

Segment CMR
Reference Manual



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Software platform v2.1 R6065

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Contents

1	Regulatory Status	1
1.1	Commercial usage of Segment CMR	1
1.2	Indications for use	1
1.3	Investigational purposes	1
2	How to Read This Manual	3
3	Conventions and Abbreviations	5
3.1	Typographic conventions	5
3.2	Trademarks	5
3.3	Abbreviations	5
4	System Requirements	9
4.1	Operating system	9
4.2	Hardware requirements	9
5	Loading Image Stacks	11
5.1	Loading DICOM files	13
5.1.1	Loading DICOM files	13
5.1.2	Tips and tricks	15
5.1.3	Graphical image series selection	15
6	Program Overview	17
6.1	Viewing image stacks	18
6.2	Montage view	19
6.3	Montage row view	21
6.4	One slice view	21
6.5	Viewing velocity encoded image stacks	21

CONTENTS

6.6	Playing images as a cine-loop	21
6.7	Synchronizing image stacks	22
6.8	Loading and storing images	23
6.9	Tool palette	23
6.9.1	Left ventricle tools	24
6.9.2	Right ventricle tools	25
6.9.3	Viability/Scar tools	25
6.9.4	Miscellaneous tool mode	26
6.9.5	ROI tool mode	27
6.10	General view and reporting functionality	27
7	Measurements and Annotations	29
7.1	Length measurements	29
8	Image settings	31
8.1	Manually set image description	31
8.2	Image description upon loading	31
9	Segmentation of the Left Ventricle	33
9.1	Definition of the left ventricle	33
9.1.1	Papillary muscles	33
9.1.2	Mitral annulus	33
9.2	Automatic LV segmentation	33
9.2.1	Before the segmentation process	33
9.2.2	Automatic LV segmentation method	34
9.2.3	Alternative automatic LV segmentation method	35
9.3	Edit the segmentation result	36
9.3.1	Undo segmentation	37
9.3.2	Refine segmentation	37
9.3.3	Expand or contract segmentation	37
9.3.4	Manually adjusting the contour by interpolation points	37
9.3.5	Manually drawing the contour	38
9.3.6	Translating the segmentation	38
9.3.7	Scale the segmentation	38
9.3.8	Manually include/exclude papillary muscles	38
9.3.9	Removing segmentation result	39
10	Segmentation of the Right Ventricle	41

11 Segmentation of Long Axis Images	43
11.1 Click an image to show point location in all views	43
12 Regional Wall Analysis	45
12.1 Radial contraction versus time	45
12.2 Report per slice	45
13 Flow Analysis	47
13.1 Automatic segmentation of flow ROI's	47
13.1.1 Refine	48
13.1.2 Refine and propagate	48
13.1.3 Shrink flow ROI	48
13.2 Plotting the result of the flow analysis	48
13.3 Compensating for eddy current effects	50
13.4 Phase unwrapping	53
13.4.1 Automated unwrapping	53
13.4.2 Manual unwrapping	53
13.5 Creating angio and velocity magnitude images	55
13.6 Coupling magnitude and flow images	55
14 Bulls eye Analysis	57
15 T2* Quantification Module	59
15.1 Module overview	59
15.2 Implementation	61
15.3 Validation	61
16 Strain Analysis	63
16.1 Strain analysis in cine or tagged images	63
16.1.1 Definition of Mean strain	63
16.1.2 Automatic strain analysis in short-axis image stacks .	63
16.1.3 Automatic strain analysis in long-axis image stacks .	67
16.1.4 Hints for Strain analysis in small animal images . .	70
16.1.5 Erase strain data	70
16.2 Strain Analysis in Velocity Encoded Images	71
16.2.1 Strain calculation	72
16.2.2 Corrections of the segmentation	73
16.2.3 Strain analysis	73

CONTENTS

17 Viability Analysis	75
17.1 Automatic mode (EWA method)	78
17.2 Old weighted	79
17.3 Manual mode	79
17.4 SD from remote	79
17.5 EM algorithm	80
17.6 Technical details	80
17.7 Grayzone Analysis	80
18 Myocardium at Risk Analysis	81
18.1 MaR from T2-weighted images	81
18.2 MaR from CE-SSFP images	82
19 Perfusion Analysis	83
19.1 Module overview	83
20 Pulse Wave Velocity Analysis	87
21 LV Sphericity Analysis	89
22 Reporting	91
22.1 Configuration	92
22.1.1 Hospital logo	92
22.1.2 Reference values	93
22.1.3 Headings for textual report	93
22.1.4 Reviewing doctor	94
23 Export Images and Results	97
23.1 Export image	97
23.2 Export screenshot	97
23.3 Export movies	97
23.4 Movie Recorder	97
24 Customization	99
24.1 Image description settings	101
24.2 Advanced and DICOM Settings	102
24.3 PACS Settings	103
24.4 Technical details	103

CONTENTS

25 Short Commands / Hot keys	105
26 Support	109
26.1 Submit bug report	109
26.2 Data privacy policy	110
26.3 General support issues	110
27 Implementation Details	111
27.1 Numeric representations	111
27.2 Loading data and interpretation of DICOM tags	111
27.3 Volume calculations	113
27.4 Mass calculations	113
27.5 Calculation of BSA	114
27.6 Peak ejection/filling rate	114
27.7 Wall thickness	114
27.8 Calculation of regurgitant volumes and shunts	115
27.9 Infarct size, extent and transmurality	115
27.10 Number of SD from remote for Scar	116
27.11 MR relaxometry calculations	116
27.12 Pulse wave velocity	117
27.13 Torsion	117
27.13.1 Least squares circle fit	117
27.13.2 Angular discontinuity detection	119
27.14 Longaxis volumes	120

1 Regulatory Status

1.1 Commercial usage of Segment CMR

Segment CMR bears the CE marking of conformity and is certified according to the ISO 13485 standard. Segment CMR is based almost entirely on the software Segment which is FDA approved with FDA 510(k) number K090833. 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. An application for FDA approval for Segment CMR is under preparation.

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 statutes, rules and regulations.

1.2 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 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.**

1.3 Investigational purposes

None of the organizations/persons named in conjunction with the software can accept any product or other liability in connection with the use of this software for investigational purposes.

2 How to Read This Manual

Technical documentation always face a certain dilemma: whether write for top-down or bottom-up learners. A top-down learner prefers to read or skim documentation, getting a large overview of how the system works; only then does she actually start using the software. A bottom-learner is a 'learn by doing' person, someone who just wants to dive into the software and figure it out as she goes, referring to book sections when necessary.

This documentation is biased towards top-down learners (And if you're actually reading this section, you're probably already a top-down learner yourself!) However, if you're a bottom-up person, don't despair. If you have patience enough to ready only one chapter then read Chapter 6. If you then get stuck you may use this manual to search for specific solutions. Most of the icons and pushbuttons in the software have tooltip strings attached to them. Simply point the mouse over a button and you will have feeling on what purpose it has.

If you do not want to read the manual at all, you can instead see the on-line video tutorials. They are available under the **Help** menu.

3 Conventions and Abbreviations

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

3.1 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.
<input type="radio"/> Endocardium	Radiobutton in the graphical user interface.
<input checked="" type="checkbox"/> Single frame	Checkbox in the graphical user interface.

3.2 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>).

3.3 Abbreviations

2CH	Two chamber view
3CH	Three chamber view
4CH	Four chamber view

CHAPTER 3. CONVENTIONS AND ABBREVIATIONS

3D	Three Dimensional
3D+T	Time Resolved Three Dimensional
AA	Ascending Aorta
ASW	Anterior Septal Wall Thickness
ARD	Aortic Root Diameter
BPM	Beats per minute
BSA	Body Surface Area
CMR	Cardiac Magnetic Resonance
CO	Cardiac Output
CT	Computed Tomography
DA	Descending Aorta
DE-MRI	Delayed Enhancement MRI
ED	End diastole
EDD	End Diastolic Dimension
EDL	End Diastolic Length
EDV	End Diastolic Volume
EF	Ejection Fraction
ES	End systole
ESD	End Systolic Dimension
ESL	End Systolic Length
ESV	End Systolic Volume
FWHM	Full Width Half Maximum
GUI	Graphical User Interface
HR	Heart Rate
LGE	Late Gadolinium Enhancement
LV	Left Ventricle
LVM	Left Ventricle Mass
MaR	Myocardium at Risk
MO	Microvascular obstruction
MB	Mega Byte
MIP	Maximum Intensity Projection
MPR	Multiplanar Reconstruction
MR	Magnetic Resonance
MRI	Magnetic Resonance Imaging
PET	Photon Emission Tomography
PER	Peak Ejection Rate
PDW	Proton Density Weighted
PFR	Peak Filling Rate

3.3. ABBREVIATIONS

PLW	Posterior Lateral Wall Thickness
PWV	Pulse Wave Velocity
ROI	Region Of Interest
RV	Right Ventricle
RVmaj	Right Ventricle Major Axis
RVmin	Right Ventricle Minor Axis
SPECT	Single Photon Emission Computed Tomography
SSFP	Steady State Free Precision
SV	Stroke volume
TOF	Time of Flight
VENC	Velocity Encoding limit

4 System Requirements

In this chapter the hardware requirements for the software are outlined. Possible bottlenecks are (in order of likelihood) lack of RAM memory, CPU speed, and I/O network or disk transfer rates.

4.1 Operating system

Microsoft Windows. It will run on any of the following Windows 2000, Windows XP, Windows 7, Windows 8, and Windows 10.

4.2 Hardware requirements

The list below are the recommended hardware requirements. To run a clinical version of Segment CMR you need at least the specifications indicated below.

- A fairly recent computer with 4 GB of memory or preferably at least 8 GB.
- Harddisk with at least 500 MB of available space. The program Matlab Compiler Runtime takes about 450 MB, another 20MB is taken by the program.
- Graphics card supporting both DirectX and OpenGL (hardware accelerated) is recommended. Systems with two screens is recommended for clinical usage of Segment CMR.

We strongly recommend using SSD disk for reading data.

5 Loading Image Stacks

The best method to load and manage studies is by using the Patient Database Module, described in Segment CMR Database Manual. For clinical use, we discourage the direct use of the DICOM loader since this is a sub optimal workflow in the clinical situation, instead please look at the Segment CMR Database and PACS connection Manual.

This section is included in the manual for reference only in case you need to load from network, CD or a USB stick. We recommend that you for clinical routine store the patients in the patient database and load them from there. When loading from CD we strongly recommend you to import the CD to the patient database, for further details, please see Patient Database and PACS Communication Manual.

The program can read DICOM, and also an internal file format. The internal file format (called `.mat` files) has the advantages that one file may contain several image stacks along with object contours and measurements, and it is also much faster and easier to load compared to loading DICOM files.

It is highly recommendable that when an image stack has been loaded from DICOM files to save the image stack(s) to the internal file format. This makes it then much easier to go back and reanalyse datasets if necessary. Note also that the internal file format requires much less storage space than the original DICOM files, mainly due to cropping of the images and to lossless compression.

How to browse your DICOM data in the easiest way is described in Section 5.1.3.

The file loading dialog box is started from the main menu, under **File**, or by pressing **Ctrl-O**. This brings up the file loader GUI shown in Figure 1.

The file loader process the selected directory and its subdirectories to find the number of files in that directory. Since this process takes some time this operation is cached, and creates a file called `folders.cache`. To recreate the cache, press . When reading from a CD-ROM it is recommendable

CHAPTER 5. LOADING IMAGE STACKS

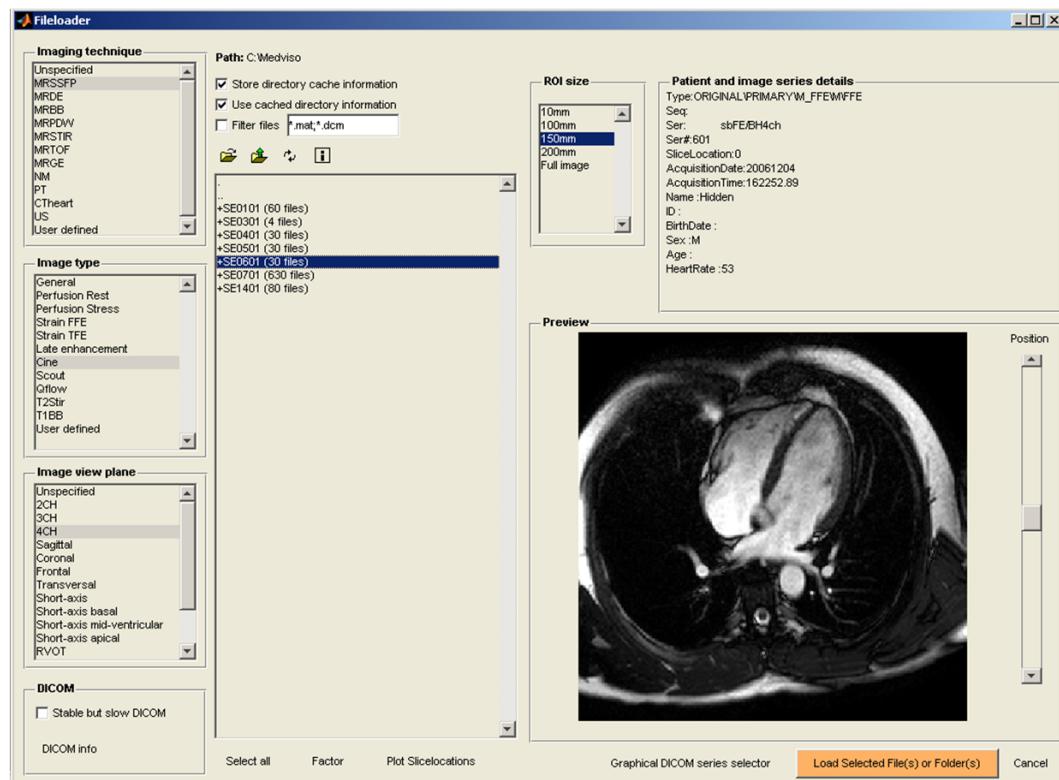


Figure 1: File loader GUI.

to copy the CD-ROM to your hard drive if you will load most of the files on the CD-ROM, since random file access from CD is very slow and caching is not possible. For further details on how to import DICOM CD-ROM's, see Patient Database Manual.

5.1 Loading DICOM files

5.1.1 Loading DICOM files

When loading DICOM files Segment CMR assumes that the files are sorted so that each image series is stored into one folder. Each folder may then contain one or many DICOM files. This is illustrated in Figure 2.

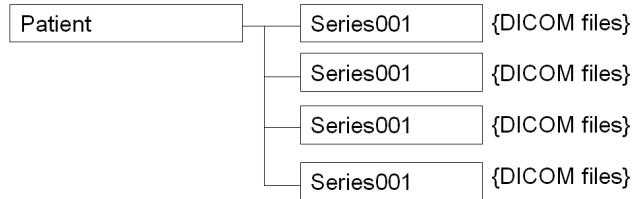


Figure 2: Files needs to be sorted so that each image series are stored into a separate folder.

If the files are not stored in this fashion then there is a sorting utility available. DICOM is a loosely structured file format and direct reading from DICOM files is slow. Currently the use of meta DICOM files is not supported (the DICOMDIR file is simply ignored).

You can either load each image series at a time or use a graphical tool to select what image stacks to load. The graphical series selector is described in Section 5.1.3. To load one image series at a time, start by selecting one folder.

To go up one directory level double click on ..., or click on the icon. To more easily get to a different folder, click on the **Browse** pushbutton. To go down one directory level double click on the folder name. Once selected one folder containing DICOM files a preview of one file in that folder is shown. To load the complete image stack, perform the following steps:

- Start by selecting the imaging technique in the top left corner of the GUI. The imaging technique sets the default segmentation parameters, and it is crucial that you select the correct imaging technique. For many scanners and sequence types this is identified automatically.
- When a valid file/folder is selected a preview of that dataset is displayed. Patient details and acquisition time are also shown.
- It is recommended, but generally not required to select **Image Type** and **Image View Plane**. This tells Segment CMR what kind of image it is. This might be required for future analysis in some applications. It is also a good idea to label image stacks upon loading when for instance doing stress analysis to be able to safely differentiate baseline from stress exams. For research purposes it is possible to set free text name as **Image Type** and **Image View Plane**.
- Select the desired region of interest size. Usually for normal hearts 100mm is sufficient to cover the left ventricle. Enlarged ventricles will need 150mm or even more.
- Click **Load** to start the loading process. This brings up a red box in the preview image. Position this box with the mouse and left click to start the loading process. If you want to use a different size of ROI right click to abort loading operation. Then click again on the **Load** button.
- Once positioned the box, left click with the mouse to start loading the files.

Once all image files are loaded a dialog box opens where you need to confirm voxel spacing and timing details. How Segment CMR interprets the DICOM information to calculate these parameters is described in Section 27.2. For users that do not use images from the three major vendors Siemens, Philips, or GE should read this section. Further technical details about how Segment CMR interprets the DICOM files are given in the Segment CMR Technical Manual.

If heart rate is not present in the DICOM file Segment CMR tries to guess that based on the time increment and the number of time frames to get R-R interval. This will fail if your image sequence is for instance one image every heart beat.

5.1.2 Tips and tricks

Often the files are not stored exactly as prerequisites above, then there are many tips and tricks available.

- You may select several subfolders. Then the program loads all the files in the subdirectories. Each subdirectory must have the same number of files. This is the case for old Siemens files and Bruker Paravision DICOM files.
- You may select what DICOM files to load directly. Note however that the files need to form a valid image stack and the result may be incorrect if slices are missing etc. When you do this, always ensure that the files are sorted properly.
- It is possible to preview different files by the **Position** slider.
- To get detailed information about DICOM tags in the files press **DICOM info**.

5.1.3 Graphical image series selection

The graphical series selector tool is shown in Figure 3. While moving the mouse pointer over the image series more information on each image series is shown in the top of the graphical interface. Select which image series to load with left mouse button. Image series outlined in yellow are selected. It is also possible to group image series to one image stack. Image series that are to be grouped are selected by holding down the **Shift** key while mouse clicking, or by using the middle mouse button. Thereafter, press the push-button **Group Selected**. Grouped image series are shown with a green outline. Multiple image stacks can be selected for loading or grouping by clicking and dragging over the selection. When finished selecting image series, press **Load**. To speed up the process this operation the generation of the thumbnails is cached.

Note that when using this tool to load the image, then there is no cropping of the images done, and that is highly recommended to crop the images during the image analysis process. Also note that if multiple directions is detected in the dicom folder all the different directions are loaded as separate image stacks.

CHAPTER 5. LOADING IMAGE STACKS



Figure 3: Graphical image series selector.

6 Program Overview

This chapter provides an overview of the program. Another good method is to view the on-line video tutorials. The tutorials are available under the Help menu.

An example of the main graphical user interface is shown in Figure 4. The major portion of the user interface is occupied by a viewing area where multiple image stacks can be visualized side by side. The current active image stack is outlined with an orange thick line. To make another image stack active, simply click on the image stack with the mouse pointer. A thumbnail image is shown for each loaded image stack. To view an image stack drag the thumbnail down to the main viewing area. To scroll through the thumbnails either use the slider or press **Ctrl** while scrolling with the mouse wheel.

The upper right corner is occupied with a reporting panel where quantitative details about the current image stacks are shown. There are two rows of icons. The top row contains icons that applies to all loaded image stacks, whereas the bottom row contains icons to applies to the current active image stack only.

Middle right part of the user interface is occupied by a volume curve and a time indicator. This graph area shows left ventricle volume versus time (red), left ventricle muscle volume (green), papillary muscle volume (blue). One easy method to adjust the displayed time frame is by clicking in this graph. You can also interactively drag which time frame that is taken as end diastole (ED) or end systole (ES). Just above the volume graph a list box with assumed long-axis motion is located. In this example the long-axis motion is automatically calculated under the assumption that the left ventricular mass is constant over time. The program selects the long-axis motion amplitude that best fits this assumption. Note that this auto detect should be disabled when manually drawing contours.

