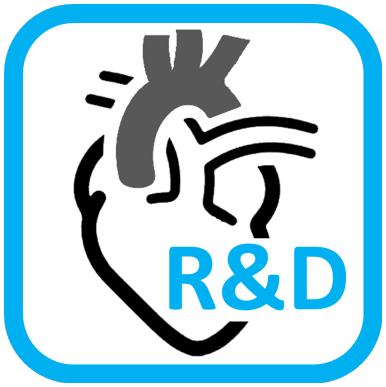
Strain analysis in Segment - User Manual



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Contents

1 Conventions and Abbreviations

This chapter describes the typographic conventions and used abbreviations in this manual and in the program.

1.1 Typographic conventions

	Caution used with the safety alert symbol, indicates a hazardous situation which, if not avoided, could result in minor or moderate injury or material damage.
	Information intended to help the user achieve optimal use of the software. Includes usage considerations, limitations, or recommendations that do not relate to safety.
	A reminder to the user of their responsibilities under applicable regulatory requirements.
`A`	Key `A` at the keyboard.
`Ctrl-A`	Control key. Hold down `Ctrl` key and `A` simultaneously.
	Icon in toolbar.
`*.mat`	Filename extension.
`C:/Program`	Folder.
File	Menu, e.g. File menu.
File→Save As	Sub menu, e.g. under the File menu the item Save As is found.
Close	Push/Toggle button in the graphical user interface.

1.2 Abbreviations

Circumf.	circumferential
CMR	Cardiac Magnetic Resonance
ED	Endo-Diastole
ES	Endo-Systole
GCS	Global Circumferential Strain
GLS	Global Longitudinal Strain
GRS	Global Radial Strain
Longit.	longitudinal
LA	Left Atrium
LV	Left Ventricle
RV	Right Atrium
RV	Right Ventricle

1.3 System requirements

- Operating System:

  - Windows 11
  - Windows Server 2019

- Processor: Any Intel or AMD x86-64 processor with a minimum of four logical cores
- Computer with 8 GB of memory or preferably 16 GB
- Harddisk with at least 5 GB of available space
- Graphics card supporting both DirectX and OpenGL
- To use the full functionality of the report function:
  - Microsoft Word
  - Adobe PDF reader
- To access full version of machine learning algorithms in Segment:
  - CUDA enabled NVIDIA graphics card with 4 GB memory or more
  - GPU architecture: Ampere, Turing, Volta, Pascal
- For users with additional modules not included in the free research version:
  - Internet connection for software license management and software download. We recommend a speed of at least 24 Mbit/s.

Recommendations

- Systems with two screens
- Using SSD disk for reading data

2 Software overview

An overview of Segment is given in Figure 1. The letters (a-p) in the figure will be used as references throughout this manual.

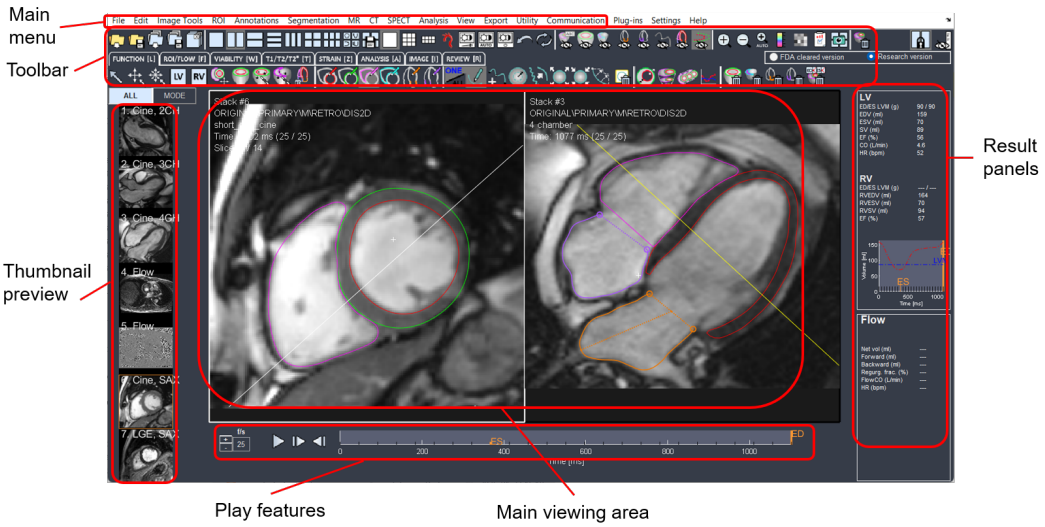


Figure 1: Main graphical user interface. The letters (a-p) in the figure will be used as references throughout this manual.

To learn more about each tool, hold the mouse over the icon in the software and a help text will be displayed.

3 Loading and storing Data

3.1 Loading data

To load patient data from the database, follow Section 3.1.1. To load patient data from PACS, follow Section 3.1.2. To load patient data from network disc, follow Section 3.1.3.

3.1.1 Loading data from database

1. Select Open from Database in the File menu (a), Figure 2 is shown.

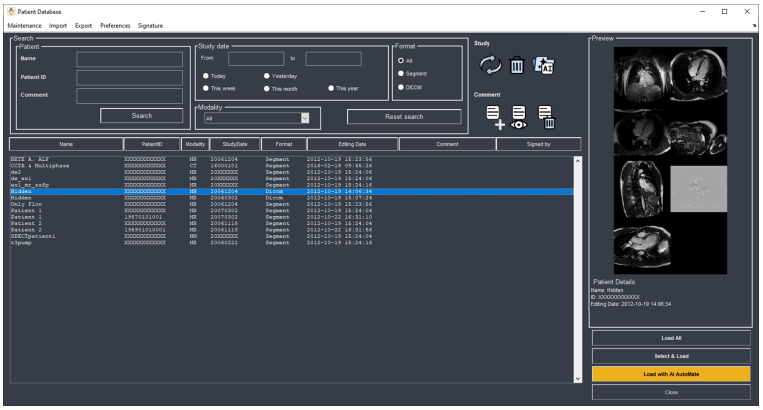


Figure 2: Graphical patient selector.

2. Select patient.

3. Patients can be stored in two formats; DICOM, or Segment format. For images in DICOM format, click Select & Load, Figure 3 is shown. For images in Segment format click Load all.

4. Select image series to load in Figure 3.

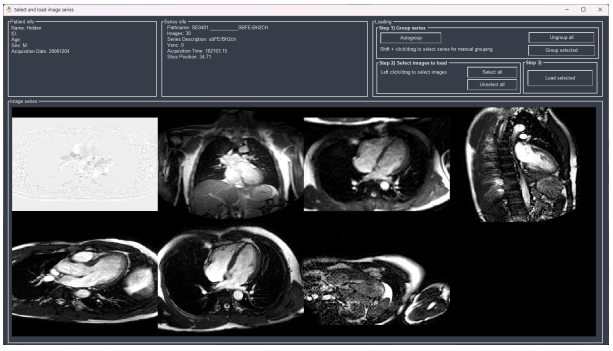


Figure 3: Graphical image series selector.

5. Click on Load.

3.1.2 Loading data from PACS

1. Select Import from PACS in the File menu, Figure 4 is shown.

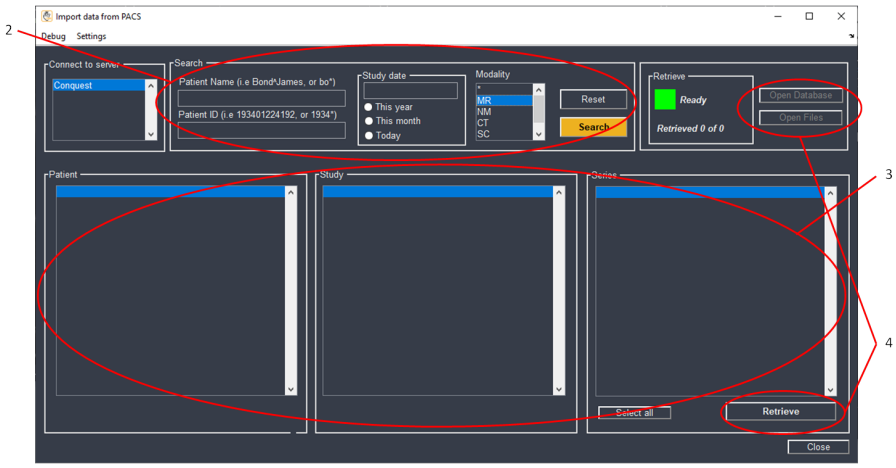


Figure 4: Interface to import image stacks from PACS.

2. Enter patient or study details and perform search.
3. Select study and series to load.
4. Load the study into Segment by select Open files.

3.1.3 Loading data from network disc

1. Click on the tool (a), or select Open from Disc in the File menu (a), Figure 5 is shown.
2. For analyzed Segment file, select image stack to load and select Load Selected Files.
3. For multiple DICOM files, select Graphical Selector and load image stacks according to Figure 3.

