

Segment CMR
Instructions For Use - English



December 14, 2017

Software platform v2.1 R6065

MEDVISO AB
<http://www.medviso.com>
Griffelvägen 3
SE-224 67 Lund
Sweden
Tel: +46-76-183 6442

Contents

1 Terms and conditions	1
1.1 Regulatory status	1
1.2 Conditions for use	1
1.3 Indications for use	1
2 Conventions and Abbreviations	3
2.1 Typographic conventions	3
2.2 Trademarks	3
2.3 Abbreviations	3
3 Getting started	5
3.1 System requirements	5
3.2 Installation	5
3.2.1 Installing Matlab Compiler Runtime	5
3.2.2 Installing Segment CMR	5
3.3 Starting Segment CMR	7
3.4 Uninstallation	7
3.5 Software overview	8
3.6 First time running Segment CMR	8
3.6.1 Setting preferences	8
3.6.2 Setting window positions	10
3.6.3 Patient database	10
3.6.4 PACS connection	10
4 Loading and storing Data - Step by step	11
4.1 Loading data	11
4.1.1 Loading data from database	11
4.1.2 Loading data from PACS	12

CONTENTS

4.1.3	Loading data from network disc	13
4.2	Storing data	13
5	Image viewing tools	15
5.1	Viewing options	15
5.2	Crop image stack	15
5.3	Zoom	15
5.4	Adjust contrast	15
5.4.1	Manual adjustment	15
5.4.2	Automatic adjustment	16
5.5	Measure distance	16
6	Image settings	17
6.1	Manually set image description	17
6.2	Image description upon loading	17
6.3	Patient details	17
7	LV segmentation - Step by step	19
7.1	Automatic LV segmentation [1]	19
7.2	Manual LV segmentation	20
7.3	Erase LV segmentation	20
7.4	Copying LV segmentation	21
7.5	Validation of LV segmentation	21
8	RV segmentation - Step by step	23
8.1	Automatic RV segmentation [1]	23
8.2	Manual RV segmentation	23
8.3	Erase RV segmentation	23
8.4	Validation of RV segmentation	23
9	ROI analysis - Step by step	25
9.1	Manual ROI analysis	25
9.2	Erase ROI segmentation	25
10	Flow analysis - Step by step	27
10.1	Automatic flow analysis [1]	27
10.2	Qp/Qs analysis [2]	28
10.3	Shunt and valve analysis [3]	28
10.4	Erase flow segmentation	29

CONTENTS

10.5 Eddy current compensation	29
10.6 Phase unwrapping	30
10.7 Pulse wave velocity (PWV) analysis [4]	31
10.8 Validation of Flow analysis	31
11 Bullseye analysis - Step by step	35
12 Report generation - Step by step	37
12.1 Reference values used in the report	38
13 Relaxometry analysis - Step by step	39
13.1 T2* analysis	39
13.1.1 Validation of T2* analysis	40
13.2 T1 analysis	40
13.3 T2 analysis	41
13.3.1 Validation of T1/T2 analysis	42
14 Strain analysis - Step by step	43
14.1 Strain analysis in cine or tagged images	43
14.1.1 Automatic strain analysis in short-axis image stacks [1-3]	43
14.1.2 Automatic strain analysis in long-axis image stacks [1-3]	46
14.1.3 Erase strain data	48
14.1.4 Validation of strain analysis	49
14.2 Strain analysis in velocity encoded images	50
14.2.1 Automatic strain analysis [1]	50
14.2.2 Erase strain data	51
14.2.3 Validation of strain analysis	51
15 Scar analysis - Step by step	53
15.1 Automatic scar analysis [1]	53
15.2 Grayzone analysis	54
15.3 Erase scar segmentation	54
15.4 Validation of Scar analysis	54
16 Myocardium at Risk (MaR) analysis - Step by step	55
16.1 Automatic MaR analysis [1]	55
16.2 Erase MaR segmentation	56

CONTENTS

16.3 Validation of MaR analysis	56
17 Perfusion analysis - Step by step	57
17.1 Automatic perfusion analysis [1]	57
17.2 Validation of perfusion analysis	59
18 ECV analysis - Step by step	61
18.1 Automatic ECV analysis	61
19 Short Commands / Hot keys	63

1 Terms and conditions

This manual contains Instructions For Use, to safely be able to use Segment CMR.

1.1 Regulatory status

Segment CMR bears the CE marking of conformity and is certified according to the ISO 13485 standard. Segment and SegmentCMR are FDA approved with FDA 510(k) numbers K090833 and K163076. Please note that there are features that are not included in the FDA approval. These functions are marked in the Instructions for Use and in the Reference Manual that they are only for investigational use.

Users are also required to investigate the regulatory requirements pertinent to their country or location prior to using Segment CMR. It is in the users responsibility to obey these statues, rules and regulations.

1.2 Conditions for use

- The software may only be used by professionals trained in Cardiac MRI.
- The software is a tool to provide relevant clinical data. The clinician is solely responsible for interpretation of clinical data and taking decisions how to manage the patients.
- The software should be used to read images from MRI Scanners from Philips, Siemens, and General Electric. Images can be supplied either by CD's or by using DICOM standard to transfer files directly from the scanner or PACS systems.

1.3 Indications for use

Segment CMR is a software that display and analyzes medical images in DICOM-format using multi-slice, multi-frame and velocity encoded MR images. Segment CMR provides features for analysis of cardiac function, such as cardiac pumping and blood flow. The ventricular analysis is provided

CHAPTER 1. TERMS AND CONDITIONS

for usage in both pediatric (from newborn) and adult population. Images and associated data analysis can be stored, communicated, rendered, and displayed within the system and across PACS system. The data produced by Segment CMR is intended to be used to support qualified cardiologist, radiologist or other licensed professional healthcare practitioners for clinical decision making. **It is a support tool that provides relevant clinical data as a resource to the clinician and is not intended to be a source of medical advice or to determine or recommend a course of action or treatment for a patient.**

2 Conventions and Abbreviations

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

2.1 Typographic conventions

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.
	Push/Toggle button in the graphical user interface.
 Endocardium	Radiobutton in the graphical user interface.
 Single frame	Checkbox in the graphical user interface.

2.2 Trademarks

Below are some of the trademarks used in this manual.

- Segment CMR is a trademark of Medviso AB.
- Segment DICOM Server is a trademark of Medviso AB.
- Sectra PACS is a trademark of Sectra Imtec AB, (<http://www.sectra.se>).
- Matlab is a trademark of the Mathworks Inc, (<http://www.mathworks.com>).

2.3 Abbreviations

CMR	Cardiac Magnetic Resonance
LV	Left Ventricle
MaR	Myocardium at Risk
PWV	Pulse Wave Velocity
RV	Right Ventricle

3 Getting started

3.1 System requirements

- Operating system: Windows 2000, Windows XP (32 bit and 64 bit), Windows Vista (32 bit), Windows 7 (32 bit and 64 bit), Windows 8 or Windows 10.
- Computer with 4 GB of memory or more.
- Harddisk with at least 500 MB of available space.
- Graphics card supporting both DirectX and OpenGL.

3.2 Installation

For first time installation, start with installing Matlab Compiler Runtime (Section 3.2.1) and thereafter installing Segment CMR (Section 3.2.2). For upgrading, only install Segment CMR (Section 3.2.2). To be able to perform the installation you need to have administrator privileges on the machine.

3.2.1 Installing Matlab Compiler Runtime

1. Download the file MCR file and double click it. The file can be downloaded from Medviso AB homepage (<http://medviso.com/download2/>).
2. Follow the instructions in Figures 1-4.
3. Reboot the computer.

3.2.2 Installing Segment CMR

1. The latest Segment CMR version can be downloaded from Medviso AB homepage (<http://medviso.com/download2/>). Download the file `install_Segment_CMR_2px_Ryyyy.exe`, double click it and follow the instructions. You need a password to download the software, which you should have received at the time of purchase. If you have lost the password, please contact `sales@medviso.com`.

CHAPTER 3. GETTING STARTED

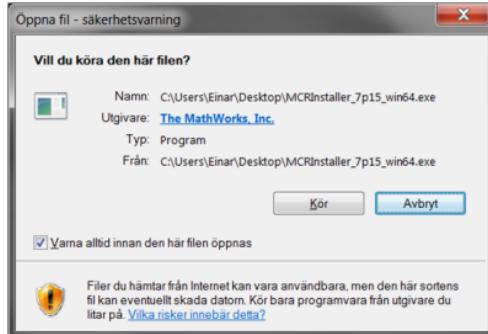


Figure 1: Click on Run.



Figure 2: Click on OK.

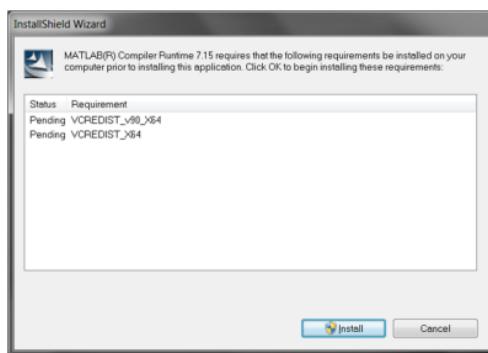


Figure 3: Click on Install.

3.3. STARTING SEGMENT CMR

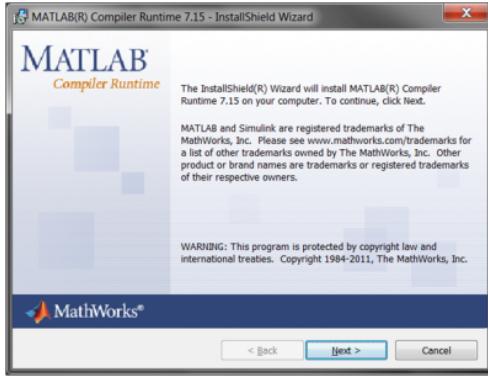


Figure 4: Click on **Next**.

2. For new installations you need to add your license code for Segment CMR. Add your license by enter your license code in the installation process. You can also add your license code after installation by starting Segment CMR and select **Generate License** under the **Help** menu in Segment CMR. Note that you have to run the software as Administrator to be able to add the license code in Segment CMR. A third way of adding your license is to add a license file (named `code.lic`) to the same folder as where Segment CMR is installed. If you do not have a license code, please contact sales@medviso.com.

3.3 Starting Segment CMR

To start the program, double click the file `C:/Program Files/Segment CMR/Segment CMR.exe`, or your shortcut to it. When starting the software, the image in Figure 5 should be displayed. If it is not displayed, then the software is not correctly installed.

3.4 Uninstallation

To uninstall Segment CMR, remove all files in the folder `C:/Program/Segment CMR` or `C:/Program Files/Segment CMR`. User preferences are stored in the `Application Data` and the subfolder `Segment CMR` under each user account. To uninstall the Matlab Compiler Runtime, use the Windows functionality `Install or Remove Programs` in the control panel menu.

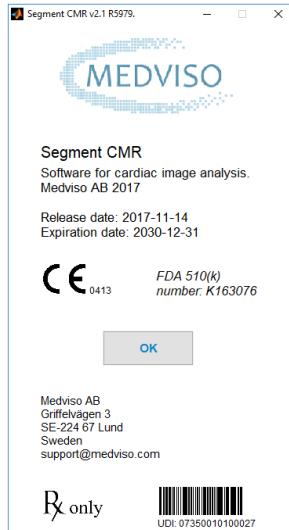


Figure 5: Startup window for Segment CMR.