If the checkbox Single frame is selected then segmentation and other operations such as translate, scale, and delete are only applied to the current time frame. To further make the user aware of this change of behavior the box

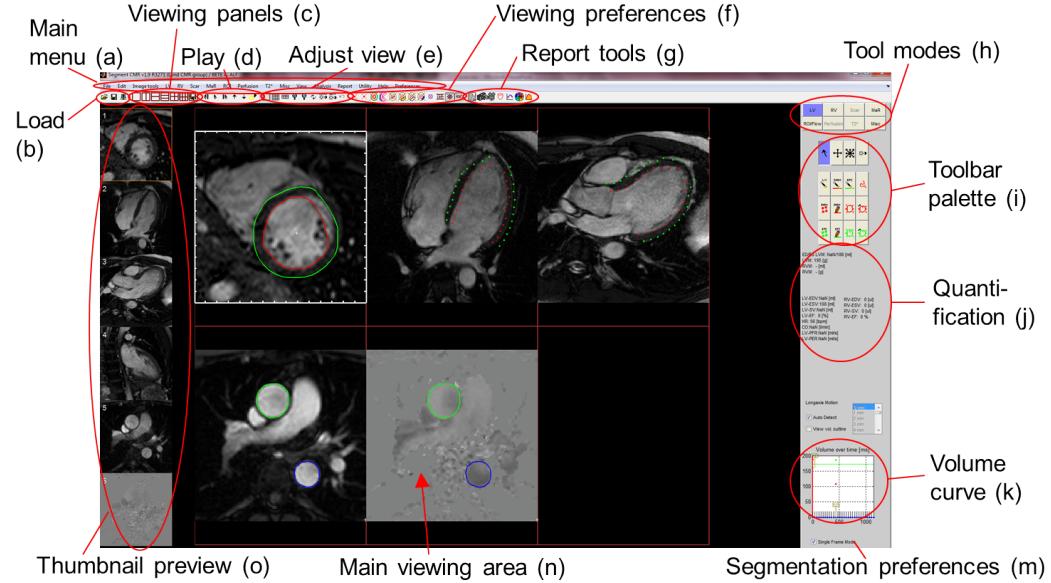


Figure 4: Main graphical user interface.

around the currently selected image panel turns to white when single frame mode is selected.

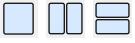
6.1 Viewing image stacks

To view a non visible image stack simply drag the thumbnail to an image panel. Right clicking on the thumbnails brings up a context menu where more options are available. To view all loaded image stacks press **Shift-A**. Only one of the image stacks are active at the same time. Around the active image stack an orange rectangle is drawn, both in the main image drawing area, and around thumbnail image.

Image stacks can be viewed in four different modes; one slice view, montage view, montage view in rows. The different modes are selected with the icons

 (one slice), (montage or all slices), (montage view in rows). Each of the different viewing modes will be described in details below. It is possible to view the same image stacks in different viewing modes simulta-

6.2. MONTAGE VIEW

neously. The number of image panels can be selected by the icons  or under the **View** menu. The icon  views information about the patient. It also possible to enter/adjust the patient information. Commonly this is used to add patient height to be able to calculate BSA.

The icon  brings up an interface for saving and loading user specified views. This allows users to save their favourite combination of stacks to view for use with any image set. It is also possible to associate each saved view with a specified hotkey. When loading a saved view for a new image set, Segment CMR automatically looks for the best matches among the current image stacks, taking into account such properties as image type, view plane, time resolution, etc.

The section  controls the visibility of pins, contours from other image stacks, endo / epicardium contours, region of interests, delineated infarct regions, measures and annotations, center point, and image plane intersections, respectively. The icons  and  zooms in/out the current active image stack. The icon  refreshes the screen which might be very useful since it also refreshed the GUI which under certain circumstances might 'hang' in case of calculations that went wrong. If the GUI seems irresponsible it is well worth to try refresh the screen. The icon  resets the light/contrast setting. The icon  automatically sets which sets contrast and brightness so that an upper and lower percentile of the intensities get saturated. The icon  undo the latest contour editing command. The icon  shows information about the current image stack.

6.2 Montage view

Figure 5 shows a screen-shot of the program in the most common view (montage view), selected by the icon . You can also switch between the montage view and the single slice view by using the hot key v. In the montage view all slices in an image stack are displayed. The slice(s) with a yellow box around are selected. Automated segmentation and many other operations are only applied to selected slices. Slices are selected by activating the tool , and by left mouse click on the desired slice and drag the mouse while the left

button is hold down.

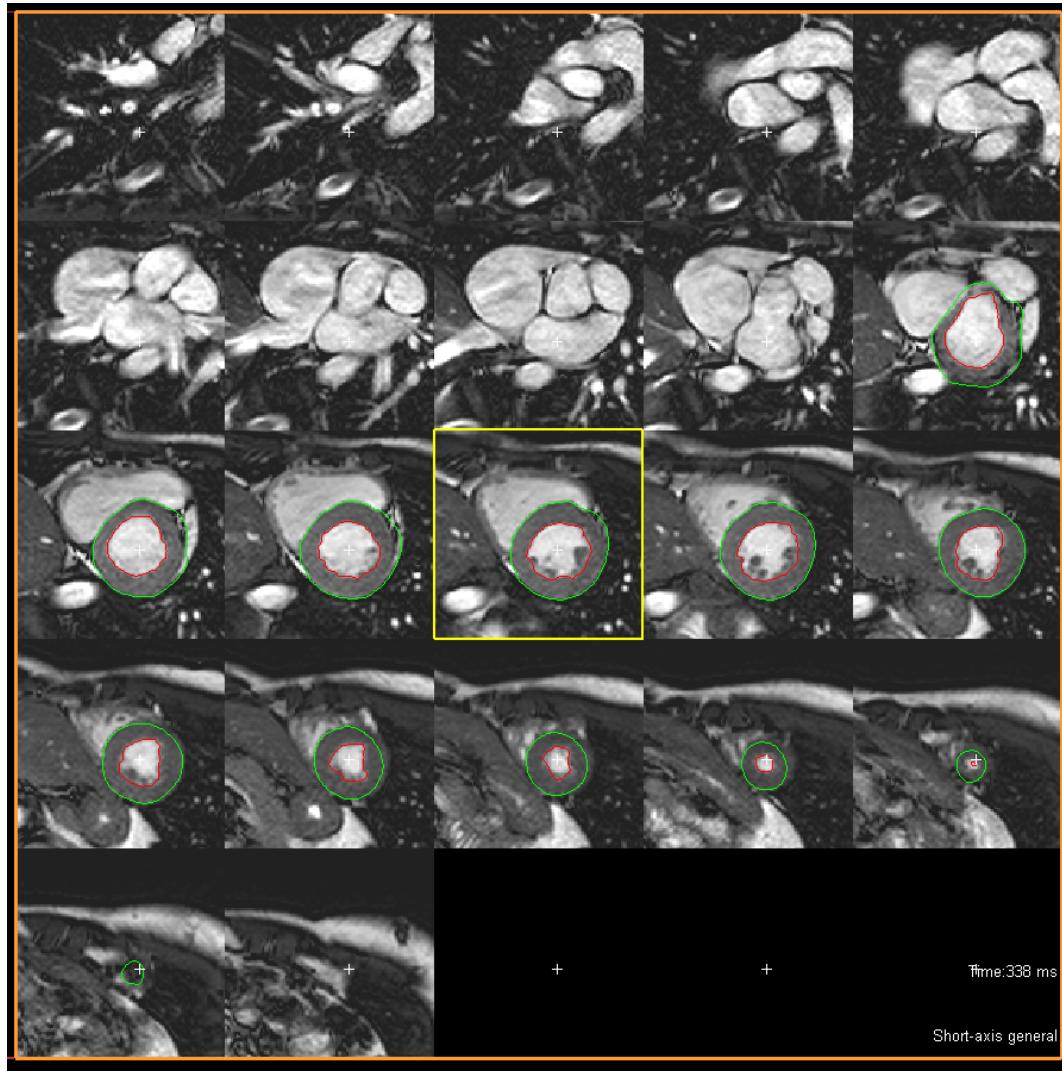


Figure 5: Screen-shot of the program showing an image stack in montage view.

6.3 Montage row view

The montage row view is same as the montage row, but with the difference that the slices are shown to minimize the number of rows that are used to display the entire image stack.

6.4 One slice view

In one slice view only one single slice are shown at a time. You can then browse between slices by up/down arrow keys. Right and left keys displays next and previous time frames. In this view intersecting image planes that also are shown. The intersection are indicated with a white or an orange line. Orange line indicate intersection with the current active image panel.

To hide/view the plane intersections use the icon . In this view intersections with contours drawn in other image stacks are also shown. For instance if the short axis stack is segmented the contour will also be visible in the long axis image. This is illustrated in Figure 6. This is very useful to delineate structures that might be difficult to see in only one image plane. The contour intersections can be hidden by using the icon . The contour intersections are only visible in one slice view mode. Note that different breathing position may cause the image stack not to align properly.

6.5 Viewing velocity encoded image stacks

For velocity encoded images it is possible to view both the magnitude image and the corresponding velocity encoded image(s). In the thumbnails a white box is drawn around magnitude and phase image to indicate what image stacks belong to each other. For more details see Chapter 13, Flow Analysis.

6.6 Playing images as a cine-loop

In the main icon toolbar the controls what time frame of the image sequence is displayed. The icon (Shift-Left Arrow) shows previous frame and applies to all visible image stacks. It displays the previous frame for the current image stack, and tries to find the corresponding time frame for all image stacks. If you just press Left Arrow then it just change

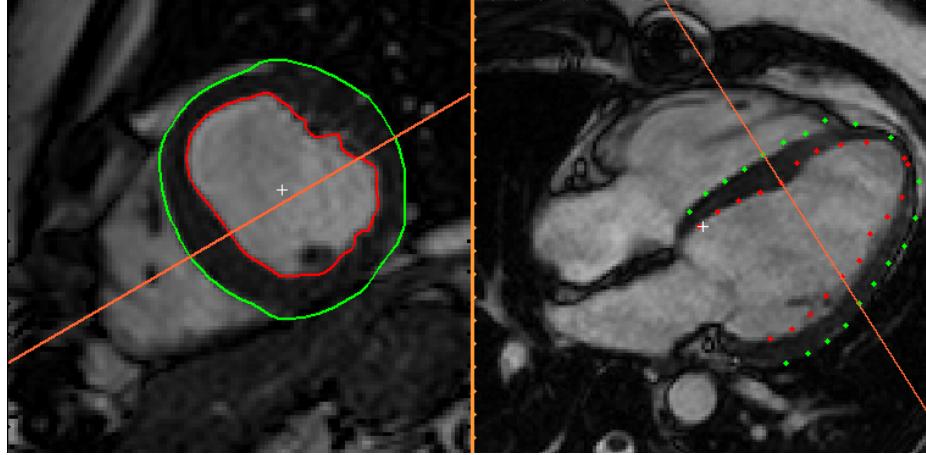


Figure 6: Contours are visible in other image stacks as dots. This is very useful to delineate structures that might be difficult to see in only one image plane.

time frame for current image stack. The icon plays all image stack sequence as a cine loop. The icon (Shift-right) performs the same operation as , but forward in time instead. Control and arrow keys show previous/next frame for all image stacks. The icon increases the playback speed, and decreases the speed. Another convenient method to quickly move between time frames is by clicking in the volume graph. Here you can also interactively drag which time frame is used as end diastole (ED) or end systole (ES). You can also switch between systole and diastole by using the hot keys **d** and **s**, respectively. Yet another way to scroll between time frames is to use the mouse wheel and at the same to press **Shift**. The icon allows the user to perform manual delineations while the current slice is played. This is very useful for a better understanding about for instance the papillary muscles.

6.7 Synchronizing image stacks

It is often required to synchronize image stacks in time and slice. This can be done by using the Shift-key. Shift-left/right key shows previous/next frame and synchronizes all visible image stacks in time. For image stacks that have

different number of time steps the nearest time frame is shown. **Shift-S** and **Shift-D** toggles between systole and diastole in all visible image stacks.

6.8 Loading and storing images

The top left section of icons contains functionality to load and save image data. The first icon  opens a file loader GUI described in Chapter 5. The second icon  opens the patient database described Segment Database Manual. The third icon  saves all the loaded image stacks to one file. The fourth icon  opens a connection to a PACS server, see Segment Database Manual.

6.9 Tool palette

The tool palette is located at the lower right corner of Segment main graphical user interface. The tool palette have several modes in which different tools become available. The current mode is indicated as black text on blue background. The current active tool is indicated by displaying the tool in a darker gray color. Generally, with few exceptions all functions in the program only applies to selected slices. Selected slices are indicated with a yellow box in the montage view. The functionality of selecting slices can only be used in the montage view. An alternative to select slices is to use the short key **Ctrl-A** that selects all slices. To pan the image use the tool  and move the mouse.

There are some general tools that is present in all tool modes, and these are;  to undo last contour edit command,  to adjust brightness and contrast (Hold down the mouse button and move left right to adjust contrast and up/down to control brightness),  to select slices or image stacks. This latter tool is the default tool. Contrast and brightness can also be adjusted without first clicking the icon , by using the middle mouse button instead. There are also in some of the modes  that translates ROI's and contours or the whole image if no ROI or contour was clicked, and  that scale ROI's and contours.

6.9.1 Left ventricle tools

The left ventricle tools are shown in Figure 7. Colors are used to indicate endocardium (red) or epicardium (green).

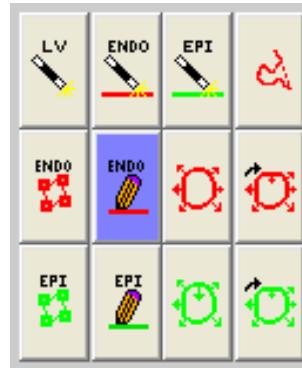


Figure 7: Left ventricular toolpalette.

On the first row (from left to right); automatically segments both endocardium and epicardium of the left ventricle. You need to ensure that the center '+' is in the middle of the ventricle and that all slices that covers the left ventricle are selected, see Chapter9. The second icon automatically segments the endocardium in the selected slices. The third icon automatically segments the epicardium of the selected slices. The fourth icon attempts to remove the papillary muscles. This can be used multiple times to successfully remove them.

On the second row (from left to right): The first icon is used for an interpolated contour mode to click out points to control the endocardial contour. To close the contour and interpolate a line between the points, shift click in the image. The points can interactively be dragged. The second tool is used to manually draw the endocardium. The third tool is to automatically refine the endocardium. The fourth tool is a tool to propagate the segmentation to next time frame.

On the third row is the same as the first row except that the tools applies to the epicardial contour instead of the endocardial contour.

6.9. TOOL PALETTE

The space key can be used to toggle between the endo and epicardial tool counterparts.

6.9.2 Right ventricle tools

The right ventricle tool palette is shown in Figure 8. The icon  is used to click out points in the interpolated contour tool for the right ventricle endocardium, and  is used for the epicardium, respectively. The icon  is used to manually draw the right ventricle (RV) endocardium. The icon  is used to automatically delineate the RV endocardium. Note that the RV tool is not as automated as the LV tools. The icon  is used to refine the RV endocardium. The icon  is used to manually draw RV epicardium.



Figure 8: Right ventricular toolpalette.

6.9.3 Viability/Scar tools

The functions described in this section is in US only for off label use and for investigational use. The viability tool palette is shown in Figure 9.

The icon  is used to automatically delineate infarct region on MR delayed enhancement images. The icon  is used to manually delineate infarction. The icon  is used to manually delineate regions with microvascular obstruction. The icon  manually removes infarction. The icon  erase manual corrections of infarction. To show the manual interactions and regions of microvascular obstruction you need to press the key  to toggle the display.



Figure 9: Viability toolpalette.

6.9.4 Miscellaneous tool mode

The miscellaneous tool mode is shown in Figure 10.



Figure 10: Miscellaneous mode toolpalette.

The icon is used to place annotation points. The icon is used to make length measurements. Left click with mouse at the starting point and hold mouse button down and move the mouse to end point. It is possible to interactively drag and refine measurements later. The icon is used to crop the current image stack. The icon is used to automatically crop all image stacks to focus on the heart, in order for it to work properly at least one time resolved short axis image stack is required. The icon allows you

6.10. GENERAL VIEW AND REPORTING FUNCTIONALITY

to find positions in 3D space for all visible image stacks.

6.9.5 ROI tool mode

The toolpalette for region of interest analysis (ROI) is shown in Figure 11.

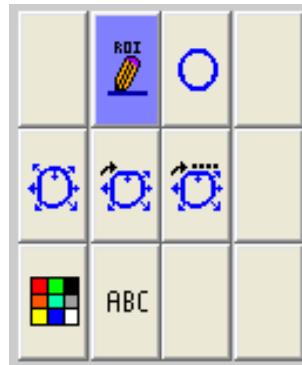


Figure 11: Region of interest mode toolpalette.

The first tool is used to manually delineate region of interests. The icon is used to automatically outline a vessel from scratch. Before using this place the center point (+) in the middle of the vessel. The icon refines a vessel. This is done in all time frames if the checkbox Single Frame mode is unchecked. The icon copies the ROI contour to next time frame and refines it. The icon tracks a ROI over the entire cardiac cycle. The icon selects current color to use to draw ROI's. The icon is used to name the current ROI.

6.10 General view and reporting functionality

The report tool creates a full text and graphical report of all the measurements for all image stacks. The icon starts a movie recorder that allows to store an image stack as an .avi movie. It is also possible to directly export a movie under the Export menu.

There are seven tools available to visualize or handle image stacks. Each of these starts separate graphical user interfaces to view and manipulate image

data. They are all available as icons on the main menu.

The icon  starts a tool to do multiple planar reconstructions. The icon  starts a three dimensional visualization tool. The icon  starts a tool to do regional wall motion per slice analysis described in Section 12.2. The icon  starts a tool to do bullseye visualization of wall motion and infarct parameters. The last icon  starts flow analysis tool, described in Chapter 13.

7 Measurements and Annotations

The whole software package Segment is designed for quantitative analysis and subsequently there are a rich variety of measurement tools available.

7.1 Length measurements

There are two possibilities to make length measurements. The easiest method is to use the measurement tool . To place a linear measurement, left click with the mouse, hold mouse button down and drag mouse to the desired location. Alternatively, or to place a measurement consisting of several line segments, hold down the **Shift** key while clicking to place end-points. Finish by clicking with **Shift** released. You are then asked to annotate and give the measurement a label. It is possible to refine the position of the measurement by click one of its end-points and drag that to the desired position. The measurement with its annotation is shown in Figure 12.

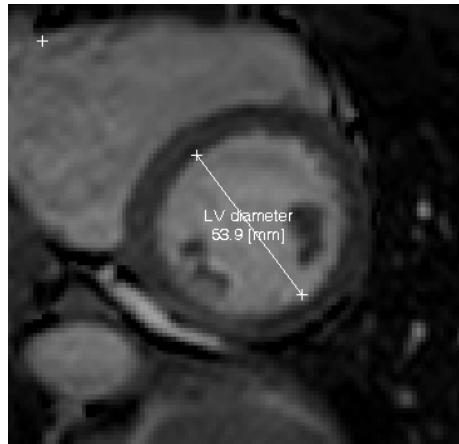


Figure 12: Example of a measurement of the left ventricle diameter.

8 Image settings

8.1 Manually set image description

To manually set the image description for an image stack, right click on the thumbnail for the image stack. Then select **Select Image Description** in the context menu and define the image description.

8.2 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`. You can manually update the text file to improve the automatical definition. This is done by open the text file, which is found in the folder where Segment CMR is installed. Then manually update the text file according to the structure as defined in the first row in the text file and store the text file.

9 Segmentation of the Left Ventricle

Before starting to describe segmentation of the left ventricle it is of importance to define what do we consider as the left ventricle.

9.1 Definition of the left ventricle

At a first thought it seems very easy to define what part of the heart should be included in the left ventricle. At a second thought the definition needs to be practical and repeatable. In the program the following decisions have been made.

9.1.1 Papillary muscles

By using the automatic LV segmentation algorithm, the papillary muscles are removed as much as possible (even if they are attached to the wall). Details on how to manually include/exclude the papillaries are given in Section 9.3.

9.1.2 Mitral annulus

Long-axis motion of the left ventricle is a very important component to achieve correct ejection fractions, and volumes. Long-axis motion is accounted for in the automatic LV segmentation algorithm. The long-axis motion direction is assumed to be orthogonal to the slice direction. The long-axis direction is shown in Figure 13. In the most basal LV slices the algorithm defines the LV segmentation with the long-axis motion in mind.