3.2 Storing data

1. To store images including delineation to Patient Database, select Save to Database in the File menu (a).
2. To store images including delineation to Disc, click on the tool (b) or select Save As ... in the File menu (a).
3. To store images including delineation to PACS, select Save to PACS in the File menu (a).

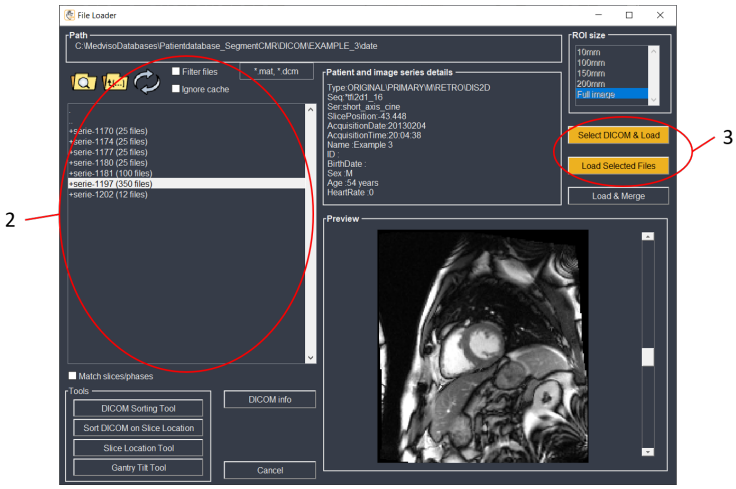


Figure 5: Image stack loading selector.

4 Image settings

4.1 Manually set image description

1. Right click on the thumbnail for the image stack.
2. Select Select Image Description in the context menu.

4.2 Image description upon loading

The image description is automatically set in the loading process by comparing information from the DICOM tags with the information in the text file `imagedescription.txt`.

1. The text file is found in the folder where Segment is installed.
2. Manually update the text file according to the structure as defined in the first row in the text file.

4.3 Patient details

Edit patient details by select  in the 

mode.

5 LV segmentation in short-axis images

5.1 LV analysis

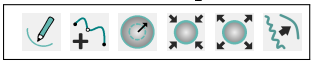
5.1.1 Automatic LV segmentation

Segmentation in all time frames

a. To run the fully automatic LV segmentation in all time frames, a CUDA enabled NVIDIA graphics card is required.

b. Start the fully automatic LV segmentation by select FUNCTION [L] (h) and select  (i).

c. The segmentation result is presented in the main window where volumes curve can be reviewed (k) and the measured LV volumes are presented, according to Figure 6 (j).

d. If needed, correction of the LV segmentation can be performed by selecting  or  , and combining with one of the tools:  (i).

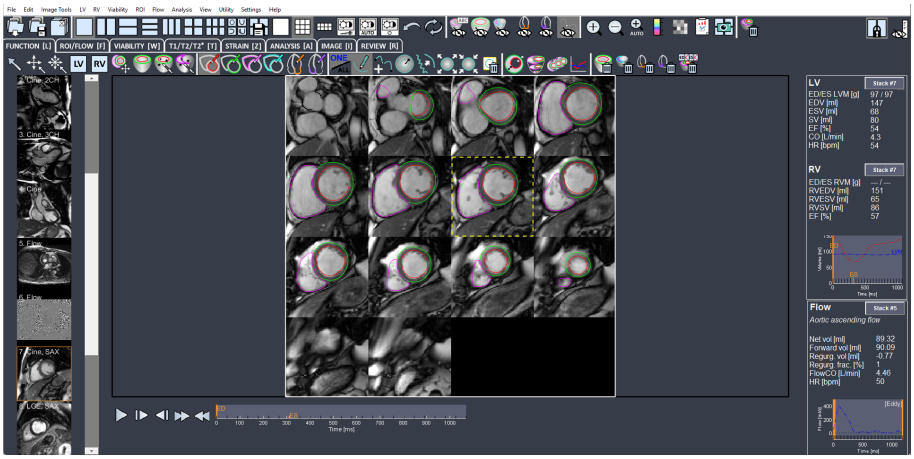


Figure 6: LV analysis result.

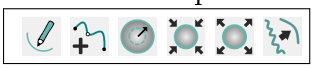
Segmentation in ED and ES time frames

a. For those not having a CUDA enabled NVIDIA graphic card, the fully automatic LV segmentation is provided for segmentation in ED and ES.

b. Start by manually define end-diastole and end-systole.

c. Start the fully automatic LV segmentation by select FUNCTION [L] (h) and select  (i).

d. The segmentation result is presented in the main window where volumes curve can be reviewed (k) and the measured LV volumes are presented, according to Figure 6 (j).

e. If needed, correction of the LV segmentation can be performed by selecting  or  , and combining with one of the tools:  (i).

5.1.2 Semi-automatic LV segmentation

(cine)

1. Start the LV analysis by select FUNCTION [L] (h) and select  (i). A new interface is open, as shown in Figure 7.

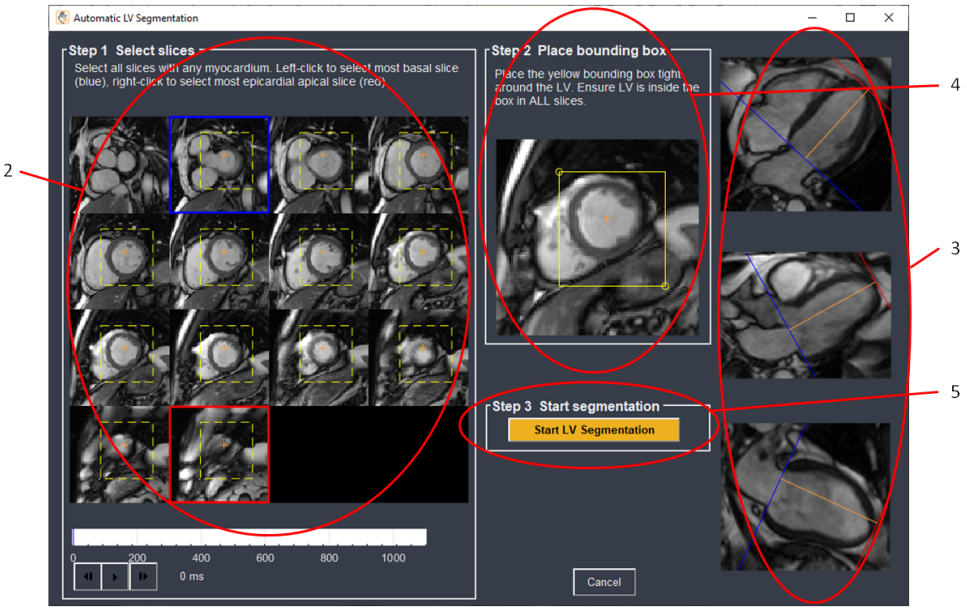


Figure 7: LV analysis GUI.

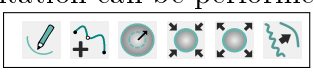
2. Select the slices covering the left ventricle by left-click to select most basal slice and right-click to select most epicardial apical slice.

3. Review the slice selection in the long-axis views.

4. Ensure that the bounding box comprises the LV in ALL slices, otherwise drag in the corners of the bounding box.

5. Start the automatic LV segmentation.

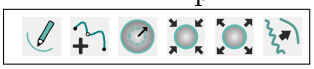
6. The segmentation result is presented in the main window where volumes curve can be reviewed (k) and the measured LV volumes are presented, according to Figure 6 (j).

7. If needed, correction of the LV segmentation can be performed by selecting  or  , and combining with one of the tools:  (i).

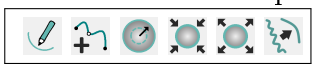
5.1.3 Automatic LV segmentation (general stack)

a. To run the fully automatic LV segmentation in all time frames, a CUDA enabled NVIDIA graphics card is required.

b. Start the fully automatic LV segmentation by select ANALYSIS [A] (h) and select  (i).

c. If needed, correction of the LV segmentation can be performed by selecting  or  , and combining with one of the tools:  (i).

5.1.4 Manual LV segmentation

Manual delineation of the LV can be performed by selecting  or  , and combining with one of the tools:  (i).

5.1.5 Clear LV segmentation

To clear the LV segmentation, select  (i) under FUNCTION [L] (h).

5.1.6 Copying LV segmentation

To copy the LV segmentation to another image stack, select Import Segmentation From Another Image Stack under menu LV (a).

5.1.7 Segmentation of papillary volume

1. To include papillary muscles in the LV myocardial segmentation, select menu item LV - Automatic Estimation of Papillary Volume.

2. Adjust the segmentation of the papillary volumes by select menu item LV - Adjust Papillay Threshold (Slider).

3. To clear the papillary segmentation, select LV - Reset Papillary Volume.

5.1.8 Validation of LV segmentation (cine)

Table 1 presents the mean bias between reference volumes by expert readers and the volumes by the automatic segmentation algorithm in 65 patients [1]. No uncertainty/error information is shown in the software together with the measurements.