3.5 Software overview

An overview of Segment CMR is given in Figure 6. 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.

3.6 First time running Segment CMR

The first time Segment CMR is started, it runs a setup process which can take a while, so be patient. To complete the setup, set preferences and window positions as described in Sections 3.6.1 and 3.6.2.

3.6.1 Setting preferences

It is recommended to set the preferences of which folders to use to avoid browsing each time you want to load or save a file. It is invoked by using the icon (p). Set Data, Export and CD folders.

3.6. FIRST TIME RUNNING SEGMENT CMR

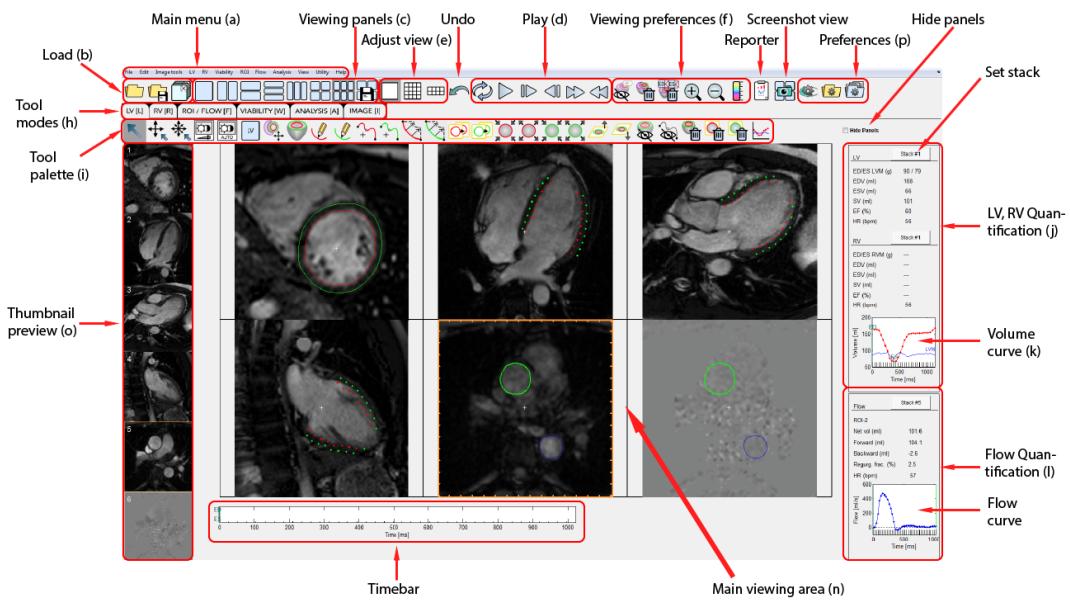


Figure 6: Main graphical user interface. The letters (a-p) in the figure will be used as references throughout this manual.

3.6.2 Setting window positions

The position of the main window for Segment CMR can be set by dragging the window to an optional position and size. The size and position will be saved so that next time Segment CMR is launched the same position will be used. In case where one have switched to another monitor, Segment CMR may move outside the screen. In this case you could press Shift-Ctrl-R to reset GUI positions. This is also available under the File menu (a).

3.6.3 Patient database

We recommend that you start by using our example patient database. Download the file **Patientdatabase.zip** from Medviso AB homepage (<http://medviso.com/download2/>). The file is quite large (1.4 GB). Unpack the file and place the contents in a folder. It is recommended to place it in a subfolder where Segment CMR is installed. In Segment CMR you need to set the location of the patient database. Click on  (p) and click on **Advanced System and DICOM Settings**. A new user interface appears and click on **Database Folder**, select the folder where the file **patientdatabase.mat** resides. To reconstruct the database, click the rebuild database icon in the database window, Figure 7.

3.6.4 PACS connection

Setting up PACS connection and Segment Server usually requires help from your local PACS support, and we recommend that you contact us to setup a telephone / web-based video conference to make this process as smooth as possible. The Database and PACS connection manual and the Sectra PACS plugin manual is found at Medviso AB homepage (<http://medviso.com/products/cmr/resources/>). The Sectra PACS plugin may require additional Microsoft Visual C++ components that can be downloaded from Medviso AB homepage (<http://medviso.com/download2/>).

4 Loading and storing Data - Step by step

4.1 Loading data

To load patient data from the database, follow Section 4.1.1. To load patient data from PACS, follow Section 4.1.2. To load patient data from network disc, follow Section 4.1.3.

4.1.1 Loading data from database

1. Click on the tool  (a), Figure 7 is shown.

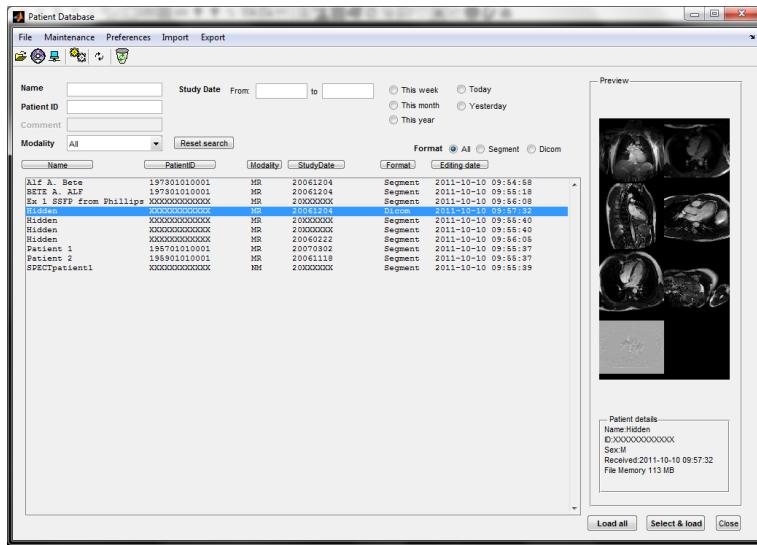


Figure 7: Graphical patient selector.

2. Select patient.
3. Patients can be stored in two formats; DICOM, or Segment CMR format. For images in DICOM format, click , Figure 8 is shown. For images in Segment CMR format click .

4. Select image series to load in Figure 8.



Figure 8: Graphical image series selector.

5. Click on **[Load]**.

4.1.2 Loading data from PACS

1. Select **Import from PACS** in the **File** menu, Figure 9 is shown.

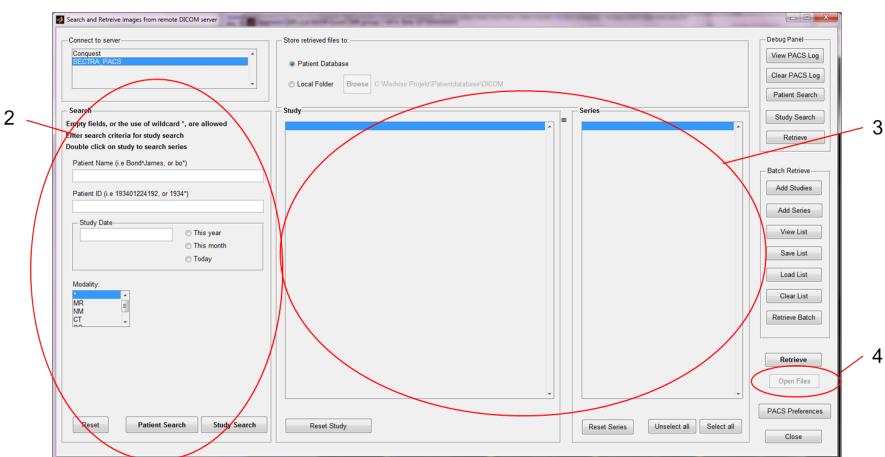


Figure 9: Interface to import image stacks from PACS.

4.2. STORING DATA

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

4.1.3 Loading data from network disc

1. Select Open from Disc in the File menu, Figure 10 is shown.

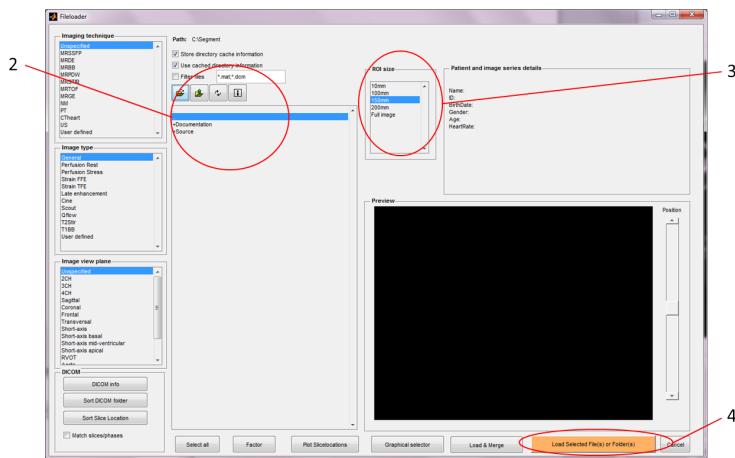


Figure 10: Image stack loading selector.

2. Select image stack to load.
3. For DICOM files, select crop size for the image stack and crop the image.
4. Click on **[Load Selected File(s) or Folder(s)]**.

4.2 Storing data

1. To store images including delineation to Patient Database, click on the tool  (b).
2. To store images including delineation to Disc, 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).

5 Image viewing tools

5.1 Viewing options

- Choose panel viewing option by using (c), (d), (e), (f), (g), (h), (i), (j), (k), (l).
- To play a movie of the image stacks, use the tools (d), (j), (k), (l).

5.2 Crop image stack

1. Click on mode (h).
2. Select the tool (i).
3. Crop an image stack by mark the region in the image stack.

5.3 Zoom

1. Select image stack.
2. Use the tools and (f) to zoom in and zoom out in the image stack.

5.4 Adjust contrast

5.4.1 Manual adjustment

1. Select image stack.
2. Select the tool (i) under mode (h).
3. Adjust the contrast and brightness by right click and drag the mouse in the image stack (right-left for contrast and up-down for brightness).

5.4.2 Automatic adjustment

- The automatic contrast and brightness adjustment is based on the intensity values inside the LV segmentation. If no LV segmentation exist, default values are used in the adjustment.
- To automatically adjust contrast and brightness in the selected image stack, select  (i) under  mode (h).

5.5 Measure distance

1. Click on  mode (h).
2. Select the tool  (i).
3. Measure a distance by dragging the mouse from start to end point in the image stack.

6 Image settings

6.1 Manually set image description

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

6.2 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 CMR is installed.
2. Manually update the text file according to the structure as defined in the first row in the text file.

6.3 Patient details

Edit patient details by select  in the  mode.