9.2 Automatic LV segmentation

9.2.1 Before the segmentation process

Before starting the automatic LV segmentation process, make sure that the basal-apex orientation is correct. The most basal slice should be in the upper left corner. If not then select **Image Tools**→**Flip z and x**, as described in detail in Chapter ???. Also make sure that correct **Image Type** is selected when loading the image stack (MR SSFP, CT...). This can also be set afterwards

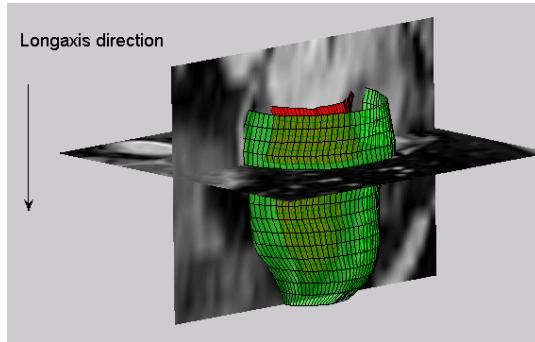


Figure 13: Three dimensional view of the left ventricle showing the long-axis direction.

by right-clicking on the image stack thumbnail image and select Set Image Description.

9.2.2 Automatic LV segmentation method

The default automatic LV segmentation method is to be applied on hearts of the similar size as human hearts (newborn to adults). For small animal hearts, please try the Alternative automatic LV segmentation method according to next section.

In order to start the automatic LV segmentation process click on  in the LV mode. A new interface is open, according to Figure 14, where you select the slices to include in the segmentation and define middle of LV lumen according to the following steps:

- The most basal slice should be the most basal slice that have left ventricular myocardium at least in some part of the heart cycle. If long-axis image stacks are available, the slice selection can be reviewed in the long-axis views. In order for Segment CMR to find the long-axis image stacks, the Image View Plane have to be defined as 2CH, 3CH or 4CH. The Image View Plane is defined by right click in the thumbnail preview and select Set Image Description.
- The next step is to ensure that the LV center cross is correctly defined in the middle of the LV lumen. This is done by review, and if needed adjust, the orange cross in the short-axis view. The center cross should

9.2. AUTOMATIC LV SEGMENTATION

be in the middle of the LV lumen for the midventricular slice and the placement in the basal and apical slices is irrelevant.

After the selection of LV slices and definition of LV center, the automatic LV segmentation is started by click on **Start LV segmentation**. The segmentation result from the automatic LV segmentation method is then displayed in the main interface for Segment CMR. If needed, manually adjustment of the LV segmentation is performed in the main interface according to Section 9.3.

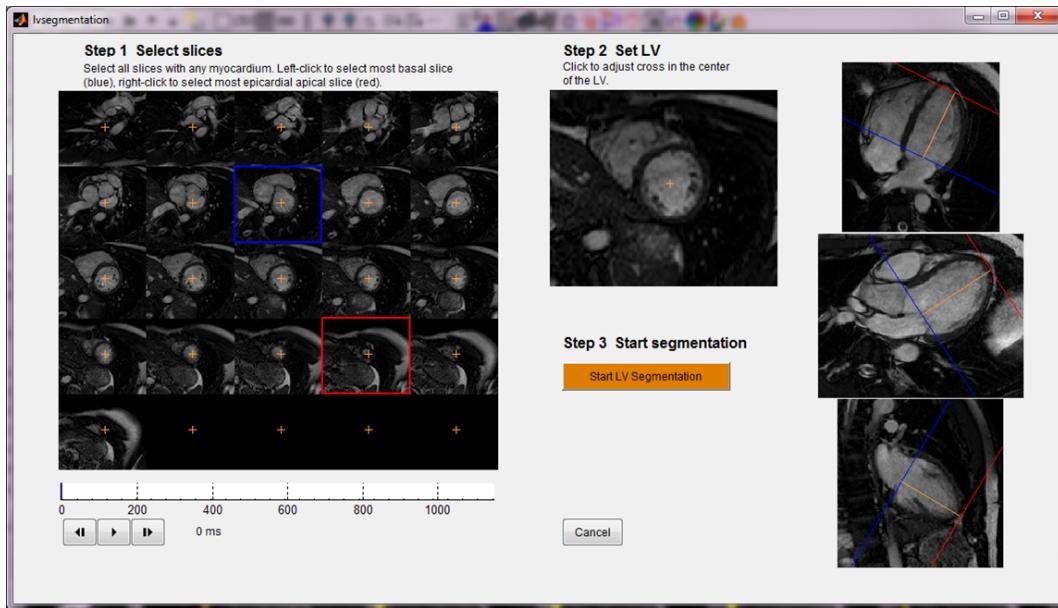


Figure 14: Interface for LV analysis.

9.2.3 Alternative automatic LV segmentation method

The Alternative automatic LV segmentation method is to prefer when doing LV segmentation in small animal images.

If the checkbox **Single Frame Mode** checkbox is checked, the LV segmentation is only performed in the current time frame. It is recommended to uncheck the checkbox and do the LV segmentation in all time frames since this leads to better conditions for the segmentation algorithm. Steps to autosegment LV.

- In the main interface of Segment CMR, move the white image center cross so it is inside LV lumen in all slices.
- Select all slices containing LV (selected slices are marked with a yellow frame around). The most basal slice should be the most basal slice that have left ventricular myocardium at least in some part of the heart cycle. If long-axis image stacks are available, the slice selection can be reviewed in the long-axis views by the intersection lines when viewing both short-axis and long-axis in different panels in Segment CMR.

Then start the alternative automatic LV segmentation method by go to menu option **Segmentation - Left Ventricle Tools - Alternative Automatic LV Segmentation - Automatic LV Segmentation in Selected Slices**. The segmentation result from the alternative automatic LV segmentation algorithm is then displayed in the main interface for Segment CMR.

AV-plane movement is automatically estimated and compensated for in the algorithm. If you would like to change the estimated AV plane movement, you can manually adjust it by go to menu option **Segmentation - Left Ventricle Tools - Alternative Automatic LV Segmentation - Set long-axis motion**. Note that this long-axis motion compensation is NOT included in the LV delination as showed as overlays to the images. The compensation only affects the LV volume measurements as presented in the result panel. By selecting AV plane movement (Long-axis motion) the LV volumes are updated automatically. If needed, manual adjustment of the LV segmentation is performed in the main interface according to Section 9.3.

9.3 Edit the segmentation result

Unfortunately the segmentation result is not always as one would desire. We have done as much as we possible can to implement and design a segmentation algorithm that is robust and accurate, but despite that the algorithm do fail in certain cases, and especially on the epicardial contour.

There are many implemented methods to manually edit the segmentation result. Different methods are good in different situations. I recommend to learn them all, and by experience learn in what situations the different types of manual interaction works best. If you experience that editing is a cumbersome task, then you are probably doing it the wrong way.

9.3. EDIT THE SEGMENTATION RESULT

When the segmentation fails completely, please check the following items:

- Double check that correct slices are selected for the LV segmentation and that a good LV center point is chosen.

There are several methods to manipulate the segmentation result. Each method have different applications where they work better, and it is a learning process to learn which tool to use in different situation.

9.3.1 Undo segmentation

To undo the latest segmentation operation select undo from the tools menu, or using the undo icon , or using the hot key **Ctrl-Z**.

9.3.2 Refine segmentation

Refine runs the segmentation algorithm a few iterations, and thus further refines the segmentation. This functionality is chosen by the two icons  and  for endocardium and epicardium, respectively. Note that the optimization is only run for the selected slices.

9.3.3 Expand or contract segmentation

If the shape of the contours is satisfactory but are inside or outside of the myocardial border, the tools , ,  or  can be used to expand or contract, respectively, the contours. The tools are applyed on selected slices and expand or contract the contour in a relative manner. If the checkbox **Single Frame Mode** is checked, then the tool is only applied in the current time frame, otherwise in all time frames.

9.3.4 Manually adjusting the contour by interpolation points

Manually correction of the contou by using interpolation points is probably the easiest way to make changes in the segmentation. This functionality is chosen by the two icons  and  for endocardium and epicardium, respectively. If there is LV segmentation in the selected slice, one left mouse click in the current slice will put interpolation points for the contour. If no LV segmentation is present in the current slice, a LV segmentation can be

performed by the interpolation points by select or tool. Then add interpolation points by left mouse click and interpolate the contour by shift-click. The LV segmentation is then corrected by move the interpolation points by dragging with the left mouse button and hold it down. New interpolation points can be added by left mouse click in at the position where you like to add the point.

9.3.5 Manually drawing the contour

This functionality is chosen by the two icons and for endocardium and epicardium, respectively. Use the left mouse button and hold it down to manually draw the complete contour or correct an existing contour. If the checkbox Single Frame Mode checkbox is checked, then the segmentation is only performed in the current time frame, otherwise in all time frames. A quick method to toggle between drawing epicardium, and endocardium is to use the space button on the keyboard.

9.3.6 Translating the segmentation

The segmentation can be translated/dragged in each slice. This is done by using the icon in the toolbar palette. Note that the usage of this translation is especially useful in conjunction with the import segmentation option in the main menu. Then a segmentation from one imaging technology can be overlaid an image of a different image stack if they were acquired using the same coordinate system. A practical application is doing the segmentation on cine gradient echo or cine SSFP images and overlay that result over late enhancement images. Under the segmentation menu it is possible to translate/move selected slices towards the base/apex.

9.3.7 Scale the segmentation

In some slices, and typically the apical slices scaling the segmentation can be very effective correction. Scaling can be done with the tool. Scaling can often successfully be combined with the refine operation.

9.3.8 Manually include/exclude papillary muscles

One approach to remove papillary muscles is to perform a few iterations with the refine tools for the LV segmentation according to Section 9.3.2. The

9.3. EDIT THE SEGMENTATION RESULT

papillary muscles can also be included/excluded in the LV segmentation by using the manual drawing tools according to Section 9.3.5.

9.3.9 Removing segmentation result

The segmentation result can be removed with the right mouse click pop-up menu (shown in the place pin section above). These function are also available in the main menu under **Segmention**.

10 Segmentation of the Right Ventricle

The right ventricle is much more geometrically complex than the left ventricle. The walls are much thinner and there are more and complex trabeculation. This is one explanation that there are currently in Segment CMR no really good automated tools to do segmentation of the right ventricle. This will be improved in future versions of Segment CMR.

Currently what is available are the same basic functionality as for the left ventricle. For the mid ventricular slices the automated methods (manual draw+refine can be used).

At the current stage we do not recommend to do time resolved segmentation of the right ventricle since the drawing and edit tools are so poor. We would suggest to remove all RV segmentation except systole and diastole. An example of segmentation of the right ventricle is shown in Figure 15.

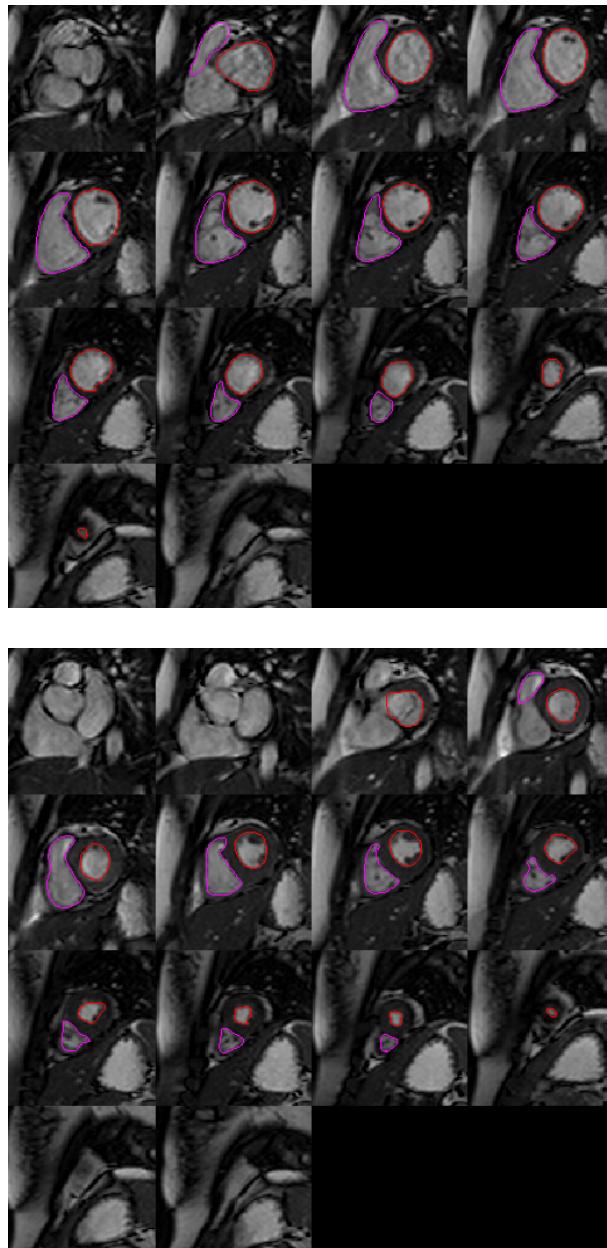


Figure 15: Top: Segmentation of the right ventricle in diastole in a short axis image stack. Bottom: Segmentation of the right ventricle in systole in the same short axis stack. Note the relative large long axis motion.

11 Segmentation of Long Axis Images

Segmentation of the left ventricle (as well as any other chamber) can be done by manually outlining the object in longaxis images. This is a fast alternative to manual drawing on short axis images.

Contours need to be present in at least two image stacks labeled 2CH, 3CH or 4CH to enable volume calculations. Please note that the image stacks needs to be labeled view the correct view. To label the images right-click on the thumbnails and select **Set Image Description**. Figure 16 illustrates the concept of segmentation in long axis images.

11.1 Click an image to show point location in all views

To provide a better estimation of the three dimensional volumes when drawing in longaxis images, there is a tool that allows the user to click an image to show the location of the clicked point in every active view. This tool  is found in the **Misc** toolbox.

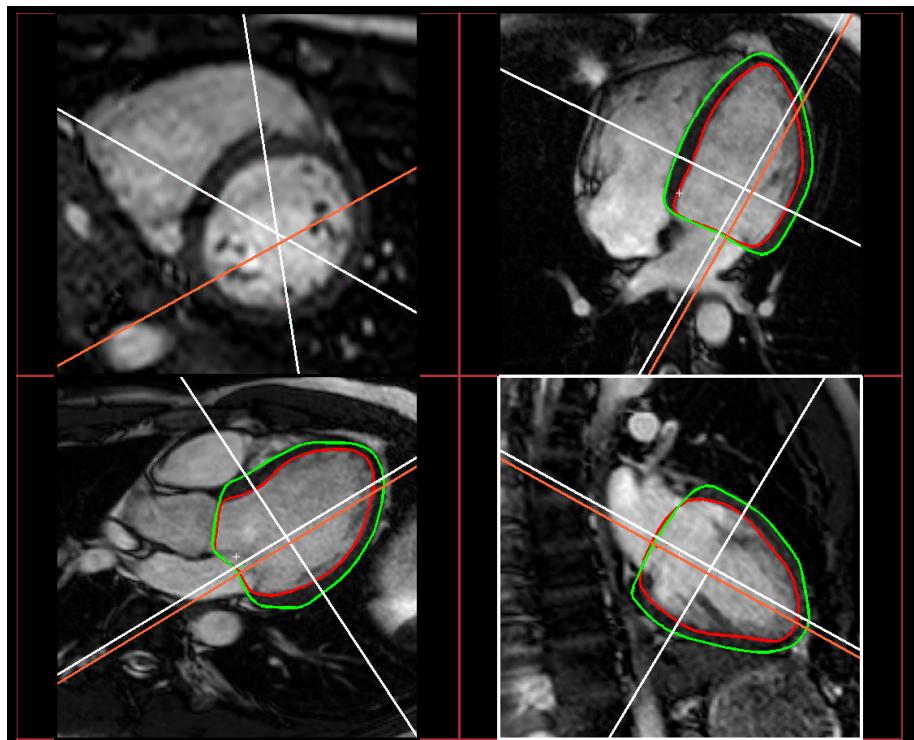


Figure 16: Illustration of the process of drawing segmentation in long axis images.

12 Regional Wall Analysis

There are a number of different analysis options available to make regional wall analysis. Please note that for regional wall motion analysis the common clinical practice is to exclude the papillaries from the segmentation, for more information on how to include/exclude the papillaries, see Section 9.3.

There are three different visualization options available for wall motion analysis:

- Radial contraction versus time
- Report per slice (icon - Bullseye plots (icon 

12.1 Radial contraction versus time

In this option the regional contraction velocity per segment is plotted over time. On the y-axis on each plot is the slices (basal to apical), and on the x-axis is time. An example is shown in Figure 17.

12.2 Report per slice

It is possible to do regional wall motion analysis on a slice by slice basis. This tool is started by the icon . Possible parameters to plot are wall thickness, fractional wall thickening, radial contraction velocity, and radius. An example showing wall thickness over time is shown in Figure 18. .

CHAPTER 12. REGIONAL WALL ANALYSIS

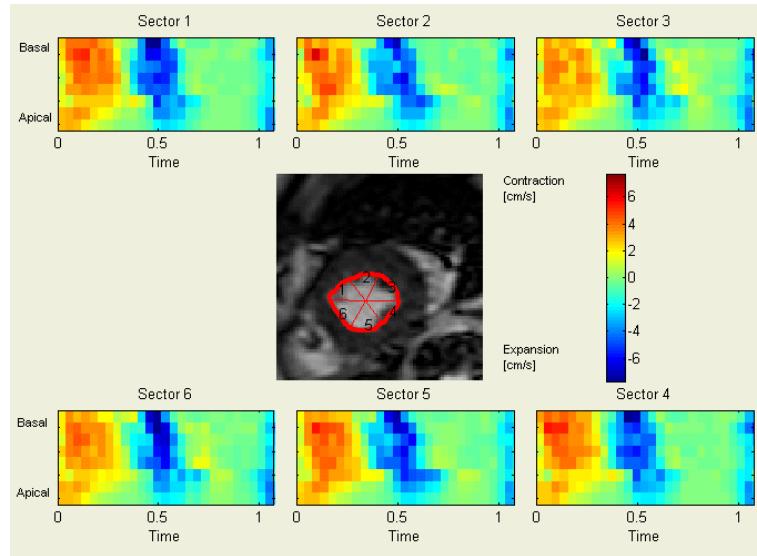


Figure 17: Radial velocity versus time in six sectors. Note the apical to basal gradient in the onset of the radial contraction.

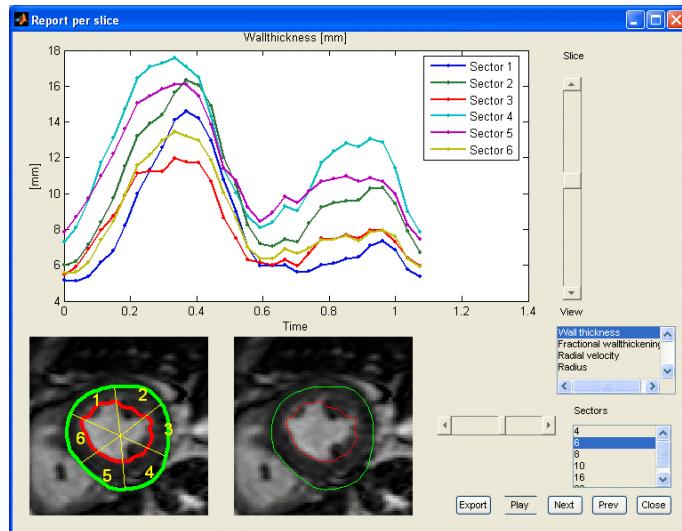


Figure 18: Wall thickness over time in a healthy subject.

13 Flow Analysis

This functionality may depend on your MRI scanner. Currently it has been tested using Siemens, Philips and GE scanners.

When flow image stacks are displayed, the screen should now similar to what is shown in Figure 19. On the left image panel the magnitude image is shown and on the right image panel the phase image is shown. When a flow image stack is selected a white frame around both the magnitude image and phase image is drawn in the thumbnail preview area. This helps to keep track of which phase images belongs to which magnitude images.

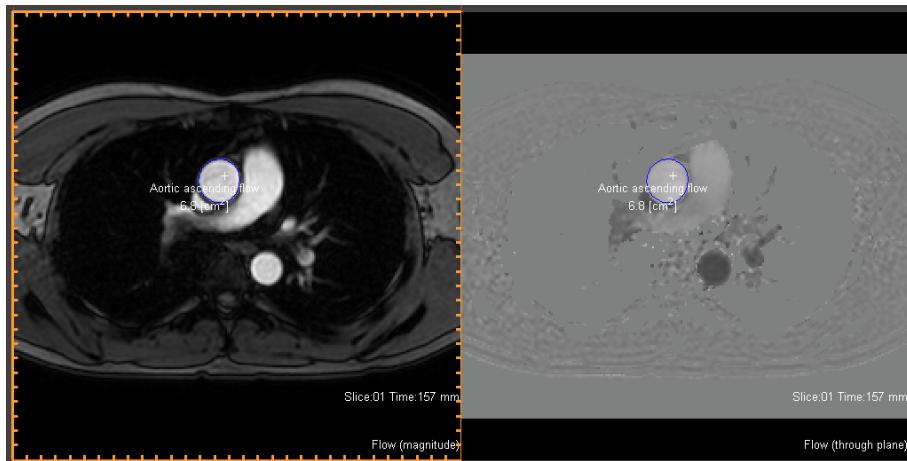


Figure 19: Example of main GUI in flow mode.

