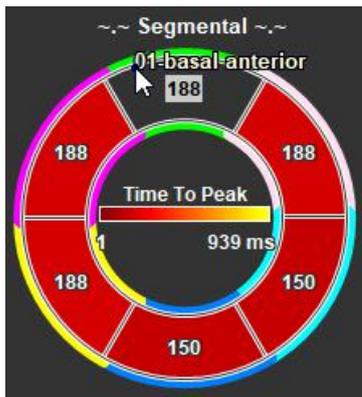


Figure 8 : Enable/Disable SAX TTP Region

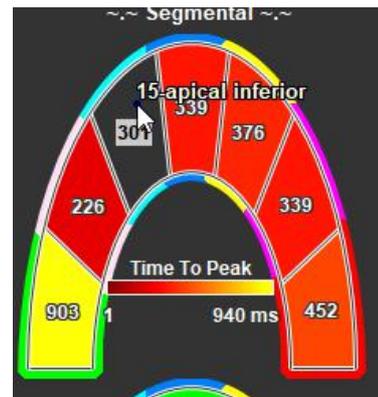


Figure 9 : Enable / Disable LAX TTP Region

In the Time to Peak analysis window.

- Click the segment to enable or disable.

To enable / disable all regions.

In the Time to Peak analysis window.

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

To switch regional analysis type.

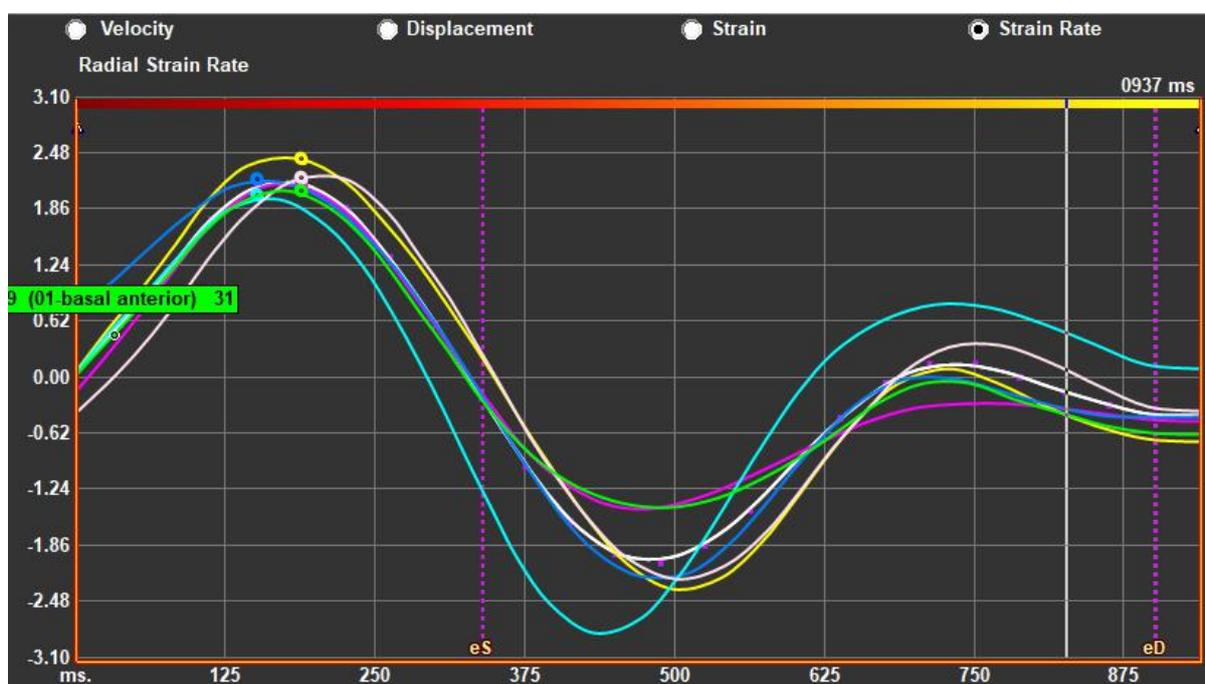


Figure 10 : Select Strain Results Type

In the Time to Peak analysis window.

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

To switch between Endocardium, Epicardium or Myocardium regional results.

In the Time to Peak analysis window.

- Click  in the vertical toolbar for the Endocardial regional results.
- Click  in the vertical toolbar for the Epicardial regional results.
- Click  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.