7 LV segmentation - Step by step

7.1 Automatic LV segmentation [1]

1. Start the LV analysis by select  mode (h) and select  (i). A new interface is open, as shown in Figure 11.

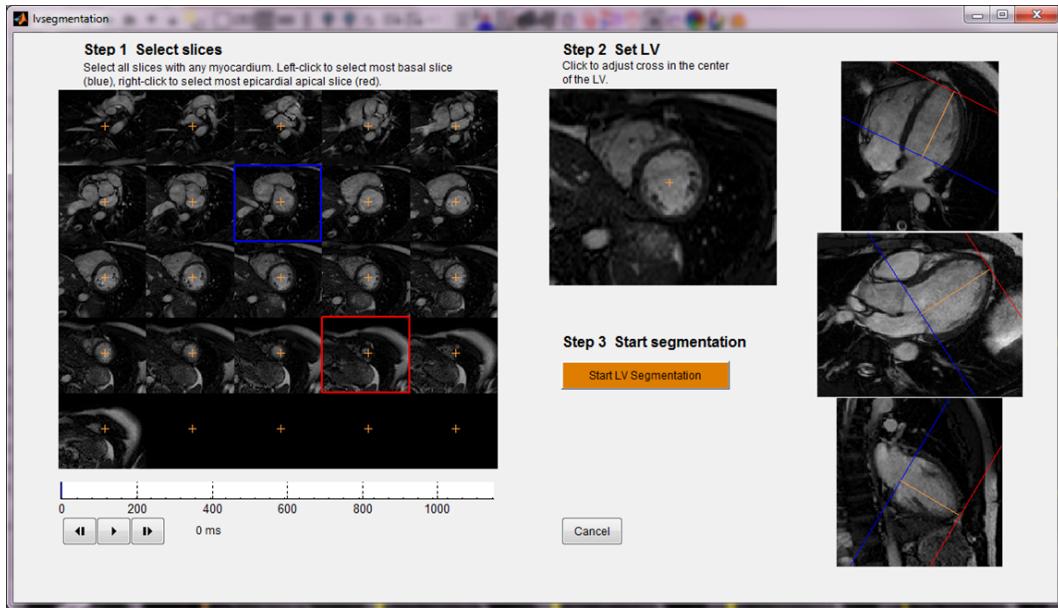


Figure 11: LV analysis GUI.

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 center cross is in the middle of the LV.
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 12 (j).

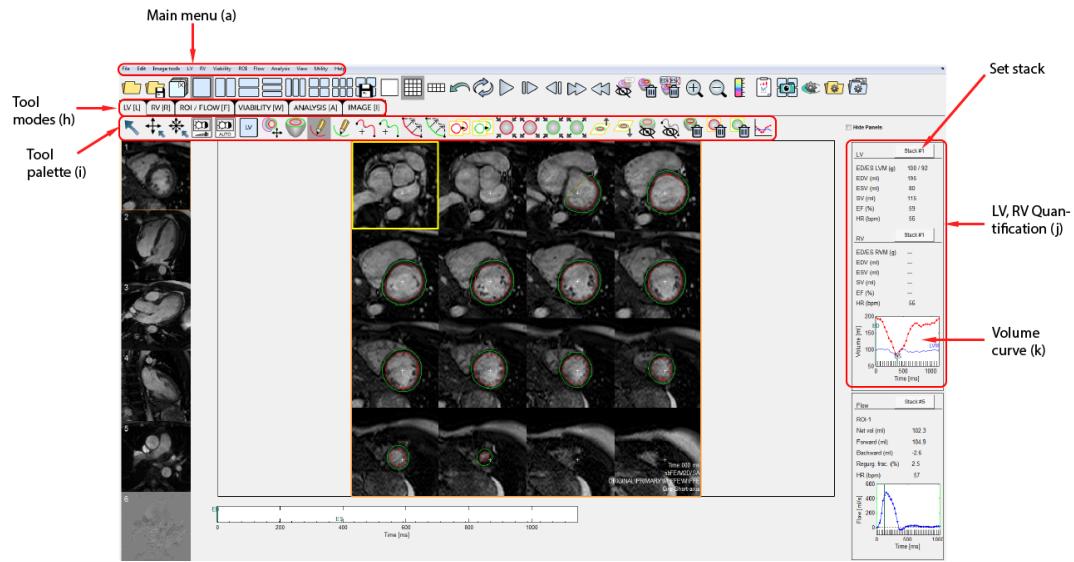


Figure 12: LV analysis result.

7. If needed, correction of the LV segmentation can be performed by using the following tools: (i), (i), (i), (i), (i), (i), (i), and (i).

7.2 Manual LV segmentation

For manual delineation of the LV, the following tools can be used: (i), (i), (i), (i).

7.3 Erase LV segmentation

To erase the LV segmentation, select (i) from mode (h).

7.4 Copying LV segmentation

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

7.5 Validation of LV segmentation

1. J. Tufvesson, E. Hedstrom, K. Steding-Ehrenborg, M. Carlsson, H. Arheden, E. Heiberg, Validation and development of a new automatic algorithm for time resolved segmentation of the left ventricle in magnetic resonance. Biomed Res Int, 2015:970357.

8 RV segmentation - Step by step

8.1 Automatic RV segmentation [1]

1. Put the center of RV indicator (white cross) in the middle of the RV cavity.
2. Select the slices covering the right ventricle. Selected slices are marked by yellow, as in Figure 12.
3. Click on  mode (h).
4. Click on  (i).
5. Select Clear All RV Segmentation Except Enddiastole/Endsystole from RV menu (a).
6. The measured RV volumes are presented (j).

8.2 Manual RV segmentation

For manual delineation or correction of automatic segmentation, the following tools can be used: , , ,  (i).

8.3 Erase RV segmentation

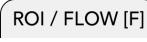
To erase the RV segmentation, select  (i) from  mode (h).

8.4 Validation of RV segmentation

1. M. A. Aneq, E. Nylander, T. Ebbers, and J. Engvall, Determination of right ventricular volume and function using multiple axially rotated MRI slices, Clin Physiol Funct Imaging 31(3) pp. 233-9, 2011.

9 ROI analysis - Step by step

9.1 Manual ROI analysis

1. Click on  mode (h).
2. To place a ROI, use one of the tools  or  (i).
3. Scale the ROI with the tool  (i).
4. Translate the ROI with the tool  (i).
5. Change the ROI segmentation by using the correction tool  (i).
6. Select ROIs with Shift-click with the tool  (i).
7. Set the label of selected ROIs with the tool  (i).
8. Set the color of selected ROIs with the tool  (i).
9. Select  (i) from  mode to perform ROI analysis according to Figure 13 (h).

9.2 Erase ROI segmentation

Delete selected ROIs by selecting , and all ROIs by selecting  in the  mode (h).

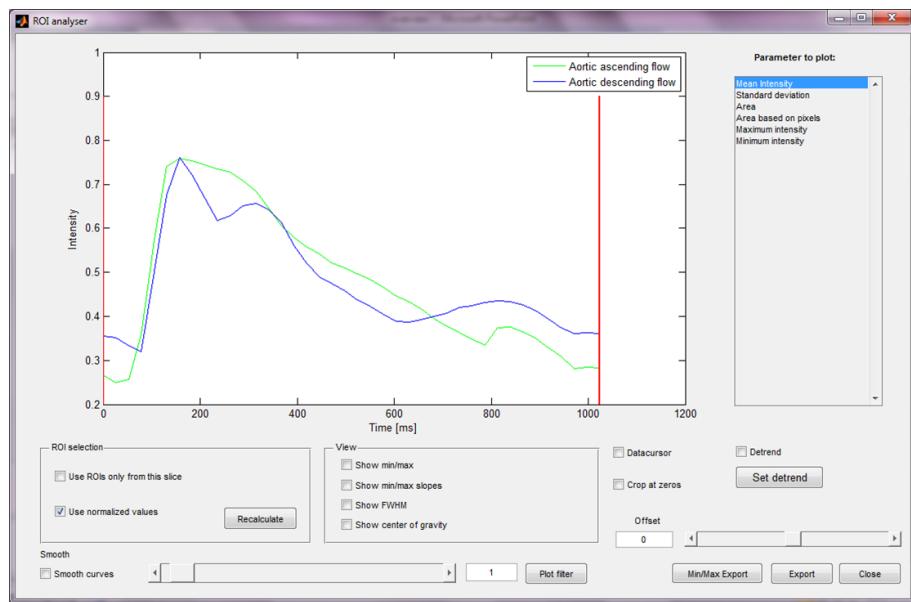


Figure 13: ROI analysis GUI.

10 Flow analysis - Step by step

10.1 Automatic flow analysis [1]

1. Display the magnitude image of the phase contrast image pair, as shown in Figure 14.

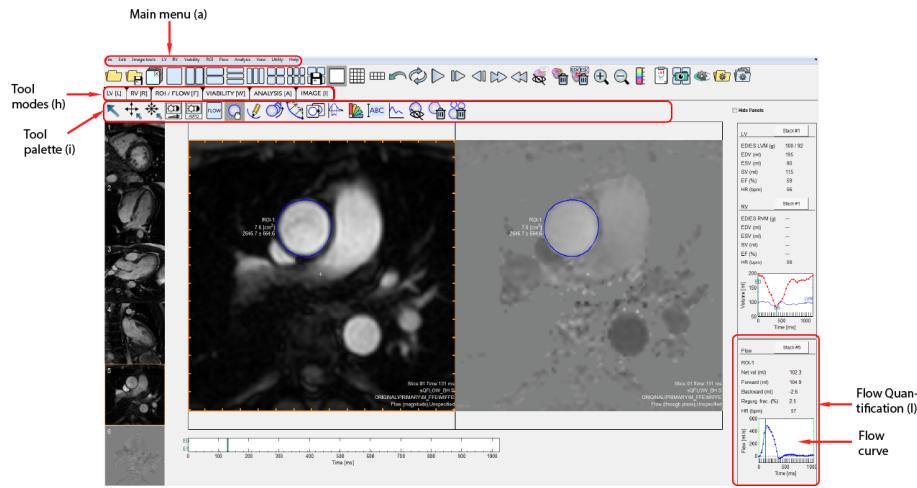


Figure 14: Flow image stack.

2. Click on **ROI / FLOW [F]** mode (h).
3. Use the tool (i), to put a ROI in the center of the vessel.
4. Scale the ROI with the tool (i).
5. Translate the ROI with the tool (i).
6. Set the label of the ROI with the tool (i).
7. Set the color of the ROI with the tool (i).
8. To track and segment the vessel, click on (i).

9. Review the segmentation. If necessary, use the correction tool  (i).
10. Click on  (i), to show flow curve, as shown in Figure 15.
11. Flow values are also presented in main gui, according to set stack, as shown in Figure 14 (l).

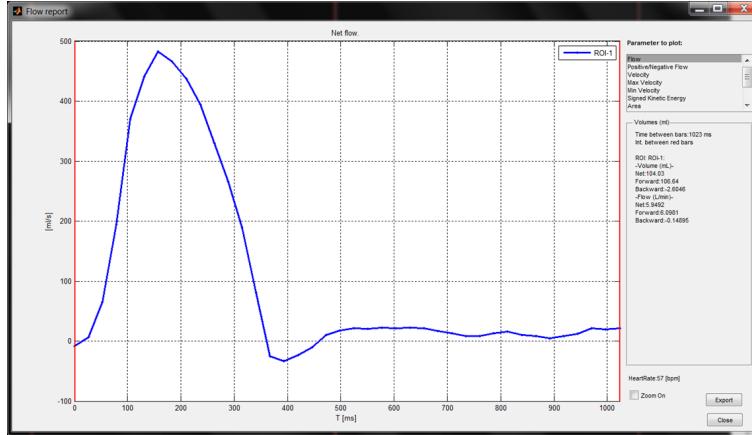


Figure 15: Flow report GUI.