13.1 Automatic segmentation of flow ROI's

The suggested method is to select the ROI tool . Then draw a ruff outline of the vessel contour. Thereafter start the automated vessel tracking and refine. This is done by pressing **Ctrl-T**.

Another method to automatically segment a vessel is to drag the center cursor (white +) to the approximate center of the desired vessel and press **Ctrl-G**,

or Auto delineate a vessel under the Segmentation→ROI and Flow Tools menu. The vessel is automatically delineated and you are asked for an appropriate label.

13.1.1 Refine

Refine operation operates on the current time frame or all time frames depending on the checkbox Single frame mode. Short key for the refine function is **Ctrl-R**. You need to have the ROI pen active when using the hot key. Refine on all time frames is particularly useful if the vessel is fairly round and not to close to other surrounding tissue.

13.1.2 Refine and propagate

Start at the first time frame of the time series. If pleased with the result simply use the right arrow key on the keyboard to proceed to next time frame. When you find a time frame where you are not pleased with the segmentation use the ROI pen  to adjust the contour or use the refine option **Ctrl-R** with the checkbox Single frame mode enabled. Continue by propagating the contour by pressing **Ctrl-F**.

13.1.3 Shrink flow ROI

If the RIO is outside the vessel then it might be advantageous to shrink the ROI followed by one ore more refine operations. Shrink flow ROI is found under the Segmentation menu and the submenu ROI and Flow tools.

13.2 Plotting the result of the flow analysis

The flow plotting utility is started by using the icon  or by using the function **Plot flow curves** under the **Flow** menu. An example of the graphical user interface is shown in Figure 20.

In the upper right area of the GUI you can select which parameter to plot. The volumes presented in Volume panel of the GUI represents flow integrated between the two vertical red bars. These bar can interactively be moved with the mouse to control the range of the integration. Forward volume is the volume of the flow integrated only over the time frames where the net flow is positive (forward). Backward volume is the volume of the flow

13.2. PLOTTING THE RESULT OF THE FLOW ANALYSIS

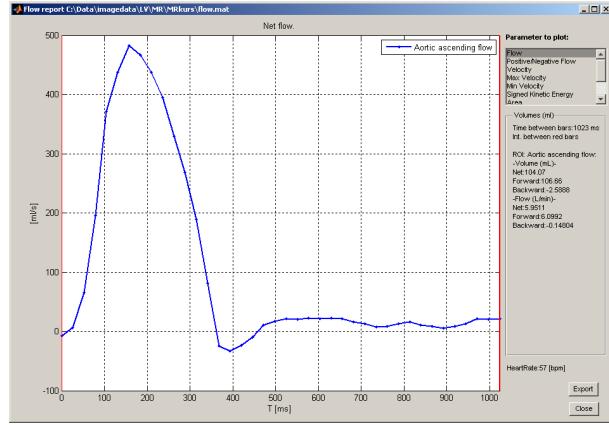


Figure 20: Example of flow plotting GUI. Plotting parameter can be selected in the upper right corner of the GUI. The flow integration is performed between the two red bars.

integrated only over the time frames where the net flow is negative (backward). This should be contrasted to the flow parameter **Forward/Backward** that plots simultaneously the flow that goes forward and backward of the region of interest. Note that there can be significant backward flow in one time frame even though the net flow is forward in that very time frame. An example on the latter is shown in Figure 21. The sum of the two curves is the same as the net flow that is shown in Figure 20.

It is also possible to plot the Velocity over time, and this is shown in Figure 22. The 'error bars' denote the standard deviation of all pixels in the ROI of that particular time frame.

Another possibility is to plot the max or min velocity in the ROI over time. It is also possible to plot the radius and diameter over time. The radius are calculated as; what diameter need a circular vessel have to have the same area as the area of the ROI. The option **Signed Kinetic Energy** calculates the kinetic energy in the blood assuming standard density of the blood.

The final possibility is to plot a 3D profile of the velocity distribution of the vessel. This can be plotted for all time frames at once or only a single time frame that later can be stepped forward/backward in time. An example of

the 3D plot is shown in Figure 23.

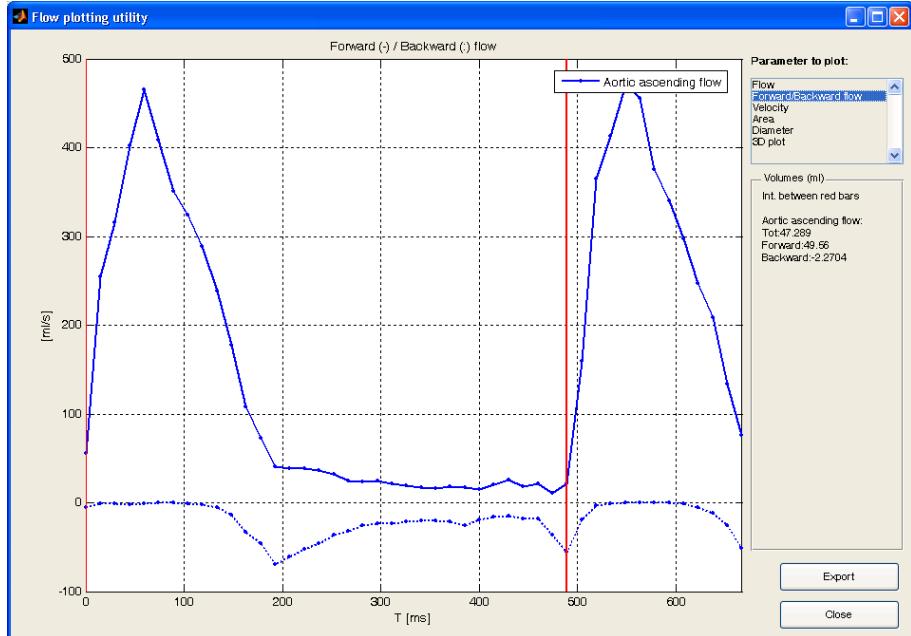


Figure 21: Example of plotting of backwards and forward flow simultaneously. The sum of the two curves will be the net flow showed in Figure 20.

13.3 Compensating for eddy current effects

To get accurate flow measurements it is important to compensate for concomitant field effects such as eddy currents, and Maxwell effects. Ideally Maxwell effects should be compensated for directly on the MRI scanner since it can be analytically calculated. Consult your MRI vendor for details about how this is implemented in your scanner. Note that when compensating for eddy current effects the image stack should not be cropped upon loading, since the algorithm need phase information of static tissue in the chest wall to function properly.

The graphical user interface for compensating for eddy current effects is shown in Figure 24.

13.3. COMPENSATING FOR EDDY CURRENT EFFECTS

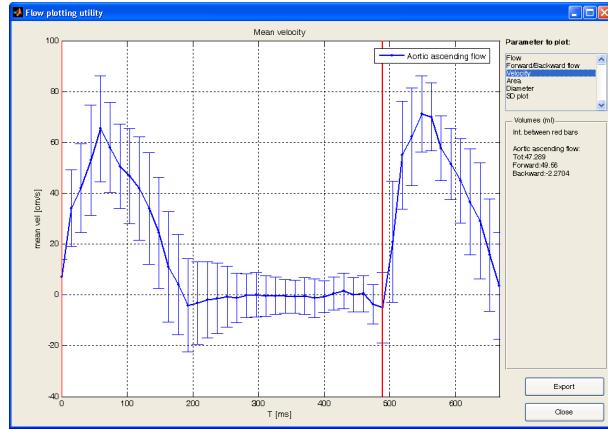


Figure 22: Example of plotting of velocity over time. The 'error' bars shown the standard deviation of the pixels within the ROI over time.

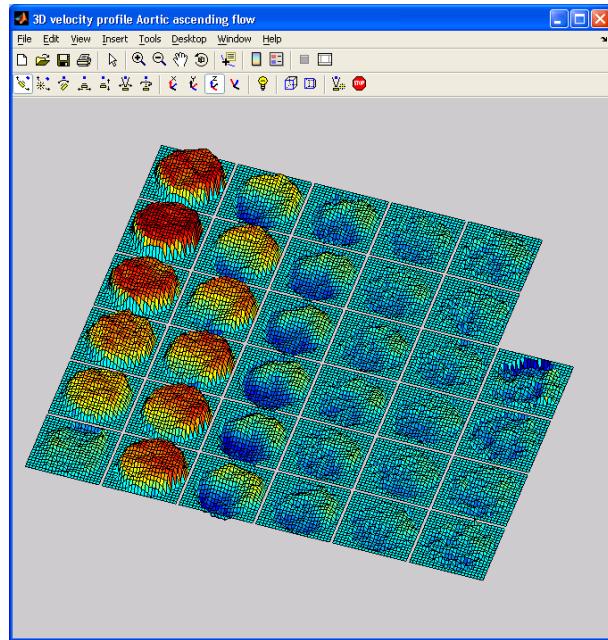


Figure 23: Example of plotting of a 3D profile of the velocity distribution.

CHAPTER 13. FLOW ANALYSIS

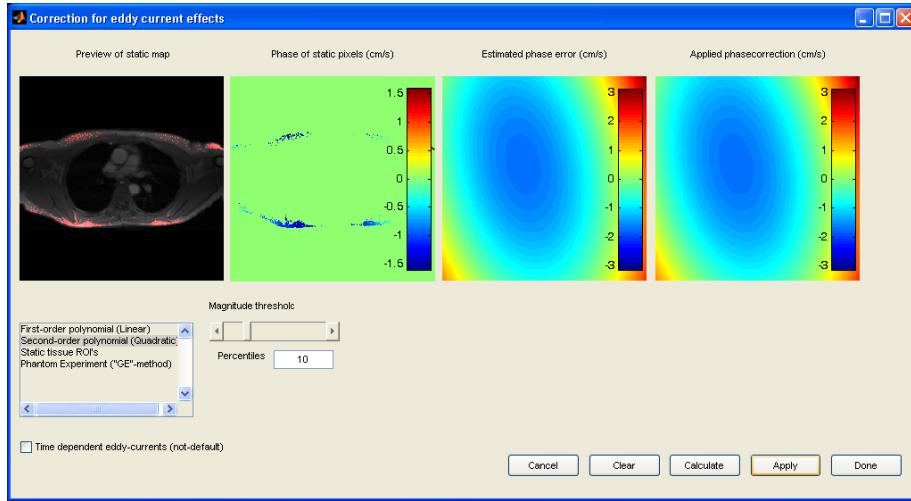


Figure 24: Example graphical user interface for compensating of concomitant field effects. In the left the identified static tissue is the displayed, and in the middle panel the corresponding phase for these pixels is shown, and in the right panel the resulting phase correction is shown.

You can select model order, and clear the phase correction. When you are pleased with the phase correction press **Apply** to proceed. The function automatically finds stationary parts in the image by selecting a percentage of the pixels whose standard deviation of the phase over time is smallest. The fraction of pixels taken can be controlled by the edit box **Percentile**. The image is divided into four quadrants and the algorithm to find stationary pixels is applied to each quadrant separately. This is done to ensure that there are about the same number of pixels from each quadrant. Pixels taken as stationary tissue are shown as red dots in the magnitude image. The **Magnitude** slider controls what magnitude the pixels need to have before being labeled as stationary. By selecting the mode of operation as **Static tissue ROI** then ROI's that are labeled **Static tissue** are taken as stationary areas. This is particularly useful when doing phantom experiments, since the automated identification of static areas fails in cases with stationary flow. The mode of operation **Phantom Experiment (GE-method)** automatically finds a flow image stacks that have the same scanning parameters this useful when a static tissue have been scanned in the same position as the patient as

recommended by GE for eddy current compensation. For usage, see paper by Alex Chernobelsky *et al.* [?].

13.4 Phase unwrapping

In cases where the velocity in the blood is higher than the VENC the velocities can wrap around. Under certain conditions these phase wraps can be uncovered and phase unwrapping can be performed to retrieve the correct velocities. The graphical user interface for the phase unwrapping tool is shown in Figure 25.

The checkbox **Show ROI pixels** shows the pixels that are used in the ROI in a red color. This is useful when one wants to know exactly what pixels are included in the ROI. The checkbox **Use magnitude mask** is used when one wants to limit the automated phase unwrapping only in pixels that have a magnitude over a certain threshold.

13.4.1 Automated unwrapping

The automated phase unwrapping algorithm works on a pixel by pixel basis and operates along the temporal dimension. It looks for pixels where the phase appears to have wrapped once up and once down. Therefore the algorithm will fail for a biphasic velocity profile if phase wrapping occurs at both phases. Furthermore, it only considers single wrap arounds (i.e the phase is assumed to have wrapped once).

13.4.2 Manual unwrapping

There are four tools available,     . The tool  is used to pan the images. The second tool  wraps the pixel up at left mouse button clicks. The third tool  wraps the pixel down at left mouse button clicks. The fourth tool  is used to plot the phase of the current pixel over time. This is mainly useful for debugging purposes. It is possible to zoom the image by usage of the zoom icons   . Undo last operation is done by pressing **Ctrl-Z** or the icon .

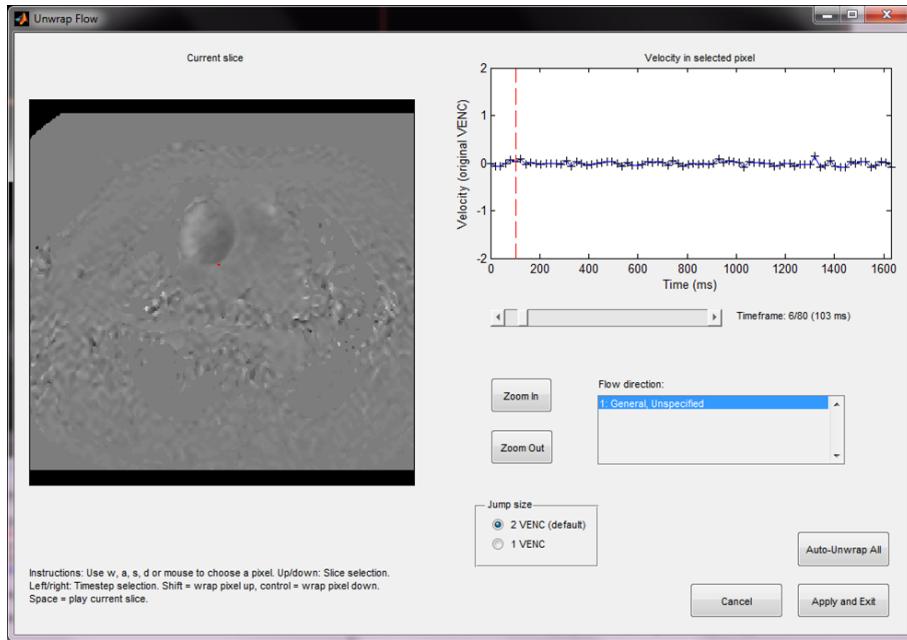


Figure 25: Example of the graphical user interface for phase unwrapping. The left image panel shows the original phase, and the right image panel shows the unwrapped phase. The long slider adjusts the current time frame.

13.5. CREATING ANGIO AND VELOCITY MAGNITUDE IMAGES

13.5 Creating angio and velocity magnitude images

It is possible to create a so called angio image that is the magnitude image times the velocity magnitude. This is available under the **Flow** menu and **Create Angio**. If you have more than one velocity encoding direction it is possible to create a velocity magnitude image that is the square root of the sum of squares of all velocity directions (velocity magnitude).

13.6 Coupling magnitude and flow images

If magnitude and flow image stacks have been loaded into Segment CMR-without being coupled to each other, it is possible to couple them using the **Couple Magnitude/Phase Flow Image Stacks** from the **Flow** menu. Available magnitude and phase image stacks are then identified and coupled using heuristics.

14 Bulls eye Analysis

The parameters that currently can be plotted as bulls eye plots are:

- Maximal expansion velocity
- Maximal contraction velocity
- Expansion velocity at PFR
- Contraction velocity at PER
- Maximal wall thickness
- ED wall thickness
- ES wall thickness
- Wall thickening (difference wall thickness ES-ED)
- Fractional wall thickness
- Myocardium volume
- Myocardial intensity (normalized or unnormalized values)
- Scar transmurality
- MaR transmurality
- Data from clipboard (each row is one slice, and each column a sector)

The graphical user interface for creating bulls eye plot is shown in Figure 26. The orientation of the bulls eye plot can be adjusted by a slider, and the number of sectors with a list box. **Note:** it is important to adjust the rotation correctly, so that the sectors corresponds with the correct anatomy. For correct AHA plots, one need to adjust the rotation so that the longest spoke in the lower right part of the GUI points to the middle of Septum wall.

The images on the right side of the GUI display one slice of the shortaxis image from which the bullseye data is extracted. The slider on the right of the image can be used to change to an image of a different slice. If a longaxis image is available, it will be displayed in the image above the shortaxis slice image. This longaxis image will contain intersection lines of the slice planes included in the analysis (displayed in white), with the current image slice in

CHAPTER 14. BULLS EYE ANALYSIS

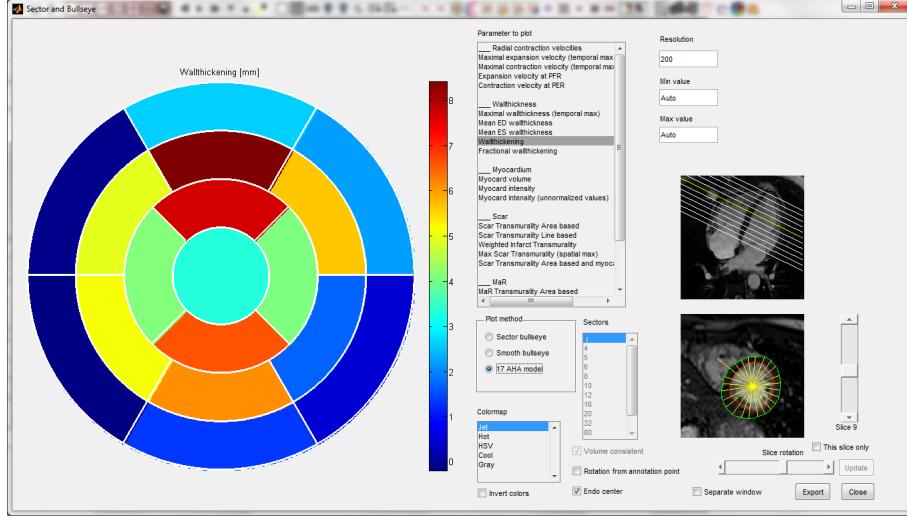


Figure 26: GUI used to create bullseye plots.

yellow. If This slice only is checked, the current image slice changes to red and the bullseye plot data is taken only from this slice.

It is also possible to export the results of the bulls eye plot to clipboard (to later past it into for instance Microsoft Excel). Note that only selected slices are plotted in the bulls eye plot. For further improve flexibility of editing and exporting it is possible to plot the bulls eye plot in a separate window. There are three possible modes of bulls eye plots, one with regular with uniform sectors displaying the 'mean' or nominal value for each sector, and one mode where the bulls eye plot is smoothed, and the final mode where the data is presented according to the AHA association model [?]. In order to make the AHA presentation meaningful you should have selected the whole LV. The smoothed bulls eye plot is done using cubic interpolation over Cartesian coordinates. The possibility to plot data from the clipboard enables to plot data as bulls-eye plots that was not created with Segment.

15 T2* Quantification Module

In magnetic resonance (MR) imaging, T1, T2 and T2* relaxation times represent characteristic tissue properties that can be quantified with the help of specific imaging strategies. The purpose of the T2* Module is to quantify T2* relaxation times in MR imaging. Quantification of T2* values follows the same underlying mathematical principles as T2, but gradient-echo (GRE) source images are used instead of spin-echo (SE) images.

T2* changes have been shown and quantified under pharmacological test in coronary artery disease [?], quantification of iron overload and of the heart and liver in Thalassaemia major [?].

T2* values can be quantified by varying GRE echo times.