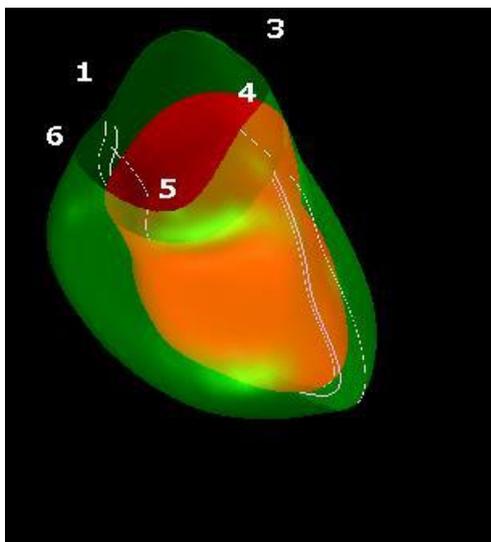


Figure 11 : 3D View of Strain

To enable 3D view

- Load and complete an analysis of at least 2 LAX series.
- In the analysis viewport, click  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  $ID/IIsv \times 100$  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.

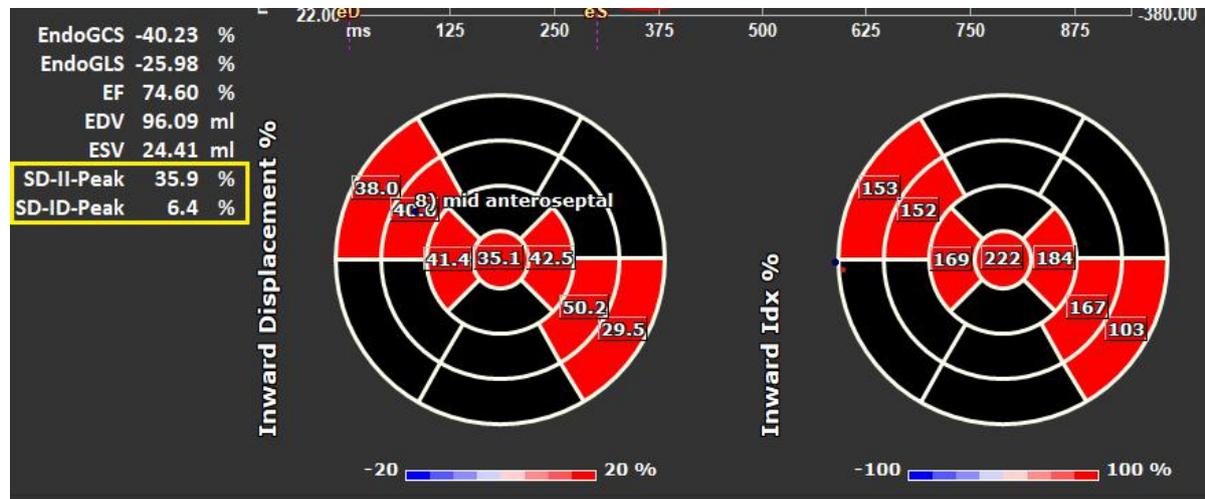


Figure 12 : Inward Displacement results

### To view the Inward Displacement 17 segment AHA model and results

- In the analysis viewport, select the “Inward Displacement” checkbox in the vertical toolbar.  Inward Displacement

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.

