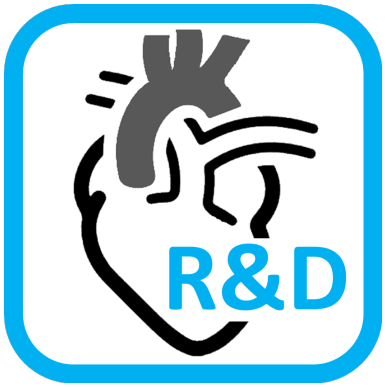
Segment - User Manual



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Contents

1 Terms and conditions

1.1 Conditions for use

- The software should be used to read images from MRI Scanners from Philips, Siemens, and General Electric. Images can be supplied either by CD's or by using DICOM standard to transfer files directly from the scanner or PACS systems.
- Users are required to investigate the regulatory requirements pertinent to their country or location prior to using Segment. The user is responsible for obeying these statues, rules, and regulations.
- The user is responsible for installing Segment. Medviso provides online assistance in the installation process if needed. To install Segment you need to be Administrator on the computer to install on.
- Users should participate in an online training session held by Medviso prior to use of Segment. This is provided by Medviso as a part of the software trial process.
- The device is for multiple patient, multiple use.

1.2 Intended users

Caution: Federal law restricts this device to sale by or on the order of medically trained professionals.

1.3 Intended purpose

Segment is a software to be used for human beings for the medical purpose of investigating a physiological state.

1.4 Indications for use

Segment is a software that analyzes DICOM-compliant cardiovascular images acquired from magnetic resonance (MR) scanners. Segment specifically analyzes the function of the heart and its major vessels using multi-slice, multi-frame and velocity encoded MR images. It provides clinically relevant and reproducible data for supporting the evaluation of the function of the chambers of the heart such as left and right ventricular volumes, ejection fractions, stroke volumes, peak ejection and filling rates, myocardial mass, regional wall thickness, fractional thickening and wall motion. It also provides quantitative data on blood flow and velocity in the arterial vessels and at the heart valves. Segment is tested on MR images acquired from both 1.5 T and 3.0 T MR scanners. The data produced by Segment 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.**

1.5 Regulatory status

Segment may be used for either investigational off label use or commercial purposes. Please see license terms which license form that applies to you. Users are also required to investigate the regulatory requirements pertinent to their country or location prior to using Segment. It is the users' responsibility to obey these statues, rules and regulations.

There are commercial, FDA approved versions of Segment with FDA 510(k) number K090833. Please contact Medviso Sales team (sales@medviso.com) to receive such a license. Please note that there are features that are not included in the FDA approval. These functions are marked in this User Manual as only for investigational use.

2 License Terms

The software can be used under three different license forms. More detailed information and pricing of the different license forms is given on Medviso AB homepage `http://www.medviso.com`.

2.1 Free or charge for non-commercial research

The software is free to use for non-commercial research or educational purposes if and only if you reference it properly and send full bibliographic information (such as Pubmed link) of your final work when published or accepted for publication. Details on how to reference the software are given in Chapter 40.

You may not use the software for clinical routine or commercial applications such as company paid pharmaceutical trials without contacting the author. Details about commercial/clinical use is given below. Note that the software is copyright and may not be redistributed/resold without permission of the author.

2.2 Clinical use

For clinical purposes medviso provides clinical software versions; Segment CMR for image analysis of Cardiac MR, and Segment CT for image analysis fo Cardiac CT. In the clinical software packages you get additional features for clincal reporting, patient database and PACS connection. Please contact `sales@medviso.com` if your are interested in a clinical version of the software.

2.3 Commercial research (non-human images)

There is a license type for Segment that is intended for commercial R & D companies, or industry sponsored trials where the majority (more than 50%) of the funding comes from a commercial sponsor. Please contact `sales@medviso.com` if you are interested in a commercial version of Segment.

3 Acknowledgements

Even if this project started as a one man project, it has grown and it would never been possible without the help of many many people.

Financial support has been received from the Swedish Heart-Lung foundation, Swedish Research Council, local founds from Östergötland County, and Region of Scania.

I would like to acknowledge all the people that have put in feed back on usability and desired functionality, algorithm etc. Among others: Andreas Otto, Andreas Sigfridsson, Erik Bergvall, Erik Hedström, Henrik Haraldsson, Henrik Engblom, Håkan Arheden, Jan Engvall, Lars Wigström, Lisa Hård af Segerstad, Karin Markenroth Bloch, Marcus Carlsson, Martin Ugander, Mikael Kanski. Finally thank to you all Segment users in the research community that has inspired and contributed to the development.

Special thanks to code providers Erik Bergvall (core routines of strain analysis), Helen Soneson (strain analysis module, SPECT module, Image fusion module), Shruti Agarwal (refactory of strain analysis module), Jonatan Wulcan (Sectra Plugin module and general improvements), Johannes Töger (3D flow and volume tracking), Måten Larsson (3D flow and kinetic energy).

Commercial development has been done by Jane Sjögren (improvements to general object segmentation, implementation of prototype based segmentation, CT functionality, and graphical seriesselector). General debugging and implementation of the new interpolated contours has been done by Johan Ugander and Erik Södervall. Report Module and general debugging have been performed by Nils Lundahl.

4 Rationale for the Software

Developing this software have required a lot of work. So what has the rationale been for producing new software where there are commercially available software packages that at least partially could do the same thing?

- At the time of writing the core of the program other existing software were simply not good enough.
- Existing software packages did not allow to store the segmentation and regions of interest in a flexible way.
- Existing software packages had no flexible exporting capabilities to allow full usage of automated delineation algorithms.
- A freely available software greatly facilitates and improves possibilities to do multi-center studies.
- There will be no company secrets we will always know, and be open and tell you exactly how things are implemented. This is crucial for doing good research.
- It can serve as a platform for experimenting and testing of various image processing ideas.
- It has been given very valuable experience of how to handle and develop a large scientific software package.

As the software grew in capabilities, there also started to be a commercial interest in the software. However, Segment will always be tightly coupled to cardiovascular research and continue to be freely available for research purposes. We hope that you will find the software useful in your research, and please do not hesitate to tell us what you think about it, and come with suggestions for improvements.

The software has been developed at:

- Home during late evenings and weekends.
- Linköping University, Sweden, Centre of Medical Image Science and Visualization & Department of Medicine and Care, Clinical Physiology (2002-2004).
- Cardiac MR Group, Lund University, Department of Clinical Physiology (2005-present).
- The company Medviso AB (2007-present).

5 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 9. 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.

6 Conventions and Abbreviations

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

6.1 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.
Close	Push/Toggle button in the graphical user interface.
◎ Endocardium	Radiobutton in the graphical user interface.
☒ Single frame	Checkbox in the graphical user interface.

6.2 Abbreviations

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

7 Getting started

7.1 System requirements

- Operating System: 64-bit Windows 10
- Computer with 8 GB of memory or preferably 16 GB
- Harddisk with at least 5 GB of available space
- Graphics card supporting both DirectX and OpenGL

To access full version of machine learning algorithms in Segment:

- CUDA enabled NVIDIA graphics card with 4 GB memory or more
  - GPU architecture: Ampere, Turing, Volta, Pascal

For users with additional modules not included in the free research version:

- Internet connection for software license management and software download. We recommend a speed of at least 24 Mbit/s.

Recommendations

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

7.2 Installation and upgrading

To install or upgrade Segment, log in on our website (https://medviso.com/download2/) and download the installation file. Run the installation file under administrator privileges on the machine and follow the instructions in the figures below. For assistance, please contact `support@medviso.com`.

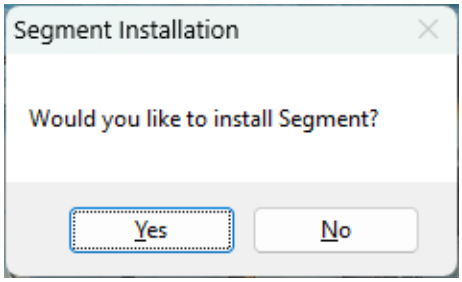


Figure 1: Click on `Yes`.

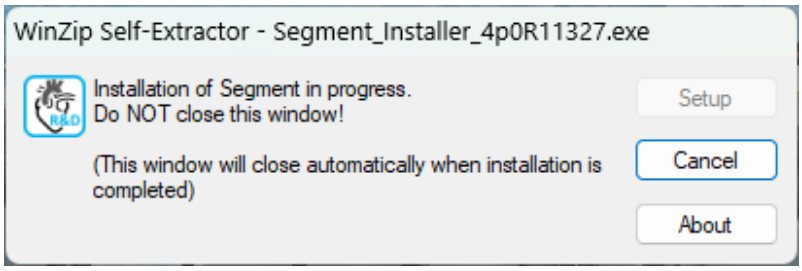


Figure 2: The installation starts automatically. Do not close this window, it will close automatically when the installation is completed.

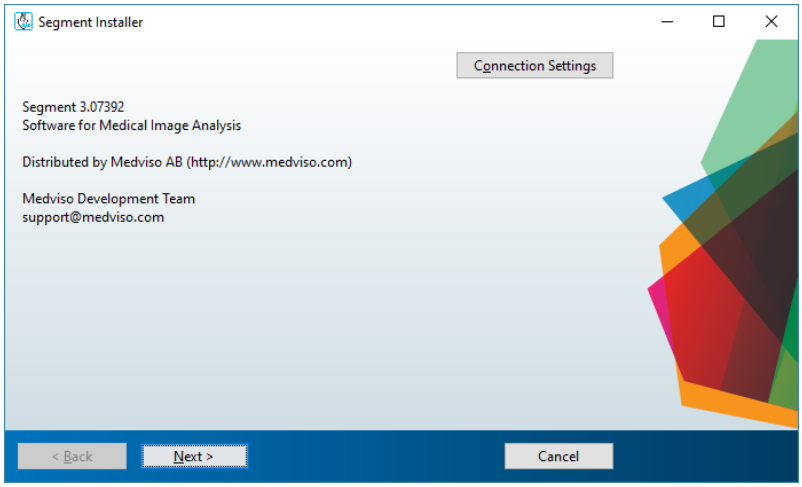


Figure 3: Click on `Next`.

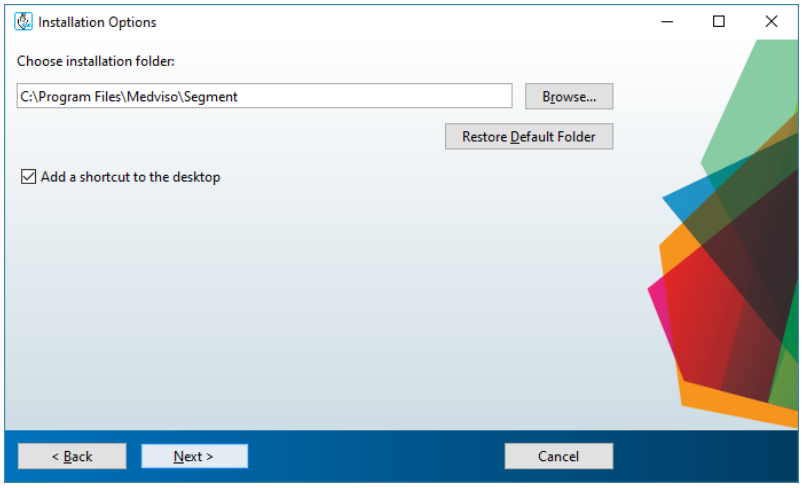


Figure 4: Select `Add a shortcut to the desktop`. Click on `Next`.

For first time installation, `Matlab Compiler Runtime (MCR)` needs to be installed according to Figure 5 - 8. For upgrading, continue according to Figure 9.

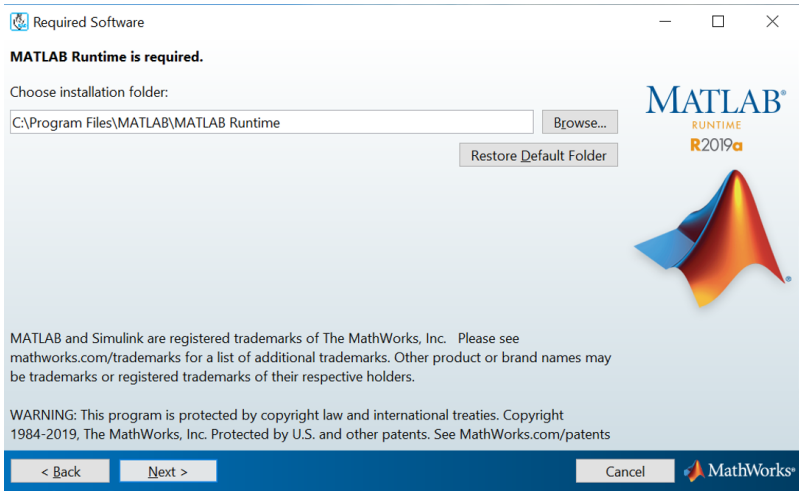


Figure 5: Click on `Next`.

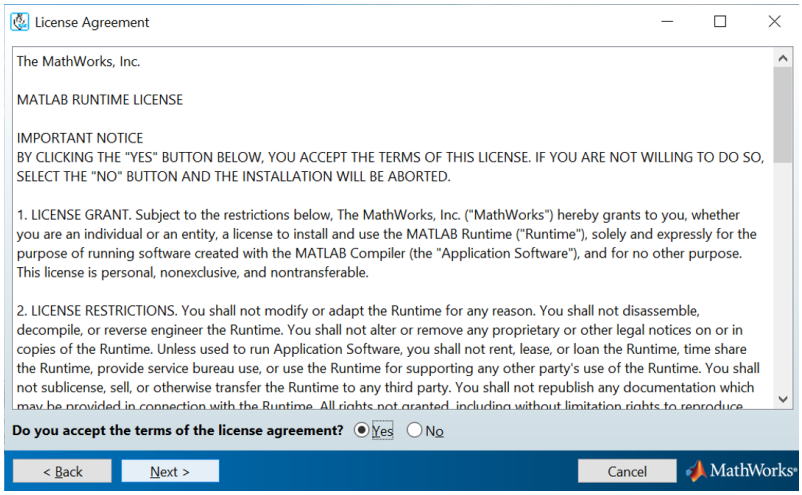


Figure 6: Select `Yes`. Click on `Next`.

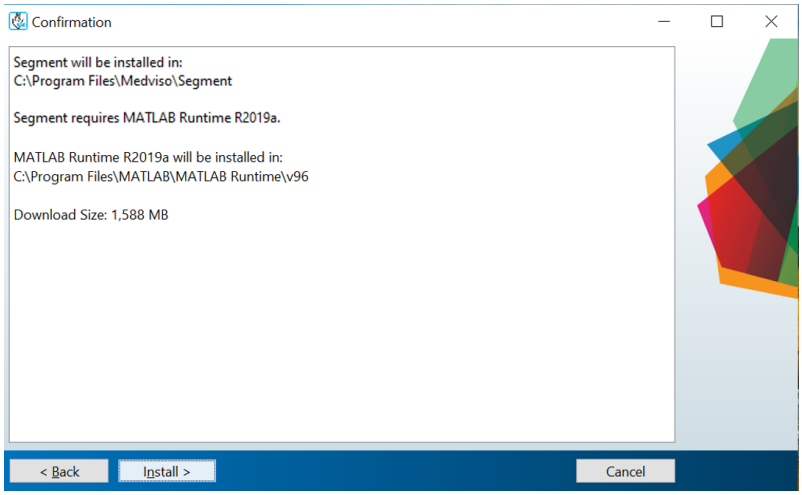


Figure 7: Click on `Install`.

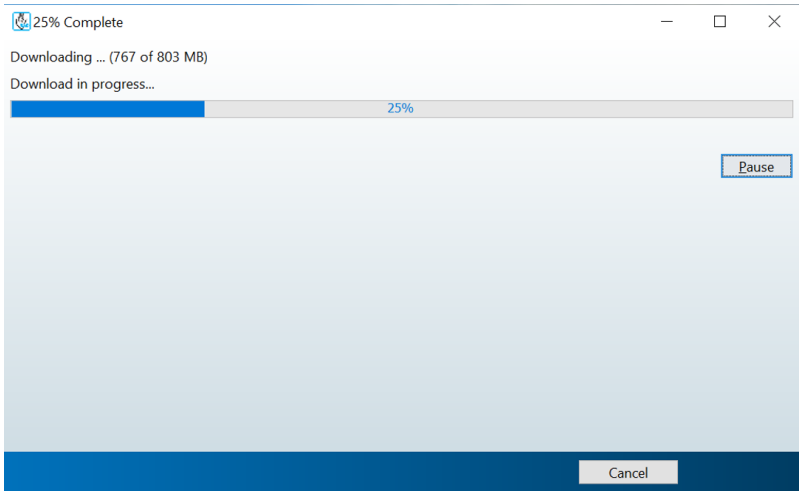


Figure 8: Wait for completed process.

For upgrading, only install Segment according to Figure 9 - 10.

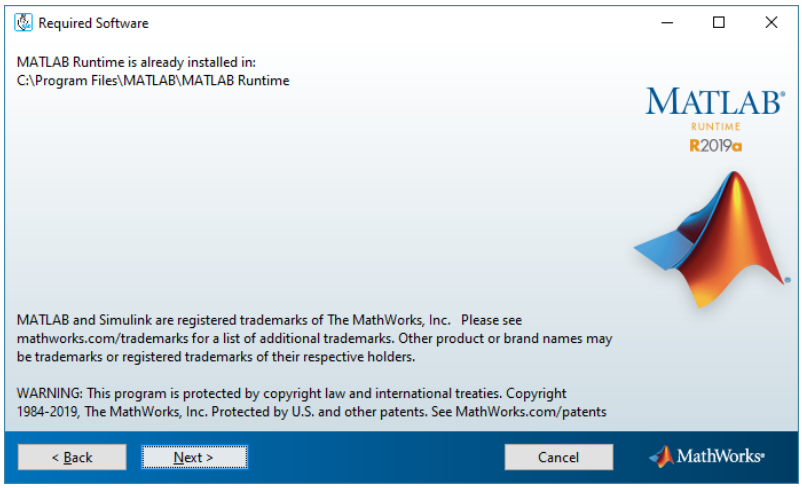


Figure 9: Click on `Next`.

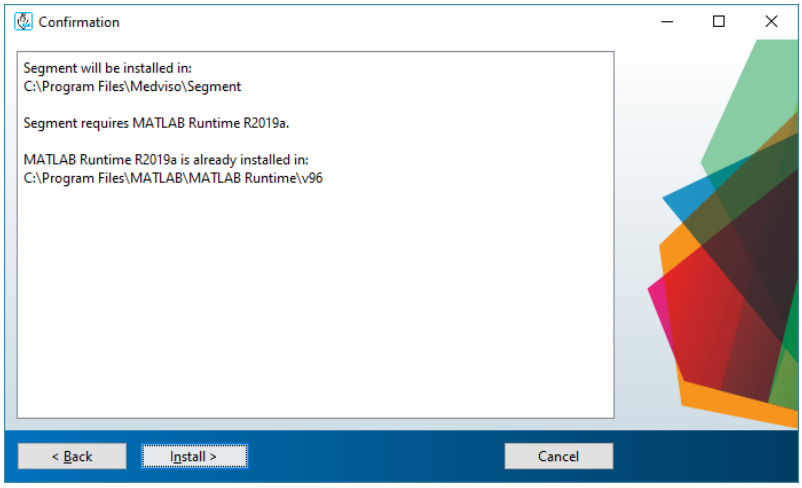


Figure 10: Click on `Install`.

For first time installation or upgrading, continue according to Figures 11 - 12.

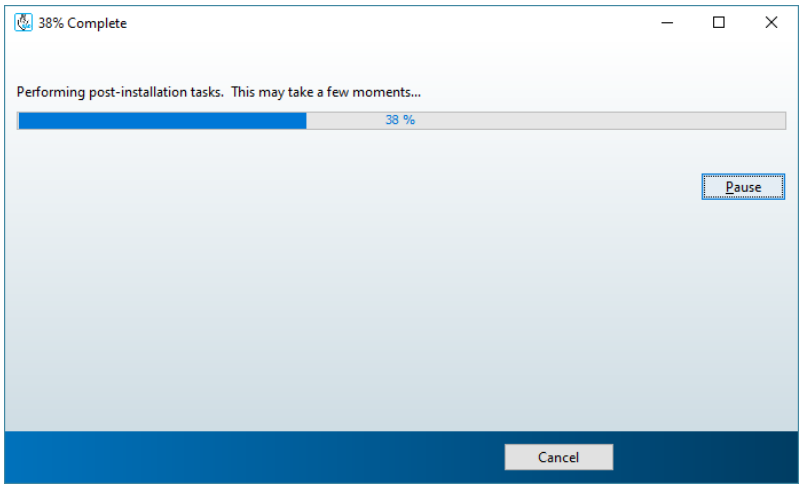


Figure 11: Wait for completed process.

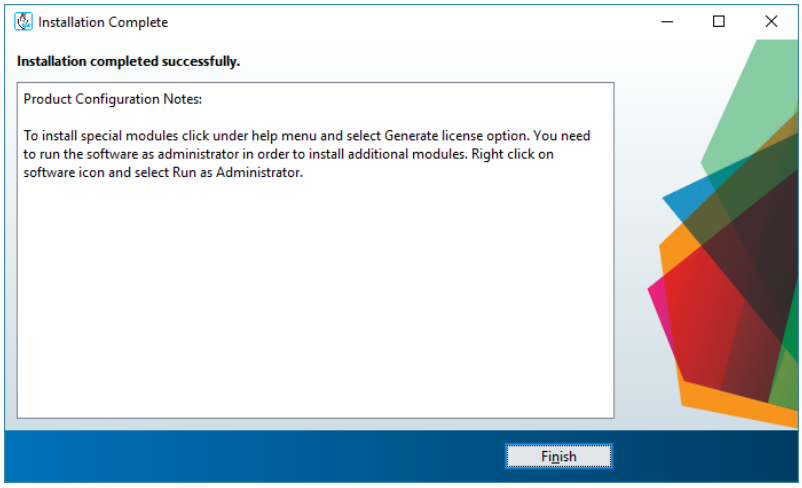


Figure 12: Click on `Finish`.

7.3 First time running Segment

The first time you run the software to configure it you need to run the software as Administrator. Right click on the shortcut to the software and select Run as administrator. Note that it is not sufficient to be logged in as administrator on the computer.

The first time Segment is started, it runs a setup process which can take a while, so be patient. When starting the software, the image in Figure 13 should be displayed. If it is not displayed, then the software is not correctly installed.

To complete the setup, set preferences and window positions as described in Sections 7.3.1 and 7.3.2.

7.3.1 Setting preferences

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

7.3.2 Setting window positions

The position of the main window for Segment can be set by dragging the window to an optional position and size. The size and position will be saved so that next time Segment is launched the same position will be used. In case where one have switched to another monitor, Segment may move outside the screen. In this case you could press `Ctrl-0` to reset GUI positions. This is also available under the File menu (a).

7.3.3 PACS connection

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

7.4 Add software license code

For new installations you need to add your license code for Segment. Add your license code after installation by starting Segment and select `Generate License` under the Help menu in Segment. Note that you have to run the software as Administrator to be able to add the license code in Segment. If you have lost the license code, please contact `sales@medviso.com`.

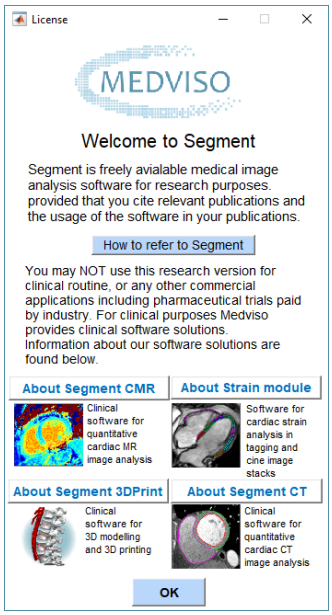


Figure 13: Startup window for Segment.

7.5 Uninstallation

To uninstall Segment, go to Control Panel and select Uninstall a program (Figure 14). Search for Segment in the programs list, right-click on it and select Uninstall/Change. Do the same steps for uninstalling MATLAB Runtime, but select MATLAB Runtime in the programs list.
User preferences are stored in `AppData`, in the subfolder `Segment` under each user account.

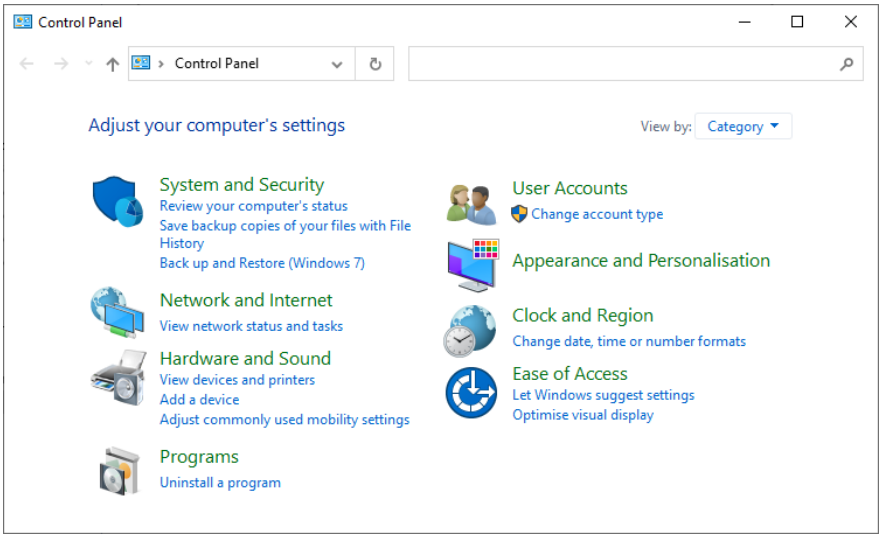


Figure 14: Control Panel

7.6 Software overview

An overview of Segment is given in Figure 19.

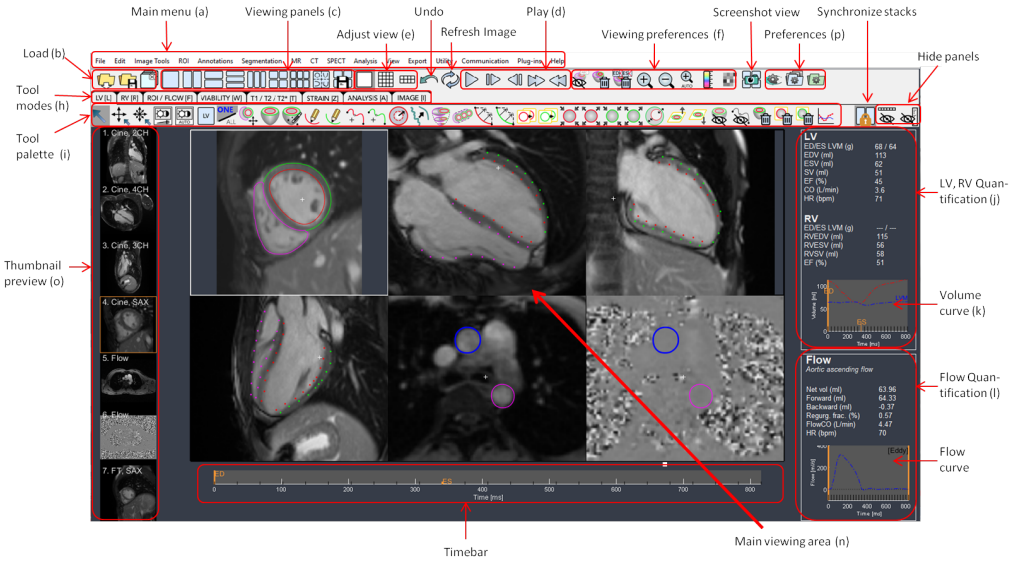


Figure 15: Main graphical user interface.

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

8 Loading Image Stacks

The best method to load and manage studies is by using the Patient Database Module, described in Segment Database Manual. For clinical use, we discurage the direct use of the DICOM loader since this is a sub optimal workflow in the clinical situation, instead please look at the Segment Database and PACS connection 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 that 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 8.1.6.

The File Loader is started from the main menu, under File, or by clicking on the icon  , or by pressing `Ctrl-O`. This brings up the File Loader GUI shown in Figure 16.

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 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 Section 18.4.

8.1 Loading DICOM files

8.1.1 Loading DICOM files

When loading MR DICOM files Segment 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 17.
If the files are not stored in this fashion then there is a sorting utility available described in Chapter 18. 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).

