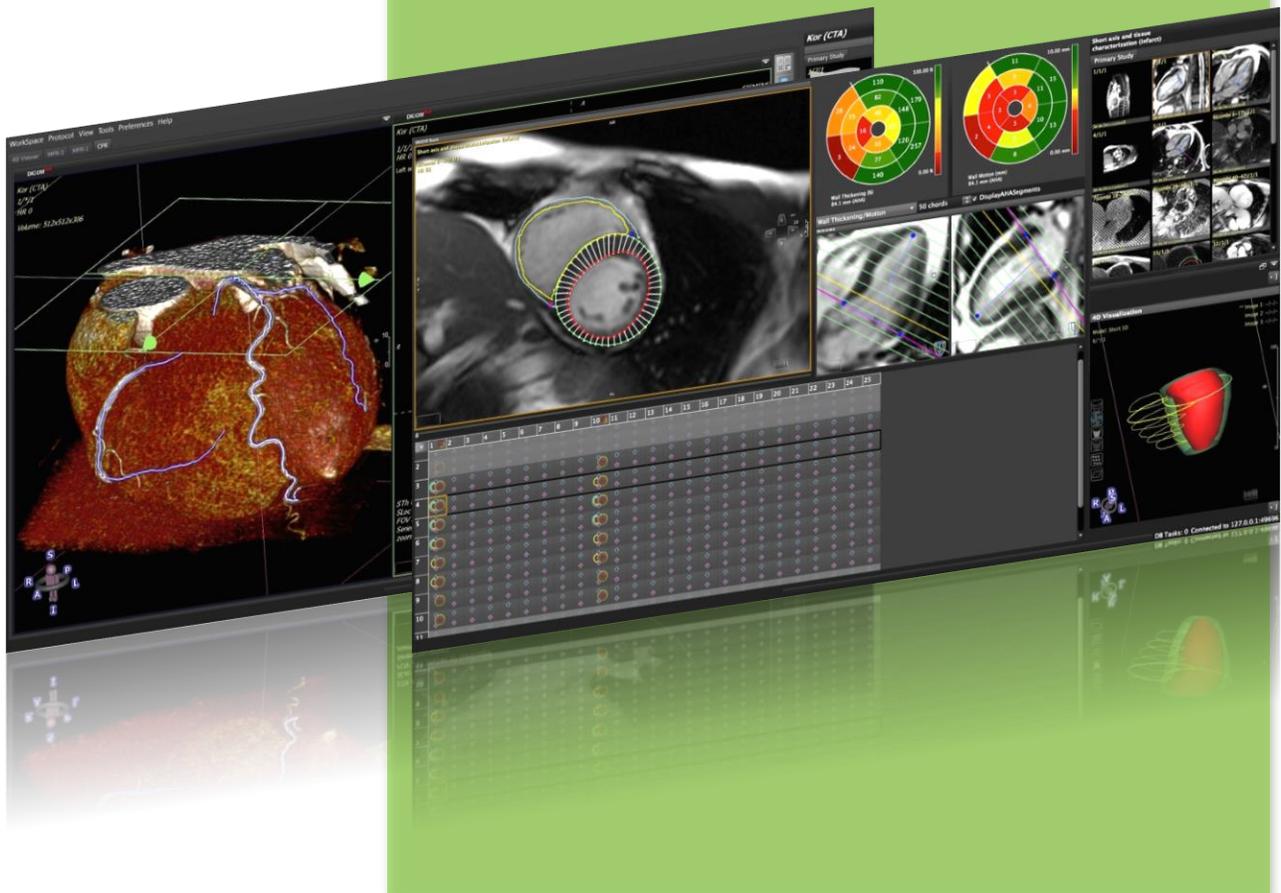




cvi⁴² / cmr⁴² / ct⁴²

Version 5.6

USER MANUAL





cvi⁴²

cmr⁴²

ct⁴²

USER MANUAL

February 2017

Regulatory Information



Manufactured by

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Canada

cmr⁴²: Health Canada device license number:
78347

ct⁴²: Health Canada device license number: 87520

United States of America

cmr⁴²: US FDA 510K number: K082628

ct⁴²: US FDA 510K number: K111373

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Australia:

ARTG Certificate No.: 177785

Sponsor: Market Access Australia Pty Lt
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European Union



cvi⁴² and cmr⁴² are qualified as a class IIa medical device. It complies with the requirements of the European Medical Device Directive 93/42/EEC



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TABLE OF CONTENTS

1	About.....	1
2	Getting Started.....	11
3	Indication Driven Workflow.....	14
4	Working with Multiple Monitors.....	17
5	Viewing.....	20
6	Contour Drawing, Labeling and Measurement Tools.....	35
7	Values Reported by cmr ⁴² and cvi ⁴² (Clinical Report).....	41
8	Patient List.....	47
9	Patient Data.....	58
10	Report Module.....	61
11	Series Overview.....	69
12	Study Viewer Module.....	74
13	4D Viewer.....	76
14	Multiplanar Reformatting.....	91
15	Coronary Module (Auto plaque).....	102
16	Vascular Module.....	111
17	Femoral Module.....	114
18	Calcium Scoring.....	119
19	Aortic Valve.....	121
20	LV/RV Function Modules.....	132
21	Tissue Characterization Module**.....	154
22	T2* Module.....	168
23	T2 Mapping.....	172
24	T1 Mapping and ECV quantification.....	176
25	First Pass Perfusion Module.....	187
26	Flow Module.....	196
27	Main Menu, Preferences and Configuration.....	201
28	Technical Support.....	217

1 About

1.1	System Requirements	2
1.1.1	cvi ⁴² Standalone and Client System Requirements ¹ v5.6	2
1.1.2	cvi ⁴² Enterprise Server System Requirements v5.6	2
1.1.3	cmr ⁴² Standalone and Client System Requirements ¹ v5.6	3
1.1.4	cmr ⁴² Enterprise Server System Requirements v5.6	3
1.1.5	ct ⁴² Standalone and Client System Requirements ¹ v5.6	4
1.1.6	ct ⁴² Enterprise Server System Requirements v5.6	4
1.2	Regulatory Information	5
1.3	Basic Components and Indication for Use	5
1.4	Abbreviations and Conventions	10

1.1 System Requirements

1.1.1 cvi⁴² Standalone and Client System Requirements¹ v5.6

Requirement	Minimum Requirements		Recommended Requirements	
Operating System	Windows 7 64-bit ² / Mac OS X 10.10		Windows 10 64-bit ² / Mac OS X 10.12	
Network (LAN)	100BaseT		1000BaseT	
Network (WAN) for client	10Mbps Downstream 2.5Mbps Upstream		1000Mbps Downstream 100Mbps Upstream	
Display	1280x800 Resolution at 24-bit color		1920x1080 Resolution or higher ³	
Processor	Intel Core i5		Intel Core i7	
Video Card	nVidia or AMD Dedicated GPU		nVidia Dedicated GPU	
	MR	CT	MR	CT
System RAM	8 GB	16 GB	8 GB	16 GB
Video RAM	1 GB	2 GB	2 GB	4 GB
	Systems without dedicated graphics⁴			
Processor / Graphics	Intel i7 with HD 3000 integrated Graphics ⁵			

¹ 3D/4D dataset viewing capability varies based on series size and amount of available RAM and VRAM. A system capable of viewing 3D is automatically capable of viewing 2D images.

² Windows 8.1, and Windows 10 are supported. Windows 8.0 and Vista are not supported at this time.

³ Multiple screens are supported up to 2560 x 1600 at 24-bit color. Landscape orientation preferred.

⁴ May affect the performance such as longer response time. It is strongly recommended to use a system with dedicated graphics card, preferably nVidia GPU.

⁵ Intel HD 520/530 Video (Skylake) with Windows 10 not supported (with current drivers as of Feb 5, 2016)

1.1.2 cvi⁴² Enterprise Server System Requirements v5.6

Requirement	Minimum Requirements	Recommended Requirements
Operating System	Windows Server 2008 R2 Mac OS X 10.10	Windows Server 2012 R2 Mac OS X 10.12
Network (LAN)	100BaseT	1000BaseT
Network (WAN) for server	25Mbps Upstream 5Mbps Downstream	1000Mbps Upstream 100Mbps Downstream
Display	24-bit color	24-bit color
Processor	Intel Core i5	Intel Core i7/Xeon
System RAM	8 GB	16 GB
Storage space	1 TB Hard Drive ⁶	2 TB RAID 1+0, 5,6,or SAN ⁶

⁶Adjust by study size, number of studies to retain prior to archival, etc. SSD drives are preferred.

1.1.3 cmr⁴² Standalone and Client System Requirements¹ v5.6

Requirement	Minimum Requirements	Recommended Requirements
Operating System	Windows 7 64-bit ² or Mac OS X 10.10	Windows 10 64-bit ² or Mac OS X 10.12
Network (LAN)	100BaseT	1000BaseT
Network (WAN) for client	10Mbps Downstream 2.5Mbps Upstream	1000Mbps Downstream 100Mbps Upstream
Display	1280x800 Resolution at 24-bit color	1920x1080 Resolution or higher ³
Processor	Intel Core i5	Intel Core i7
Video Card	nVidia or AMD Dedicated GPU	nVidia Dedicated GPU
System RAM	8 GB	8 GB
Video RAM	1 GB	2 GB
	Systems without dedicated graphics⁴	
Processor / Graphics	Intel i7 with HD 3000 integrated Graphics ⁵	

¹ 3D/4D dataset viewing capability varies based on series size and amount of available RAM and VRAM. A system capable of viewing 3D is automatically capable of viewing 2D images.

² Windows 8.1 is supported and Windows 8.0 and Vista are not supported at this time.

³ Multiple screens are supported up to 2560 x 1600 at 24-bit color. Landscape orientation preferred.

⁴ May affect the performance such as longer response time. It is strongly recommended to use a system with dedicated graphics card, preferably nVidia GPU.

⁵ Intel HD 520/530 Video (Skylake) with Windows 10 not supported (with current drivers as of Feb 5, 2016)

1.1.4 cmr⁴² Enterprise Server System Requirements v5.6

Requirement	Minimum Requirements	Recommended Requirements
Operating System	Windows Server 2008 R2 Mac OS X 10.10	Windows Server 2012 R2 Mac OS X 10.12
Network (LAN)	100BaseT	1000BaseT
Network (WAN) for server	25Mbps Upstream 5Mbps Downstream	1000Mbps Upstream 100Mbps Downstream
Display	24-bit color	24-bit color
Processor	Intel Core i5	Intel Core i7/Xeon
System RAM	8 GB	16 GB
Storage space	1 TB Hard Drive ⁶	2 TB RAID 1+0, 5,6 or SAN ⁶

⁶Adjust by study size, number of studies to retain prior to archival, etc. SSD drives are preferred.

1.1.5 ct⁴² Standalone and Client System Requirements¹ v5.6

Requirement	Minimum Requirements	Recommended Requirements
Operating System	Windows 7 64 bit ² or Mac OS X 10.10	Windows 10 64-bit ² or Mac OS X 10.12
Network (LAN)	100BaseT	1000BaseT
Network (WAN) for client	10Mbps Downstream 2.5Mbps Upstream	1000Mbps Downstream 100Mbps Upstream
Display	1280x800 Resolution at 24-bit color	1920x1080 Resolution or higher ³
Processor	Intel Core i5	Intel Core i7
Video Card	nVidia or AMD Dedicated GPU	nVidia Dedicated GPU
System RAM	16 GB	16 GB
Video RAM	2 GB	4 GB
Systems without dedicated graphics⁴		
Processor / Graphics	Intel i7 with HD 3000 integrated Graphics ⁵	

¹ 3D/4D dataset viewing capability varies based on series size and amount of available RAM and VRAM. A system capable of viewing 3D is automatically capable of viewing 2D images.

² Windows 8.1 is supported and Windows 8.0 and Vista are not supported at this time.

³ Multiple screens are supported up to 2560 x 1600 at 24-bit color. Landscape orientation preferred.

⁴ May affect the performance such as longer response time. It is strongly recommended to use a system with dedicated graphics card, preferably nVidia GPU.

⁵ Intel HD 520/530 Video (Skylake) with Windows 10 not supported (with current drivers as of Feb 5, 2016)

1.1.6 ct⁴² Enterprise Server System Requirements v5.6

Requirement	Minimum Requirements	Recommended Requirements
Operating System	Windows Server 2008 R2 Mac OS X 10.10	Windows Server 2012 R2 Mac OS X 10.12
Network (LAN)	100BaseT	1000BaseT
Network (WAN) for server	25Mbps Upstream 5Mbps Downstream	1000Mbps Upstream 100Mbps Downstream
Display	24-bit color	24-bit color
Processor	Intel Core i5	Intel Core i7/Xeon
System RAM	8 GB	16 GB
Storage space	1 TB Hard Drive ⁶	2 TB RAID 1+0, 5,6, or SAN ⁶

⁶ Adjust by study size, number of studies to retain prior to archival, etc. SSD drives are preferred.

1.2 Regulatory Information

AGENCY	cmr ⁴²	ct ⁴²	cvi ⁴²
US FDA 510K #	K082628	K111373	K141480
Europe CE Certificate #	CE 539277		
Health Canada Device License #	78347	87520	93385
Australia TGA ARTG #	177785	pending	
Brasilian ANIVSA			094337/14-1
South Korea KFDA	14-1334	pending	
Japan	227ADBZX00153000		227ADBZX00157000

1.3 Basic Components and Indication for Use

cvi⁴² is intended to be used for viewing, post-processing and quantitative evaluation of cardiovascular magnetic resonance (MR) and computed tomography (CT) images in a Digital Imaging and Communications in Medicine (DICOM) Standard format.

- Module: Patient List
 - Browse and filter database
 - Import and Export of Cardiac MR Images in DICOM format
 - Anonymization

- Module: Patient Data
 - View Patient related DICOM Header information
 - Edit patient biometrical data and history
 - Choose BSA calculation method
 - View collected images for Case Review

- Module: *Report*
 - View clinical and scientific report
 - Send and/or save report

- Module: Series Overview
 - View all images/series in an overview
 - Filter for specific images/sequences
 - Series Composer to rearrange or combine series and to delete or add images, slices or phases

- Module: *Viewer*

- Custom viewing in up to 12 viewer frames
 - Basic measurements like length, area and SI
 - Option to view two scans side-by-side
- ⊙ Module: 4D Viewer
- DVR, MIP, Angio and Surface rendering
 - Dataset clipping, cutting and cropping
 - Endoluminal and external view
 - Segmentation via " 3D region growing" based on 3D threshold segmentation
 - Segmentation options for the heart and left ventricle (CT only)
 - Calculation of ESV, EDV, SF, EF in multiphase series (CT only)
 - Movie export in multiple formats (AVI, QuickTime)
 - Secondary DICOM capture saving options include rotation images and cines
- ⊙ Module: Multiplanar Reformatting
- 3D data resampling in any oblique plane
 - Customizable interface with the option of three MPR viewers and a 4D reference view.
 - Thick and thin slab rendering
 - Synchronized zoom, windowing, slab thickness
 - Multiple preset views designed for cardiac and vascular imaging
 - Create secondary DICOM captures as cine or stack of any view
 - Automatic generation of a short axis stack, including long axis reference of CT images for LV function assessment
 - Volume navigation and/or vessel segmentation can be done directly on the 4D reference image
 - Free form rotation option allows to navigate through the volume in all directions
 - A report panel will provide predefined measurement profiles and allows for reporting of measurements and respective images. Measurements and MPR locations will be saved and can easily be reviewed
- ⊙ Module: Vascular
- The *Vessel* module workflow includes sub modules for *Centerline* and *Curved MPR* and *Cross Section* of vessel segmentations
 - vessel segmentation and/or extension can be done via seed-points or region-growing.
 - Vessel displays include projected, stretched and straightened CPR views as well as multiple cross sectional views
 - Artifact-free viewing option
 - Endoluminal view options including animated centerline fly-through
 - Automatic contour detection for vessel lumen.
 - Automatic min/max/average diameter as well as stenosis percentage calculation of the vessel lumen
 - Contours will be saved automatically

- Multiple export options include recording of fly through videos
 - Centerlines can be restored and saved from workspaces
- Modules: Coronary and Autoplaque (plug-in)
- Same as vascular but specific for coronary arteries.
 - *Autoplaque* is a plug in and requires a separate license. It is part of the *Analysis* sub-module and performs an automated plaque analysis providing a color overlay and a report panel displaying all plaque measurements
- Module:
- *Femoral* see vascular but specific for access path planning
- Module: Aortic Valve
- Annulus specific measurement tools calculate perimeter, area, and minimum and maximum diameters
 - Assisted height measurement of the coronary ostia perpendicular to the annulus plane
 - Display of a circular device simulation with adjustable diameter and height values
 - Optimal viewing curve provides different viewing angles in the synchronized 4D and MPR views. Preset and customizable angles can be included in the report
 - Optional planning of transapical access route
 - Flexible reporting options allow for customized selection of images and measurements
- Module: Ca scoring
- Quantification of plaque load in coronary arteries
 - Automatic calculation of Agatston score, including risk classification and percentile ranking based on age and gender
 - Customizable threshold setting and correction factor
 -
- Module: Biplanar/Triplanar LAX
- Global LV function in 2 or 3 planes
 - Atrial Volumetry (area length)
- Module: Multiple Long LAX
- Global LV function
 - Time resolved LV volume curves
- Module: Short Axis 3D
- Global and regional LV function analysis including polar map display
 - Global RV function assessment

- Volume Curves
- Atrial volumetry (disc summation technique)
- Color coded 3/4D contour model

- Tissue Tracking
 - 2D and 3D left ventricular Tissue Tracking
 - 2D RV Tissue Tracking
 - Calculation of various strain values
 - Color coded strain display in 2,3 and 4D
 - Display of Polar Maps
 - Generation of strain curves

- Module: Perfusion
 - Semi quantitative Perfusion analysis of rest and stress images
 - Qualitative Perfusion analysis compared to LGE and Function images
 - Polar Map display

- Module: Tissue Characterisation**
 - Late Gd Enhancement analysis (viability)
 - T2 analysis (edema)
 - Early Gd Enhancement (inflammation)
 - Color coded 3D mesh model
 - Polar Map display

- Module: T2*
 - Analysis of gradient echo sequences for the assessment of myocardial iron overload; Color coded overlay and graphical display of decay curve.

- Module T2 mapping
 - Global and segmental T2 times
 - T2 and R2 map with customizable color LUT

- Module: T1 mapping
 - Assessment of native and post contrast T₁ Relaxation times
 - T1, T1*and R2 maps with customizable color LUT and polar map display
 - Assessment of ECV % per slice and segment including polar map display and map generation with customizable color LUT
 -

- Module: Flow Analysis

- Color-coded flow display with semi-automatic contour detection, synchronization and forwarding
 - Option to perform flow analysis on ROI's of different series and derive values such as flow difference, sum and ratio.
 - Graphical Display of flow rate and flow velocity (mean/max/min)
 - Background and Phantom correction options
 - Automatic calculations include volumes, velocities, regurgitant fraction and mean/max pressure gradient
- ⊙ Module: Calcium Scoring (cvi⁴² and ct⁴² only)
- Quantification of calcium load in coronary arteries
 - Automatic calculation of Agatston score, incl. risk classification and percentile ranking based on age and gender
 - Threshold and Correction factor can be customized
- ⊙ Module Aortic Valve
- Pre-procedural planning of transcatheter aortic valve replacement.
 - Assessment of the access path for catheter selection and guidance
 - Measurement of the aortic annulus for device sizing
 - Ancillary measurements such as the distance between the coronary ostia and the annulus to avoid obstruction
 - Device simulation
- ⊙ Reporting
- All analyses (and screenshots) in one report
 - Clinical and scientific reports
 - Export reports in multiple formats (PDF, ODF, TXT, XML or DICOM)

It shall be used by qualified medical professionals, experienced in examining and evaluating cardiovascular MR images, for the purpose of obtaining diagnostic information as part of a comprehensive diagnostic decision-making process. cvi⁴² /cmr⁴² is a software application that can be used as a stand-alone product or in a networked environment.

The target population for the cvi⁴² /cmr⁴² is not restricted, however the image acquisition by a cardiac magnetic resonance scanner may limit the use of the device for certain sectors for the general public.

WARNING:

Quantitative analysis is dependent on the quality and correctness of the image source data.

WARNING:

**The Tissue Characterization and Perfusion modules are not available in the USA since the FDA does not approve the use of contrast agents for cardiac MR procedures. A non-diagnostic version of cvi⁴²/cmr⁴², intended to be used only for scientific research is available upon request.

1.4 Abbreviations and Conventions

References to buttons or icons and modules are written in *italic*.

If the selection of a menu or function, requires multiple clicks, it will be notated as follows: E.g. *Configuration > Contours > Rounded SAX Endocardial Contours* (which explains how to get to the selection of using rounded contours for the automatic contour detection)

Tooltips, names of menus and icons are written the same as in the interface, e.g. the button for the Short axis 3D volume module is described as *Short3D*

CMR	Cardiovascular imaging
EGER	Early Gadolinium Enhancement Ratio
dc	Double click
EGE	Early Gadolinium Enhancement
LMB	Left mouse button
lc	Left click
LGE	Late Gadolinium Enhancement
LV	Left ventricle
MB	Mouse button
MMB	Middle mouse button
RMB	Right mouse button
rc	Right click
ROI	Region of interest
TC	Tissue Characterization
SAX	Short axis

2 Getting Started

2.1	Installation	11
2.2	Request and/or Add License (if prompted)	12
2.3	Load Images	13
2.4	Analysis	13

2.1 Installation

Running cvi⁴² /cmr⁴² on a local server

1. Download from the website
2. Run installer application
3. Open the client (cvi⁴² or cmr⁴²)
4. Client Login
5. Connect to the local server. You will find the server.app (Mac) or server.exe (Windows) in the same folder as the cvi⁴² Client .app (or .exe)

Default Server Setup Connection settings:

- Name: "Local Server"
- Server Address: 127.0.0.1
- Server Port: 49696

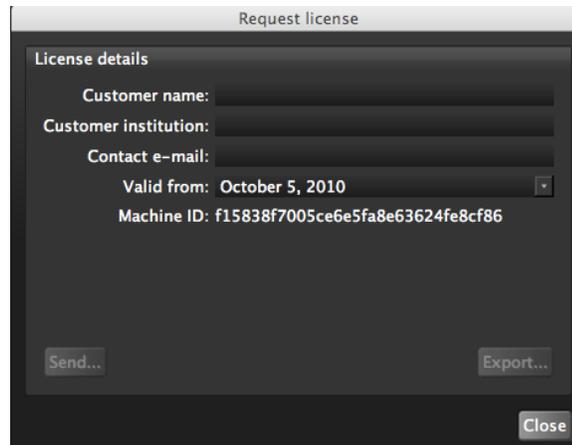
Default *UserId* and *Password*:

- username: admin
- password: passwordThe first time you run cvi⁴²/cmr⁴² to your local server and/or if you move or rename the path to the server, you may be asked to locate the cvi⁴²/cmr⁴² server .app or .exe on Windows

Depending on how fast the computer is you may need to repeat step 4 and re-enter your name and password and press Login.

2.2 Request and/or Add License (if prompted)

Clicking the "Request" button opens a dialog



Machine ID: All cmr⁴² and cvi⁴² licenses are tied to an individual workstation, which is identified by this number that is calculated from the hardware of the workstation it runs on. To avoid licensing problems, prior to running the "Request License" dialog, please turn off or remove any hardware from your machine that is not permanently turned on or connected to your machine during cmr⁴²/cvi⁴² usage.

After you have entered your information you can proceed by two options:

- Send: If you have an e-mail client configured on your workstation, you can click the "Send" button in order to e-mail the information to the Circle CVI Sales Department
- Export: You can export the information to a file by clicking the "Export" button in order to transfer it to another machine and send it to the Circle CVI Sales Department.

An E-mail with a license file attached will be send to you. Save the file on the desktop and re-open the licenses window. There are two options:

- a) *Import:* Import the license from the desktop
- b) *Add:* Open the license file and copy /paste into the license string window

If the license has been added successfully the application will open the *Image Database*, ready to import studies.

Note: cvi⁴² will still show the old license expiry date after a new license has been installed. As soon as the expiry date has elapsed, the new license will automatically take over.

Alternatively:

1. Manually remove the license files / lines that are superseded by the newly installed license
2. Restart the server

2.3 Load Images

1. Click on the *Import Images* button and select the image file on the local system, the network or CD/DVD.
2. After the import is completed, the study will be added to the *Main DB* tab.
3. One LMB click loads the study in the preview window. Double LMB click opens the study in the *Series Overview*
4. Select the indication to open a workflow or go to *No Indication*
5. From here choose your series and drag it in the analysis module

2.4 Analysis

1. Contouring tools can be found in the top tool bar. Hovering over a tool will display a brief description.
2. A LMB click selects the tool.

 Icons with a star perform semiautomatic contour detection

 Icons with a little arrow provide additional options.

3. Trace with a LMB drag
4. Drop a tool:
 - LMB click somewhere in the background of the analysis window
 - Pick up a different tool
 - Click on the arrow *Leave Draw Mode* in the toolbar
5. Correct a contour: Double-click on the contour and re-trace
6. Short-cut keys for different drawing modes
 - c - click draw
 - p - nudge contours
 - d - drag contours (rubber band)
 - alt - threshold segmentation

3 Indication Driven Workflow

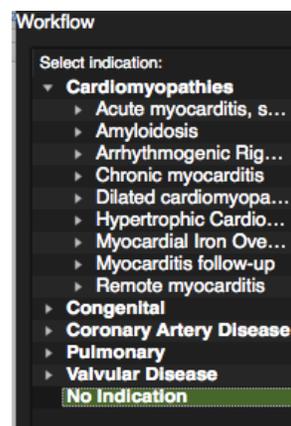
3.1	How to use an Indication Driven Workflow	14
3.2	Customize Tools and Working Modules	15

Indication driven workflow shall facilitate a standardized workflow from referral to reporting. cvi⁴² will automatically set up a guideline based workflow for a selected indication.

Indication driven workflow can be disabled in *Preferences>Workflow*

The benefits:

- Time saving due to automated selection of modules
- Guarantees a standardized, complete work-up even for the less experienced user
- Adherence to guidelines for post-processing and reporting
- Synchronization with report⁴², prompting indication specific configuration of report sections, normal ranges, citations and more.



Upon opening a study, a workflow panel in the *Series Overview Module* will list the indications which are grouped into disease clusters.

Tied to the indications are ‘protocols’. Protocols contain the modules used for the work up of the selected indication. For report⁴² users, there is additional reporting information assigned to a protocol.

The software ships with a default set of indications, however these can be easily customized for any site-specific standard(s).

3.1 How to use an Indication Driven Workflow

For cases where there is no indication, go directly to *No Indication*. For cases with a specific indication, follow the steps below:

1. LMB Click to expand relevant disease cluster
2. RMB click on an indication to display the associated modules (optional)
3. To add more modules, check the box in the list, or, once an indication is selected and in the workflow pane, add modules using the “+” button. These changes will apply to the study only. A user with administrator rights can additionally save any changes to the protocol by pressing the “save” button.

4. Disease clusters, indications, and their associated protocols are public and can be configured by an administrator user only. Go to *Preferences> Workflow*

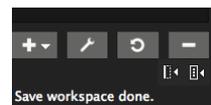
3.2 Customize Tools and Working Modules

cvi⁴²/cmr⁴² offers a wide range of functionality and tools. In the clinical routine not everything is needed, thus toolsets, window frames reserved for specific evaluations and certain functionality can be turned on or off. In addition, you are able to set your preferred thresholds and analysis options, like for e.g. greyzone analysis. The following modules do not provide interface customization: Patient Data, Report, Series Overview, 4D viewer,

Customize the Interface



1. In the protocol list select the module you would like to customize
2. Click on the wrench (bottom)
3. You can hide/display view ports, single buttons or entire groups of buttons. Green indicates they will be displayed in the interface, purple indicates they are hidden.
4. Hovering with the mouse over the buttons will display a tool tip.
5. Click the 'eye'-icon to hide/de-activate functionality.
6. To re-activate click on the 'x'.



7. To return to default click 
8. To exit the edit mode click the wrench again.



9. The selection can be saved to the protocol, by clicking the save button in the workflow pane

For activating or deactivating more functions (e.g. include exclude papillaries) or to customize settings (e.g. metric vs. imperial units), please go to *Preferences*.

When disabled in the protocol, display options (such as the below) will be available in the *Context Menu*:

- Exclude Papillaries
- Show Cross View
- LV volume curve
- Reference
- View Regional Function and
- Mitral Valve Plane correction



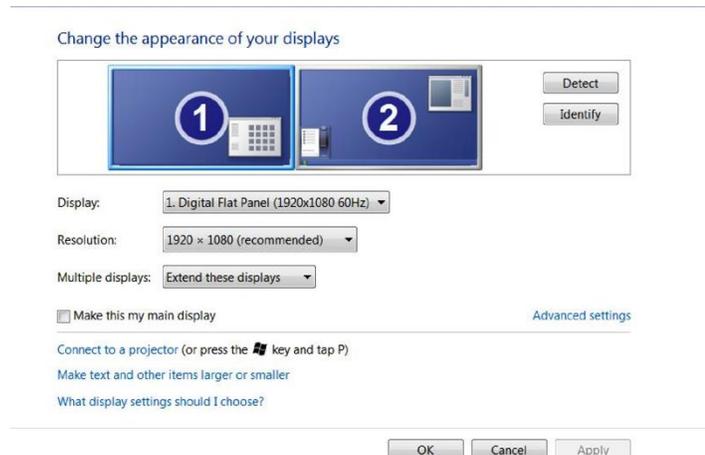
4 Working with Multiple Monitors

4.1	Set up your displays	17
4.2	Activate multiple screen functionality	17
4.3	Locating the main screen	18
4.4	Choose a module for the other screen	18
4.5	How to handle protocol and thumbnail panel in a multi monitor set-up	19

4.1 Set up your displays

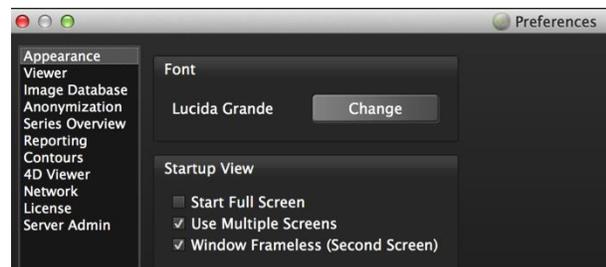
▶ Control Panel ▶ All Control Panel Items ▶ Display ▶ Screen Resolution

In your Windows settings open up your *display* controls, arrange your monitors and determine your main monitor.