Table 1:

LVM	-2.1 ± 8.9 g
EDV	-2.0 ± 10.2 ml
ESV	-1.9 ± 7.0 ml
EF	0.2 ± 4.6 %

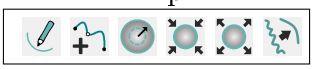
6 RV segmentation in short-axis images

6.1 Fully automatic RV segmentation

a. To run the fully automatic RV segmentation, a CUDA enabled NVIDIA graphics card is required.

b. Start the fully automatic RV segmentation by select FUNCTION [L] (h) and select  (i).

c. The segmentation result is presented in the main window where the measured RV volumes are presented, according to Figure 8 (j).

d. If needed, correction of the RV segmentation can be performed by selecting:  or  , and combining with one of the tools:  (i).

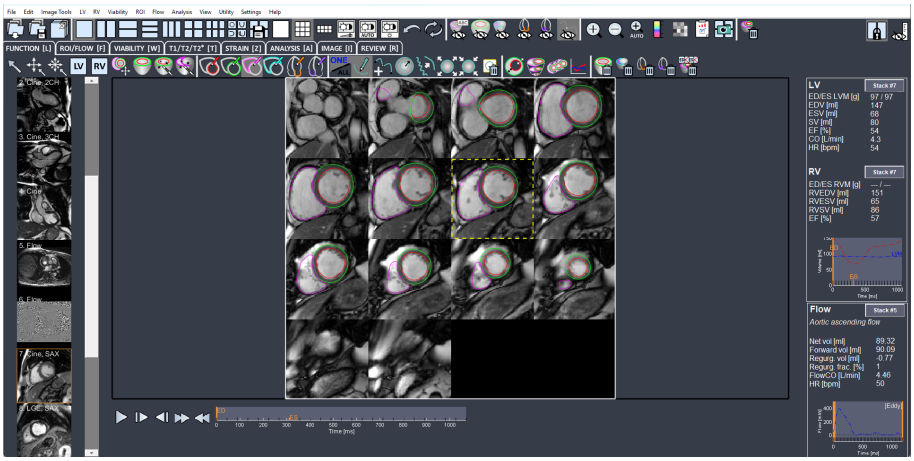


Figure 8: RV analysis result.

6.2 Semi-automatic RV segmentation

1. For those not having a CUDA enabled NVIDIA graphic card, the semi-automatic RV segmentation is provided instead of the fully automatic RV segmentation.

2. Start the semi-automatic RV segmentation by select FUNCTION [L] (h) and select  (i). A new interface is open, as shown in Figure 9.

3. Set RV center and select the slices covering the right ventricle by left-click to select most basal slice and most apical slice.

4. Review the slice selection and center line in the long-axis views.

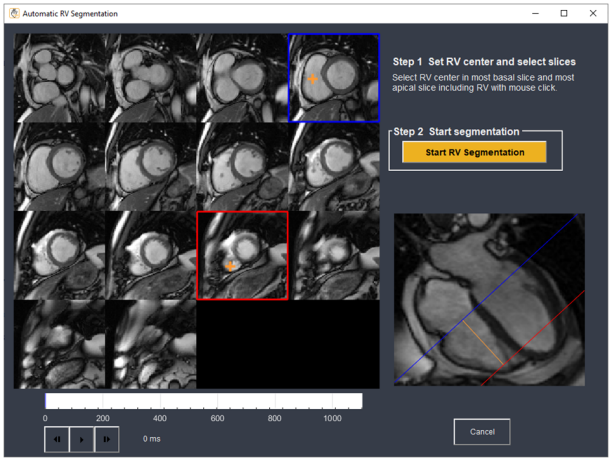
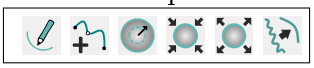


Figure 9: RV analysis GUI.

5. Start the RV segmentation process.

6. The segmentation result is presented in the main window where the measured RV volumes are presented, according to Figure 8 (j).

7. If needed, correction of the RV segmentation can be performed by selecting:  or  , and combining with one of the tools:  (i).

6.3 Manual RV segmentation

Manual delineation of the RV can be performed by selecting:  or  , and combining with one of the tools:  (i).

6.4 Clear RV segmentation

To clear the RV segmentation, select  (i) under  (h).

6.5 Validation of RV segmentation

Table 2 presents the mean bias between reference volumes by expert readers and the volumes by the automatic segmentation algorithm in 50 patients [1]. No uncertainty/error information is shown in the software together with the measurements.

Table 2:

RVEDV	-6.0 ± 10.0 ml
RVESV	-1.0 ± 5.8 ml

1. J. Akesson, E. Ostenfeld, M. Carlsson, H. Arheden, and E. Heiberg, Deep learning can yield clinically useful right ventricular segmentations faster than fully manual analysis, Sci. Rep., vol. 13:1216, pp. 1–10, 2023.

7 Segmentation in long-axis images

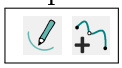
7.1 Fully automatic LV, RV, LA and RA segmentation

1. Ensure that `Image View Plane` is set correctly (`2CH`, `3CH` and `4CH`), respectively. Otherwise set it according to Section 4.

2. Ensure that end-diastole (ED) time frame is defined correctly in all three views. If not, correct it manually by dragging ED marker to the end-diastole time frame in the time bar.

3. Start the fully automatic segmentation by select FUNCTION [L] (h) and select  (i).

4. The segmentation is performed at the ED time frame for all long-axis images (2CH, 3CH and 4CH). See Figure 10.

5. If needed, correction of the segmentation can be performed by selecting  ,  ,  , or  , and combining with one of the tools:  (i).

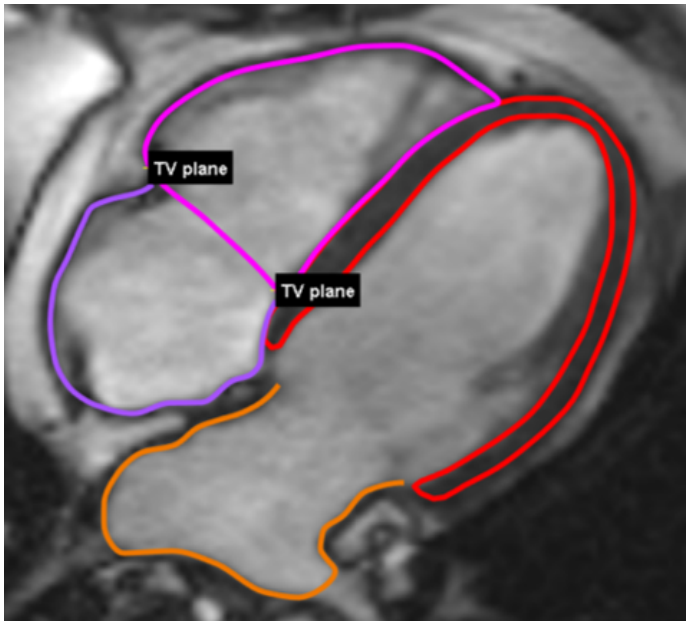


Figure 10: LV, RV, LA and RA segmentation in 4CH.

7.1.1 Validation of LV, RV, LA, and RA segmentation

Table 3 presents the mean bias between reference volumes and strain values by expert readers and the volumes and strain values based on the automatic segmentation algorithm in 91

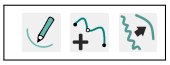
Table 3:

LV-GLS	-0.13 ± 0.44 %
RV-GLS	-0.60 ± 1.46 %
LA Total Strain	0.65 ± 2.47 %
RA Total Strain	-0.66 ± 2.98 %
LAV-ED	-1.18 ± 3.34 ml
RAA-ED	-0.52 ± 0.70 cm^2

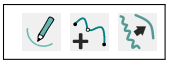
patients [1]. No uncertainty/error information is shown in the software together with the measurements.

1. Medviso White Paper, LV, RV, LA, and RA LAX validation, 2025. [Available through https://medviso.com/documents/LAXAI.pdf]

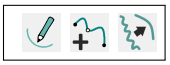
7.2 Manual LV segmentation

Manual delineation of the LV can be performed by selecting  , and combining with one of the tools:  (i). The tools are found in the tab FUNCTION [L]. The LV segmentation should be horseshoe shaped according to Figure 10. The same principle goes for all long-axis images (2CH, 3CH and 4CH).

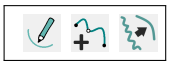
7.3 Manual RV segmentation

Manual delineation of the RV can be performed by selecting  , and combining with one of the tools:  (i). The tools are found in the tab FUNCTION [L]. The RV segmentation should be a closed contour and be done in the 4CH view according to Figure 10.

7.4 Manual LA segmentation

Manual delineation of the LA can be performed by selecting  , and combining with one of the tools:  (i). The tools are found in the tab FUNCTION [L]. The LA segmentation should be an open contour and be done in the 2CH and/or the 4CH view according to Figure 10.