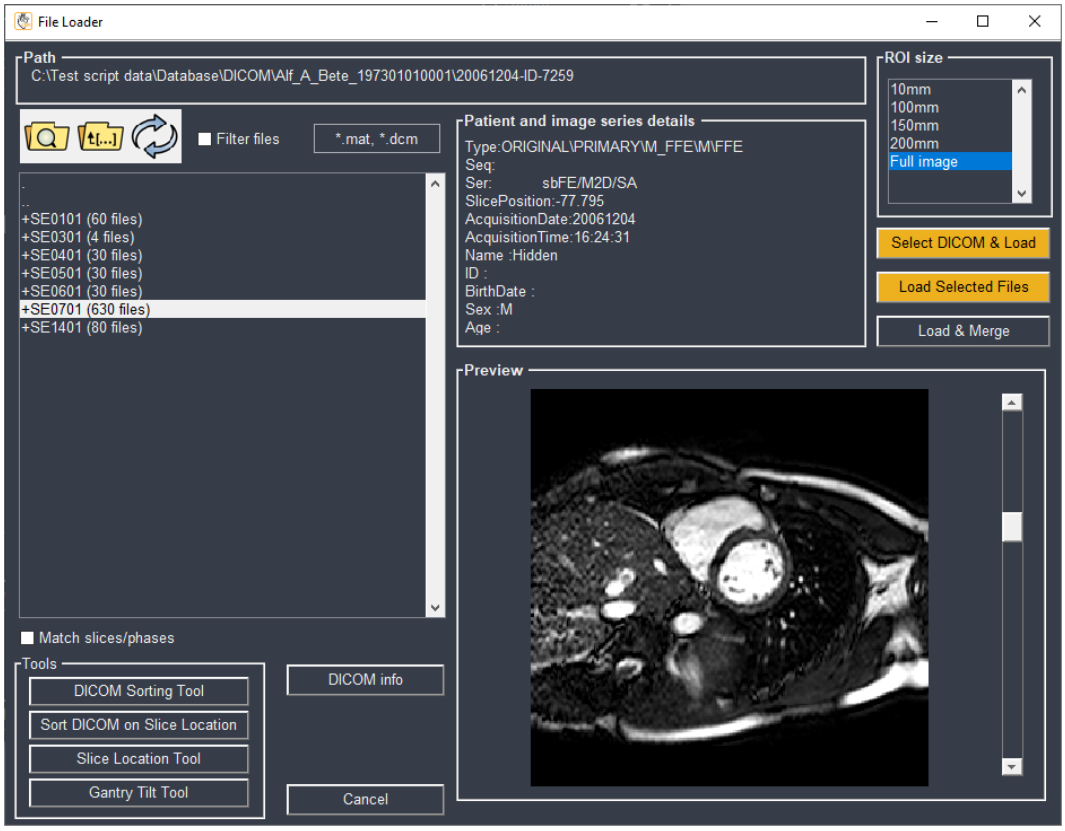


Figure 16: File Loader GUI.

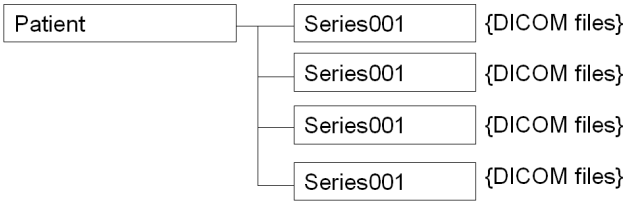


Figure 17: Files needs to be sorted so that each image series are stored into a separate folder.

8.1.2 Loading SPECT DICOM files

When loading SPECT DICOM files Segment assumes that the files are reconstructed into a short axis stack.

8.1.3 General loading DICOM files

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 8.1.6. 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 image stack, use the Graphical DICOM Selection tool as described in Section 8.1.6.
Further technical details about how Segment interprets the DICOM files are given in the Segment Technical Manual.

If heart rate is not present in the DICOM file Segment 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.

8.1.4 Tips and tricks

Often the files are not stored exactly as prerequisited 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. It is possible to compare DICOM tags between two DICOM files by pressing Compare.

8.1.5 Loading images from CD

When loading images from a CD it is highly recommended to import the files from the CD to your image data directory. This is done by using the utility described in Section 18.4.

8.1.6 Graphical image series selection

The graphical series selector tool is shown in Figure 18. 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 pushbutton 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 selected.

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.

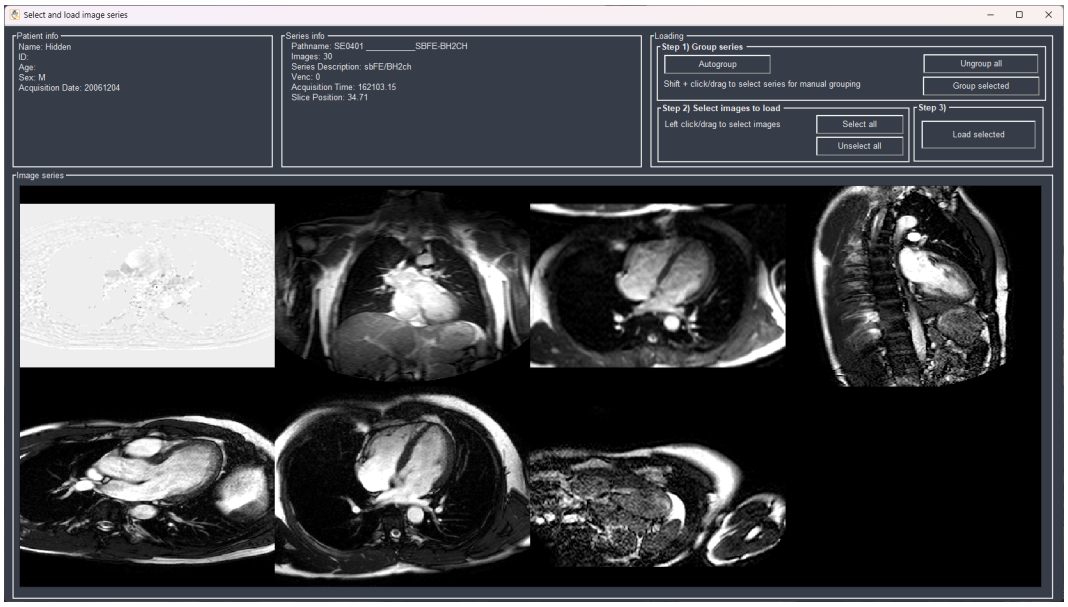


Figure 18: Graphical image series selector.

8.1.7 DICOM - details

First of all remember that DICOM is not a well defined standard. I have tried hard to make Segment to work with DICOM files from different imaging device manufacturers. It is currently tried on General Electric MR-scanners, Siemens CT/MR/PET, and Philips MR scanners, Bruker MR, Suinsa PET. Furthermore various PACS manufacturer might 'corrupt' the files in different ways.

The DICOM reader does not support JPEG encoded images, or big endian DICOM files. However, when images are imported into the patient database or sorted by the DICOM sorter they are converted on the fly and can be read by Segment DICOM reader.

There are some short cuts taken in the fast loader:

- The spacing in time is assumed to be equal between all frames when loading time resolved images. This may be violated if the scanner rejects some beats in a perfusion image serie for instance.
- The spacing in slice is assumed to be equal between all slices when loading image stacks with multiple slices.
- When you have loaded a rotated image stack you need to tell Segmentabout it. It is done under Image Tools and View Adjust and Image Details. A rotated image stack is a set of slices that are rotated around a central axis. Then subsequent analysis will assume that the data is a rotated image stack. When you view the data in single slice view  a cyan line are drawn with the rotational axis indicated. To get correct volume estimates it is crucial that this line co-incides with the true axis of rotation. To achieve this you may have to flip the image stack, see details in Section 15.7.

8.1.8 Unstructured files

Some systems (Siemens depending on platform version, or how you do it or what PACS you are using) outputs files in a completely unstructured way (all patients and all time frames, and all slices) are mixed into the same folder. In Segment there is a sorting utility that can be accessed on the main menu that can sort the files. This is described in Chapter 18.

8.2 Matlab format - details

Internal format used by the program. The image needs the be stored in the variable `im` or `setstruct`, and must be in single precision format. The dimensions must be x, y, t, z. If you do not have time resolved data make sure to make the temporal dimension singleton, i.e. always put in a 4D-array. It is possible to also give dimensions, and patient specific information as well as a preview image. To learn about this, load an image stack from DICOM images, and select Save Both Image Stacks and Segmentation As under the File menu. Then load the file in Matlab, and study the variables in the file. Details about the file format is given in the Segment Technical Manual.

9 Program Overview

This chapter provides an overview of the program. Yet a good method is to view the on-line video tutorials. The tutorials are available on our website http://medviso.com/tutorial-videos/.

An example of the main graphical user interface is shown in Figure 19. 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.

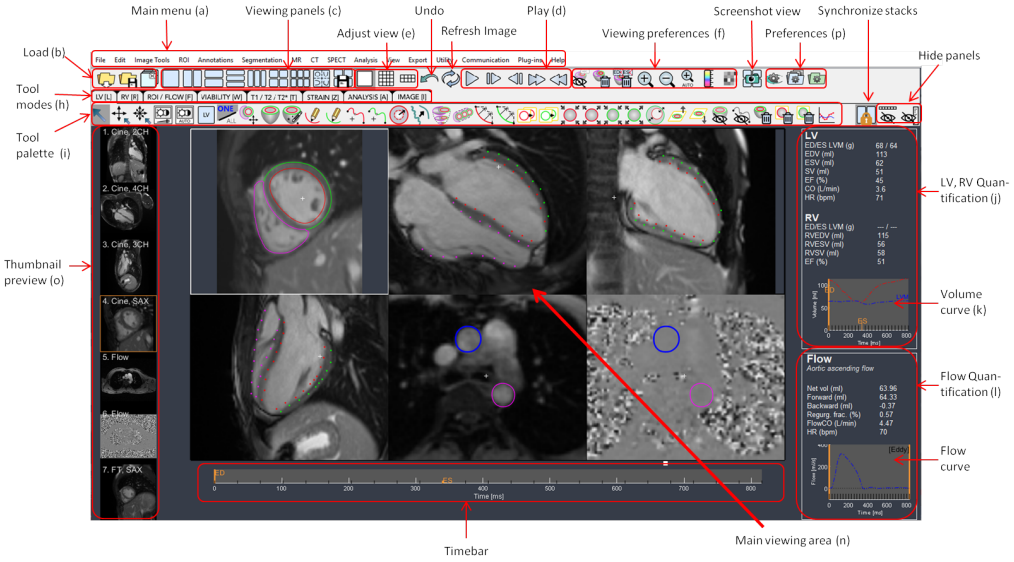


Figure 19: Main graphical user interface.

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. For further details, see Section 11.1.2.

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

9.1 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, and m-mode view. 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 simultaneously. 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 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 automatically looks for the best matches among the current image stacks, taking into account such properties as image type, view plane, time resolution, etc. This interface also enables the user to save and load specific contrast/brightness settings, in absolute values, which can also be assigned a hotkey.

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 irresponsive 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.

9.2 Montage view

Figure 20 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.

9.3 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.

9.4 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 21. 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.

9.5 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 21, Flow Analysis.

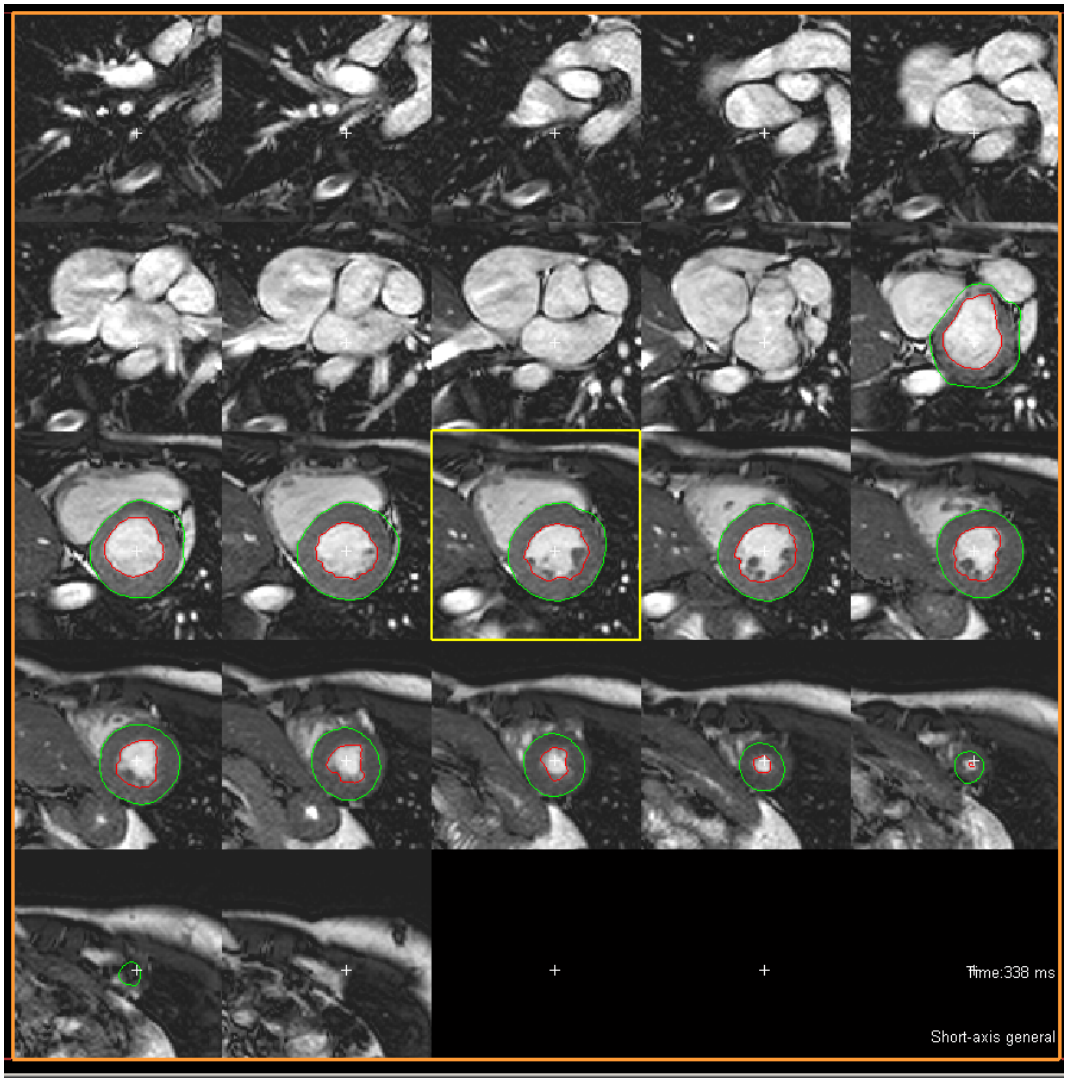


Figure 20: Screen-shot of the program showing an image stack in montage view.

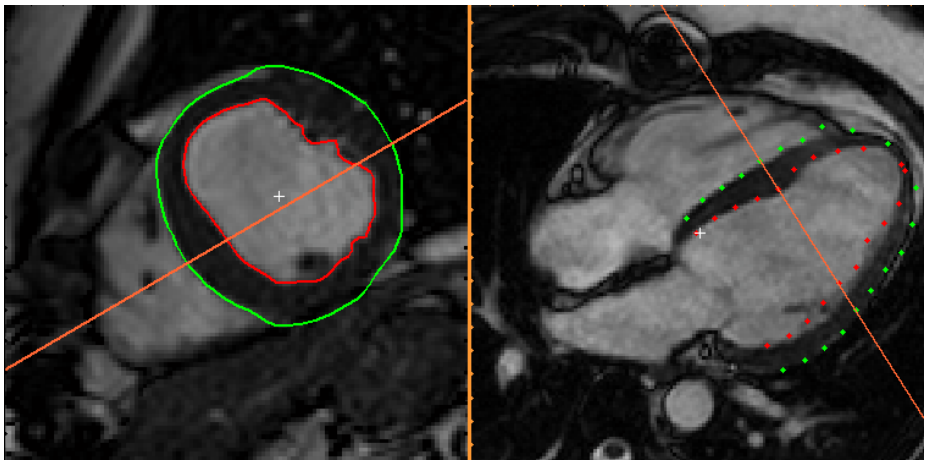


Figure 21: Contours are visible in other image stacks as dots. This is very useful to delineate structures that might be difficult to see in only one image plane.

9.6 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`) shows previous frame but 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. They `left` key displays the previous time frame for the active image stack. You can also use left arrow button. The icon  plays the active image stack sequence as a cine loop. The key `right` shows the next frame for the active image stack. You can also use right arrow button to show the next frame. 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.

9.7 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.

9.8 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 8. The second icon  opens the patient database described Segment Database User 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 User Manual.

9.9 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 are present in all tool modes, and these are:

Select slices or image stacks. This is the default tool.

Translate ROI's and contours or the whole image if no ROI or contour was clicked.

Change the size of ROI's and contours.

Undo last contour edit command.

Adjust brightness and contrast. Hold down the mouse button and move left/right to adjust contrast and up/down to adjust brightness of the current image stack. By holding down the `Shift` key while pressing the mouse button, the adjustments also affect every other image stacks in the current view, and sets the absolute values of their contrast and brightness to be equal to those of the active image stack. Contrast and brightness of the current image stack can also be adjusted without first clicking the icon, by instead using the middle mouse button.

9.9.1 Left ventricle tools

The left ventricle tools are shown in Figure 22. Colors are used to indicate endocardium (red) or epicardium (green).

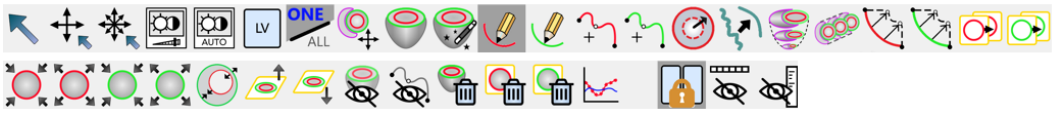


Figure 22: Left ventricular toolpalette.

On the first row (from left to right): Automatic LV- segmentation tools:
The icon  automatically segments both endocardium and epicardium of the left ventricle in the selected slices.The algorithm is AI-based and it is available for computers with and without a NVIDIA GPU card, see Section11.2.2 in Chapter11. The second icon  automatically segments the endocardium and epicardium. The algorithm is AI-based and automatically selects slices for segmantation. For computers equiped with a NVDIA GPU card the alorithm perfroms segmentation of left ventricle for all time frames. For computers

without a NVIDA GPU card segmentation of left ventricle is performed for endo-diastole and endo-systole time frames, and the icon changes to . Please refer to Section11.2.1 in Chapter11 for details.

On the first row (from left to right): Manual drawing tools: The tool under this icon is used to manually draw the endocardium. The 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, click on the right-mouse button. The points can interactively be dragged by using left-mouse button. The icon is to semi-automatically draw endocardium with a left-mouse button. Press the left-mouse button in the middle of the blood pool and drag outwards the endocardium contour that matches best the border between blood and LV-wall. The icon is to automatically refine the endocardium.

The icons , , applies to the epicardial contour instead of the endocardial contour. Generally, the space key can be used to toggle between the endo and epicardial tool counterparts.
The icon is used to smooth the ednocardial or epicardial contour depending on which colour of the manual drawing tool is selected.

9.9.2 Right ventricle tools

The right ventricle tool palette is shown in Figure 23. Colors are used to indicate endocardium (magenta) or epicardium (cyan).

Figure 23: Right ventricular toolpalette.

The icon automatically segments endocardium of the right ventricle and its availabale for computers with a NVIDA GPU card. Refer to Section 12.1 for details. For computers without a NVIDIA GPU card, the icon is used to automatically delineate the RVendocardium. Refer to Section 12.2 for details.

The icon is used to manually draw the right ventricle (RV) endocardium. The 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, click on the right-mouse button. The points can interactively be dragged by using left-mouse button. Generally, the space key can be used to toggle between the endo and epicardial tool counterparts. The icon is to semi-automatically draw the RV endocardium with a left-mouse button. Press the left-mouse button in the middle of the blood pool and drag outwards the endocardium contour that matches best the border between blood and RV wall. Note: To use this tool, LV epicardial contour is needed to be drawn first. The icon is used to refine the RV

endocardium.

The icons , applies to the epicardial contour instead of the endocardial contour. The icon is used to smooth the endocardial or epicardial contour depending on which colour of the manual drawing tool is selected.

9.9.3 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 24.

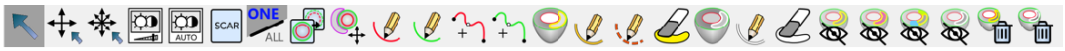


Figure 24: Viability toolpalette.

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 show the manual interactions and regions of microvascular obstruction you need to press the key `o` to toggle the display.

9.9.4 Image tool mode

The miscellaneous tool mode is shown in Figure 25.

Figure 25: Image 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 to find positions in 3D space for all visible image stacks.

9.9.5 ROI tool mode

The toolpalette for region of interest analysis (ROI) is shown in Figure 26.

The first tool is used to automatically outline a vessel from scratch. The icon is used to manually delineate region of interests. The icon is to semi-automatically outline a left-mouse button. Press the left-mouse button in the middle of the blood pool and drag

Figure 26: Region of interest mode toolpalette.

outwards the vessel edges. The icon refines a vessel. This is done in all time frames if is set to All mode. 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.

9.10 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, described in Chapter 28. The icon starts a three dimensional visualization tool, and an example of a such visualization is shown in Figure 27. The icon starts a tool to do regional wall motion per slice analysis described in Section 24.2. 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 21.

10 Image settings

10.1 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.

10.2 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 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.

11 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.

11.1 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.

11.1.1 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 11.3.

11.1.2 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 27. In the most basal LV slices the algorithm defines the LV segmentation with the long-axis motion in mind.

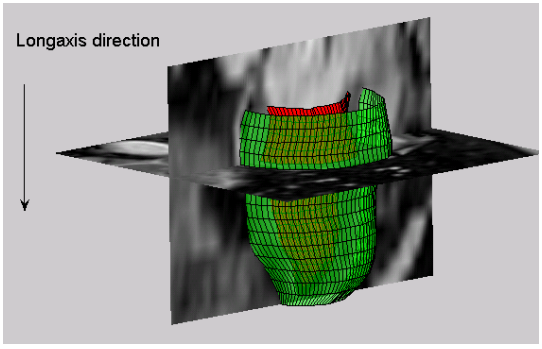


Figure 27: Three dimensional view of the left ventricle showing the long-axis direction.

11.2 LV analysis

11.2.1 Fully automatic LV segmentation [1]

Segmentation in all time frames

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

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

c. The segmentation result is presented in the main window where volumes curve can be reviewed (k) and the measured LV volumes are presented, according to Figure 28 (j).

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

Segmentation in ED and ES time frames

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

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

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

d. The segmentation result is presented in the main window where volumes curve can be reviewed (k) and the measured LV volumes are presented, according to Figure 28 (j).

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

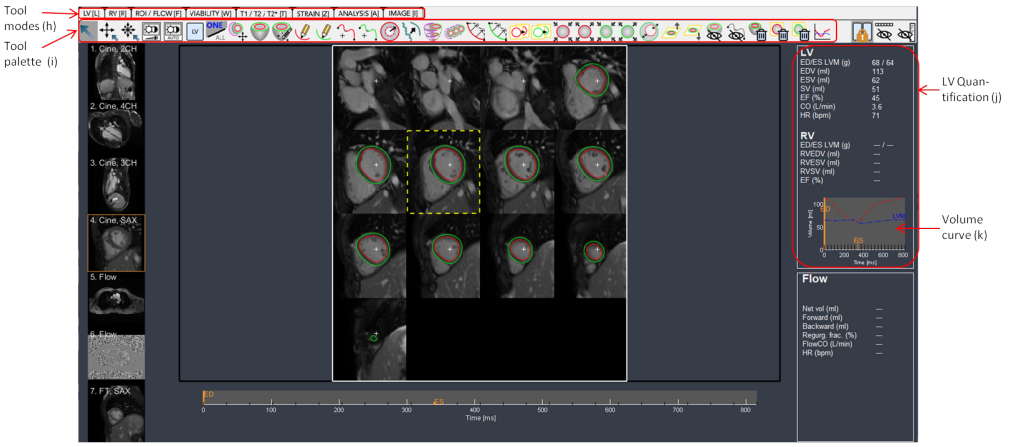


Figure 28: LV analysis result.

11.2.2 Semi-automatic LV segmentation [1]

1. Start the LV analysis by select LV [L] (h) and select (i). A new interface is open, as shown in Figure 29.

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

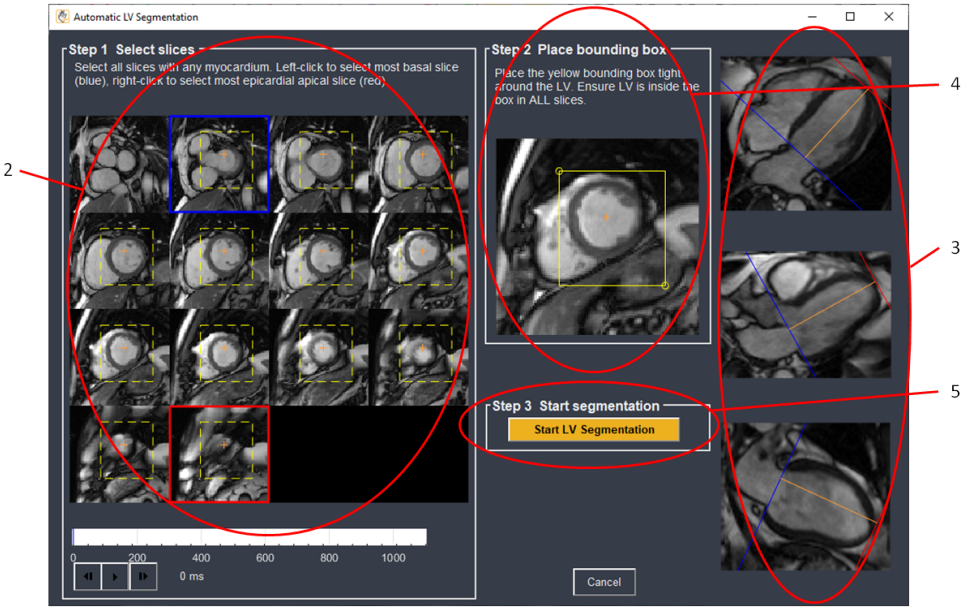


Figure 29: LV analysis GUI.

3. Review the slice selection in the long-axis views.
4. Ensure that the bounding box comprises the LV in ALL slices, otherwise drag in the corners of the bounding box.
5. Start the automatic LV segmentation.
6. The segmentation result is presented in the main window where volumes curve can be reviewed (k) and the measured LV volumes are presented, according to Figure 28 (j).
7. If needed, correction of the LV segmentation can be performed by using the following tools: , , , , , , , , , , and (i).

11.2.3 Manual LV segmentation

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

11.2.4 Erase LV segmentation

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

11.2.5 Copying LV segmentation

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

11.2.6 Validation of LV segmentation

Table 1 present the mean bias between reference volumes by expert readers and the volumes by the automatic segmentation algorithm in 63 patients [1]. No uncertainty/error information is shown in the software together with the measurements.

Table 1:

LVM	3.4 ± 7.0 g
EDV	-9.5 ± 8.2 ml
ESV	-1.3 ± 6.3 ml
EF	-1.8 ± 3.0 %

1. Medviso White Paper, LV validation, 2023. [Available through https://medviso.com/documents/LVAI.pdf]

11.2.7 Batch segmentation of LV

In the Utility menu there is an option to perform LV segmentation in multiple image stacks in a batch process. This option enables LV segmentation with the fully automated LV segmentation algoritm in all time frames, independent if there are a CUDA enabled NVIDIA graphics card on the computer or not. To prepare for the batch process, load the short-axis LV stack into Segment and save it as a Segment file. Do this for all cases where you would like to apply the LV segmentation and place all Segment files in one folder. Then select Batch LV segmentation in the Utility menu. This will provide you with LV segmentation in all selected files.

11.3 Edit the segmentation result

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.

11.3.1 Smart endo segmentation tool

The smart endo segmentation tool is accessed by  . Perform endo segmentation in a slice by select the tool, push down left-mouse button in the middle of LV lumen and drag out. Release when the endo segmentation line is at the endo border.

11.3.2 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.

11.3.3 Propagate segmentation

An efficient way of handling erroneous slice is to copy the LV segmentation results from an adjacent slice. This is especially efficient in the more basal slices. The program copies the LV segmentation in selected slices and refines the position of the contours by a few iterations. To propagate a segmentation forward in time one time frame, press Ctrl-F. If the endocardial pen is selected  then the endocardium is propagated, and if the epicardial pen is selected  , then the epicardium is propagated. The hot key Ctrl-F also applies to ROI's if the ROI pen  is selected. You can also use the tools  or  to propagate the endocardium or epicardium, respectively.