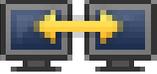
4.2 Activate multiple screen functionality

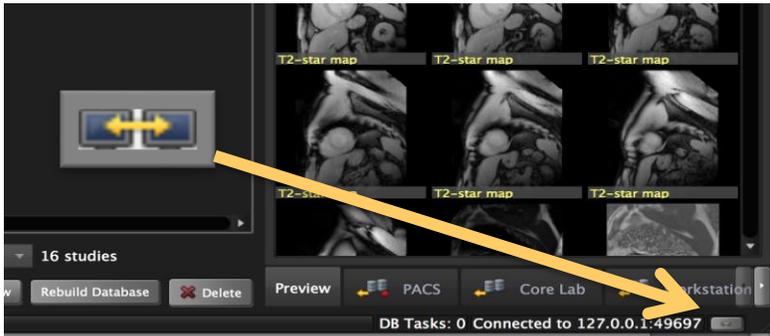
1. In cvi⁴², go to the Preferences>Appearance >Startup View and check Use Multiple screens click ok
2. Quit cvi⁴² and restart the application



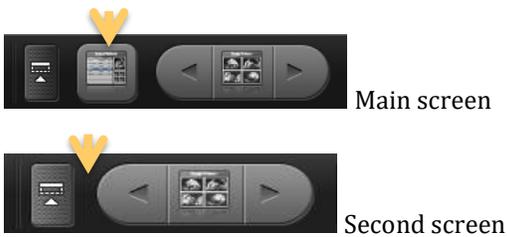
4.3 Locating the main screen

The main screen is the only screen that displays the following icons:

- 
 Move current module to screen x icon will be shown on the bottom right corner of the Patient List module



- 
 Patient List module icon in the top tool bar



4.4 Choose a module for the other screen

There are 2 ways to switch to a different module (default Viewer Module) on the second screen

- On the second screen: simply use the arrow keys on the top toolbar



- On the home screen:
 - Select the module you would like to push to the second screen and click the button in the lower right corner *Move current module to screen no. x*



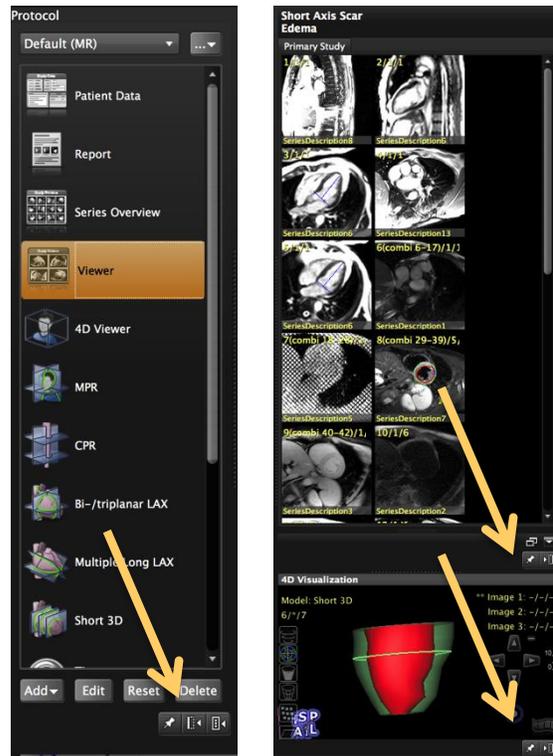
4.5 How to handle protocol and thumbnail panel in a multi monitor set-up



When working with multiple screens, the panes will always follow your mouse cursor.



If you want them fixed on a specific monitor, use the pin on the bottom of the pane.



5 Viewing

5.1 View Ports - Overview	21
5.1.1 Viewer Overlays, Annotations	22
5.1.2 Sequence Parameter	22
5.2 Thumbnail pane	24
5.3 Image Editing, Viewer Controls	24
5.3.1 Panning	24
5.3.2 Windowing	24
5.3.3 Main Viewer Controls Table	25
5.3.4 Shortcut and modifier keys	26
5.3.5 Context Menu Table	27
5.4 Additional Viewing	30
5.4.1 Floating Viewer	30
5.4.2 Reference Viewer	31
5.4.3 4D Visualization Viewer	32
5.4.3.1 Mesh Model Options	33
5.5 Compare Two Studies	34

There are 3 dedicated viewer modules

- Series-Overview module
- Viewer module
- 4D viewer including

(For a detailed description please refer to the respective module chapter)

Next to the main viewer frames within the modules, there are additional frames embedded that allow for optimal assessment by displaying different aspects and/or orientations

- Reference frames
- 4D Visualization frames
- Floating viewer
- Multiview display option

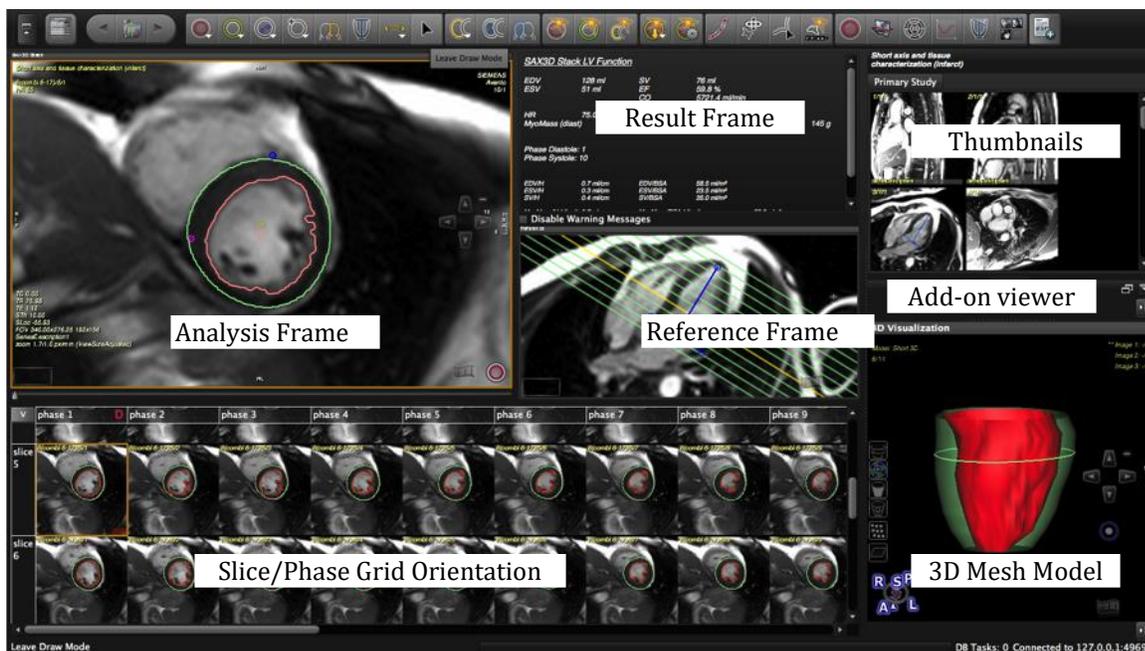
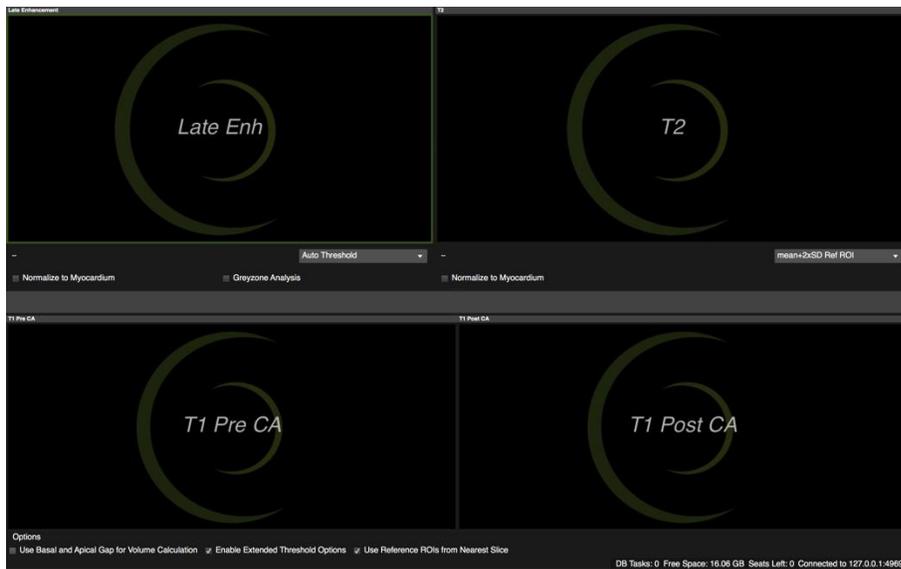
(For more detail, please refer to the respective chapter below)

You will start your assessment by loading an image into the viewer

5.1 View Ports - Overview

Each module provides viewer frames for image post-processing.

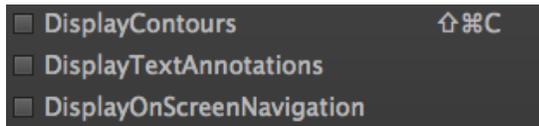
The frames are tagged and prepared for specific image sets (e.g. T2-weighted images).



5.1.1 Viewer Overlays, Annotations

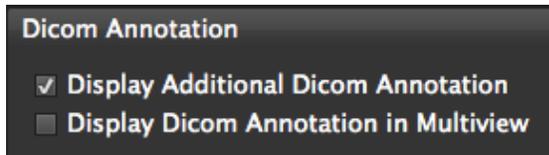
Overlays consist of information retrieved from the DICOM Header, on-screen tools and contours.

You can remove all overlays e.g. for screenshots, via context menu (opens with a RMB click in the viewer frame)



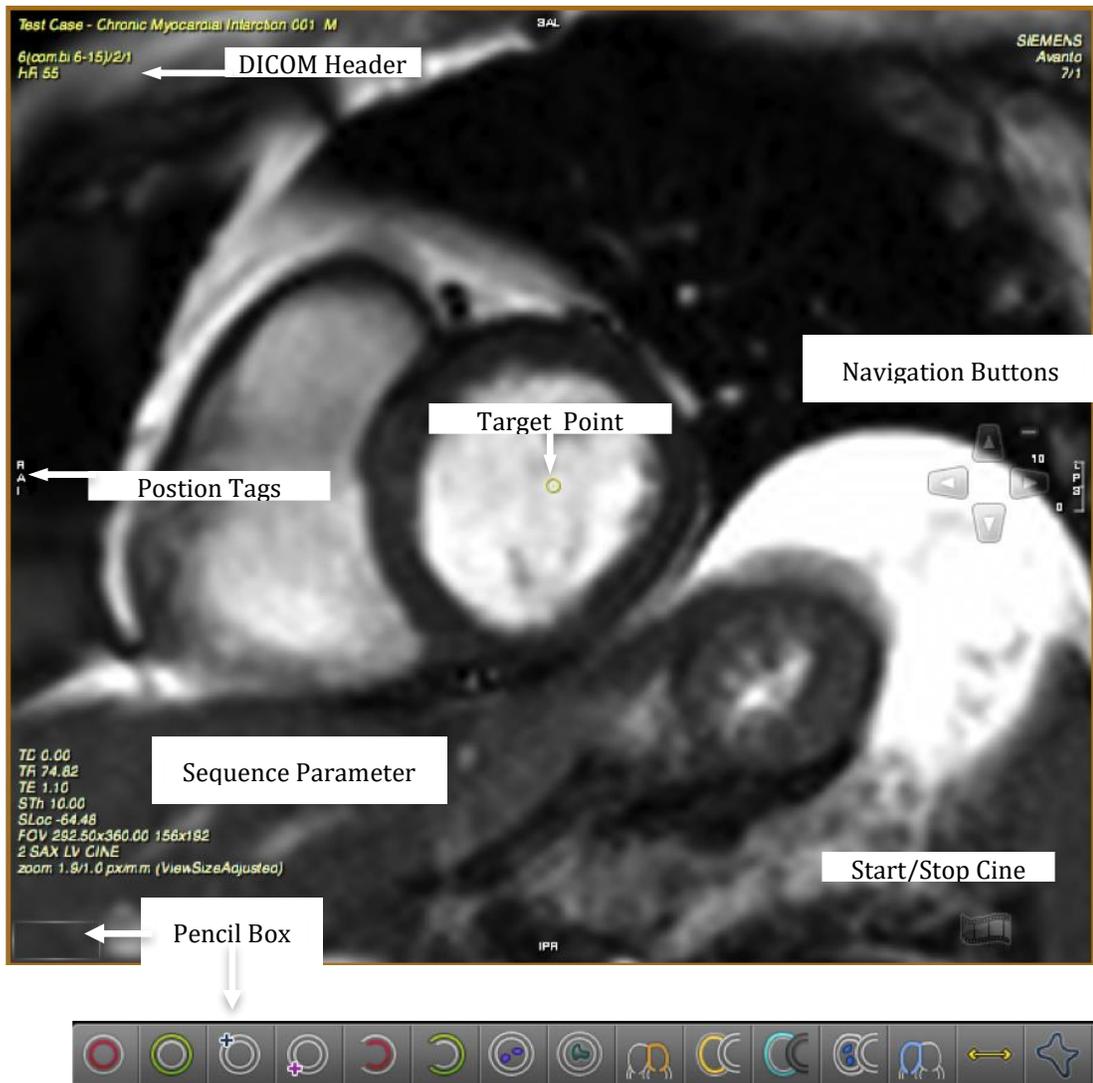
5.1.2 Sequence Parameter

Sequence Parameter settings are found in the *Preferences/Viewer/DICOM annotations*



- If checked DICOM Annotations will be **visible** on all images
- If unchecked, they are **hidden**, but can still be retrieved with a LMB click in the left bottom corner of the image frame. Parameters will be displayed for 3 seconds.

To increase **font size**, go to *Preferences/Appearance/Font*



Cines will be displayed in real time speed

By pressing the "S" key during cine display the speed shall be reduced to half of the real time speed.

5.2 Thumbnail pane

If enabled in *Preferences*, cvi⁴² performs a smart series sorting: To help the user find the correct sequence more quickly, relevant images are moved to the top of the list and are marked with a green checkmark.

- A red cross indicates that the series cannot be loaded.
- Images without a checkmark or cross are not preferred but can be loaded.
- Secondary DICOM captures and manually created series can be found at the end of the list.

To turn off the Smart Series Handling, go to *Preferences>Appearance>Smart Series Handling*



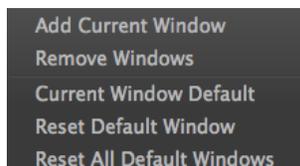
5.3 Image Editing, Viewer Controls

5.3.1 Panning

- ☉ Center your image with the LMB held.
- ☉ All signal intensities within the frame border (= frame input area) will be included into signal intensity calculation. By default the *Contour Detection Connect to View* is activated in the *Preferences*, which means the frame input area automatically adjusts with the zoom.
- ☉ Zoom in to your region of interest (ROI) using the scroll wheel.

5.3.2 Windowing

- ☉ **Mouse:** The mouse allows for direct window adjustments
While holding the shift-key, click and drag the LMB (up/down and left/right)
 - Clicking the MMB of a 3-button mouse will auto-window
- ☉ **Context menu:** Allows to apply or to save custom presets
 - *Windowing Presets* and *Auto-Windowing* options can be found in the context menu.
 - Keyboard short-cut keys for presets are: 1, 2, 3, 0
 - To change the default *Windowing Preset* and/or to add a custom windowing preset choose *Edit* from the *Window...* menu:



A newly defined Window will be added to the *Window...* menu

- ☉ **Toolbar:** Synchronizes window settings within the module



The *Sync Window* button  will automatically sync the window settings to the other frames

- **Preferences:** Changes apply to all modules

Change the default setting in the *Preferences/Viewer* menu (preset is 8%).



5.3.3 Main Viewer Controls Table

ICON	FUNCTION	MOUSE CLICKS	ALTERNATIVE
	Windowing	Window: push mouse wheel and drag Auto adjust: double click MMB Holding shift-key+LMB and drag	Windowing presets: keyboard keys 1-2-3-0 Windowing presets: context menu Define your own preset via <i>Edit</i> in the context menu
	Panning	Hold LMB down and pan	
	Zooming	Scroll mouse wheel	Move cursor to the right frame border until symbol appears; LMB drag up/down Context menu: Image/Auto adjust Zoom
	Cine mode	LMB click	
	Navigation	Open on-screen navigation buttons	
	Scroll through phases/slices and series	Hold the shift key and scroll the mouse wheel	Keyboard arrow keys Customize your mouse wheel: Preferences/Viewer/Mouse Wheel function

5.3.4 Shortcut and modifier keys

COMMAND KEY COMBINATIONS	WINDOWS	MAC
Undo	Control + Z	⌘ + Z
Redo	Control + Y	⌘ + Y
Delete Contour	Control + X	⌘ + X
Delete All Contours	Control + Del	⌘ + ⌫
Delete Contour (slice)	Control + D	⌘ + D
Delete All Contours (slice)	Control + M	⌘ + M
Delete Contour (phase)	Control + O	⌘ + O
Delete all Contours (phase)	Control + P	⌘ + P
Hide contours	Shift	Shift
Select a contour & jump to the next contour	Tab	Tab
Contours On/Off	Control + Shift + C	⌧ + ⌘ + C
Copy Contour	Control + C	⌘ + C
Copy All Contours	Control + A	⌘ + A
Paste	Control + V	⌘ + V
Forward Contour (slice)	Control + F	⌘ + F
Forward All Contours (slice)	Control + E	⌘ + E
Smooth contour	Control + S	⌘ + S
Round contour	Control + L	⌘ + L
Add to Case Review	Control + R	⌘ + R
Default Window (set in the preferences)	Control + W	⌘ + W
Auto Windowing (type I)	1	1
Auto Windowing (type II)	2	2
Auto Windowing (type III)	3	3
Auto Windowing (Min Max)	0	0
Change mouse wheel from zoom to phase	Shift	Shift
Hide cmr ⁴²	Control + H	⌘ + H
Hide others	⌘Control + H	⌘ + H
Click-Draw Contours	c + LMB click	c + LMB click
Threshold segmentation contour definition	Alt + LMB drag	Alt + drag
Drag Contours	d + LMB click	d + LMB click
Push Contours	p + LMB click	p + LMB click
Contour reposition (all at once)	Control + LMB drag	⌘ + LMB drag
View all images of a series next to each other	space bar	space bar
Full Screen	⌘F11	(fn) ⌘F11
Refresh study list	⌘F5	(fn) ⌘F5
Preferences	Control + " ,"	⌘ + " ,"
Quit	Control + Q	⌘ + Q
Contour refinement ()	press 	press 

5.3.5 Context Menu Table

The context menu allows you to make changes to the active viewer frame.

CONTEXT MENU	COMMAND	DESCRIPTION
Undo	⌘Z	Deletes last action e.g. last drawn contour
Redo	⌘Y	Retrieves deleted action
Copy Contour	⌘C	Copies a selected contour
Paste Contour(s)	⌘V	Pastes previously copied contours
Delete Contour	⌘X	Deletes a selected contour (double click)
Copy/Forward		
Copy All Contours	⌘A	Copies all contours that are drawn on the selected image
Forward Contour (Slice)	⌘F	Forwards a selected contours across all phases
Forward All Contours (Slice)	⌘E	Forwards all contours of a selected slice across all phases
Delete		
Delete All Contours	⌘⌘	Deletes all contours in the active frame
Delete Contour (Slice)	⌘D	Deletes a selected contour in all phases per slice
Deletes All Contours (Slice)	⌘M	Deletes all contours in one slice across all phases
Delete Contour (Phase)	⌘O	Deletes a contour in all slices of a selected phase
Delete All Contours (Phase)	⌘P	Deletes all contours in all slices of a selected phase
Delete Contour (Series)		Deletes a selected contour within a series
Delete All Contours (Series)		Deletes all contour of the selected series
Contours		
Smooth Contour	⌘S	Smooths a shivery contour
Round Contour	⌘L	Contour will assume a round shape
Derive Cardiac Contours		Existing contours in short axis can be retrieved in other series
Derive Cardiac Contours Phase		Existing contours in short axis can be derived for an entire phase
Forms - Tools for planimetry		
Freehand		⌘
Line		⌘
Box		⌘
Circle		⌘

Annotate		
Annotation Text		Type in text
Annotation Arrow		Point out a structure with an arrow
Annotation Arrowhead		Point out a structure with an arrowhead
Annotation Circle		Point out a structure by encircling it
Closed Contour Rotation ¹		Adjust a selected contour for heart twisting
Display Contours	⇧⌘C	Hide or display drawn contours
Display Text Annotations		Removes all overlays from the image
Display On Screen Navigation		Shows navigation arrows
Windowing Preset	⌘W	Auto windowing
Windowing		
AutoWindowingImage Type I	1	Ignoring outliers, the system automatically provides you with an optimized setting for window contrast
AutoWindowingImage Type II	2	
AutoWindowingImage Type III	3	
AutoWindowing MinMax	0	Calculates the optimal windowing by taking all (minimal and maximal) grayscale values into account
AutoWindowingImageRegion	4	See auto windowing, but only calculated for display window
AutoWindowingImageRegion MinMax	5	Auto windowing min/max but only calculated for display window
Edit		
Add Current Window		Adds a custom window preset to the menu
Remove Windows		Allows to remove one or all custom presets
Current Window Default		Sets the window as a default for the chosen image type
Reset Default Window		
Reset All Default Windows		If there are multiple defaults they will be reset
Export As		
Export Image		Opens a window that allows the user to save the active frame to a different location
Export Image Multiview		Exports the images in a multiview format and displays them all at once side-by-side
Copy Image To Clipboard		Copies the image and allows the user to paste it into any other application

Export Cine Current Slice		Exports the cine of a selected slice to a new file as AVI movie
Export Movie All Slices Multi View		Exports all slices and phases of a selected cine as one movie file (AVI)
Export Movie All Slices Stacked		Separates the slices of a cine and exports them as a sequential stack of movie files (AVI)
Add Current Series To Case Review	⌘R	Adds a complete series to the case review in the <i>Patient-Data</i> module
AddFrameToReport		Adds the active frame to the report
Image		
Rotate Image		Allows the user to rotate the image e.g. for better comparison
Reset Image Rotation		Resets previous rotations
Interpolate Image		Shows the image with its raw data
Invert Image		If checked, the image will be displayed with inverted grayscales (negative image)
Display Overlay		Displays existing color-coded overlays e.g. LE
Display Cursor Signal Intensity		Display of SI in according to the cursor position
Use Open GL		Optimization for video cards that increases performance
AutoAdjustZoom		Optimizes the zoom
Display & Localizer		
Display Localizer		Turns localizer in the reference window on/off
Display Localizer Cut Line		Display of a cut line
Display Localizer Box		Localizer is checked this will display a box
Display Current Localizer Box		
Histogram		
Display Image Histogram		
Display Contour Histogram		
Other		
Display Additional DICOM Tags		Turns on/off sequence parameter
Display Pos Tags		Displays position tags

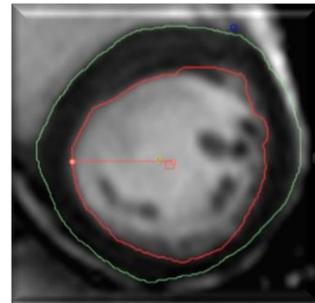
Display Scale		Displays scale located on the right middle frame border
Display Window		Displays window width (contrast) and window center (window level, brightness) located in the left bottom corner
Display Cine Tags		
Clear Frame		Removes image from frame
Show DICOM Dump		Shows complete DICOM header information

Note: Changes only apply to the active frame; general settings have to be changed in the Preference Menu

Closed Contour Rotation¹:

Contours can be corrected for ventricular twist motion by a simple rotation of the contour set.

1. Click on the contour that has to be rotated,
2. Open the context menu with a right mouse click
3. Grab the red dot on the contour
4. Rotate the contour



5.4 Additional Viewing

5.4.1 Floating Viewer

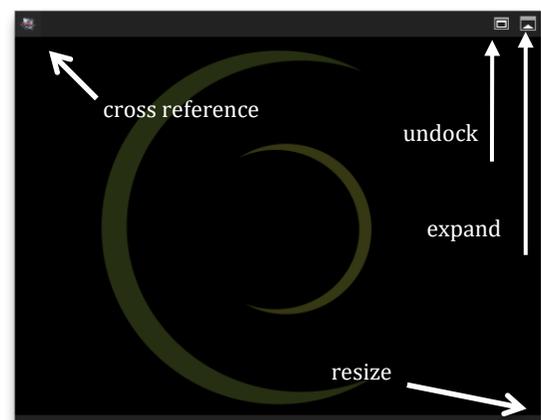
Located underneath the thumbnail panel is an additional detachable viewer, that can be changed in size and that will stay on the screen even when switching to a different module.

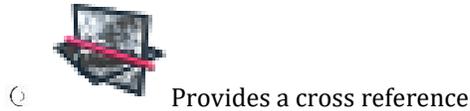


- ⊙ Expand/Collapse Viewer: Opens an additional viewer frame. Select an image via drag-and-drop from the thumbnail panel



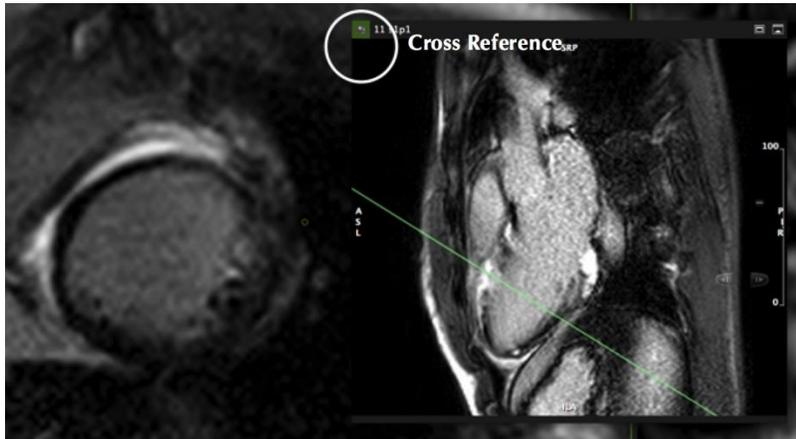
- ⊙ Undock/Dock Viewer: Creates a floating viewer



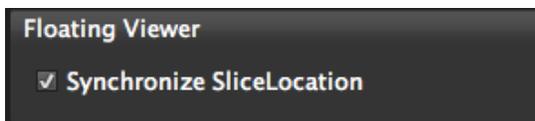


By default the slice location of the main viewer frame is synchronized with the slice location of the floating viewer.

In addition you can *Show/Hide a Cross Reference* in the floating viewer

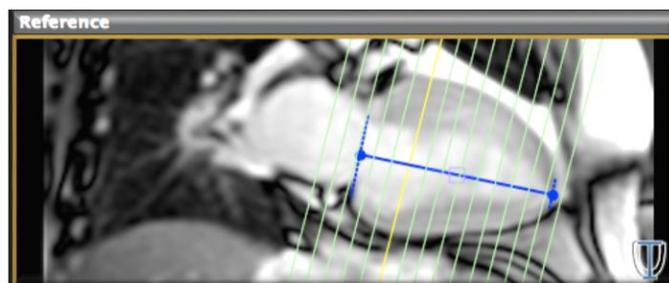


To disable the synchronization go to the *Preferences/Viewer* and turn off *Synchronize Slice Location*



5.4.2 Reference Viewer

Reference Viewer requires an orthogonal plane to display the slice orientation of the main viewer frame. In addition, it allows for defining the range of slices to be included into the analysis by marking the basal and apical edges of the anatomical long axis.



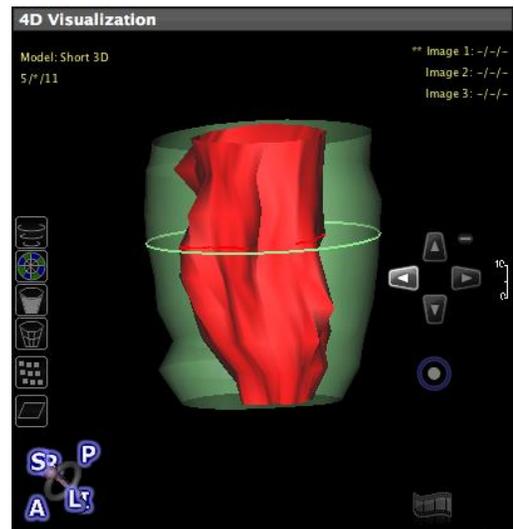
5.4.3 4D Visualization Viewer

Modules with **4D Visualisation** frames

- Short3D
- Tissue Characterization
- Perfusion
- T2*
- T1

Note:

No mesh model will be displayed, when images are not parallel or have variable slice distances.