# Results

## 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

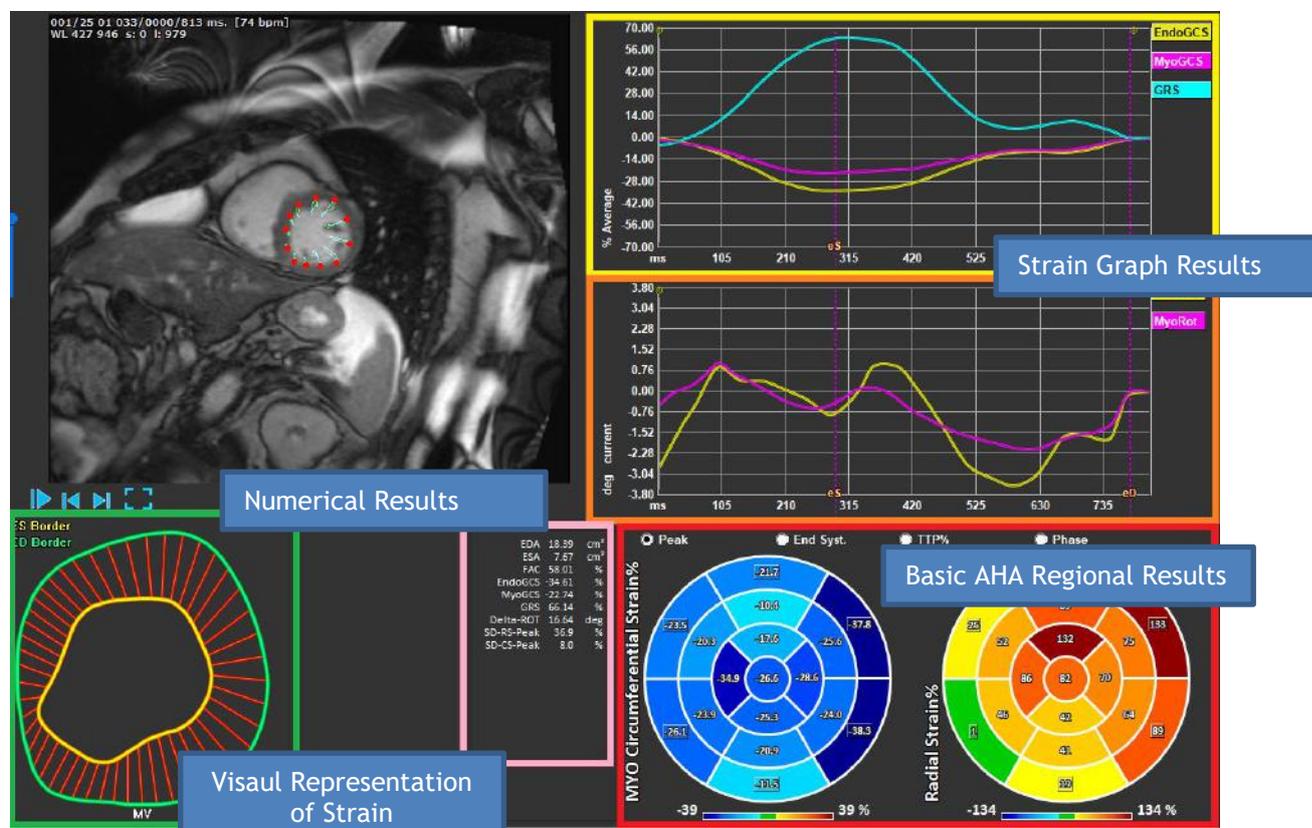


Figure 13 : Results Sections Overview

## 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 lower shows Rotational Strain curves in SAX analysis and Area Curves in the LAX, Atrium and RV analysis.

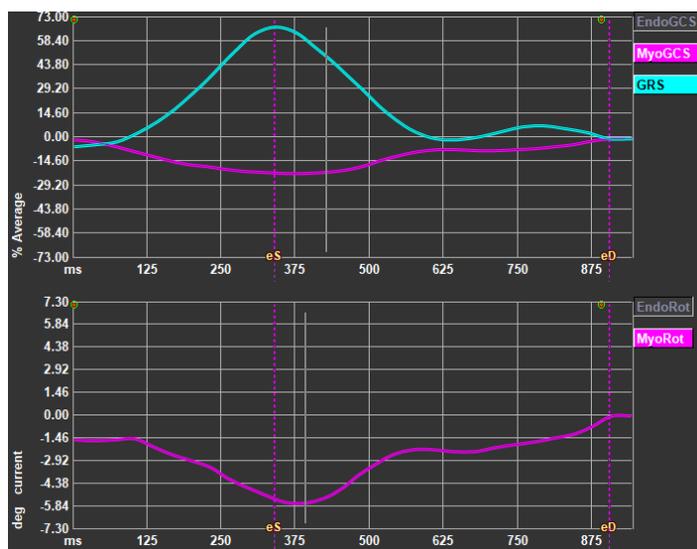


Figure 14 : Analysis Strain Graphs

### To enable Strain Rate curve

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

- ⓘ 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.ndo

## 3.2 Global Strain Numerical Results

The numerical global results are accessible from the analysis window.