11.3.4 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.

11.3.5 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.

11.3.6 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. A quick method to toggle between drawing epicardium, and endocardium is to use the space button on the keyboard.

11.3.7 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.

11.3.8 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.

11.3.9 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`.

11.3.10 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 11.3.2. The papillary muscles can also be included/excluded in the LV segmentation by using the manual drawing tools according to Section 11.3.6.

11.3.11 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.

11.4 Alternative automatic LV segmentation method

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

If ALL is selected in the icon  , the LV sementation is only performed in all time frames, which is the recommended setting. Steps to segment LV with the alternative semi-automatic algorithm.

- In the main interface of Segment, 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.

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 segmenation result from the alternative automatic LV

segmentation algorithm is then displayed in the main interface for Segment.

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 11.3.

12 Segmentation of the Right Ventricle

12.1 Fully automatic RV segmentation [1]

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

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

c. The segmentation result is presented in the main window where the measured RV volumes are presented, according to Figure 30 (j).

d. If needed, correction of the RV segmentation can be performed by using the following tools: , , , , (i).

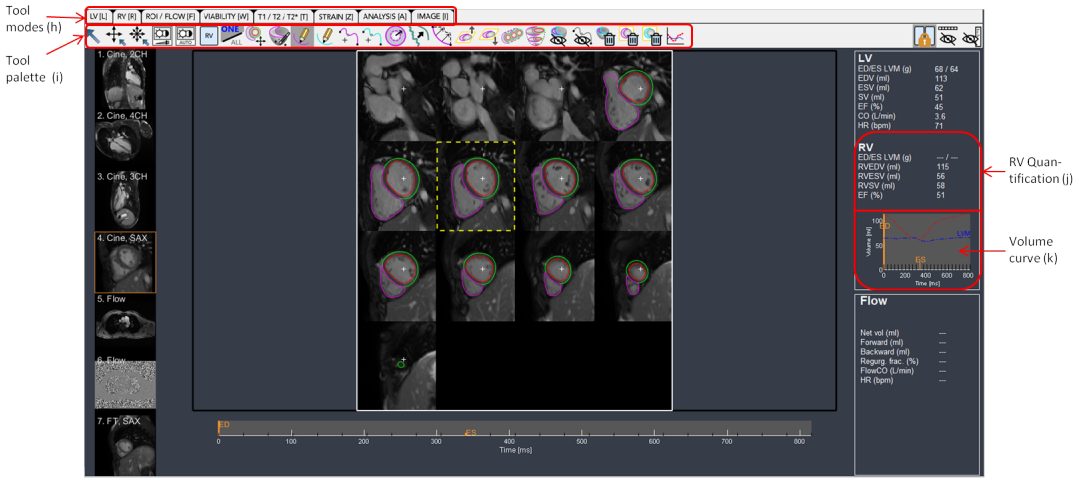


Figure 30: RV analysis result.

12.2 Semi-automatic RV segmentation [1]

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

2. Start the semi-automatic RV segmentation by select RV [R] (h) and select (i). A new interface is open, as shown in Figure 31.

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

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

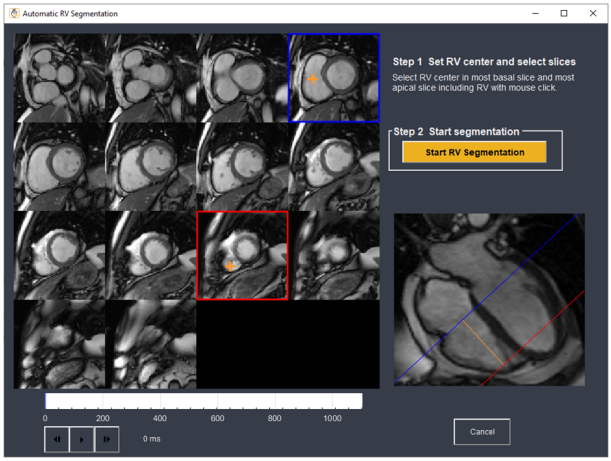


Figure 31: RV analysis GUI.

5. Start the RV segmentation process.
6. The segmentation result is presented in the main window where the measured RV volumes are presented, according to Figure 30 (j).
7. If needed, correction of the RV segmentation can be performed by using the following tools: , , , , (i).

12.3 Manual RV segmentation

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

12.4 Erase RV segmentation

To erase the RV segmentation, select (i) under RV [R] (h).

12.5 Validation of RV segmentation

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

Table 2:

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

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

13 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 32 illustrates the concept of segmentation in long axis images.

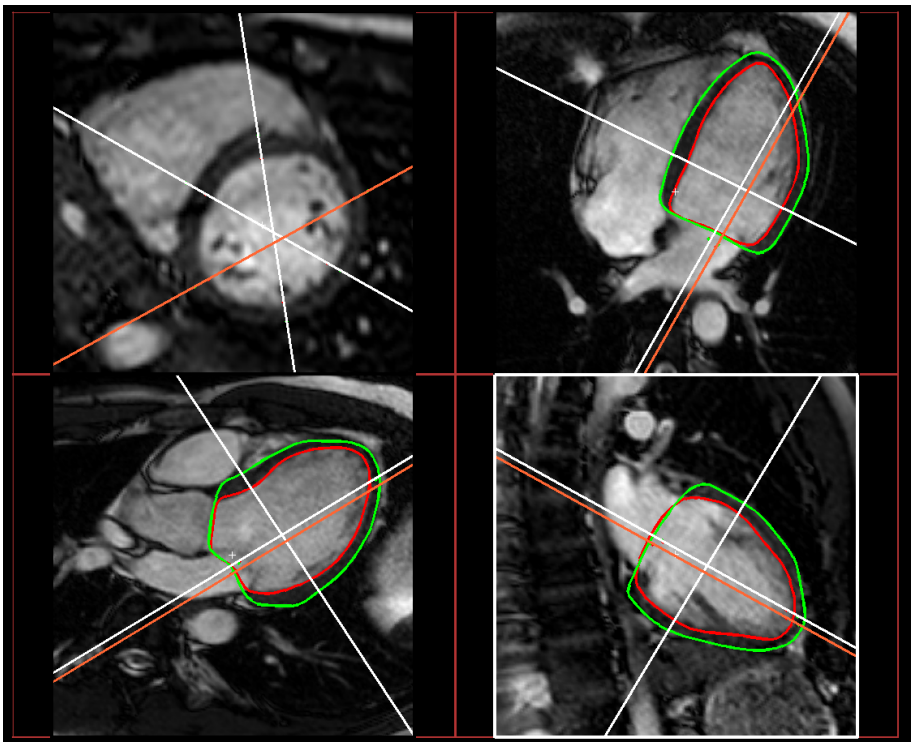


Figure 32: Illustration of the process of drawing segmentation in long axis images.

13.1 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.

13.2 Fully Automatic LV Segmentation

This tool is assigned to the Strain module workflow. See Chapter 34 or 35 for details.

1. Ensure that `Image View Plane` is set correctly (`2CH`, `3CH` and `4CH`), respectively. Otherwise set it according to Section 10.
2. Ensure that end-diastole (ED) time frame is defined correctly in all three views. If not, correct it manually by dragging ED marker to the end-diastole time frame in the time bar.
3. Start the fully automatic LV segmentation by select STRAIN [Z] (h) and select (i).
4. Ensure that the bounding box comprises the LV in ALL views, otherwise drag in the corners of the bounding box. Click on OK. See Figure 33 for details.
5. The segmentation is performed at the ED time frame for all long-axis images (2CH, 3CH and 4CH).
6. If needed, correction of the LV segmentation can be performed by using the following tools: or .

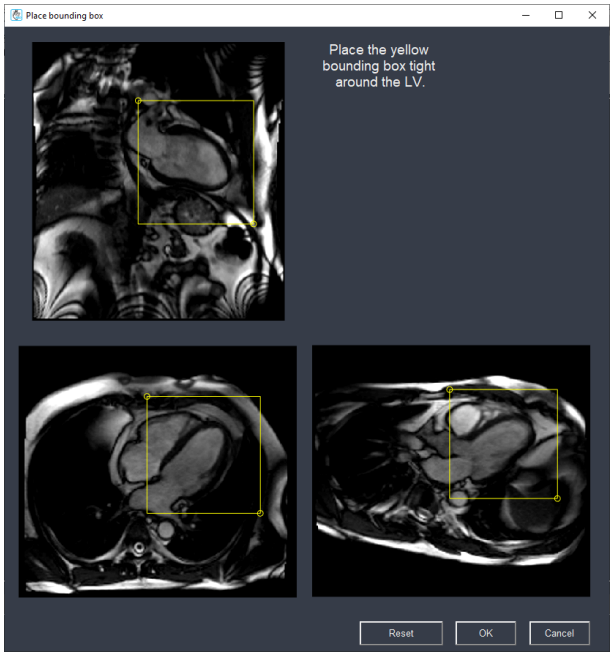


Figure 33: AI-based LV LAX segmentation GUI

13.3 Validation of LV segmentation

Table 3 present the mean bias between reference strain values by expert readers and the strain values based on the automatic segmentation algorithm in 91 patients [1]. No uncertainty/error information is shown in the software together with the measurements.

1. Medviso White Paper, LV LAX validation, 2023. [Available through https://medviso.com/documents/LVLAXAI.pdf]

Table 3:

GLS	0.42 ± 0.40 %
GRS	0.79 ± 1.70 %

14 Save and Load Segmentation

A key feature in Segment is that all measurements and user interaction can be saved so that is possible to go back and see how the analysis was done.

Saving and loading works differently in the Clinical mode or in the research mode. In the clinical mode then Ctrl-S automatically saves to the patient database, and in the research mode you will be prompted where to store the file. Loading operations in the clinical mode opens the patient database, whereas in the research mode it opens the file loader GUI.

14.1 Save images

Segment is able to save files in three diffrent formats. One old and soon to be obsoleted that stores only the image information of one single image stack, one that stores all image stack with all segmentation into one single file and one that stores all images stacks with all segmentation into one single file that is also a valid DICOM file. The second format is the most stable and is recommended when one observer is reviewing the images, and one would like to have the opportunity to go back and check how the analysis where made. If one needs to store the file in an enviroment which only accepts DICOM images, such as a PACS, one can use the third format.

14.1.1 Save both image stacks and segmentation to one file

This function saves both the image stacks and the segmentation to one file. This is the recommended way to save the images.

14.1.2 Save both image stacks and segmentation as

Same as above, but asks for a filename.

14.1.3 Save only segmentation

To save the segmentation results (including the measurements of mass, distance measurements, viability, and volumes etc), select the function Save Segmentation under the File menu (hot key is `Ctrl-S`). Then the program asks for a filename. The file extension should always be set to `*.seg`. Note that the segmentation file also contains scar delineations, roi's for flow analysis etc. When comparing segmentation results for different observers it is usually better to store them as separate image files with segmentation. Note this function only saves the segmentation, **not** the images. This function is kept for backwards compability and may be dropped in future versions of Segment.

14.1.4 Save as DICOM

To save as DICOM file select Special save in the File menu. Then select Save as Dicom. You will be prompted for location and filename. Note that the file is saved as a DICOM file, but

essentially it is an internal file format with a DICOM wrapper. It can not be used to load and study segmentations with other DICOM compliant softwares.

14.2 Load segmentation

To load a segmentation select Load Segmentation under the File menu. The current limitations of this operation is that you should not have removed / reordered any slices compared to when you saved the file. This limitation might be removed in the future. When loading some elementary error checking is done to ensure that the loaded segmentation indeed was done on the same image stack. To disregard this safety check see importing segmentation, below.

14.3 Importing segmentation result

The difference between loading and importing segmentation is that the error checking is disabled. This means that it is possible to load a segmentation from another dataset, and overlay that on the current image stack. This could be especially useful for instance with late enhancement image where the delineation can be performed on gradient echo and SSFP cine images, and then be overlaid on a late enhancement images. See Section 11.3 on details how to translate the segmentation loaded segmentation.

14.4 Hints

Setting the data path and export path in the preferences menu (see Chapter 27) saves a lot of work when frequently loading or saving images. When performing studies where the observer should be blinded to the identity of the patient, you can use the option to hide patient ID when loading the images. For more details see under Chapter 27.

15 Image Tools

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

There are numerous possibilities to manipulate image stacks. This chapter describes the tools found under the Image tools menu in the main menu. Many of these operations are not undoable. One workaround is to before applying the intended tool, right click on the image stack thumbnail and select duplicate image stack. By doing so you do not need to reload the image stack at least.

15.1 Crop image stack

This functionality is useful to crop the images to reduce memory requirement. This functionality is not available under the image tools menu, but as a tool in the tool palette  . Note that this function is not undoable.

15.1.1 Autocrop all image stacks

There is also a functionality to automatically crop all image stacks. The icon for this 

is found next to the crop icon.

15.2 Remove time frames

There are several suboptions to select exactly which time frames you wish to delete. Note that when you have removed time frames, you should also save the image volume since it is not possible to directly load the segmentation if it is stored as a separate `.seg` file. Note that this function is not undoable.

15.3 Remove slices

It is possible to remove all selected slices or all slices except the selected slices. When removing slices, note that you may not be able to import a segmentation to the current image stack since the number of slices will not match. When removing slices and you want to use the data set later be sure to save the image stack. Note that this function is not undoable.

15.4 Fake in extra apical or basal slice

In some instances the most basal or the apical slice may be missing due to improper scan planning. This should be avoided and be reported back to the scanning operator. However, if it still occurs the image set might be possible to rescue the image stack with this operation. It inserts a copy of the basal or apical slice and the segmentation. The reason that this might

work is that it might be possible to copy the delineation of the basal slice in end diastole to the second most basal slice in end systole.

15.5 Manipulate light/contrast

Once loading image data from DICOM files Segment internally converts the image data to the range [0..1]. The conversion factors are stored and the original pixel intensities can thus always be recovered.

15.5.1 Permanently apply light setting

When adjusting contrast and brightness the changes only affect the on screen appearance. With this option the current light setting is permanently applied to the image stack. This will then have impact on subsequent image quantification. Note that this functionality is not undoable.

15.5.2 Normalize image data

When loading image stacks from `.mat` files this check is not performed. Normalize image data will do this process. This process is currently not undoable even though all the required data is stored.

15.5.3 Invert colors

Invert colors remaps all pixels with the equation $s_{new} = 1 - s_{old}$, where s denotes pixel intensity. This functionality is undoable by repeating the operation.

15.5.4 Precompensation

This functionality might be useful for gradient echo MR images to minimize inflow artefacts. This option scales each time frame such as the mean image intensity is constant over time. Note that this function is not undoable.

15.5.5 View intensity mapping

Brightness and contrast settings are implemented so that the pixel intensity is remaped before being rendered. Currently this remaping function is a cropped linear function, but will be extended to a sigmoid function in future versions of Segment. This functionality plots the current intensity mapping.

15.5.6 View true image intensity

The function displays the current slice and time frame, and a color scale coupled to the original pixel values in the DICOM file.

15.6 Set colormap for current image stack

This function sets the used colormap for the selected image stack. Supported colormaps are shown in Figure 34.

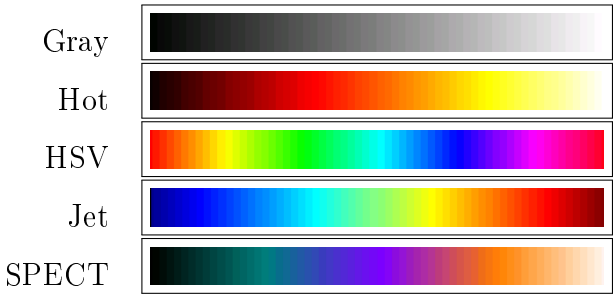


Figure 34: Colormaps.

15.7 Flip/Rotate image stack

By using this function it is possible to swap the direction of one axis. For instance if want to flip an image stack upside-down (apex/base) use Flip z. Flip x corresponds to what one usually would call y-axis, and for a short axis image stack this would usually be frontal/dorsal, and Flip y corresponds to left/right. Note that to preserve a right hand coordinate system it is not possible to flip in one image direction alone. Therefore, a flip in x directions also flips in the z direction. The simple flip's above is possible to do when there is an existing segmentation. If you require to make rotations (flip between two axis) you must not have an existing segmentation. Flip x&y transposes the image, Flip x&z switch between basal/apical to up/down direction, and Flip z&t change between time frames and slices. The later option is very useful when loading non standard images. This option does not update coordinate axes so this might be dangerous to use if combining with non flipped image stacks. If you need to rotate image volume and maintain correct voxel dimensions, please use the multiplanar reconstruction (MPR) functionality described in Chapter 28. Note that currently the option to rotate 90 degrees right is not working properly.

15.8 Resample image stack

There are different methods to resample the original image stack.

15.8.1 Reformat multiplanar reconstruction)

This option invokes the multiple planar reconstruction tool described in Chapter 28.

15.8.2 Upsample/downsample image

By using this option it is possible to upsample or downsample the image stack. Note that resampling is only done in the in-plane direction. When downsample an appropriate anti-alias

filter is applied. The used interpolation algorithm is bicubic interpolation. This functionality is not undoable.

15.8.3 Upsample/downsample slices

The number of slices can be upsample of downsampled. This functionality is not undoable.

15.9 Add noise

By using this functionality it is possible to add noise Gaussian white noise to the current image stack. The amount of noise is regulated by the std of the noise.

15.10 Calculate temporal mean image

This function creates a new image stack that is the temporal mean of the current image stack.

15.11 Set current frame as first frame

This function shifts the time series (cyclic shift) such as the current time frame becomes the first time frame in the time series. Note that it only applies to selected slices.

15.12 View K-space

This menu option shows the k-space for the current frame and slice.

15.13 Set image description

By using this menu option the image type, image view plane and imaging technique is displayed and a menu is shown where new image descriptions can be selected. Image type and image view plane is used by Segment to find what image stacks to take measurements from. This applies to the utility to summarize multiple `.mat` files and the report sheet generator. Imaging technique is used to find segmentation parameters and are therefore critical for a good automated segmentation. For further details, see Section 11.3.

15.14 View Image details

This function copies the most important image details to the clipboard. It is the same as the icon  .

15.15 View and adjust image details

By using this menu option it is possible to adjust image details. Parameters that can be adjusted are Slice thickness, Slice gap, Resolution in x direction, Resolution in y direction, and time increment.

15.16 View and adjust patient details

This menu option starts a graphical user interface where it is possibly to view/adjust: Patient Name, ID, birth date, acquisition date, age, height, weight, sex. The pushputton Apply to all applies the changes to all image stacks that are loaded to memory. By entering height and weight, BSA is automatically calculated.

15.17 Remove subject identity

By using this menu option all patient data are removed from all image stacks. This is useful when sending data to a different center or for bug report purposes. This function is not undoable. Removed items are patient name, id, birth date, acquisition date, filename, and original filename.

15.18 Calculating image histogram

Image histogram can be calculated by using tools found under the ROI-menu. For further details, see Section 16.6.

16 Region of Interest Analysis

The region of interest (ROI) functionality can be used for a wide range of possibilities. To select the ROI mode you can use the hot key `Shift-F`.

You can label and color each ROI individually. For flow measurements each ROI can also be assigned with a sign that will be multiplied with the velocities inside the ROI. The default sign is positive. The following names of ROI's are reserved for various purposes:

- Remote ROI (used to implement 2SD from remote as described by [1]).
- Scar region ROI (used to implement 2SD from remote as described by [1]).
- Static tissue (used for concomitant field correction, described in Chapter 21).
- Aortic ascending flow
- Aortic descending flow
- Pulmonary artery
- Vena cava inf
- Vena cava sup
- Vena pulmonalis inf
- Vena pulmonalis sup
- Vena pulmonalis dex
- Vena pulmonalis sin
- Sinus coronarius
- Lung
- Heart

16.1 Creating ROI's

There are several possibilities to add ROI's. Perhaps the most intuitive method is to draw the ROI by using the  . The ROI will be given the same name, and color as the latest modified/drawn ROI. This is very useful if you would like to draw several ROI's of the same kind. Start by drawing the first ROI, name and color it. Thereafter you can continue to draw the remaining ROI's.

It is also possible to add fix sized ROI's by using the Add fix size ROI under the ROI menu. This will add a fix size ROI and you will be prompted to enter the diameter. This function applies to the current slice. Another approach is to add ROI's in the myocardium between the endocardium and epicardium. This is done by using the function Add ROI's in sector (selected slices). You will be prompted for center angle, width in degrees, percent from the wall. Zero center angle corresponds to three o clock and counting counter clock-wise. This

function only adds sectors in selected slices. An example of automatic ROI placement is shown in Figure 35.

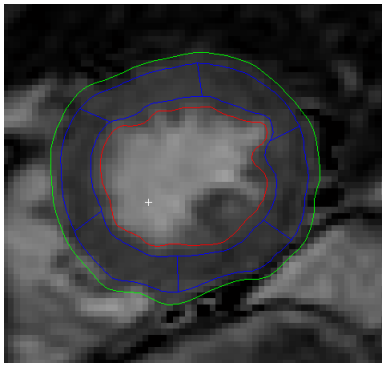


Figure 35: Automatic placement of ROI's inside the myocardium.

Another possibility to create ROI's is to convert the endocardial, epicardial or scar surface to a ROI. This is done by the option Copy endocardium to a ROI, Copy epicardium to a ROI or copy scar to a ROI. This only includes the selected slices.

16.2 Modifying and deleting ROI's

By right clicking on a ROI a pop-up menu appears where it is possible to:

- Delete ROI
- Set ROI label (change the name/function of the ROI).
- Set ROI color (change the color of the ROI).
- Copy ROI upwards
- Copy ROI downwards
- Copy ROI outline to all timeframes
- Refine ROI (for flow purposes, see Chapter 21).
- Switch ROI sign (useful for flow analysis).

16.3 Translating and scaling ROI's

ROI's are translated with the icon and scaled with . Point on ROI contour and drag while mouse button kept down to adjust to correct position/size.

16.4 Deleting ROI's

Under the ROI menu it is also possible to Delete ROI, Delete ROI's Using Template, and Clear All ROI's. The first menu option deletes the current (last drawn or modified ROI). The second menu option deletes ROI's with a name matching a specified template. A menu of possible ROI's that can be deleted are shown.

16.5 ROI analysis

It is possible to plot and export the following parameters over time:

- Mean signal intensity
- Standard deviation of signal intensity
- ROI area
- ROI area based on pixels
- Minimal signal intensity
- Maximal signal intensity

Figure 36: Graphical user interface for ROI analysis.

An example of the user interface is shown in Figure 36. In the ROI-selection panel the ROI's to plot can be selected. If the checkbox ☒ Use ROI's only from this slice is selected, then only ROI's in the current slice are shown. If the checkbox Use normalized values is selected the the values are shown in the `Segment's` own internal normalized representation. Otherwise the values

are recalculated back to the pixel values in the DICOM files. In the View panel it is possible to select to plot min/max values, min/max slopes, or Full-Width-Half-Maximum (FWHM). If the checkbox ☒ Smooth curves is selected, then the curves are smoothed before slopes, and min/max values are calculated. The smoothing is applied is a Gaussian smoothing kernel. The smoothing parameter σ is adjustable with the slider, and the edit box. By using the Plot filter button it is possible to plot the filter in the temporal domain. Currently the filter is applied directly to the ROI curve. Finally, the Export button exports all parameters to the clipboard. The Max/Min Export button exports the values and timing of min/max, min/max slopes, and FWHM. Note that that when changing plotting options the plot is not updated until you click Update.

16.6 ROI histogram

This function plots the histogram of ROI(s). When initiated the program asks for a selection criteria on what ROI's to include. If no ROI's are present then the histogram for the whole image (current slice and time frame) is displayed. The most common percentiles are also calculated and exported to clipboard. An example is shown in Figure 37.

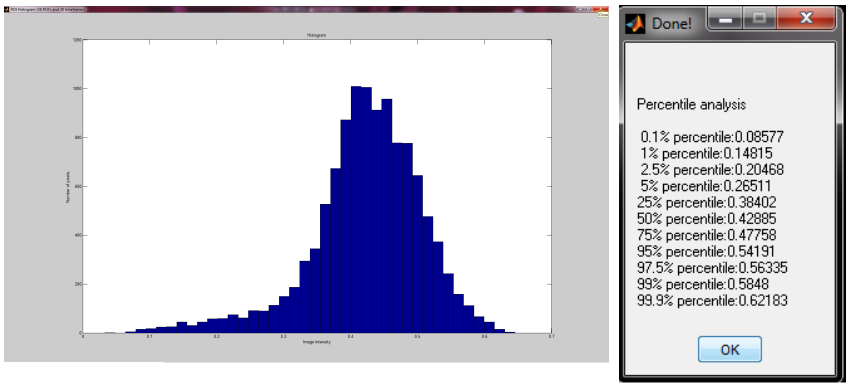


Figure 37: Example of ROI histogram.

16.7 Multiple threshold analysis

This function calculates the number of pixels inside the ROI's above the selected threshold. Before starting the program prompts for start threshold, end threshold and number of levels. All curves are plotted at the same level. The offset of each curve is displayed. All numeric data are copied to clipboard. There is also a visual mode where the pixels above a certain threshold are color-coded. An example of the visual analysis is shown in Figure 38. You are also prompted whether to use the internal normalized image pixel values or the original data from the file. The non-normalized range can be found by plotting the image intensity mapping (found under Image tools). By selecting Multiple threshold analysis - numeric the same analysis is performed for each time frame and numeric values are exported to the clipboard.

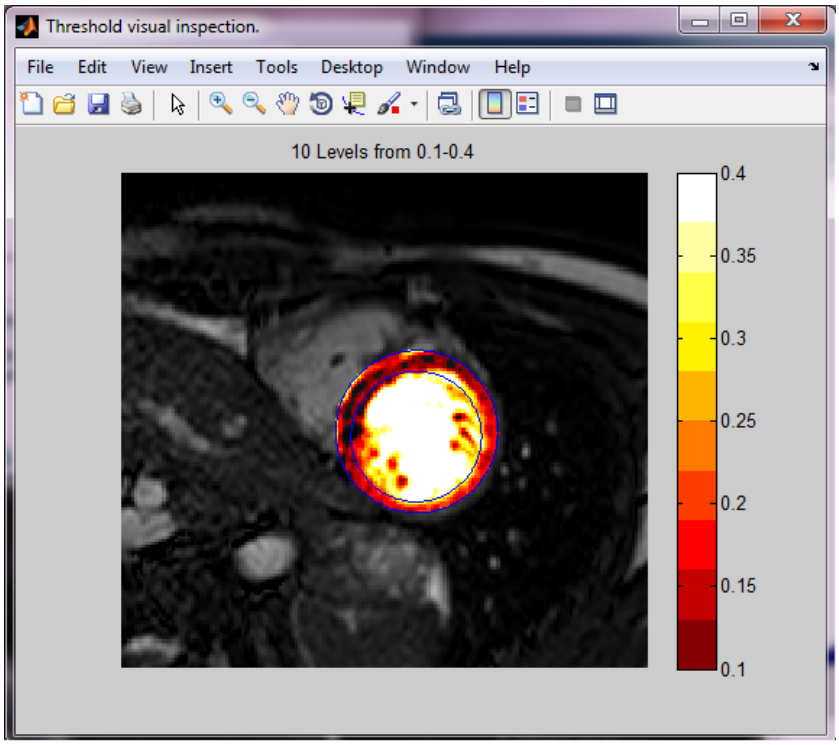


Figure 38: Example of multiple threshold analysis.

17 Measurements and Annotations

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

17.1 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 39. Under the Annotations menu it is possible to clear or export all measurements to the clipboard. Measurements of ventricular wall thickness is best performed by using the tools for region wall motion analysis described in Chapter 24.

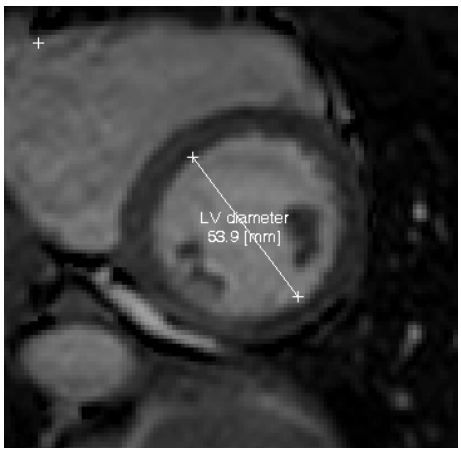


Figure 39: Example of a measurement of the left ventricle diameter.

Another method to get distances (or timing intervals) by adding annotation points at different points in space and time. Annotation points are added with the icon  and export the coordinates and time points of the annotation points to Excel or another spread sheet program and there calculate the distance. Annotation points is also useful for marking anatomical landmarks etc. For further details, see Section 17.7.