7.5 Manual RA segmentation

Manual delineation of the RA can be performed by selecting  , and combining with one of the tools:  (i). The tools are found in the tab FUNCTION [L]. The RA segmentation should be an open contour and be done in the 4CH view according to Figure 10.

8 Strain analysis - MITT

The strain analysis module uses MR images to calculate myocardial strain. The module has been developed in close collaboration with researchers at Katholieke Universiteit Leuven, Belgium and University of Minho, Portugal.

If you only have access to the 1st Generation of Strain module, please refer to Chapter 9. For strain parameters defintions please refer to Chapter 8.5

8.1 Strain analysis in short-axis image stacks

1. Ensure that `Image View Plane` is set correctly (`SAX`). Otherwise set it according to Section 4

2. **LV:** Perform LV segmentation. The LV segmentation should be performed in the end-diastole (ED) time frame in the cine image stack, according to Chapter 5.

3. **RV:** Perform RV segmentation. The RV segmentation should be performed in the ED time frame in the cine image stack, according to Chapter 6.

4. Ensure that the `data type` found under STRAIN is correctly defined to ensure proper tissue tracking. Otherwise select a proper `data type` on the list shown in Figure 11. The label "beta" indicates that the parameter setting for that data type is currently under validation.

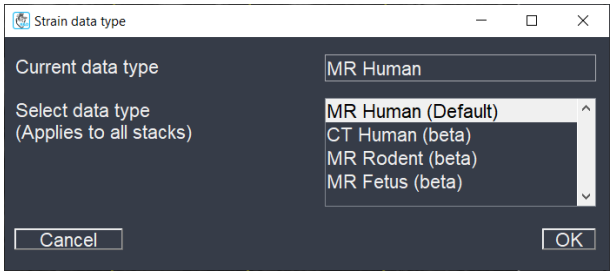


Figure 11: Strain data type interface.

5. Start the strain analysis by clicking on under STRAIN [Z] (a).

6. If ED time frame is not the first time frame, images will automatically be shifted in time so ED will be the first time frame.

7. The Strain interface is shown (Figure 12).

8. **LV:** Define LV rotation by setting the white line in the middle of the RV lumen, using the slider. The myocardial strain quantification is updated automatically.

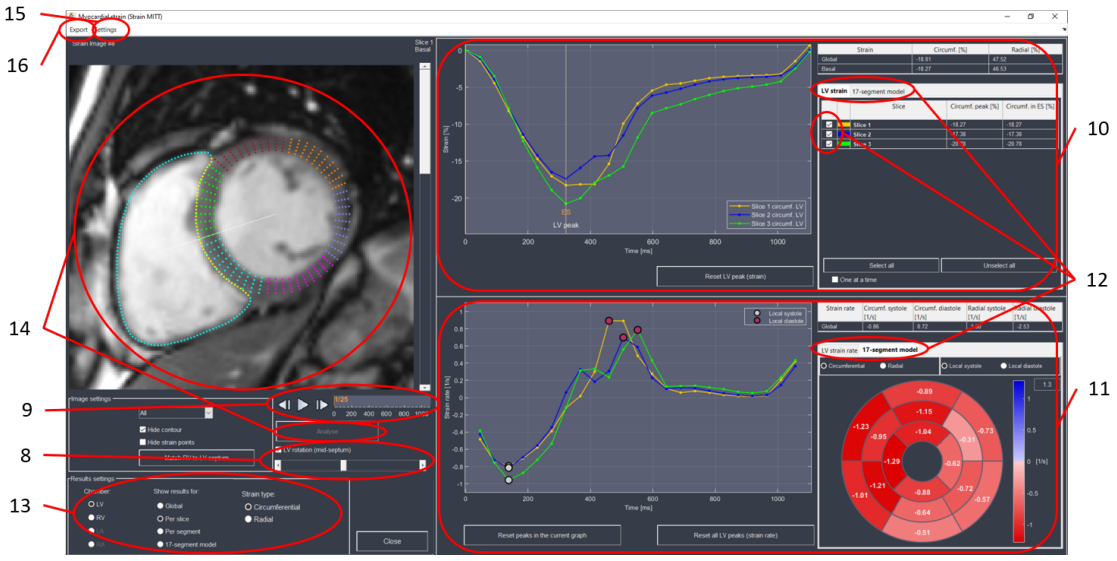


Figure 12: Strain analysis GUI.

9. Verify the strain tracking by using the movie tools.
10. Strain over time and peak strain is shown in the panel to the right.
11. Strain rate over time and peak strain rate is shown in the panel to the right.
12. The result presentation can be shifted between table view and bullseye view. The different curves in the graphs can be hided by using the checkboxes.
13. Switch between the different result views by using the radiobuttons.
14. If needed, manual correction can be performed by moving the segmentation interpolation points, in the initial time frame in the image stack. Then run the strain quantification again by selecting Analyse.
15. Manually change the short-axis slices for the bullseye division by selecting Settings.
16. Select menu item under Export to export strain result.

8.2 Strain analysis in long-axis image stacks

1. Ensure that `Image View Plane` is set correctly (`2CH`, `3CH` and `4CH`), respectively. Otherwise set it according to Section 4.
2. Ensure that end-diastole (ED) time frame is defined correctly in all three views. If not, correct it manually by dragging ED marker to the end-diastole time frame in the time bar.

3. **LV:** The LV segmentation should be performed in the end-diastole (ED) time frame in the cine image stack, according to Chapter 7.1, 7.2.

4. **RV:** The RV segmentation should be performed in the ED time frame in the cine 4CH image stack, according to Chapter 7.1, 7.3. Set two annotation points to define the Tricuspidalis valve plane and name them TV plane, according to Figure 13. The annotation point tool is found under STRAIN [Z].(a)

5. **LA/RA:** The LA and RA segmentation should be performed in the end-diastole (ED) time frame in the cine image stack, according to Chapter 7.1, 7.4, 7.5.

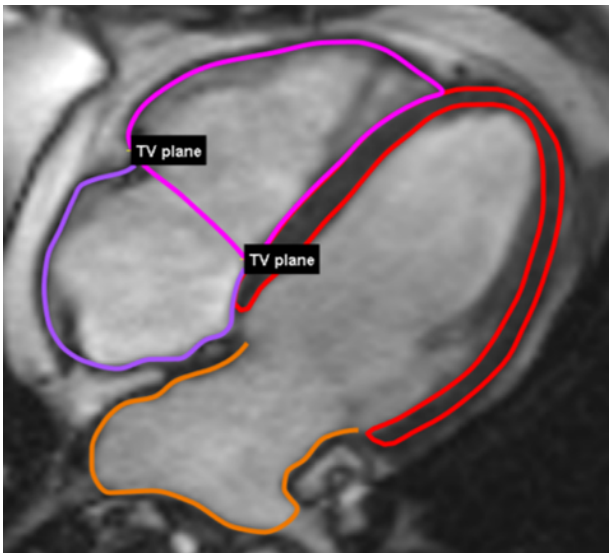


Figure 13: LV, RV, LA and RA segmentation in 4CH.

6. Ensure that `data type` found under STRAIN is correctly defined to ensure proper tissue tracking. Otherwise select a proper `data type` on the list shown in Figure 11).

7. Start the strain analysis by clicking on under STRAIN [Z]. (a).

8. If ED time frame is not the first time frame, images will automatically be shifted in time so ED will be the first time frame.

9. The Strain interface is shown (Figure 14).

10. Verify the strain tracking by using the movie tools.

11. Strain over time and peak strain is shown in the panel to the right.

12. Strain rate over time and peak strain rate is shown in the panel to the right.

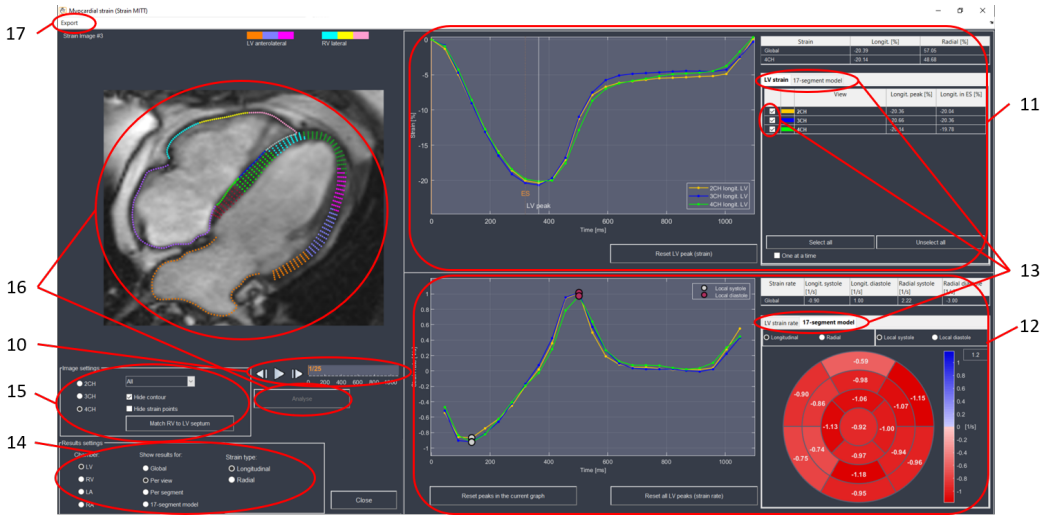


Figure 14: Strain analysis GUI.