10.2 Qp/Qs analysis [2]

1. Start with vessel segmentation of both the pulmonary and aorta as described in the previous section. Check the labels so they are correct (**Pulmonary artery** and **Aortic ascending flow**). Otherwise, set the label of the ROIs with the tool  (i).
2. Select **Qp/Qs Analysis** from **Flow** menu (a).
3. The **Qp/Qs** ratio is presented in a new message box.

10.3 Shunt and valve analysis [3]

1. Start with vessel segmentation of the pulmonary and/or aorta as described in the Section 10.1. Check the labels so they are correct

10.4. ERASE FLOW SEGMENTATION

(Pulmonary artery and Aortic ascending flow). Otherwise, set the label of the ROIs with the tool  (i).

2. Select **Shunt and Valve Analysis** from **Flow** menu (a).
3. The regurgitant fractions are presented in a new message box.

10.4 Erase flow segmentation

Delete current ROI by selecting  (d), and all ROIs by selecting  (e) in the **ROI / FLOW [F]** mode (h).

10.5 Eddy current compensation

The eddy current compensation algorithm is a method to reduce background phase errors in MR phase contrast images. Note that it is important that when compensating for eddy current effects the image stack should not be cropped, since the algorithm need phase information from the whole image stack.

1. Select **Eddy Current Compensation** from **Flow** menu (a), to open the interface for compensating for eddy current effects, as shown in Figure 16.
2. If necessary, adjust threshold parameters to only include static tissue regions.
3. Select compensation method.
4. Click on **Calculate**.
5. Click on **Apply** to apply the compensation on the image stack.
6. Click on **Done** to close the interface.

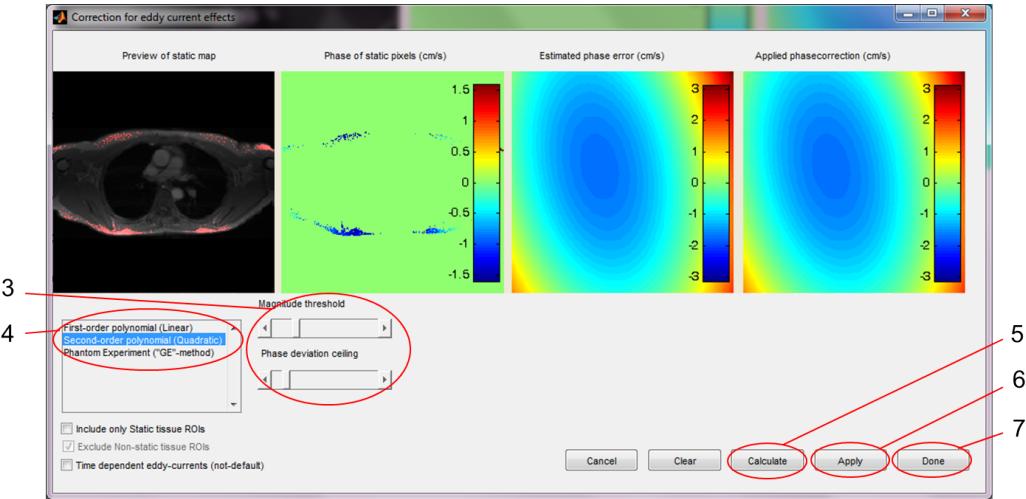


Figure 16: Eddy current compensation GUI.

10.6 Phase unwrapping

The unwrap algorithm is a method to correct wrapped phase values in MR phase contrast images.

1. Select from **ROI / FLOW [F]** mode (h).
2. Enter the original VENC for the dataset.
3. The interface for phase unwrapping is shown, as in Figure 17.
4. Choose a pixel (represented by a red dot in the image).
5. Click on **Auto-Unwrap All**, to apply the automatic phase unwrapping algorithm to the whole image stack.
6. If needed, use the manual tools to unwrap single pixels.
7. Click on **Apply and Exit**, to store the unwrapping in the dataset and to return to the main GUI.

10.7. PULSE WAVE VELOCITY (PWV) ANALYSIS [4]

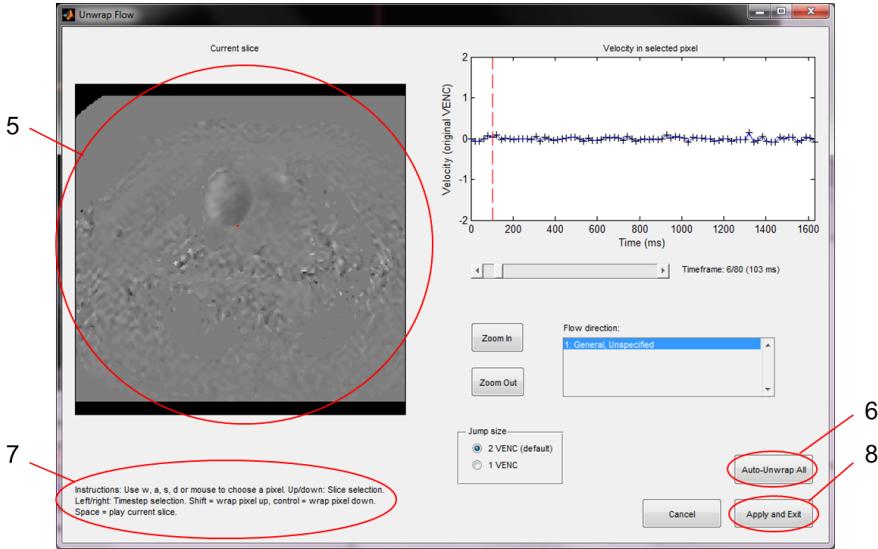


Figure 17: Phase unwrap GUI.

10.7 Pulse wave velocity (PWV) analysis [4]

1. Start with a measurement labelled **Aortic Length** and two ROIs labelled **Aortic ascending flow** and **Abdominal aorta**. This is done by using the measurement tools as described in section 5.5 and flow ROI tools as described in Chapter 10.
2. Select **Pulse Wave Velocity Analysis** under **Analysis (a)**, to start pulse wave velocity analysis.
3. To the left the measurement is displayed in yellow and the intersections with images containing flow are displayed as white lines. On the right is a plot of flow curves along with their respective calculated tangents. The sigma parameter in the calculation can be adjusted using the slider.

10.8 Validation of Flow analysis

1. S. Bidhult, M. Carlsson, K. Steding-Ehrenborg, H. Arheden, and E. Heiberg, A new method for vessel segmentation based on a priori input from medical expertise in cine phase-contrast Magnetic Resonance

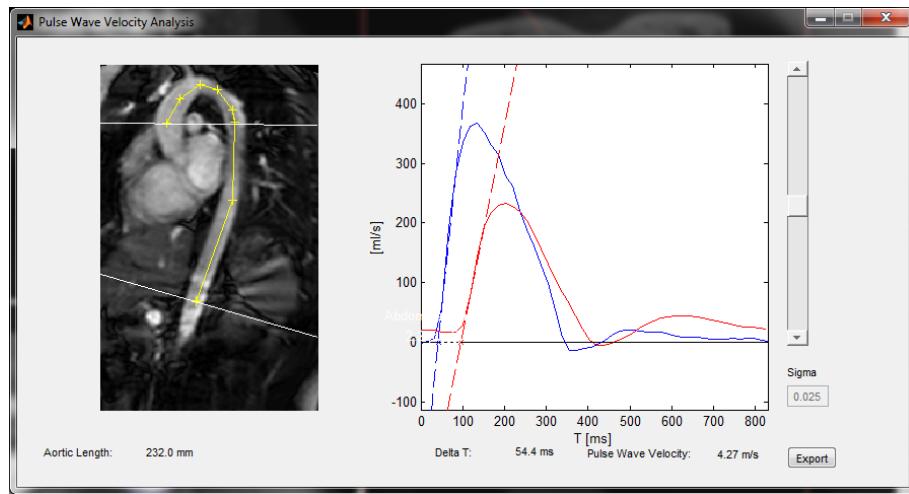


Figure 18: GUI for Pulse wave velocity analysis.

Imaging. In Proceedings of Seventeenth Annual SCMR Scientific Sessions, New Orleans, USA, 2014.

2. P. Munkhammar, M. Carlsson, H. Arheden, and E. Pesonen, Restrictive right ventricular physiology after Tetralogy of Fallot repair is associated with fibrosis of the right ventricular outflow tract visualized on cardiac magnetic resonance imaging, *Eur Heart J Cardiovasc Imaging* 14(10) pp. 978-85, 2013.
3. G. Barone-Rochette, S. Pierard, S. Seldrum, C. de Meester de Ravenstein, J. Melchior, F. Maes, A. C. Pouleur, D. Vancraeynest, A. Pasquet, J. L. Vanoverschelde, and B. L. Gerber, Aortic Valve Area, Stroke Volume, Left Ventricular Hypertrophy, Remodeling and Fibrosis in Aortic Stenosis Assessed by Cardiac MRI: Comparison Between High and Low Gradient, and Normal and Low Flow Aortic Stenosis, *Circ Cardiovasc Imaging*, 2013.
4. K. Dorniak, E. Heiberg, M. Hellmann, D. Rawicz-Zegrzda, M. Wesierska, R. Galaska, A. Sabisz, E. Szurowska, M. Didziak and E. Hedstrom, Required temporal resolution for accurate thoracic aortic pulse wave velocity measurement by phase-contrast magnetic resonance imaging

10.8. VALIDATION OF FLOW ANALYSIS

and comparison with clinical standards applanation tonometry. BMC Cardiovasc Disord, 16(1):110, 2016.

11 Bullseye analysis - Step by step

1. Start with manual or automated segmentation of the LV as described in Chapter 7.
2. Select the image stack to perform bullseye analysis of.
3. Click on the tool  (i) in mode  (h) to open Bullseye analysis interface, as shown in Figure 19.

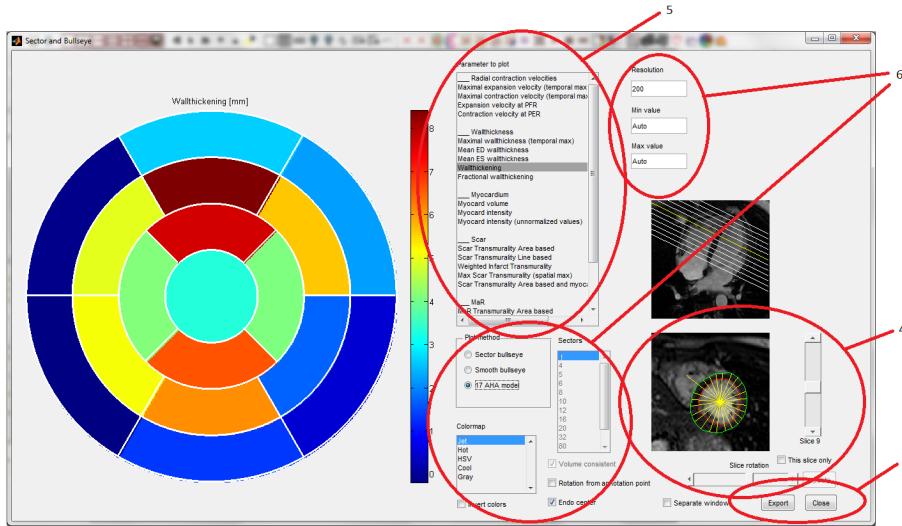


Figure 19: Bullseye analysis GUI.