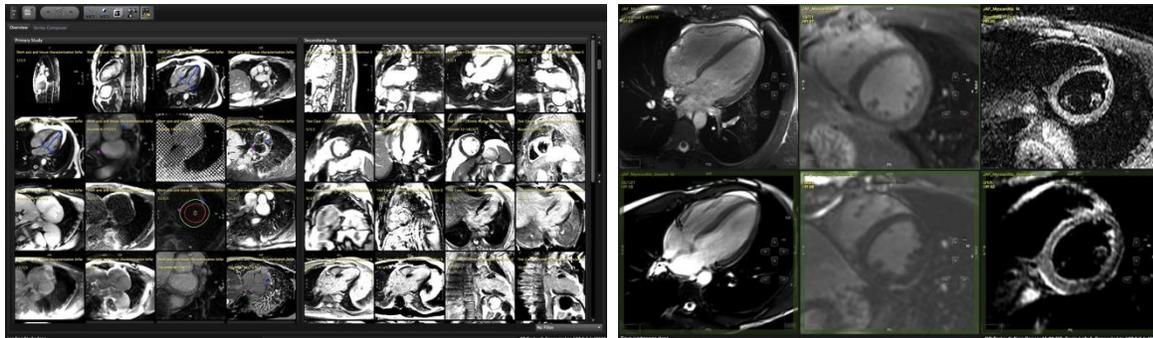
CONTEXT MENU MESH MODEL	SHORTCUT
Reset View	⌘R
Follow Module Selection	
Display Volume Frame	⇧F
Display All Overlay	O
Export as file...	
Export Image	
Export Image Multiview	
Copy Image to Clipboard	
Export Video Rotation	
Export Video Cine	
Save as DICOM Secondary Capture...	
Save Single Image	⌘⇧1
Save Rotation Images	⌘⇧2
Save Cine Images	⌘⇧3
Save Cine Rotation Images	⌘⇧4

5.4.3.1 Mesh Model Options

MESH MODEL Options			
	<input checked="" type="radio"/> Short 3D Model <input type="radio"/> Tissue Char. (Late Enh.) Model <input type="radio"/> Tissue Char. (T2) Model <input checked="" type="radio"/> Perfusion (Rest) Model <input type="radio"/> Perfusion (Stress) Model <input checked="" type="checkbox"/> Display Mesh Model M	Choose a set of contours to create a 3D Model	
	<input type="radio"/> Wall Thickening <input type="radio"/> Wall Motion <input type="radio"/> Wall Thickness Diastole <input type="radio"/> Wall Thickness Systole <input checked="" type="checkbox"/> Apply Polarmap Color C	Choose the analysis to visualize, or simply click on the corresponding polar map	
	<input checked="" type="checkbox"/> Show Endocardium D <input checked="" type="checkbox"/> Show Epicardium E <input checked="" type="checkbox"/> Show RV G <input checked="" type="checkbox"/> Show Slice Highlight H	Choose which contour to display	D - on/off endocardial contour E - on/off endocardial contour
	<input type="checkbox"/> Endocardium Wireframe Q <input type="checkbox"/> Epicardium Wireframe W	Switch to a wireframe display	Q - on/off endo wireframe W - on/off epi wireframe
	<input type="radio"/> Tissue Char. (Late Enh.) Volume <input type="radio"/> Tissue Char. (T2) Volume <input checked="" type="checkbox"/> Display Volume V	Display color overlay for LGdE and T2	
	<input checked="" type="radio"/> Image Plane 1 1 <input type="radio"/> Image Plane 2 2 <input type="radio"/> Image Plane 3 3 Unload Selected Plane U Unload All Planes %U <input checked="" type="checkbox"/> Display Image Planes N	Select the image plane to scroll through	1-3 select a plane: planes are numbered according to the order they have been loaded
		Click to pan the model	

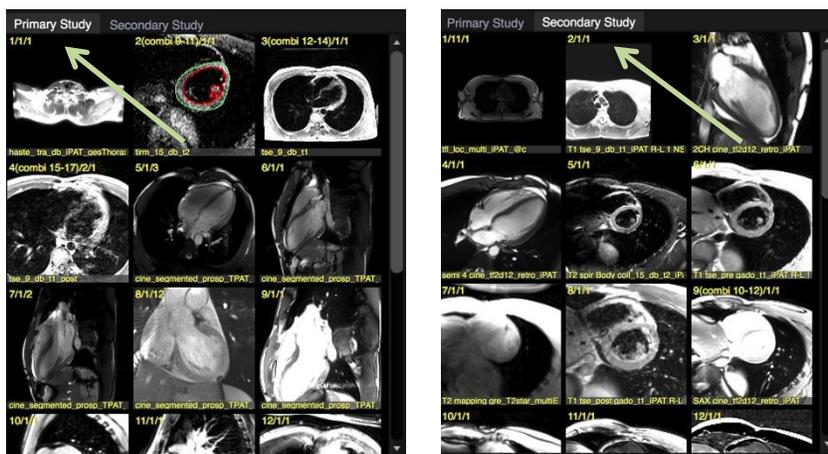
5.5 Compare Two Studies

cvi⁴² and cmr⁴² allow for the comparison of two studies side by side, even of two different modalities.



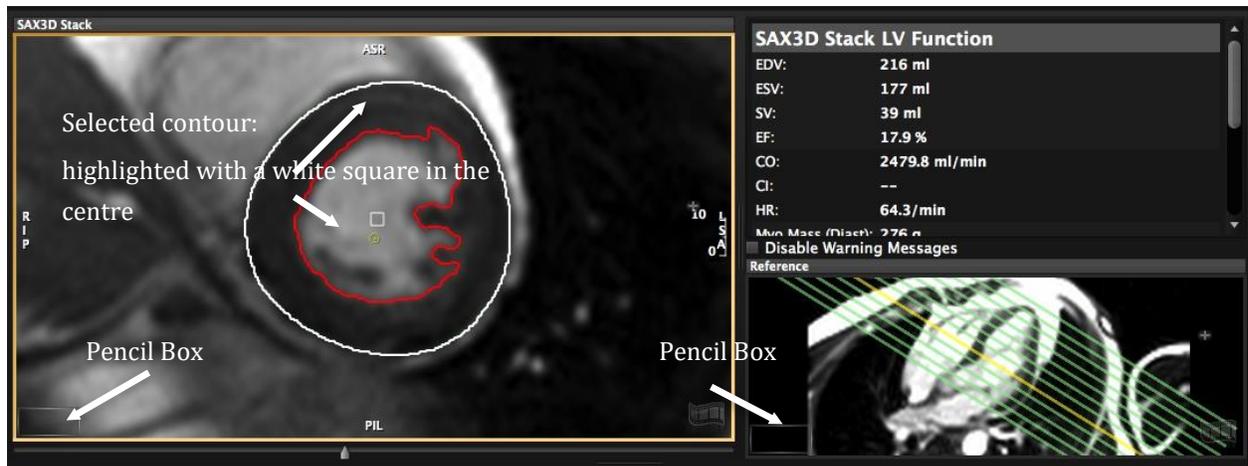
1. Load the first study (double-click)
2. Go back to the *Patient List* and load (double-click) a second study from the patient list **while holding the shift key**. (Repeating this process will substitute the second study)
3. In the *Series Overview* Module, both studies will be shown side by side.
4. In the *Viewer* Module click on the *Primary Study* tab above the thumbnails and select your images for viewing
5. Go to the *Secondary Study* tab and make your selection. Images from the secondary study are highlighted with a thicker frame
6. In the *4D Viewer* you can load either the primary or the secondary study

Analyses are only allowed for primary studies



6 Contour Drawing, Labeling and Measurement Tools

6.1 Measurement tools	36
6.1.1 Manual Contouring	36
6.1.1.1 Free-Hand Drawing	36
6.1.1.2 Free-Hand Drawing Using a Selected Drawing Mode (e.g. by setting points)	37
6.1.2 Semiautomatic Contour Detection	37
6.1.3 Automatic Contour Detection	38
6.1.4 Contour Review	38
6.1.4.1 Tips for a rapid review	38
6.1.5 Contour Propagation	38
6.1.6 Contour Saving	39
6.1.7 Contour Deletion	39
6.1.8 Add the Analysis to the Report	39



- Drawing tools are located in the top toolbar or the on-screen pencil box and in the context menu. In addition, the context menu provides multiple options for contour editing and display, export and more.
- Tooltip: All buttons show a brief description on mouse hover.
- You can label contours or the respective anatomical structure via context menu.



An overview as well as a short description of all toolbar buttons is provided in the chapter "*Toolbar Buttons*".

Tools that seem to be missing might be deactivated: Go to the *Protocol* panel, select the module and go into Edit mode by clicking the wrench and check if they are turned off.

6.1 Measurement tools

There are 2 tools that can be customized in the *Configuration or Preferences/Viewer*

1.  An angle measurement tool: By default the angle measurement will use angles within 180 degrees. Unchecked it will provide all angles. It will pick the smaller or larger angel depending on the order you set the 3 measurement points (from left to right it will measure the smaller angle and vice versa)

2.  *Perimeter* tool: By default the *Calculate Ellipse Perimeter* will measure perimeter and area of a drawn contour and in addition it will estimate a strict elliptical perimeter including it's area .

6.1.1 Manual Contouring

The toolbar is sorted into tool-sets:



for the left heart chambers;



the right heart chambers;



Buttons with a little white triangle indicate, that there are more options provided: Click and hold the LMB for displaying more options. To select, drag the cursor to the desired function and release the mouse button

6.1.1.1 Free-Hand Drawing

1. Select a tool with a LMB click.
2. To draw, click and hold the left mouse button.
3. To switch to another tool, simply click on the new tool.
4. To drop the tool, double click LMB anywhere within the frame (to change settings to leave draw mode

after drawing, go to Preferences/Viewer). Alternatively LMB click on the Leave draw mode icon  in the toolbar

6.1.1.2 Free-Hand Drawing Using a Selected Drawing Mode (e.g. by setting points)

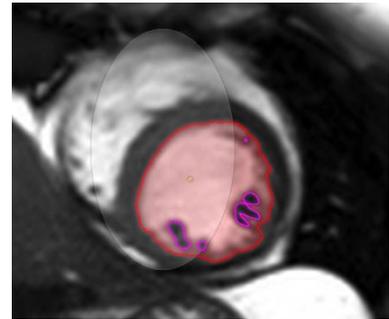
1.  Start with selecting the contouring mode,
2.  Select the contour (e.g. endocardial) you would like to draw.



Drawing Mode Options:

- *Click-Draw-Contour:* sets a series of points for edge definition. This mode is a great option when you have limited contrast, e.g. epicardial contours.
Modifier Key: "c"

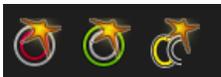
- *Threshold segmentation:* allows to define borders by dragging with the LMB downwards and sideways until you have found the threshold that best defines your border. A great contour detection mode for close contours that have distinct contrast. (e.g. endocardial and vessel contours).
Modifier Key: "alt"



- *Nudge Contour:* allows to drag part of the contour in a defined direction. The section of the contour that will be affected by dragging will be depicted by a thicker contour line. This area can be mini-/maximized using arrow keys on the keyboard.
Modifier Key: "d" for drag
- *Push Contour:* Shape the contour by pushing the circle. The circle becomes larger the further away you are from the contour when engaging the contouring mode. Alternatively you can use the arrow keys on the keyboard to in-/decrease the size.
Modifier Key: "p" for push

Click the contouring mode button or the freehand mode to exit the way of drawing. Instead of entering and exiting the mode by clicking the buttons, hold down the modifier keys while contouring.

6.1.2 Semiautomatic Contour Detection



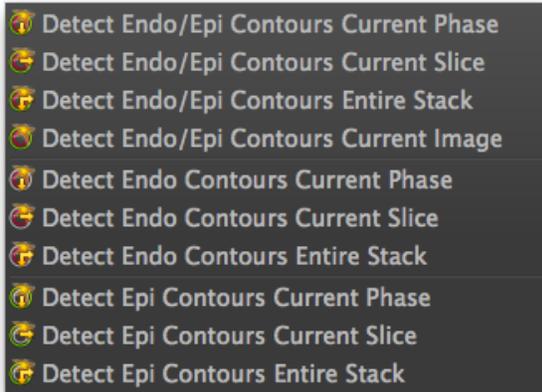
This will perform a automatic detection for either endo- (left and right ventricle) or epicardial contours

1. Target your area of analysis (LV or RV) by centering the small yellow circle (target point) in the respective chamber cavity
2. Click the button ones to apply a contour detection
3. Click and hold to adjust

6.1.3 Automatic Contour Detection



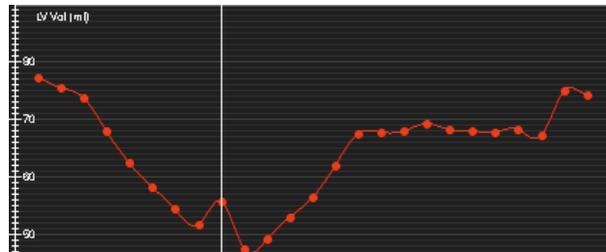
The automatic contour detection is specific to the LV function assessment in a short axis stack and allows for performing a contour detection for a group of images. Please refer to the respective chapter.



6.1.4 Contour Review

There are multiple ways to review the quality of your edge detection:

- The 4D Viewer will instantly provide a 3D model of your contours.
- Display all slices in a tile view by clicking the spacebar.
- Use the *shift-key* to toggle contours.
- Check contours of all relevant images, by using the on-screen navigation buttons or the arrow keys.
- Check by viewing a cine loop (double-click on the film-icon).
- In case you have contours in all phases, use the *LV volume curve* or the *LV myocardial mass curve* to detect misplaced contours.



6.1.4.1 Tips for a rapid review

- Holding the "shift"-key hides contours and allows checking the borders.
- Refine the contour by moving the cursor over the contour and pushing the RMB.
- Key- combination command + L rounds a contour (e.g. vessels in the Flow module)
- Key- combination command + S, smoothens out a wiggly contour

6.1.5 Contour Propagation

You can forward a contour via *Context Menu/Contours/Forward (All) Contours (slice)* or via shortcut ⌘F

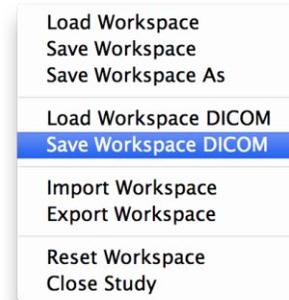
This will copy the contour across all phases within a slice. You may need to manually adjust the contours.

6.1.6 Contour Saving

Contours are saved automatically. You have the option to save a second workspace via workspace menu in the main menu bar.

A simple drag and drop of the image to the thumbnail panel will save it as a screenshot (DICOM secondary capture)

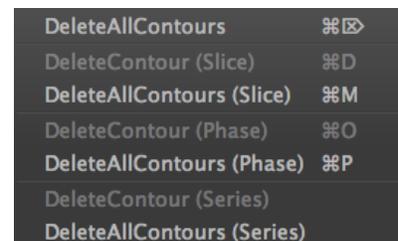
(Please refer to the *Main Menu>Workspace* chapter)



6.1.7 Contour Deletion

Shortcut ⌘X deletes a selected contour.

More options can be found in the context menu (RMB click)



6.1.8 Add the Analysis to the Report

- Measurements will be displayed either on-screen at the bottom of the viewer frame or in a reporting window
- Measurements change simultaneously with your drawing



- Add the measurements of the reporting frame to the report by clicking on the *Add to Report* button
- Add an image to your report via context menu (right mouse click and left click on *Add Frame To Report*)
- See more detailed information in the module Chapters
 -

Note: A warning message will be displayed in the results frame (and the exported reports), if

- Only one phase has been evaluated,
- The number of evaluated slices differ between systole and diastole,
- Less than 3 slices are used for calculations.

At the readers discretion, warning messages can be turned off. They will re-appear after contour alteration

WARNING: Automatic Contour Detection

The automatic contour detection provides an initial assumption of contour definitions. It is the responsibility of the user to verify and correct the results.

7 Values Reported by cmr⁴² and cvi⁴² (Clinical Report)

7.1	Left Ventricular Function	42
7.2	Right Ventricular Function	42
7.3	Atrial Volumetry	43
7.4	Late Gd Enhancement	43
7.5	T2 Signal Intensity Analysis	43
7.6	T1 Early Gd Enhancement	44
7.7	Perfusion	44
7.8	T2*	44
7.9	T1mapping	44
7.10	Flow Analysis	45
7.11	Auto Plaque	45

More values will be found in the scientific report.

PARAMETER	UNIT	REMARK
7.1 Left Ventricular Function		
LV EDV	(ml)	End diastolic volume
LV ESV	(ml)	End systolic volume
LV SV	(ml)	Stroke volume
LV EF	(%)	Ejection fraction
LV EDV/H	(ml/cm)	End diastolic volume indexed to height
LV ESV/H	(ml/cm)	End systolic volume, indexed to height
LV SV/H	(ml/cm)	Stroke volume, indexed to height
LV EDV/BSA	(ml/m ²)	End diastolic volume indexed to body surface area
LV ESV/BSA	(ml/m ²)	End systolic volume, indexed to body surface area
LV SV/BSA	(ml/m ²)	Stroke volume, indexed to body surface area
LV CO	(l/min)	Cardiac output
LV CI	(ml/min/m ²)	Cardiac index
LV MyoMass (diast)	(g)	Myocardial mass (diastolic)
LV MyoMass (syst)	(g)	Myocardial mass (systolic)
LV PapMass	(g)	Papillary mass
LV MyoMass/H (diast)	(g/cm)	Myocardial mass, indexed to height (diastolic)
LV MyoMass/H (syst)	(g/cm)	Myocardial mass, indexed to height (systolic)
LV MyoMass/BSA (diast)	(g/m ²)	Myocardial mass, indexed to body surface area (diastolic)
LV MyoMass/BSA (syst)	(g/m ²)	Myocardial mass, indexed to body surface area (systolic)
Peak Diastolic Wall Thickness (scientific report)	(mm)	
Peak Ejection Rate (scientific report)	(ml/s)	Requires contours in all slices and phases
Peak Filling Rate (scientific report)	(ml/s)	Requires contours in all slices and phases
7.2 Right Ventricular Function		
RV EDV	(ml)	End diastolic volume
RV ESV	(ml)	End systolic volume
RV SV	(ml)	Stroke volume
RV EF	(%)	Ejection fraction
RV EDV/H	(ml/cm)	End diastolic volume indexed to height
RV ESV/H	(ml/cm)	End systolic volume, indexed to height
RV SV/H	(ml/cm)	Stroke volume, indexed to height
RV EDV/BSA	(ml/m ²)	End diastolic volume indexed to body surface area
RV ESV/BSA	(ml/m ²)	End systolic volume, indexed to body surface area
RV SV/BSA	(ml/m ²)	Stroke volume, indexed to body surface area
RV CO	(l/min)	Cardiac output

RV CI	(ml/min/m ²)	Cardiac index
RV MyoMass (diast)	(g)	Myocardial mass (diastolic)
RV MyoMass (syst)	(g)	Myocardial mass (systolic)
RV PapMass	(g)	Papillary mass
RV MyoMass/H (diast)	(g/cm)	Myocardial mass, indexed to height (diastolic)
RV MyoMass/H (syst)	(g/cm)	Myocardial mass, indexed to height (systolic)
RV MyoMass/BSA (diast)	(g/m ²)	Myocardial mass, indexed to body surface area (diastolic)
LV MyoMass/BSA (syst)	(g/m ²)	Myocardial mass, indexed to body surface area (systolic)

7.3 Atrial Volumetry

EDV (left and right atrium)	(ml)	Disc summation (Short 3D Module) and area length technique (Bi-, Tri-Planar Module)
ESV (left and right atrium)	(ml)	

7.4 Late Gd Enhancement

Myocardial Volume	(ml)	Myocardial volume
Myocardial Mass	(g)	Myocardial mass (g)
Total Enhanced Volume	(ml)	Total enhanced volume
Total Enhanced Mass	(mg)	Total enhanced mass
No Reflow Volume	(ml)	No reflow volume
No Reflow Mass	(g)	No reflow mass
Enhanced Volume/Mass (relative)	(%)	Enhanced volume related to myocardial mass as calculated in the TC module
Enhanced Volume/Mass (rel SAX mean diast/syst)		Enhanced volume related to myocardial mass as calculated in the short 3D Module
Salvaged area at risk	(ml)	T2 enhanced volume - LGdE enhanced volume
Manually excluded Volume	(ml)	
Manually excluded Volume/Mass	(%)	
Greyzone volume	ml	
Greyzone mass	g	
Greyzone Volume/Mass (rel)	%	

7.5 T2 Signal Intensity Analysis

Myocardial Volume	(ml)	Myocardial volume
Myocardial Mass	(g)	Myocardial mass (g)
Total Enhanced Volume	(ml)	Total enhanced volume
Total Enhanced Mass	(mg)	Total enhanced mass
No Reflow Volume	(ml)	No reflow volume
No Reflow Mass	(g)	No reflow mass
Enhanced Volume/Mass (relative)	(%)	Enhanced volume related to myocardial mass
Salvaged area at risk	(ml)	
Manually excluded Volume	(ml)	

Manually excluded Volume/Mass (rel)	(%)	
T2 Signal Intensity Ratio		
Total Ratio		SI myocardium/SI skeletal muscle
<i>Per slice:</i>		
T2 SI Ratio		
Myocardial SI \pm SD		
Skeletal Muscle SI \pm SD		
7.6 T1 Early Gd Enhancement		
Myocardial Early Enhancement	(%)	Mean SI and standard deviation in T1
EGER		Early Gadolinium Enhancement ratio: myocardial enhancement/skeletal muscle enhancement
<i>Per slice, pre and post CA</i>		
EGER	(%)	
Myocardial Enhancement		Myocardial SI enhancement
Myocardial SI \pm SD		Myocardial SI \pm standard deviation
Skeletal Muscle SI \pm SD		Skeletal muscle SI \pm standard deviation
7.7 Perfusion		
<i>For Rest and Stress:</i>		
Baseline SI		
Max SI		
Time to max SI		
Time to 50% max SI		
Time between 20% and 80% max SI		
Maximum upward slope		The user has the possibility to specify the number of graph points used for this.
Perfusion Index (PI)		Upslope (tissue)/Upslope (LV)
Myocardial Perfusion Reserve Index (MPRI)		(PI (stress)/PI (rest))
7.8 T2*		
T2* Relaxation time	(m/s)	
R ² value		Estimation of accuracy (coefficient of determination)
7.9 T2 mapping		
Global and Regional Segmental T ₂ time	(ms)	
R ² value		Estimation of accuracy (coefficient of determination)
7.10 T1mapping		
Global and regional and segmental T ₁ time	(ms)	
R ² value		Estimation of accuracy (coefficient of determination)
ECV per slice and segment	(%)	

7.11 Flow Analysis		
Total Forward Volume (TFV)	ml	positive + negative velocities = positive value (above x-axis)
Total Backward Volume (TBV)	ml	positive + negative velocities = negative value (below x-axis)
Total Volume	ml	TFV + TBV
Net positive Volume	ml	only positive velocities (above x-axis)
Net Negative Volume	ml	only negative velocities (below x-axis)
Regurgitation Fraction	%	
Volume/min	ml/min	
Volume/min effective	ml/min	
Heart rate	bpm	
Maximum pressure gradient	mmHg	
Mean pressure gradient	mmHg	
Maximum velocity	cm/s	
Maximum mean velocity	cm/s	The phase with the maximum velocity out of all calculated mean (per phase) velocities
Minimum velocity	cm/s	
Maximum Flow	ml/s	
Minimum Flow	ml/s	
Inside Ruler Volume	ml	
Outside Ruler Volume	ml	
Comparison of two flow studies (Qp/Qs)		
Difference total volume (Flow 1-Flow 2)	ml	
Difference volume/min (Flow 1-Flow 2)	ml/min	
Ratio Total Volume (Flow1/Flow2)		
Ratio Total Volume (Flow2/Flow1)		
Ratio vol/min (Flow1/Flow2)		
Ratio vol/min (Flow2/Flow1)		
7.12 Auto Plaque		
NCP Volume	(mm ³)	
CP volume	(mm ³)	
Total Plaque Volume	(mm ³)	
Low-density NCP Volume	(mm ³)	
NCP Perc	(%)	
Low-density NCP Perc.	(%)	
NCP Burden	(%)	
CP Burden	(%)	
Total Plaque Burden	(%)	
Low-density NCP Burden	(%)	

ANALYSIS INPUT/OUTPUT

Dm Stenosis (Vessel Taper)	(%)	
Minimal Luminal Area	(mm ³)	
Mean Ref. Dist. Stenosis	(%)	
Area Stenosis	(%)	
Remodeling Index	(FU)	
Contrast Density Drop	(%)	
NCP X-sections		
CP X-sections		
Total X-sections		
Plaque lenght	(mm)	
Proximal Dm.	(mm)	
Distal Dm.	(mm)	
Max. Stenosis Dm.	(mm)	
NCP Threshold	(HU)	
Peak Threshold	(HU)	
CP Threshold	(HU)	

Modules

8 Patient List

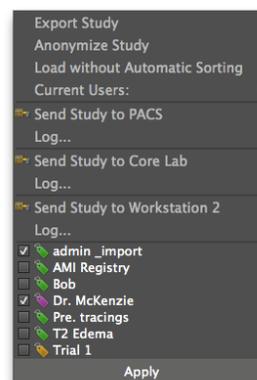
8.1	Study List	48
8.1.1	Series List	49
8.1.2	Image List	49
8.2	Study Import	49
8.3	Study Filter	51
8.4	Study Export	52
8.5	Delete Study or Series	53
8.6	Sort your Studies by Applying a Tag	53
8.7	Anonymize Studies	54
8.8	"View" Buttons	57
8.9	Rebuild Database	57

All images will be imported into the main database.

The number of studies contained in your database is displayed next to the date filter at the bottom

- It is possible to browse the database and look at images, including cines, and sequence parameter without loading a study.

- A right click on the study line opens a menu
 - Export study
 - Anonymize study
 - Load with Automatic sorting
 - Send Study to XYZ (DICOM Node)
 - Log...



In case the study has been tagged, the tags will be listed in the menu as well

The screenshot displays the 'Image Database' interface in an 'Extended View'. It features several panels:

- Study List:** A table listing studies with columns for Patient Name, Study Tags, Study Date, Patient ID, Birth Date, Import Date, Study Description, Sex, Manufacturer, and Mode. A green dot next to 'Acute MI with no reflow' indicates it is a new study.
- Series List:** A table listing series with columns for No., Receive Coil, Transmit Coil, Series Descripto, Sequence Name, Protocol Name, Contrast Bolus, Patient Position, Series Time, and Image Comments.
- Image List:** A table listing images with columns for No., Slice Location, Slice Thickness, Slice Spacing, Trigger Time, TR, TE, Flip Angle, Angio Flag, and Image Comments.
- Preview:** A large area on the right showing a preview of MRI scans, including a main view and a grid of thumbnails.

Image Database: Extended view, showing the level of information without loading

- A double LMB click opens the study and displays it in a new module, called Series Overview.

8.1 Study List

- Green dots indicate a "new study", this study has not been loaded yet.
- White highlights the study currently loaded.
- **Select the attributes** that will be displayed in the header line:

RMB click on the column header provides a context menu that allows to choose a study attribute and hide or unhide the selected column

- **Sort** the columns alphabetically with a click on the attribute in the study-list header. The sorting will be stored and will be applied at the next start up.

This screenshot shows a close-up of the Study List table. Annotations include:

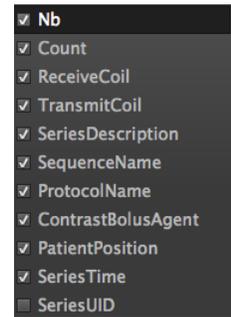
- Sorting:** A callout box with a left mouse drag icon pointing to the 'Sex' column header, with the text "Sorting: left mouse drag".
- Select attributes:** A callout box with a right mouse click icon pointing to the 'Sex' column header, with the text "Select attributes: right mouse click".

The table columns are: PatientName, PatientID, Sex, BirthDate, Age, StudyDate, AccessionNumbr, StudyTime, and StudyDescrip. The rows show various study entries with their respective values.

8.1.1 Series List

1. Click on the button *Extended View* at the bottom left will open the series and image level. Here you find series and sequence related data.

2. A RMB click on the series header row opens a menu from which the displayed parameter can be chosen.

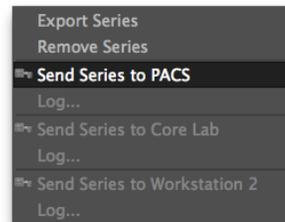


3. LMB Click on a series line to:

- display respective image parameters in the image level (section below)
- display the images of that series in the thumbnail section to the right. The selected image will be framed in green.

4. RMB click on a series allows to export, remove and send a series

5. Clicking on the *View Preview* button on the bottom right of the operation panel will open/close a preview frame on top of the thumbnail panel, displaying the first picture of the selected series.



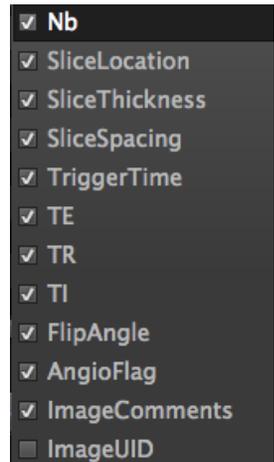
6. Click on *View Preview Cine* starts a cine in the Preview window

8.1.2 Image List

The image level displays values related to the image of a selected series.

1. A RMB click on the series header row opens a menu from which the displayed parameter can be chosen.

2. Click on an image line will frame the corresponding image in the thumbnail panel in orange and displays the corresponding image in the *Preview* frame.



8.2 Study Import

○ Import images from a folder on the computer:

1. Click on Import Images
2. Browse the computer for the images and click to activate
3. Click on “choose”
4. The status bar on the bottom left shows the progress of the download

-

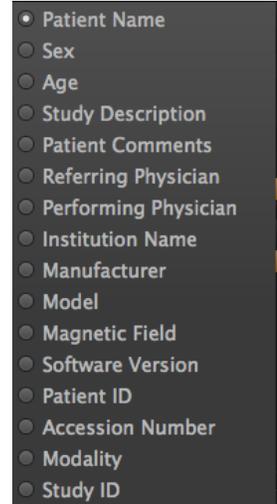
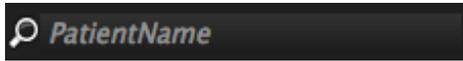
○ Import DICOM files as a command line attribute:

cmr⁴² and cvi⁴² allow the definition of a list of absolute file paths or directories to DICOM files as a command line attribute. These images will be loaded from the file system after the startup of the software. In case of an existing process, these files will be loaded by the existing cmr⁴² instance

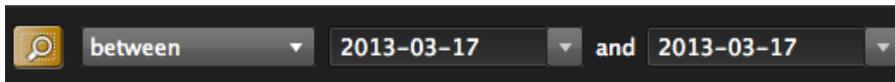
-
- Find your study:
 1. In the Patient List files are sorted according to the date. Unread files are marked by a green dot
 2. Use the filter options on the bottom of the screen (magnifying glass)
 3. Use the *Query* filter to retrieve a study from a remote DICOM server (e.g. PACS)

8.3 Study Filter

- A customizable filter is located at the left bottom corner. A RMB click on the magnifying glass opens a drop down menu, that will provide filter options

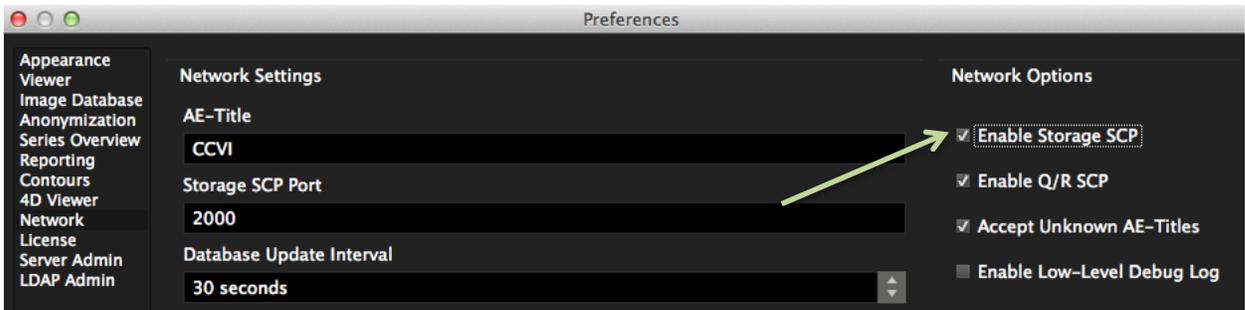


- **Date filter**, again a RMB click opens a menu to filter for
 - Birth Date
 - Study Date
 - Import Date

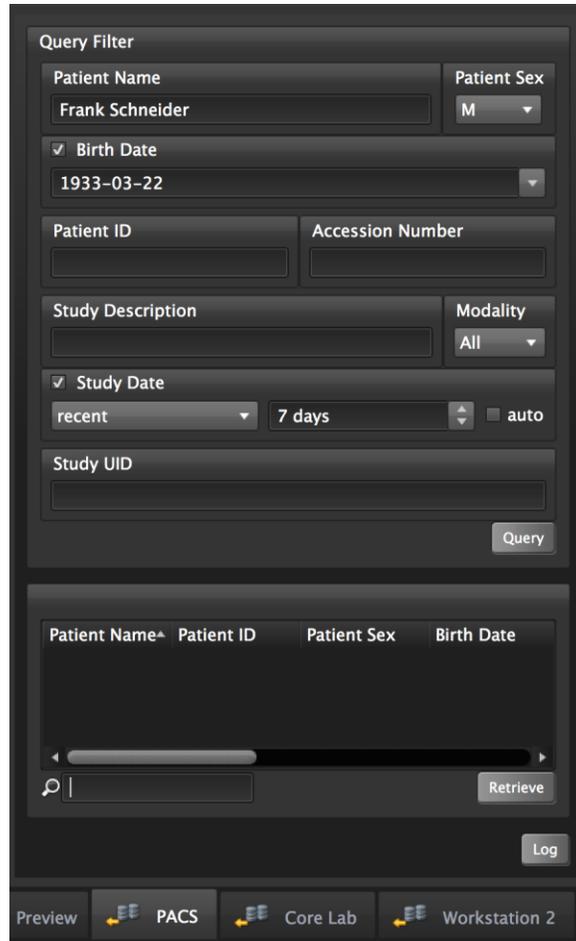


- **A Query Filter** to search a connected DICOM node.