13. The result presentation can be shifted between table view and bullseye view. The different curves in the graphs can be hided by using the checkboxes.

14. Switch between the different result views by using the radiobuttons.

15. Switch between the different long-axis views by using the radiobuttons.

16. If needed, manual correction can be performed by moving the segmentation interpolation points, in the initial time frame in the image stack. Then run the strain quantification again by selecting Analyse.

17. Select menu item under Export to export strain result.

8.3 Clear strain data

To clear the strain data, click on  to clear Strain in selected image stack, or  to clear Strain in all image stacks (a).

8.4 Strain export options

8.4.1 Patient exports

For exporting strain results and graphs for one patient, use the Export functions found in the Strain analysis interface numbered 16 in Figure 12.

8.4.2 Batch exports

The batch export script for strain is found under main menu Utility - Batch Export from .mat files - Export Strain MITT where you find functions for export of Feature Tracking Strain from multiple files. The result is exported to spreadsheet for further processing.

8.5 Strain Analysis Module definition

This chapter presents definition of main strain results obtained in Strain MITT.

8.5.1 Definition of Strain

Strain is defined according to Lagrangian formula as (L-L0)/L0 with L the instantaneous length and L0 is the baseline length in end-diastole. The values for Strain are expressed in [%]. The length is calculated for the set of points, based on conturs drawn in end-diastole phase. Strain is calculated for circumeferential, radial and longitudinal direction. Both Global and Segmental strain values are provided.

8.5.2 Definition of Global strain

Global Strain is defined as the mean of all strain values within the entire chamber wall. The values for global Strain are expressed in [%]. Reported values for "GRS", "GCS" and "GLS" (global radial strain, global circumferential strain, global longitudinal strain respectively) are the values of global strain at the time point defined as the global peak time frame. The global peak time frame is the time point of peak strain for entire chamber wall by default. Illustrated in Figure 15. The 'Peak' marker can adjusted by dragging and moving to another time frame.

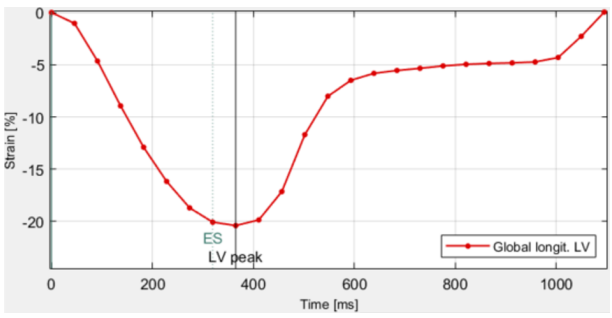


Figure 15: Illustration of strain at global peak time frame, which is the strain values at the vertical black line.

8.5.3 Definition of Time vector

- For SAX view: Time vector of SAX stack. Unit of time vector is [ms].
- For LAX views: Time vector is a mean value of time vector/time increment in LV LAX views (2ch, 3ch, 4ch) that are used for Strain analysis. For example, if all three (2ch, 3ch, 4ch) views are used, than the mean value of the time vectors of the three views is calculated. Unit of time vector is [ms].

8.5.4 Definition of Strain for slice/view

"Strain for slice/view" is defined as the strain value in each view or slice (long axis or short axis respectively) at the time point defined as the global peak time frame. The values for

Strain are expressed in [%]. The global peak time frame is the time point of peak strain for entire chamber wall (as illustrated in Figure 15).

8.5.5 Definition of Strain plots

This section presents definitions of strain plots displayed on the graph in the Results panel of the Strain window.

Strain plot

”Strain plot" presents values of all strain values within the entire chamber wall over the heart cycle. Radial, circumferential or longitudinal strain plots can presented on the graph.

Strain for slice/view plot

"Strain for slice/view plot"presents all strain value within selected view or slice over the heart cycle. Radial, circumferential or longitudinal strain plots can presented on the graph.

Segmental Strain for slice/view plot

"Segmental Strain for slice/view plot" presents strain values for each segment within selected view or slice over the heart cycle. Segments corresponds to bullseyplot diagram according to AHA 17 standard.

8.5.6 Definition of Strain bullseye plots

This section presents definitions of strain values displayed on bullseye diagram according to AHA 17 standard in the Results panel of the Strain window.

Peak circumferential/radial/longitudinal strain

"Peak circumferential/radial/longitudinal strain" is defined as the strain value for each segment at the time point defined as the global peak time frame. This is strain at the same time point for all segments. Illustrated in Figure 16. The *Peak* marker can adjusted by dragging and moving to another time frame.

Peak circumferential/radial/longitudinal strain at ES

"Peak circumferential/radial/longitudinal strain" is defined as the strain value in each segment at the ES time point. This is strain at the same time point for all segments. The *ES* marker can be adjusted by dragging and moving to another time frame.

8.5.7 Definition of Strain Rate

Strain rate is a rate of shortening of a length and it is defined as (1/L0)*(dL/dt) with L the instantaneous length and L0 is the baseline length in end-diastole. The values for Strain Rate are expressed in [1/s]. Strain Rate values are presented in the lower right panel in the Strain window.

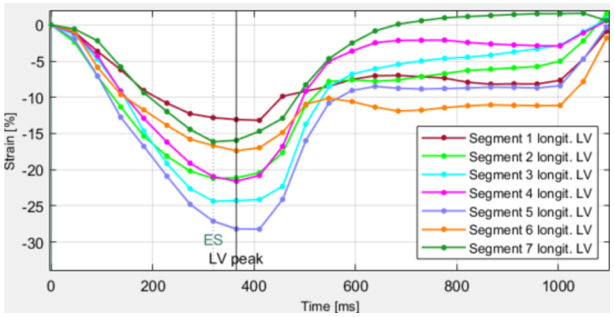


Figure 16: Illustration of Segmental strain at global peak time frame, which is the strain values at the vertical black line in each segment.

8.5.8 Definition of Global Strain Rate

"Global Strain Rate" is defined as the mean of all strain rate values within the entire chamber wall at the diastole and systole peaks. The values for global Strain Rate are expressed in [1/s]. Illustrated in Figure 17

- In radial direction: systole strain rate peak is defined as the maximal value, and diastole strain rate peak is defined as the minimal value.
- In longitudinal/circumferential direction: systole strain rate peak is defined as the minimal value, and diastole strain rate peak is defined as the maximal value.

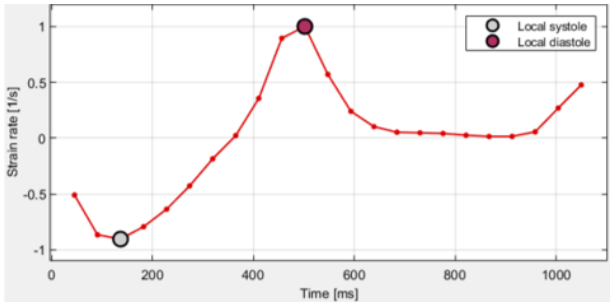


Figure 17: Illustration of diastole and systole strain rate, where systole strain rate is defined by the grey dot, and diastole strain rate is defined by the red dot.

8.5.9 Definition of Strain Rate plots

This section presents definitions of strain rate plots displayed on the graph in the Strain Rate window. The values of the diastole and systole strain rate peaks are presented in the table in the Strain Rate window.

Strain Rate

"Strain Rate" is defined as the mean of all strain rate values within the entire chamber wall at the diastole and systole peaks. The *diastole* and *systole* strain rate marker can be adjusted by dragging and moving to another time frame.

Strain Rate per slice/view

"Strain Rate per slice/view" is defined as values of diastole and systole strain rate peaks for each LAX views or SAX slices. The values of Strain Rate are expressed in [1/s]. The *diastole* and *systole* strain rate marker can be adjusted by dragging and moving to another time frame.

Strain Rate per sector

"Strain Rate per sector" is defined as values of diastole and systole strain rate peaks for each segment independently. The values for global Strain Rate are expressed in [1/s]. The *diastole* and *systole* strain rate marker can be adjusted by dragging and moving to another time frame.

8.6 Validation of strain analysis

Table 4 presents the inter-vendor reproducibility for the device when comparing to the mean of four strain vendors in 45 subjects [1]. No uncertainty/error information is shown in the software together with the measurements.