4. Set the slice rotation by dragging the slider so the yellow line is in the middle of septum. Click on **Update**. This step is important to have a correct bullseye plot.
5. Select the parameter to plot.
6. Set the viewing parameters.

7. Click on **Export**, to export data to spreadsheet.

12 Report generation - Step by step

1. After performing measurements, click on the reporter  to show the report generator.

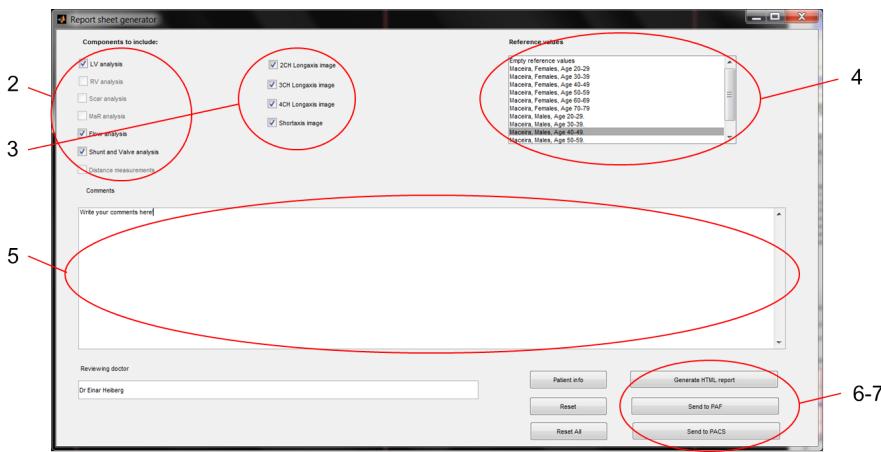


Figure 20: Report generator.

2. Select the desired sections to include in the report. Sections that are grayed out is not available since measurements, or images are missing.
3. Select the images to include in the report.
4. Ensure that the appropriate reference values are chosen.
5. Write your impression about the patient.
6. Click on **Generate HTML report**, to generate a HTML report.
7. Click on **Send to PACS**, to send the report to PACS.

12.1 Reference values used in the report

1. A. M. Maceira, S. K. Prasad, M. Khan, and D. J. Pennell, Normalized Left Ventricular Systolic and Diastolic Function by Steady State Free Precession Cardiovascular Magnetic Resonance. *J Cardiovasc Magn Reson.* 2006;8(3).

13 Relaxometry analysis - Step by step

13.1 T2* analysis

1. Start with manual or automated segmentation of the LV in all time frames as described in Chapter 7.
2. Place a ROI in the image stack to define the region for applying T2* calculation, as described in Chapter 9.
3. Start the T2* module by selecting  (i) under  menu (h).

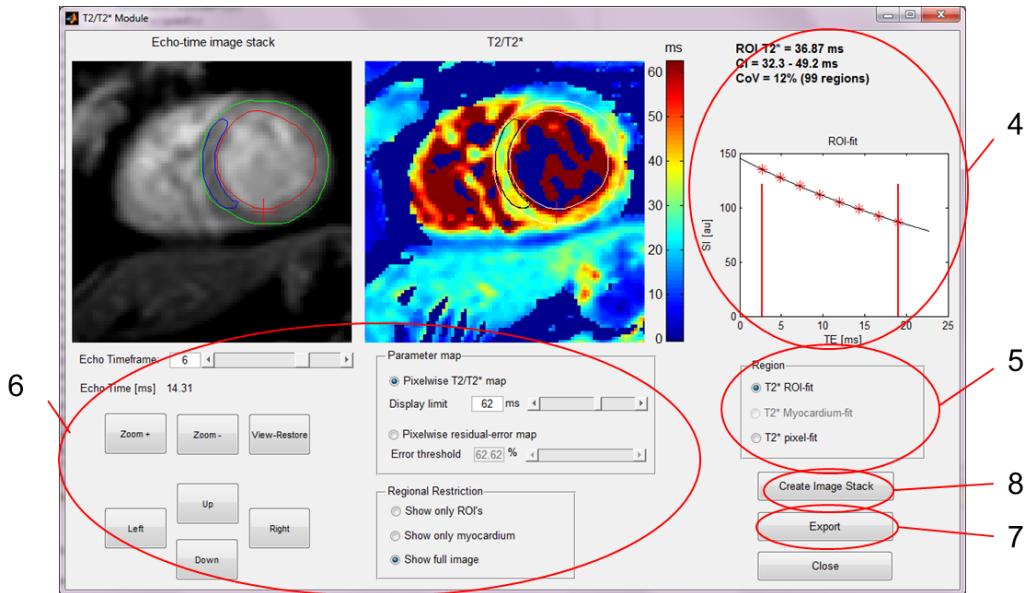


Figure 21: T2* analysis GUI.

4. The regional mean T2* value is presented above the graph. The regional mean T2* values has been shown to closely correlate to iron concentration [2, 3].

5. A pixelwise T2* value is provided by selecting **T2* pixel-fit**, and moving the red cross in the acquired image on the left, or in the T2* map.
6. Image viewing parameters are defined by using the sliders and checkboxes in the bottom left part of the panel.
7. Click on **Export** to export result to spreadsheet.
8. Click on **Generate Image Stacks** to add the T2* map to the main GUI of Segment CMR.

13.1.1 Validation of T2* analysis

1. S. Bidhult, C. G. Xanthis, L. L. Liljekvist, G. Greil, E. Nagel, A. H. Aletras, E. Heiberg, E. Hedstrom, Validation of a New T2* Algorithm and Its Uncertainty Value for Cardiac and Liver Iron Load Determination from MRI Magnitude Images. *Magn Reson Med*, May 22, 2015.

13.2 T1 analysis

1. Place a ROI in the image stack to define the region for applying T1 calculation, as described in Chapter 9.
2. Start the T1 module by selecting  (i) under **ANALYSIS [A]** menu (h).
3. The regional mean T1 value is presented above the graph.
4. A pixelwise T1 value is provided by selecting **T1 pixel-fit**, and moving the red cross in the acquired image on the left, or in the T1 map.
5. Image viewing parameters are defined by using the sliders and checkboxes in the bottom left part of the panel.
6. Click on **Export** to export result to spreadsheet.
7. Click on **Generate Image Stacks** to add the T1 map to the main GUI of Segment CMR.
8. Click on **options** to change number of parameters in the T1 fitting model, change ROI for analysis and plot T1 histogram within currently selected restriction.

13.3. T2 ANALYSIS

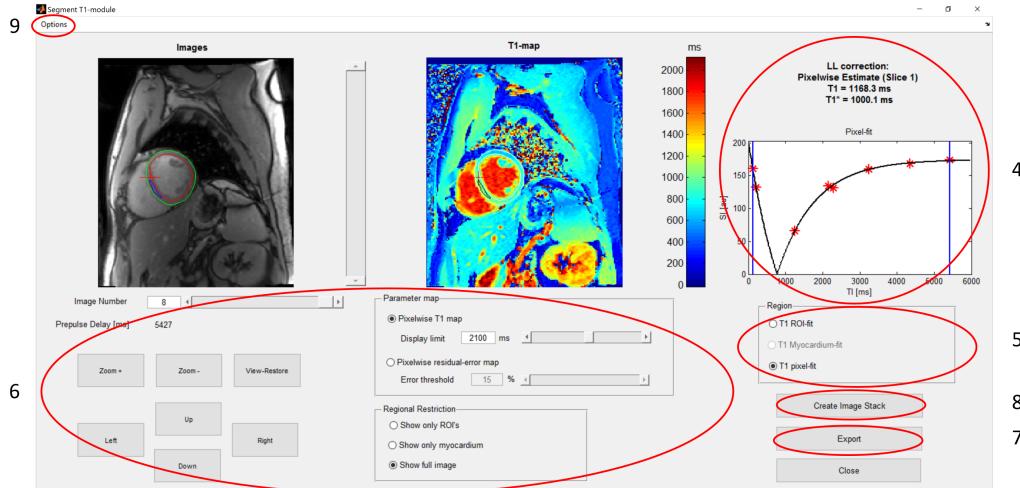


Figure 22: T1 analysis GUI.

13.3 T2 analysis

1. Place a ROI in the image stack to define the region for applying T2 calculation, as described in Chapter 9.
2. Start the T2 module by selecting [T2] (i) under [ANALYSIS [A]] menu (h).
3. The regional mean T2 value is presented above the graph.
4. A pixelwise T2 value is provided by selecting [T2 pixel-fit] , and moving the red cross in the acquired image on the left, or in the T2 map.
5. Image viewing parameters are defined by using the sliders and checkboxes in the bottom left part of the panel.
6. Click on [Export] to export result to spreadsheet.
7. Click on $\text{[Generate Image Stacks]}$ to add the T2 map to the main GUI of Segment CMR.
8. Click on [options] to change number of parameters in the T2 fitting model, change ROI for analysis and plot T2 histogram within currently selected restriction.

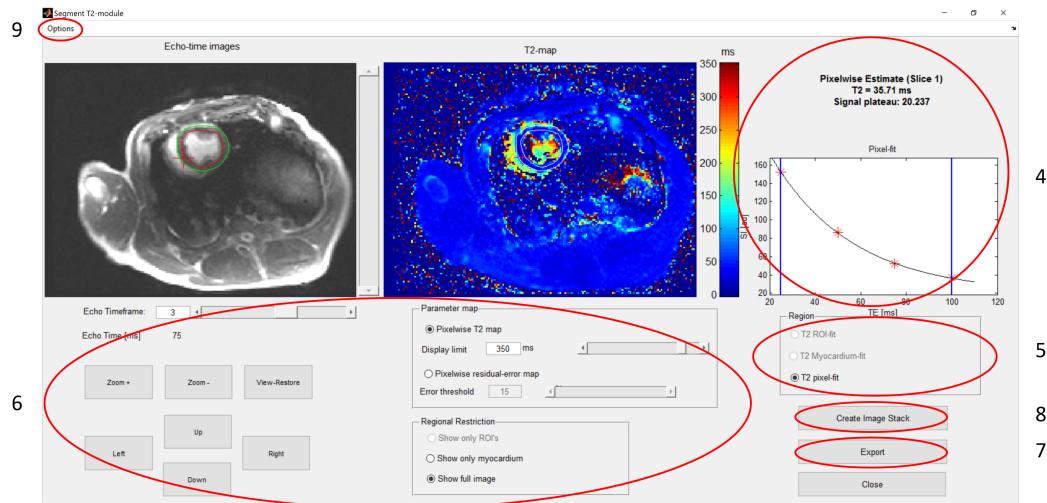


Figure 23: T2 analysis GUI.

13.3.1 Validation of T1/T2 analysis

1. S. Bidhult, G. Kantasis, A. H. Aletras, H. Arheden, E. Heiberg, E. Hedstrom, Validation of T1 and T2 algorithms for quantitative MRI: performance by a vendor-independent software. BMC Medical Imaging, August 8, 2016.