15.1 Module overview

An overview of the T2* quantification module is shown in Figure 27. The top left image panel shows the magnitude images for the different echo times, adjustable with the echo time slider. The lower left panel allows zooming functionality, the lower middle panel allows to make regional restriction on what regions to quantify. There are three modes and in the first mode **Use only myocardium** the pixels inside the myocardium is included in the quantification. The second mode **Use only ROI** includes only pixels that are inside region of interests. In the last mode **Use full image** all pixels are included in the quantification. The delineation of ROI's and myocardium is taken from the first time frame in the image series. The right image panel shows the pixelwise T2* values.

CHAPTER 15. T2* QUANTIFICATION MODULE

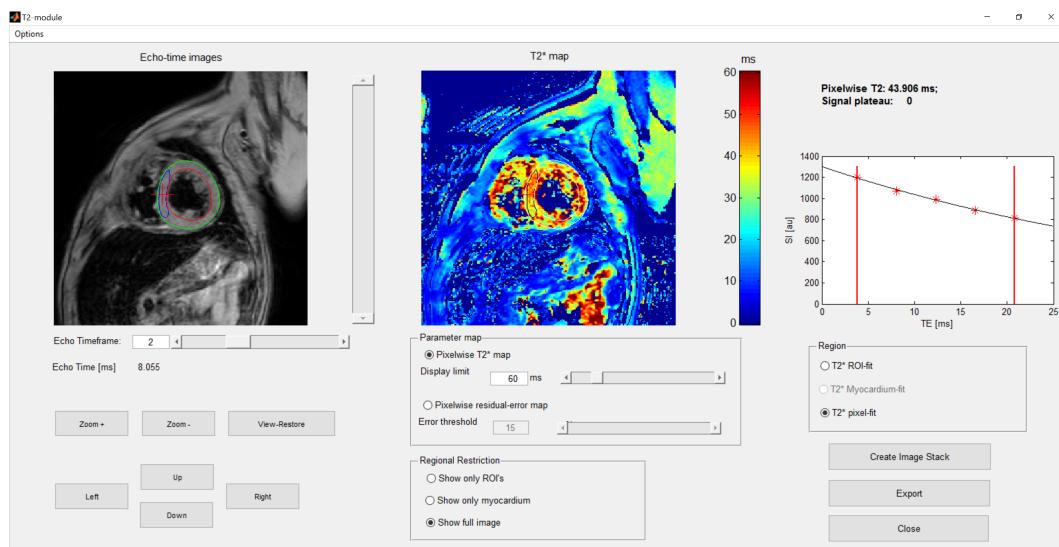


Figure 27: GUI for quantification of T2* values. The top left image panel shows the magnitude images for the different echo times, adjustable with the echo time slider. The right image panel shows the pixelwise T2* values.

15.2. IMPLEMENTATION

The right lower panel shows the fitting curve over time. The mean T2* value is presented in the graph and the associated graph title. The region for the mean value calculation is according to the selection of the checkboxes to the right, either T2* ROI-fit or T2* pixel-fit. The T2* pixel-fit takes the T2* values according to the red cross in the right image panel.

T2* values can be exported to spreadsheet by using the **Export** button. To create the T2* image stack in the main GUI of Segment CMR use the **Create Image Stacks** button.

15.2 Implementation

The detailed implementation of the T2* calculation is given in Chapter 27. In short the calculation is performed with standard exponential curve fitting that is calculated in the least square sense.

15.3 Validation

The module has been validated comparing to the open source software MRmap [?]. More validation details is available in a separate report from Medviso AB.

16 Strain Analysis

16.1 Strain analysis in cine or tagged images

The strain analysis module uses tagging 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.

16.1.1 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" from echocardiography. We are not using the same nomenclature due to the slight differences in calculation methods. In echocardiography, "Global strain" is defined as $(L-L_0)/L_0$ with L the instantaneous length of the endo- or mid-myocardial contour and L_0 the length of the contour in end-diastole. In Segment CMR, "Mean strain" is defined as the mean of all strain value within the entire LV wall.

16.1.2 Automatic strain analysis in short-axis image stacks

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 8. Manually start the automatic strain analysis by Select **Tagging Strain Short-axis** under **Strain** menu.

Cine: First perform LV segmentation. The automatic strain analysis starts by Select **Feature Tracking Strain Short-axis** under **Strain** menu.

2. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 28.
3. 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 segmentation.

Tagging: The segmentation should be performed in one of the first

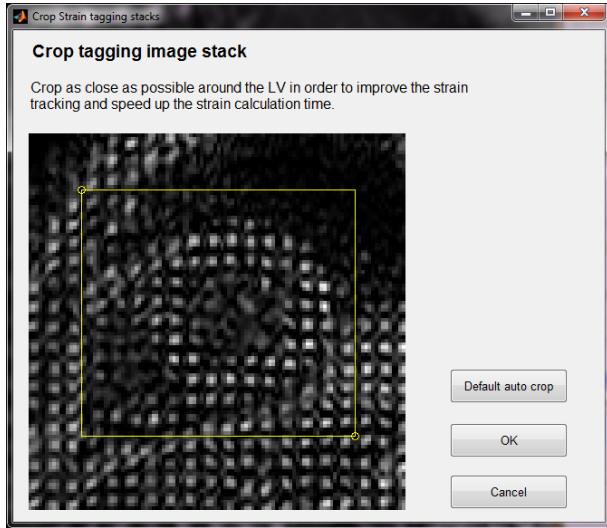


Figure 28: Strain cropping interface.

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 stack.

This time frame with segmentation will be the initial time frame for the strain tracking.

LV: Perform the LV segmentation according to Figure 29, using methods described in Chapter 9.

RV: Perform the RV segmentation according to Figure 29, using methods described in Chapter 10.

4. 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 at Current Timeframe in menu Edit.
5. **Tagging:** Start the strain module by selecting Tagging Strain Short-axis under Strain menu (a). The Strain interface is shown (Figure 30). **Cine:** Start the strain module by selecting Feature Tracking Strain Short-axis under Strain menu (a). The Strain interface is shown (Figure

16.1. STRAIN ANALYSIS IN CINE OR TAGGED IMAGES

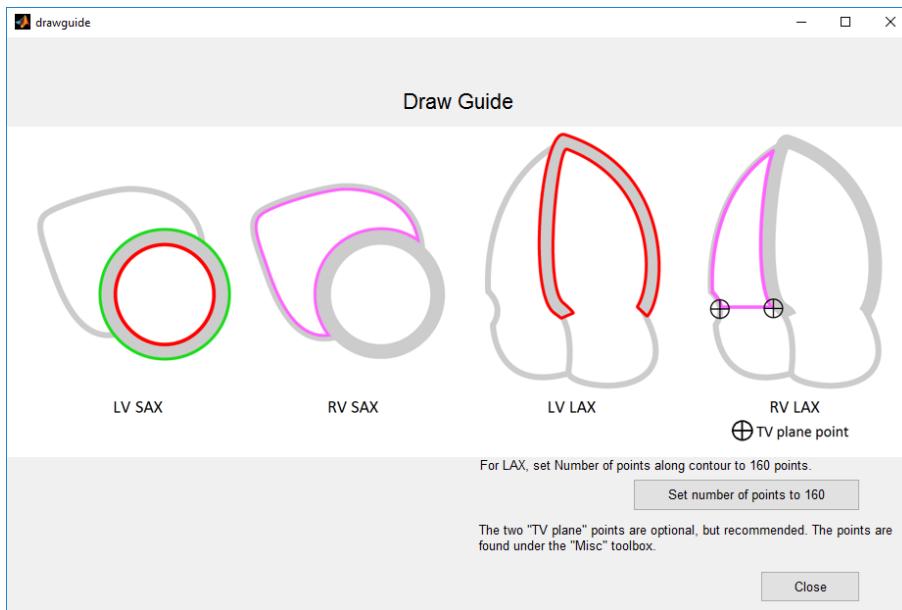


Figure 29: Strain drawing guidance.

30).

6. **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.
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. You can choose which segments to be presented in the graph with the radiobuttons below the graph.
10. 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 select **Analyse**.

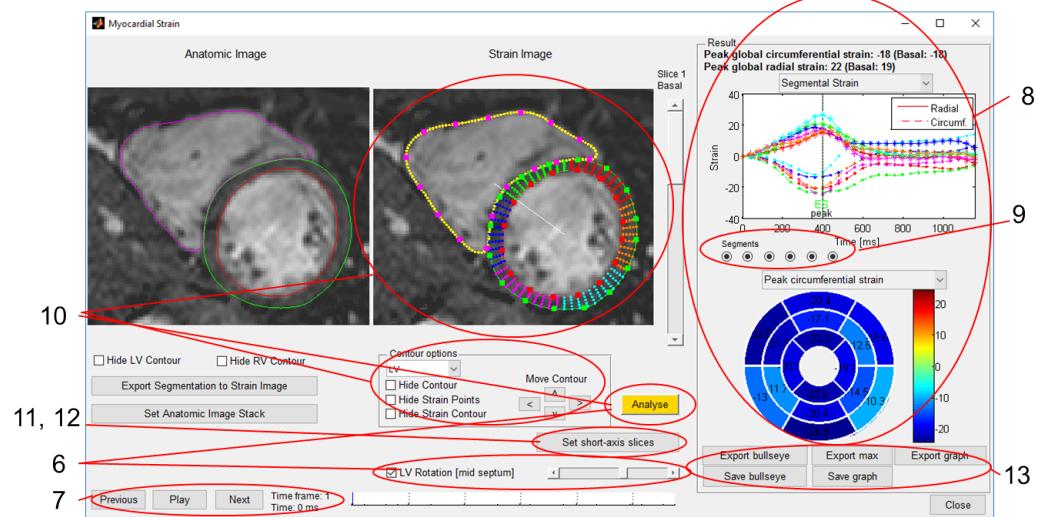


Figure 30: Strain analysis GUI.

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

Torsion

For short axis images torsion can be calculated. 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. For details on how the torsion measure is obtained see section 27.13.

16.1. STRAIN ANALYSIS IN CINE OR TAGGED IMAGES

16.1.3 Automatic strain analysis in long-axis image stacks

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 8. Manually start the automatic strain analysis by Select **Tagging Strain Long-axis** under **Strain** menu.
Cine: The automatic strain analysis starts 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 8.
3. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 31.

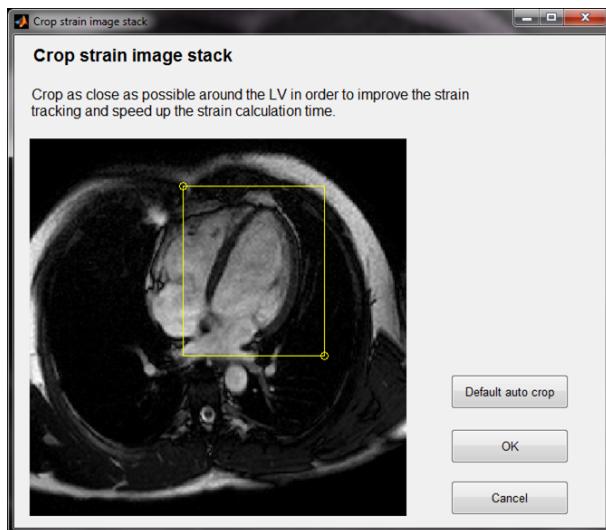


Figure 31: Strain cropping interface.

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 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.

5. **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 stack.

This time frame with segmentation will be the initial time frame for the strain tracking.

LV: Perform the LV segmentation according to Figure 32 by using the LV endo segmentation tools or in all three long-axis views.

RV: Perform the RV segmentation according to Figure 32 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.

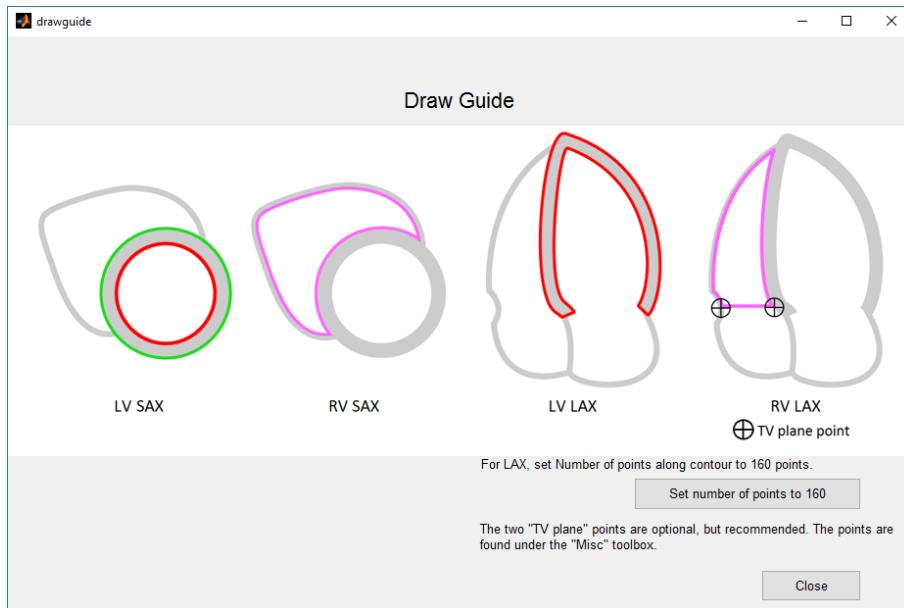


Figure 32: Strain drawing guidance.

16.1. STRAIN ANALYSIS IN CINE OR TAGGED IMAGES

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 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 33).
Cine: Start the strain module by selecting Feature Tracking Strain Long-axis under Strain menu (a). The Strain interface is shown (Figure 33).

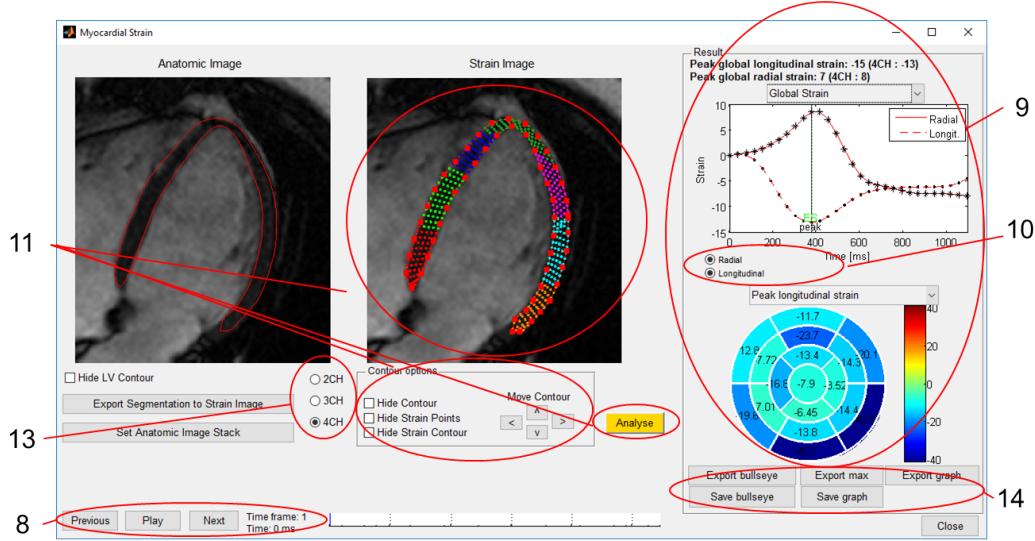


Figure 33: Strain analysis GUI.

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 segmentation interpolation points, in the initial time frame in the tagging image stack. Then run the strain quantification again by select **Analyse**.
12. **Tagging:** Manually change the initial time frame by select **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.

16.1.4 Hints for Strain analysis in small animal images

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 CMR you do that by Select **Upsample/Downsample 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 CMR you do that by Select **Upsample/Downsample 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.

16.1.5 Erase strain data

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

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

16.2 Strain Analysis in Velocity Encoded Images

The strain analysis module uses velocity encoded MR images to calculate myocardial strain. The module have been written by Helen Soneson as her Master thesis work [?], and resides on the work by Erik Bergvall for strain calculations and myocardial tracking [?]. This module is not available yet to researchers since it is under development and will be released as soon as the underlying method is properly published. Preliminary results about the method was presented at SCMR 2008 [?], [?].

Strain calculations require velocity encoded MR images with two velocity components. An example of such an image stack are shown in Figure 34. The leftmost panel is the magnitude image stack the two rightmost are the velocity image stacks.

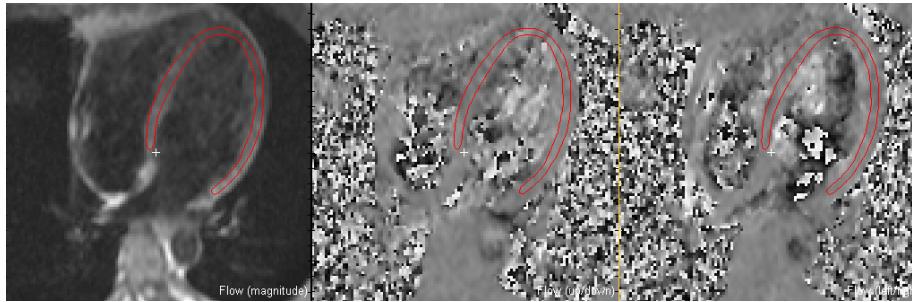


Figure 34: Example of a velocity encoded magnitude image stack and two directional velocity encoded image stacks.

Before starting strain calculation the myocardium of the left ventricle need to be manually outlined in end-diastole. One method to do this is to use the endocardium tool directly in the velocity encoded image stack. One tip before outline the myocardium in a long-axis image is to first set the "Number of points along the contour" in **Preferences** under the **Preferences** menu to 300. This make it easier to do small changes in the segmentation. The other method is to segment the myocardium in the anatomical (balanced or SSFP) image stack and then export it to the velocity encoded image stack. The exportation is done with the function **Import From Cine Stack** under the menu **Strain From Velocity Encoded Imaging** under the **Strain** menu. Before calculating strain the image type have to be set to either "Strain

2CH TFE” or ”Strain 2CH FFE” (and similar for 3CH and 4CH). This is done either upon loading or by right clicking on the corresponding thumbnail images and select Set Image Type.

16.2.1 Strain calculation

The strain in a long-axis velocity encoded image stack is calculated by using the function **Strain Tool** under the **Strain From Velocity Encoded Imaging** under **Strain** menu. Note that you need to manually outline the myocardium in end-diastole first. The function calculates segmentation and strain in all time frames. It also opens a new graphical user interface that make it possible to analyse/visualize strain in the image. An example of such a GUI can be seen in Figure 35.

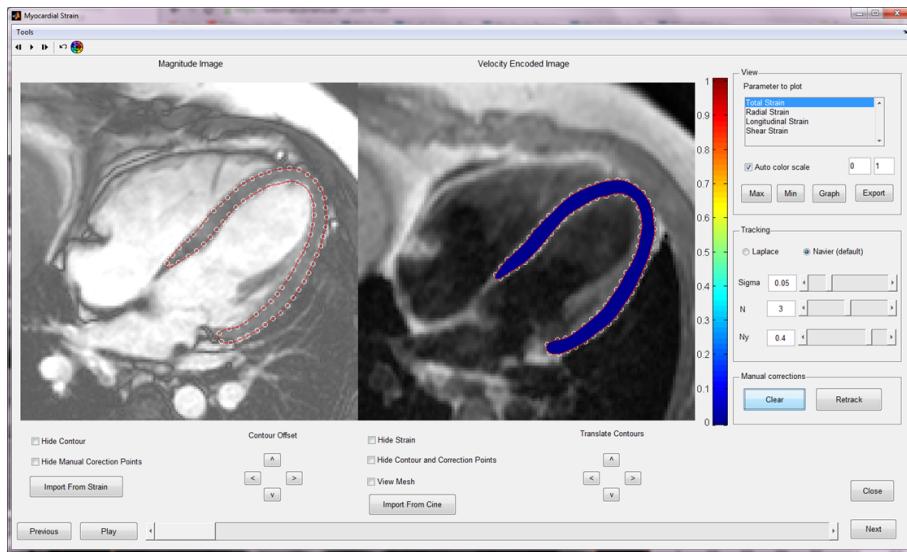


Figure 35: Example of the strain GUI.