1. In order to use the Query/Retrieve functionality, the option *Enable Storage SCP* in the Preferences, must be enabled.



2. Click on the respective server button on the bottom right, underneath the thumbnails.
3. LMB-click on *Preview* next to the server buttons to switch back to the thumbnail panel



Query Filter: The *Study Date* filter can be set to *auto*. This way you will always be presented with the chosen setting. E.g. Always filter for patients of the recent 7 days.

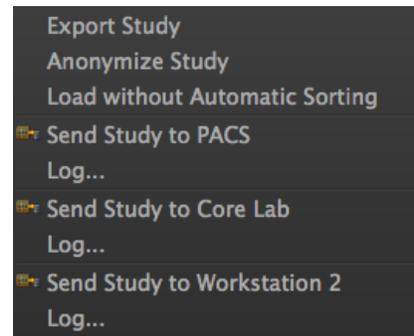
8.4 Study Export

A right mouse button click on the study opens the menu that will allow to export, anonymize or send a study:

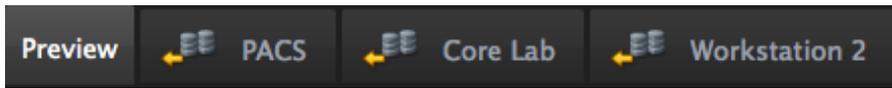
- ☉ *Export Study:* opens a browser to determine the destination

DICOM file set writer:

Activate 'Write DICOMDIR' in the *Preferences>Image Database* menu. *cmr⁴²* and *cvi⁴²* will now export studies in a directory that contains, in addition to the DICOM objects, a DICOMDIR file.



- *Send Study to...:* If you are embedded in a network the DICOM nods will be listed in the menu or underneath the thumbnail panel.

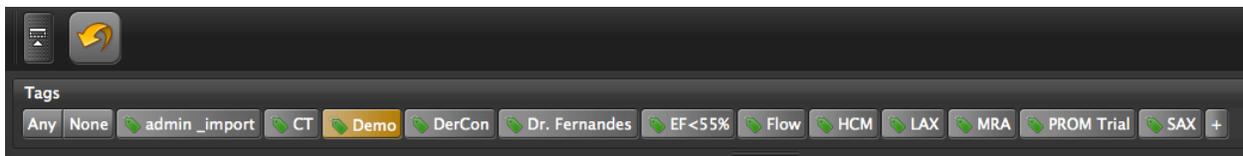


8.5 Delete Study or Series

- Delete an entire study: Click on the study, (a study that is currently open can not be deleted! Go to the *Workspace* menu and close study) and click the delete button on the bottom of the screen.
- Remove a single series: In *Extended View*, select the series from the series list , right-click on the series and select *Remove Series*

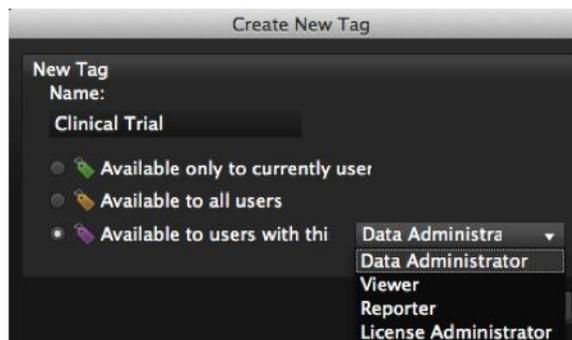
8.6 Sort your Studies by Applying a Tag

Instead of creating sub-databases you are able provide one or multiple tags to a study.

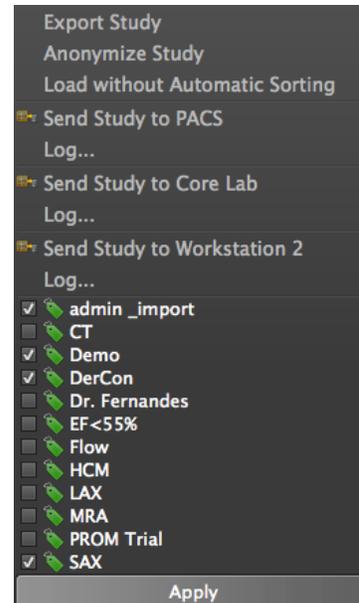
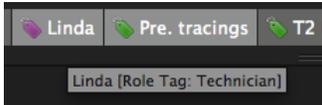


All available tags are listed above the patient list.

- To create a new tag click "+"
In the *Create New Tag Menu* provide a name and assign a user to the tag.



- There are 3 ways **to assign a tag** to a patient
 - Drag the applicable tag on the highlighted line of the patient study
 - Drag the patient study on the tag
 - RMB on the patient name opens a menu that allows to *check* and *apply* an existing tag
 -
- To **remove a tag from a study**, open the context menu and uncheck.
- To **delete a tag**, RMB click on the tag and select
- To **review assigned users** hover over the tag (tag name is "Linda" assigned role "Technician")



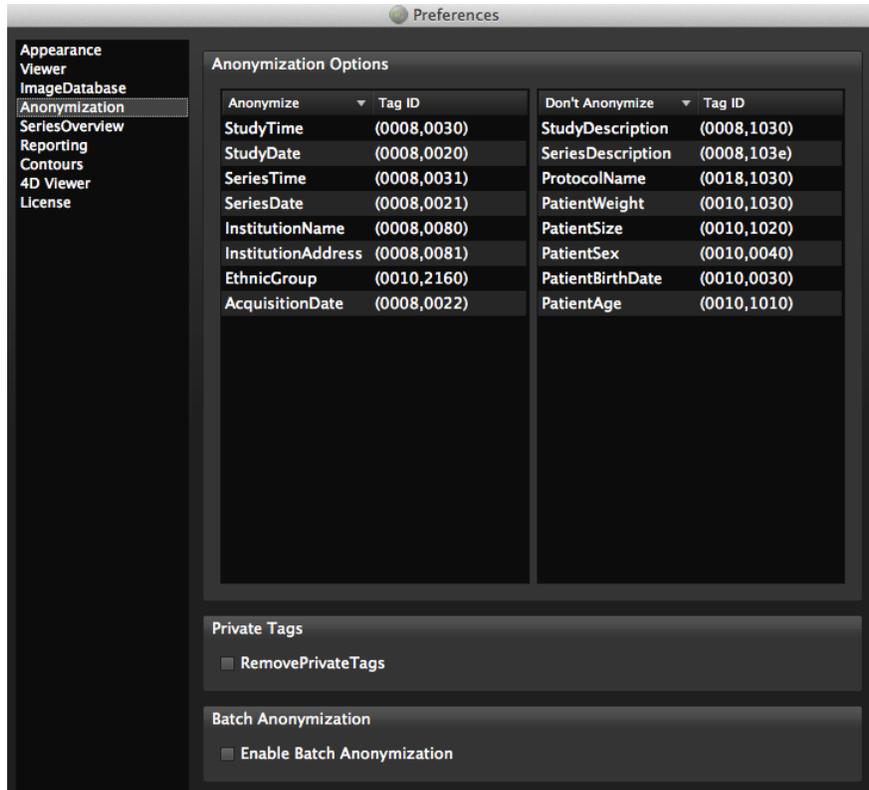
- To filter for multiple tags, hold down the command key and select as many as you wish

8.7 Anonymize Studies

Anonymization is conforming to the DICOM standard. However, depending the requirements, you have the option to disable certain attributes. (*Preferences>Anonymization*).

On all accounts the DICOM attribute *Patient Address* will be removed.

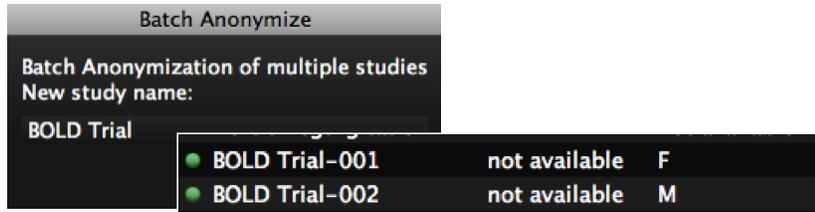
All available tracings will be included into the anonymization procedure; DICOM Secondary Captures will be re-created.



1. Customize anonymization: Set the attributes in *Preferences/Anonymisation* by dragging the attributes that you wish to keep into the right column.
2. RMB click on the Patient study in your database to open a context menu
3. Click on *Anonymize*
4. Provide an identifier
5. Click ok
6. The old study will be kept, the anonymized study will be appended to your patient list

○ Anonymizing multiple studies at once (*Batch Anonymization*):

1. Go to Preferences/Anonymization and check Batch Anonymization
2. Multiple studies can now be selected from the image database (holding the shift key selects continuous studies, cmd/ctrl selects multiple non sequential studies).
3. LMB click on Anonymize opens a dialog: provide a name.



4. Anonymized studies will be labeled with the name provided (e.g Snow Trial) and a number will be assigned

- Snow Trial 2014-001
- Snow Trial 2014-002
- Snow Trial 2014-003
- Snow Trial 2014-004
- Snow Trial 2014-005

5. Track anonymization: You will find a list of your anonymized studies in the folder *cvi42/ServerLogs/logAcces.txt*.

- Open the file in *Text Edit* and search for the Identifier (e.g Snow Trail 2014):
- Mc Carthy - Snow Trial 2014 -001
- Mayer - Snow Trial 2014 -002...

```

logAccess.txt
Snow Trial 2014
Sun Feb 16 15:37:30 2014 Success,127.0.0.1,127.0.0.1,admin,AnonymizeStudy(unknownu
McCarthy, Snow Trial 2014-001, [default]MainDB,, false, StudyTime, StudyDescription,
ProtocolName, InstitutionName, InstitutionAddress, EthnicGroup)
Sun Feb 16 15:37:30 2014 Success,127.0.0.1,127.0.0.1,admin,DatabaseStatistics()
Sun Feb 16 15:37:30 2014 Success,127.0.0.1,127.0.0.1,admin,GetStudyList()
Sun Feb 16 15:37:30 2014 Success,127.0.0.1,127.0.0.1,admin,EnumerateWorkspaces(adm
Sun Feb 16 15:37:30 2014 Success,127.0.0.1,127.0.0.1,admin,GetStudyHashes(MainDB,u
Adam Ashton)
Sun Feb 16 15:37:41 2014 Success,127.0.0.1,127.0.0.1,admin,AnonymizeStudy(unknownu
Mayer, Snow Trial 2014-002, [default]MainDB,, false, StudyTime, StudyDescription, Stu
ProtocolName, InstitutionName, InstitutionAddress, EthnicGroup)
Sun Feb 16 15:37:43 2014 Success,
127.0.0.1,127.0.0.1,admin,SaveWorkspace(admin, unknownunknown1.2.276.0.7230010.3.1.
.0.549.1361383803.450575, {00000000-0000-0000-0000-000000000000}, false, false, ByteAr
Sun Feb 16 15:37:50 2014 Success,127.0.0.1,127.0.0.1,admin,DatabaseStatistics()
Sun Feb 16 15:37:51 2014 Success,127.0.0.1,127.0.0.1,admin,AnonymizeStudy(unknownu
Morgan, Snow Trial 2014-003, [default]MainDB,, false, StudyTime, StudyDescription, St
ProtocolName, InstitutionName, InstitutionAddress, EthnicGroup)
Sun Feb 16 15:37:54 2014 Success,127.0.0.1,127.0.0.1,admin,AnonymizeStudy(unknownu
Smith, Snow Trial 2014-004, [default]MainDB,, false, StudyTime, StudyDescription, Stu
ProtocolName, InstitutionName, InstitutionAddress, EthnicGroup)
    
```

- When using the option *Remove Private Tags* a warning will be displayed in case velocity encoded images are about to be removed (applies GE and Philips).

Caution: For clinical trial purposes anonymization has to be validated by the readers/core lab)

WARNING: Anonymize

The Anonymization/Pseudonymization of DICOM data sets removes all data that are selected. In addition to the DICOM information, cmr⁴² removes another subset of DICOM tags with private information. The end user must decide whether this level of removal satisfies the local regulations/policies of the institute.

8.8 "View" Buttons

- *ExtendView*: displays series and image information
- *View Preview*: A Preview Window above the thumbnails will open
LMB click on the pencil box in the left bottom corner will provide tools for simple measurements.
- *View Preview Cine*: allows to play a cine loop in the *Preview* window

8.9 Rebuild Database

In case the database seems to be corrupt it has to be rebuild. Therefore the system will re-read the content of the sub database folder into the cmr42-image database.

You have to have administrator rights to rebuild. In the *Preferences>Server Admin>Rebuild Database* you will find the following option

Update Image File Path - This option rebuilds paths to the images in the cvi42 database without having to perform a full database rebuild. Typically used when images are not displaying due to migration of existing images and/or migration of the cvi42 database to a different drive or machine.

Import Orphaned Workspaces - This option rebuilds the linkage between user workspaces and studies. If there are workspace files that the cvi42sql db does not know about in the /ProgramData/cvi42/users folders (in each user's workspace folder) then the association is rebuilt, without having to perform a full database rebuild. Typically used when workspace associations have been broken due to migration of the database/workspaces to a different drive or machine.

Full Database Rebuild - Complete rebuild of the cvi42 database. Includes rebuild of the workspace associations and updating the image data file paths. This option can take a long time to complete, as it needs to re-read every image in the database. Use with caution, as cvi42 will not be available during this time. Before starting a full database rebuild, we recommend to use the *Go Offline* button to place the cvi42 server in an "offline" state so that client connections are not permitted during the rebuild process.

9 Patient Data

9.1 View DICOM Header Information	58
9.2 Enter Patient Data	58
9.2.1 Enter Patient Related Comments.....	59
9.2.2 Create a Case Review Presentation.....	59

Patient-Data Module: Editing patient data and annotations, and creating a case review report

9.1 View DICOM Header Information

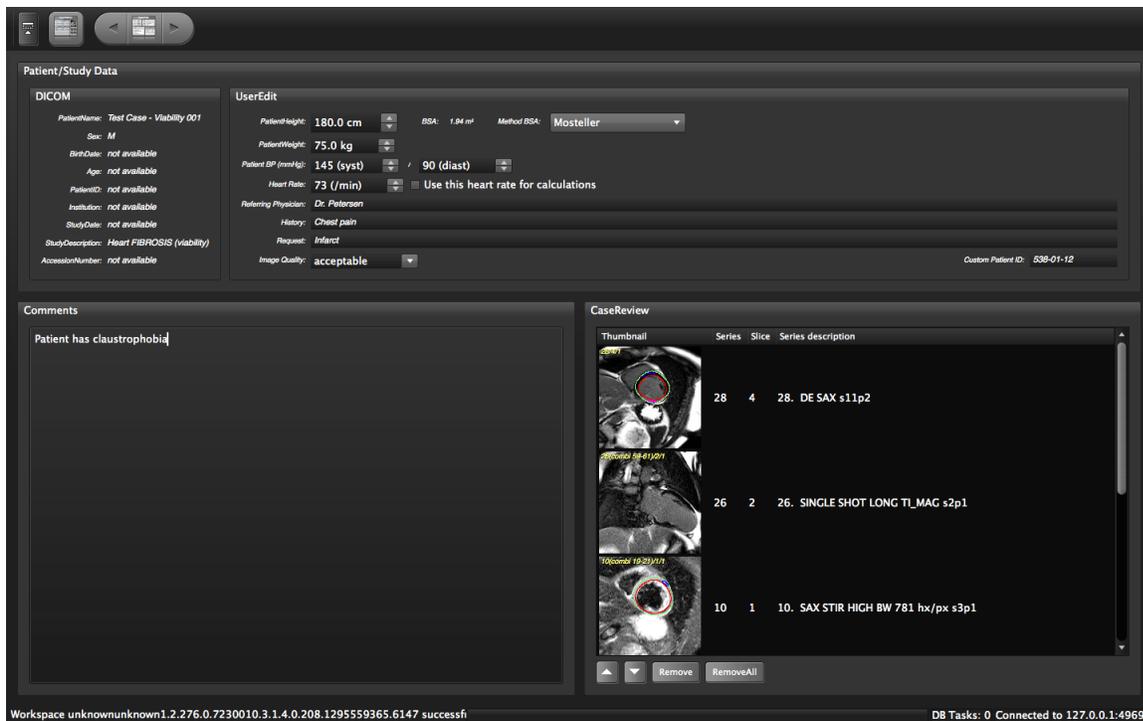
DICOM Frame on the top left, displays DICOM Header information

WARNING: Patient Data

The displayed study/patient data is initially derived from the DICOM information if available. Note that editing these values affect the calculations of all modules. It is the responsibility of the user to verify these data before releasing final results.

9.2 Enter Patient Data

The User Edit Frame allows you to enter patient related data, which are necessary for calculation, documentation and reporting.



You have the option to change the units from metric to imperial. Go to *Preferences/Appearance/Patient Data Metric*. Settings will be updated as soon as you load the next patient.

Note: The software retrieves the heart rate from the first image of a series. Please check for probability and make sure the correct heart rate is entered, before you tick the “use this heart rate for calculation” box.

A heart rate over 250 bpm will not be displayed. The value remains at 250 bpm.

9.2.1 Enter Patient Related Comments

The Comments Frame allows you to type in comments for internal purposes.

9.2.2 Create a Case Review Presentation

The Case Review Frame displays the images, which had previously been selected for a case review.

1. **Select an Image for Case Review:** Select your image for review via context menu Add Current Series to Case Review or .
2. **Change the Order of the Images:** Select an image and click on the arrow buttons underneath or simply drag and drop the image to the desired position.
3. Present Your Case Review
 - If the study is already open: Go to *Overview* and select *Case Review* in the Filter.

- If you would like to present the case at a later time point: Before you leave cmr⁴², go to the *configuration/Series Overview* and check *Case Review*. The next time you open the study, the *Study Overview* windows will display the previously selected Case Review Images

10 Report Module

10.1	The Clinical Report	62
10.2	Review the Scientific Report	63
10.3	Edit the Report	63
10.4	Customize the Header and Generate Canned Text	64
10.4.1	Writing the Text File	65
10.4.2	Create canned Text (Example)	65
10.4.3	Adding a Logo	66
10.4.4	Add Your Phrase to the Report	66
10.5	Save and Export the Report	66
10.5.1	Save and Export the Clinical Report	67
10.5.2	Save and Export the Scientific Report	67
10.5.3	Export the Scientific Report into Excel or Numbers.	68

10.1 The Clinical Report

1. In the Analysis modules click the *Add to Report* button . This will add measurements, images, and polar maps to the report.

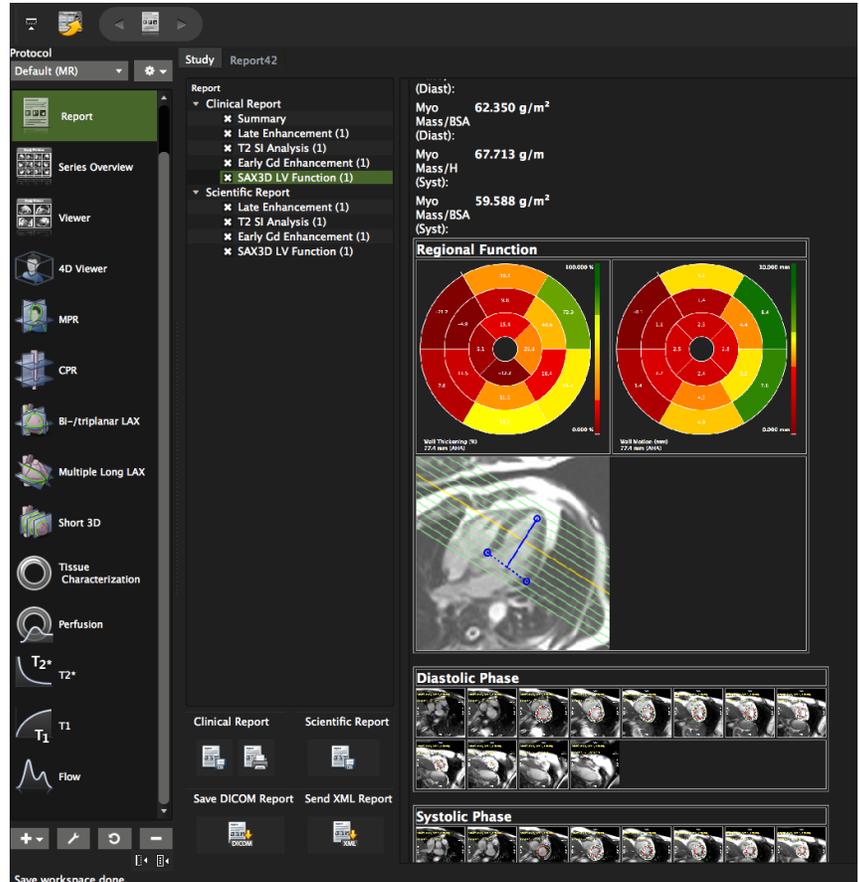
4. The **AddFrameToReport** command in the *Context Menu* allows adding additional images.

5. To review report additions, navigate to the *Report* module.

6. You will find a report panel next to the protocol pane. *cvi/cmr⁴²* automatically generate a *Clinical* and a *Scientific Report*.

7. Click on the line, e.g. *Late Enhancement* to view the report.

8. To remove a certain part, do a RMB click on , e.g. *Late Enhancement* the and select **Delete**

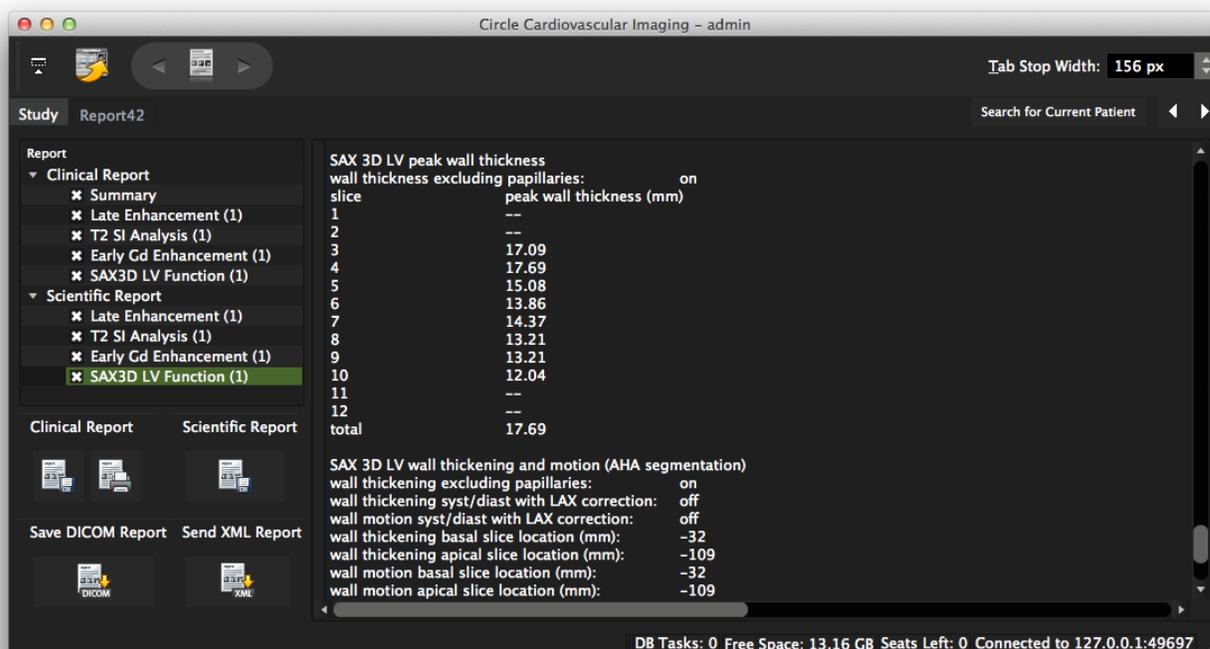


9. To remove warning messages from the report, go back to the analysis module and check the box in the report window: **Disable Warning Messages**

10.2 Review the Scientific Report

For scientific purposes, cvi/cmr⁴² has the option to display all calculated values (e.g. each SI per phase).

For further analysis the scientific report can easily be transferred into a spreadsheet. See below: export the scientific report



10.3 Edit the Report

Clicking on the Summary in the left panel will display the editing frames for the:

- Header frame
- Patient related data
- Findings frame
- Summary frame (if you are not in Full Screen mode, you need to scroll to get to it)
- Text Module frame

cvi/cmr⁴² automatically retrieves the patient related data from the DICOM Header as well as from the Patient-Data module where the patient specific data is entered.

42

Robert Koch
Charité
Berlin-Mitte

Cardiovascular Magnetic Resonance Study Report

Patient Name:	JAF_Myocarditis	Institution:	not available
Patient Sex:	M	Study Date:	HERZ Herz
Birth Date:	1993-04-11	Study Description:	2013-03-21
Age:	19 Y.	AccessionNumber:	not available
Patient ID:	not available	cv42 Version:	4.1.0
Custom Patient ID:			
Height:	187 cm		
Weight:	85.0 kg		
BSA:	2.10 m ² (Mosteller)		

10.4 Customize the Header and Generate Canned Text

cmr⁴²/cvi⁴² provides the option to customize the header and to define 'pre-canned' text modules.

Findings

Normal LV function with regional wall motion abnormality
Left ventricle not enlarged (EDV ml/cm, ESV ml/cm),

Summary

Normal LV function with regional wall motion abnormality
No evidence for stress-inducible wall motion abnormality

TextModules

- ▼ Myocardial ischaemia
 - Adenosine
 - Dobutamine
 - Aortic valve stenosis
 - Hypertrophic Cardiomyopathy
 - ARVC
 - Viability/infarction
 - LV thrombus
 - Aortic regurgitation
 - Pericardial effusion

No evidence for stress-inducible wall motion abnormality
Stress-inducibility mild/moderate/severe wall motion abnormality in the basal/mid/apical anterior/lateral/posterior/inferior/inferoseptal/anteroseptal region
Mild wall motion abnormality at rest without aggravation at stress, not typical for significant coronary artery stenosis.
Mild wall motion abnormality at rest with aggravation at stress, but not typical for significant coronary artery stenosis.
Significant perfusion deficit at rest with aggravation at stress, compatible with significant coronary artery stenosis.
Significant perfusion deficit at stress without abnormalities at rest, indicating significant coronary artery stenosis.

10.4.1 Writing the Text File

1. Create a text file (see example below)
2. Save it with the suffix ".conf"
3. Copy the file (e.g. "cmr42ReportText.conf") into the Documents/cvi42 (or cmr42) folder
4. Restart the software

10.4.2 Create canned Text (Example)

Indentations and empty lines will be ignored.

☉ The first "tag" will be your **name/affiliation/institution**

1. Type [InstitutionName] in rectangular brackets in the first line
2. Next line will be your free text: Institution name and address
3. [/InstitutionName] ends the command

☉ Standard phrases (example):

1. Type [LV function] in rectangular brackets in the first line
2. Next line will be your free text: e.g. Left ventricle not enlarged, no hypertrophy
3. [/LV function] ends the command

[InstitutionName]

Sunshine General Hospital

Success Rd

Somewherenice, 2013

[/InstitutionName]

[Standard phrases for reports]

[LV function]

Left ventricle not enlarged (EDV ml/cm, ESV ml/cm), no hypertrophy (LV mass g/cm) with normal/globally mildly/moderately/severely reduced left ventricular systolic function; regional mild hypokinesis/moderate hypokinesis/severe hypokinesis/akinesis/dyskinesis in the basal/mid/apical anterior/lateral/posterior/inferior/inferoseptal/anteroseptal region / without regional wall motion abnormalities; Ejection fraction normal/mildly impaired/moderately impaired (45 to 55%)/severely impaired, % (triplanar evaluation).

[/LV function]

[/Standard phrases for reports]

[Standard phrases for report summaries] _____

[LV function]

Normal LV function

Normal LV function with regional wall motion abnormality

Impaired LV function with global hypokinesia

Impaired LV function with basal/midventricular/apical anterior/lateral/posterior/inferior/septal/anteroseptal hypokinesia

Severely impaired LV function with global hypokinesia

[/LV function]

[/Standard phrases for report summaries]

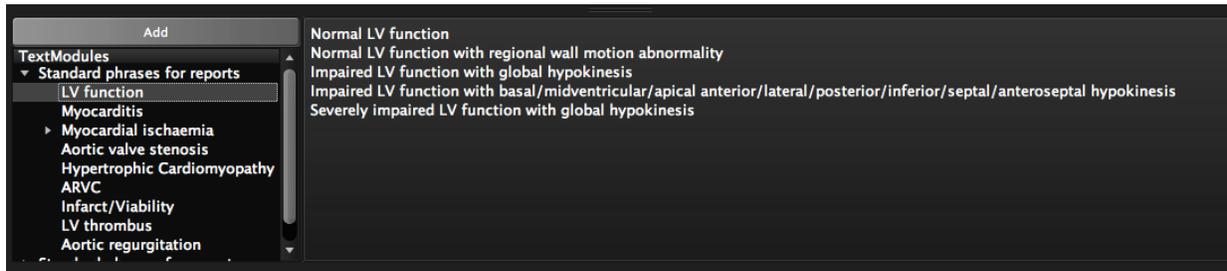
Repeat for other modules in the same way.