14 Strain analysis - Step by step

14.1 Strain analysis in cine or tagged images

14.1.1 Automatic strain analysis in short-axis image stacks [1-3]

1. **Tagging:** The automatic strain analysis starts upon loading a tagged image stack. Segment CMR identifies a tagged image stack according to the DICOM tag Series Description. The associated Series Description names can be customized by the user according to Section 6. Manually start the strain analysis by select Tagging Strain Short-axis under Strain menu.
2. **Cine:** First perform LV segmentation. The LV segmentation should be performed in the first time frame in the cine image stack, according to Chapter 7. Start the strain analysis by select Feature Tracking Strain Short-axis under Strain menu.
3. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 24.
4. 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 CMR. During the registration process the user can perform LV segmentation. The LV segmentation should be performed in one of the first seven time frames in the tagged image stack, or potential cine image stack, according to Chapter 7. This time frame will be the initial time frame for the strain tracking.
5. 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 CMR go to the time frame representing end-diastole, then select Set First Timeframe for Selected Slices at Current Timeframe in menu Edit.
6. **Tagging:** Start the strain module by selecting Tagging Strain Short-axis under Strain menu (a). The Strain interface is shown (Figure 25).

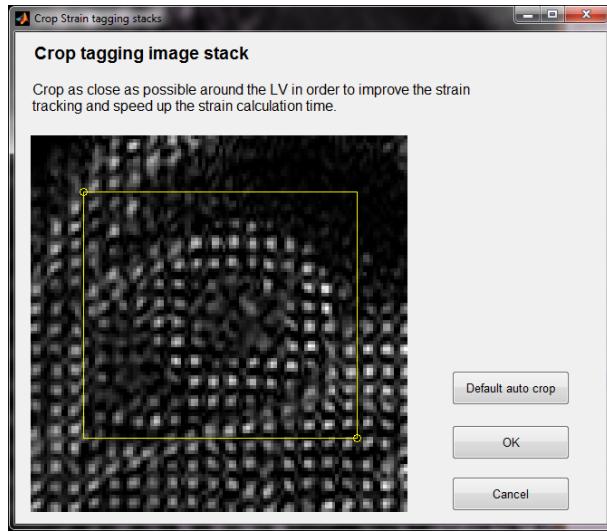


Figure 24: Strain cropping interface.

Cine: Start the strain module by selecting **Feature Tracking Strain Short-axis** under **Strain** menu (a). The Strain interface is shown (Figure 25).

6. Define LV rotation by setting the white line in the middle of the RV lumen, using the slider, and press **Analyse** to run the myocardial strain quantification.
7. Verify the strain tracking by using the movie tools.
8. Strain over time and peak strain is shown in the figures to the right according to the selected parameters.
9. The different curves in the graphs can be hided by using the radiobuttons below the graph.
10. 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 image stack. Then run the strain quantification again by select **Analyse**.

14.1. STRAIN ANALYSIS IN CINE OR TAGGED IMAGES

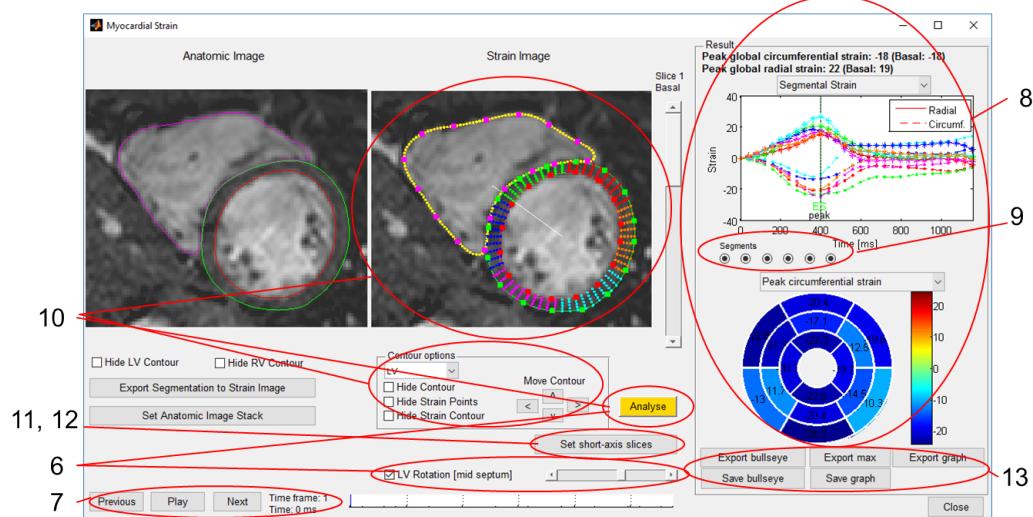


Figure 25: Strain analysis GUI.

11. Manually change the short-axis slices for the bullseye division by select **Set short-axis slices**.
12. Manually change the initial time frame by select **Set initial time frame**.
13. Click on export buttons to export result to spreadsheet.

14.1.2 Automatic strain analysis in long-axis image stacks [1-3]

1. **Tagging:** The automatic strain analysis starts upon loading a tagged image stack. Segment CMR identifies a tagged image stack according to the DICOM tag Series Description. The associated Series Description names can be customized by the user according to Section 6. Manually start the strain analysis by select Tagging Strain Long-axis under Strain menu.
- Cine:** Start the strain analysis by select Feature Tracking Strain Long-axis under Strain menu.
2. Ensure that Image View Plane is set correctly (2CH, 3CH and 4CH), respectively. Otherwise set it according to Section 6.
3. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 26.

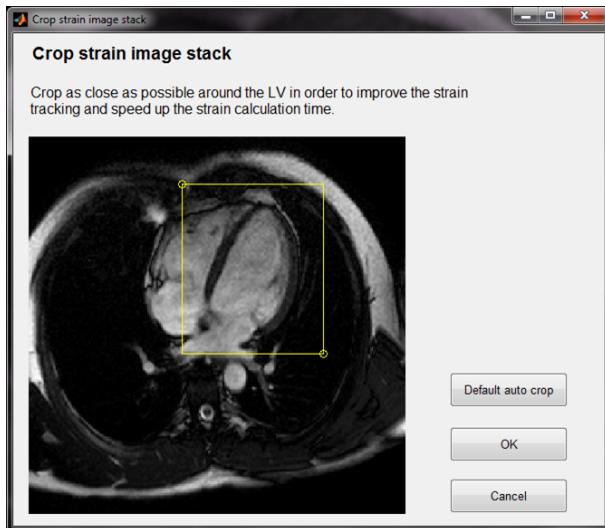


Figure 26: Strain cropping interface.

4. 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 CMR. During the registration process the user can perform LV segmentation.

14.1. STRAIN ANALYSIS IN CINE OR TAGGED IMAGES

5. Before performing the LV segmentation, ensure that the parameter **Number of points along contour** in general settings  (p) is set to 160, in order to have a smooth segmentation. The LV segmentation should be performed in one of the first seven time frames in the tagged image stack, or potential cine image stack, by using the endo segmentation tools  or , according to Figure 27. This time frame will be the initial time frame for the strain tracking.

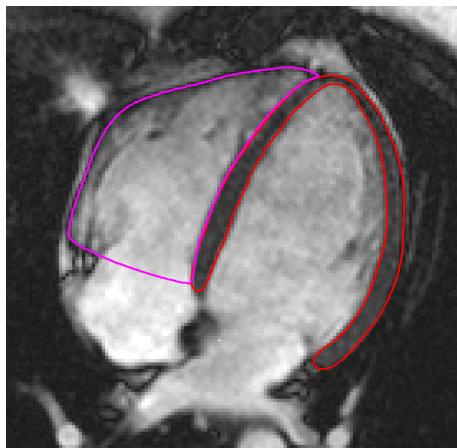


Figure 27: LV segmentation in long-axis image stack.

6. 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 CMR go to the time frame representing end-diastole, then select **Set First Timeframe for Selected Slices at Current Timeframe** in menu **Edit**.
7. **Tagging:** Start the strain module by selecting **Tagging Strain Long-axis** under **Strain** menu (a). The Strain interface is shown (Figure 25).
Cine: Start the strain module by selecting **Feature Tracking Strain Long-axis** under **Strain** menu (a). The Strain interface is shown (Figure 25).
8. Verify the strain tracking by using the movie tools.

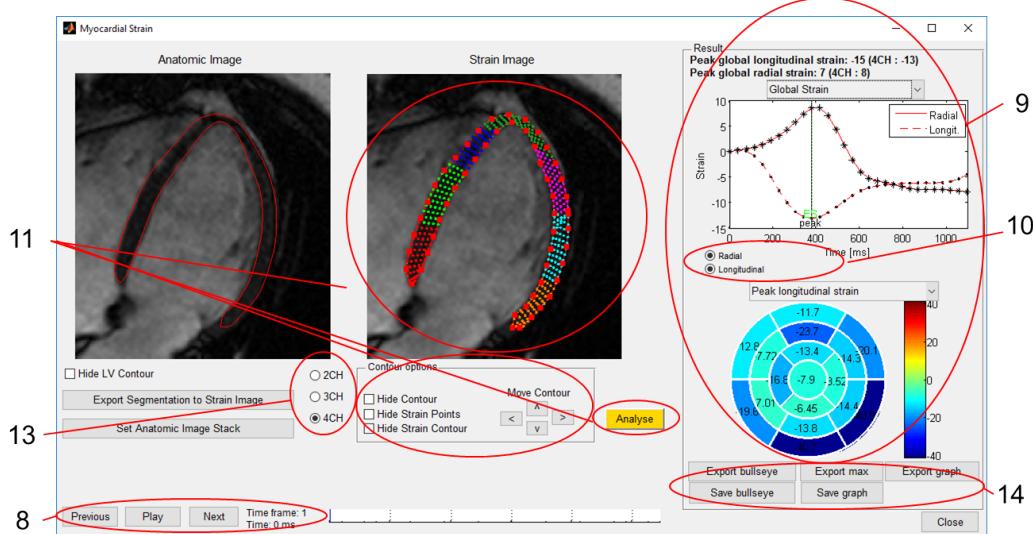


Figure 28: Strain analysis GUI.

9. Strain over time and peak strain is shown in the figures to the right according to the selected parameters.
10. The different curves in the graphs can be hided by using 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 image stack. Then run the strain quantification again by select **Analyse**.
12. Manually change the initial time frame by select **Set initial time frame**.
13. Shift between the different long-axis views by using the radiobuttons below the images.
14. Click on export buttons to export result to spreadsheet.

14.1.3 Erase strain data

Tagging: To erase the strain data, select **Clear Tagging Data** under **Strain** menu (a).