To select which strain or displacement parameter to analyse, mark one of the parameters in the listbox in the figure. The 4 alternatives are:

- Total Strain
- Radial Strain

16.2. STRAIN ANALYSIS IN VELOCITY ENCODED IMAGES

- Longitudinal Strain
- Shear Strain

To see how strain changes over time there are three buttons in the figure to use. **Prev** that step one time frame backward in the heart cycle. **Next** that step one time frame forward in the heart cycle and **Play** plays a movie of strain over the whole heart cycle. The buttons **Min** and **Max** produce a figure of minimal respectively maximal strain in each pixel over time.

The **Export** button export strain values to a clipboard. These values are only given section-wise, and the values in each sector corresponds to the mean value of the pixels in the sector. The sectors are divided according to American Heart Associations 17-segments model.

16.2.2 Corrections of the segmentation

To make manual corrections in the calculated segmentation select use left mouse click in the image to move contour points. Delete manual point by right click on the added point. When you are satisfied with the manual correction in all time frames push the **Retrack** button. The **Delete** button deletes all manual corrections.

16.2.3 Strain analysis

One method to evaluate the strain calculation is to export the segmentation from the velocity encoded image stack to the SSFP image stack after the strain calculation is done. This is done with the button **Import From Strain**. The motion of the myocardium can then be compared to the myocardial movement in the SSFP image stack. It should be noticed that the two images (SSPF and velocity encoded) are not acquired during the same heart beat which can result in differences in position of the myocardium.

With strain calculated in the current velocity encoded image stack it is possible to produce a graph over time for strain by the button **Graph**.

In a file that consist of velocity encoded image stacks with calculated strain in all the three long-axis views it is possibly, by clicking the icon of a bullseye

plot to produce a bullseye plot of strain.

The function **Export From Multiple .mat Files** under the menu **Strain From Velocity Encoded Imaging** under the **Strain** menu export strain values to clipboard in all **.mat** files in the selected folder.

17 Viability Analysis

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

The viability tools can be found under the MR menu in Segment CMR. The method used for automated delineation of infarct is described in [?]. It uses a new paradigm in analyzing delayed contrast enhancement MRI. Instead of treating each pixel as dichotomously infarcted or not infarcted pixels are weighted with their signal intensity to compensate for partial volume effects [?]. The algorithm have been extensible validated against independent reference standards; TTC in animals 7 days after accute coronary occlusion, high resolution ex vivo MRI, and expert delineations in a multi-centre, multi-vendor cohort [?]. Please note that the presented algorithm is the only algorithm that is validated experimentally and in a multi-centre setting available (including all commercial alternatives).

The method delineates a larger area than would be outlined manually. It should be noted that even though it delineates a slightly larger area, this should not be compared to manual delineation, since the darker pixels are given a lower weight. As a graphical illustration of this a pink line is also shown in the weighted mode. An example of this is illustrated in Figure 36. This line graphically represent the corresponding non weighted area. Please note that this line is only provided for visual feed-back and should not be used for any quantification purposes.

The first step to do viability analysis of late gadolinium enhancement MRI (LGE) images is to delineate both endo- and epicardium. This can be done either manually or by a semiautomated method. In many cases however, it may be faster to manually draw the endo- and epicardial contours. Then select **Auto Delineate Viability (EWA method)** to delineate infarct. The automated delineated infarct is now shown with a yellow contour. After the delineation you can select the mode of operation. The default mode to use is the EWA scar delineation, although there are other options for specific research purposes (see below for details).

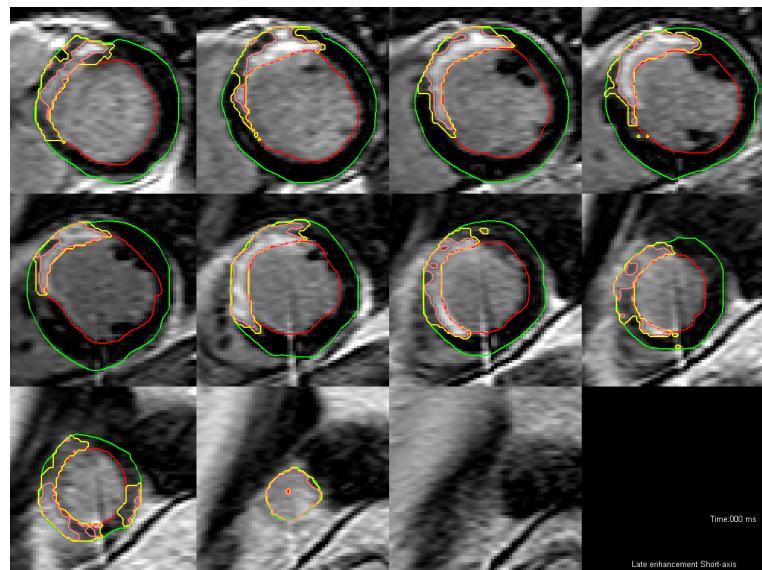


Figure 36: Example of scar delineation in the weighted mode. The yellow line denotes the complete affected area, and the pink line a graphical representation of the corresponding weighted area.

In the **Viability** menu you can select mode of operation, reset all scar delineation, reset user corrections, control visibility and automatic parameters. It is possible to add infarct regions by using the pen tool and remove infarcts with the rubber tool regardless of the mode of scar delineation. The tool removes the manual corrections made with the or . By default manually added scar regions shows up in green and manually deleted areas in blue. The tool is used to manually draw regions of microvascular obstruction. Microvascular obstruction is indicated in red. User interaction (and microvascular obstruction) can be showed/hided by clicking the key . Note when using the EWA method, regions with microvascular obstruction needs to be manually drawn if not automatically detected, since otherwise they are weighted incorrectly.

The following modes of scar delineations is available:

- **EWA method - Default.** Automatic scar delineation as described in [?].
- **Old weighted.** Automatic scar delineation as described in [?]. Kept only for backwards compability during ongoing research projects.
- **SD from remote.** Implementation of taking two 2-SD from remote myocardium as proposed by Kim *et. al* [?]. You need to place ROI's in the myocardium and label them ase 'remote'. Note that this method is not encouraged.
- **Otsu.** Implementation of Otsu method. No post-processing is performed. Note that this method is not encouraged.
- **EM algorithm.** Implementation of EM-algorithm. No post-processing is performed. Note that this method is not encouraged.
- **FWHM algorithm.** Implementation of FWEM-algorithm. No post-processing is performed. Details on FWHM implementation details is given in [?]. Note that this method is not encouraged.
- **Manual mode.** Manual drawing of hyper enhanced regions.

Each of the different methods are further described below.

17.1 Automatic mode (EWA method)

The automatic mode with EWA (Expectation Maximization, Weighted Intensity, *A* priori) is the default mode. This method has the ability to use a priori information on the vessel terrotori to aid the delineation. This is selected as a first step in a graphical user interface shown in Figure 37. If no assumption of affected vessel is to be used, then select No vessel assumption.

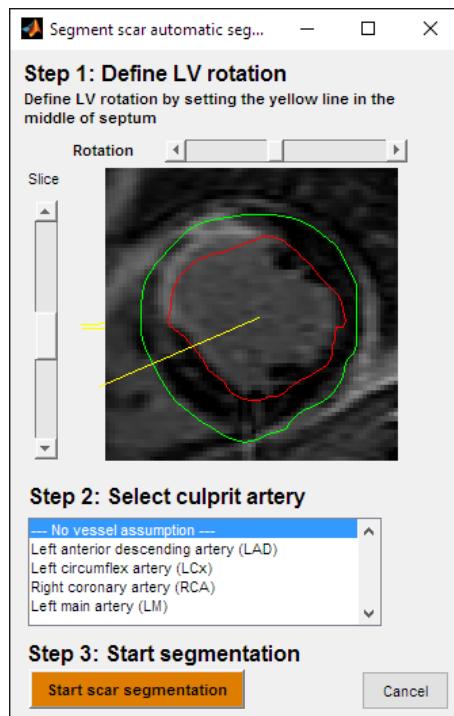


Figure 37: User interface to select vesselterrotori. First adjust sector rotation to point towards the mid point of septum. Secondly select known affected vessel. If this is not known or not applicable just select No vessel assumption.

In cases where the algorithm fails or make small mistakes manual corrections can be applied by using the tools and , respectively. Note that including extraneous black regions in the weighted method only marginally changes the result, since the infarct is weighted with pixel intensity. It may be necessary to manually mark regions of microvascular obstruction to get

these regions weighted correctly. If this is not performed the infarct will be weighted lower and the infarct mass will be incorrect.

17.2 Old weighted

The old weighted method is retained only for backwards compatibility during ongoing research projects. It will eventually be removed. Manual corrections are performed in the same manner as for the EWA algorithm.

17.3 Manual mode

In this manual mode the infarct area is not automatically updated and the only way to change the delineation is by doing manual interactions. If you want to start from scratch to manually draw your infarct regions, then first select **Clear all scar data**. This option also resets the viability mode to **Automatic mode** so you need to choose **Manual mode** before starting to draw the infarct regions.

17.4 SD from remote

It is possible to do scar delineation as proposed by Kim *et. al* where the infarct is determined as pixels with an image intensity that is higher than the mean plus two standard deviations from the mean in a non infarcted remote region. In the original method by Kim et al when one read the paper carefully they used two types of ROI's, both remote ROI's and also a scar region ROI in which the thresholding was applied. Therefore, the same approach is also applied in Segment CMR.

To draw remote region use the ROI drawing tool  or Add ROI's in sector under the **ROI** menu. The latter option adds ROI's in a sector in selected slices with a position specified as an angle, the width as and angle and finally the distance from the endo- and epicardium as percentage of the wall thickness. This option automatically flags the ROI's to be remote regions, but if you use the ROI drawing tool  you need to manually flag that by right clicking on the ROI and select **Select ROI label** on the pop-up menu. When drawing a subsequent ROI the label of the ROI is copied from the last modified ROI so you only need to first draw one ROI, then label it and draw all remaining ROI's. If you do not draw a remote region in the

threshold for that slice is then intra/extrapolated from adjacent slices. Using the default viability options this approach will only set a threshold to the level set algorithm based on the drawn ROI's.

To draw the scar region ROI's (**Scar region ROI**) use the same approach as described above. It is often advantagous to first draw all the remote ROI's and then the scar ROI's since you do not need to alternate with labeling the ROI's.

17.5 EM algorithm

This mode is to be used only for evaluating different infarct quantification algorithms, especilly ex-vivo studies. In cases where it fails make necessary manual corrections by using the tools  and , respectively. It may be necessary to manually mark regions of microvascular obstruction to get these regions delineated.

17.6 Technical details

It is possible to control the parameter Beta, Min volume, Standard deviation from remote. The parameter **Beta** controls the smoothness 'curvature' forces on the level set surface and in practice it controls the smoothness of the result. The parameter **Min volume** controls the minimum size allowed for an infarct in ml. These parameters are not recommended to change and are further described in [?, ?]. The parameter **Standard deviations from remote** controls is the only variable that we recommend to change, and then for the SD from remote method.

17.7 Grayzone Analysis

The menu item **Gray Zone Analysis** enables the user to divide the scar area into core and grayzone based on the scar segmentation. The result is displayed in the image view as colored overlays of dark red (core) and dark yellow (grayzone) pixels. The quntitative core and grayzone values are presented in a message box.

18 Myocardium at Risk Analysis

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

There are two algorithms to quantify myocardial at risk (MaR) from MR images. There is also one tool to quantify MaR on SPECT images and this is described in Section ??.

The maR tools can be found under the **MR** menu in Segment CMR. The first step to do MaR analysis of T2-weighted MRI (T2w-MRI) images is to delineate both endo- and epicardium. This can be done either manually or by a semiautomated method. In many cases however, it may be faster to manually draw the endo- and epicardial contours. Then select **Auto Detect MaR** to delineate MaR, see below for details. Depending on the number of timeframes either of the two methods below is selected. If there is only one time frame available, then MaR from T2-weighted images are chosen.

It is possible to add infarct regions by using the pen tool and remove infarcts with the rubber tool . The tool removes the manual corrections made with the or . By default manually added mar regions shows up in green and manually deleted areas in blue.

18.1 MaR from T2-weighted images

The method used for automated delineation of MaR from T2-weighted is described by Sjogren et al [?]. It uses an Expectation Maximization algorithm to calculate a probability of MaR based on intensity instead of using a threshold and models of the perfusion territories are used as a priori information to constrain the segmentation.

In the graphical user interface choose the culprit artery in the list box and rotate the yellow line to indicate the center of the septum and press OK. The automated delineation of MaR is now shown with a white contour. Note that you need to select culprit artery. The coronary perfusion distributions may be

different for different species and special care needs to be taken into account in such cases.

18.2 MaR from CE-SSFP images

Using contrast enhanced standard cine images acquired directly after contrast injection can be used to determine MaR, [?]. This technique is the technique recommended to use by Medviso AB as it has been shown to be more stable across vendors and in multi-centre setting compared to T2-weighted techniques [?]. The algorithm for automated MaR delineation from CE-SSFP images is developed by Tufvesson (maiden name Sjogren) [?]. The algorithm is based on expectation maximization (EM) and a vessel tree model for accurate segmentation. We recommend to use both systole and diastole images and that their result should be compared as in internal consistency check.

Just as for MaR from T2-weighted images you need to select a vessel model and ensure correct rotation with the yellow-line pointing towards the centre of septum.

19 Perfusion Analysis

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

The perfusion module is used for performing analysis of perfusion image stacks. Quotes between maximum upslopes of rest and stress images can be calculated for each sector of the myocardium.

19.1 Module overview

Before opening the perfusion analysis GUI, make sure to have one open image stack whose image type is set to Perfusion Rest and one whose image type is set to Perfusion Stress. An overview of the perfusion analysis GUI, as it appears when launched, is shown in Figure 38. From left to right, each image column contains Stress, Rest, Cine and LGE images respectively. Image slices are shown with the most basal at the top and the most apical at the bottom. If the perfusion stacks contain more than three slices, a scrollbar allows the user to toggle between them. Segmentation contours are shown, but can be disabled by unchecking the **Contour** box. The **Rotate** checkbox is used to set images in rotation mode. This causes the images to zoom in on the contour, and displays the borders for myocardial sectors as well as a horizontal yellow line from the center to the left of each image. By dragging this yellow line, the user can rotate the images to align them properly with the sector partition. When the mouse button is released, the line will rotate back to its original leftward position and drag the image with it.

The timebars below the Stress, Rest and Cine images enable the user to step in time. The Stress and Rest timebars each have one bar labelled **Start** and one labelled **End**. These are used to set the start and end points of motion correction. They also affect use of the playback functionality, which can be done one image at a time using the playback panel with buttons  and , or making Stress and Rest images play synchronously by using the **Play all** button.

CHAPTER 19. PERFUSION ANALYSIS

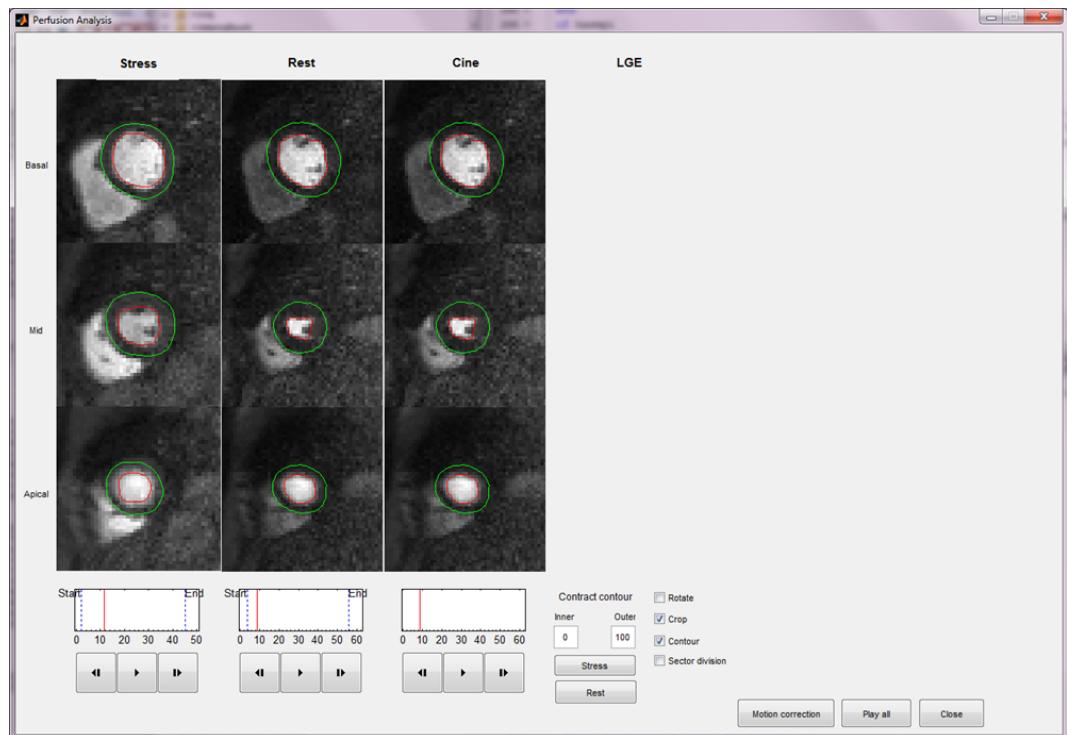


Figure 38: GUI for perfusion analysis.

19.1. MODULE OVERVIEW

Once an interval has been set using the Start and End bars and all slices of one timeframe have been outlined in both Stress and Rest image stacks, hit the **Motion correction** button to start the automatic motion correction. This process can take several minutes. The result is shown in Figure 39. If intensity from the right ventricle or elsewhere spills into the myocardium segmentation as a result of the motion correction, the contour of the respective image stack can be adjusted contraction percentages in the **Inner** and **Outer** textboxes and using the **Contract Contour** pushbuttons labelled **Stress** and **Rest**.

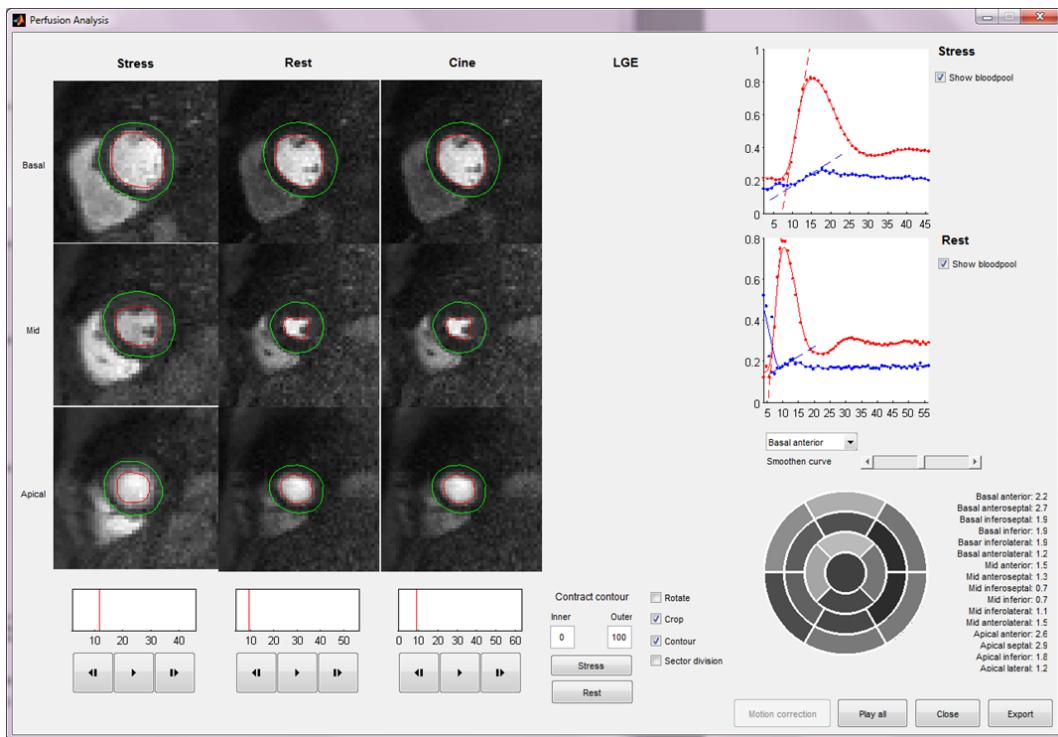


Figure 39: GUI for perfusion analysis after motion correction.

The two plots on the right side of the GUI show the upslope curves of the current sector (selected from the pop-up menu), which are calculated using a Gaussian filter on the measured values. The width of this filter can be adjusted using the slider labelled **Smoothen curve**, making the curve sharper or smoother. By checking the box **Show bloodpool**, a curve of the blood-

CHAPTER 19. PERFUSION ANALYSIS

pool is shown in red in the same plot. The bullseye plot below the curve plots displays the sectorwise quote between the maximum stress and rest up-slopes, normalized with respect to the respective maximum upslopes of the bloodpool curves. The quote values are also shown in text next to the bulls-eye plot, and can be exported to a spreadsheet by clicking the **Export** button.