17.2 Timing

By using the M-mode viewing mode it is possible to make measurements of both timing and distances. This is illustrated in Figure 40.

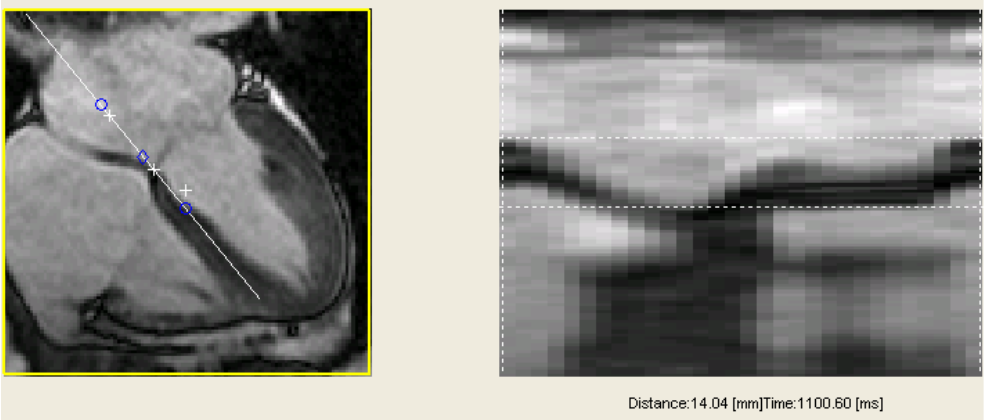


Figure 40: Example of a measurement in M-mode.

17.3 Volumes

Volume of the left ventricle is displayed and updated as soon as you have delineated some slices. If the volume was calculated from segmentation in longaxis images, this is indicated in a line of text above. Volumes of ROIs can be derived by using the numeric multiple threshold analysis described in Section 16.7. On possible mistake when doing manual delineation of the left ventricle in only diastole and systole is the failure to indicate what time frames that are end-diastole and systole respectively. This will cause `Segment` not to show any volumes. Selecting diastole and systole can be done by interactively dragging ED and ES in the volume graph or using the Autodetect End systole and End diastole under the Edit menu.

17.4 Area

Area of ROI's can be derived by using the region of interest analysis tool in Chapter 16. In certain cases area can also be derived by dividing volumes by the slice thickness. The area of the ROI's is shown for each ROI in the one slice view. In the near future a general area tool will also be added to Segment.

17.5 Flow and volumes

Measurements of flows and volumes are covered in Chapter 21.

17.6 Signal intensity

Signal intensity can be measured by using the region of interest analysis tools described in Chapter 16.

17.7 Annotation and anatomical landmarks

Annotations are added with the  icon or under the Annotation menu. The points can either be stationary or time resolved (i.e have different positions in different time frames). The stationary points are marked with a bold font. To make a pointtimeresolved right click on it and select Make point timeresolved from the pop-up menu. Note that this operation is undoable. It is possible to Clear All Annotation Points, Clear Annotation Points Using Template, Rename Annotations Using Template, and Export All Annotation Points. When deleting or renaming using a template you are prompted for a template. The template must be an exact match since no wildcards are allowed.

To propagate the location of a time resolved point, press `Ctrl-F`. Note that you need to have the annotation tool  active when doing this.

18 Utilities

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

The differentiation between a utility and a function/feature is that the utility does not necessary apply to an image stack. Utilities also include batch script.

18.1 Pseudonymize data

The pseudonymize features are found under the Utility menu. There are both options to apply the psydonymization on the current open file in the software, or to apply it as a batch feature on multiple studies.

There are two levels of psedonymization, partial or extensive. Partial pseydonymization will remove patient name, ID and birthdate, filename, original filename, and pathname. Extensive pseudonymization will remove patient name, ID, birthdate, sex, age, length, weight, and BSA, acquisition institution and date, filename, original filename, and pathname. The level is selected in the pseudonymization interface.

To apply the pseudonymization on the current open file in Segment, select Pseudonymize subject in the Utility menu. To run batch pseudonymization, select in the Utility menu for DICOM files Batch Pseudonymize DICOM Files, and for .mat files Batch Pseudonymize .mat Files. This will open the Pseudonymization interface where to add files to pseudonymize and the level of pseudonymization.

18.2 Clear segmentation from multiple `.mat` files

This utility is useful when one want to clear the segmentation from multiple .mat files at once. One particular example when it is useful is when a second observer should reanalyse all files. In such cases copy all files, rename them and run this function.

18.3 Sort Folder of DICOM files

This utility is useful when you a have a large collection of DICOM files that are in a strange order. This is often the case from certain Siemens scanners. The program will sort them up in folders that are arranged as patientname+patientid, studydate+stydyid, and series number. Each folder will contain sorted files according to instance number and trigger time.

The graphical user interface is shown in Figure 41.

Start by selecting input and output folders/path/directories. If the checkbox ☒ Recursively take sub dirs is selected then the program will take all files below the selected input directory including its subdirectories. The input/output folders should preferably not overlap. Each file will be named according to the name template followed with a 5 digit number. The function

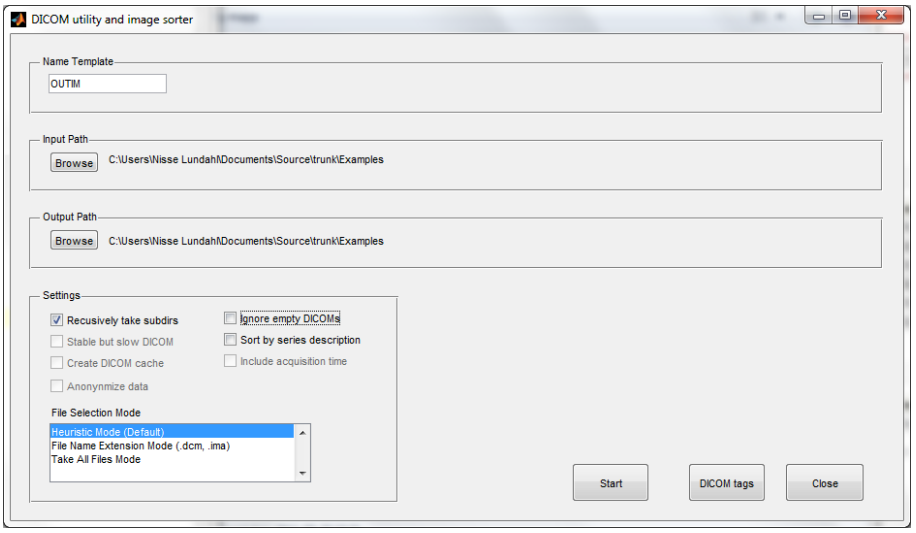


Figure 41: Graphical user interface for the DICOM sorter.

DICOM tags asks for a filename and displays all DICOM tags in that particular file. The checkbox ☒ Stable but slow DICOM controls what DICOM interpreter is used in the sorting operation.

If you select the checkbox ☒ Create DICOM cache then the program will create cache files that are used when loading DICOM data into Segment. This will significantly speed up loading and is therefore recommended. For more details of caching of DICOM files, see Chapter 8. The checkbox ☒ Ignore empty DICOMs allows the user to leave out files where the Acquisition-Date tag is either empty or broken, which is an indication of an empty file. If a series is broken up into parts with separate series numbers, ☒ Sort by series description sorts all files with the same series description into the same directory. If this is selected, ☒ Include acquisition time can be used to include acquisition time in filenames, thus making the time order of files in the series directory easy to follow.

18.4 Copy and Sort Images from CD to Data Folder

This function is ideal to use when you have images on a CD (structured or not) that you want to copy to your harddrive and subsequent analyze. This function assumes that you have set the location of your CD drive in the preferences (see Chapter 27). This function sorts and name the files in the same manner as the sorting utility. DICOM cache and thumbnails are also created.

18.5 Create DICOM cache for folders recursively

This function ask for a folder and creates DICOM cache files for all subdirectories. This functionality is highly useful when you have copied large sets of DICOM files to your local harddrive that you need to load into Segment. It takes a long time to run so a good idea

is to start this function over lunch. Once this is done loading of your DICOM files will go much faster.

18.6 Create thumbnails preview recursively

Analog to creating of DICOM cache files but creates thumbnail preview for all subdirectories. Depending on the number of subfolders this function may also take quite long time to run.

18.7 Find patient details in .mat files

This utlity allows to scan your entire harddrive (or network drive) for patient details in .mat files. Output is a list of all patients occuring in the directory tree. This feature is useful when you want to ensure that you have not stored any sensitive information on your local computer/laptop for instance. The output is an Excel file where each row .mat file with patient information.

18.8 Find patient details in DICOM files

Analog to the above function, but instead looks in all your DICOM files. The following heuristics is used to classify a file as DICOM or not:

- Files that ends with `.dcm`.
- Files that only contains digits and no extension.
- Files with name that contains more than 7 dots and the two first letters corresponds DICOM identification of an imaging modality.

The output of this function is an Excel file where each line is one unique patient identity and the number of files in which the patient name was found. Note that to be completly certain about the are no DICOM files with the patient details you need to count the number of files that are deleted / pseudonymized for each patient or simply run the function twice.

18.9 Export from multiple `.mat` files

This function summarize multiple `.mat` files into one summary. This is very useful for research studies. For instance by placing `.mat` files, one for each patient in one folder. It is possible to summarize all patient data into one Excel sheet. Note that each `.mat` file can contain several image stacks. The program automatically determines what image stack is for instance short-axis slices, and what image stack is viability images. If this automatic image stack detection fails it may be necessary to load the image stacks and select correct image type. For further details see Section 15.13. Currently the following data is outputed for each files; File name, Patient name, Patient ID, Age, Length, Weight, Sex, BSA, Heart rate, R-R interval, LVM in ml, LVM in g, EDV, ESV, EF, LVM from viability images, Scar percentage, Scar in ml measured on viability images. Furthermore, for each ROI in the image stack the name of the ROI and the total volume is reported. When EDV, and ES is not exported see Section 17.3 for hints.

18.10 Export Information from multiple .mat files

This function exports imaging information from multiple .mat files. Example on exported information is:

- ImageType
- Image size
- Resolution
- Slice thickness and slice gap
- Time increment between
- Information whether the file contains infarct sizing, flow information, segmentation

19 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. The method used for automated delineation of infarct is described in [2]. 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 [3]. 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 [2]. 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 slighly 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 illustraded in Figure 42. 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.

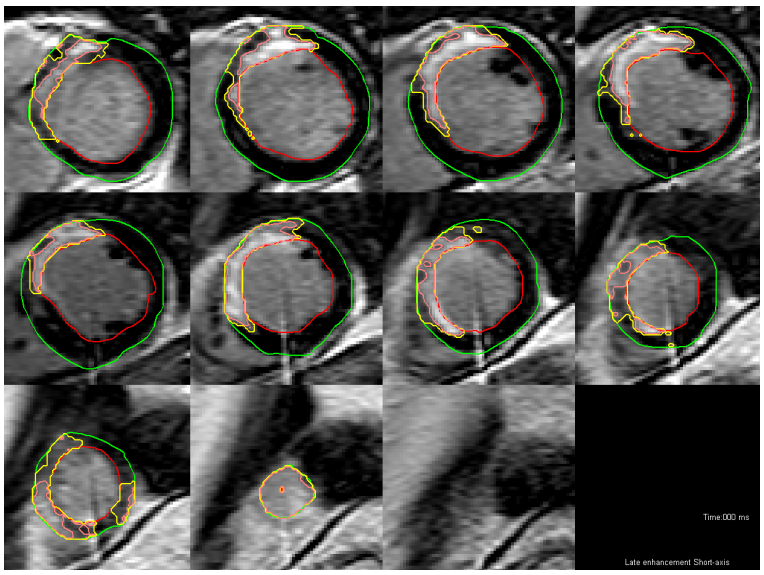


Figure 42: Example of scar delineation in the weighted mode. The yellow line denotes the complete affected area, and the pink line a graphical representation of the corresponding weighted area.

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).

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. 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 o. 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 [2].
- Old weighted. Automatic scar delineation as described in [3]. 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* [4]. 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 [2]. Note that this method is not encouraged.
- Manual mode. Manual drawing of hyper enhanced regions.

Each of the different methods are further described below.

19.1 Automatic mode (EWA method)

The automatic mode with EWA (*E*xpectation Maximization, *W*eighted 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 43. If no assumption of affected vessel is to be used, then select No vessel

assumption.

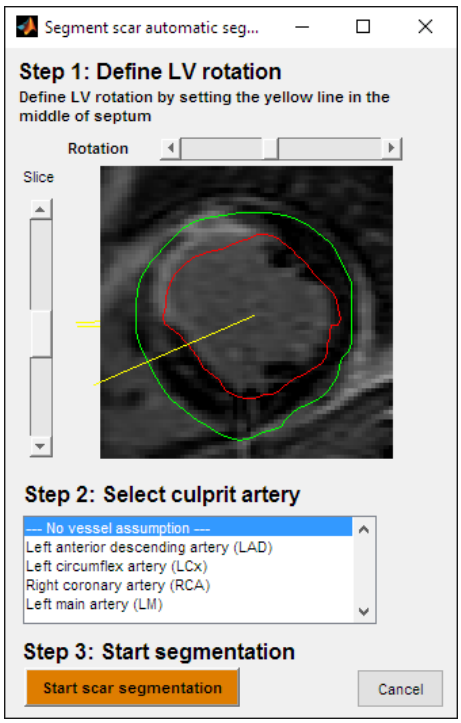


Figure 43: User interface to select vesselterrotori. First adjust sector rotation to point towards the mid point of septum. Secondly select known affected vessel. If this is not known or not applicable just select No vessel assumpion.

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.

19.2 Old weighted

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

19.3 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.

19.4 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.

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 advantagoues 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.

19.5 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.

19.6 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 [5, 3]. The parameter Standard deviations from remote controls is the only variable that we recommend to change, and then for the SD from remote method.

19.7 Grayzone Analysis

Two different methods for Gray Zone analysis is provided in Segment. The two methods are the Weighted method and the ROI method.

19.7.1 Gray Zone default analysis

The menu item Gray Zone Analysis - Default 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. It uses either EWA method or the old weighted algorithm depending whichever method was used for infarct quantification.

19.7.2 Gray Zone analysis by ROI method

The menu item Gray Zone Analysis (ROI Method) enables the user to divide the scar area into core and grayzone based on ROI segmentations and a user selected threshold. The result is displayed in the image view as colored overlays of dark red (core) and dark yellow (grayzone) pixels. The Grayzone Analysis GUI displays a histogram of the pixel intensities of the currently segmented scar volume. By dragging the red bar, the user can change the threshold for what identifies as grayzone (intensity values lower than that of the bar) and core (the remainder). The user can also change the threshold for scar segmentation, given as number of standard deviations from remote value, by clicking the Increase or Decrease buttons. After changing either of these thresholds, the values are recalculated by clicking the Recalculate button. The sizes of the core and grayzone volumes are calculated based on pixel volume and displayed in the GUI, and can be exported along with the threshold values by clicking the Export button.

20 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 33.4.

The maR tools can be found under the MR menu in Segment. 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  and  removes the manual corrections made with the  or  . By default manually added mar regions shows up in green and manually deleted areas in blue.

20.1 MaR from T2-weighted images

The method used for automated delineation of MaR from T2-weighted is described by Sjogren et al [6]. 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.

20.2 MaR from CE-SSFP images

Using contrast enhanced standard cine images acquired directly after contrast injection can be used to determine MaR, [7]. 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 [8]. The algorithm for automated MaR delineation from CE-SSFP images is developed by Tufvesson (maiden name Sjogren) [9]. 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.

21 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 44. 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.

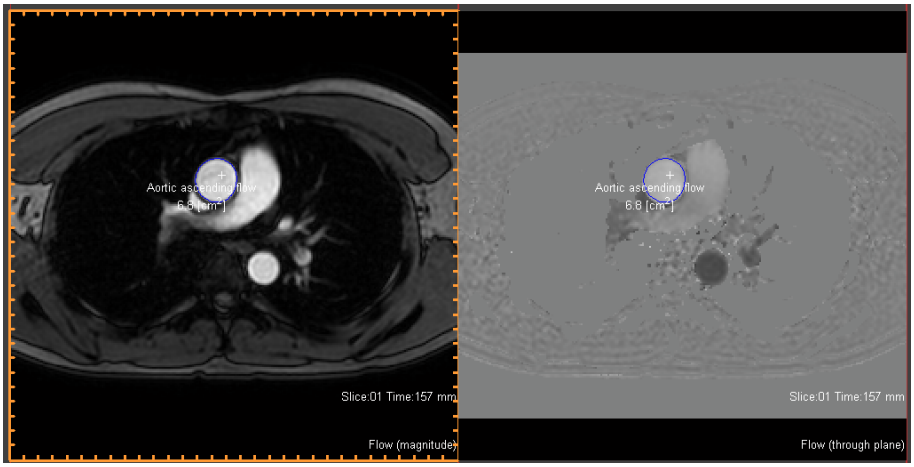


Figure 44: Example of main GUI in flow mode.

21.1 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. Deleting, renaming, recoloring the region of interest is described in Chapter 16. If you are not satisfied with the ROI there are two methods that can be applied.

21.1.1 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.

21.1.2 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`.

21.1.3 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.

21.2 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 45.

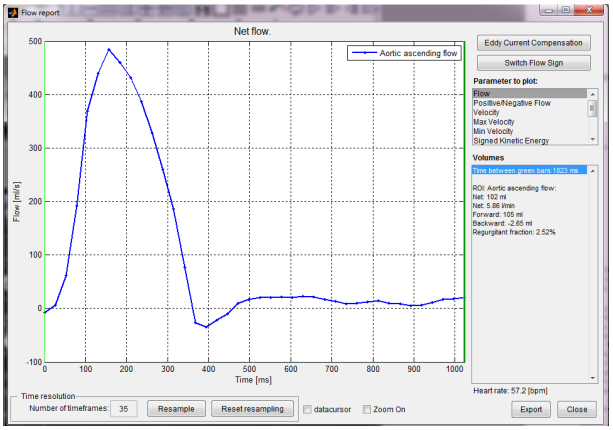


Figure 45: Example of flow plotting GUI. Plotting parameter can be selected in the upper right corner of the GUI. The flow integration is performed between the two red bars.

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 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 46. The sum of the two curves is the same as the net flow that is shown in Figure 45.

It is also possible to plot the Velocity over time, and this is shown in Figure 47. 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 48.

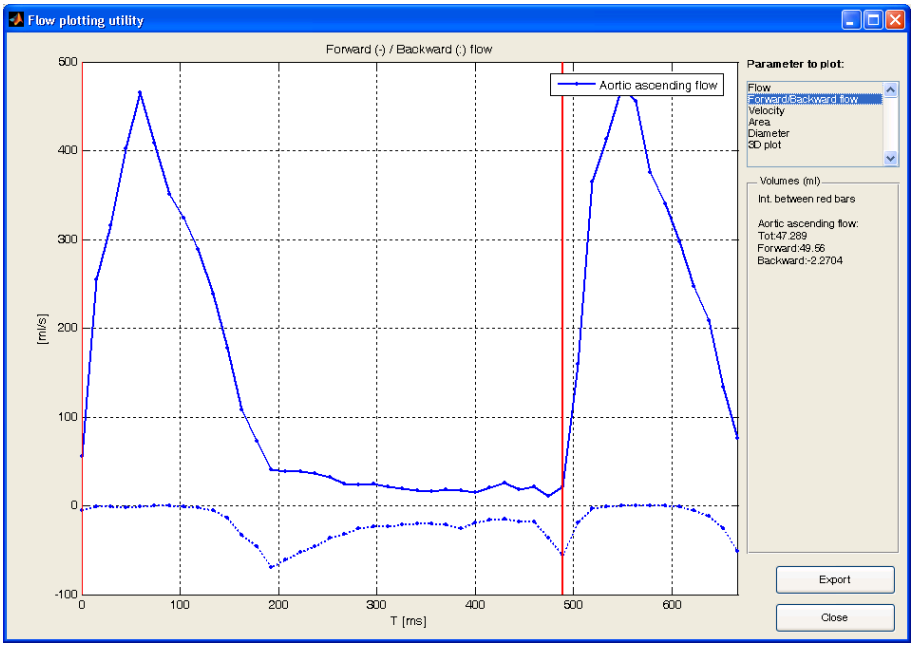


Figure 46: Example of plotting of backwards and forward flow simultaneously. The sum of the two curves will be the net flow showed in Figure 45.

21.3 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

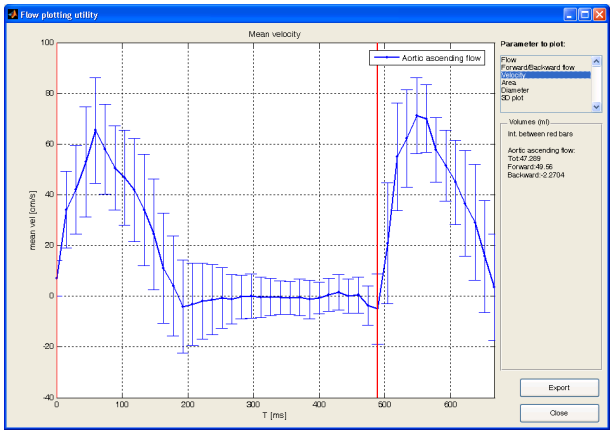


Figure 47: Example of plotting of velocity over time. The 'error' bars shown the standard deviation of the pixels within the ROI over time.

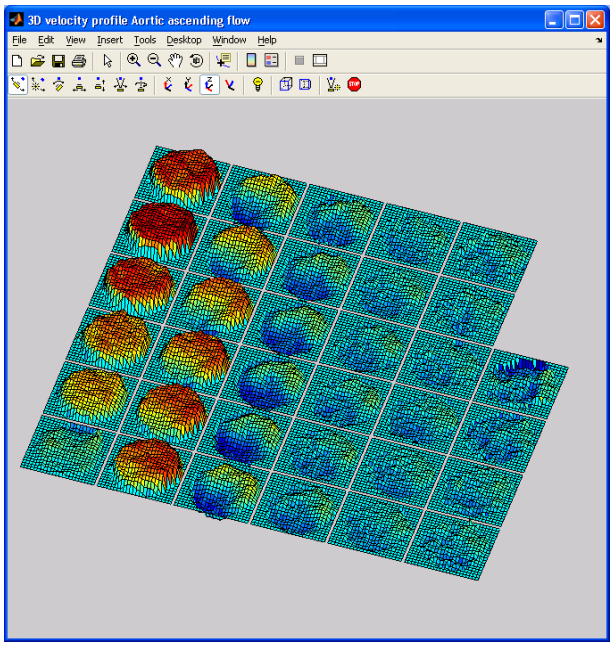


Figure 48: Example of plotting of a 3D profile of the velocity distribution.

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 49.

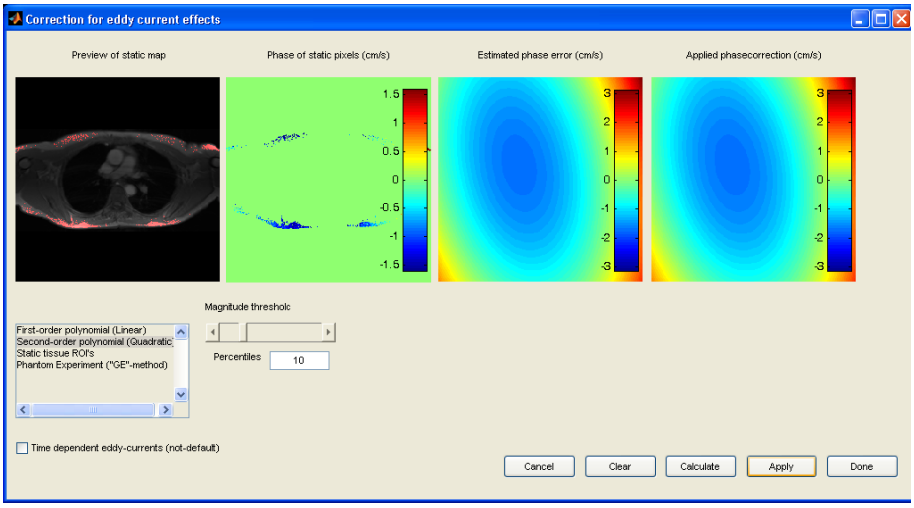


Figure 49: Example graphical user interface for compensating of concomitant field effects. In the left the identified static tissue is the displayed, and in the middle panel the corresponding phase for these pixels is shown, and in the right panel the resulting phase correction is shown.

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.* [10].

21.4 Phase unwrapping

In cases were 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 50.

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

21.4.1 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).

21.4.2 Manual unwrapping

Instructions for the manual unwrapping are given in the user interface.

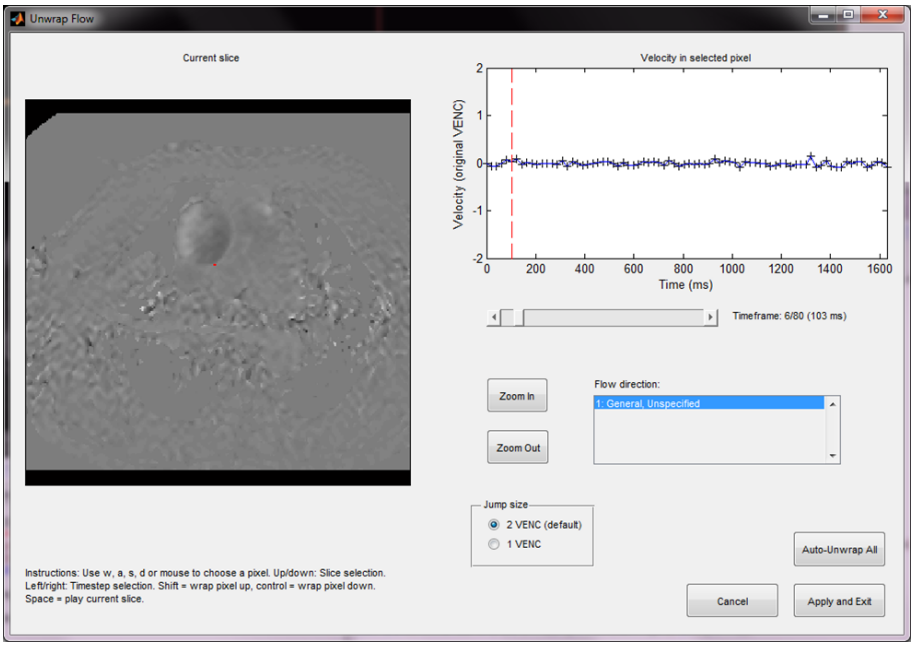


Figure 50: Example of the graphical user interface for phase unwrapping. The left image panel shows the original phase, and the right image panel shows the unwrapped phase. The long slider adjusts the current time frame.

21.5 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).

21.6 Coupling magnitude and flow images

If magnitude and flow image stacks have been loaded into Segmentwithout 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.

22 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 51. 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.

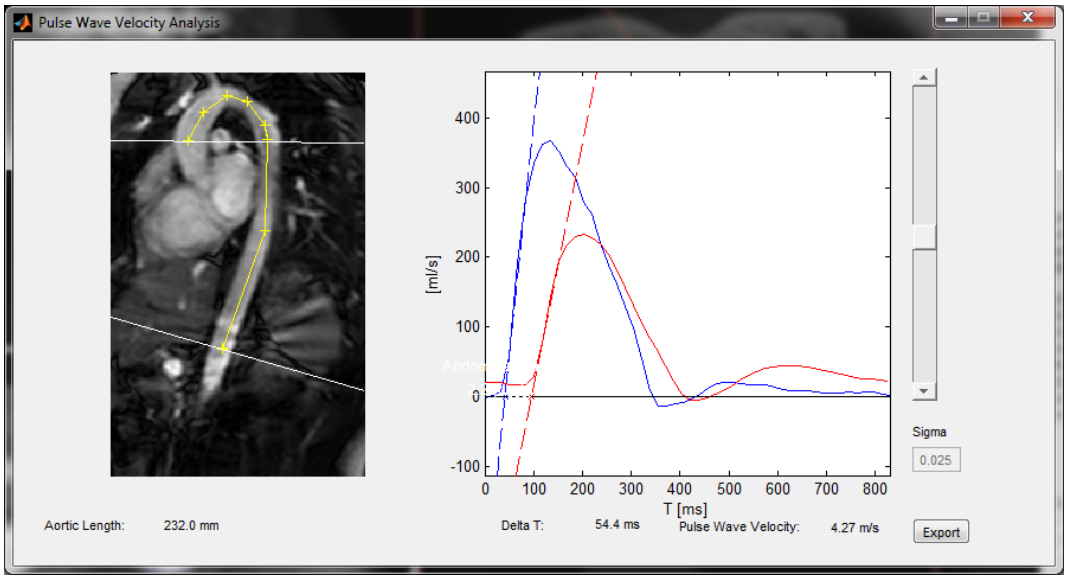


Figure 51: GUI for Pulse Wave Velocity Analysis. On the left is the image containing the measurement of Aortic Length. On the right is a plot of flow curves along with their respective tangents.