Table 4:

LV-GCS	$0.14 \pm 1.16\%$
LV-GLS	$1.11 \pm 1.30\%$
LV-GRS	$-5.17 \pm 4.99\%$

1. Medviso White Paper, Strain MITT LV Validation, 2022. [Available through https://medviso.com/documents/StrainMITTvalidation.pdf]

Table 5 presents the difference between the mean strain values for the device in 94 healthy subjects and the mean strain values from three other feature tracking vendors in groups of LV:2472 subjects, RV:673 subjects, LA:747 subjects, and RA: 311 subjects.[1]

1. Medviso White Paper, Strain MITT Validation, 2024. [Available through https://medviso.com/documents/StrainMITTvalidation2.pdf]

Table 5:

LV-GCS	1.7%
LV-GRS	0.2%
LV-GLS	−1.4%
RV-GLS	5.0%
LA-total	−6.2%
LA-passive	−4.1%
LA-active	−2.8%
RA-total	−5.1%

9 Strain analysis - 1st Generation

9.1 Strain analysis in cine or tagged images

The strain analysis module uses tagged MR images or cine MR images to calculate myocardial strain. The module has been developed in close collaboration with researchers at KU Leuven in Belgium.

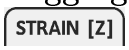
9.2 Strain analysis in short-axis image stacks

1. Ensure that `Image View Plane` is set correctly. Otherwise set it according to Section 4
   Tagging: The correct label is `Tagging, SAX`
   Cine: The correct label is `Cine, SAX`

2. Ensure the end-diastole (ED) time frame is the first time frame (or close to), since the first time frame will be the base for the strain calculation and strain will be defined as 0 in this time frame. You can correct this by in Segment go to the time frame representing end-diastole, then select Set First Timeframe at Current Timeframe in menu Edit.

3. Start the automatic strain analysis.

   - If you have licence **only** for Strain 1st Generation then:

     Tagging: Manually start the automatic strain analysis by clicking on  under  (a).
     Cine: First perform LV segmentation. Manually start the automatic strain analysis by clicking on  under  (a).

   - If you have licence for **both** Strain 1st Generation and Strain MITT then:

     Tagging: Manually start the automatic strain analysis by selecting Tagging Strain SAX analysis under menu Analysis - Strain 1st Generation.
     Cine: First perform LV segmentation. Manually start the the automatic strain analysis by selecting FT Strain SAX analysis under menu Analysis - Strain 1st Generation.

4. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 18.

5. The automatic strain registration is then performed in the background. The progress is shown in a progressbar at the bottom of the main interface of Segment. During the registration process the user can perform segmentation.
   Tagging: The segmentation should be performed in one of the first seven time frames in the tagged image stack, or potential cine image stack.

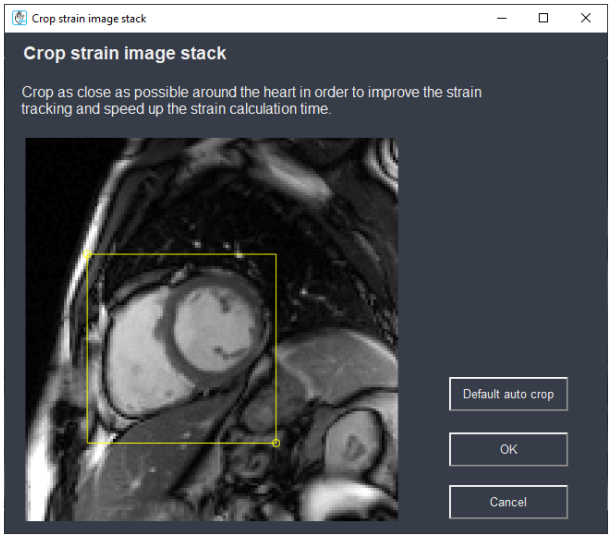


Figure 18: Strain cropping interface.

Cine: The segmentation should be performed in the first time frame in the cine image stack.
This time frame with segmentation will be the initial time frame for the strain tracking.
LV: Perform the LV segmentation according to Figure 19, using methods describe in and Chapter 5.
RV: Perform the RV segmentation according to Figure 19, using methods describe in Chapter 6.

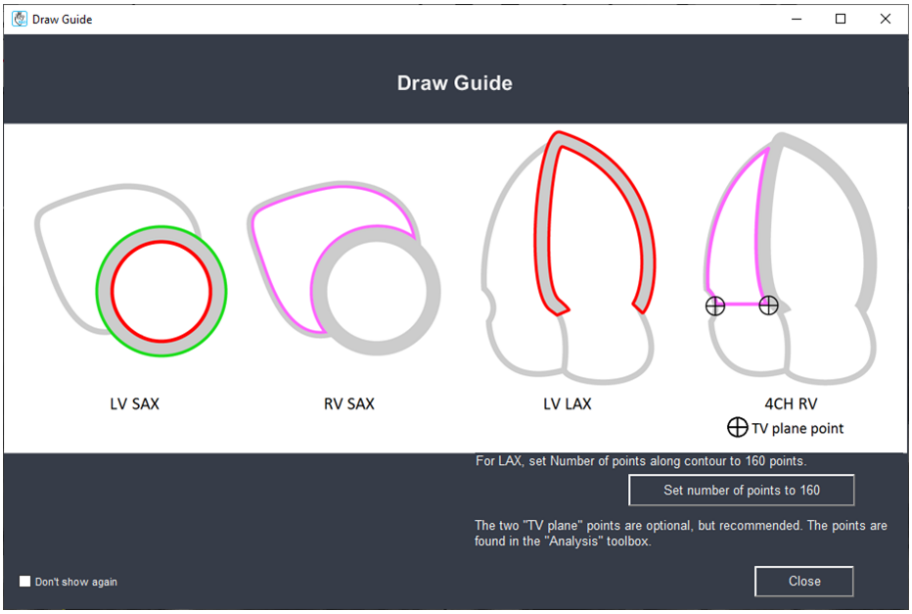


Figure 19: Strain drawing guidance.

6. When the registration and delineation is performed open the window with strain analysis. The Strain interface is shown (Figure 20).

   - If you have licence **only** for Strain 1st Generation then:

     Tagging: Start the strain module by clicking on  under STRAIN [Z] (a).
     Cine: Start the strain module by clicking on  under STRAIN [Z] (a).

   - If you have licence for **both** Strain 1st Generation and Strain MITT then:

     Tagging: Start the strain module by by selecting Tagging Strain SAX analysis under menu Analysis - Strain 1st Generation.
     Cine: Start the strain module by selecting FT Strain SAX analysis under menu Analysis - Strain 1st Generation.

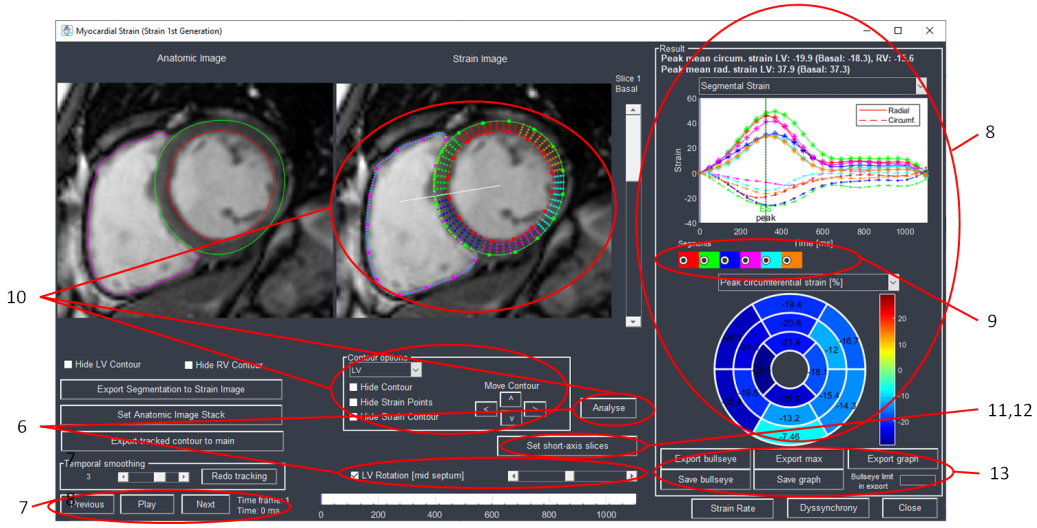


Figure 20: Strain analysis GUI.

7. **LV:** Define LV rotation by setting the white line in the middle of the septum, using the slider, and press Analyse to run the myocardial strain quantification.

8. Verify the strain tracking by using the movie tools.

9. Strain over time and peak strain is shown in the figures to the right according to the selected parameters.

10. You can choose which segments to be presented in the graph with the radiobuttons below the graph.

11. If needed, manual correction can be performed by using the `Move Contour` arrows, or moving the LV segmentation interpolation points, in the initial time frame in the strain image stack. Then run the strain quantification again by selecting Analyse.

12. Manually change the short-axis slices for the bullseye division by selecting Set short-axis slices.
13. **Tagging:** Manually change the initial time frame by selecting Set initial time frame.
14. Click on export buttons to export result to spreadsheet and save buttons to store graph and bullseye to image files.