[First Pass Perfusion]

text

[/First Pass Perfusion]

After restarting, a window will appear with the text modules next to the save and export buttons.



10.4.3 Adding a Logo

- The filename has to have the extension ".png" .
- Depending on which side of the report the logo should be placed, add "Right" or "Left" to the name e.g. : *RockyMountainHospitalLogoLeft.png*
- The file has to be copied into the *cvi⁴²* folder within the documents folder.
- Restart the software

10.4.4 Add Your Phrase to the Report

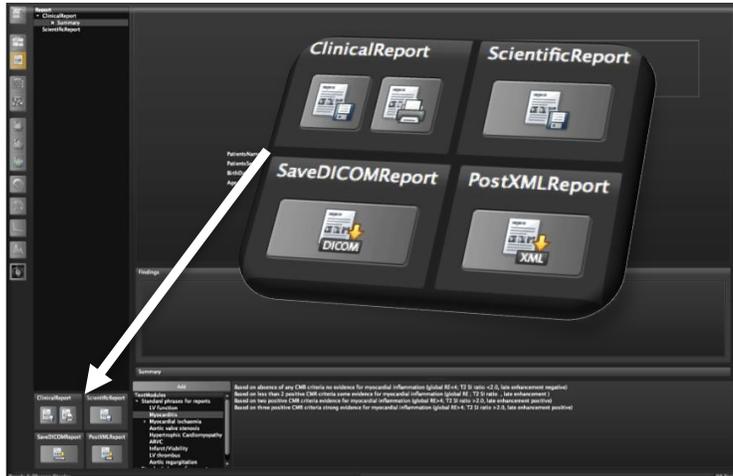
- To select a phrase, select an editing window (*Findings* or *Summary* box) with a left mouse click.
- From the menu, select the Text Module. The complete text will be shown in the right window. Click *Add*
- To preview the report: go to Print Clinical Report/PDF/Preview

10.5 Save and Export the Report

Unlike the tracings, reports will not be saved automatically in the patient study. **Closing the study will result in losing previously added analyses, text editions in the Findings and the Summary frame.**

To save the report, either save it as a separate file to the desired location or take a DICOM Secondary Capture. The secondary capture will be added to the image series and will reside within the study for future review.

On the bottom of the reporting panel there are several options to save, print and export reports.



10.5.1 Save and Export the Clinical Report

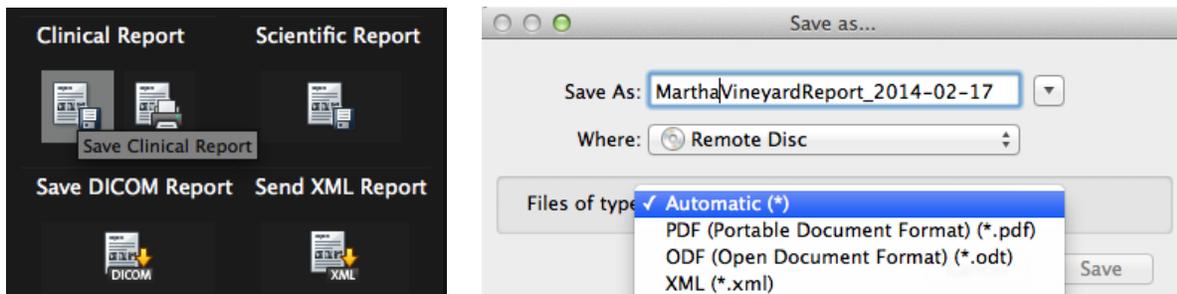
Clicking on the Save Clinical Report button provides the following options:

- Automatic
- PDF
- XML

Saving it in an open text format allows to make changes.

10.5.2 Save and Export the Scientific Report

Clicking on the button on the bottom left, lets the user save the scientific reports in different formats



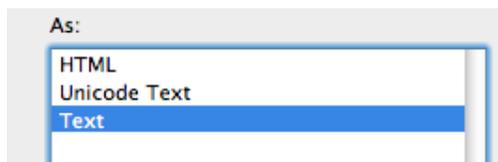
10.5.3 Export the Scientific Report into Excel or Numbers.

The Report can be copy-pasted into Excel (Microsoft) or Numbers (Mac).

To transfer the analysis into Numbers, simply copy and paste the measurements into Numbers.

To transfer the report into Excel, one extra step is required otherwise all numbers will be pasted into one column:

- a) Copy the Report
- b) Open Excel
- c) In Excel go to the Edit menu
- d) Choose Paste Special
- e) A dialog will open, choose Text



11 Series Overview

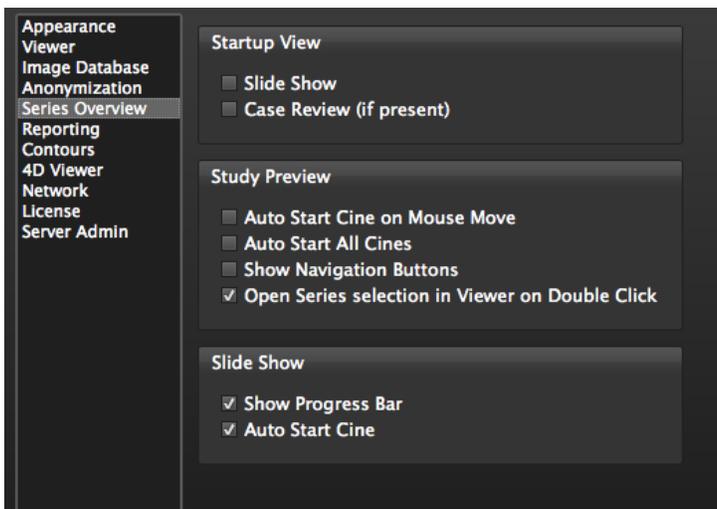
11.1	Series-Overview configuration	69
11.2	Features	70
	How to open a series in one of the analysis module	70
	How to use a multiview window as an add-on viewer in other modules	70
11.3	Series Composer	72

Intended use:

- Get a quick, in-depth overview of sequences and images
- Choosing the right image/ series for evaluation.
- Series Composer sub-unit allows for recomposing studies

11.1 Series-Overview configuration

Settings for the Series Overview can be changed in the *Preference>Series Overview*



11.2 Features

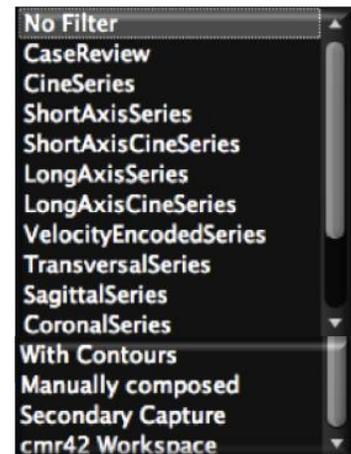
- Synchronization options (toolbar)
 - Zoom
 - Windowing: series that shall be synched should be selected first. Press the command key while selecting with a LMB click
- Display options (toolbar)
 - Slide Show Mode: Will always present the first image of the series use the on-screen navigatin buttons to move to the next slice/phase or series
- Multiview Mode: opens a series and displays all images next to each other (Short-cut-key: spacebar). The *Multiview* layout can be added to the report via context menu (*Add Frame To Report*)



- **Cines** are tagged with this symbol .
By default cines start as soon as you move the mouse over the image. To stop the cine, click on the icon.
- **Stacks** will always display the first image of that series.
- Click on the spacebar will open the stack and display all images in a **multi-view** fashion (see below Multiview) . Click again to go back
- Double-click on the image will display it in the **Viewer** module
- A **filter** is located at the bottom right of the toolbar

How to open a series in one of the analysis module

1. Select the series
2. Drag and drop it into one of the modules in the module pane *or*
Open the context menu with a RMB click and select the module from here *or*
Go to the toolbar and use the module selection button *or*
Open the analysis module and drag and drop the series from the thumbnail



How to use a multiview window as an add-on viewer in other modules

A *Multiview* display shows all images of a selected series in a new window. The window can be undocked and shifted

Select a series with a left mouse click.

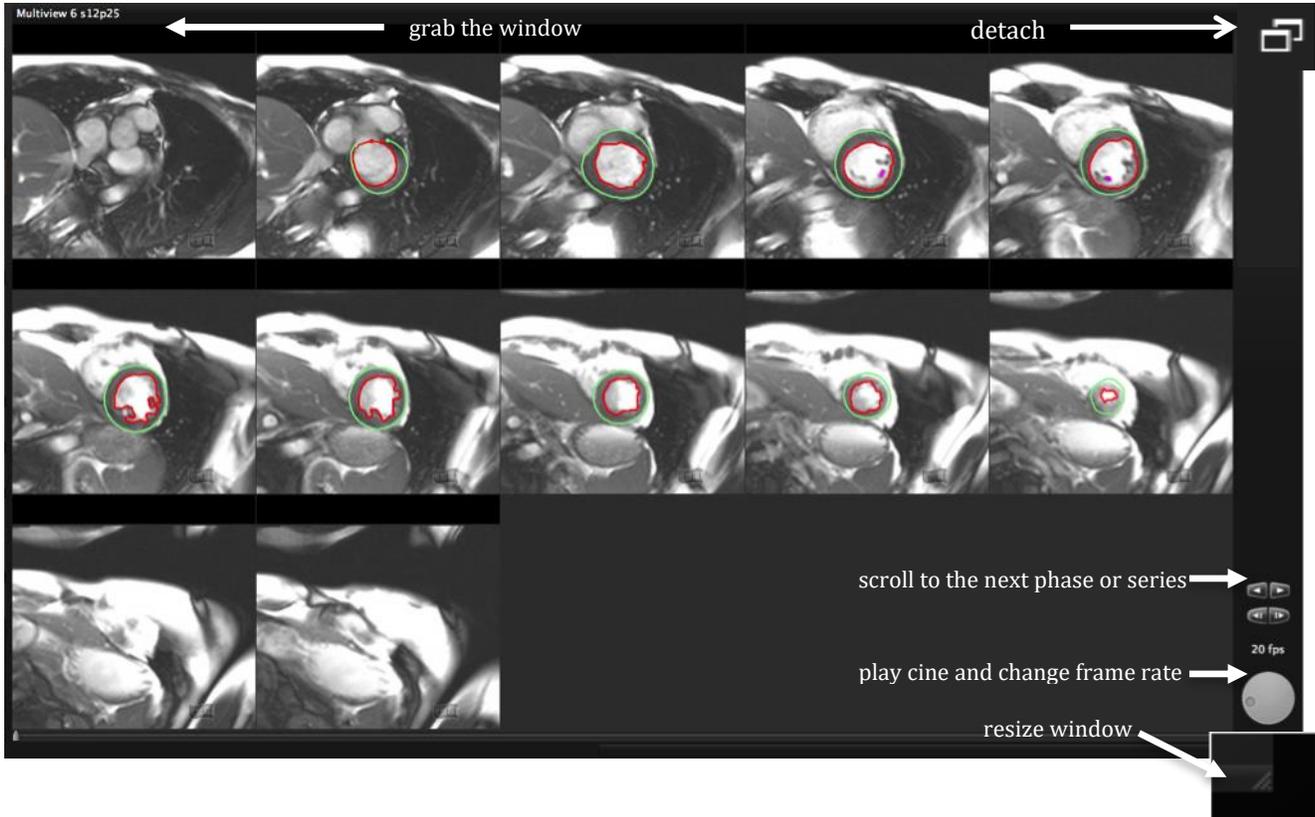


To open up the series either use the *Multiview button* (if present) or simply click the spacebar of your keyboard to open the selected series.



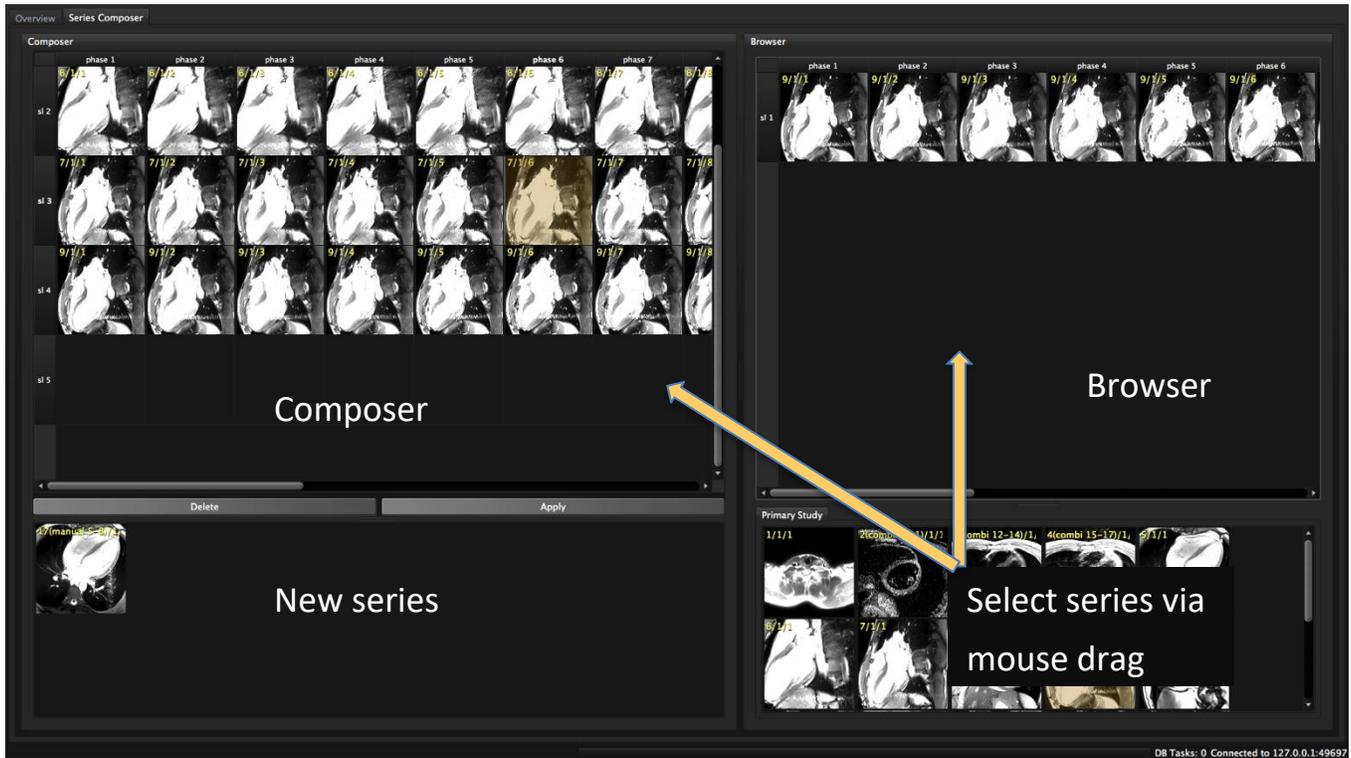
The window can be undocked and resized. It will now stay on screen even if you change modules.

Contours in the *Multiview* can be altered. With the short-cut-keys you can even engage a certain drawing mode (*threshold segmentation="alt"* or *click-draw="c"*).



11.3 Series Composer

The Series composer allows to generate new manually composed series



1. Drag a series to the *Browser*, choose slices or phases and drag them into the composer:
Click on the slice or phase number to select all. To select a row of images press the the control key; or for multiple individual images the command key, while selecting via left mouse click.
A complete series can be dragged directly to the composer
2. For sequence information (e.g. trigger time or slice location) hover over an image.
3. In the *Composer* select the phase/slice or series and use the context menu to remove, insert or sort images
4. Click *Apply* to assemble the newly composed series. The lower window provides a showcase for newly composed series.
5. A newly composed series will automatically be appended to the list of series. Manually composed series can be identified by their tag (e.g. 28 (manual 9/1/1))

Clear Cells	⌘X
Remove Slices	⌘D
Remove Phases	⇧⌘D
Insert Slice	⌘I
Insert Phase	⇧⌘I
Sort by Slice Location	
Sort by Time	

Plausibility check: cmr/cvi⁴² performs a plausibility check before it assembles a new series.

Composition refused if the following check fails:

1. all images have the same frame of reference
2. for stacks containing velocity encoded images:
 - series has exactly two slices,
 - both slices have the same slice location,
 - both slices have the same acquisition time,
 - only images in the first slice are velocity encoded.
 - both slices have the same number of phases,
 - trigger times in every phase is equal between both slices,
 - all images have the same orientation normal.
- Warnings will be shown if one of the following checks fails:
 3. same number of phases in each slice
 4. parallel slices or slices with a central rotation axis
 5. for parallel stacks:
 6. equal slice distances,
 7. sort order from basal to apical.

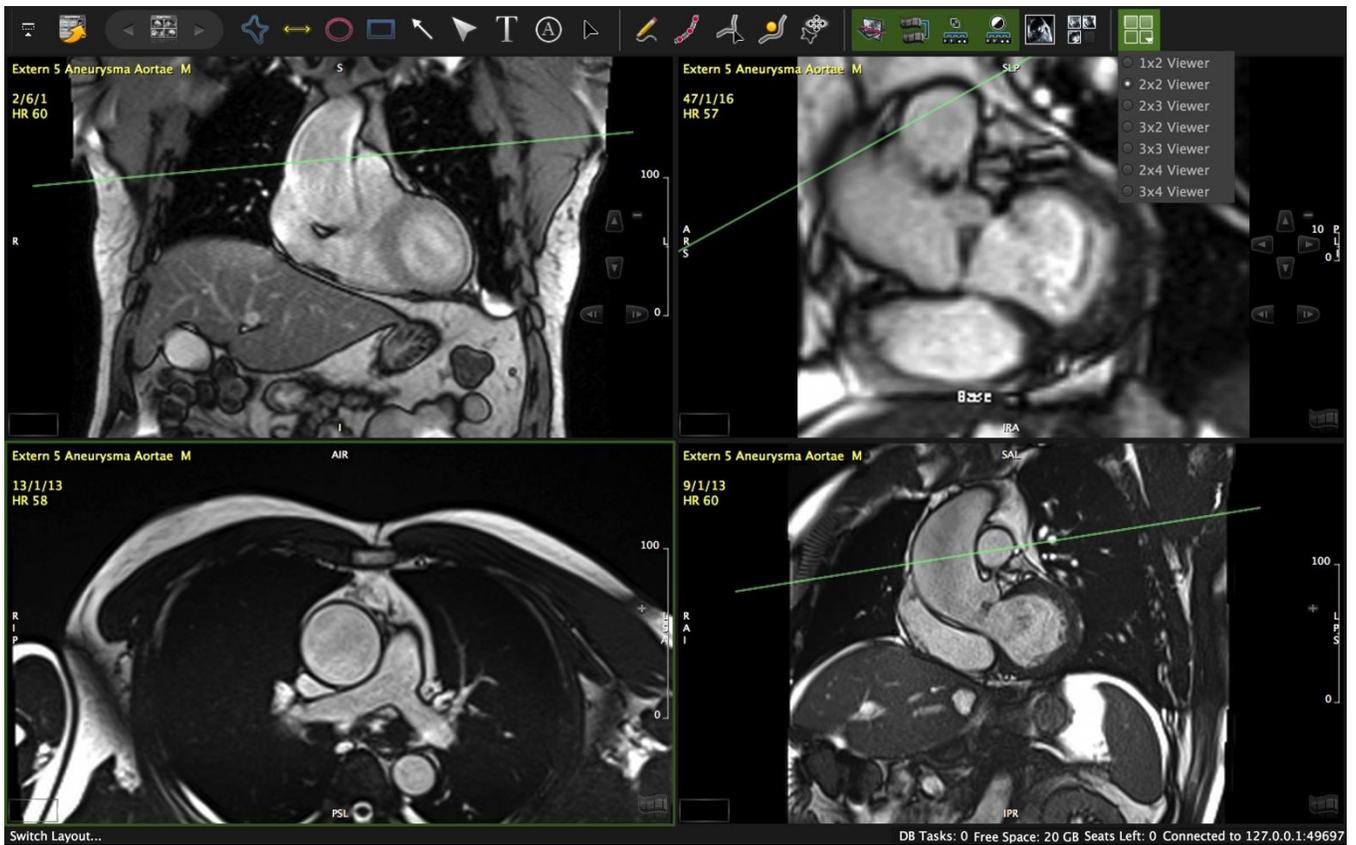
In some cases, the user is offered the choice to continue or to ignore the warning. It is at the users discretion to accept.

12 Study Viewer Module

12.1	Change the number of view ports	74
12.2	Optimize Image Viewing	75

12.1 Change the number of view ports

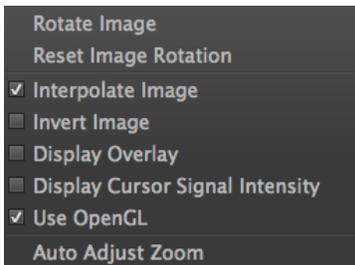
The study viewer offers different layout views from 2 to 12 view ports.



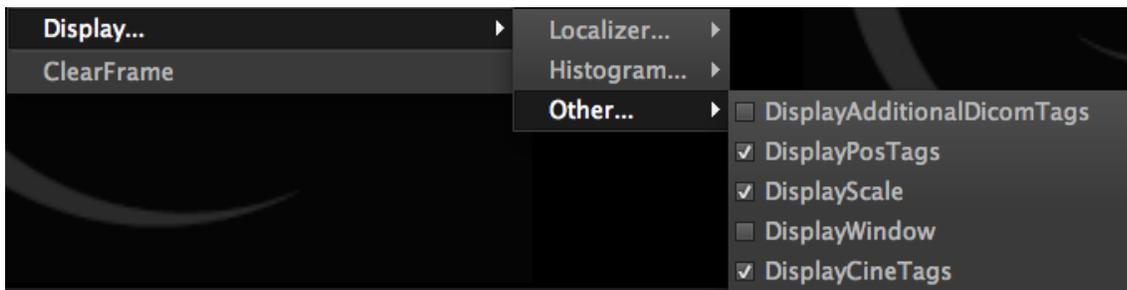
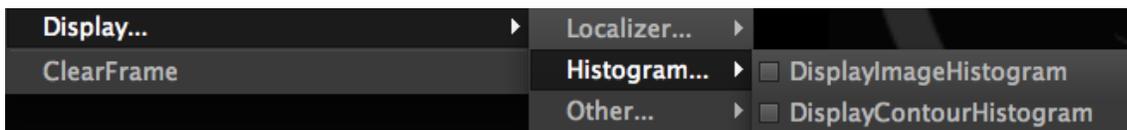
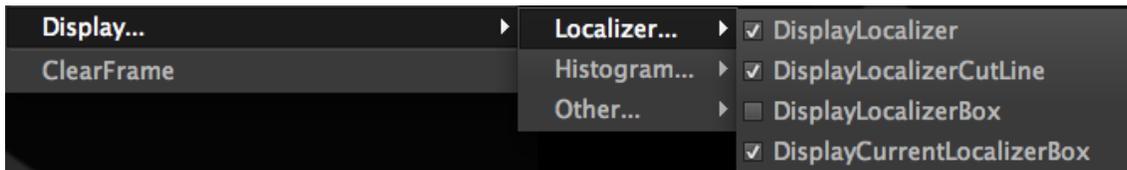
12.2 Optimize Image Viewing

- Images can be synchronized for cines, zooming and windowing.
- Cines will be displayed in real time speed. By pressing the “S” key during cine display the speed shall be reduced to half of the real time speed.
- In addition there are cross reference displays, contouring and annotation options.
- A context menu that opens with a right mouse click, allows for more features including multiple *Display* and *Export* options.

○ *Image* menu



○ *Display* menu



13 4D Viewer

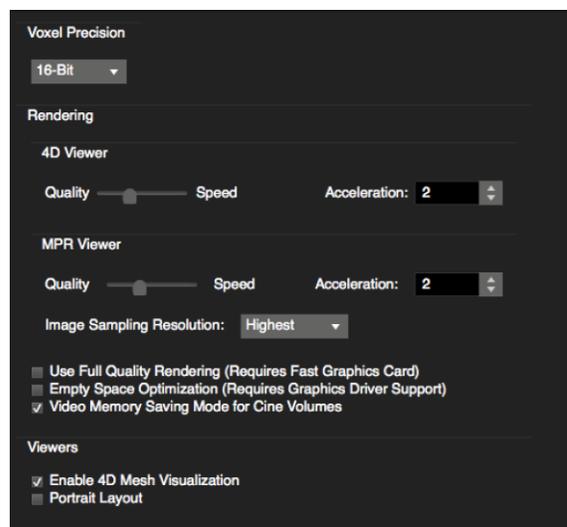
13.1	Edit	77
13.1.1	4D Viewer Control Features (Table)	78
13.1.2	How to use the measurement option	81
13.1.3	Rendering Options	82
	How to do a Segmentation in the 4D Viewer Module	83
13.1.4	Segmentation Options (CT only)	83
13.1.5	Manual Segmentation	84
	How to use clipping and cropping	84
	How to create a custom Background MIP	84
	How to use the growing tool	85
13.2	Color	87
	How to Save and Export 3D/4D Rendered Images	90

This viewer is designed to analyze 3D and 4D data such as MR and CT (cvi⁴² only) angiography.

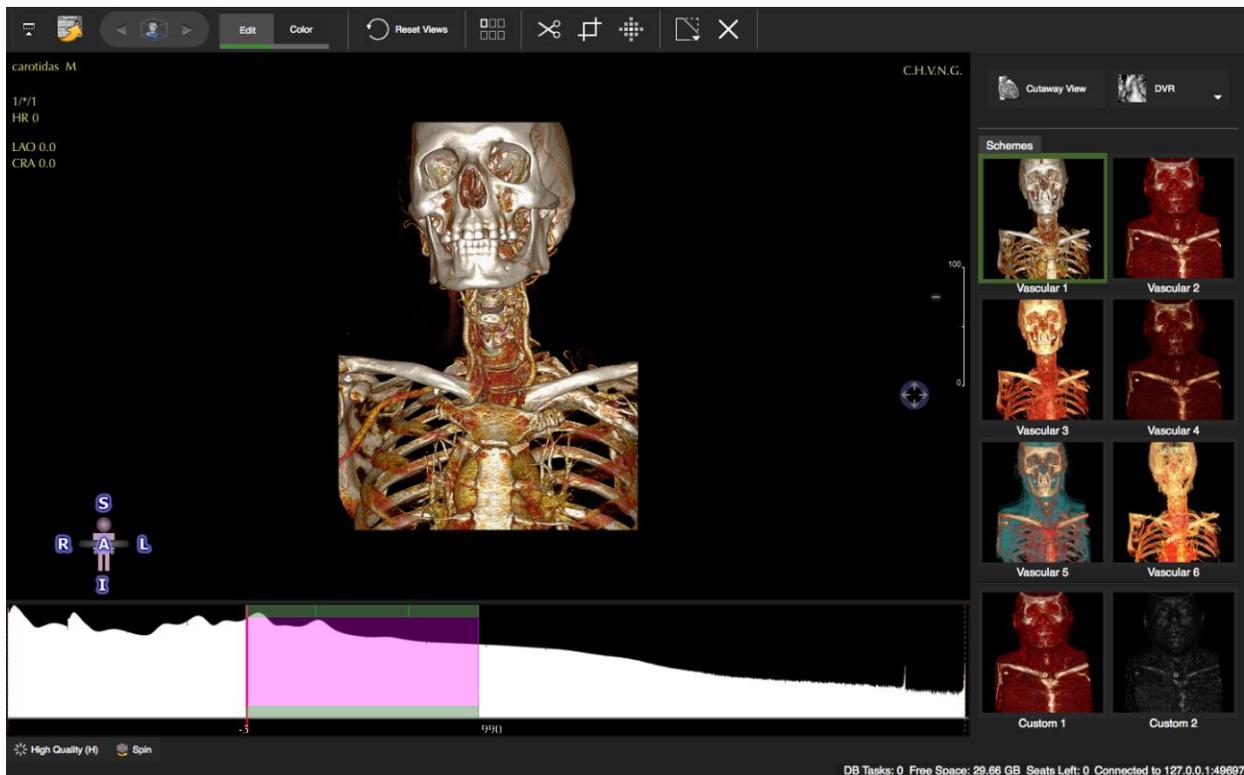
The *Preferences* offer several 4D Viewer configuration options

- ☉ *Voxel Precision*: If you encounter problems loading large series due to limited VRAM on the graphics card, you can decrease the spatial resolution of the displayed volume from 16 bits to 8 bits. Changes require reloading of the series.

Note: A change in voxel precision may affect apparent image quality.



The *4D Viewer* module provides 2 sub-modules: *Edit* and *Color*



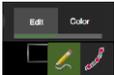
13.1 Edit

Drag a 3D, 4D or stacked 2D image data set into the viewer frame.