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.

23 Stress Analysis

In earlier versions of Segment there were a special stress viewer available. This have been removed since it's functionality is now directly available in the normal viewing capabilities of Segment (synchronized viewing of several image stacks). It is possible to place four (or more) image stacks on the screen simultaneously and play them synchronized in the same speed by the icon  . Other functionality in Segment that could be used to analyse stress images is the report per slice functionality, described in Section 24.2 which allows quantitative studies of wall motion abnormalities.

Further hints on doing stress analysis is to label your image stacks. Then it is easy for the viewer to see which image stack is stress and which is rest. This is done by right click on the image thumbnail and select Set Image Type in the pop-up menu.

24 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 11.3.

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

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

24.1 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 52.

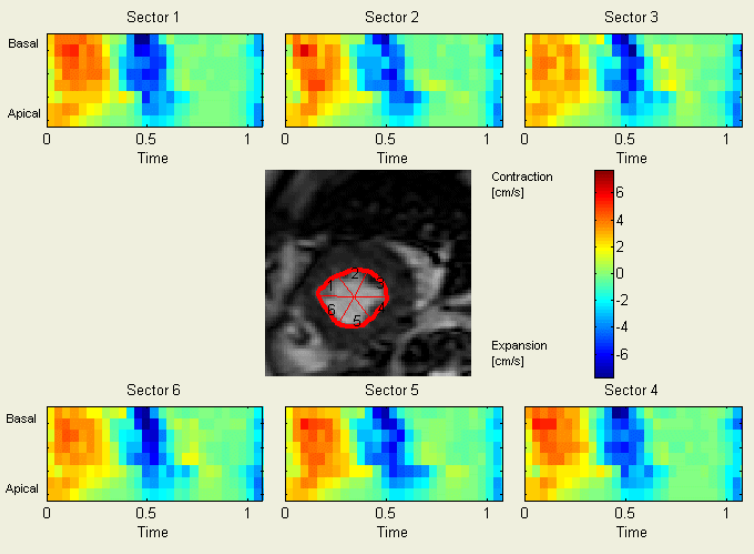


Figure 52: Radial velocity versus time in six sectors. Note the apical to basal gradient in the onset of the radial contraction.

24.2 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 53. You can adjust the start of the sectors by using the rotation slider or take the starting sector as the sector that is closes to the annotation point `Start Sector`. How to place annotations, see Section 17.7.

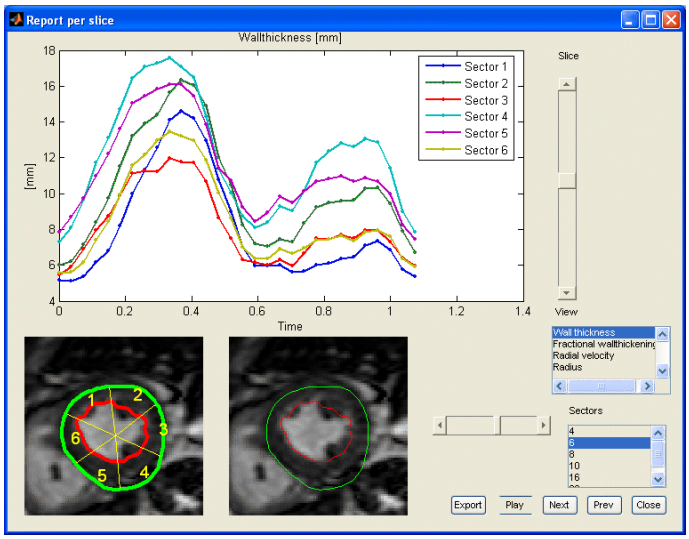


Figure 53: Wall thickness over time in a healthy subject.

25 LV Sphericity Analysis

LV sphericity can be calculated from the Report 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.

26 Export Images and Results

There are many options to do batch exporting from multiple `.mat` files. Please see Chapter 18 for further details.

26.1 Export results to clipboard

These functions export results such as LV mass, ejection fraction, volumes etc, to the clipboard. Data is outputed in a format so that it directly can be pasted into Microsoft Excel (by usage of `Ctrl-V` in Excel) or other spread sheet softwares. When you need to export data from multiple files, it is strongly recommended to use the utility to summarize `.mat` files described in Section 18.9.

26.1.1 All stacks with header

This function exports the results of all image stacks and includes a header line above. Segment tries to use the image type to determine which image stacks are short axis cine images which are used for mass and ejection fraction, flow image stacks, delayed enhancement image stacks and so forth.

26.1.2 All stacks

Same as above but no header line is included in the output.

26.1.3 This stack with header

This function only outputs results from the current image stack and includes a header line.

26.1.4 This stack

Same as above but without including a header line.

26.2 Export volume curve to clipboard

The volume curve (both) endocardial volume, and epicardial volume is copied into two columns.

26.3 Export contour to clipboard

This function ask what contours to export and export the internal representation to the clipboard. You can currently chose to export LV endo-, epicardium, RV endo- and epicardium, respectively.

26.4 Export volume of contours per slice

This function export the volume of each contour per slice. Data is exported for all contours and all time frames. If you instead want to have the area per slice you can divide the result with the slice thickness in cm to get the area in cm^3.

26.5 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`.

26.6 Export screenshot

Using this option, you can choose from which GUI you want to take a screenshot or if you want only the current dsiplayed image. You can also crop the image before exporting. 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 27 for further details.

26.7 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).

26.8 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 54.

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 54 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

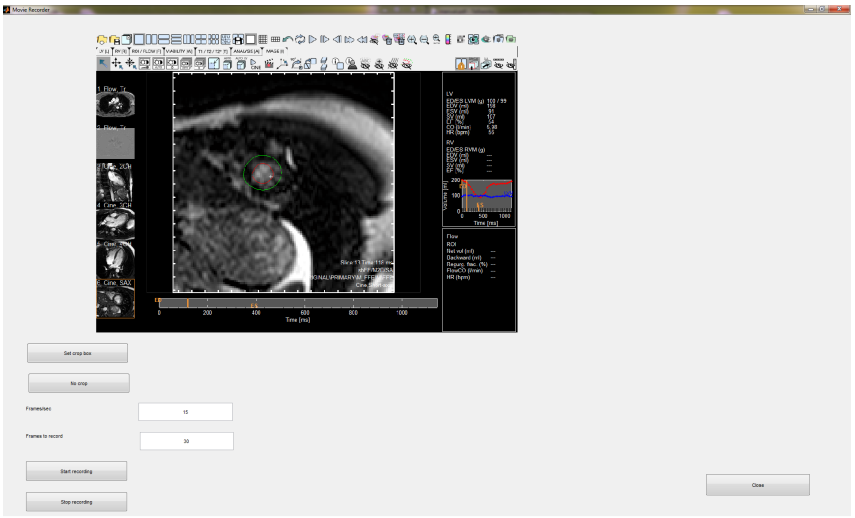


Figure 54: Movie Recorder GUI.

movie compressor, since all compressors might not be available on your computer. Personal experiences are that the cine-pak encoder are pretty stable.

27 Customizing Segment

This chapter describes how to customize Segment. 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 55. It is invoked by using the menu Preferences on the main menu.

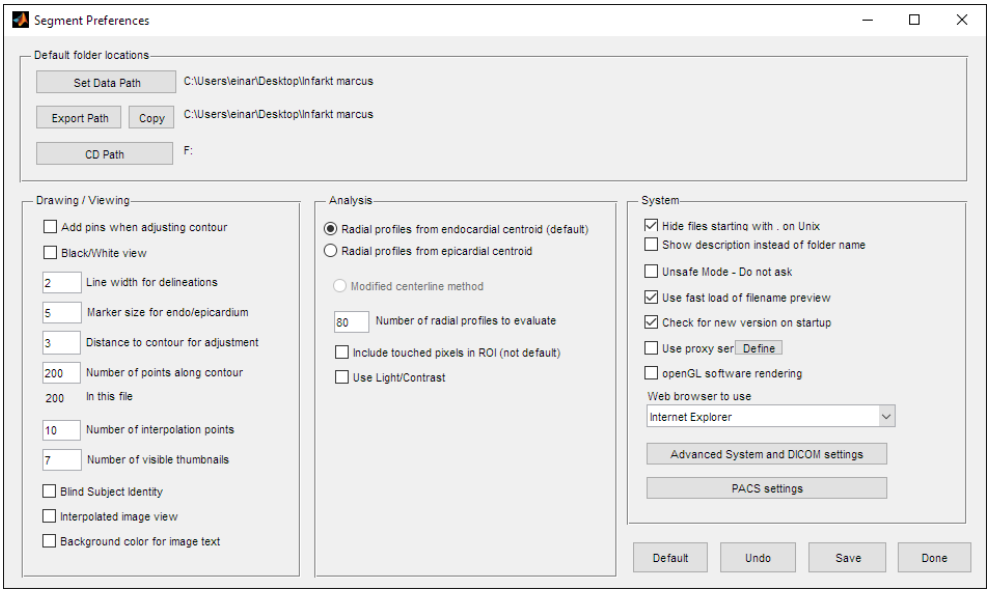


Figure 55: Preferences GUI.

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.

The option ☒ Add pins when adjusting contour controls weather 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 43. 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 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 38.

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.

27.1 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 56.

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

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

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

Figure 56: 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 `imagedescption.txt` according to Figure 56. 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 57, 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 57: Example of a parse file for image description settings.

27.2 Advanced and DICOM Settings

The graphical interface for advanced settings is shown in Figure 58. 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 beeing 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 interprets DICOM files. The checkbox ☒ Force 16 bit DICOM enforces Segment 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. For further details see about loading DICOM files in Chapter 8.

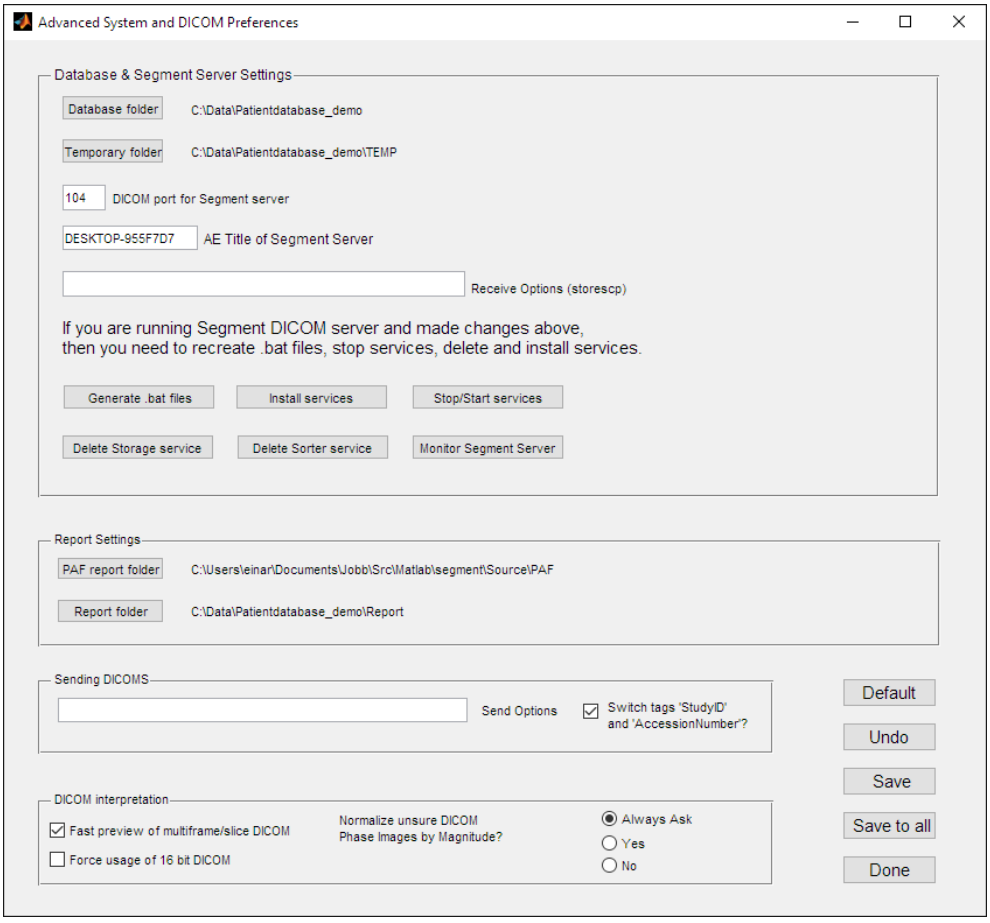


Figure 58: Advanced and DICOM Settings GUI.

27.3 PACS Settings

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

27.4 Technical details

On Windows platform, the preferences are stored under the local user folder and the sub-directory `Application Data/Segment`. 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 is installed. This will also override all PACS and Segment Server settings for all users. In the preferences folder Segment also stores a log file for debugging purposes, and small temporary files that are used in the PACS communication batchdownload process.

28 Image Reformat (MPR)

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

It is possible to reformat an image stack along any axis. The main purpose of this tool is to be able to resample the data volume to short axis slices (if they are for instance scanned in an axial direction). The reformater can also be used to construct a long-axis image from a stack of short-axis slices. The user interface is shown in Figure 59.

One limitation with the multiplanar reconstruction is that it does not utilize the patient image coordinate system. This means that image stacks created with the reformater does not display image plane crossings. This will be addressed in future versions of Segment. Furthermore, the MPR routine does not currently support non-isotropical voxels (i.e voxels of dimension 3x4x8 mm). Voxels where x and y size are equal do work, i.e 3x3x8 mm works fine.
The functions are:

New cut	Resamples into parallel slices to the selected line. The cuts are also perpendicular to the viewing direction.
Previous cut	Backs up one level in the cut history. The current cut is not saved.
Done/Export	Exports the resample image stack back to Segment.
Play	Then this toggle button is selected then the image is played as a movie.
Close	Closes the dialog resampler without storing any information.

Parameter slice determines the slice distance in mm, and output determines the output resolution in the new 'short-axis' plane.

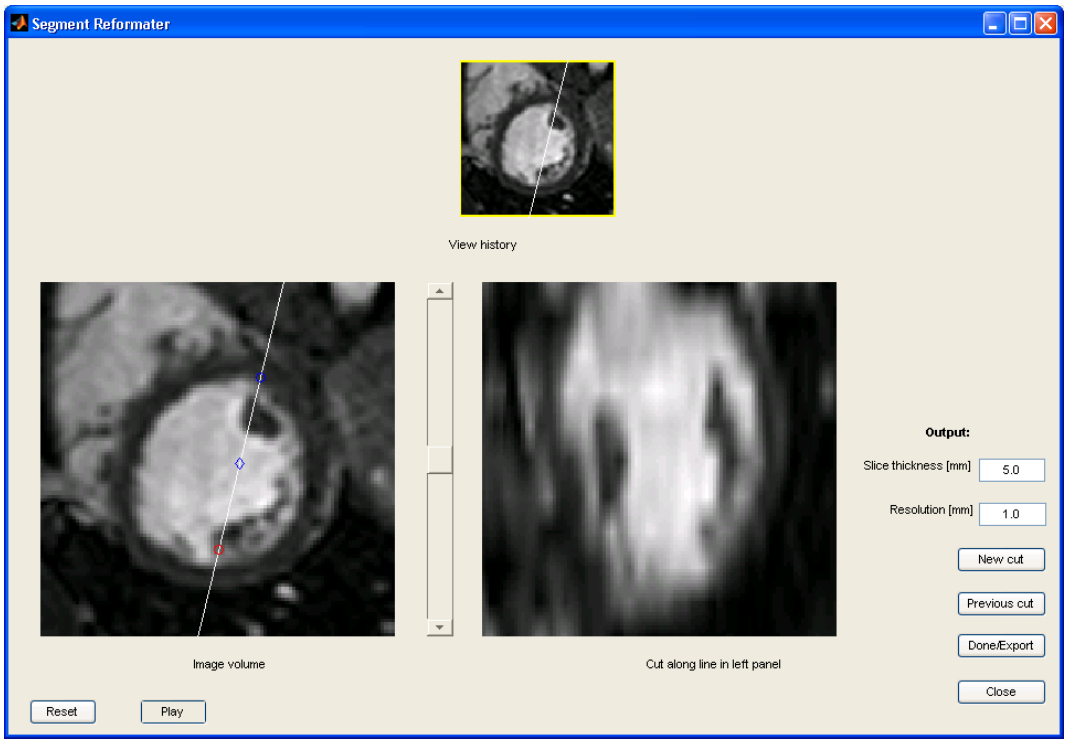


Figure 59: Image reformater GUI.

29 T2* Quantification Module

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

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 [11], quantification of iron overload and of the heart and liver in Thalassaemia major [12].

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

29.1 Module overview

An overview of the T2* quantification module is shown in Figure 60. 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.

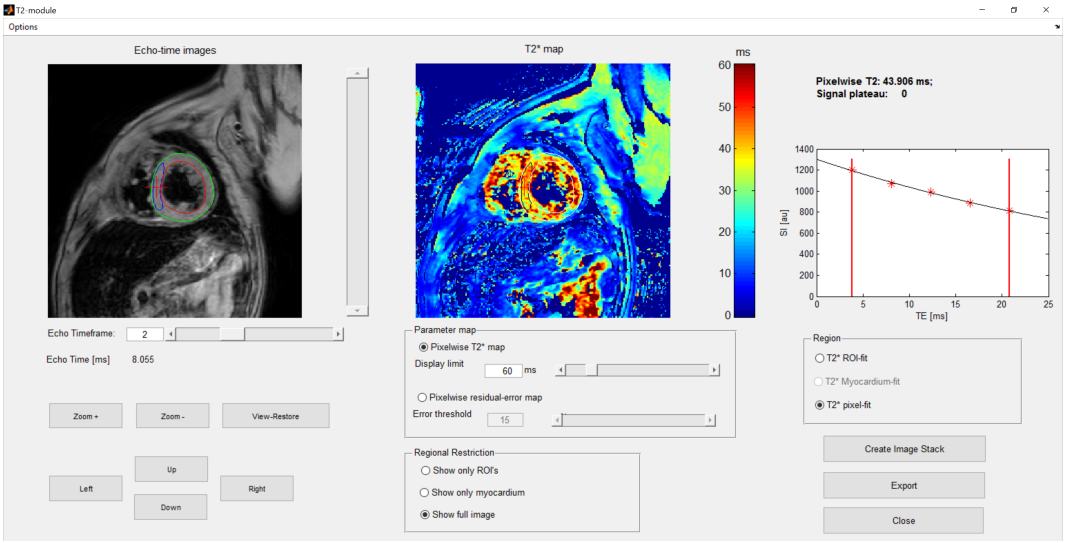


Figure 60: GUI for quantification of T2* values. The top left image panel shows the magnitude images for the different echo times, adjustable with the echo time slider. The right image panel shows the pixelwise T2* values.

The right lower panel shows the fittig 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.

If there are more than one ROI in the current image stack, you can select which ROI to perform analysis on in the T2* interface by go to the menu Options and Switch ROI for analysis.

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

29.2 Implementation

The detailed implementation of the T2* calculation in given in Chapter 43. In short the calculation is performed with standard exponential curve fitting that is calculated in the least square sense.

29.3 Validation

The module has been validated comparing to the open source software MRmap [13]. More validation details is available in a separate report from Medviso AB.

30 T2 Quantification Module

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

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 corresponds to finding the time constant of the exponential signal decay of refocused spin-echo imaging.

T2 changes have been shown to correlate with water content.

T2 values can be quantified by varying spin-echo times.

30.1 Module overview

An overview of the T2 quantification module is shown in Figure 61. 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.

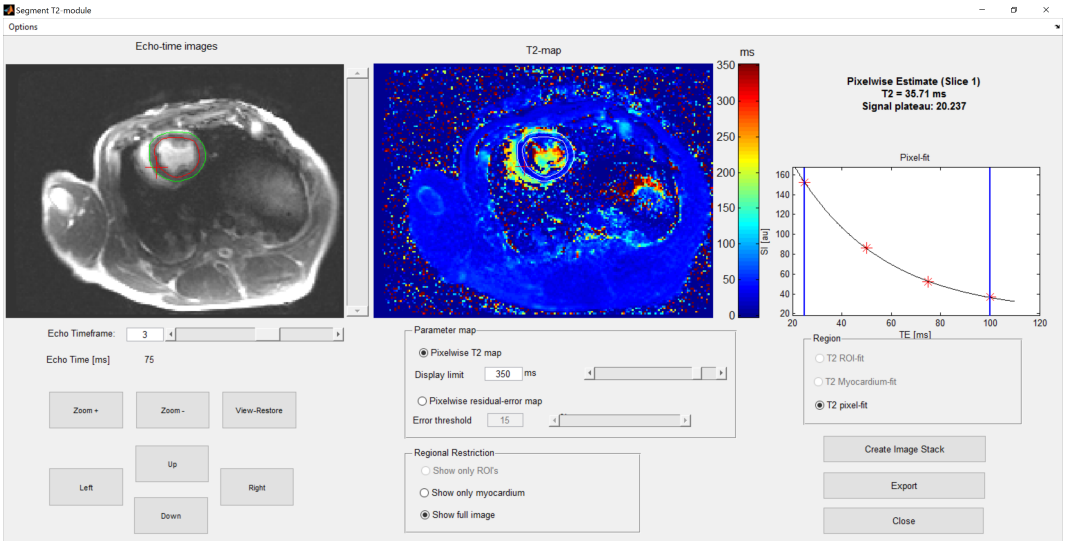


Figure 61: GUI for quantification of T2 values. The top left image panel shows the magnitude images for the different echo times, adjustable with the echo time slider. The right image panel shows the pixelwise T2 values.

The right lower panel shows the fittig 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.

If there are more than one ROI in the current image stack, you can select which ROI to perform analysis on in the T2 interface by go to the menu Options and Switch ROI for analysis.

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

30.2 Implementation

The detailed implementation of the T2 calculation in given in Chapter 43. In short the calculation is performed with standard exponential curve fitting that is calculated in the least square sense.

30.3 Validation

The module has been validated in an open access publication.

31 T1 Quantification Module

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

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 T1 Module is to quantify T1 relaxation times in MR imaging. Quantification of T1 values corresponds to finding the time constant of the exponential regrowth of longitudinal relaxation MR-signal strength.

T1 values can be quantified by varying inversion- or saturation-times.

31.1 Module overview

An overview of the T1 quantification module is shown in Figure 62. The top left image panel shows the magnitude images for the different inversion/saturation times. 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 T1 values.

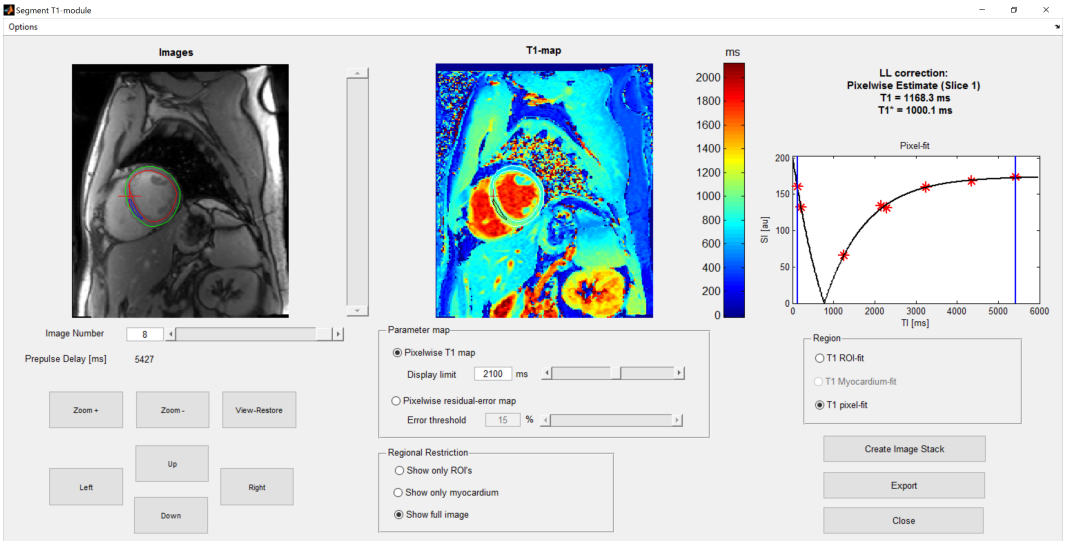


Figure 62: GUI for quantification of T1 values. The top left image panel shows the magnitude images for the different inversion/saturation times, adjustable with the inversion/saturation time slider. The right image panel shows the pixelwise T1 values.

The right lower panel shows the fittig curve over time. The mean T1 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 `T1 ROI-fit` or `T1 pixel-fit`. The T1 pixel-fit takes the T1 values according to the red cross in the right image panel.

If there are more than one ROI in the current image stack, you can select which ROI to perform analysis on in the T1 interface by go to the menu Options and Switch ROI for analysis.

T1 values can be exported to spreadsheet by using the Export button. To create the T1 image stack in the main GUI of Segment use the Create Image Stacks button.

31.2 Implementation

The detailed implementation of the T1 calculation in given in Chapter 43. In short the calculation is performed with standard exponential curve fitting that is calculated in the least square sense.

31.3 Validation

The module has been validated in an open access publication.

32 ECV Analysis Module

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

32.1 Automatic ECV analysis

1. Start with pre T1 map image stack(s) and post T1 map image stack(s). The ECV analysis can be performed for multiple image stack pairs or multiple slices in the same analysis. Make sure `Image Type` is correctly defined (`T1 map Pre` and `T1 map Post`). Otherwise set it according to Section 10.

2. Perform segmentation of the LV in one time frame in both pre and post image stacks as described in Chapter 11.

3. Place a ROI defining the blood pool in both pre and post image stacks and label it `Blood` as described in Chapter 16.

4. Optional: Define regions for ECV quantification by placing ROIs in the pre T1 map.

5. Select  . The post T1 maps are then aligned with to the pre T1 maps.

6. The result is presented in a new interface, according to Figure 63.

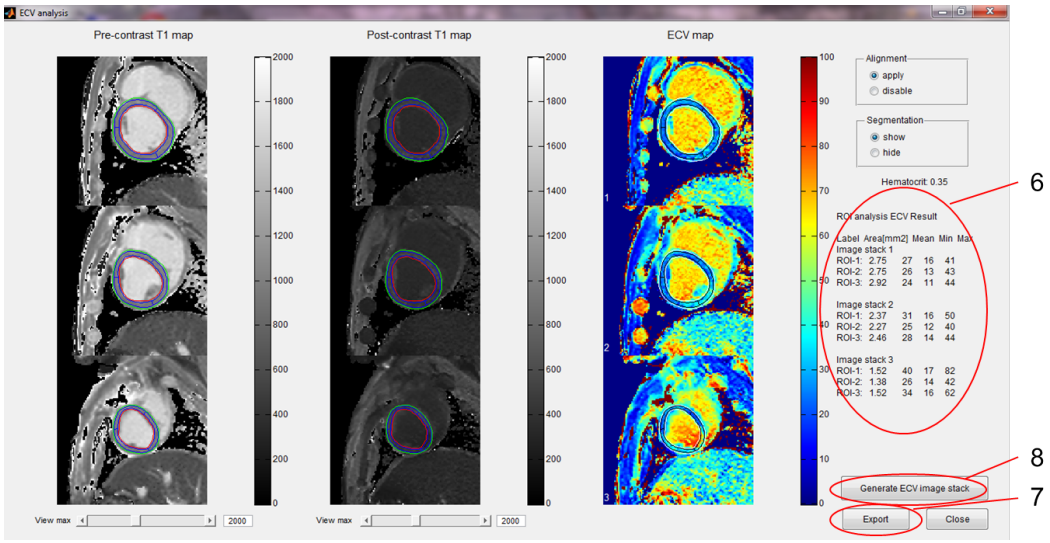


Figure 63: ECV analysis result.

7. Click on Export to export result to spreadsheet.

8. Click on Generate Image Stack to add the ECV map to the main GUI of Segment.

9. Bullseye of the ECV map can be obtained according to Section **??**.

33 SPECT Analysis Module

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

The SPECT Analysis Module is work in progress and therefore are not all automatic analysis tools currently freely available. The SPECT analysis module can be used in both gated and non-gated image stacks for analysis of left ventricular mass and volumes, quantification of stress-induced ischemia, myocardial infarction and myocardium at risk. To use the automatic analysis tools, the `Imaging Technique` has to be defined as NM.