20 Pulse Wave Velocity Analysis

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

An overview of the Pulse Wave Velocity module is shown in Figure 40. Upon launch, the module automatically finds the image stack that contains a measurement labelled **Aortic Length** and the two flow image stacks that contain ROI's labelled **Aortic ascending flow** and **Abdominal aorta**. The image on the left of the GUI shows the image containing the measurement. This measurement is displayed in yellow and the intersections with images containing flow are displayed as white lines. The plot on the right side shows the flow curves of the **Aortic ascending flow** ROI (in blue) and the **Abdominal Aorta** (in red). For each flow curve, the tangent of the upslope is calculated using a Gaussian smoothing function and displayed as a dashed line in the corresponding color. The sigma parameter of the smoothing function can be adjusted using the slider on the right of the plot.

Pulse wave velocity is calculated using the length of the **Aortic Length** measurement and the time between the upslopes of the flow curves. The time is measured as the temporal distance from the moment when the tangent of the **Aortic ascending flow** curve is equal to zero to the moment when the tangent of the **Abdominal Aorta** curve is equal to zero. This distance is displayed as a dotted portion of the black line along $y = 0$ in the plot. The values for aortic length, time between upslopes and calculated velocity are displayed in the GUI and can be exported to a spreadsheet by clicking the **Export** button.

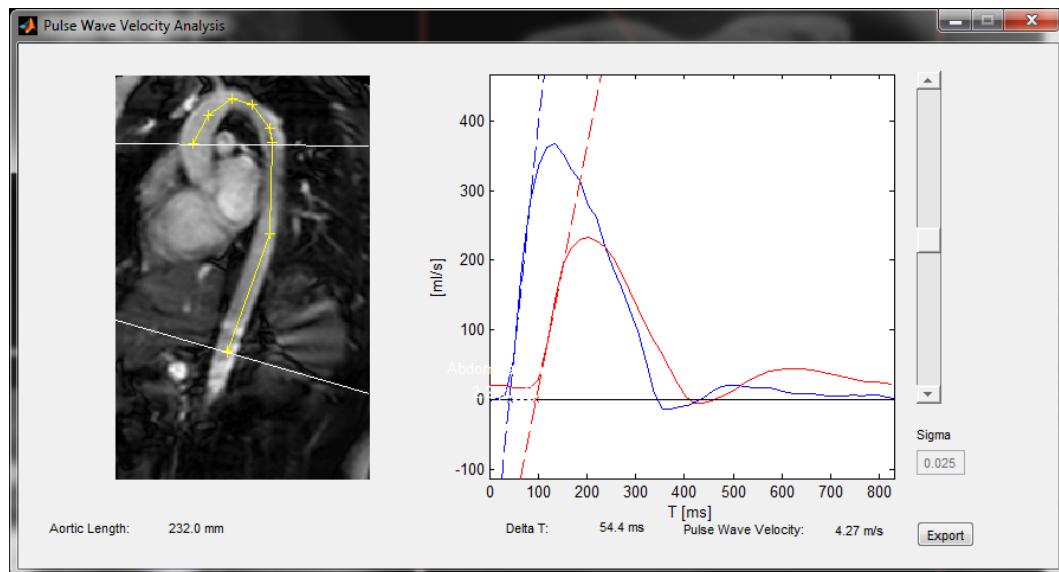


Figure 40: GUI for Pulse Wave Velocity Analysis. On the left is the image containing the measurement of Aortic Length. On the right is a plot of flow curves along with their respective tangents.

21 LV Sphericity Analysis

LV sphericity can be calculated from the **Analysis** menu.

The sphericity of the left ventricle is defined as the maximum short-axis diameter divided by the length of the ventricle. This calculation is performed separately for ED and ES and for each of these timeframes, it is required that there exists LV endocardium segmentation in an open short-axis image stack, as well as an image stack containing a measurement labelled **End Diastolic Length** and **End Systolic Length** respectively.

The values of diameter and length of the ventricle and the calculated sphericity are displayed in a messagebox and copied to the clipboard, allowing the user to paste them into a spreadsheet.

22 Reporting

The report tool is a report generator is a tool to generate reports of a study. The tool is started by the icon  or under the Report menu. The graphical user interface is illustrated in Figure 41. The report can be generated in one of three formats:

- HTML format. The **Generate HTML report** is used to generate a HTML report, complete with images and plots. Each page can be printed and together they contain a detailed report of an exam. An example of the final output is given in Figure 42.
- JPEG format. A simplified graphic report, containing only text and tables, can be created using the **Send to PAF** button. This report is saved as a collection of JPEG files for easy upload to PAF. The output folder can be set in the **Advanced System and DICOM settings** under the **Preferences** menu.
- DICOM format. The simplified graphic report can also be saved as a collection of DICOM files and automatically uploaded to PACS by clicking the **Save to PACS** button.

Hospital logo, patient data, signature field and current date are automatically included in the report. The checkboxes are used to select which details of the analysis are to be included in the report. A checkbox is grayed out if data is unavailable.

- LV Analysis, this section contains a table of global LV parameters and, if the images are time-resolved, a volume curve.
- RV Analysis, this section contains a table of global RV parameters.
- Scar Analysis, this section contains a table of data from scar analysis and an image of scar delineation.
- MaR Analysis, this section contains a table of data from myocardium at risk analysis.
- Flow Analysis, this section contains flow data from phase contrast images and a plot of net flow over time. If there are several image stacks containing different flow data, one section will be added for each such stack.

CHAPTER 22. REPORTING

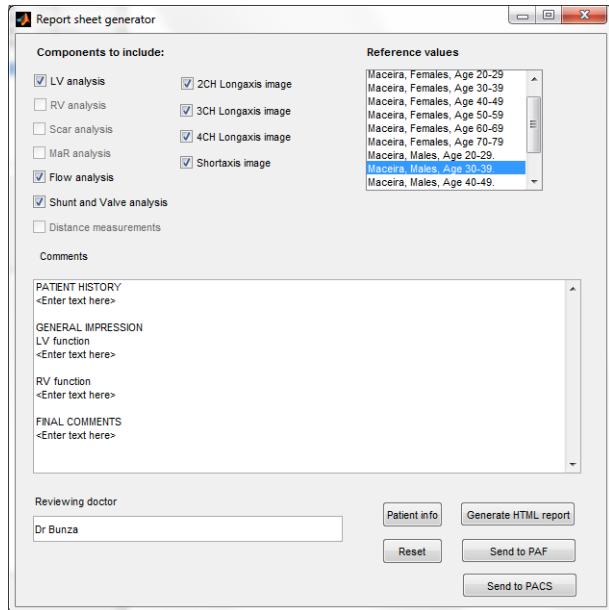


Figure 41: GUI for patient report generator.

- Shunt and Valve analysis, this section contains the Qp/Qs ratio and regurgitant volumes and fractions for the mitralis and tricuspid, insofar as the data necessary for calculation is available.
- Distance measurements, this section contains a table that lists all distance measurements performed on the current set of image stacks.
- 2CH/3CH/4CH Longaxis Image, this section contains a user selection of longaxis images in end-diastole.
- Shortaxis Image, this section contains a montage view of all shortaxis image slices in end-diastole with delineations included.

22.1 Configuration

This section describes how the Report Module can be configured.

22.1.1 Hospital logo

This is an image header that is supplied by Medviso AB to each customer separately. Place this file in the folder where Segment CMR is installed.

22.1.2 Reference values

Reference data used in LV and RV analysis can be selected from a listbox. If patient age and sex are present in the patient info, the listbox will automatically suggest a suitable set of reference values. If reference data is used in the report, patient values outside the range specified by the reference data will be marked in red. The name of the used reference data set will also be included in the report.

A directory contains each reference data set as a text file with the following structure:

```
Name: 'Maceira, Males, Age 30-39.' %Title to display in listbox.  
ImagingType: 'SSFP' %Describes used imaging type.  
LowerAgeBound: 30  
UpperAgeBound: 39  
Sex: 'M' %should be either M or F.  
LVM: [109 185]  
EDV: [121 204] %range  
...  
EDV_BSA: [66 101] %BSA means normalized with BSA.  
...
```

22.1.3 Headings for textual report

There is also a large textbox where it is possible to enter free text comments on the study. This text is then stored together with the segmentation. A few formatting tricks can be used in this box:

- To divide the text into paragraphs, enter a blank line between the text blocks to be used as paragraphs.
- To start a paragraph with a headline in bold print, simply begin the paragraph with the text to be used as headline, then insert a new line where the text body is entered.
- To insert a super headline, do the same as above except that the text is entered in all upper-case letters. A super headline may be followed by a regular headline.

CHAPTER 22. REPORTING

For simplification, standard text templates are supplied by Medviso AB. An example of such a template is the following:

PATIENT HISTORY
<Enter text here>

GENERAL IMPRESSION
LV function
<Enter text here>

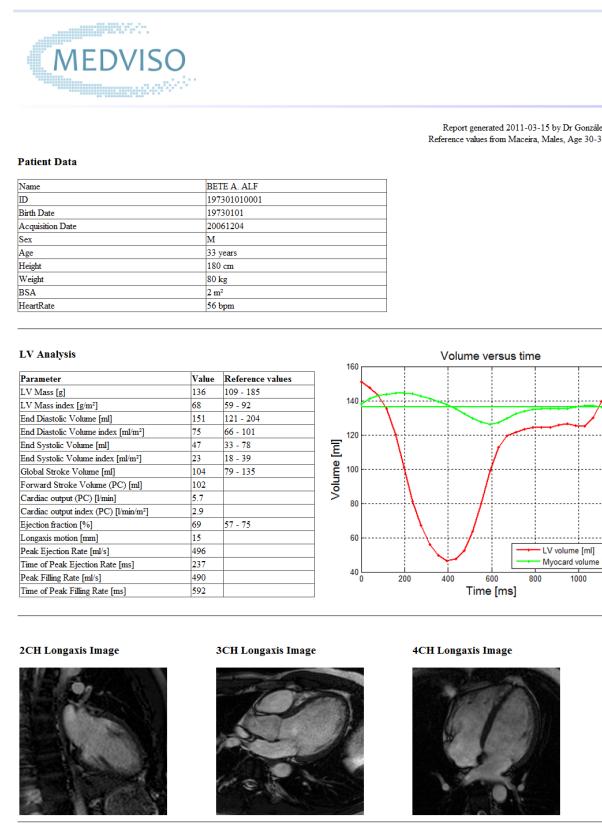
RV function
<Enter text here>

FINAL COMMENTS
<Enter text here>

22.1.4 Reviewing doctor

The final textbox in the GUI allows for including the name of the doctor performing the analysis and generating the report. If entered, the name of the doctor appears by the logo image at the beginning and by the signature field at the end of the report.

22.1. CONFIGURATION



GENERAL IMPRESSION

This patient looks normal..

Date: 2011-03-15

Reviewing doctor:

Dr González

Figure 42: Example of a report.

23 Export Images and Results

23.1 Export image

Using this option, only the current frame without segmentation is exported as a file. You need to select file format, and the following formats are supported: `.jpg`, `.bmp`, `.png` (portable network graphics), and `.tiff`. The recommended image format to use is `.png`.

23.2 Export screenshot

Using this option, the current frame including segmentation is exported as a file. The following image formats are supported: `.jpg`, `.bmp`, `.png` (portable network graphics), and `.tiff`. The recommended image format to use is `.png`. There is also an option to save the screenshot file to a PACS system.

When preparing images for publication it is often helpful to change the color of the contours to black/white and increase line width to increase visibility. This can be done under the preferences menu, see Chapter 24 for further details.

23.3 Export movies

Exporting movies can be done by either using the built-in movie recorder in Segment or by exporting the current image stack as a movie ([Export Movie](#)).

23.4 Movie Recorder

This is an experimental functionality that take screen captures and store them in a movie format. The movies can be done in two ways and either to `.avi`-files or a sequence of `.png` files (that later can be converted to different file formats). In future versions it will also be possible to export to animated `.gif` format. You can create movies of the main view, zoom view, 3D plot view, report per slice view. First select **Movie Recorder** under the **Export** menu. This brings up a user interface shown in Figure 43.

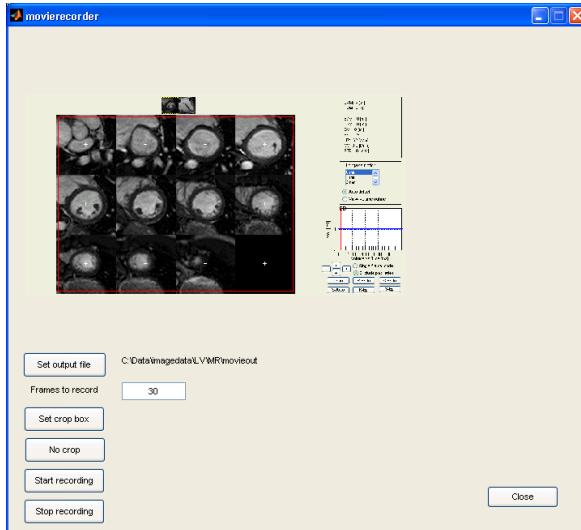


Figure 43: Movie Recorder GUI.

The movie recorder is when started unpopulated. To do a first screen capture force an image update by view next frame. You can now set a crop box (shown in Figure 43 as a red box), set number of frames to record, and start to record the movie. Usually you should set the number of frames to record to the same number of time frames as there are frames in the image stack. When all frames are recorded then a file selection pop up menu appears and where you can select storing options. When exporting to .avi files you need also to select a movie compressor, since all compressors might not be available on your computer. Personal experiences are that the cine-pak encoder are pretty stable.

24 Customization

This chapter describes how to customize Segment CMR. 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. The GUI for setting preferences is shown in Figure 44. It is invoked by using the menu **Preferences** on the main menu.

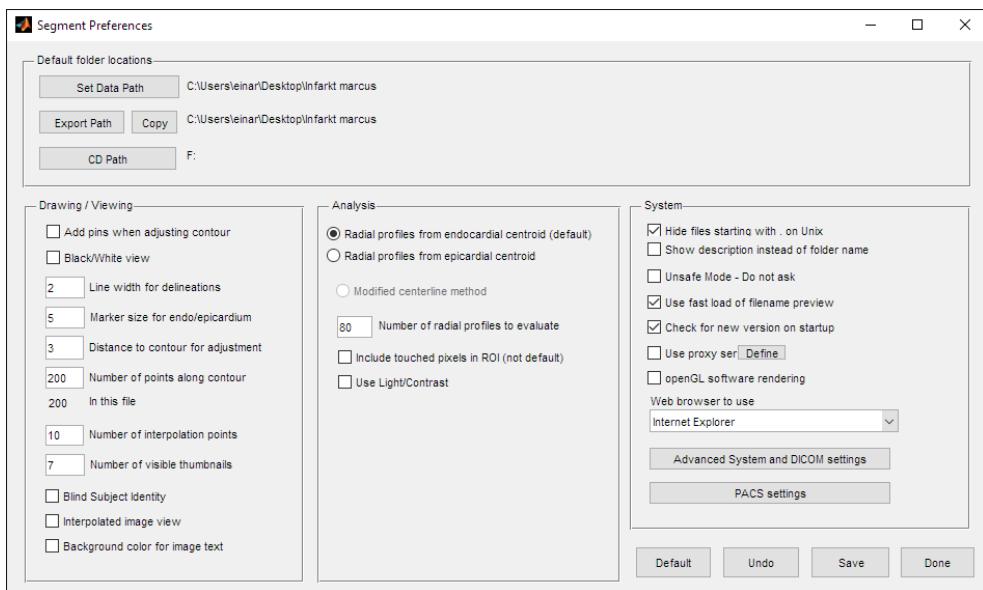


Figure 44: Preferences GUI.

There are four panels in total. The top most panels sets default folder locations for loading, and saving, respectively. It is also possible to indicate which drive / path that corresponds to your CD-drive. Then, the left most panel sets preferences for editing and drawing contours, the middle panel sets preferences for regional analysis, and the right most panel sets system preferences. The button **Advanced System and DICOM Settings** opens a new interface with settings for base image path for patient database, and DICOM communication parameters. The button **PACS Settings** opens an interface with settings for PACS communication.

CHAPTER 24. CUSTOMIZATION

The option **Add pins when adjusting contour** controls whether points should be placed when manually correcting a contour. This option should be checked when modifying time resolved images, but unchecked otherwise.

Black/White view plots the endocardium and epicardium with white lines. This is useful for making screen captures for illustrations that are not printed in color. The edit box **Line width for endo/epicardium** sets line width for the contours. This again is useful for making screen captures. Default line width is 1. The edit box **Distance to contour for adjustment** adjust how close to a contour one need to click before this contour is activate. When using the interpolate tool it is recommended to set this to quite small, typically 1-2. The edit box **Number of Points Along Contour** sets the number of points that are stored along a contour for endocardium and epicardium. When using automated segmentation this value should be set to 80. When manually drawing complicated objects this can be set to a higher number. If the option **Blind Subject Identity** is checked then the program will not show patient info on screen this is useful for making screen shots etc for presentations. It is highly useful when doing research and the observer should be blinded to the patient identity. The edit box **Number of visible thumbnails** sets the maximum number of thumbnails visible. When the number of image stacks exceeds this number a slider will be visible to scroll through all the thumbnails.

The radio buttons **Radial profiles from endo/epicardial centroid** controls how regional wall measures are placed. The radio button **Modified centerline method** is reserved for future use when the modified centerline method will be implemented. The edit box **Number of radial profiles to evaluate** sets the number of radial spikes that are evaluated before sector means are calculated. For more details on how the regional parameters are calculated see Chapter 27. The checkbox **Include touched pixels in ROI** sets how the edge pixels of a ROI are treated. When selected all pixels that are touched by the ROI are included. The default behavior is to include only the pixels where the center of the pixel lies within the ROI.

The checkbox **Allow DICOM cache** allows creation of cache files for tags in DICOM files to be generated.

The web browser to be used can be chosen in the drop list by either choosing

24.1. IMAGE DESCRIPTION SETTINGS

a program if it is installed in the default location or choose other to browse for the program file to use for example select `chrome.exe`, or `firefox.exe`.

Customization of the Report Module is described in Chapter 22.

The `Use proxy server` checkbox allows for usage of a proxy server. When clicking the checkbox you are given a message indicating if there is a proxy server defined. If not, you are given a form in which you can specify a proxy server. The lower two fields are optional. There is also a define button in which you can specify your desired proxy server.

You can configure which OpenGL rendering to use via the checkbox `openGL software rendering`. If it is checked you are using OpenGL software, if not you are using the OpenGL hardware rendering.

24.1 Image description settings

The automatical definition of image description parameters upon loading is controlled by a parse file. A schematic view of the parse file is shown in Figure 45.

```
#Imaging technique
'output', 'string matched against sequence name', 'string matched against seriesdescription',
'string matched against modality', 'string matched against filename', matlab code

#Image type
'output', 'string matched against sequence name', 'string matched against seriesdescription',
'string matched against modality', 'string matched against filename', matlab code

#Image type
'output', 'string matched against sequence name', 'string matched against seriesdescription',
'string matched against modality', 'string matched against filename', matlab code
```

Figure 45: Schematic view of the parse file for image description settings.

Correctly defined image description parameters is important in the use of automatic analysis tools. The image description is divided into three parameters; Imaging technique, Image type and Image view plane. The definition of image description parameters is controlled by manually change the parse file

`imagedescription.txt` according to Figure 45. This make it possible to adjust the definition of image description parameters to different acquisition parameters settings. There are no limitations in the number of specifications below each image description parameter. An example of a parse file is shown in Figure 46, and is also helpful to study the default file `imagedescription.txt`. If you have questions, please contact `support@medviso.com` for further details.

```
#Image type
General,,,
Perfusion Rest,,rest,,,
Perfusion Rest,,,REST,
Late enhancement,,DE,,,
Late enhancement,,Viabilitetm3d,,,
Late enhancement,,3D viab,,,
Cine,,sbFE,,isempty(SET(no).Flow)
Cine,,M2D,,,

#Image view plane
Unspecified,,,
2CH,,2ch,,,
3CH,,3ch,,,
4CH,,4ch,,,
Sagittal,,sag,,,
Coronal,,cor,,,
Frontal,,front,,,
Transversal,,trans,,,

#Imaging technique
Unspecified,,,
MRSSFP,,SSFP,,,
MRSSFP,,TF2d,,,
MRSSFP,,Fiesta,,,
MRDE,,DE,,,
MRDE,,psir,,,
NM,,,NM,,,
PT,,,PT,,,
CTheart,,,CT,,,
US,,,US,,
```

Figure 46: Example of a parse file for image description settings.