14.1. STRAIN ANALYSIS IN CINE OR TAGGED IMAGES

Cine: To erase the strain data, select **Clear Feature Tracking Data** under **Strain** menu (a)

14.1.4 Validation of strain analysis

1. Medviso White Paper, Strain tagging Validation, 2015. [Available through <http://medviso.com/documents/straintagging.pdf>]
2. Medviso White Paper, Strain Feature tracking Validation, 2016. [Available through <http://medviso.com/documents/strainfeaturetracking.pdf>]
3. P. Morais, A. Marchi, JA. Bogaert, T. Dresselaers, B. Heyde, J. D'hooge and J. Bogaert. Cardiovascular magnetic resonance myocardial feature tracking using a non-rigid, elastic imageregistration algorithm: assessment of variability in a real-life clinical setting. *J Cardiovasc Magn Reson* 2017 Feb 17;19(1):24.
4. Medviso White Paper, Strain Feature tracking Validation, 2017. [Available through <http://medviso.com/documents/strainmodule.pdf>]
5. Heyde B, Jasaityte R, Barbosa D, Robesyn V, Bouchez S, Wouters P, Maes F, Claus P, D'hooge J. Elastic image registration versus speckle tracking for 2-D myocardial motion estimation: a direct comparison in vivo. *IEEE Trans Med Imaging*. 2013 Feb;32(2):449-459
6. P. Morais, B. Heyde, D. Barbosa, S. Queiros, P. Claus, and J. D'hooge. Cardiac motion and deformation estimation from tagged MRI sequences using a temporal coherent image registration framework. *Proceedings of the meeting on Functional Imaging and Modelling of the Heart (FIMH), Lecture Notes in Computer Science*, vol. 7945, pages 316-324, London, 2013.

14.2 Strain analysis in velocity encoded images

14.2.1 Automatic strain analysis [1]

1. Ensure that the feature **Number of points along contour** under is set to 300 (a).
2. Start with manual segmentation of the LV in end-diastole in the magnitude long-axis image stack by using the tool . The LV segmentation can also be performed in the Cine image stack and thereafter be imported to the magnitude image stack by **Import From Cine Stack** under **Strain From Velocity Encoded Imaging** under **Strain** menu (a).
3. Start the strain module by selecting **Strain Tool** under menu **Strain From Velocity Encoded Imaging** under **Strain** menu (a). The Strain interface is shown (Figure 29).

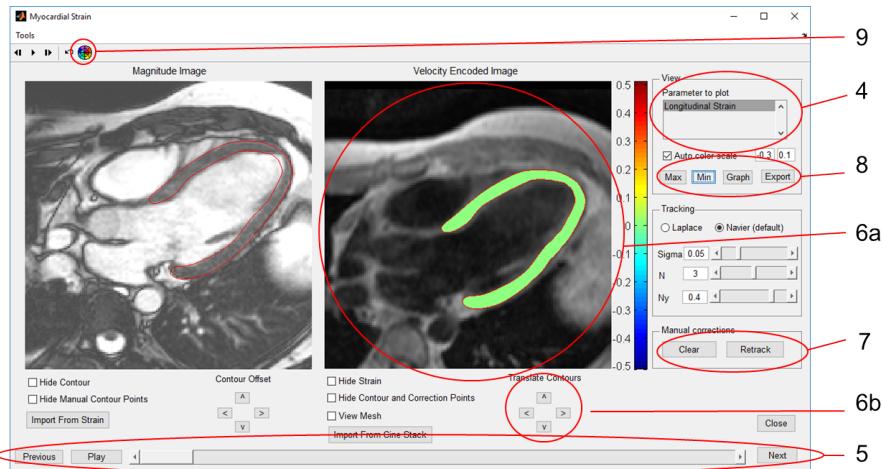


Figure 29: Strain analysis GUI.

4. Select **Parameter to plot**.
5. Verify the strain tracking by using the movie tools.
6. If needed, manual correction can be performed in two ways:
 - (a) Use the left click of the mouse to move a contour point, and use the right click of the mouse to delete a manual contour point.

14.2. STRAIN ANALYSIS IN VELOCITY ENCODED IMAGES

- (b) Manually transfer the contour by using the arrow buttons in the interface.
- 7. Use **Retrack** to calculate strain after manual correction. Use **Clear** to delete all manual corrections.
- 8. The tool enables visualization of maximal strain, minimal strain and strain over time and export to clipboard.
- 9. Click on  for bullseye plot of strain.

14.2.2 Erase strain data

To erase the strain data, select **Clear Strain Data** from **Strain From Velocity Encoded Imaging** under **Strain** menu (a).

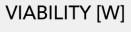
14.2.3 Validation of strain analysis

- 1. E. Heiberg, U. Pahlm-Webb, S. Agarwal, E. Bergvall, H. Fransson, K. Steding-Ehrenborg, M. Carlsson and H. Arheden, Longitudinal strain from velocity encoded cardiovascular magnetic resonance: a validation study. *J Cardiovasc Magn Reson*, 15:15, 2013.

15 Scar analysis - Step by step

The functions described in this chapter is in US only for off label use and for investigational use.

15.1 Automatic scar analysis [1]

1. Start with manual or automated segmentation of the LV as described in Chapter 7.
2. Click on  mode (h).
3. Click on  (i).

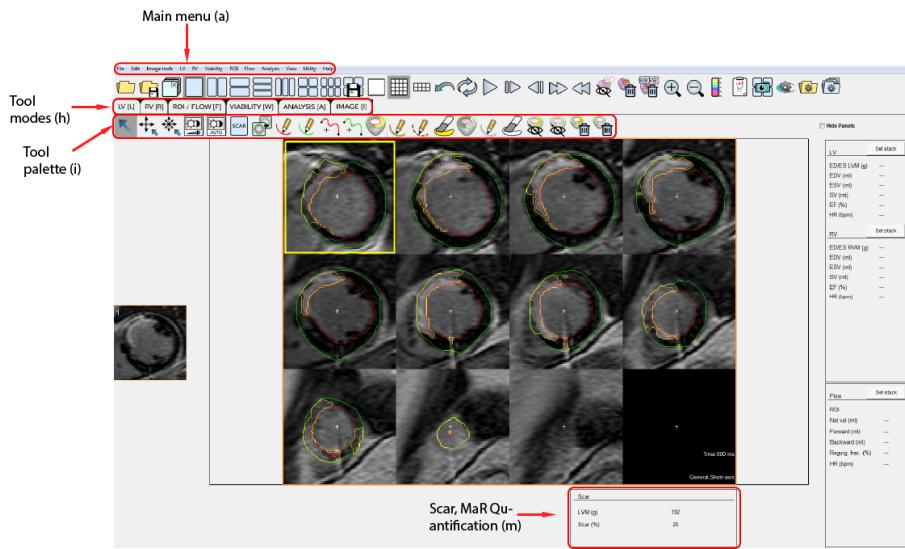


Figure 30: Scar segmentation.

4. If necessary, use the tools  (i), to add scar region, and  (i), to remove scar region.
5. The yellow line demarks the scar region, and the pink line demarks a visual representation of the mass of the infarct. This would be the

corresponding area to include if just counting pixels instead of using the automatic weighted approach.

6. The measured Scar volumes are presented in (m).

15.2 Grayzone analysis

1. Start with manual or automated segmentation of the scar as described in the section above.
2. Select **Gray Zone Analysis** from **Scar** menu (a).

15.3 Erase scar segmentation

To erase the Scar segmentation, select  from **VIABILITY [W]** mode (h).

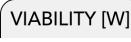
15.4 Validation of Scar analysis

1. E. Heiberg, M. Ugander, H. Engblom, M. Gotberg, G. K. Olivecrona, D. Erlinge, and H. Arheden, Automated quantification of myocardial infarction from MR images by accounting for partial volume effects: animal, phantom, and human study, *Radiology* 246(2) pp. 581-8, 2008.

16 Myocardium at Risk (MaR) analysis - Step by step

The functions described in this chapter is in US only for off label use and for investigational use.

16.1 Automatic MaR analysis [1]

1. Start with manual or automated segmentation of the LV as described in Chapter 7.
2. Click on  mode (h).
3. Click on  (i).

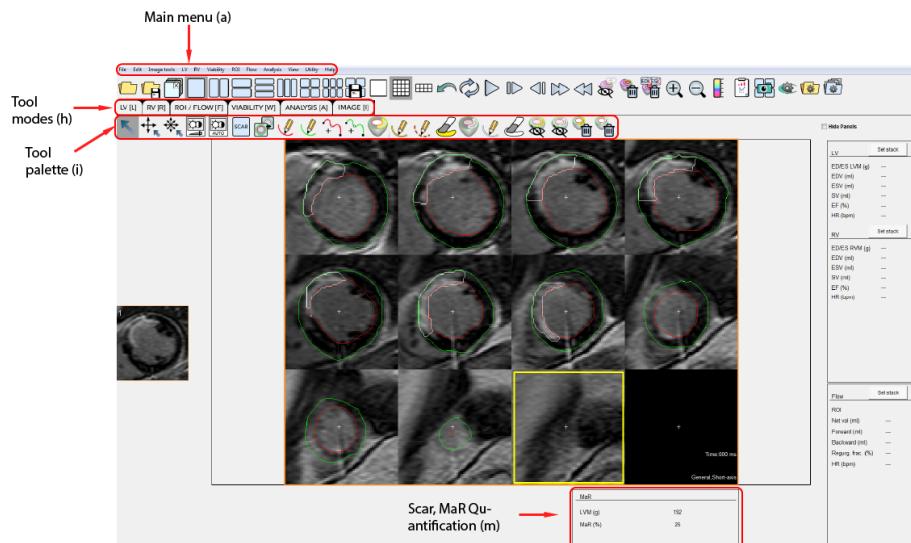


Figure 31: MaR segmentation.

4. Use the tools  (i), to add MaR region, and  (i), to remove MaR region, if necessary.

5. The white line demarks the MaR region.
6. The measured MaR volumes are presented in (m).

16.2 Erase MaR segmentation

To erase the MaR segmentation, select  from  mode (h).

16.3 Validation of MaR analysis

1. J. Sjogren, J. F. Ubachs, H. Engblom, M. Carlsson, H. Arheden, and E. Heiberg, Semi-automatic segmentation of myocardium at risk in T2-weighted cardiovascular magnetic resonance, *J Cardiovasc Magn Reson* 14(1) p 10, 2012.

17 Perfusion analysis - Step by step

The functions described in this chapter is in US only for off label use and for investigational use.

17.1 Automatic perfusion analysis [1]

1. Start with a rest image stack and a stress image stack. Both image stacks need to have LV segmentation in all slices in one time frame, as described in Chapter 7. Make sure **Image Type** is set correctly (**Perfusion Rest** and **Perfusion Stress**). Otherwise set it according to Section 6.
2. Start the perfusion module by selecting  from **ANALYSIS [A]** mode (h).

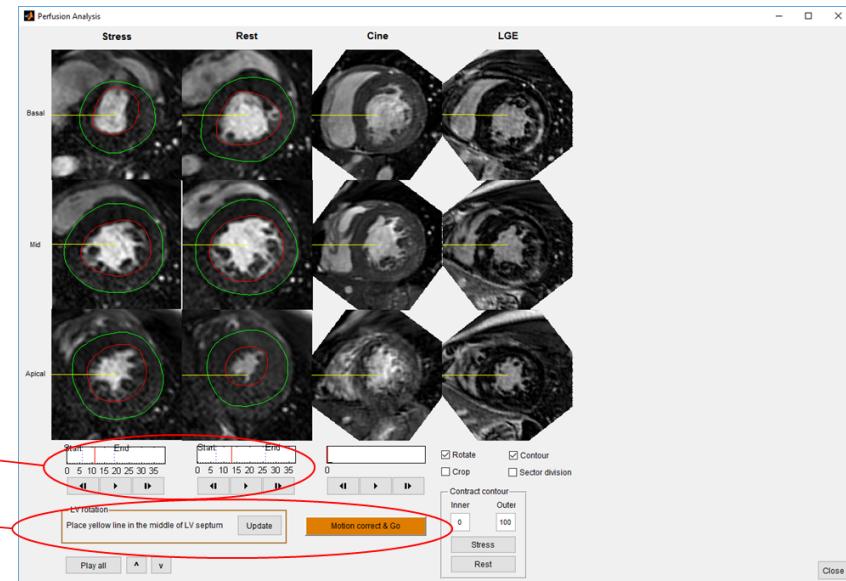


Figure 32: Perfusion analysis GUI.