33.1 Visualization

In addition to the regular view of image stacks within Segment there are two visualization views specific for SPECT images. By using Plot 2D View under the SPECT menu a seperate graphical user interface is opened with three short-axis slices (one basal, one midventricular and one apical slice) and horizontal and vertical long-axis projections. The user interface is shown in Figure 64. In the left panels the stress image stack are shown and in the right panels the rest image stack. For Segment to be able to identify the rest and stress image stack, the `Image Type` has to be defined as Perfusion Stress and Perfusion Rest, respectively. By using the + and - buttons in the lower panel the LV segmentation for each image stack can be manually corrected by include / exclude basal or apical SA-slices in the LV segmentation. For gated image stacks the visualization is time resolved and the left ventricular blood volume is illustrated as a curve over time to the right in the interface.

A three dimensional view of the counts within the LV myocardium is presented by using Plot 3D Surface under the SPECT menu. This will open a separate graphical user interface, shown in Figure 65.

33.2 Automatic segmentation of the left ventricle

The function Auto Delineate LV under the SPECT menu automatically segment the left ventricle in the current image stack. To use the function the image stack must fulfill the following requirements.

- The image stack need to be in short-axis projection.
- The "Number of points along the contour" must be greater then or equal to 50 (define in the Preferences menu).
- The slices have to be in the order basal to apex when go through the slices from the top to the bottom. If this requirement is not fulfilled use the function Flip z (also Flip in x) under Flip & Rotate→Image tools.
- The septal part of the heart have to be in the left side of the image.

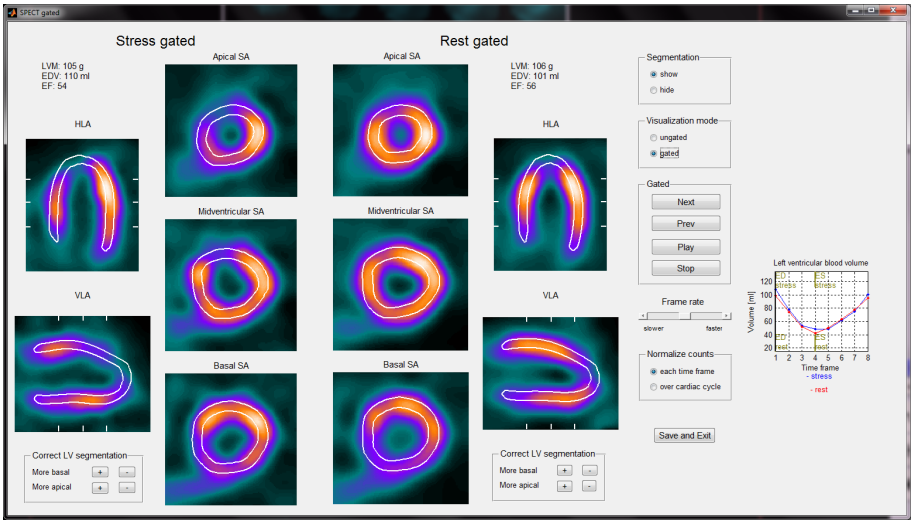


Figure 64: Graphical user interface of the 2 dimensional visualization for SPECT images.

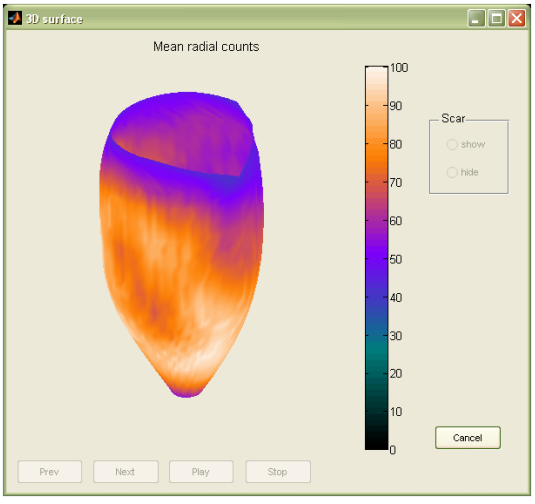


Figure 65: Graphical user interface of the 3 dimensional visualization for SPECT images.

A segmented left ventricle is shown in Figure 66. The endocardial segmentation is illustrated as red lines and the epicardial segmentation as green lines.

33.2.1 Manual corrections

If the results from the automatic left ventricular segmentation algorithm is not satisfying, the user can do manual corrections. This can be done in four ways:

- Crop the image stack using the icon  (find in the lower right panel in the main interface). If there are extra-cardiac activity this can affect the segmentation.
- Manually select short-axis slices for the LV segmentation. This is done by select the slices in question for the segmentation by using the icon  (find in the lower right panel in the main interface).
- Manually point out the center point of the left ventricle. Use the icon  (find in the lower right panel in the main interface) and place two points in the middle of the left ventricle in two different image slices. The program then adjust a center point line through all slices by adjusting a straight line to these two center points. It is important that it is just two points because otherwise the segmentation algorithm ignores them and automatically select center point.
- Manually change the finished segmentation with the pen for endocardium segmentation  and epicardium segmentation  .

33.3 Automatic quantification of myocardium at risk

To perform automatic segmentation of the myocardium at risk (MaR) in the segmented left ventricle use the function Auto Detect MaR under the Myocardium at Risk and SPECT menu. The MaR in the SPECT image are defined as a region with low intensity. The intensity limit that define the perfusion defect are set by the MaR preferences, as described in the next section. An example of outlined MaR are shown in Figure 66. From the segmentation, the MaR is quantified by percentage extent, absolute volume in ml, severity of the defect and total perfusion deficit (TPD). The TPD value includes both extent and severity of the MaR and ranges between 0 (no perfusion defect) to 100 (severe perfusion defect in the whole LV).

33.3.1 Define RV center

In order to calculate the TPD value for each of the sections of the LV supplied by the three main coronary arteries (LAD, RCA, and LCx), the placement of the right ventricle in relation to the left ventricle need to be defined. This is done by estimating the RV center straight to the left of the LV center. This estimation can then be corrected manually in the interface shown in Figure 67. The RV center definition is performed as one step in the quantification of myocardium at risk. In the interface, use the button "Set manually" to correct the RV center definition and the button "Confirm" when the RV center definition is sattisfying.

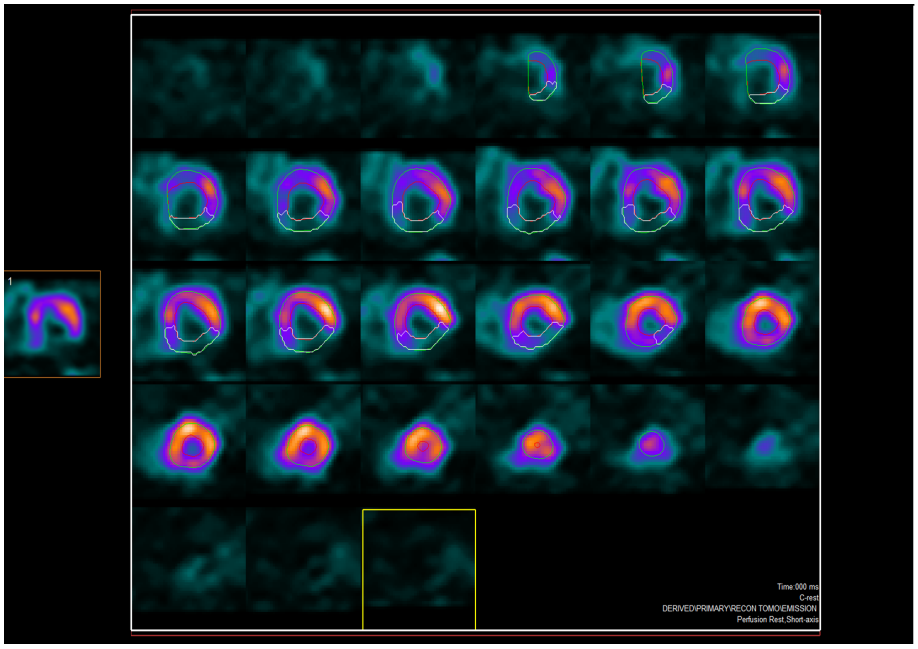


Figure 66: An example of a segmented left ventricle with myocardium at risk outlined. The red line is the endocardium, the green line the epicardium and the yellow line the perfusion defect.

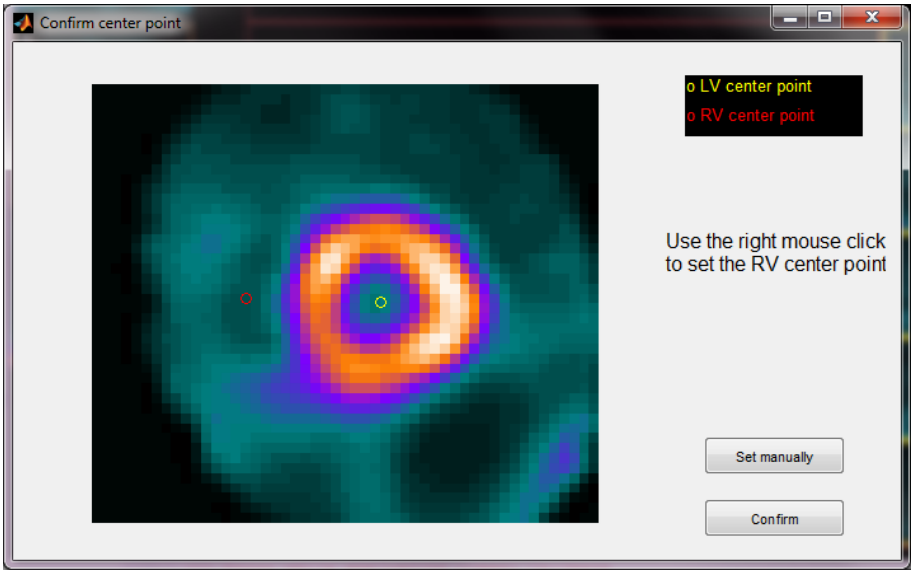


Figure 67: The interface for definition of the right ventricular center point.

33.3.2 Set preferences

The MaR preferences are set by the function Set MaR preferences under the Myocardium at Risk and SPECT menu. The preferences are set for each image stack which make it possibly to have different preferences for different image stacks.

The MaR preferences interface is shown in Figure 68. The choice made in the upper panel determine the region for which the count calculations are done in. The two selections are ROI (the default value) and Image. The Image selection include all pixels in the image in the defect calculation while the ROI selection only include the pixels within the LV segmentation in the calculations. The "Count Maximum" number is defining the percentile (the default value is 100%). The "Threshold" number is determined the percent of Count Maximum which defined a defect (the default value is 55%). All pixels with a count lower than this value are included in the MaR segmentation process. The "Minimum volume" number determined the smallest volume for a defect, expressed as percentage of the LVM (the default value is 10%). All defects with a volume smaller than this number are excluded from the MaR segmentation. The two selection for the subdivision of the LV used in the a priori model are the default model (based on normal coronary artery perfusion territories) and the standard 17-segment model. The choice in the lowest panel determine if the a priori model of the coronary distribution should be used in the MaR segmentation or not.

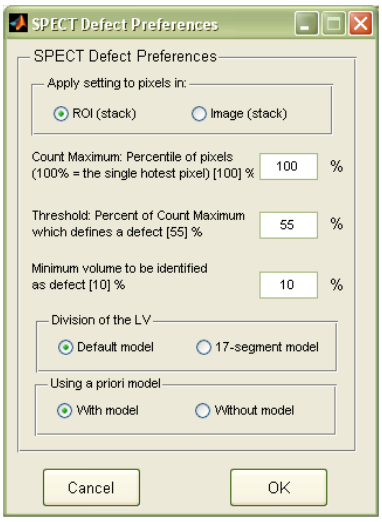


Figure 68: The MaR preferences interface.

33.3.3 Reset MaR

To reset the MaR quantification use the function Reset MaR under the Myocardium at Risk and SPECT menu. This function reset both the MaR segmentation and the MaR preferences for the current image stack.

33.4 Perfusion analysis

The automatic analysis of myocardial perfusion is work in progress and will be made freely available upon publication of these algorithms.

33.4.1 Automatic quantification of stress-induced ischemia and infarction

To perform automatic quantification of stress-induced ischemia and infarction both a rest and stress image stack need to be present. For Segment to be able to identify the rest and stress image stack, the `Image Type` has to be defined as Perfusion Stress and Perfusion Rest, respectively. The automatic quantification of stress-induced ishcemia and infarction in SPECT images is performed by two steps. First, an image registration is performed between the rest and the stress image stacks. Secondly, segmentation and quantification of the perfusion defects is performed by using the rest and stess counts, the stress-rest count change and the rest wall thickening (if a gated rest image stack is present). The following sections describe the two steps.

Image registration

The image registration between the rest and the stress image stacks is performed by use the function Auto Image Registration under the Perfusion and SPECT menu. The registration method is based on statistical optimization and the result can therefore vary slightly each time registration is performed on the same image stacks. To only show the registration result, use the function Show Image Registration under the Perfusion and SPECT menu. Figure 69 show the result by the automatic registration algorithm. From the interface, it is possibly to manually correct the registration by using the tools to the right in the interface. To reset the manual corrections and go back to the automatic registration, use the button "Reset registration" in the interface. To continue with the automatic perfusion analysis, use the button "Perfusion analysis".

Segmentation and quantification

The quantification of stress-induced ischemia and infarction is performed by using the function Auto Perfusion Analysis under the Perfusion and SPECT menu. A pre-request to perform perfusion analysis is image registration between rest and stress image stacks, as described in the previous section. Figure 70 illustrate the interface for showing the perfusion analysis result. The defect quantification is presented for both the rest and the stress study as well as for the stress-rest change. The rest defect is the quantification of myocardial infarction and the stress-rest change is the quantiafication of stress-induced ischemia. The defect quantifications are presented both as percentage extent of the LV, absolute volume in ml and by Total perfusion deficit (TPD). TPD is a measure of the perfusion defect including both the extent and the severity of the defect. It is presented for the whole LV as well as for each of the three coronary arteries (LAD, LCx, and RCA). To be able to calculate the TPD for LAD, LCx and RCA, the RV center need to be defined. This is done as described in the previous section "Define RV center".

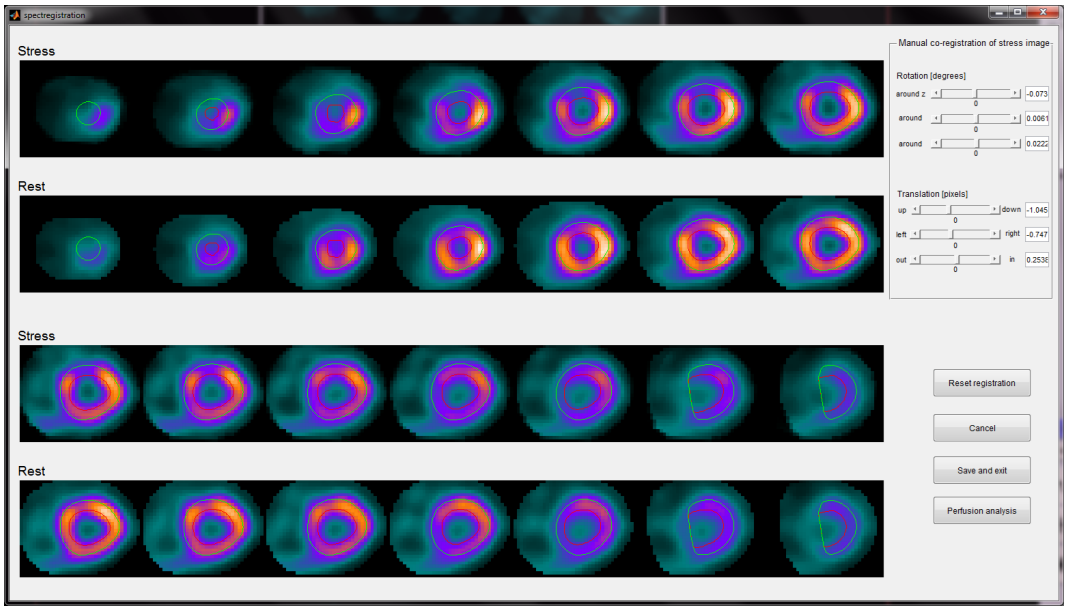


Figure 69: The rest-stress registration interface.

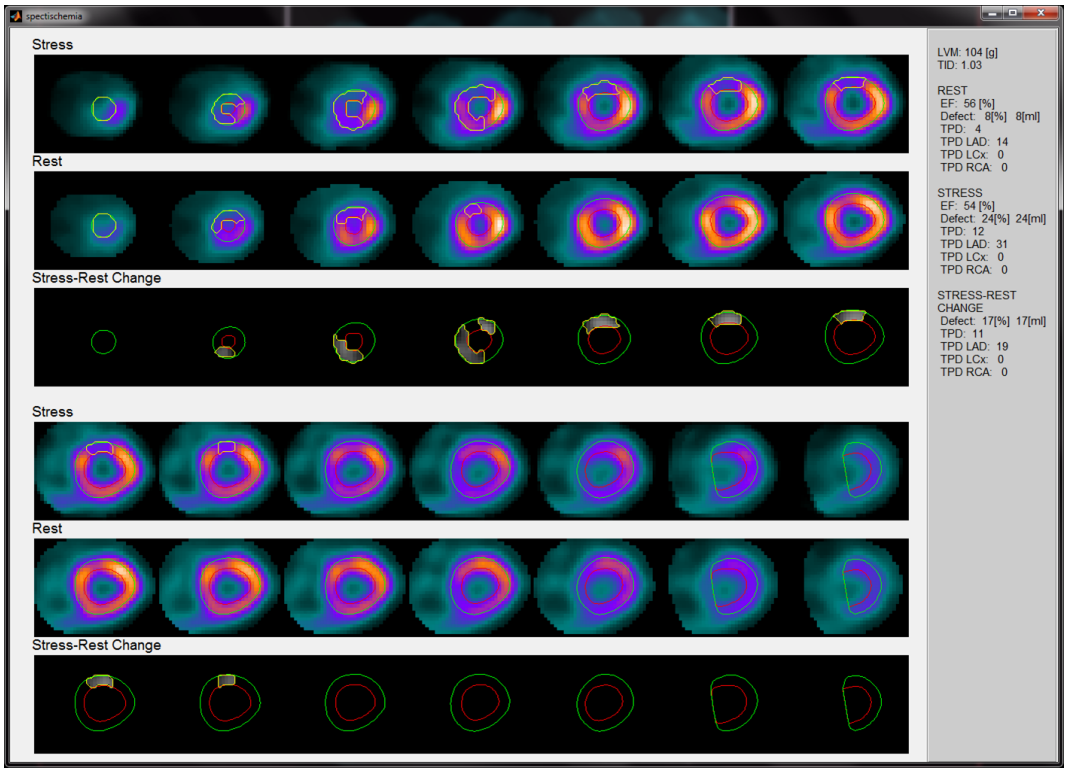


Figure 70: The perfusion analysis interface. The red line is the endocardium, the green line the epicardium and the yellow line the perfusion defect.

33.4.2 Automatic quantification of stress perfusion defect

When there is only a stress MPS image stack present, the perfusion analysis tool (Auto Perfusion Analysis under the Perfusion and SPECT menu) can only quantify stress perfusion defects. The automatic quantification is performed by using the counts in the stress image stack and the result is illustrated in an interface similar to the interface shown in Figure 70. The defect quantification is presented both as percentage extent of the LV, absolute volume in ml and by Total perfusion deficit (TPD). TPD is a measure of the perfusion defect including both the extent and the severity of the defect. It is presented for the whole LV as well as for each of the three coronary arteries (LAD, LCx, and RCA). To be able to calculate the TPD for LAD, LCx and RCA, the RV center need to be defined. This is done as described in the previous section "Define RV center".

33.4.3 Manual perfusion scoring

Segment provides an inferface for manual scoring of tracer uptake and myocardial infarction. The inferface is illustrated in Figure 71. The scoring is performed for each of the segments in the AHA 17 segment model. Summed scores are calculated for stress (SSS), rest (SRS) and stress-rest difference (SDS). There are two modes for the scoring, the first illustrating the rest and the stress ungated images and are for scoring of the tracer uptake. The scoring values should be between 0 and 4 as described to the right in the interface. The second scoring mode is found by choosing "gated" under the Visualization mode. This opens the interface for scoring the precens of myocardial infarction. For this pupose, the rest gated and ungated image stacks are used and the scoring values should be between 0 and 2 as described to the right in the interface.

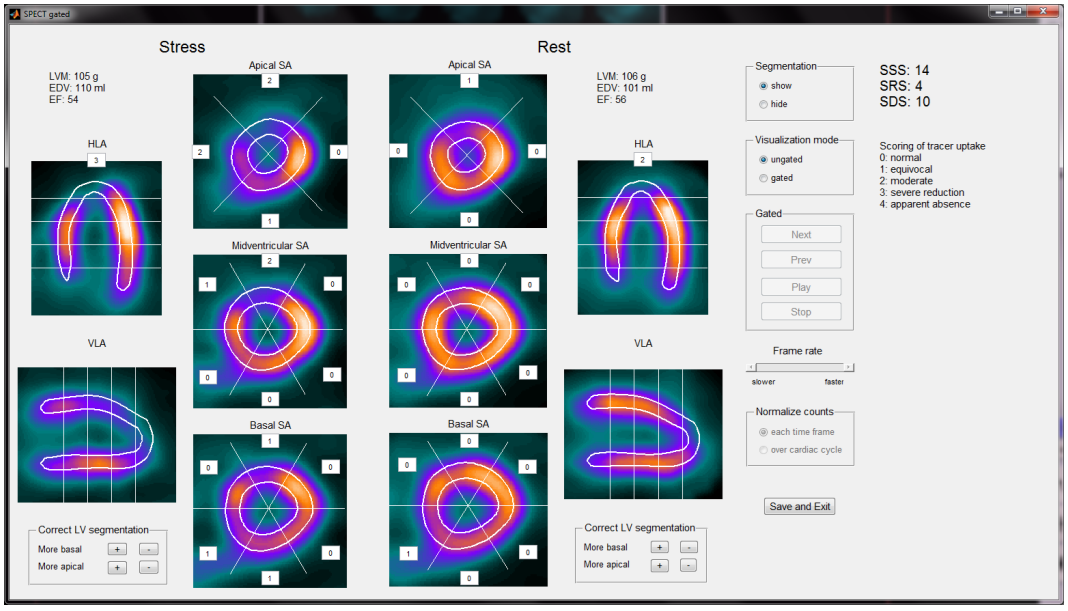


Figure 71: The perfusion scoring interface. The LV is divided into 17 segments accoring to AHA model.

34 Strain MITT module

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

If you only have access to the 1st Generation of Strain module, please refer to Chapter 35. For strain parameters defintions please refer to Chapter 34.6

34.1 Automatic strain analysis in short-axis image stacks

1. Ensure that `Image View Plane` is set correctly (`SAX`). Otherwise set it according to Section 10

2. **LV:** Perform LV segmentation. The LV segmentation should be performed in the end-diastole (ED) time frame in the cine image stack, according to Chapter 11.

3. **RV:** Perform RV segmentation. The RV segmentation should be performed in the ED time frame in the cine image stack, according to Chapter 12.

4. Ensure that `data type` found under STRAIN is correctly defined to ensure proper tissue tracking. Otherwise select a proper `data type` on the list shown in Figure 72).

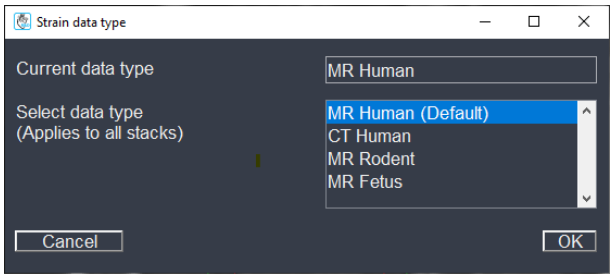


Figure 72: Strain data type interface.

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

6. If ED time frame is not the first time frame, a dedicated message window will pop-up. Accept moving ED time frame to the first time frame by clicking on Yes button.

7. The Strain interface is shown (Figure 73).

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

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

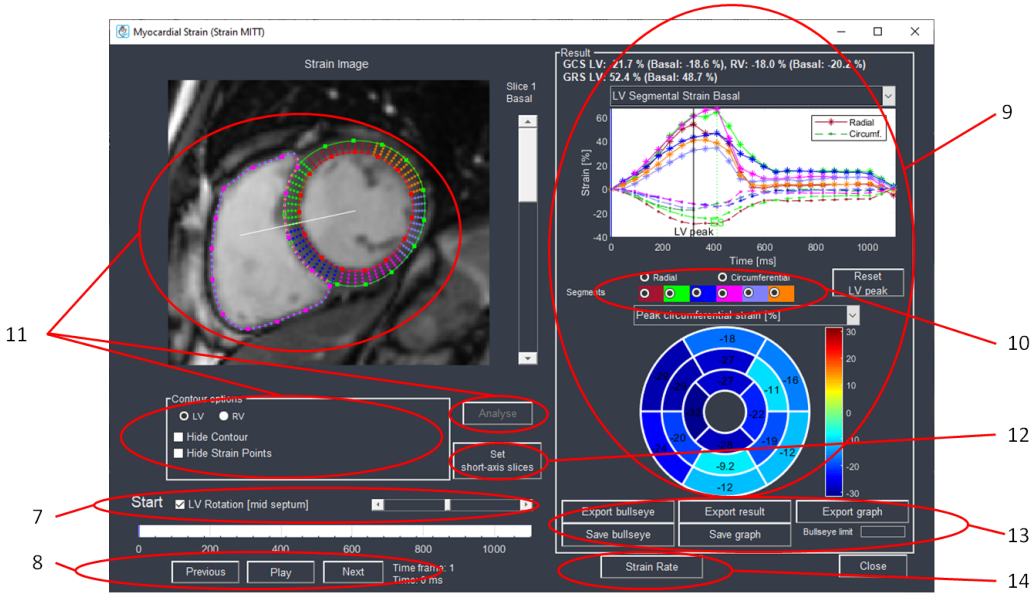


Figure 73: Strain analysis GUI.

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

11. The different curves in the graphs can be hided by using the radiobuttons below the graph.

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

13. Manually change the short-axis slices for the bullseye division by selecting Set short-axis slices.

14. Click on export buttons to export result to spreadsheet.

15. Click on Strain Rate to open Strain rate interface. Refer to Chapter 34.3 for details.

34.2 Automatic strain analysis in long-axis image stacks

1. Ensure that `Image View Plane` is set correctly (`2CH`, `3CH` and `4CH`), respectively. Otherwise set it according to Section 10.

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

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

4. **RV:** The RV segmentation should be performed in the ED time frame in the cine 4CH image stack, according to Chapter **??**. Set two annotation points to define the Tricuspidalis valve plane and name them TV plane, according to Figure 74. The annotation point tool is found under STRAIN [Z].(a)

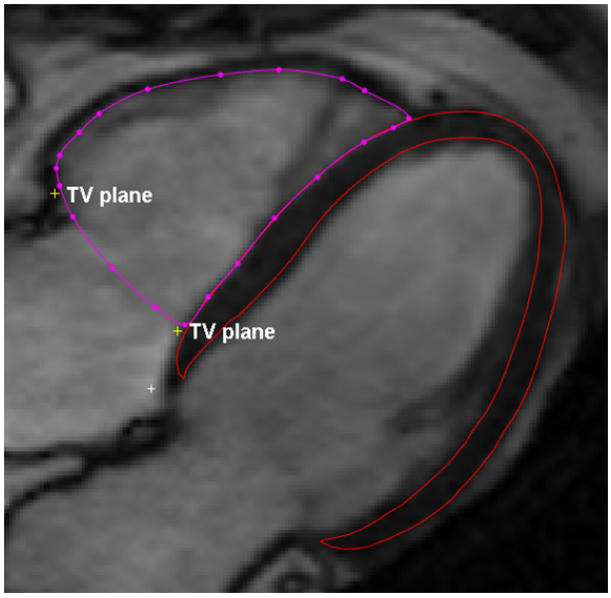


Figure 74: LV and RV segmentation in long-axis image stack.

5. Ensure that `data type` found under STRAIN is correctly defined to ensure proper tissue tracking. Otherwise select a proper `data type` on the list shown in Figure 72).