24.2 Advanced and DICOM Settings

The graphical interface for advanced settings is shown in Figure 47. The GUI is divided into four sections; Database settings and Segment Server settings; Report settings, Sending DICOM files; and DICOM interpretation. Please note that these operations may require that you run the software as Administrator (not only being logged in as Administrator). This is done by right clicking on the icon of the software and then select "Run as administrator".

In this section we will only describe Report settings and DICOM interpretations as the other settings are explained in conjunction with Segment Server documentation, and Patient Database Module which are described in the

Patient Database and PACS communication Manual.

The Reporter Settings adjust where the temporary reports are stored. By default this is done in a subfolder called **Report** in the folder where the Patient Database is located. The folder PAF report folder is a Swedish Client Patient Administrative Report and can be ignored.

The DICOM interpretation adjusts how Segment CMR interprets DICOM files. The checkbox **Force 16 bit DICOM** enforces Segment CMR to assume usage of 16 bit DICOM files, regardless what is stated in the file. This option is helpful when images looks like chessboard when read into Segment CMR. For further details see about loading DICOM files in Chapter 5.

24.3 PACS Settings

PACS Settings are described in the Patient Database and PACS Communication Manual.

24.4 Technical details

On Windows platform, the preferences are stored under the local user folder and the subdirectory **Application Data/Segment CMR**. This means that each user have can set their own preferences. It is possible to create a set of default settings by using the option **Save to all** where the preferences are saved to a file called **default_preferences.mat** in the folder where Segment CMR is installed. This will also override all PACS and Segment Server settings for all users. In the preferences folder Segment CMR also stores a log file for debugging purposes, and small temporary files that are used in the PACS communication batchdownload process.

CHAPTER 24. CUSTOMIZATION

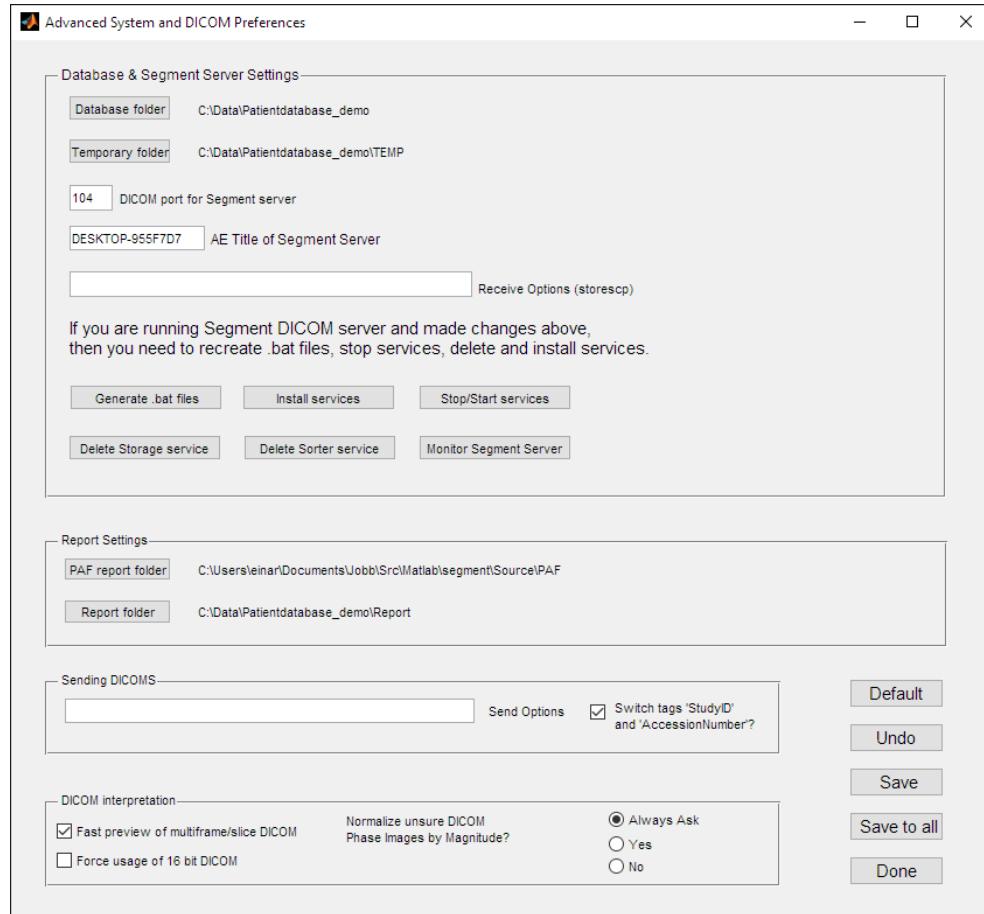


Figure 47: Advanced and DICOM Settings GUI.

25 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

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 25. 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)

26 Support

26.1 Submit bug report

When submitting a bug report it is very important to describe how to reproduce the bug and to provide the log file for the session. In many cases it is also necessary to provide some files that can be used to analyse the problem. It may either be .mat files or DICOM files when the problem is loading data into Segment.

To submit a bug report, select the function **Support Request** under the **Help - Support** menu. This will open the graphical user interface where you can describe the bug and attach log files and data such as .mat files or DICOM files. When all information is entered you press the **Send support request** and the description entered and the attached files are submitted to Medviso.

By changing the type you can also submit general questions or enhancement requests.

Hints to remember:

1. Even though the submitted files are encrypted your files should be anonymized. Anonymization of .mat files are available under either **Image Tools** menu or the **Utilities** menu. Anonymization of DICOM files are available under the **Utilities** menu.
2. Additional files to submit should be placed in a folder and the folder is then submitted.
3. Remember to name your files wisely, otherwise we will not be able to identify which file belongs to which support request.
4. Remember to mention the filename uploaded in your support question/request.

26.2 Data privacy policy

Medviso AB will strictly keep the data safe and **not** distribute it and any data or information from it (such as possible pulse-programming ideas, post-processing ideas, etc etc). Medviso will **not** utilize it for other purposes than debugging purposes or to answer the specific questions unless other is agreed upon. When the support case has been closed, then the data will be deleted. If you have questions, please contact support@medviso.com for further details.

26.3 General support issues

To get into contact with developers at Medviso AB, send email to support@medviso.com.

27 Implementation Details

In this chapter a few implementation details are given. There are much more details that are interesting, but this is as far as we have got with the documentation. If you have specific questions, please do not hesitate to ask us.

27.1 Numeric representations

All numbers are stored and used internally as double precision floating points with the following exceptions:

- Images are stored as single floats (normalized) or as integers (uint8), and then as they are stored in the DICOM files. Most functions in Segment will automatically convert the data to floats.
- Edge detection results are stored as integers (16 bits, 'normalized')
- Character strings are stored in 8bit ASCII format
- Infarct maps are stored as int8 (manual interaction), and uint8 (result).
- General segmentation tool store objects as levelset function with an uint8 representation where the zero levelset resides at 128.

Internally the image stack is normalized upon loading by a global maximum intensity such that all values are [0..1]. Offset and scaling is also calculated so that the image stack can be reconverted back to original signal intensities.

27.2 Loading data and interpretation of DICOM tags

This section describes how Segment interprets DICOM information to calculate important parameters suchs as geometric properties of the images.

- Number of slices. This is calculated from the presence of different slices based on the DICOM tags `ImagePosition` and `ImageOrientation`.
- Number of timeframes. This is based on dividing the total number of images with the number of slices.

- Time increment in ms between each timeframe. If uniform, this is based on the difference between the number of timeframes divided by largest and the smallest value of the DICOM tag **TriggerTime**. If the DICOM tag **TriggerTime** is not present then the DICOM tag **TR** is used as time increment. Note that this might depend on your k-space acquisition scheme so for scanners that do not report **TriggerTime** you really need to double check the estimated value of time increment. For perfusion and other image stacks with non-uniform time increment, this is calculated using differences in **AcquisitionTime**.
- Heart rate. The heart rate is taken from the DICOM tag **HeartRate** if present. Note that many vendors (including Siemens) does not specify this. As a fall back Segment tries to calculate the heart rate assuming full R-R intervall coverage by using of trigger time (i.e it does not work for prospective imaging series). For long image acquisitions where one image is taken approximately for each heart beat then the heart rate is taken as the time between start of image acquisition and end of image acquisition adjusted for the number of frames. Note that in many cases this heart rate calculation will fail. Heart rate can be adjusted under patient details. Note also that heart rate may vary between image stacks therefore do not press Apply for all when manually changing heart rate. Heart rate is not used in any calculation, instead time increment between image frames is used in all calculations.
- Slice thickness in mm. The slice thickness is taken from the DICOM tag **SliceThickness**. If this tag is not present then the information is taken from same DICOM tags as number of slices, and assuming slice gap to be 0.
- Gap between slices in mm. This is taken from the DICOM tag **Spacing BetweenSlices**.
- Pixelspacing in X-direction in mm (vertical direction in Segment). This is taken from the DICOM tag **PixelSpacing**.
- Pixelspacing in X-direction in mm (horizontal direction in Segment). This is taken from the DICOM tag **PixelSpacing**.
- Velocity encoding (VENC) in cm/s. For non velocity encoded images this should be 0. How this is interpreted involves proprietary information of different scanner vendor information.

- Rotated image stack. This should by default be false. If your image stack is rotated, then change this to true. Currently this parameter is not taken from information in the DICOM tags and the user needs to manually change this when loading rotated image stacks.
- Cyclic image. If the image stack is cyclic, i.e covers the whole heart cycle this should be true (default). For prospectively gated image series this should be false. This affects mainly the automated segmentatin algorithm. Currently this information is not read from the DICOM information.

27.3 Volume calculations

The volume calculations are done by a summing the area in each slice. The main reason for not using a more advanced volume integration method is that no one else is using that and therefore it might be difficult to compare the results. Segmentation (i.e. delineation of endocardium and epicardium) is stored on a sub-pixel accuracy and subsequent calculations are on a sub-pixel basis. For viability the classification into viable or scar is done on a pixel-wise basis and there the volume calculations are done by summing the number of pixels.

For the rotated image stacks the volume is given by a integration method. The volume contribution of each outline is given by :

$$\delta V = \frac{\pi}{2 * Z} \int y(s)^2 \text{sign}(y(s)) \frac{dy}{ds} ds \quad (1)$$

where the curve is given on a parametric representation $(x(s), y(s))$, Z is the number of slices in the rotated image stack. No long-axis compensation is performed for the rotated image stacks.

27.4 Mass calculations

When converting volume to mass the density is assumed to be 1.05 g/ml. Note that this number differs in the literature between 1.04 to 1.05. Furthermore, note that these numbers are valid for healthy myocardium ex-vivo, what happens in for instance infarcted regions is not shown in the literature. Therefore usually it is better to report volume instead of mass.

27.5 Calculation of BSA

The formula used is based on Mosteller.

$$BSA = \sqrt{\frac{w * h}{3600}} \quad (2)$$

where w is the body weight in kg, and h is height in cm.

27.6 Peak ejection/filling rate

When calculating peak ejection and peak filling rate the volume curve is differentiated using forward difference approximation. For cyclic datasets cyclic convolution is used for the calculation.

27.7 Wall thickness

Currently wall thickness is defined as the thickness along a radial spike from the endocardial or the epicardial center (depending on setting in the preferences. In the future I plan to also include the modified center line method. Note that the centers are calculated for each timeframe separately.

Wall thickening is defined as the wall thickness in end-systole minus the wall thickness in end-diastole. Note that it is possible to manually or automatically select what timeframes that are diastole or systole respectively.

Fractional wall thickening is defined as:

$$WT_f = \frac{WT - WT_{ED}}{WT_{ED}} \quad (3)$$

Where WT_f is fractional wall thickness and WT is wall thickness and WT_{ED} is wall thickness in end-diastole. In the bulls eye plot then fractional wall thickening is showed in end-systole.

27.8. CALCULATION OF REGURGITANT VOLUMES AND SHUNTS

27.8 Calculation of regurgitant volumes and shunts

The regurgitant fraction for the aortic valve and the pulmonary values are calculated as:

$$r = 100 \frac{v_{back}}{v_{forward}} \quad (4)$$

where r is regurgitant fraction, v_{back} is backward volume, and $v_{forward}$ is forward volumes. Backward volumes is taken as timeframes where the net flow is negative and integrated over the entire cardiac cycle.

The regurgitant fraction for the tricuspid and mitral valve are calculated as:

$$r = 100 \frac{SV - v_{forward}}{SV} \quad (5)$$

where r is regurgitant fraction, and SV is stroke volume for left or right ventricle, respectively. $v_{forward}$ is forward volume.

The Q_p/Q_s ratio is defined as

$$Q_p Q_s = \frac{Q_p}{Q_p} \quad (6)$$

where Q_p is the stroke volume of the pulmonary artery and Q_s is the stroke volume of the aortic artery.

27.9 Infarct size, extent and transmurality

Calculations of infarct sizes etc are based on 'counting' pixels, i.e. each pixel has a binary classification. There are two methods for regional analysis available, one are based where the percentage of the pixels that are inside the sector. The other method is based on radial spikes from the center (endo- or epicardial depending on setting in the preferences). The line between endocardium and epicardium is resampled in 50 steps and the percentage of infarcted pixels are counted.

Infarct extent is defined as the projected infarcted area on the endocardial surface [?].

$$I_{ext} = \sum_i \frac{T_i R_i}{R_i} \quad (7)$$

where I_{ext} is the infarct extent, T_i is the transmurality of sector i and R_i is the mean endocardial radius of sector i .

27.10 Number of SD from remote for Scar

The number of SD from remote for an existing scar segmentation is calculated by the function found in the main menu in Segment under MR menu Viability menu and then the menu option Get SD from Remote. The presented value is calculated by first calculate the mean and sd in the remote area ($Mean_{remote}$ and SD_{remote}). If there exist ROIs named **Remote ROI**, these regions define the remote area. Otherwise the whole myocardium except for the scar region defines the remote area. The presented SD from remote value is then calculated by

$$SDfromRemote = \frac{T_{optim} - Mean_{remote}}{SD_{remote}} \quad (8)$$

The optimal threshold value (T_{optim}) represent the optimal threshold for separating the remote and the scar regions based on the existing scar segmentation. This value is defined by an exhaustive search where the threshold is set to all intensities represented in the image stack. For each threshold, the number of missclassified pixels are counted (total of both missclassified remote pixels and missclassified scar pixels). The optimal threshold value is then defined as the threshold corresponding to the minimal number of missclassified pixels.

27.11 MR relaxometry calculations

The MR relaxometry calculation for T1/T2 mapping is given in the paper [?]. Implementation of the ADAPTS T2* mapping is given in the paper [?].

27.12 Pulse wave velocity

The implementation of the pulse wave velocity unit is described in the paper [?].

27.13 Torsion

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.

27.13.1 Least squares circle fit

The circle is fitted by minimizing the global squared radial difference between all tracking points for all timeframes, (x_i, y_i) , $i = 1, \dots, N$ and a circle with radius $r = \sqrt{a}$ for each slice. For nicer calculations we make the tracking point cloud zero mean and define a new coordinate system

$$u = x - \frac{1}{N} \sum_i^N x_i, \quad v = y - \frac{1}{N} \sum_i^N y_i \quad (9)$$

The properties of the circle determining the fit is the radius r and center (u_c, v_c) . The circle equation we are going to work with is

$$f(u, v) = (u - u_c)^2 + (v - v_c)^2 - a = 0 \quad (10)$$

which yields the least squares expression we want to minimize.

$$M(a, u_c, v_c) = \sum_i^N f^2(u_i, v_i) = \sum_i^N ((u_i - u_c)^2 + (v_i - v_c)^2 - a)^2 = 0 \quad (11)$$

The minima is found by solving,

$$\frac{dM}{da} = 0 \quad (12)$$

$$\frac{dM}{du_c} = 0 \quad (13)$$

$$\frac{dM}{dv_c} = 0 \quad (14)$$

for all parameters of M . From (12) we get that

$$\frac{dM}{da} = 2 \sum_i^N f(u_i, v_i) \frac{df(u_i, v_i)}{da} = -2 \sum_i^N f(u_i, v_i) = 0. \quad (15)$$

Resulting in

$$\frac{dM}{da} = 0 \iff \sum_i^N f(u_i, v_i) = 0. \quad (16)$$

Then consider (13). As (13) (14) only differ in notation, any result for (13) is applicable to 14.

$$\frac{dM}{du_c} = 2 \sum_i^N f(u_i, v_i) \frac{df(u_i, v_i)}{du_c} = 4 \sum_i^N (u_i - u_c) f(u_i, v_i) \quad (17)$$

Since 16,

$$\frac{dM}{du_c} = 0 \iff \sum_i^N u_i f(u_i, v_i) = 0. \quad (18)$$

and the same goes for 14.

$$\frac{dM}{dv_c} = 0 \iff \sum_i^N v_i f(u_i, v_i) = 0. \quad (19)$$

expanding equation (18) yields

$$\frac{dM}{du_c} = \sum_i^N u_i (u_i^2 - 2u_i u_c + u_c^2 + v_i^2 - 2v_i v_c + v_c^2 a) = 0 \quad (20)$$

Define $S_u = \sum_i^N u_i$ and $S_v = \sum_i^N v_i$ then

$$\frac{dM}{du_c} = S_{u^3} - 2u_c S_{u^2} + u_c^2 S_u + S_{uv^2} - 2v_c S_{uv} + v_c^2 S_u - a S_u = 0 \quad (21)$$

In making the coordinates zero mean $S_u = 0$ we get the equation

$$u_c S_{u^2} + v_c S_{uv} = \frac{1}{2} (S_{u^3} + S_{uv^2}) \quad (22)$$

After doing the same for (19) we obtain the system

$$\begin{cases} u_c S_{u^2} + v_c S_{uv} = \frac{1}{2}(S_{u^3} + S_{uv^2}) \\ u_c S_{uv} + v_c S_{v^2} = \frac{1}{2}(S_{v^3} + S_{vu^2}) \end{cases} \quad (23)$$

which can be converted into a matrix equation

$$\begin{bmatrix} S_{u^2} & S_{uv} \\ S_{uv} & S_{v^2} \end{bmatrix} \begin{bmatrix} u_c \\ v_c \end{bmatrix} = \begin{bmatrix} \frac{1}{2}(S_{u^3} + S_{uv^2}) \\ \frac{1}{2}(S_{v^3} + S_{vu^2}) \end{bmatrix} \quad (24)$$

This gives us an easy way to get the least squares fitted circle center. For the center in the original (x, y) domain translate with the previously subtracted mean. Finally for the radius, expanding equation (16) and simplifying yields

$$a = u_c^2 + v_c^2 + \frac{S_{u^2} + S_{v^2}}{N}, \quad (25)$$

where

$$r = \sqrt{a}. \quad (26)$$

27.13.2 Angular discontinuity detection

After fitting a circle to each time frame with tracking points we can translate the points in each time frame so that the fitted circle center i.e the AoR is in origo. With this in place a polar coordinate change results in an approximate line like formation of the points, lets call it a worm. Who's movement along the θ axis is the rotation of the heart muscle. Here a problem arises. Since $\theta \in [-\pi, \pi]$, $\theta_t + \Delta\theta > |\pi|$ results in a sign change and the point appears at the lower limit if it passed the upper and vice versa. This needs to be mended if we are to measure angular distance from a starting point. This is done by examining

$$\Delta\theta_t = \theta_t - \theta_{t+1} \quad (27)$$

for each tracking point, adjusting the point with $\pm\pi$ (sign depends on border transition) if $|\Delta\theta_t| > 5$.

Torsion is then found as the difference between the rotation in a apical and a basal slice normalized with the distance along the long axis of the heart between the slices and the mean radius.

27.14 Longaxis volumes

Volumes can be calculated using segmentation from longaxis images. The algorithm begins with automatically locating images labeled 2CH, 3CH and 4CH that contain segmentation. If the same kind of segmentation is found in two such images, the volume is calculated by rotating each segmentation area one full revolution around the axis of intersection and taking the mean of these volumes. If there are three images that contain the same segmentation, the volumes are calculated as described above for each pair of images, and the mean of these three values is used.