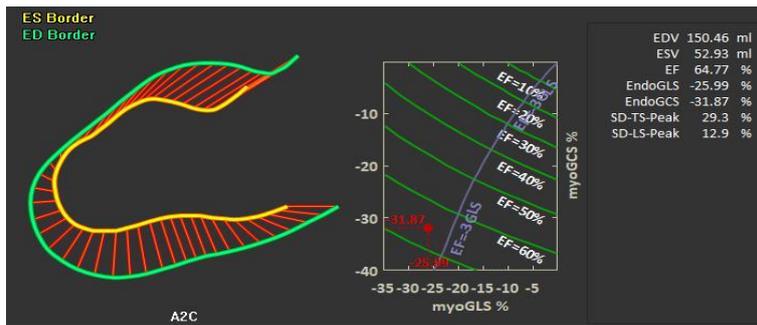


Figure 15 : LAX Numerical Results

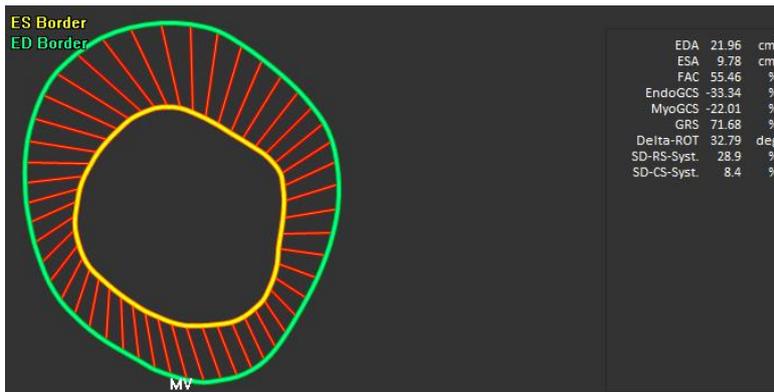


Figure 16 : SAX Numerical Results

### 3.3 Standard Regional Strain Results

The standard regional results are accessible from the analysis window.

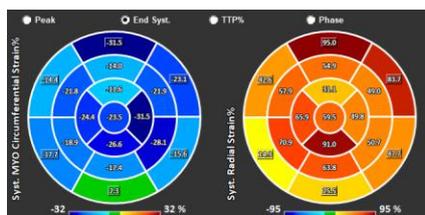


Figure 17 : Standard Regional Results

### 3.4 Detailed Regional Results (Time To Peak)

Detailed regional results are accessible from the analysis window.



Figure 18 : 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 (Apical) 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)

### 4.2 Short axis (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 SAX-LV 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 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.

The screenshot displays the Medis Suite Report interface. On the left is a navigation pane with sections like Patient Study Info, Reason for Referral, Technique, Viewer, and V QFlow 4D Stable Daily 1.0 #1. The main area shows the report content, including Patient Study Info, Reason for Referral, and QFlow 4D Stable Daily 1.0 #1. The QFlow section details background correction and flow volume data for two slices.

QFlow 4D Stable Daily 1.0 #1			
Background Correction			
Fitting Order:	1		
Std Threshold:	25%		
Reconstruction 01 Results ROI 1:[ROI 1] slice 1			
ROI 1:[ROI 1] slice 1	per HB	per Minute	
Net flow volume	34.17 ml/beat	3.04 l/min	
Forward flow volume (S.1)	34.45 ml/beat	3.06 l/min	
Backward flow volume (S.1)	0.27 ml/beat	0.02 l/min	
Regurgitant fraction (S.1)	0.80 %		
Reconstruction 01 Results ROI 2:[ROI 2] slice 1			
ROI 2:[ROI 2] slice 1	per HB	per Minute	
Net flow volume	-14.14 ml/beat	-1.26 l/min	
Forward flow volume (S.1)	18.95 ml/beat	1.68 l/min	
Backward flow volume (S.1)	4.81 ml/beat	0.43 l/min	
Regurgitant fraction (S.1)	25.39 %		

Figure 19 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 button.
- Select the Medis Suite main menu button in the upper right corner  > **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**

## 7 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
<b>Layout</b>	
F11	Show or hide the workspace windowpanes
<b>Image control</b>	
Scroll wheel	Zoom
<b>Procedures</b>	
<b>Navigation Controls</b>	
Arrow left	Display the previous time point
Arrow right	Display the next time point

## 8 Parameters / Measurements

### 8.1 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

### 8.2 Velocity Parameters

Pk	Peak velocity
S-Pk	Velocity at ES
TTP ms	Time to the peak velocity in milliseconds

### 8.3 Displacement Parameters

Pk	Maximum displacement
S-Pk	Displacement at ES
TTP ms	Time to the maximum displacement in milliseconds

### 8.4 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

## 8.5 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