9.3 Strain analysis in long-axis image stacks

1. Ensure that `Image View Plane` is set correctly (`2CH`, `3CH` and `4CH`), respectively. Otherwise set it according to Section 4.
2. Ensure the end-diastole (ED) time frame is the first time frame (or close to), since the first time frame will be the base for the strain calculation and strain will be defined as 0 in this time frame. You can correct this by in Segment go to the time frame representing end-diastole, then select Set First Timeframe at Current Timeframe in menu Edit.
3. Start the automatic strain analysis.

   - If you have licence **only** for Strain 1st Generation then:

     Tagging: Manually start the automatic strain analysis by clicking on  under STRAIN [Z].
     Cine: First perform LV segmentation. Manually start the the automatic strain analysis by clicking on  under STRAIN [Z].

   - If you have licence for **both** Strain 1st Generation and Strain MITT then:

     Tagging: Manually start the automatic strain analysis by selecting Tagging Strain LAX analysis under menu Analysis - Strain 1st Generation.
     Cine: First perform LV segmentation. Manually start the the automatic strain analysis by selecting FT Strain LAX analysis under menu Analysis - Strain 1st Generation.

4. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 21.
5. The automatic strain registration is then performed in the background. The progress is shown in a progressbar at the bottom of the main interface of Segment. During the registration process the user can perform segmentation. Before performing the segmentation, ensure that the parameter `Number of points along contour` in Preferences is set to at least 160, in order to have a smooth segmentation.
6. **Tagging:** The segmentation should be performed in one of the first seven time frames in the tagged image stack, or potential cine image stack.
   Cine: The segmentation should be performed in the first time frame in the cine image

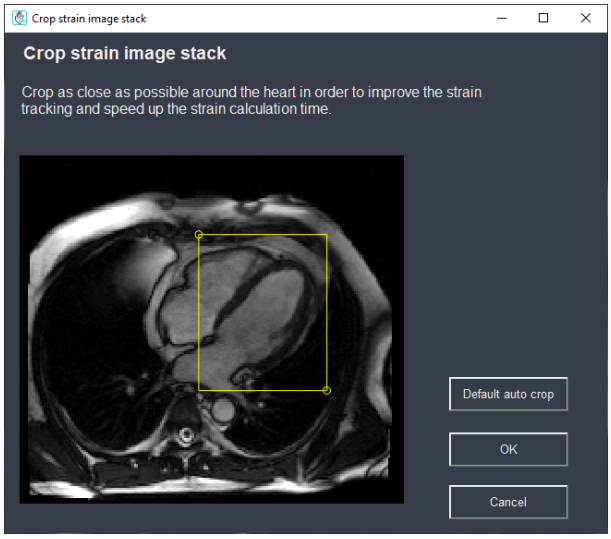


Figure 21: Strain cropping interface.

stack.
This time frame with segmentation will be the initial time frame for the strain tracking.
LV: Perform the LV segmentation according to Figure 22 by using the LV endo segmentation tools or in all three long-axis views.
RV: Perform the RV segmentation according to Figure 22 by using the RV endo segmentation tools or in the 4CH view. Set two annotation points to define the Tricuspidalis valve plane and name them TV plane. The annotation point tool is found under the Misc toolbox.

7. When the registration and delineation is performed open the window with strain analysis. The Strain interface is shown (Figure 23).

   - If you have licence **only** for Strain 1st Generation then:

     Tagging: Start the strain module by clicking on under STRAIN [Z] (a).
     Cine: Start the strain module by clicking on under STRAIN [Z] (a).

   - If you have licence for **both** Strain 1st Generation and Strain MITT then:

     Tagging: Start the strain module by selecting Tagging Strain LAX analysis under menu Analysis - Strain 1st Generation.
     Cine: Start the strain module by selecting FT Strain LAX analysis under menu Analysis - Strain 1st Generation.

8. Verify the strain tracking by using the movie tools.

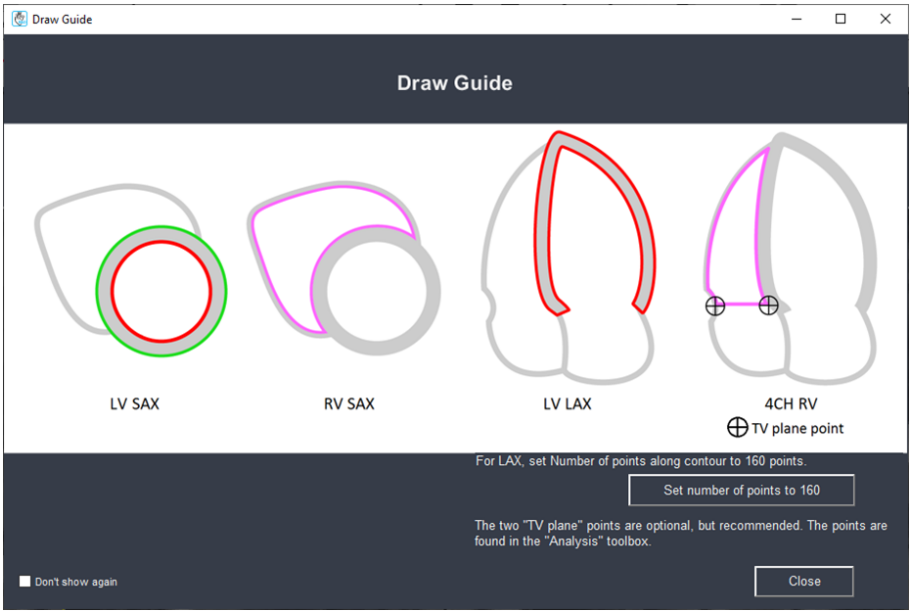


Figure 22: Strain drawing guidance.

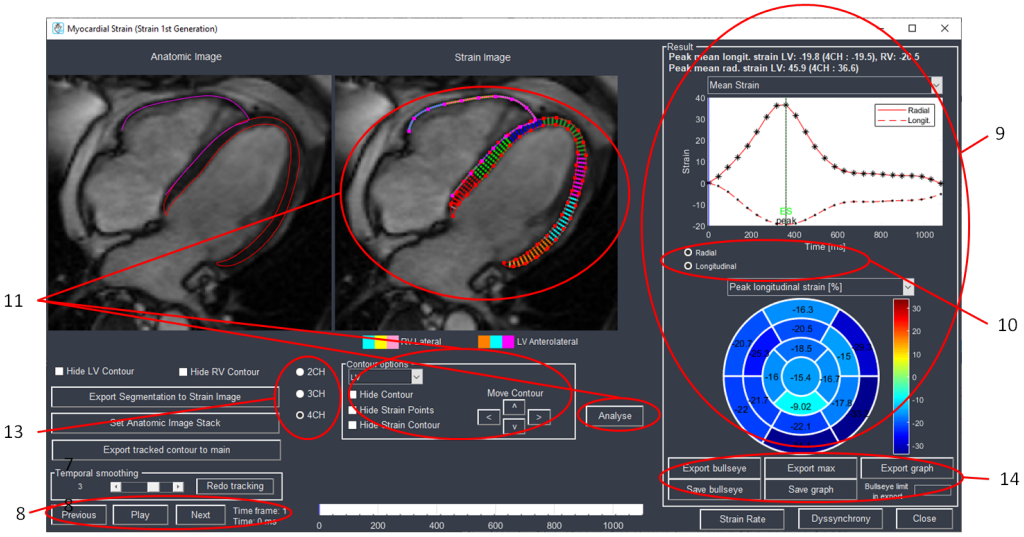


Figure 23: Strain analysis GUI.

9. Strain over time and peak strain is shown in the figures to the right according to the selected parameters.

10. You can choose which segments to be presented in the graph with the radiobuttons below the graph.

11. If needed, manual correction can be performed by using the `Move Contour` arrows, or moving the segmentation interpolation points, in the initial time frame in the tagging image stack. Then run the strain quantification again by selecting Analyse.

12. **Tagging:** Manually change the initial time frame by selecting Set initial time frame.

13. You can toggle between existing views by using the radiobuttons labeled with the chamber views.

14. Click on export buttons to export result to spreadsheet and save buttons to store graph and bullseye to image files.

9.4 Strain analysis of the left atrium

To perform strain analysis in the left atrium use the RV endo tools. It is work in progress to add tools specific for left atrial strain, but meanwhile it works perfectly fine to use the RV endo tools to measure strain in the left atrium.

1. Start with manually peform left atrial segmentation in the first time frame in the 4CH view using the  according to Figure 24.