3. Select the Start and End slice for motion correction.

CHAPTER 17. PERFUSION ANALYSIS - STEP BY STEP

4. Set the LV rotation by dragging the yellow line to point at the middle of septum. Click on **Motion correction & Go**, to start the analysis. This generates motion corrected image stacks with LV segmentation in all selected time frames.

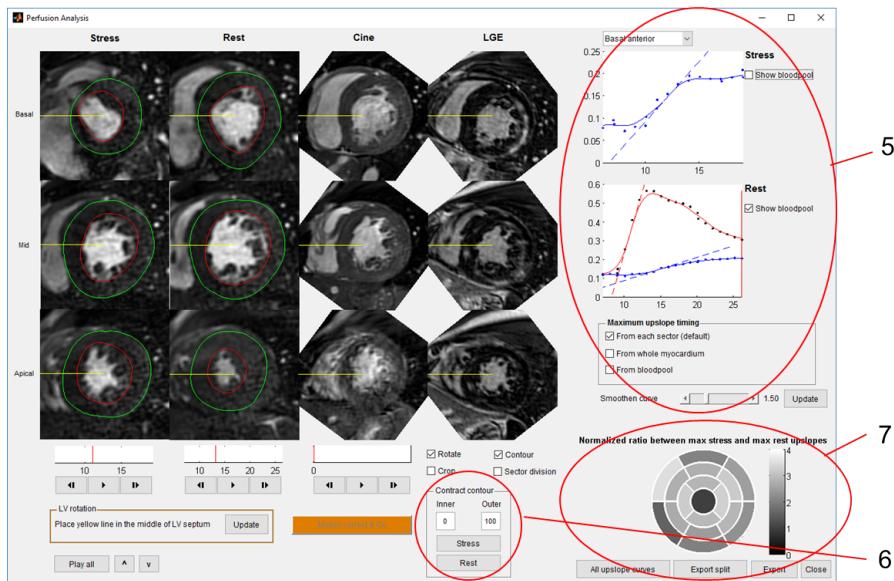


Figure 33: Perfusion analysis result.

5. Select LV region to plot, and the level of smoothing of the Gaussian filter used in the curve fitting process.
6. If intensity from outside of the LV spills into the LV segmentation, the LV contour can be contracted for each image stack by setting the inner and outer values [0 100] and clicking on **Stress** or **Rest**.
7. The bullseye plot displays the sectorwise quote between the maximum stress and rest upslopes, normalized with respect to the respective maximum upslopes of the bloodpool curves. Click on **Export** to export result to spreadsheet.

17.2. VALIDATION OF PERFUSION ANALYSIS

17.2 Validation of perfusion analysis

1. M. Saeed, S. W. Hetts, L. Do, and M. W. Wilson, MRI study on volume effects of coronary emboli on myocardial function, perfusion and viability, *Int J Cardiol*, 2011.

18 ECV analysis - Step by step

The functions described in this chapter is in US only for off label use and for investigational use.

18.1 Automatic ECV analysis

1. Start with pre T1 map image stack(s) and post T1 map image stack(s). The ECV analysis can be performed for multiple image stack pairs or multiple slices in the same analysis. Make sure **Image Type** is correctly defined (**T1 map Pre** and **T1 map Post**). Otherwise set it according to Section 6.
2. Perform segmentation of the LV in one time frame in both pre and post image stacks as described in Chapter 7.
3. Place a ROI defining the blood pool in both pre and post image stacks and label it **Blood** as described in Chapter 9.
4. Define regions for ECV quantification by placing ROIs in the pre T1 map.
5. Select **ECV From Registration** under **ECV** menu from the **Analysis** menu. The post T1 maps are then aligned with to the pre T1 maps.
6. The result is presented in a new interface, according to Figure 34.
7. Click on **Export** to export result to spreadsheet.
8. Click on **Generate Image Stack** to add the ECV map to the main GUI of Segment CMR.

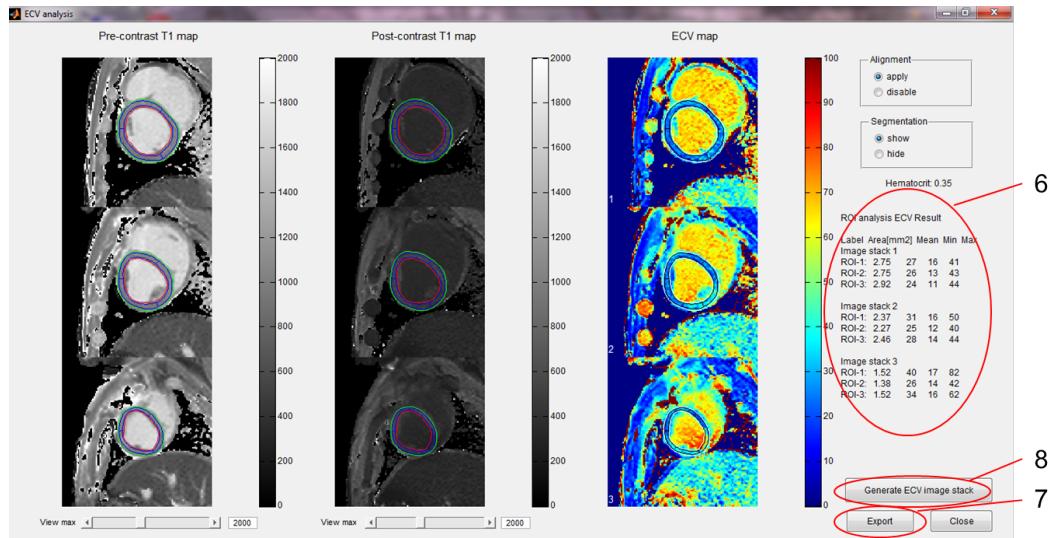


Figure 34: ECV analysis result.

19 Short Commands / Hot keys

This chapter describes the hot keys that can be used in Segment CMR.

Stack navigation commands

Left arrow	Previous frame or pan left
Right arrow	Next frame or pan right
Up arrow	View next slice in basal direction
Down arrow	View next slice in apical direction
D	Go to end diastole
S	Go to end systole
Shift-D	Go to end diastole all visible image stacks
Shift-S	Go to end systole all visible image stacks
C	Start to play cine thumbnail
P	Start to play movie

Viewing commands

R	Refresh screen
H	Hide/show all contours and markers
V	Shift mode in panel between montage and one slice
Ctrl-A	Selects all slices
Shift-U	Unselect all slices
Shift-A	View all image stacks
Shift-1	View one image panel
Shift-2	View two image panels
Alt-2	View two image panels as rows
Shift-3	View three image panels
Alt-3	View three image panels as rows
Shift-4	View three image panels
Shift-6	View six image panels
Alt-6	View six image panels as rows
Shift-9	View nine image panels
Ctrl-1	One view

CHAPTER 19. SHORT COMMANDS / HOT KEYS

Ctrl-2	M-mode view
Ctrl-3	Montage view
Ctrl-4	Montage row view
Ctrl-5	Montage fit view
Ctrl-plu	Zoom in
Ctrl-minus	Zoom out
Segmentation commands	
<hr/>	
- LV -	
Ctrl-L	Perform fully automatic LV segmentation
Ctrl-M	Segment LV endocardium
Ctrl-Shift-M	Segment LV epicardium
Ctrl-R	Refine LV endocardium
Ctrl-Shift-R	Refine LV epicardium
Ctrl-F	Propagate LV endocardium forward and refine
Ctrl-Shift-F	Propagate LV epicardium forward and refine
Ctrl-U	Copy LV endocardium upwards and refine
Ctrl-Shift-U	Copy LV epicardium upwards and refine
Ctrl-D	Copy LV endocardium downwards and refine
Ctrl-Shift-D	Copy LV epicardium downwards and refine
Ctrl-E	Expand LV Endo
Ctrl-K	Contract LV Endo
Ctrl-Alt-E	Expand LV Epi
Ctrl-Alt-K	Contract LV Epi
Ctrl-V	Exclude papillary muscle from LV endocardium
Shift-Alt-R	Refine LV endocardium for Alternative LV segmentation method
- RV -	
Ctrl-Alt-M	Segment RV endocardium
Ctrl-Alt-R	Refine RV endocardium
Ctrl-Alt-F	Propagata RV endocardium forward, do not refine
Ctrl-Alt-U	Copy RV endocardium upwards and refine
Ctrl-Alt-D	Copy RV endocardium downwards and refine
- Flow -	
Alt-T	Track tool for Flow ROI
Alt-R	Refine Flow ROI
Alt-F	Propagate Flow ROI forward and refine
Ctrl-T	Plot flow

- General -

0	Smooth current segmentation
Ctrl-Z	Undo segmentation

Analysis commands

Alt-D	Set end diastole at current time frame
Alt-S	Set end systole at current time frame
Ctrl-B	Bullseye plot

Translation commands

Alt-A	Translate contours left (selected slices)
Alt-X	Translate contours right (selected slices)
Alt-W	Translate contours up (selected slices)
Alt-Z	Translate contours down (selected slices)
Shift-Alt-A	Translate contours and image left (selected slices)
Shift-Alt-X	Translate contours and image right (selected slices)
Shift-Alt-W	Translate contours and image up (selected slices)
Shift-Alt-Z	Translate contours and image down (selected slices)

Tool toggling commands

Space	Toggle tool in toolbar menu (depending on tool and mode)
Shift-L	Select LV mode
Shift-R	Select RV mode
Shift-F	Select ROI/Flow mode
Shift-V	Select Scar(Viability) mode
Shift-M	Select MaR mode
Shift-I	Select Misc mode
Shift-N	Select LV Endo pen
Shift-B	Select LV Epi pen
Shift-G	Select LV Endo interp
Shift-H	Select LV Epi interp

File menu commands

Ctrl-N	Load next .mat file
---------------	---------------------

CHAPTER 19. SHORT COMMANDS / HOT KEYS

Ctrl-O	Load image stack
Ctrl-P	Open patient data base
Ctrl-O (zero)	Reset GUI Position
Ctrl-S	Save all image stacks
Ctrl-W	Close current image stack
Ctrl-Shift-W	Close all image stacks
Ctrl-Q	Quit program

Mouse commands

Mouse wheel	Scroll through slices
Shift-Mouse wheel	Scroll through time frames
Ctrl-Mouse wheel	Scroll through visible thumbnails
Alt-Mouse wheel	Zoom
Left+Right mouse button	Pan / Windowing (dependent on selected tool)