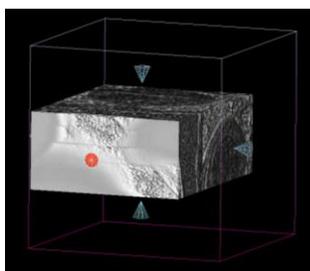
Note: The image will be rejected and a warning will be displayed if slices

- are not parallel
- have different slice thickness
- contain DICOM secondary captured images
- have an inconsistent phase count for each slice (time-resolved data sets)
- contain invalid or inconsistent image parameters (i.e. width/height, pixel spacing, image orientation patient, slice thickness, or slice locations)

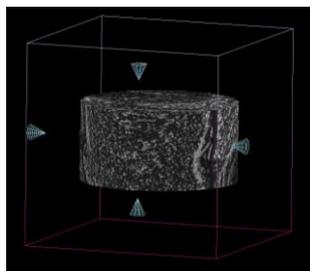
13.1.1 4D Viewer Control Features (Table)

4D VIEWER SPECIFIC COMMANDS	SYMBOL	WINDOWS	MAC
High Quality (bottom left)			
Applying a shorter sampling distance while ray casting allows for capturing finer details within the volumetric data.		H	H
Spin			
control speed with the fps wheel in the top tool bar		Y	Y
Windowing			
Use the LMB and the shift key to window. 3 button mouse: press the MMB and move the mouse to fine tune grayscale settings. Alternatively change window width and center using the histogram			
Zooming		+/-	+/-
Use the mouse wheel to zoom in (scroll down) or out (scroll up)			
Phase/Slice Navigation			
Open the navigation bar to use the on screen widgets			
Panning			
Move the cursor over the icon and drag			
Rotation			
When in clipping or cutting mode, use the 'Rotate Volume' icon. With the left mouse held, you can rotate the image in all directions. The center of the view port will be the center of rotation.			
Aspect			
Navigator: clicking on the navigator in the bottom left corner switches to different aspects		(S) (I) (A) (P) (L) (R)	(S) (I) (A) (P) (L) (R)
Segmentation (see below <i>How to do</i>)			
			
Clipping the Volume			
When activated, the clip tool displays cones. Grab a cone with the left mouse button to clip the volume in orthogonal directions. The process does not affect the actual 3D data, so the visible volume can be reset at any time.		Axial	C
		Cylindrical	⇧C
		View	C
Freehand Cut		Ctrl+D	⌘ D
Freehand Crop		Shift+Ctrl+D	⇧⌘ D
To open the tool-pop-up, move the cursor to the box in the top-middle of the viewer frame. You have the option between <i>Free hand</i> drawing and <i>Click-</i>			

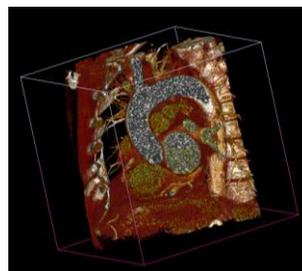
<i>Draw</i>			
3D Threshold growing: move the mouse over your ROI and drag downwards. (sideways will increase the threshold)		Ctrl+G	
<i>Reset View</i> : Resets to default pan/zoom/orientation. (keeps segmentation and clipping)		Ctrl+E	⌘ E
<i>Undo all clippings and reset to original volume</i>			(⌘Z)
<i>Clipping options (axial/cylindrical)</i>			



Axial



Cylindrical



Cutaway View

Context Menu 4D View Ports		
Measurement Add Marker Measurement Manager		see below
View Reset View Cutaway Endoluminal Internal* Spin Volume Link MPR Rotation	⌘R V	
Rendering DVR MIP Angio Surface High Quality Background Set as background	⌘F1 ⌘F2 ⌘F3 H B	
Display Display Volume Resolution Display Volume Frame Display all Overlay Display MPR Reference	↑F ☑ ↑M	
Select ROI	⌘I	
Clipping Unclip All Axial Cylindrical Freehand Cut Freehand Crop 3D Region Growing	⌘E C ↑C ⌘D ↑⌘D ⌘G	
Windowing Preset	⌘W	
Windowing... (MR) Type I Type II Type III Vessel Min-Max	↑1 ↑2 ↑3 ↑4 ↑0	
Windowing...(CT) CTA CT Heart CT Lung CT Bone CT Soft Tissue Auto Windowing Image Type Min - Max	↑5 ↑6 ↑7 ↑8 ↑9 ↑0	
Export as file...		
Export Image		Settings for: Size and format (jpeg, tiff,...)
Export Image Multiview		Format (jpeg, png,...) and size
Copy Image to Clipboard		

<i>Export Video Rotation</i>		Format (mov,Quicktime,avi)
<i>Export Video Cine</i>		Settings for: Format and Size, Video Speed
Save as DICOM Secondary Capture		
<i>Save Single Image</i>	⌘1	
<i>Save Rotation Images</i>	⌘2	Settings for: No. of Images, Rotation Angle
<i>Save Cine Images</i>	⌘3	
<i>Save Cine Rotation Images</i>	⌘4	Settings for: No. of Images, Rotation Angle
Unload Volume		Clears the frame

*Internal View: When the volume is clipped or showing a segmented region of interest, switching to the internal view may display empty content. Adjust window width/level or switch off segmentation from the context menu, segmentation option.

13.1.2 How to use the measurement option

Measurement is an option that can be found in the context menu.

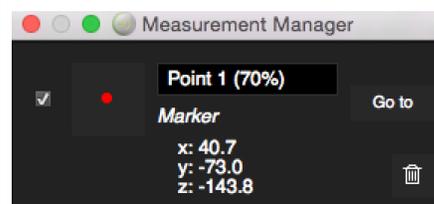
It allows to set a marker which will indicate the position within the volume that can be viewed across pages and modules:

Point the cursor to a point of interest, open the context menu *and select* Measurement: a red dot will be set at the cursor location

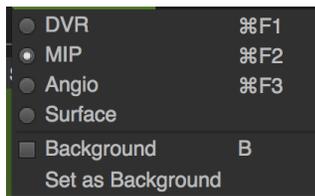
Measurement Manager:

- A checkmark allows to show/hide the point
- Click on the colored dot to change the color
- The percentage of the heart cycle in which the point has been set will be indicated
- The coordinates are indicated
- A go-to option will display the location in the 3/4D volume
- The point can be deleted with a click on the garbage can

Marker points are automatically saved to a workspace



13.1.3 Rendering Options



Select a rendering option from the side-panel



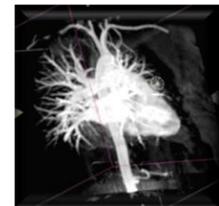
○ Direct Volume Rendering (DVR)

This technique can be effective at depicting arteries and veins even when these structures are adjacent.

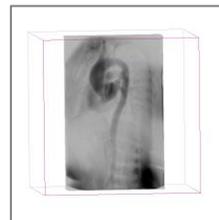


○ Maximum Intensity Projection (MIP)

The MIP connects pixels with maximal signal of the blood vessels in three dimensions, providing an angiogram that can be viewed from any projection.

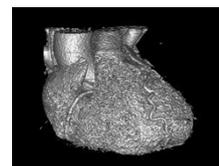


○ Angio Rendering:



○ Surface Rendering:

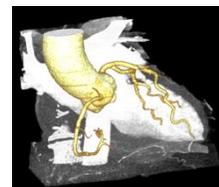
This technique is mainly used to visualize complex anatomical details.



○ Background MIP

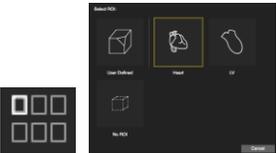
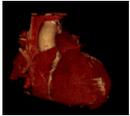
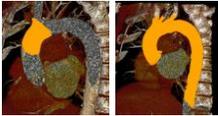
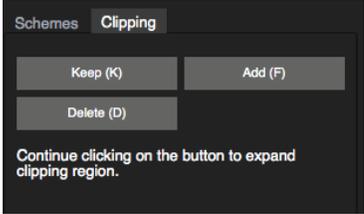
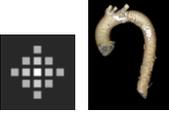
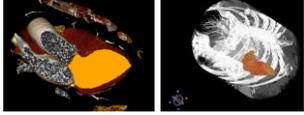
A fusion between DVR and MIP rendering

Set Background Mask allows for creating a custom Background MIP (can be done in DVR)



13.1.4 Segmentation Options (CT only)

How to do a Segmentation in the 4D Viewer Module

<p>Select the <i>Region of Interest</i></p> <p>Select one of 4 options</p>	
<p>ROI-Heart:</p> <p>The heart will be segmented automatically</p>	
<p>ROI - User defined:</p> <p>1. Activate the <i>Cutaway</i> button (former <i>View Clip</i>)</p>	
<p>2. Activate the <i>3D Region Grow Clip</i></p>	
<p>3. Point the cursor in the middle of your ROI and drag</p>	
<p>4. When you are done, go to the clipping pane and click <i>Keep</i></p>	
<p>5. Turn off the grow button</p>	
<p>6. Optionally, add a background: <i>Context menu>Rendering>Background</i></p>	
<p>ROI-LV</p> <p>Repeat steps 1-6</p>	
<p>No Region of Interest</p> <p>Will display the original volume</p>	

13.1.5 Manual Segmentation

The toolbar offers cutting cropping and growing tools.

How to use clipping and cropping

1. Select the tool from the tool bar and select a drawing mode from the tool pop-up menu (default=freehand).



2. *Cut*: Drag the mouse cursor to encircle structures you would like to remove



3. *Crop*: Drag the mouse cursor to encircle things you would like to keep



4. To rotate or pan the volume while in clipping mode move the mouse over the icons and drag

How to create a custom Background MIP

A cvi⁴² specific feature allows the displaying of a segmented structure with a MIP background.

In addition, the background MIP allows continuous growth of the segmented structure e.g. vessels after segmentation.

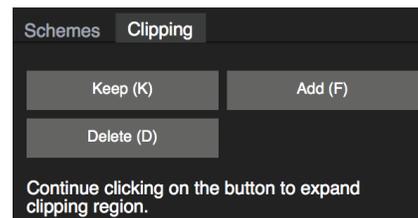
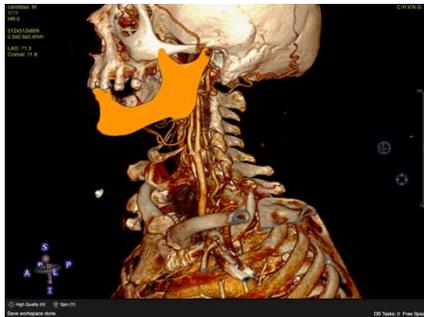


1. In DVR create an image that you would like to use as background MIP via auto-segmentation, growing, clipping or cutting.
2. Save the segmentation by clicking *Set as Background Mask* in the DVR drop down menu.
3. Now carry on to segment your structures of interest, e.g. vessels. As soon as you click *keep* the structure will be displayed isolated with the surrounding clipped away.
4. Go back to the DVR drop down menu and select *Background MIP*. This will add the previously saved MIP and will allow for further vessel growing.

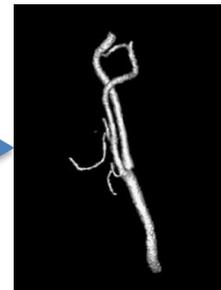
How to use the growing tool



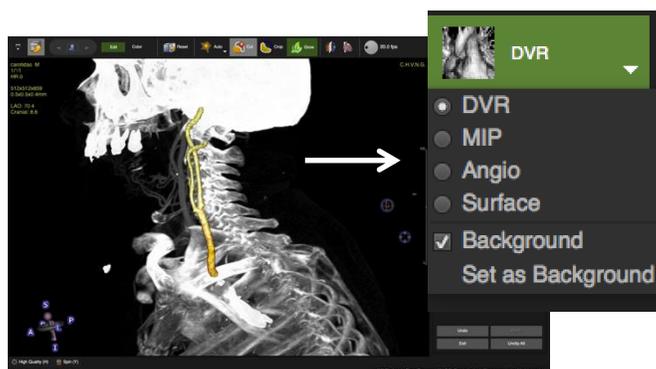
1. Grow will open a clipping menu next to the color schemes.
2. Move the cursor over the region of interest. A black dot will indicate the software has detected a structure that can be segmented. A red square will appear over a structure that has already been segmented.
3. Dragging the cursor downwards will define the region of interest according to the SI threshold.
4. Dragging the cursor sideways will increase the threshold, taking more SI into account.
5. The clipping menu to the right allows for the following options:
 - Define a structure and click *Delete (D)*: click the button several times to continuously delete the surrounding structures.



- Define a structure and click *Keep (K)*: this will isolate the vessel, removing all other structures.



- To continue with the segmentation, add a *Background MIP (B)* (see above)

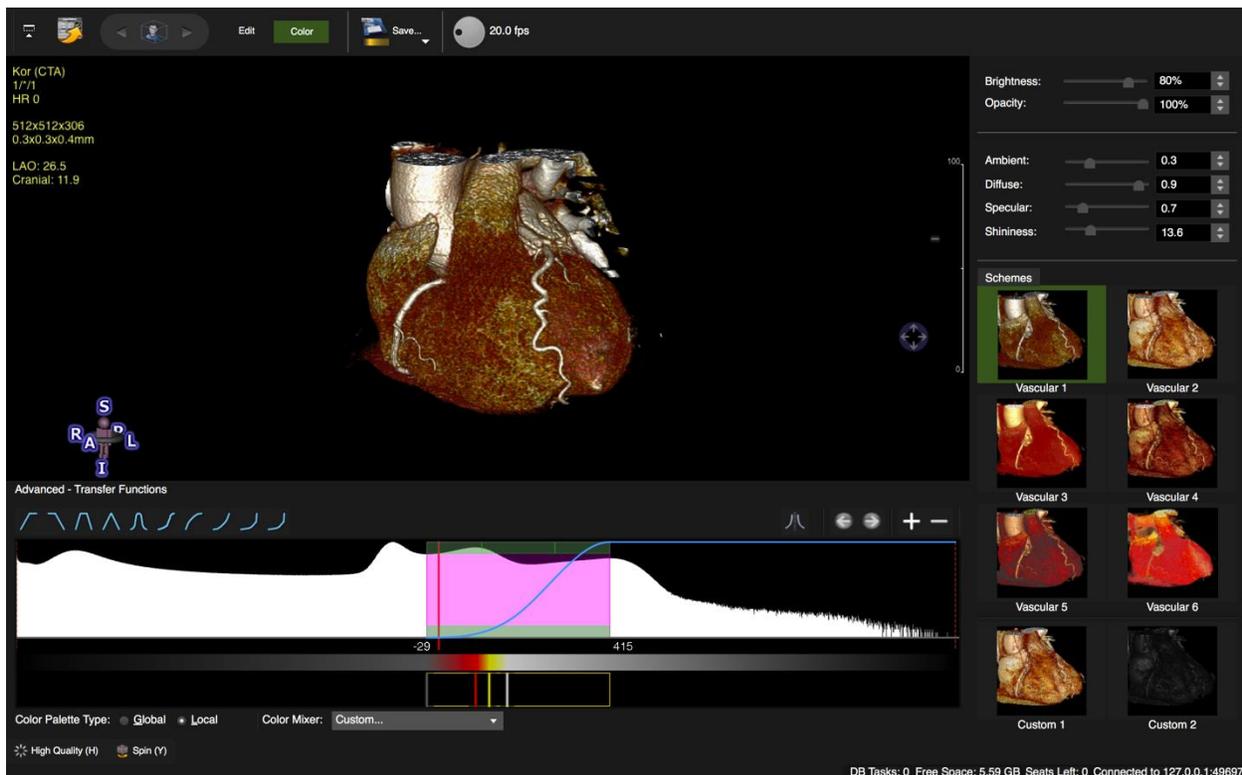


6. Continue segmentation and click *Add*



7. In addition you can undo/redo/exit/unclip all

13.2 Color



- **Opacity and Brightness:** In DVR mode, move the slider or use up/down arrows.
- **Lighting:** In DVR mode different lighting scenarios are available. Changing the lighting modifies the appearance of surfaces and textures and allows for better definition of certain structures. Increasing the **opacity** will lead to a stronger impact of the lighting adjustment on the image.
 - **Ambient Light:** simulates surrounding light
 - **Diffuse Light:** light that reflects into all directions.
 - **Specular Light:** simulates the light reflection on the surface depending on the vantage point.
 - **Shininess:** increases the highlights.
- **Color Schemes:** cmr⁴² and cvi⁴² provide 6 predefined color schemes (vascular 1-6) and 2 custom schemes

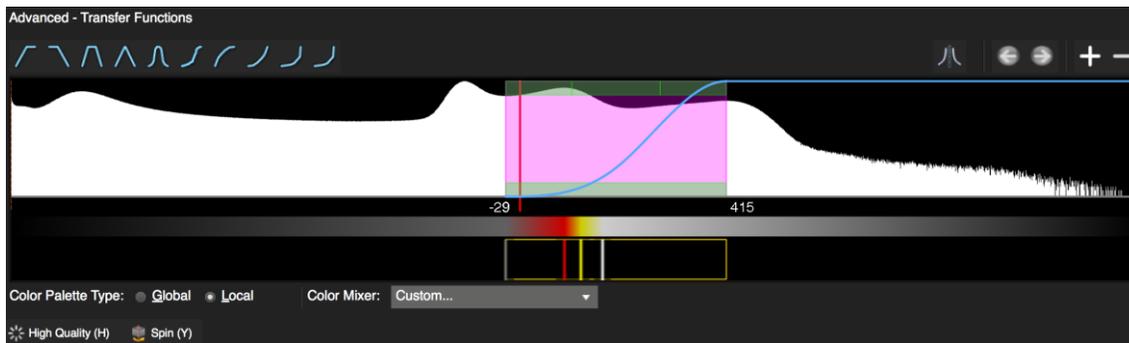


To save a custom scheme, use the save button in the top tool bar.

Override Custom Scheme 1

Override Custom Scheme 2

Advanced Transfer functions



Histogram: Within the Signal Intensity Histogram the window range is displayed as a purple shaded area. The vertical red line marks the signal intensity value at zero.

The window is separated into three horizontal regions, which are shaded slightly differently. The upper horizontal region is divided into 3 sections.

1. Top: Dragging the left or right sections on the top of the shaded area allows adjustment of the window boundaries (i.e. minimum and maximum); dragging the middle section expands or minimizes the entire window
 2. Middle: The middle horizontal section: Dragging up/down changes the window width; left/right changes the window center
 3. Bottom horizontal section, changes the window center
- *Opacity curves and color palettes:* The transfer function maps SI values to a 4-component color lookup table (i.e. red, green, blue, and alpha) for color-coding of DVR images.

1. Add/Remove: the plus and minus button on the top right lets you add/remove transfer functions. By default pushing the '+' button will display a triangular opacity curve with white color palette



2. Clicking on one of the opacity curves in the selection on the top left (above the graph) substitutes the current opacity curve with the selected preset



3. Switch between curves: click on the left/right arrow



4. Invert opacity curves in interior views.

Color Palette

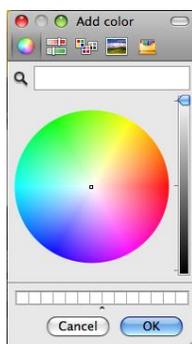
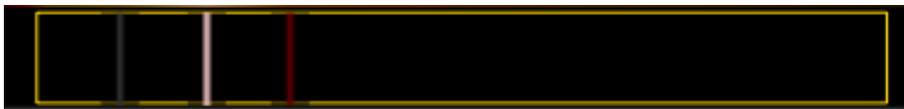
There are 2 types of color palettes

- *Global*: A global palette applying a color to a specific signal intensity value, thus representing a specific texture. If Global is checked, moving the window center will only change the opacity curve not the color.
- *Local*: window-center adjustment will reposition the attached color palette, thus changing color and opacity
- Setting the Color Palette



The Color mixer provides a pre-defined color palette. The preset will be positioned relatively to the active window.

- Add a color: double-click in the palette and choose a color from the palette



Mac



Windows

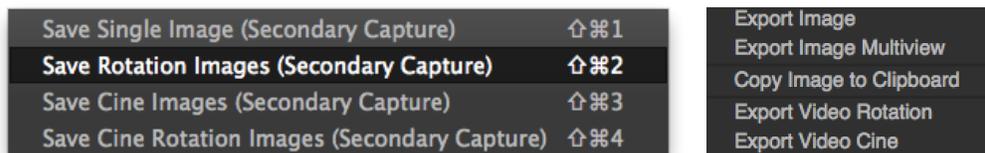
- Remove a color: Move the cursor in the palette and with the LMB drag over the bar that you would like to delete;
- Reposition color bar: Grab and drag the bar with the LMB
- Change the color of existing color bars: double click on the bar and choose a new color from the palette

Note for Windows Vista and Windows 7 users:

Using anything other than the Windows Aero Color Scheme might result in images partially refreshed after certain actions (e.g. after closing context menu, dialogs, and minimizing other windows on top of cmr⁴²/cvi⁴²).

How to Save and Export 3D/4D Rendered Images

- The easiest way to save an image is creating a secondary DICOM capture by dragging it to the thumbnail panel:
- *Workspace>Save Workspace* will remember all clipping, rotation and the segmentation
- More options for saving and exporting are provided in the context menu



14 Multiplanar Reformatting

14.1	Double Oblique	91
14.1.1	Layout	92
14.1.2	Phase Indicator	92
14.1.3	Toolbar	92
14.1.4	MPR Control feature	93
14.1.5	MPR Viewer Controls	95
14.1.6	Reporting and saving of image captures and measurements	95
	How to save, restore and clear images/measurements	96
	How to add multiple MPR frame sets to the report	97
	How to generate a short axis stack and a long axis reference:	97
14.1.6.1	The context menu options	99
14.2	"Navigation" tab	100

The Multi-planar reformatting (MPR) technique reconstructs a slice in any position and orientation through the 3D Volume. It can reconstruct the axial images into coronal, sagittal and oblique anatomical planes but also it can specify a plane off an oblique image.

-
- The MPR Module provides 2 tabs:



Double Oblique

Free Form Navigation

14.1 Double Oblique

By default there are 4 view ports

14.1.1 Layout

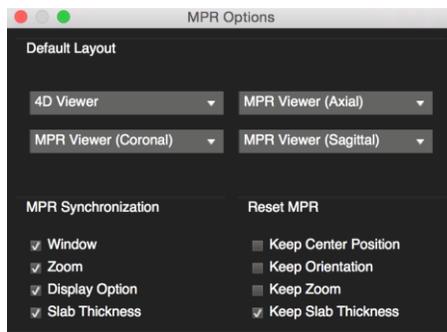
Colors of the cross-hairs correspond to the orientation framed in the same color.

The short-cut <M> hides the cutting lines

- Axial view (top right **blue** frame)
- Coronal view (bottom left, **red** frame)
- Sagittal view (bottom right, **yellow** frame)
- 3D reference view (MIP, Surface or Direct Volume Rendering)



MPR Options (bottom left of the interface)



- Change the layout
- Set Synchronization
- Set Reset



- For a Portrait layout view please go to *Preferences>4DViewer>Viewers*

14.1.2 Phase Indicator

When loading a multi-phase 3D data set, a schematic ECG will be display.

The time points of the images will be indicated as percentage of the cardiac cycle.

You can run a cine and change the frame rate.

The valve modules allow to mark systole and diastole by simply clicking S/D



14.1.3 Toolbar

-  Reset MPR Reset volume resets clipping and segmentation and zoom and defaults back to the original volume.

-  *Reslice* will save multi-slice images as DICOM or DICOM capture (screenshot). Choose between parallel or rotational slicing (see below)
-  Links the 4D view with the MPR orientation
-  Pan MPR; Toggles between panning and scrolling
-  Save layout view. You have the option to Save a DICOM secondary capture or to export the view as a file (see below: *Export/Save MPR Images and videos*)

14.1.4 MPR Control feature

- **Switching Between Viewer Frames**
A single LMB click at the top-left corner in one of the 3 viewers brings the view port into focus.
A LMB click anywhere else in the view port will additionally reposition the MPR-center
- **Panning the MPR centre:**
Moving the center point will move the entire image plane through the 3D data

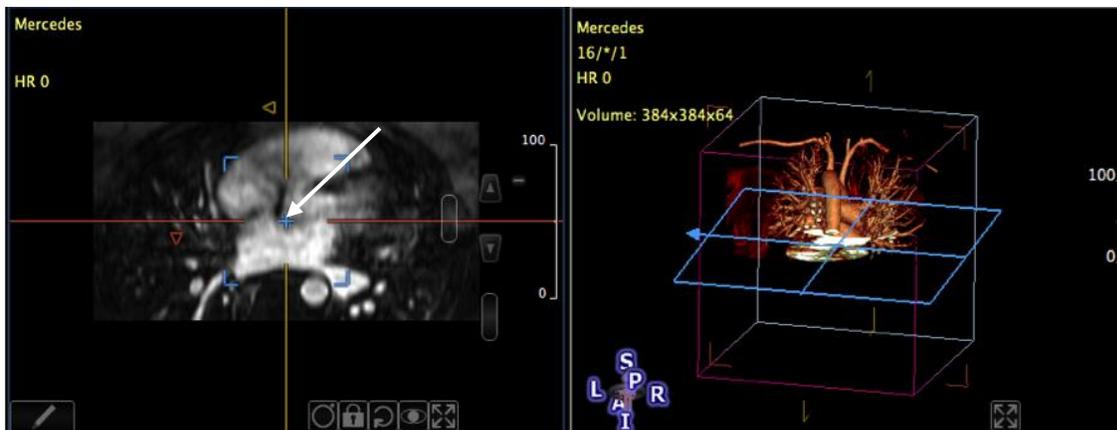
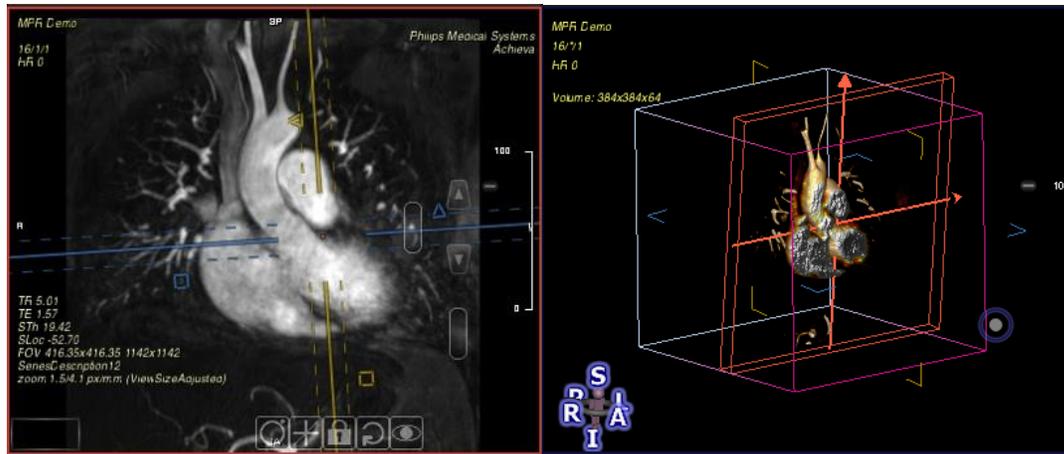


Figure 4: Panning the MPR center

A single left click on the image in the MPR viewer repositions the MPR center.

- **Adjust the Slab-Thickness:**
 1. Slab-thickness handle (colored squares next to cutting line):
Moving the little square up and down next to the MPR plane cross-reference lines allows you to change the slab thickness

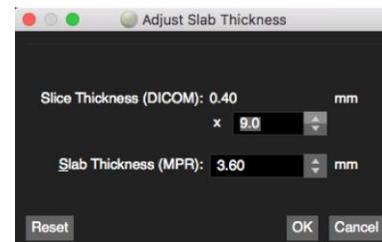
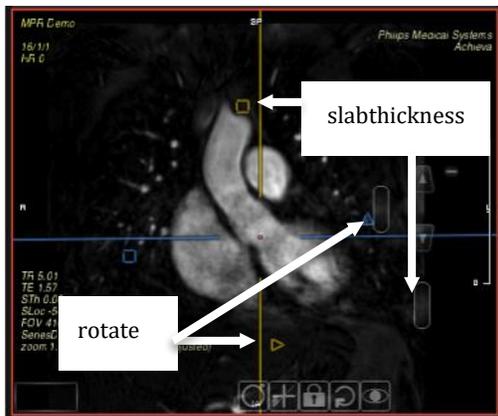


Zero slab thickness depicts thin-slab MPR. Positive thickness uses thick-slab volume rendering. The slab volume will be displayed in the cross-reference viewer frame.

2. Slab-thickness scroll bar (see screenshot):

Dragging the scroll bar with LMB increases/decreases the slab thickness using the smallest amount of data increment available for the loaded volume.

3. LMB double-click on the scroll bar opens up the Adjust Slab Thickness dialog. The slab thickness can be entered in mm or set by the multiplicity of the originally acquired DICOM slice thickness.



Note: Slice thickness (DICOM) multiplying factor will be blank if slab thickness is not a multiple of the slice thickness.



Maximize View

Move the mouse cursor to the right top corner until 2 opposing triangles appear, click LMB

- Take a DICOM secondary capture: move the cursor to the top left until a hand appears. Now you can simply drag and drop the image in the thumbnail panel.

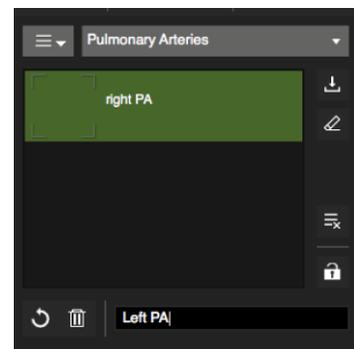
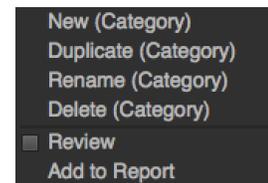
14.1.5 MPR Viewer Controls

MPR VIEWER CONTROL FEATURE		
FUNCTIONALITY	DESCRIPTION	BUTTONS
<i>Show Rotation Circle</i>	Rotating the little circle at one o'clock, will rotate the image in all 3 view ports Rotating the big circle, rotates the image in the frame	
<i>Orthogonalize Planes</i>	Displays an orthogonal view to selected orientation	
<i>Lock Plane orientation</i>	Locks orientation (respective cutting line becomes dotted) and will not follow adjustment in other planes	
<i>Rotate View</i>	<i>Rotate Left 90</i> <i>Rotate right 90</i> <i>Rotate 190</i> <i>Flip Horizontal</i> <i>Flip Vertical</i>	
<i>Preset Views</i>	<i>Axial View</i> <i>Coronal View</i> <i>Sagittal View</i> <i>Cranial LAO View</i> <i>Lateral View</i> <i>Caudal RAO View</i> <i>Short Axis View (CT Only)</i> <i>Long Axis View (CT Only)</i> <i>Custom View</i>	
<i>Enlarge View</i>	Click space bar	

14.1.6 Reporting and saving of image captures and measurements

How to set up a categories and respective measurement lists

-  Open the menu and chose an option: Create a new, duplicate, rename or delete an existing category
- For a new list select *New*, type a name in the window and click *Enter*
- To add an item to the list, go to the bottom of the panel, type a new label and click *Enter*.



4.  To remove an item, select and click the trash can.
5.  Lock the list when you are done.
6.  *Save to protocol* will save the categories and measurement lists into the current workflow protocol (e.g. Default (CT))

How to save, restore and clear images/measurements

1. Select the item in the group you are about to measure.
2. Use the measurement tools in the toolbox of the respective MPR viewport and perform a measurement. To enlarge the image click *spacebar*.
3. If you wish you can label a contour in the image for future reference via *context menu/contour labels*

4.  Clicking *Fill* (hot-key F4) will fill in the measurement and record MPR location including double-oblique images. Alternatively you can simply drag and drop an image from the MPR viewer

5.  To remove image captures and related measurements from an item, click *clear*

6.  Clear all images/measurements

7.  To review a capture or a measurement select it from the list go to the menu and check the box next to *Review*.

8. The context menu offers several options to save secondary DICOM captures and to export images and cines to a specified location.