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

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

8. The Strain interface is shown (Figure 75).

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

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

11. The different curves in the graphs can be hided by using the radiobuttons below the graph.

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

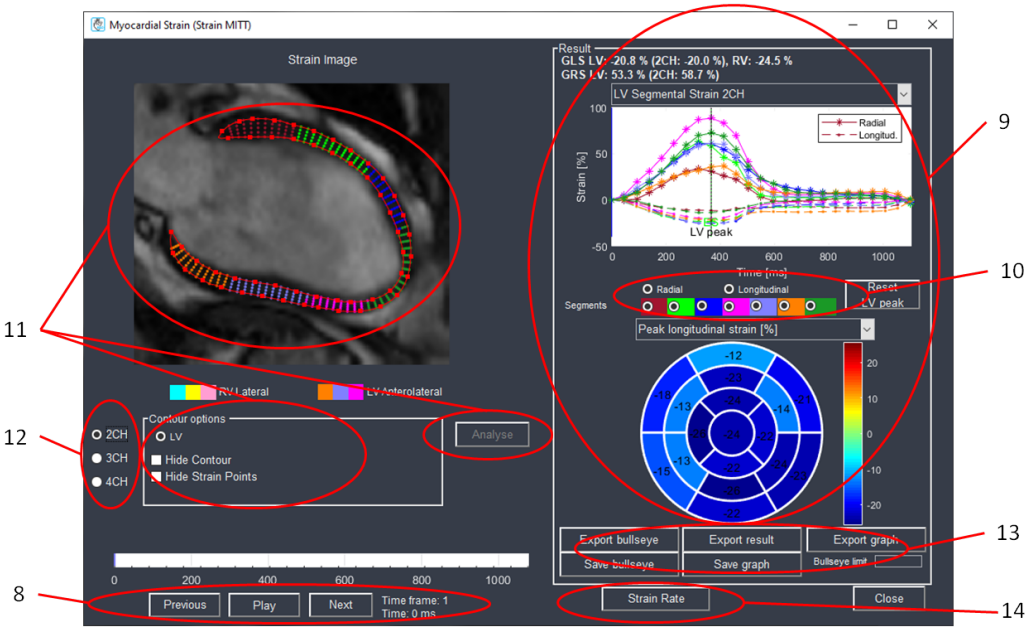


Figure 75: Strain analysis GUI.

13. Shift between the different long-axis views by using the radiobuttons below the images.

14. Click on export buttons to export result to spreadsheet.

15. Click on Strain Rate to open Strain rate interface. Refer to Chapter 34.3 for details.

34.3 Strain rate analysis

1. Perform strain analysis for SAX or LAX views according to Chapter 34.1 or Chapter 34.2 respectively.

2. Click on Strain Rate in the Strain analysis interface to open Strain rate interface. (Figure 76)

3. Inspect carefully strain rate peaks in Strain rate interface.

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

4. If needed, adjust *diastole* and *systole* strain rate marker by dragging and moving to another time frame.

5. Strain rate global values are shown in the summary table.

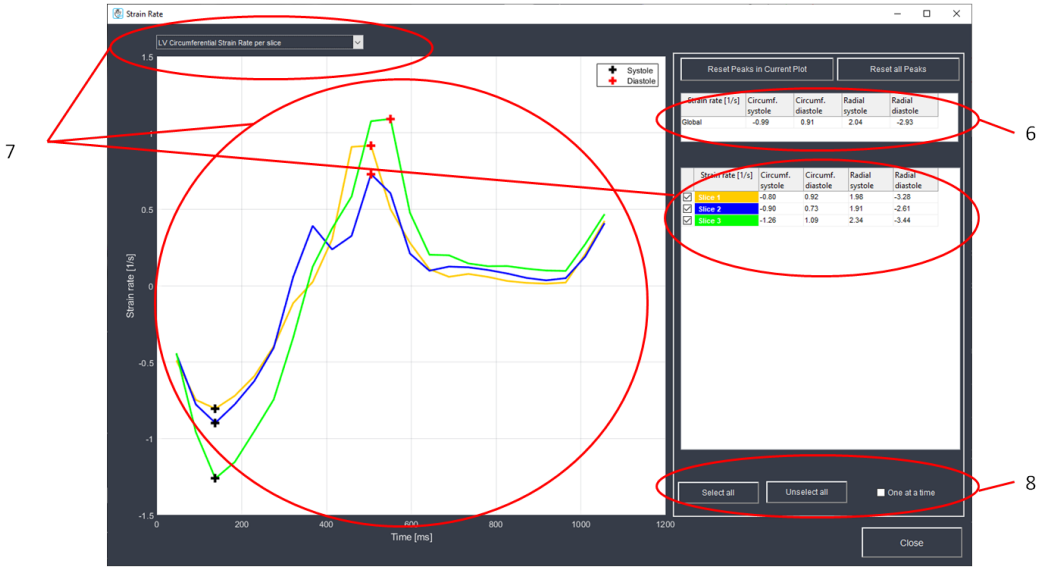


Figure 76: Strain rate interface.

6. Strain rate plots and Strain rate values are shown according to the selected parameter.

7. Strain rate values per segment are also presented on the bullseye diagram in the Strain analysis interface. (Figure 73)

34.4 Erase strain data

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

34.5 Strain export options

34.5.1 Patient exports

For exporting strain results and graphs for one patient, use the Export functions found in the Strain analysis interface numbered 10 in Figure 73.

34.5.2 Batch exports

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

34.6 Strain Analysis Module definition

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

34.6.1 Definition of Strain

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

34.6.2 Definition of Global strain

Global Strain is defined as the mean of all strain values within the entire chamber wall. The values for global Strain are expressed in [%]. Reported values for "GRS", "GCS" and "GLS" (global radial strain, global circumferential strain, global longitudinal strain respectively) are the values of global strain at the time point defined as the global peak time frame. The global peak time frame is the time point of peak strain for entire chamber wall by default. Illustrated in Figure 77. The 'Peak' marker can adjusted by dragging and moving to another time frame.

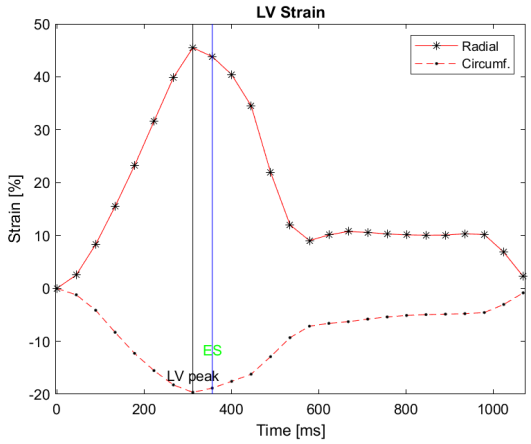


Figure 77: Illustration of strain at global peak time frame, which is the strain values at the vertical black line.

34.6.3 Definition of Time vector

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

34.6.4 Definition of Strain for slice/view

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

Strain are expressed in [%]. The global peak time frame is the time point of peak strain for entire chamber wall (as illustrated in Figure 77).

34.6.5 Definition of Strain plots

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

Strain plot

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

Strain for slice/view plot

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

Segmental Strain for slice/view plot

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

34.6.6 Definition of Strain bullseye plots

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

Peak circumferential/radial/longitudinal strain

"Peak circumferential/radial/longitudinal strain" is defined as the strain value for each segment at the time point defined as the global peak time frame. This is strain at the same time point for all segments. Illustrated in Figure 79. The *Peak* marker can adjusted by dragging and moving to another time frame.

Peak circumferential/radial/longitudinal strain at ES

"Peak circumferential/radial/longitudinal strain" is defined as the strain value in each segment at the ES time point. This is strain at the same time point for all segments. Illustrated in Figure 79. The *ES* marker can be adjusted by dragging and moving to another time frame.

34.6.7 Definition of Strain Rate

Strain rate is a rate of shortening of a length and it is defined as (1/L0)*(dL/dt) with L the instantaneous length and L0 is the baseline length in end-diastole. The values for Strain Rate are expressed in [1/s]. Strain Rate calculations are availble under Strain Rate. Strain Rate values are also presented in the bullseye diagram in the Strain window. Note: Before

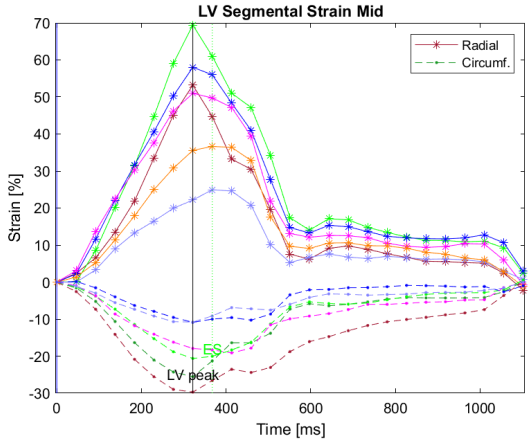


Figure 78: Illustration of Segmental strain at global peak time frame, which is the strain values at the vertical black line in each segment.

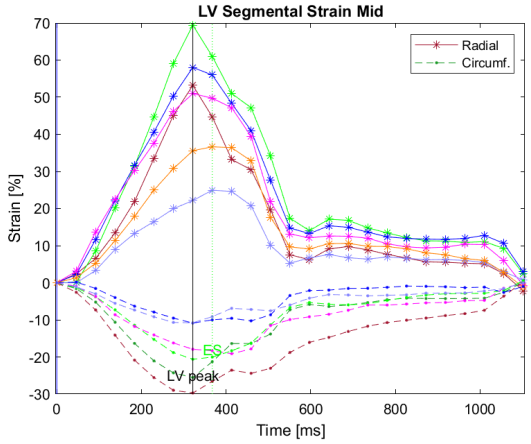


Figure 79: Illustration of Segmental strain at ES time frame, which is the strain values at the vertical green line in each segment.

diplaying Strain Rate in the bullseye diagram inspect carefully strain rate peaks in Strain Rate window.

34.6.8 Definition of Global Strain Rate

"Global Strain Rate" is defined as the mean of all strain rate values within the entire chamber wall at the diastole and systole peaks. The values for global Strain Rate are expressed in [1/s]. Strain Rate calculations are available under Strain Rate. Illustrated in Figure 80

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

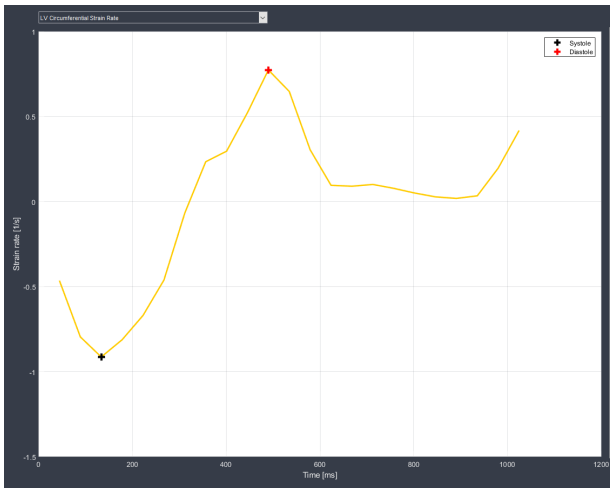


Figure 80: Illustration of diastole and systole strain rate, where systole strain rate is defined by the black cross and diastole strain rate is defined by the red cross on the plot.

34.6.9 Definition of Strain Rate plots

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

Strain Rate

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

Strain Rate per slice/view

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

Strain Rate per sector

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

34.7 Validation of strain analysis

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

Table 4:

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

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

35 Strain analysis - 1st Generation

35.1 Strain analysis in cine or tagged images

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

35.2 Automatic strain analysis in short-axis image stacks

1. Ensure that `Image View Plane` is set correctly. Otherwise set it according to Section 10
   Tagging: The correct label is `Tagging, SAX`
   Cine: The correct label is `Cine, SAX`

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

3. Start the automatic strain analysis.

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

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

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

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

4. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 81.

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

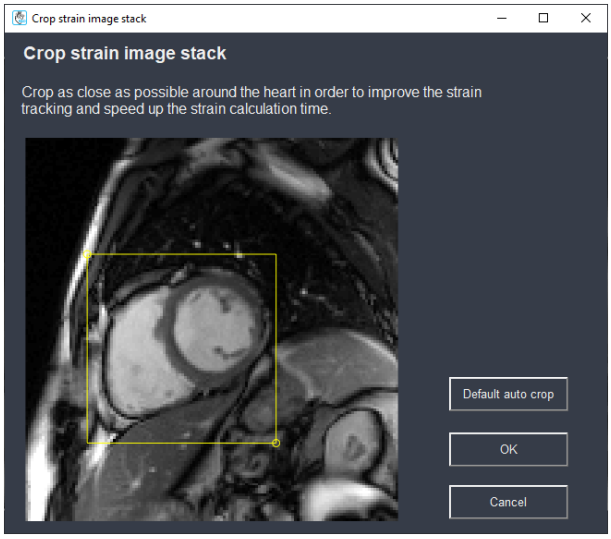


Figure 81: Strain cropping interface.

Cine: The segmentation should be performed in the first time frame in the cine image stack.
This time frame with segmentation will be the initial time frame for the strain tracking.
LV: Perform the LV segmentation according to Figure 82, using methods describe in and Chapter 11.
RV: Perform the RV segmentation according to Figure 82, using methods describe in Chapter 12.

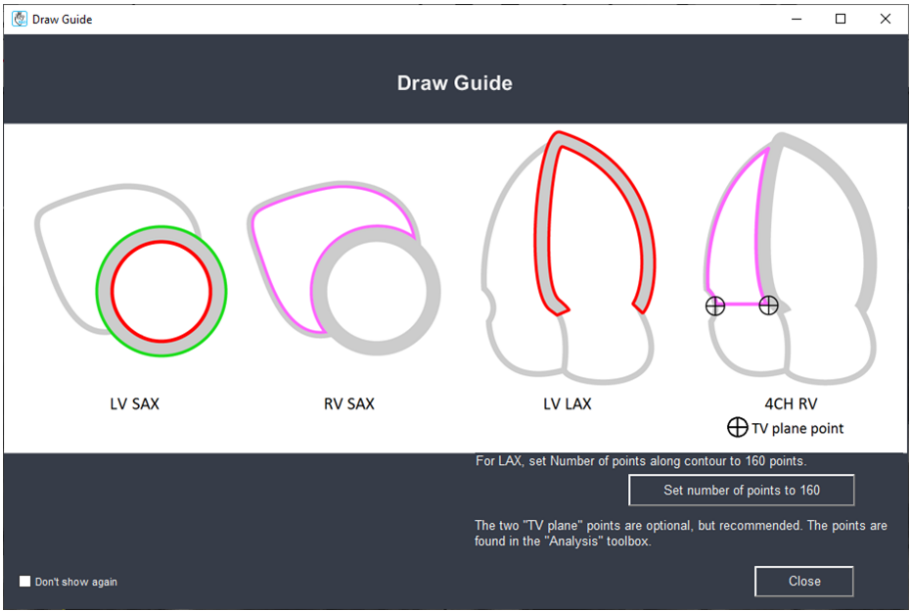


Figure 82: Strain drawing guidance.

6. When the registration and delineation is performed open the window with strain analysis. The Strain interface is shown (Figure 83).

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

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

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

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

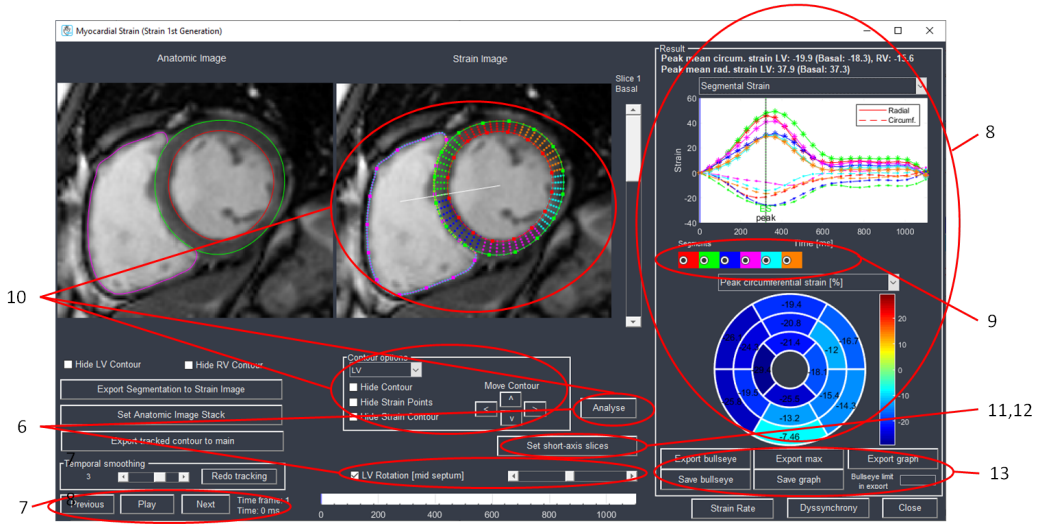


Figure 83: Strain analysis GUI.

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

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

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

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

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

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

35.3 Automatic strain analysis in long-axis image stacks

1. Ensure that `Image View Plane` is set correctly (`2CH`, `3CH` and `4CH`), respectively. Otherwise set it according to Section 10.
2. Ensure the end-diastole (ED) time frame is the first time frame (or close to), since the first time frame will be the base for the strain calculation and strain will be defined as 0 in this time frame. You can correct this by in Segment go to the time frame representing end-diastole, then select Set First Timeframe at Current Timeframe in menu Edit.
3. Start the automatic strain analysis.

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

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

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

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

4. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 84.
5. The automatic strain registration is then performed in the background. The progress is shown in a progressbar at the bottom of the main interface of Segment. During the registration process the user can perform segmentation. Before performing the segmentation, ensure that the parameter `Number of points along contour` in Preferences is set to at least 160, in order to have a smooth segmentation.
6. **Tagging:** The segmentation should be performed in one of the first seven time frames in the tagged image stack, or potential cine image stack.
   Cine: The segmentation should be performed in the first time frame in the cine image

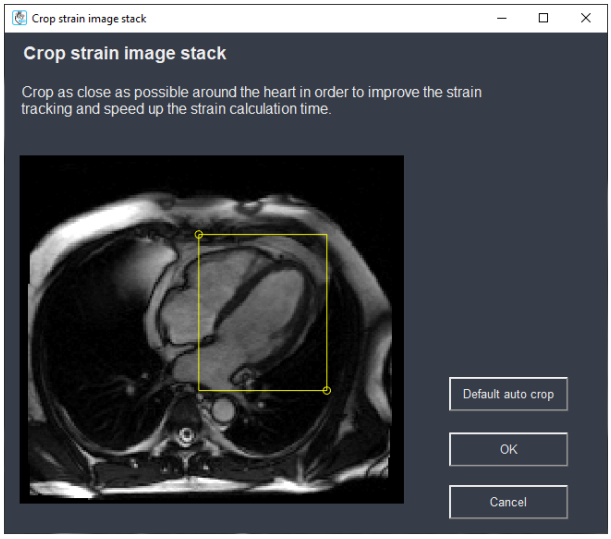


Figure 84: Strain cropping interface.

stack.
This time frame with segmentation will be the initial time frame for the strain tracking.
LV: Perform the LV segmentation according to Figure 85 by using the LV endo segmentation tools or in all three long-axis views.
RV: Perform the RV segmentation according to Figure 85 by using the RV endo segmentation tools or in the 4CH view. Set two annotation points to define the Tricuspidalis valve plane and name them TV plane. The annotation point tool is found under the Misc toolbox.

7. When the registration and delineation is performed open the window with strain analysis. The Strain interface is shown (Figure 86).

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

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

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

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

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

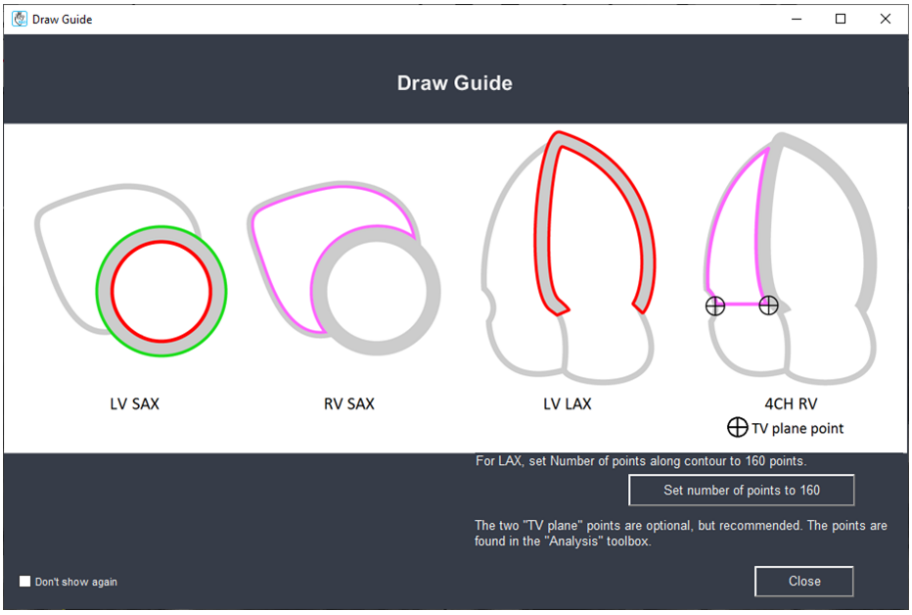


Figure 85: Strain drawing guidance.

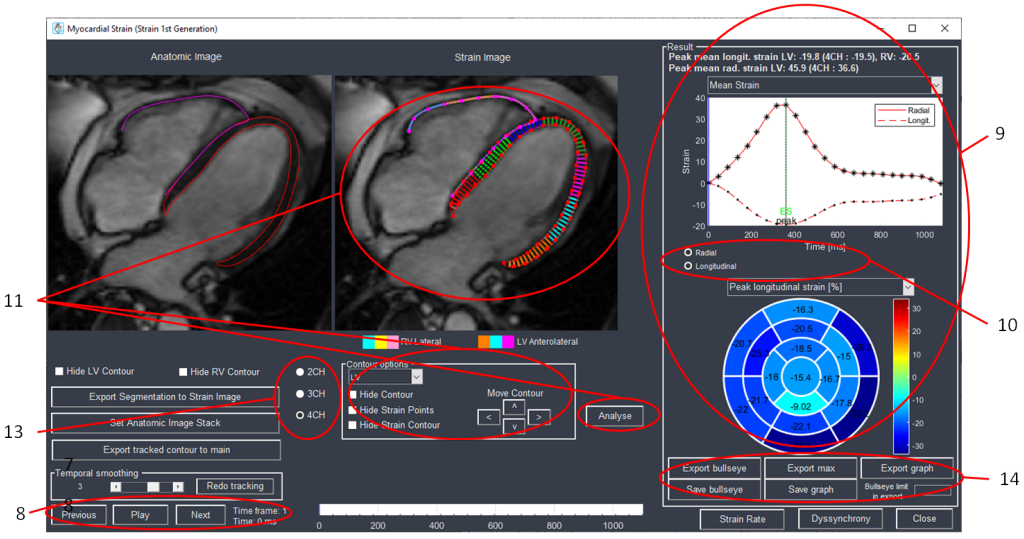


Figure 86: Strain analysis GUI.

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

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

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

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

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

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

35.4 Automatic strain analysis of the left atrium

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

1. Start with manually peform left atrial segmentation in the first time frame in the 4CH view using the  according to Figure 87.

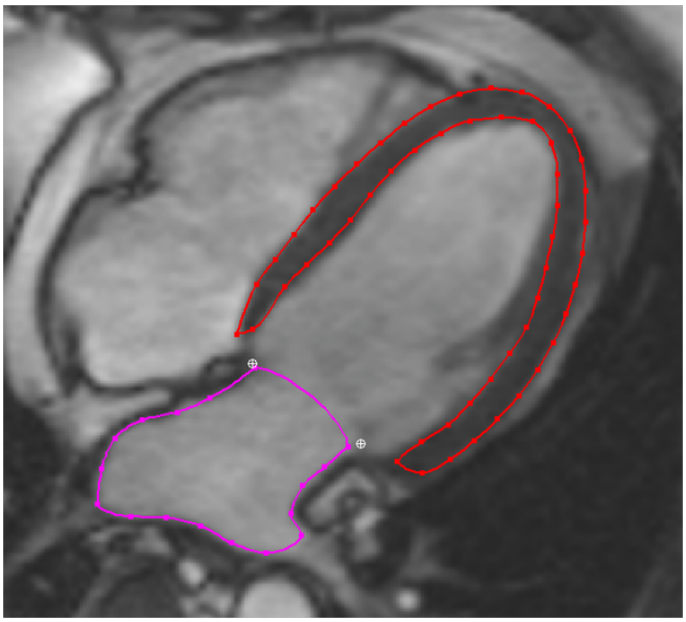


Figure 87: Segmentation of the left atrium to be used for strain analysis.

2. Ensure that `Image View Plane` is set correctly (`4CH`). Otherwise set it according to Section 10.

3. Start the automatic strain analysis.

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

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

4. When the registration and delineation is performed open the window with strain analysis. The Strain interface is shown (Figure 88)

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

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

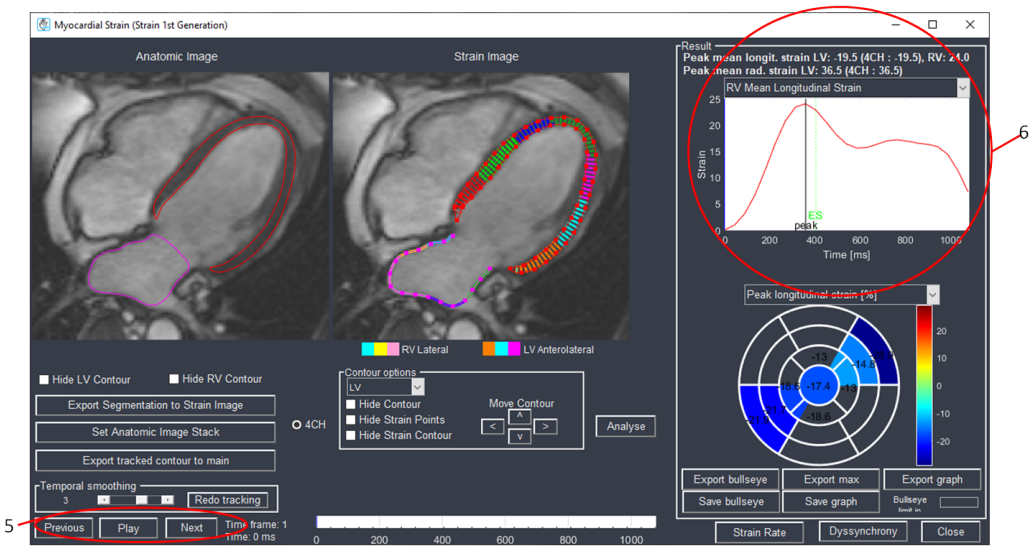


Figure 88: Strain analysis GUI.

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

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

35.5 Hints for Strain analysis in images of small animals

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

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

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

35.6 Erase strain data

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

35.7 Strain export options

35.7.1 Patient exports

For exporting strain results and graphs for one patient, use the Export functions found in the Strain analysis interface numbered 13 in Figure 83.

35.7.2 Batch exports

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

35.8 Strain parameters definition

This chapter presents definition of main strain results obtained in Strain 1st generation module, see chapter 35 for details on how to perform analysis.

35.8.1 Definition of Mean strain

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

35.8.2 Definition of Peak strain

Segmental strain at global peak time frame

"Segmental strain at global peak time frame" is defined as the strain value in each segment at the time point defined as the global peak time frame. This is strain at the same time point for all segments. Illustrated in Figure 89

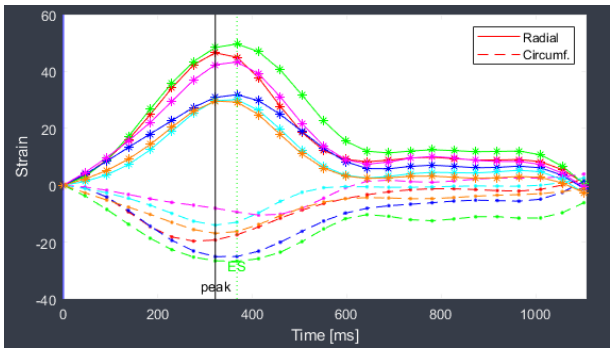


Figure 89: Illustration of Segmental strain at global peak time frame, which is the strain values at the vertical blue line in each segment.