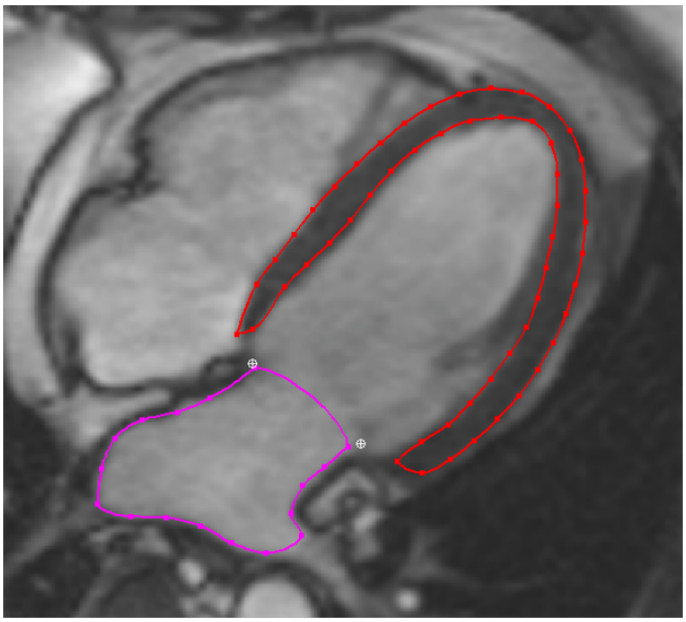


Figure 24: Segmentation of the left atrium to be used for strain analysis.

2. Ensure that `Image View Plane` is set correctly (`4CH`). Otherwise set it according to Section 4.

3. Start the automatic strain analysis.

   - If you have licence **only** for Strain 1st Generation then:
     Start the strain module by clicking on  under STRAIN [Z] (a).
   - If you have licence for **both** Strain 1st Generation and Strain MITT then:

     Start the strain module by selecting FT Strain LAX analysis under menu Analysis - Strain 1st Generation.

4. When the registration and delineation is performed open the window with strain analysis. The Strain interface is shown (Figure 25)

   - If you have licence **only** for Strain 1st Generation then:
     Start the strain module by clicking on  under STRAIN [Z] (a).

   - If you have licence for **both** Strain 1st Generation and Strain MITT then:
     Start the strain module by selecting FT Strain LAX analysis under menu Analysis - Strain 1st Generation.

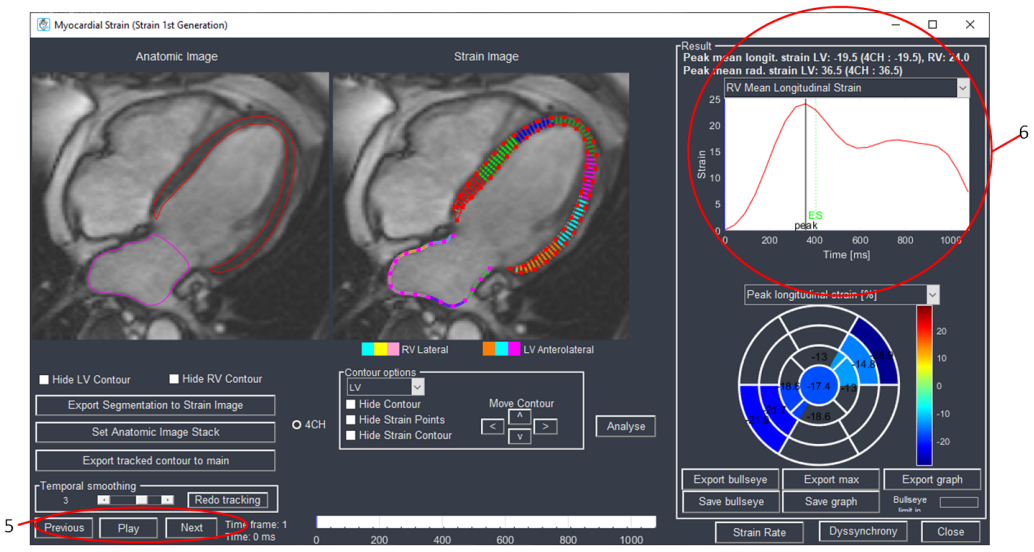


Figure 25: Strain analysis GUI.

5. Verify the strain tracking by using the movie tools.

6. Strain over time and peak strain is shown in the result panel to the right in the interface labeled with RV.

9.5 Hints for Strain analysis in images of small animals

The Strain analysis module is known to work well for analysis of Strain in small animals. However, there are two things to consider:

1. **Time resolution** The time resolution should be good enough. If you have less than 15 time frames for the whole cardiac cycle it is recommended to upsample the image stack. In Segment you do that by selecting Upsample/Downsaple Temporal under menu Resample image stack under menu Image tools.

2. **Image resolution** The strain tracking in human hearts is optimal for a pixel resolution of 0.5 mm. If you have small animal hearts of for example say 5 times as small as human hearts, you need to upsample the image to a pixel resolution of 0.1 mm (0.5/5). In Segment you do that by selecting Upsample/Downsaple Image (In Plane) under menu Resample image stack under menu Image tools. Also crop the image properly before starting the Strain analysis. Crop it so you only have the LV and a little bit surrounding around the LV left in the image.

9.6 Erase strain data

To erase the strain data, select Clear Strain in selected image stack or Clear Strain in all image stacks under STRAIN [Z] (a).

9.7 Strain export options

9.7.1 Patient exports

For exporting strain results and graphs for one patient, use the Export functions found in the Strain analysis interface numbered 13 in Figure 20.

9.7.2 Batch exports

The batch export script for strain is found under main menu Utility - Batch Export from .mat files - Export Strain (1st Generation) where you find functions for export of Feature Tracking Strain and Tagging Strain from multiple files. The result is exported to spreadsheet for further processing.

9.8 Strain parameters definition

This chapter presents definition of main strain results obtained in Strain 1st generation module, see chapter 9 for details on how to perform analysis.

9.8.1 Definition of Mean strain

In the Strain module the mean value of strain in the whole heart is defined as "Mean strain". This measures the same character as "Global strain". "Global strain" is defined as (L-L0)/L0 with L the instantaneous length and L0 is the baseline length in end-diastole. The length is calculated for the set of points, based on conturs drawn in endo-diastole phase. In Segment, "Mean strain" is defined as the mean of all strain value within the entire LV wall.

9.8.2 Definition of Peak strain

Segmental strain at global peak time frame

"Segmental strain at global peak time frame" is defined as the strain value in each segment at the time point defined as the global peak time frame. This is strain at the same time point for all segments. Illustrated in Figure 26

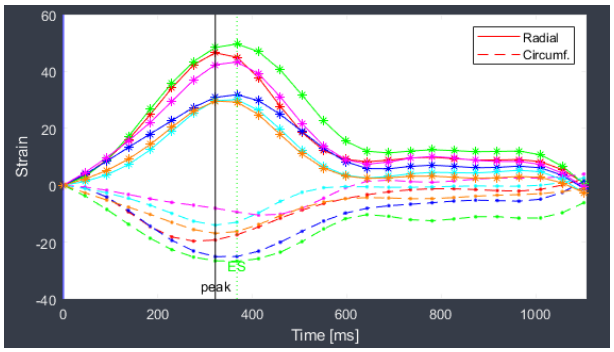


Figure 26: Illustration of Segmental strain at global peak time frame, which is the strain values at the vertical blue line in each segment.

Segmental peak strain for each segment

"Segmental peak strain for each segment" is defined as the peak strain for each segment. This could be strain at different time points for the different segments. In radial direction peak is defined as the maximal value and in longitudinal/circumferential direction peak is defined as the minimal value. Illustrated in Figure 27

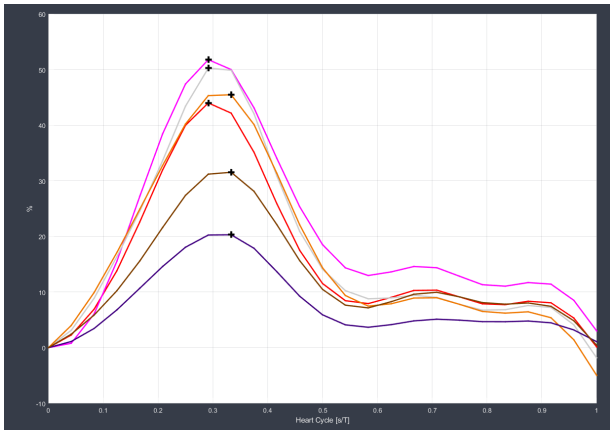


Figure 27: Illustration of Segmental peak strain for each segment, which is the peak strain in each segment defined by the black cross in the images.

9.9 Rotation

Calulations for Rotation are provided for short axis images.
To derive torsion one must consider rotation, this is something that also is available in the strain gui, as well as segmental rotation and endocardial and epicardial rotation. Rotation is quantified as the mean angular distance for all the tracking points in a chosen group, from the current timeframe to the end diastolic timeframe. With torsion we consider the normalized rotational difference of the heart for the most basal and apical slices in data. The rotational difference is normalized with the mean radius divided by the slice distance along the longaxis.

9.9.1 Implementation details

In short axis cardiac images the heart muscle wall of the left chamber is well approximated by a circle. The method finds the axis of rotation, AoR, for the left chamber as the center of a circle fit to the tracking points generated by the segment strain module. For the circle fitting a least squares method is used.