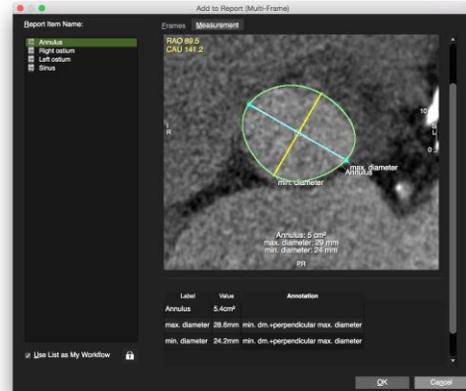
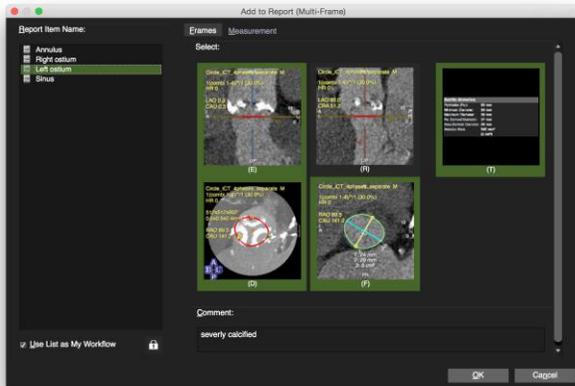
Save Single Image	⌘1	Export Image
Save Multi-Slice Images	⌘2	Export Image Multiview
Save Cine Images	⌘3	Copy Image to Clipboard
Save Cine Multi-Slice Images	⌘4	Export Cine Current Slice
Save Single Image (Secondary Capture)	⇧⌘1	Export Movie All Slices Multiview
Save Multi-Slice Images (Secondary Capture)	⇧⌘2	Export Movie All Slices Stacked
Save Cine Images (Secondary Capture)	⇧⌘3	
Save Cine Multi-Slice Images (Secondary Capture)	⇧⌘4	

9.  Select and add multiple frames to the report. (see below)

10.  Save a Layout View to the report



How to add multiple MPR frame sets to the report



1. To report a measurement with an appropriate identifier, the contour for this measurement has to be labeled: in the analysis frame activate the contour and open the context menu. Select *Contour Labels*. Labels will be remembered and compiled into a list in the contour label menu



2. In the toolbar click the *Add to Report (Multi Frame)* button
3. Provide a description
4. In the *Frame* page select the frames for the report. Optionally provide a comment.
5. In the *Measurement* page items can be annotated.
6. Go to the *Report* module to find your measurements for reporting.
7. Check *Use List as My Workflow* to save the list for futures reference. In your next patient study the list of values or items will be preset. The set of frames will be linked to an item by simply selecting it in the list.

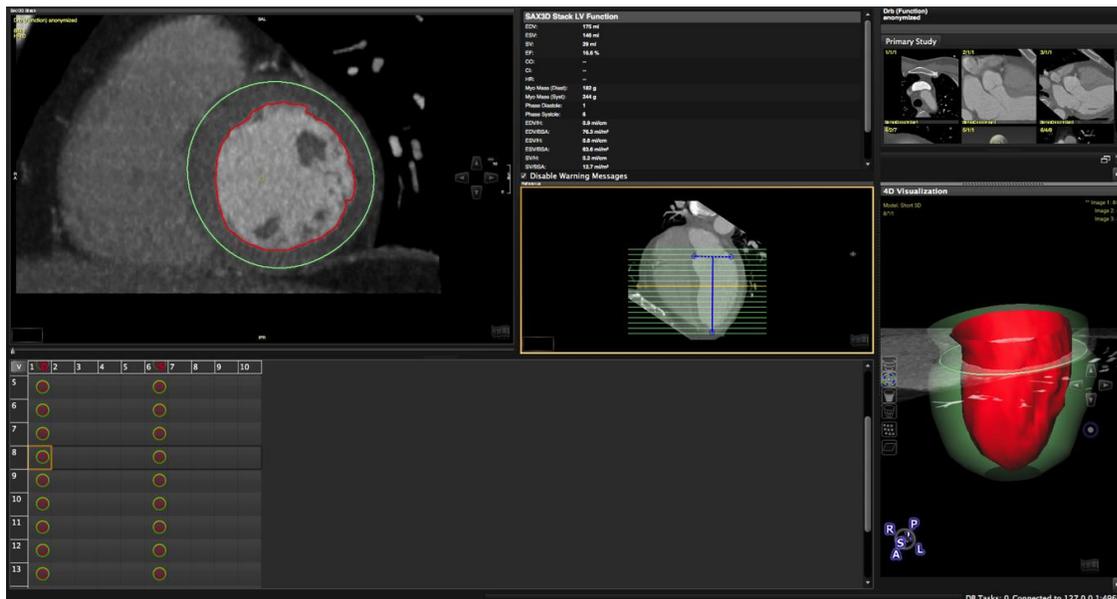
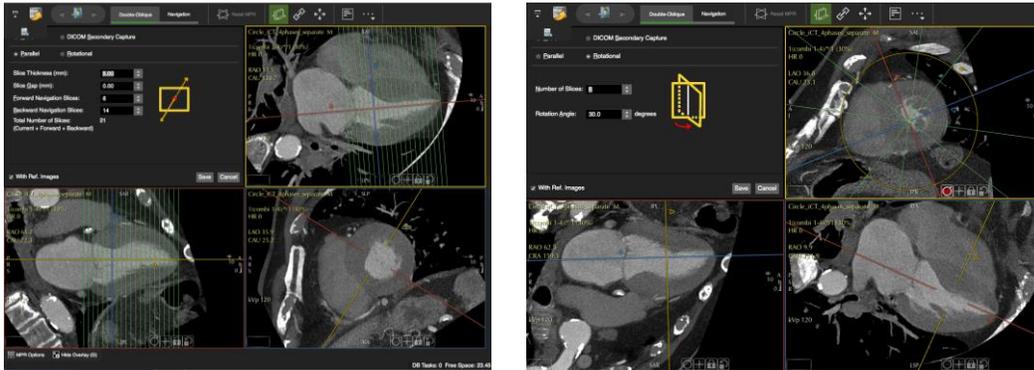
How to generate a short axis stack and a long axis reference:



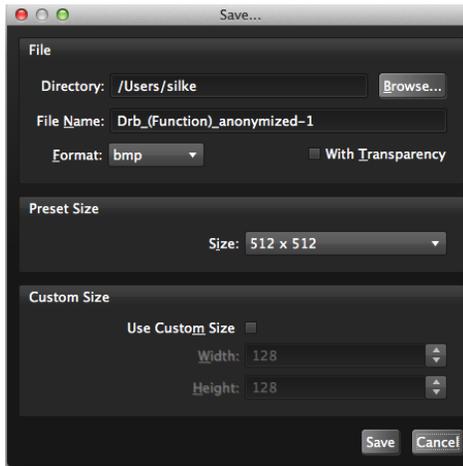
1. Click *LV* automatically creates a 4 CV, 2CV and SAO orientation.
2. Double click the view port to change to the desired reference slice
3. Select the *Slice Thickness* (e.g. 7mm) and *Gap* (e.g. 3 mm)

MULTIPLANAR REFORMATTING (MPR)

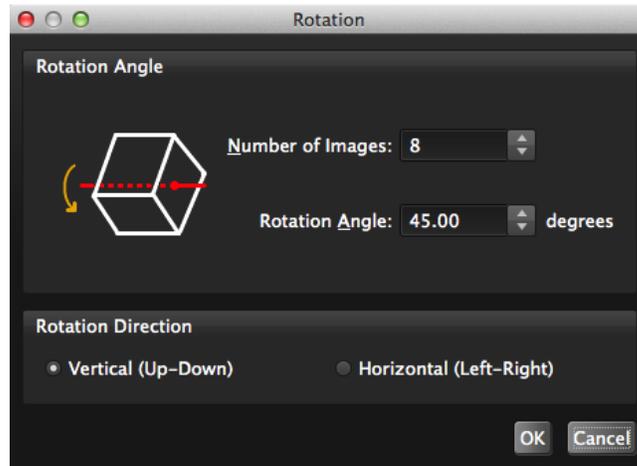
4. Set *Forward/Backward* slices and make sure to cover the entire LV.
5. Check *With Ref. Images* to generate a reference image in LAO
6. The stack will be appended to the thumbnail panel and could be used for LV function assessment



14.1.6.1 The context menu options



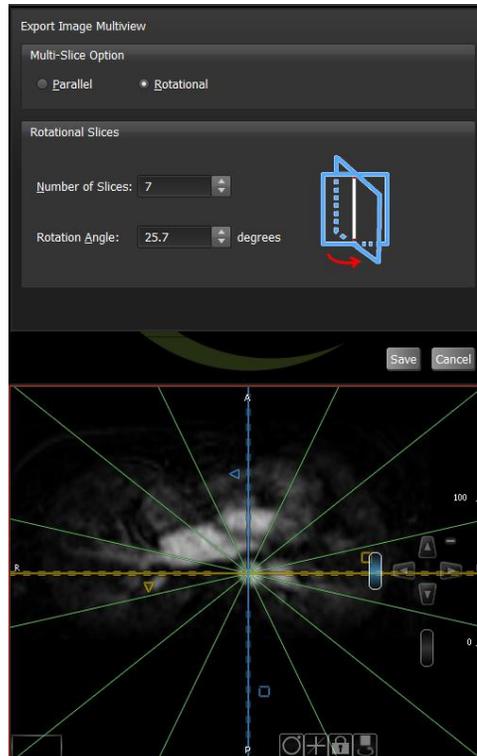
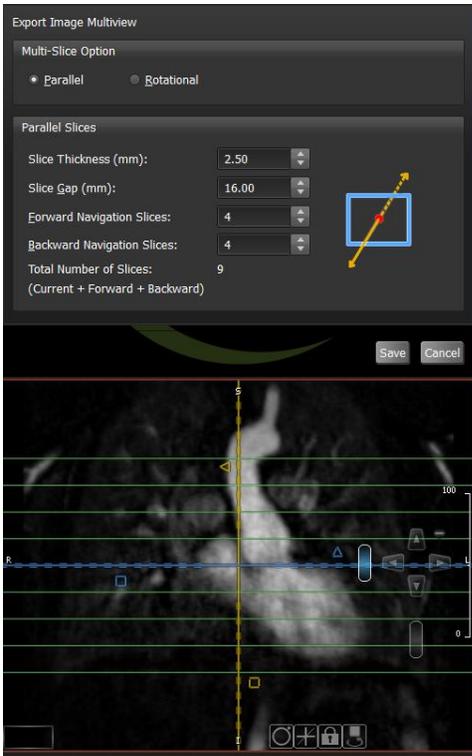
Export Image



Export Image Multiview

Export Image/Video in Multi View

You can export either a parallel stack (*Parallel* option) or images rotated along the y-axis of the selected frame (*Rotational* option).



The color of the frame corresponds with the orientation you are about to export (here red: the images will be exported in a coronal view.)

- In *Parallel* multi-slice option, you can modify or limit the number of forward/backward navigation slices, i.e. moving the target MPR image plane along the view direction by clicking on the up/down navigation arrows.

In the target frame, adjustment of the slab thickness affects the number of the exported slices.

Slice gap could be specified to reduce the number of slices created.

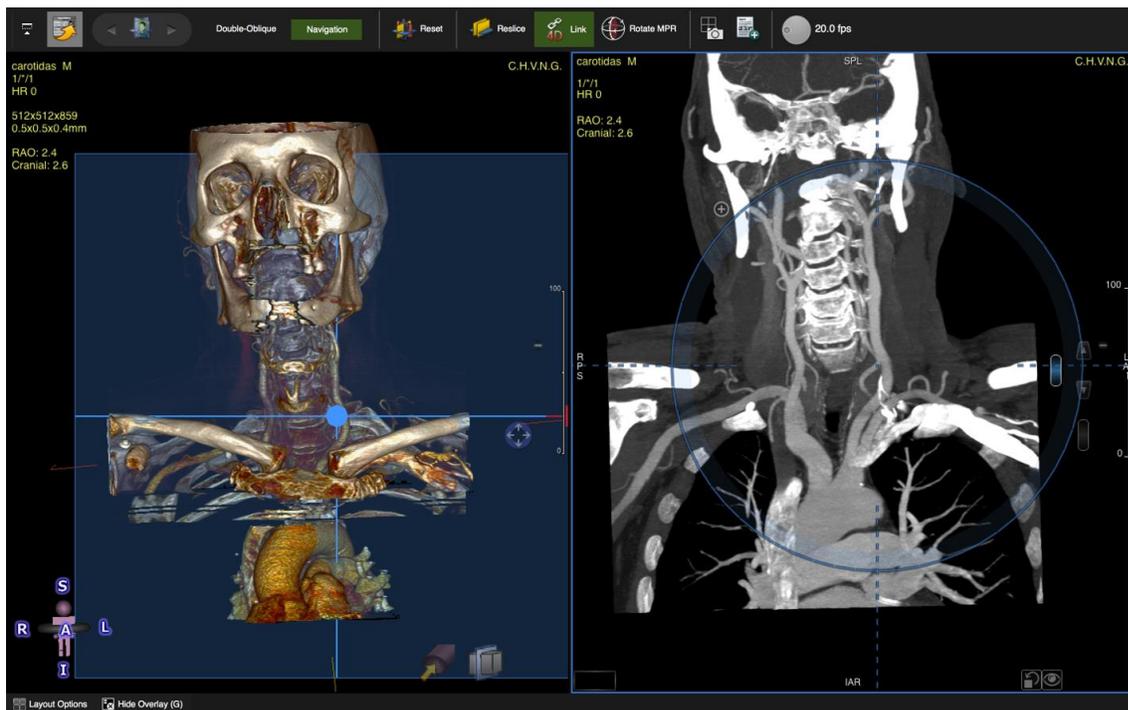
- In *Rotational* multi-slice option, you can specify either the number of slices or the incremental angle of rotation*: clicking on the up/down navigation arrows rotates the target MPR plane by the specified angle of rotation, the other parameter will be automatically calculated.

Example: if the incremental angle of rotation is 15 degrees, the plane is rotated about the y-axis of the plane by 15 degrees increment and the image is obtained with 15, 30, 45, ... degrees rotation with respect to the original image.

Number of slices * incremental rotation angle= 180 degrees, e.g. 10 slices * 18 degrees = 180 degrees

14.2 "Navigation" tab

Select the MPR viewer that you would like to move into the *Navigation* sub-module and click the button. Or drag and drop the viewer on the button



- **Panning:** LMB drag outside the circle
- **Free form navigation:** drag within the circle.
- **Hold the centre of rotation** during free-form navigation :
 - Click the "+" at around 11 o'clock or use the modifier key "Shift"
- **Slice scrolling:** toggle between scrolling and free-form navigation by clicking on the slice navigation slider.

Use CTRL/Command key to allow accelerated slice navigation.

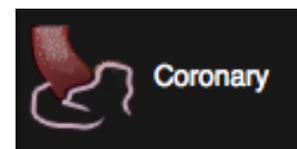
When in slice scrolling mode, you can still freely navigate initiating your mouse drag in the shaded area, of the circle.

15 Coronary Module (Auto plaque)

15.1	Landmark Page	103
15.2	Centerline Page	103
15.2.1.1	How to define a centreline via region growing	104
15.2.2	Main Viewer	105
15.2.2.1	How to create a centerline via seed points:	105
15.2.2.2	Clip Menu	106
15.2.2.3	Save Options	106
15.3	Curved MPR	107
15.4	Cross Section	107
15.4.1.1	How to calculate the stenosis using 2 reference points	107
15.4.1.2	How to use the centerline graph	108
15.4.1.3	How to display and endoluminal view and a fly through	109
15.4.1.4	How to perform Plaque Analysis	110

The Coronary Module includes the following pages:

- Landmark: aids the coronary segmentation,
- Centerline: Create a centerline for CPR
- Curved MPR: Correct the centerline
- Cross Section: Evaluation

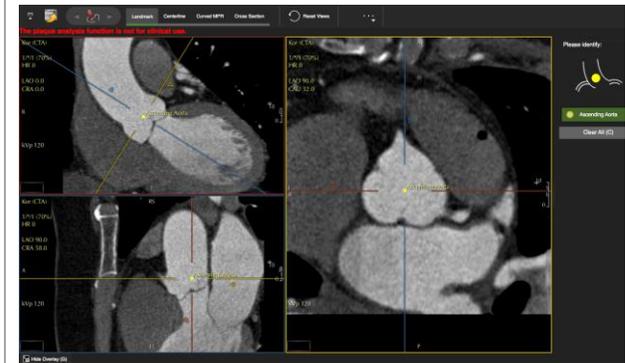


Auto-plaque assessment requires a separate license.

15.1 Landmark Page

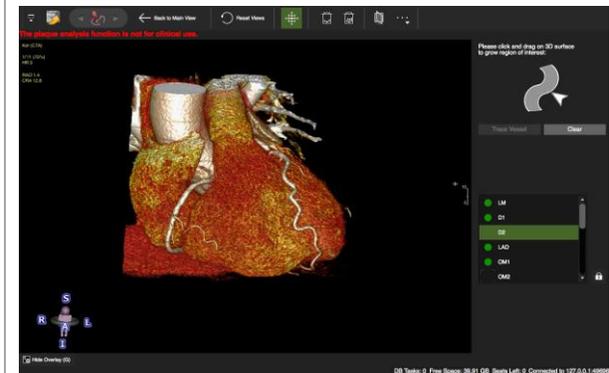
Place a Landmark in the ascending Aorta

Move to the next page



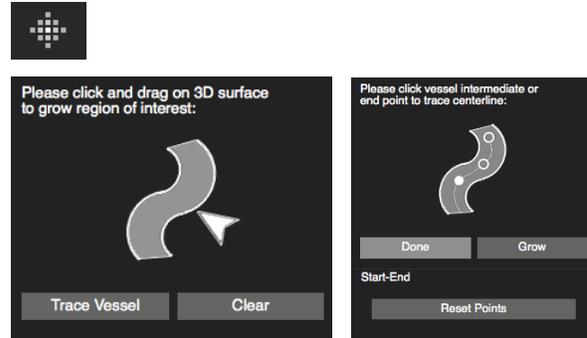
15.2 Centerline Page

- The centerline page is designed to extract a centerline via 3D region growing.
- Using the landmark, the system will automatically segment the heart.

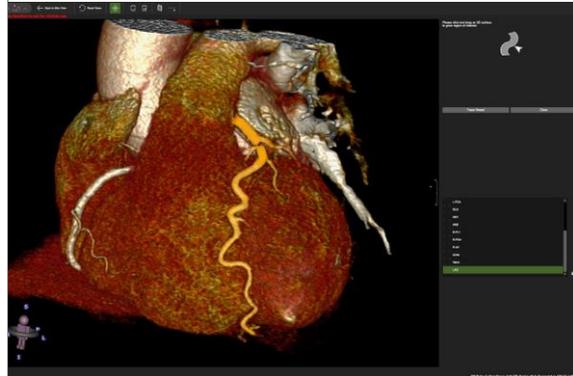


15.2.1.1 How to define a centreline via region growing

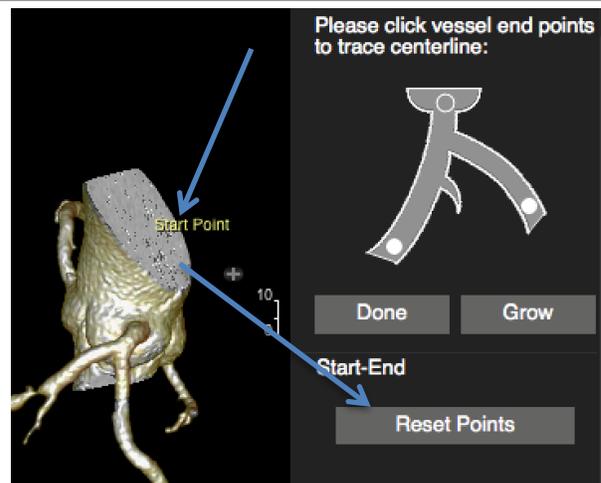
1. The Grow Region Interface provides a guide diagram to indicate the next user action



2. Select the vessel from the list
3. The *Region Growing* tool is activated by default. Define a single vessel or the entire coronary tree.
4. Clear will delete the grown vessel. Start over again or move to the main page use the seed method.



5. *Trace Vessel* will segment the artery
6. To extract the centerline place a start and endpoint: The system will automatically set a starting point at the proximal end of the segment..
7. *Reset the Points* if the Start Point is not in the correct position



- Set a start and an end point. The software will automatically trace the vessel, and will move to the next item in the list. Check that this is actually the vessel you would like to trace next.



- To redo, re-select the vessel in the list and click *Delete Current Vessel Centerline*.



15.2.2 Main Viewer

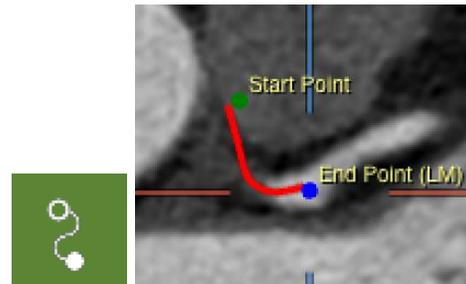
Click *Back to main View*. The main viewer allows to

- trace a centerline by setting control points
- edit control points

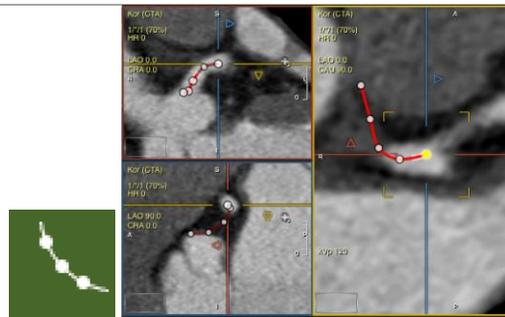
15.2.2.1 How to create a centerline via seed points:

- Select a vessel from the list
- Place a start and an end point. Sometimes it is necessary to set several seeds along the way to guide the system.

3.

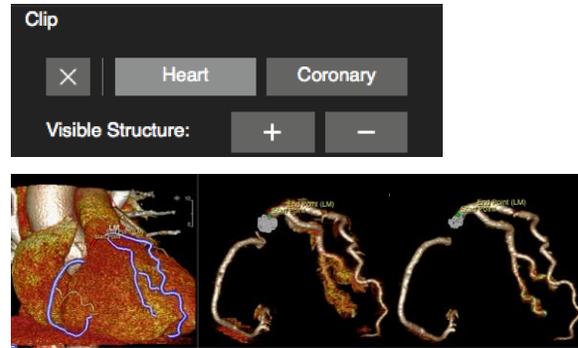


- Edit control points using the MPR viewer



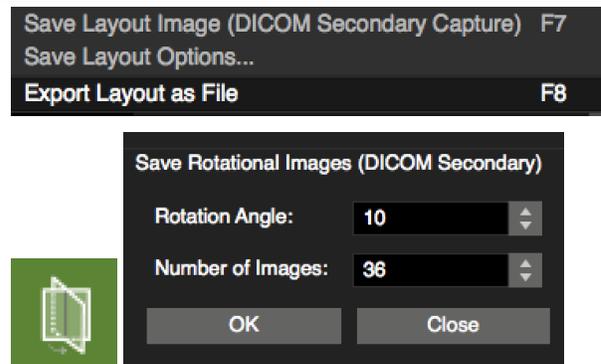
15.2.2.2 Clip Menu

- You can reset the clipping (x), or
- Toggle between *Heart* and *Coronary* tree segmentation
- *Visible Structure* (+/-) allows for volume adjustment



15.2.2.3 Save Options

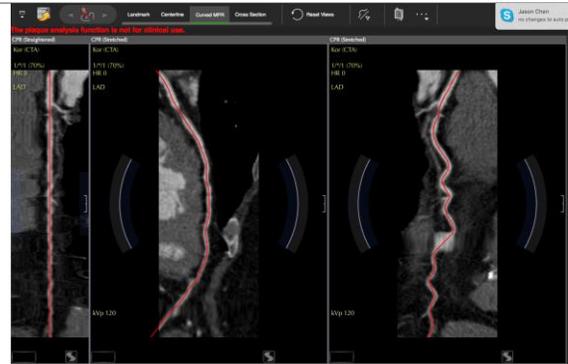
- Save a layout view
- Save rotational images: The button will open a menu on the bottom of the right panel, underneath the Clip menu. The number of images will define the rotation angle and vice versa. The series of rotational images is attached to the thumbnails and can be viewed in the Viewer module.



15.3 Curved MPR



Edit the centerline

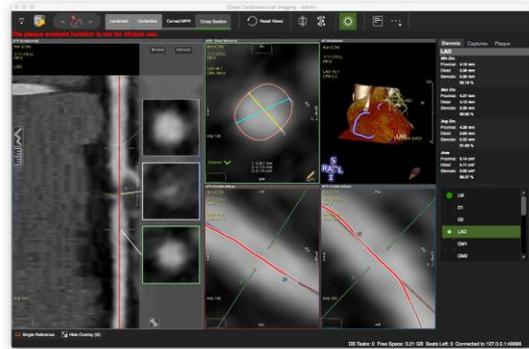


15.4 Cross Section

The page is designed to visually and quantitatively assess the vessels with existing centerlines

15.4.1.1 How to calculate the stenosis using 2 reference points

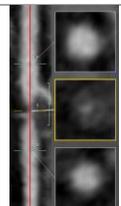
5. Select the vessel from the list.
6. Set the straightened MPR to *Stenosis*.
7. Click in the stenosis to place the stenosis marker, the distal and proximal marker are placed automatically.



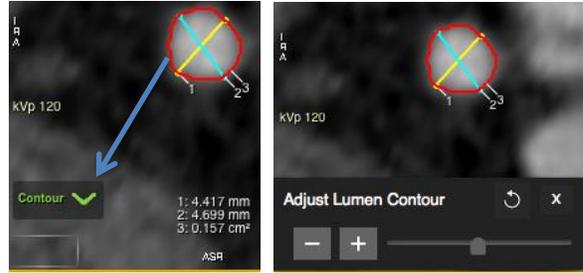
8. Select the proximal cross-reference image and turn on the *Auto Vessel Lumen Contour*.



9. Move to the stenosis image. The contour should be generate automatically if the *Auto Vessel Lumen Contour* is still active (green).



10. To adjust the threshold, click the green *contour* label. It will open up a slider that allows to adjust the contour.



11. Stenosis measurements will be filled in automatically.

Stenosis	Captures
LAD	
Min Dm.	
Proximal: 4.37 mm	Avg Dm.
Distal: 3.41 mm	Proximal: 4.51 mm
Stenosis: 2.16 mm	Distal: 3.65 mm
44.52 %	Stenosis: 2.58 mm
	36.69 %
Max Dm.	
Proximal: 4.69 mm	Proximal: 0.16 cm²
Distal: 3.91 mm	Distal: 0.10 cm²
Stenosis: 3.12 mm	Stenosis: 0.05 cm²
27.51 %	63.20 %

Select images and measurements to the report.



Warning:

The use of the *Auto-Plaque* is not FDA approved and is for non-clinical, scientific use only.

15.4.1.2 How to use the centerline graph

Centerline Graph displays min./max./average lumen diameter, lumen area and tortuosity. It will automatically detect the minimum and maximum point along the centerline graphs.

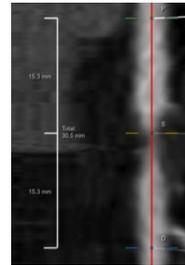
- *Lumen*: Clicking on the lumen title will bring up a dropdown menu allowing the user to switch between the different centerline graphs.
- *Options* item in the dropdown menu allows the user to define the increments (in mm) for each angle measurement in the tortuosity graph.



- Dragging the yellow handle allows to set a *cut off*, such that anything above/below the set threshold for lumen and/or that exceeds the cutoff threshold for tortuosity will be highlighted. (e.g. for catheter selection (1 Fr = 0.33mm)). Double clicking on the yellow handle brings up a dialog where the user can specify a precise cutoff threshold (in mm or degree).

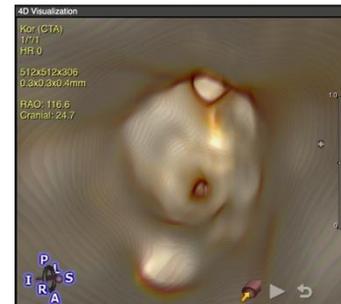
Note: The stenosis graph is calculated based on auto contour detection for each cross-sectional image along selected vessel centerline. Each image series may require different SI threshold. Please adjust auto lumen threshold in the threshold tuner to update the stenosis graph accordingly.