Segmental peak strain for each segment

"Segmental peak strain for each segment" is defined as the peak strain for each segment. This could be strain at different time points for the different segments. In radial direction peak is defined as the maximal value and in longitudinal/circumferential direction peak is defined as the minimal value. Illustrated in Figure 90

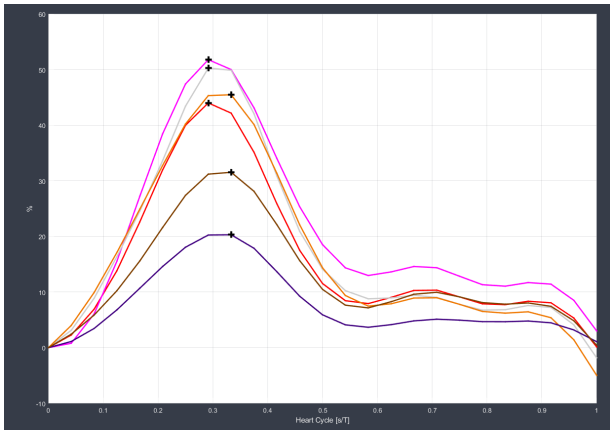


Figure 90: Illustration of Segmental peak strain for each segment, which is the peak strain in each segment defined by the black cross in the images.

35.9 Rotation

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

35.9.1 Implementation details

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

36 Image Fusion Module

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

Details of this Fusion Module is given in Ugander et al [14].

The image fusion tool is used to compare and fuse one anatomical and one functional image stack. Currently the tool is restricted to rigid body translation and rotation.

An example of the fusion GUI is shown Figure 91. The leftmost panel is the anatomical image stack, the middle the functional image stack and the rightmost the fusion image stack.

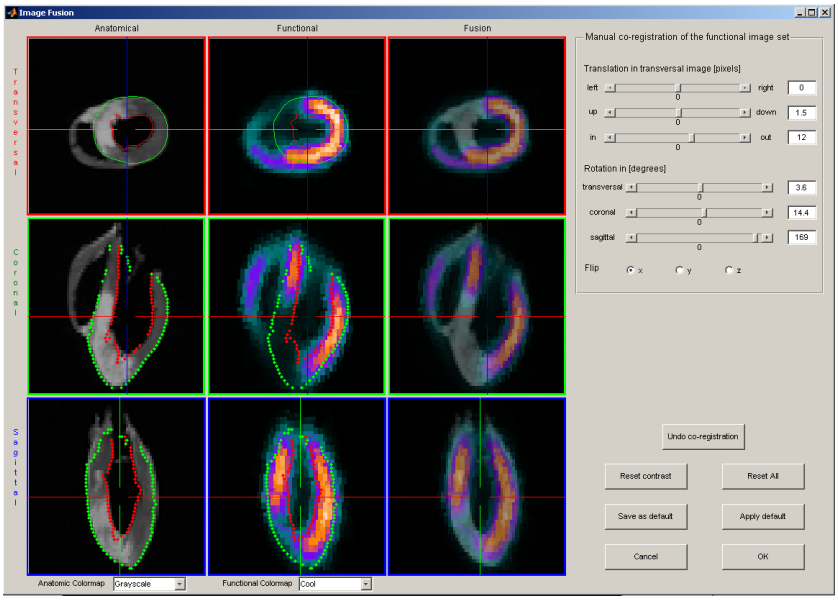


Figure 91: Example of the image fusion GUI.

To start the fusion tool select Fusion of Two Image Stacks under the Fusion menu. You will then be prompted for which anatomical and functional image stacks to fuse. You select by entering a number that are the same as the thumbnail order (from left) in the main Segment GUI. If the anatomical image stack contains a segmentation this will be shown both in the anatomical and the functional image stack.

Below each image stack the user can manually select color map. The two selections are gray and cool and can be different for the two image stacks. To change the transparency in the fusion image stack hold the right mouse button down and move up or down. In the anatomical and functional image stack the right mouse button will change the brightness

(up/down) and contrast (right/left). Click on the left mouse button define the current slice in the image stack. Same slices are always shown in anatomical and functional image stack. The arrow buttons on the desktop can then be used to step in the slices in the last clicked image. If the last click was in one of the co-registration sliders the arrow key buttons will change the position of the slider.

The manually co-registration of the functional image stack is done by changing the parameters in the right box in the GUI. The three sliders and editboxes on the top translate the image stack. The sliders and editboxes in the middle make a rotation in the image stack. The three radiobuttons below the sliders flip the image stack in x- y- and z-direction, respectively.

The Undo co-registration button undoes the last translation or rotation. It also undo the Reset all button. This button reset both co-registrations, colormaps, current slices, contrast and brightness in all image stack to the start values. The Reset contrast button only reset contrast and brightness in the anatomical and functional image stack, and the transparently in the fusional image stack to initial values.

If you need to fuse many data-sets with approximately the same parameter settings, the default buttons can be helpful. The Save as default button saves the current translation, rotation, flip and colormap choices. These settings are then available to use on another data-set. The settings are applied to the image stack by using the button Apply default.

When you are satisfied with the fusion use the Ok button. This results in a new image stack with image type "Fused" and contains the functional images stack, with the anatomical image stack size, and the segmentation from the anatomical image stack. Example of such an image stack are shown in Figure 92. The parameter settings are also saved and the fusion GUI with the old parameter choices can be open again by select Fusion of Two Image Stacks under the Fusion menu when having an image with image type "Fused" selected. When an image stack with another type than "Fused" is selected, a new fusion GUI always open. Pushing the Ok button in the fusion GUI always result in a new fused image stack.

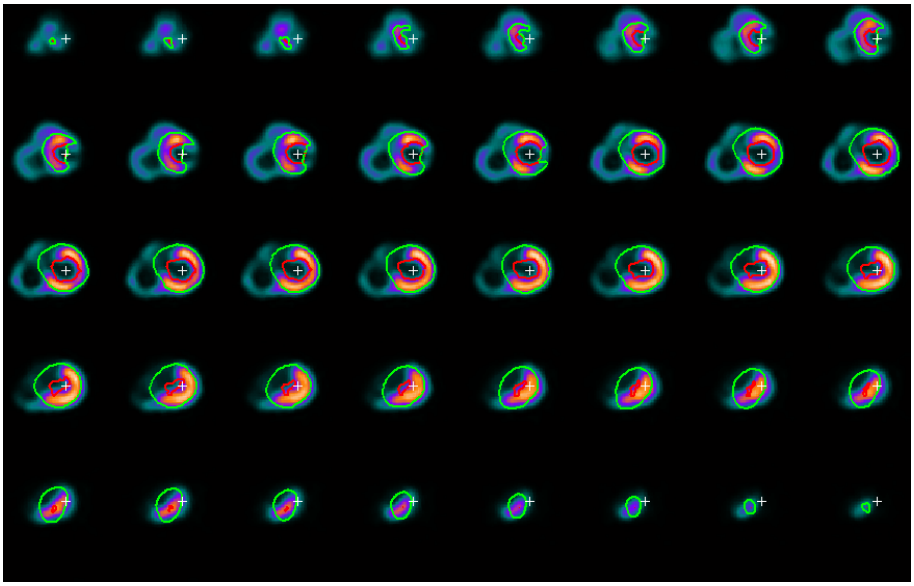


Figure 92: Example of a fused image stack.

37 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.

37.1 Perfusion upslope analysis

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 93. 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.

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 94. 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.

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 mea-

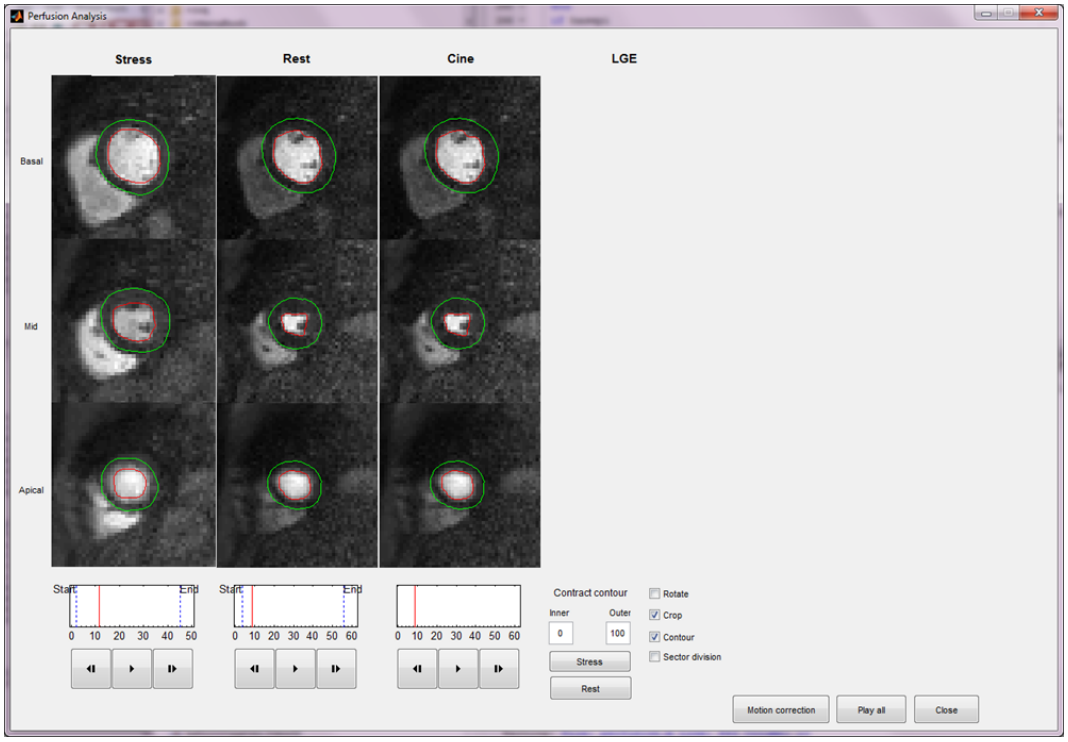


Figure 93: GUI for perfusion analysis.

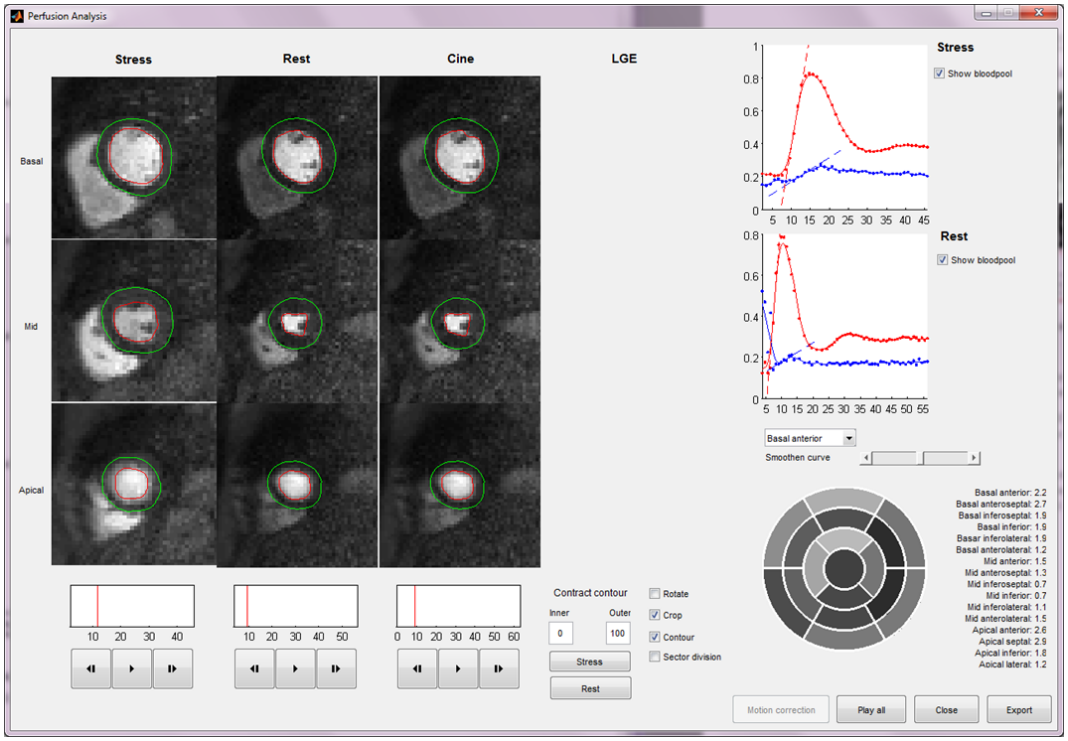


Figure 94: GUI for perfusion analysis after motion correction.

sured 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 bloodpool 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 upslopes, normalized with respect to the respective maximum upslopes of the bloodpool curves. The quote values are also shown in text next to the bullseye plot, and can be exported to a spreadsheet by clicking the Export button.

37.2 Perfusion scoring

Rest and/or stress perfusion image stacks can be manually scored using the integrated perfusion scoring tool.

1. Start with a rest image stack and a stress image stack. Make sure `Image Type` is set correctly (`Perfusion Rest` and `Perfusion Stress`). Otherwise set it according to Section 10.
2. Start the perfusion module by selecting under ANALYSIS [A] (h).

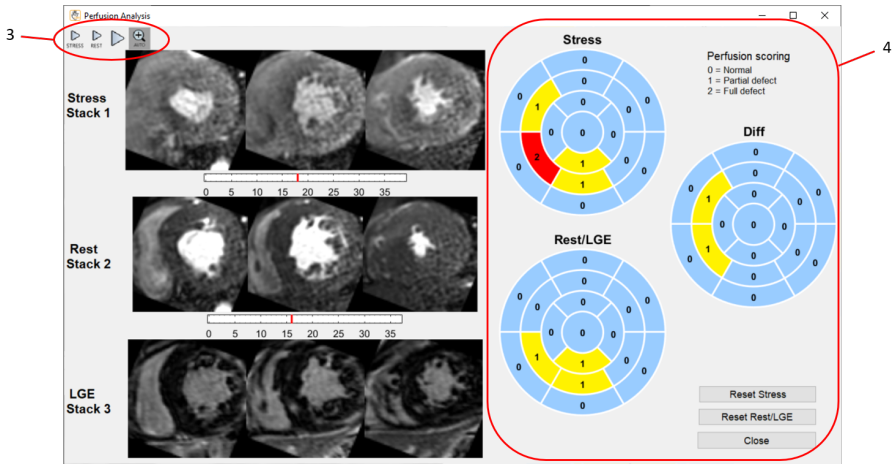


Figure 95: Perfusion analysis GUI.

3. Use the play icons to play a movie of the perfusion image stacks.
4. Click in the bullseyeplots for manual scoring of stress perfusion and rest perfusion.

37.3 Gadgetron perfusion analysis

Perfusion image stacks that are in-line post-processed with the image reconstruction software Gadgetron, can be loaded and displayed in Segment.

- The quantitative perfusion results from the Gadgetron data set can be exported from Segment using the feature Export All Gadgetron Data under the menu Analysis.

- Perfusion values can also be obtained directly in the Gadgetron image stack by perform ROI analysis in Segment according to Chapter 16. Note that the ROI must be drawn in the Gadgetron image stack that have an integrated colorbar, as shown in Figure 96.

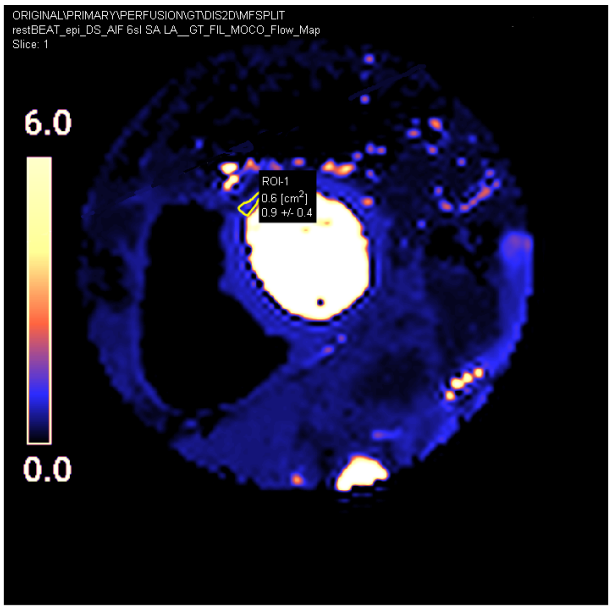


Figure 96: Gadgetron image stack where to perform perfusion ROI analysis.

38 Report Module

This functionality is only available as an additional commercial module to Segment.

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 97. 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 98.
- 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.

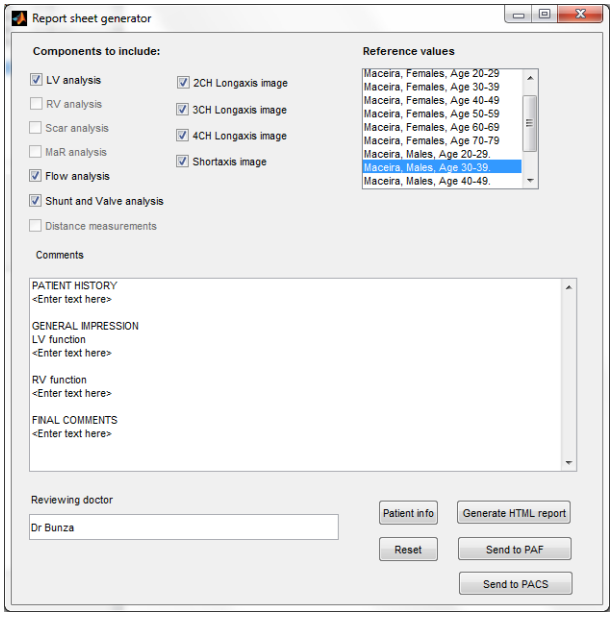


Figure 97: GUI for patient report generator.

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.
- Shunt and Valve analysis, this section contains the Qp/Qs ratio and regurgitant volumes and fractions for the mitralis and tricusp, 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.

38.1 Configuration

This section describes how the Report Module can be configured.

38.1.1 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 is installed.

38.1.2 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.
...
```

38.1.3 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:

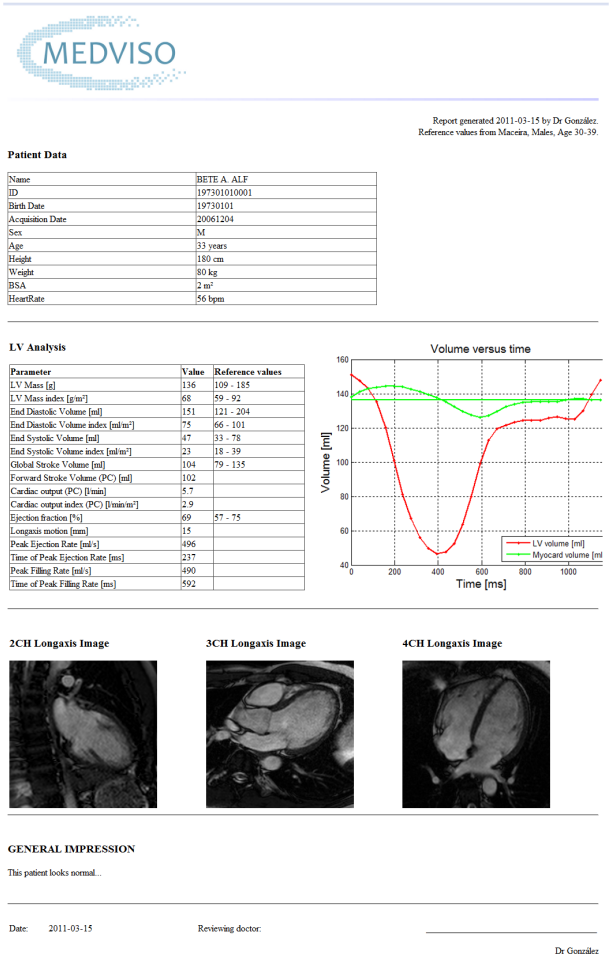
- To divide the text into paragraphs, enter a blank line between the text blocks to be used as paragraphs.
- To start a paragraph with a headline in bold print, simply begin the paragraph with the text to be used as headline, then insert a new line where the text body is entered.
- To insert a super 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.

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>
```

38.1.4 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.



MEDVISO

Report generated 2011-03-15 by Dr González.
Reference values from Maceira, Males, Age 30-39.

Patient Data

Name	BETE A. ALF
ID	197301010001
Birth Date	19730101
Acquisition Date	20061204
Sex	M
Age	33 years
Height	180 cm
Weight	80 kg
BSA	2 m²
HeartRate	56 bpm

LV Analysis

Parameter	Value	Reference values
LV Mass [g]	136	109 - 185
LV Mass index [g/m²]	68	59 - 92
End Diastolic Volume [ml]	151	121 - 204
End Diastolic Volume index [ml/m²]	75	66 - 101
End Systolic Volume [ml]	47	33 - 78
End Systolic Volume index [ml/m²]	23	18 - 39
Global Stroke Volume [ml]	104	79 - 135
Forward Stroke Volume (PC) [ml]	102	
Cardiac output (PC) [l/min]	5.7	
Cardiac output index (PC) [l/min/m²]	2.9	
Ejection fraction [%]	69	57 - 75
Longaxis motion [mm]	15	
Peak Ejection Rate [ml/s]	496	
Time of Peak Ejection Rate [ms]	237	
Peak Filling Rate [ml/s]	490	
Time of Peak Filling Rate [ms]	592	

2CH Longaxis Image

3CH Longaxis Image

4CH Longaxis Image

GENERAL IMPRESSION

This patient looks normal...

Date: 2011-03-15 Reviewing doctor:

Dr González

Figure 98: Example of a report.

39 Short Commands / Hot keys

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

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-plus`	Zoom in
`Ctrl-minus`	Zoom out

Segmentation commands

- 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 -	
`O`	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
`Ctrl-O`	Load image stack
`Ctrl-P`	Open patient data base
`Ctrl-0 (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)

40 How to Reference the Software

To be permitted to use the software for research purposes you need to reference the usage of the software properly. This is very important since it is necessary that we can prove to granting organisations that this project returns scientific output and has a significant impact to the scientific community.
A reference should encompass both the name and version of the software, **and** a reference to the suitable scientific publication about that function in Segment. It should also be indicated that the software is free for research purposes, and the address homepage of the software (`http://segment.heiberg.se`).

You should reference the software differently depending on what part of the software that have been used. This list is subject to change after submitted papers are accepted. *Always* check the website https://medviso.com/how-to-refer/ for the latest information about proper references. In doubt, please do not hesitate to contact us at support@medviso.com, or place the generic Segment reference [15].

Note that referencing the software is mandatory also for short abstracts to scientific conferences. In case of shortage of space, please reference the software as something like:

... Images was analyzed using the freely available software Segment (`http://segment.heiberg.se`).

In extreme shortage of space, such as conferences where the word limit is < 350 words then reference may be omitted in the abstract text, but should be included in the oral presentation and / or poster.

40.1 Examples of possible formulations

- *... Infarct size were determined using Segment v4.0 R12067 (`http://segment.heiberg.se`) [2].*
- *... Image analysis was performed using the freely available software Segment v4.0 R12067 (`http://segment.heiberg.se`) [15].*

41 Support

On Medviso website you find solutions to the most frequently asked questions on the page https://medviso.com/faq/.

If you have any questions or support requests about our software products, please send us request to support@medviso.com.

We love to get feedback and are happy to hear from you about new software feature request and any potential question or software issue. We see our users as collaboration partners and always do our best to meet your requests. You can at any time upgrade to the latest software version found at our download page. Our unique software development platform allows us to have a quick turnaround time and provide updated software versions in a short time.

41.1 How to make a support request

If the support request is related to a data set, the easiest way to send us a support request is to use the Support Request feature under the Help menu in the software. Fill in the form and do not forget to attach the DICOM / .mat-file associated with the support request. You can also send your support questions to support@medviso.com. As applicable, please include the following:

- Issue description
- Error log
- DICOM data
- Analyzed files (.mat-files)

Even though the submitted files are encrypted your files should be pseudonymized. Pseudonymization of `.mat` files and DICOM files are available under the Utilities menu. If you have large data files to attach, you can send the data with Medvisos ftp account or file sharing services such as Dropbox, WeTransfer, etc. Email us to support@medviso.com for getting login details to our FTP server.

41.2 Additional support

As we have several hundreds of research group using the software daily, the time for supporting the free research only version of Segment is limited. However, we encourage all users to submit any possible questions or problems and we'll try our best to help out. Researchers can purchase an academic support contract for additional software support. Please contact sales@medviso.com for further details or to request a quote.

42 Plugins

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

In Segment it is possible to create own plugins and extensions. This is further described in [15] and the Technical Manual. Currently there are two plugins that are shipped with the stand-alone version of Segment.

42.1 Image Loader Plugin

The image loader plugin is used to load diffrent kinds of images into segment. The plugin currently supports the following image formats.

- JPEG (*.jpg)
- PNG (*.png)
- TIFF (*.tif)

There are two diffrent ways of loading images in the image loader plugin. The first way, called Load single file, load a single image file in a new image stack. The second way, called Load files from directory, loads all files in a directory and places them in a single image stack. The images are ordered according to filename and placed in z-depth.

Some information, such as resolution, that exist in dicom files are not present in these general image formats. The image loader plugin will simply guess on default values for these values. Sometimes one can use the calibrate plugin to set the resolution to a correct value.

42.2 Image Calibration Plugin

Sometimes the correct resolution for an image stack isn't known. However if one knows the area of some region of the image beforehand one can calculate the correct resolution. This plugin helps one do that.

When loading the plugin one is presented with a red square. By moving the corners of the square one can select the region. One is also presented with a input box where it's possible to enter the area of this region. When pressing the ok button the plugin calculate the correct resolution and updates the image stack accordingly. Note that this plugin assumes isotrope images.

43 Implementation Details

In this chapter implementation details for Segment are given.

43.1 Version handling

A proper version handling is employed when developing Segment. A detailed version history of Segment is found in the revision log of Segment SVN.

43.2 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.

43.3 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 depent 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 working 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 calculaion, 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 (horisontal 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 interpretated involvs proprietry information of different scanner vender 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.

43.4 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 :

$$\delta V = \frac{\pi}{2 * Z} \int y(s)^2 \texttt{sign}(y(s)) \frac{dx}{ds} ds \tag{1}$$

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.

43.5 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.

43.6 Calculation of BSA

The formula used is based on Mosteller.

$$BSA = \sqrt{\frac{w * h}{3600}} \tag{2}$$

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

43.7 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.

43.8 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:

$$WT_f = \frac{WT - WT_{ED}}{WT_{ED}} \tag{3}$$

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.

43.9 Calculation of regurgitant volumes and shunts

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

$$r = 100\frac{v_{back}}{v_{forward}} \tag{4}$$

where r is regurgitant fraction, v_{back} is backward volume, and v_{forwd} 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:

$$r = 100\frac{SV - v_{forwd}}{SV} \tag{5}$$

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

The Q_p/Q_s ratio is defined as

$$Q_pQ_s = \frac{Q_p}{Q_p} \tag{6}$$

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

43.10 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 [16].

$$I_{ext} = \sum_i \frac{T_iR_i}{R_i} \tag{7}$$

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.

43.11 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

$$SDfromRemote = \frac{T_{optim} - Mean_{remote}}{SD_{remote}} \tag{8}$$

The optimal threshold value (T_{optim}) represent the optimal threshold for seperating 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.

43.12 MR relaxometry calculations

The MR relaxometry calculation for T1/T2 mapping is given in the paper [17]. For clarification, the implementation of Look Locker correction uses the standard formula as is used in previous literature: T1=T1*(B/A-1). The formula in [17] gives the same result as the standard formula. Implementation of the ADAPTS T2* mapping is given in the paper [18].

43.13 Pulse wave velocity

The implementation of the pulse wave velocity unit is described in the paper [19].

43.14 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.

43.14.1 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), $i = 1, ..., N$ 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

$$u = x - \frac{1}{N}\sum_{i}^{N} x_i, \quad v = y - \frac{1}{N}\sum_{i}^{N} y_i \tag{9}$$

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

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

which yields the least squares expression we want to minimize.

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

The minima is found by solving,

$$\frac{dM}{da} = 0 \tag{12}$$

$$\frac{dM}{du_c} = 0 \tag{13}$$

$$\frac{dM}{dv_c} = 0 \tag{14}$$

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

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

Resulting in

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

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

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

Since 16,

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

and the same goes for 14.

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

expanding equation (18) yields

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

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

$$\frac{dM}{du_c} = S_{u^3} - 2u_c S_{u^2} + u_c^2 S_u + S_{uv^2} - 2v_c S_{uv} + v_c^2 S_u - aS_u = 0 \tag{21}$$

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

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

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

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

which can be converted into a matrix equation

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

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

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

where

$$r = \sqrt{a}. \tag{26}$$

43.14.2 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

$$\Delta\theta_t = \theta_t - \theta_{t+1} \tag{27}$$

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.

43.15 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.

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