- ①  The ruler measures the distance between vessel markers along the centerline

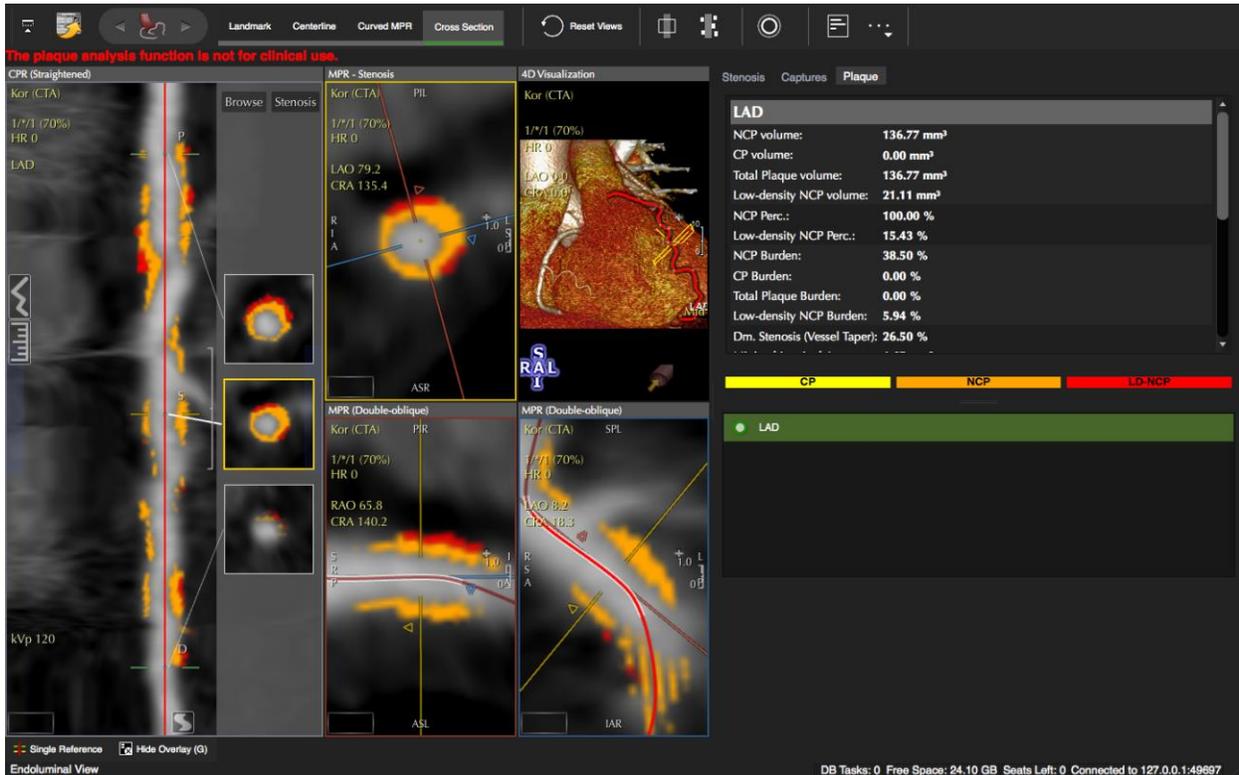


15.4.1.3 How to display and endoluminal view and a fly through

1. In the reference viewer click the *Endoluminal* view.
2. To move slowly through the vessel, drag the stenosis marker in the CPR viewer.
3. Clicking the *Play* button, will display a fly through animation of the vessel. This view can be exported via Context Menu>Export>Export Video Immersion.
4. The context menu offers, viewing, rendering, saving, export and more options



15.4.1.4 How to perform Plaque Analysis



1. Load the study into the Vessel module.



2. Define a *Lesion* range by dragging the shaded area over the lesion.



3. Click on auto plaque.

4. The plaque will be color coded and your report is available in the *Plaque* tab of the reporting panel



5. Select frames and add them to the report

Troubleshooting:

3D/4D module cannot be enabled even though the computer has a video card that meets the minimum system requirements (nVidia 520M GT):

Some laptops (Mac 15", 17", HP, Dell with nVidia) have integrated graphics cards to help save battery life and dedicated GPU's for Games. Always make sure the dedicated graphics card (GPU) is turned **ON** and that the video drivers (windows) are up to date.

Settings for the GPU can usually be enabled in the control panel for the Display or Energy Saver settings.

16 Vascular Module

16.1	Centerline page:	112
16.1.1	Main Page	112
16.1.2	Region Growing Page	112
16.2	Curved MPR	113
16.3	Cross Section	113

The module has 3 pages

- Centerline: create and edit a centerline of any vessel using orthogonal MPR views
- Curved MPR: view and edit the centerline in CPR views
- Cross Section: do a visual and quantitative assessment



16.1 Centerline page:

16.1.1 Main Page

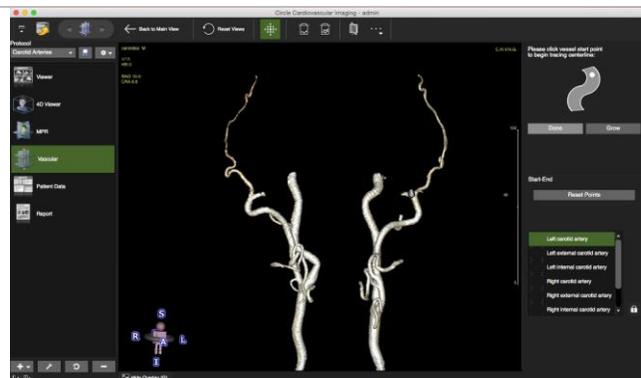
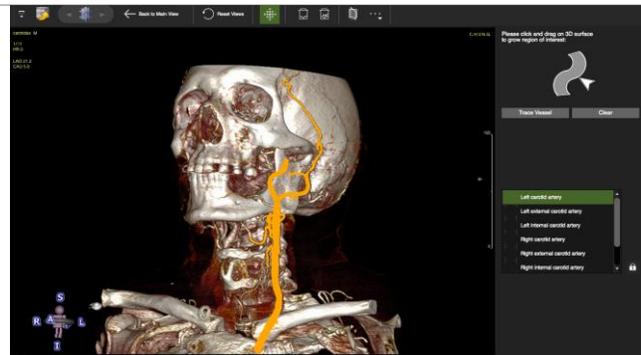
- Trace a centerline by setting a start and an end seed point in one of the MPR views
- Define a vessel (see above)



16.1.2 Region Growing Page

Alternatively, trace a centerline via region growing.

1. Click the *Region Growing* button in the top toolbar. The software will open the image in an enlarged view. The top right panel will guide you through the steps
2. Grow the vessel by dragging on the 3D surface
3. Click *Clear* to deleted the tracing
4. Click *Trace vessel*, to extract the vessel
5. To add more segments click *Grow*.
6. If you are satisfied click *Done*.



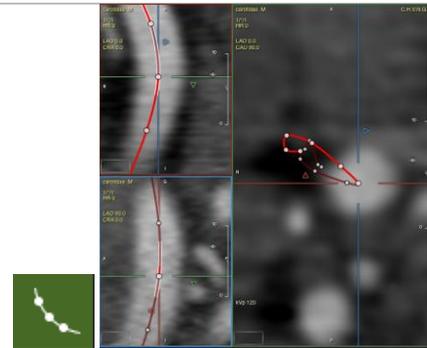
- In the segmented vessel, extract the centerline by placing a start and an endpoint.



- Will delete a selected centerline and allows to start over again
- Move to the next vessel and repeat

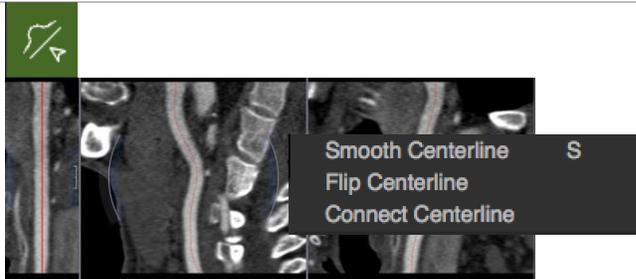


- Done* will go back to the Main page. Here you can edit the centerline.
- Click Edit Centerline Control points



16.2 Curved MPR

Use the context menu and the *Edit* button to retrace the centerline



16.3 Cross Section

See Coronary Module

17 Femoral Module

17.1	Landmark Page	115
17.2	Centerline Page	115
17.2.1.1	How to generate a centerline.....	115
17.2.1.2	How to assess calcifications	117
17.3	Curved MPR	117
17.4	Cross Section	118
17.4.1.1	How to analyze the vessel	118

The Femoral Module allows to assess the access for cardiac interventions

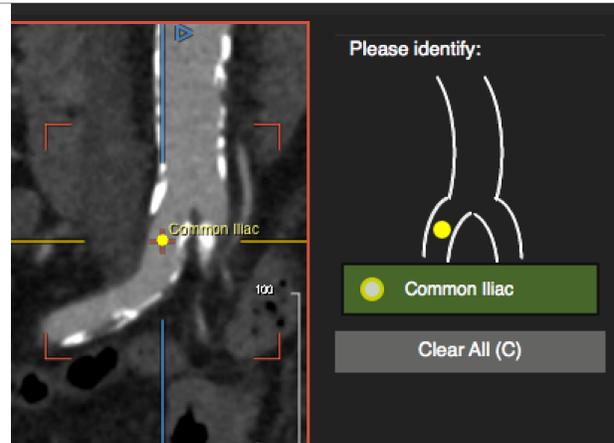


17.1 Landmark Page

Setting landmark will help the software to segment a region of interest.

Using the MPR views display the A. iliaca and set a point in the middle of the vessel

Move to the Centreline Page



17.2 Centerline Page

- Generate a centerline via *Region Growing*
- Edit the centreline control points
- Assess the calcium load of Aorta A. iliaca and Femoralis

17.2.1.1 How to generate a centerline

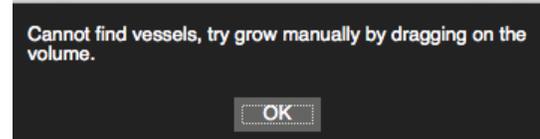
1. Trace a centreline via *Region Growing*
2. Activating the button...



...will automatically switch to an *Aortic View* .



3. A warning message will pop up if the system is not able to segment the vessels



4. Try to grow the vessels manually:



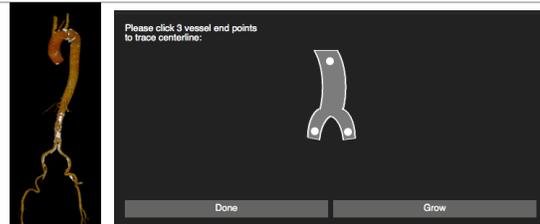
5. Point the cursor in the vessel. A black dot will appear as soon as the system detects a traceable structure.
6. Drag on the surface to grow the Femoralis, Iliaca and Aorta. If doesn't seem to pick up the vessel, try to window to better display the vessel.



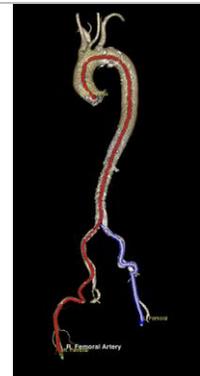
7. As soon as you have grown a region you have the option to
 - *Clear* the grown region
 - Click *Trace* when you are done



8. The system extracts the vessel. If you are not satisfied, you can go back to the growing mode, click *Grow*



9. Otherwise, define a centerline by setting 3 endpoints: In the Aorta, the left and the right femoral artery. If it does not seem to pick up the seed point, try to window the image.
 The system will automatically detect if you are in the right or in the left iliofemoral artery.
 In addition, you can set intermediate points and elongate if you wish

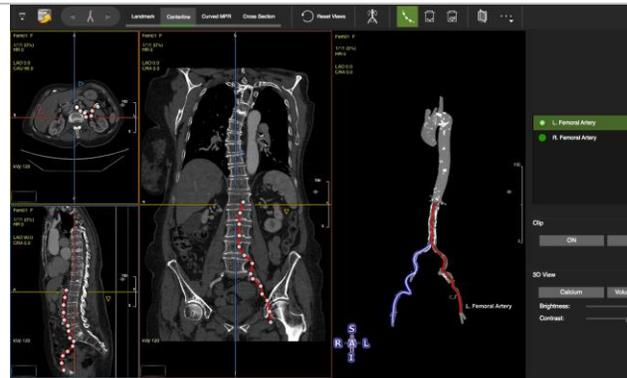


17.2.1.2 How to assess calcifications

1. Go to the 3D View menu and click on Calcium. Change Brightness and/or Contrast to optimize the image



2. Done will bring you back to the centerline. (clip off) For the reference image you have the choice to see the entire volume or (clipp on) a clipped view, that only displays the vessel



Here you can edit the centerline in 3 orthogonal orientations

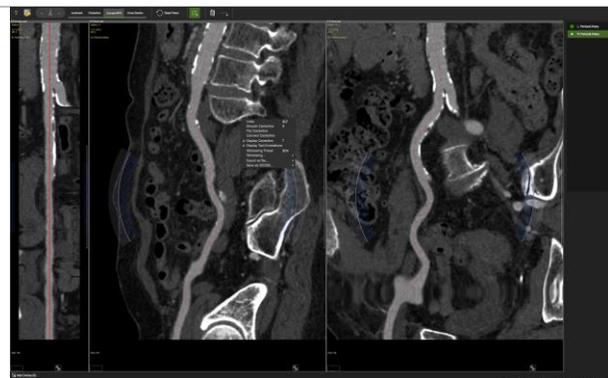
Edit/Define Centerline Control Points (E)



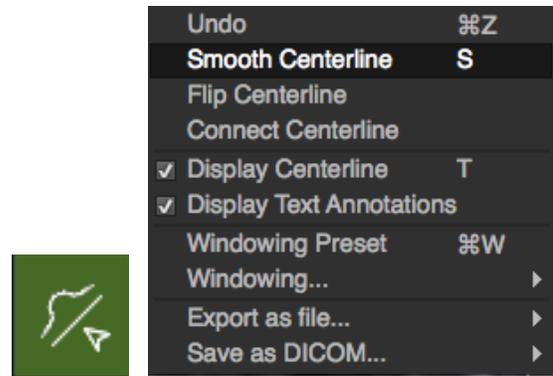
17.3 Curved MPR

Edit Centreline

Centrelines are displayed in Straightend and Stretched view



The *Edit* button and options in the context menu allow to further refine the centreline



17.4 Cross Section

Quantitative Analysis

- Caliber
- Stenosis
- Tortuosity

17.4.1.1 How to analyze the vessel

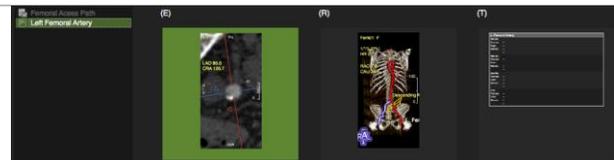
1. Set the stenosis marker.
2. Select a cross reference image.
3. Adjust the MPR viewer
4. Click the Auto Vessel lumen Contour to measure



5. Adjust the threshold if necessary



6. Add to report



18 Calcium Scoring

18.1	Toolbar	119
	How to do Calcium Scoring	119

Calcium scoring is a method to quantify the plaque load of the coronary arteries.

Post processing for Calcium Scoring requires the detection of calcium and assignment to a coronary

18.1 Toolbar

The toolbar provides 4 buttons to identify Calcium in the different coronary arteries.

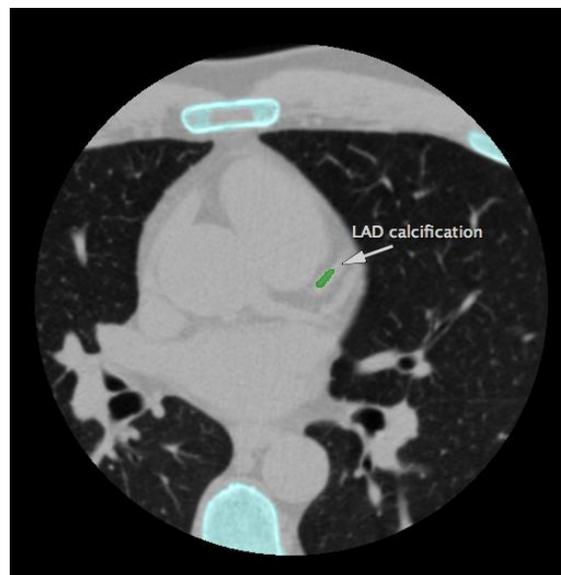
The following Region Of-Interest buttons should be selected to depict calcification

- Left Main Artery (LM)
- Left Anterior Descending Artery (LAD)
- Left Circumflex Artery (CX)
- Right Coronary Artery (RCA)

Ca Mass calibration factor: Using a phantom with calcium inserts of known mass allows for determination of a calibration factor for different MDCT scan protocols.

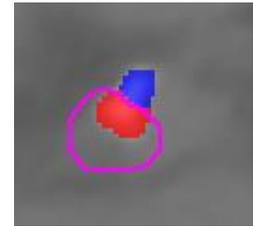
How to do Calcium Scoring

- Open the on screen navigation buttons or use your keyboard arrow keys to scroll through the slices.
-  Toggle the Overlay Display and scroll through the volume
- When you have detected Ca, select the respective coronary ROI-button and simply click in the calcified area.
- To re-do the region selection, click again
-  To re-set all region selections use the *Reset Selection* button in the toolbar





- To assign calcification to two different coronaries:
 - split the lesion with the Ca Scoring Selection Contour ,
 - select the first matching ROI (e.g. LM) and click into the respective section,
 - then select the second ROI (e.g. LAD) and click into the other part of the lesion



- Add the analysis to your report.

- Set the **Threshold** (default 130) (on the bottom of the reporting panel, underneath the Percentiles)..
- The calibration factor will be retrieved from the DICOM header or can be entered manually (calibration factors are specific to scanner, protocol and patient weight)

Ca Threshold (HU) 130

Manual Calibration 1.000

- Volume, Mass and Agatston Score and **Agatston Classification** determined automatically.
- To determine the **Percentiles** of the patients Agaston Score per coronary, select the ethnic group

Ca Scoring Report

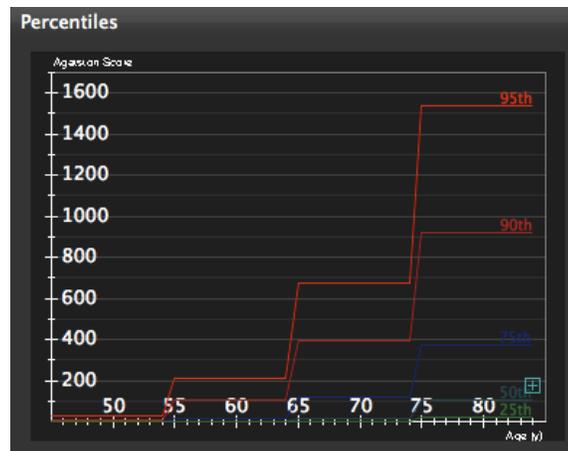
Artery	Volume mm ³	Mass mg	Score Agatston
LM	0.00	0.00	0.00
LAD	75.44	27.55	100.59
CA	0.00	0.00	0.00
RCA	54.44	19.51	72.59
Total	129.88	47.06	173.18

Ca Threshold: 130.00

Ca Mass Calibration Factor: 1.00

Agatston Score Classification:

Moderate Coronary Artery Calcification



19 Aortic Valve

19.1	Calculated values	121
	Landmark page	122
19.1.1	How to define the cusp insertion points	123
19.2	Annulus page	123
19.2.1.1	How to analyze the aortic annulus	124
19.2.1.2	How to save and report images and measurements	125
19.3	Ancillary Page	127
19.3.1.1	How to measure the ostium height	127
19.3.1.2	How to measure the sinus of valsalva	128
19.3.1.3	How to measure the sino-tubular junction	128
19.3.1.4	How to report calcification and additional findings	128
19.3.1.5	How to simulate a device	128
19.3.2	Device Simulation:	128
19.4	Fluoro page	129
19.4.1.1	How to identify angulation for fluoroscopy	129
19.5	Access page	130
19.6	References	130

Intended Use

cvi⁴² – The Aortic Valve modul offers a structured workflow for pre-procedural planning of transcatheter aortic valve replacement. Accurate measurements of the access path, the aortic annulus, the left ventricular outflow tract (LVOT) and ancillary measurements such as the distance between the coronary ostia and the annulus allow for accurate device type and sizing.

19.1 Calculated values

For multiple phases:

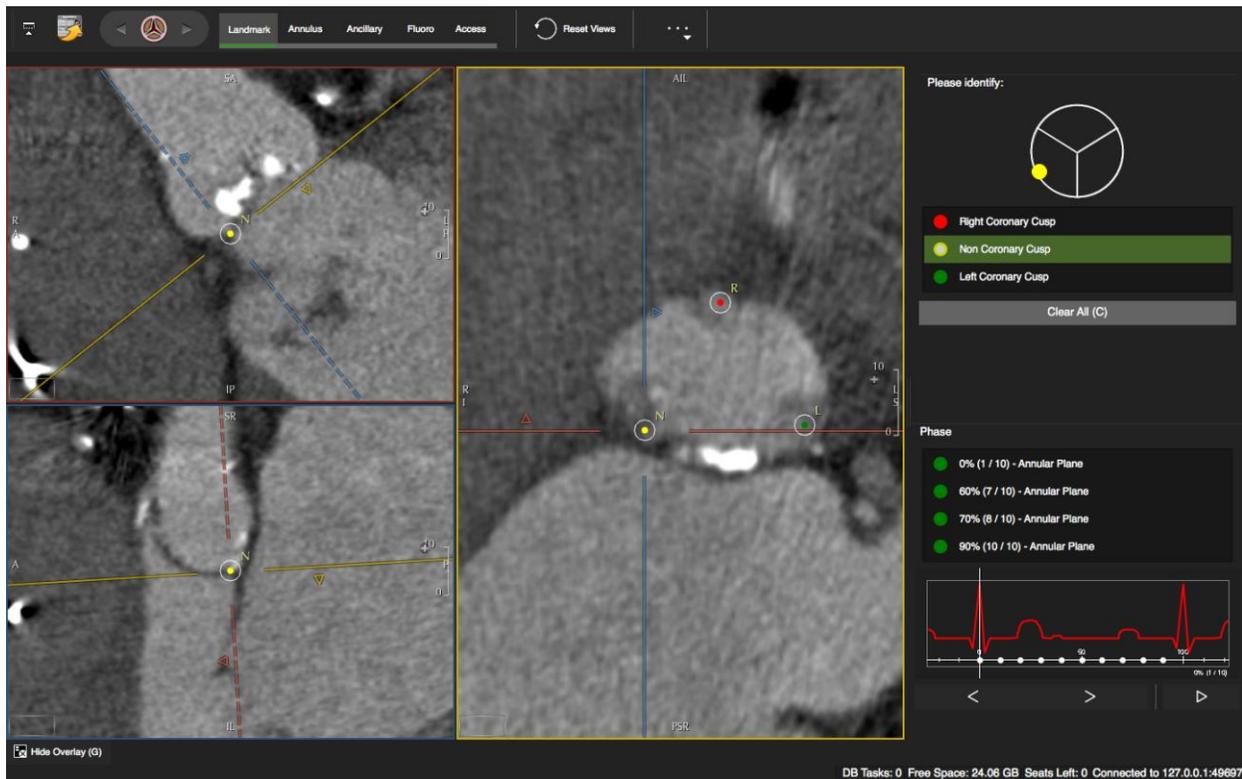
- Perimeter (mm)
- Annulus Area (mm²)
- Minimum Diameter (mm)
- Maximum Diameter (mm)
- Perimeter Derived Diameter (mm)
- Area Derived Diameter (mm)
- Ellipse Perimeter (mm)

- Ellipse Area (mm²)

Ancillary Measurements:

- Ostium height
- Custom measurements

Landmark page



The annulus page is designed to identify the annulus plane by defining the cusp insertion points.

According to the recommendations for measurement of aortic annulus dimensions ¹, systolic measurements (30% of the R-R-cycle) may be preferable to diastolic measurements of aortic annulus size. ^[1]

The software however allows definition of the basal ring in multiple phases. Landmarks and measurements will be saved per phase and it is possible to easily switch between the phases in each page.

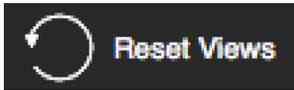
19.1.1 How to define the cusp insertion points

1. In case you have a multiphase data set, start with selecting the appropriate phase.
2. Display the annulus plane in the *Annulus* view port.
3. Select a cusp in the *Point of Interest* pane, move the MPR center in the *Annulus* view port to the cusp insertion point, check the location in the orthogonal views
4. Click the insertion point in the axial view port to define the cusp insertion point

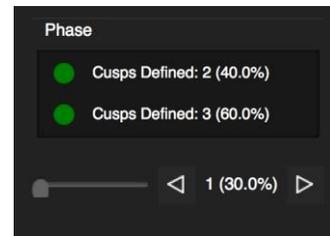
To correct, simply click again.

For a step by step approach please refer to Achenbach S., Determination of the Aortic Annulus Plane in CT Imaging²

•

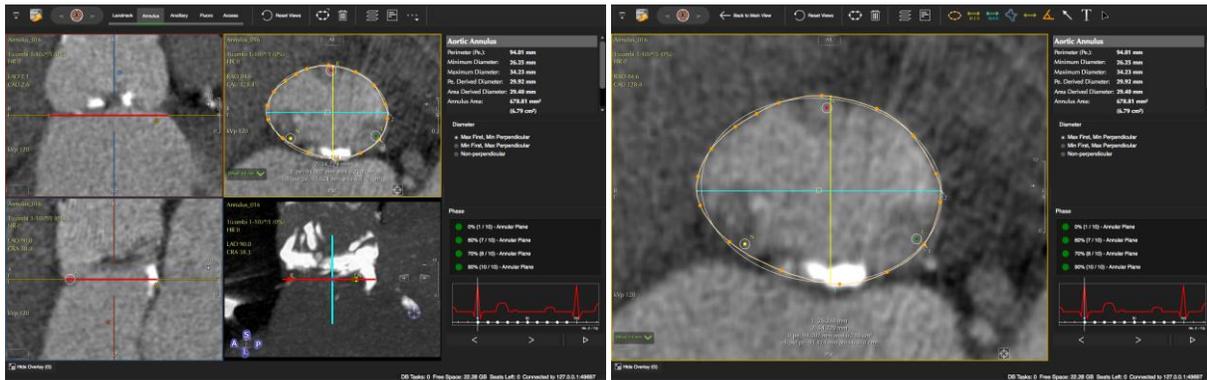


5. Allows to reset the view



6. Go to the next phase and repeat. You can easily switch back and forth between the phases by clicking on the phase line or using the arrow keys.

19.2 Annulus page



Measurement tools

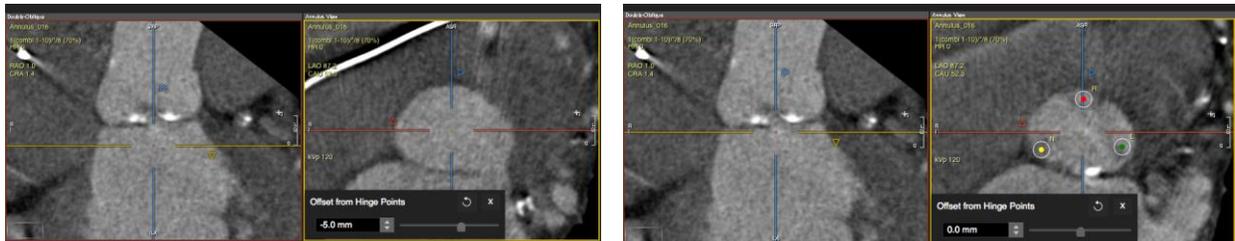
	Perimeter control points	By default the <i>Calculate Ellipse Perimeter</i> will measure perimeter and area of a drawn contour. In addition it will estimate a strict elliptical perimeter including it's area
	Maximum Length	
	Minimum Length	
	Freehand Contour (On/Off)	Area in cm ² and SI
	Line Contour	Length in mm (LMC, drag and release)
	Angle Measurement	By default the angle measurement will use angles within 180 degrees. Unchecked in the <i>Preferences</i> it will provide all angles.

19.2.1.1 How to analyze the aortic annulus

1. Measurements will be performed in the annulus view frame.



2. The axial view port allows to open an offset menu, which displays the distance from the hinge points when you scroll up or down .



3.  Maximize the frame for better viewing. Use the *Back to Main View* button in the toolbar to get back.

4.  Pick up the perimeter tool and set points around the annulus. The following values will be calculated:

- Perimeter (Pe) (mm)
- Minimum Diameter (mm)
- Maximum Diameter (mm)

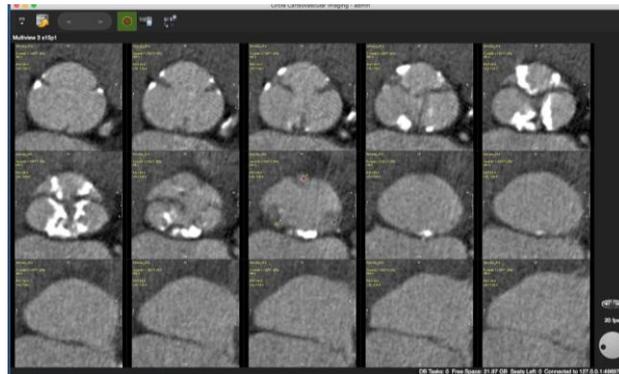
- Pe Derived Diameter (mm)
- Area Derived Diameter (mm)
- Annulus Area (mm², cm²)

The ellipse perimeter will be displayed in the annulus view port.

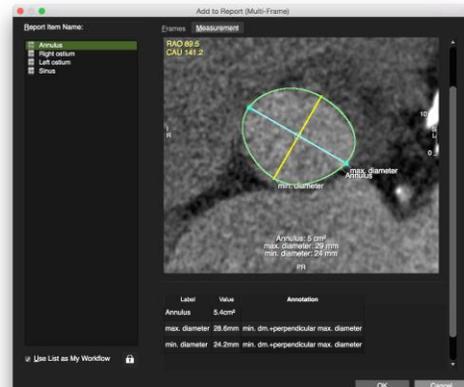
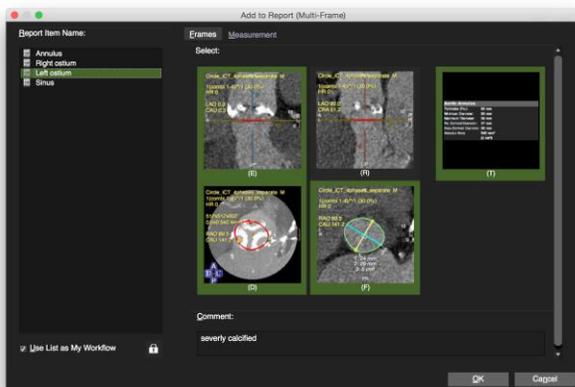
5.  Click to edit the perimeter

19.2.1.2 How to save and report images and measurements

1.  Save a stack of images as a secondary DICOM capture



2.  Select and add multiple frames and measurements to the report



- To report a measurement with an appropriate identifier, the contour for this measurement has to be labeled: in the analysis frame activate the contour and open the context menu. Select *Contour Labels*. Labels will be remembered and compiled into a list in the contour label menu
- In the toolbar click the *Add to report* button
- Provide a description
- In the *Frame* page select the frames for the report. Optionally provide a comment.
- In the *Measurement* page items can be annotated.
- Go to the *Report* module to find your measurements for reporting.
- Check *Use List as My Workflow* to save the list for futures reference. In your next patient study the list of values or items will be preset. The set of frames will be linked to an item by simply selecting it in the list.

3.  Save the Layout view.

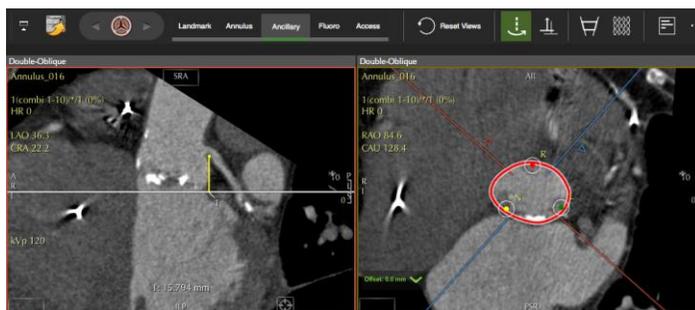


19.3 Ancillary Page



19.3.1.1 How to measure the ostium height

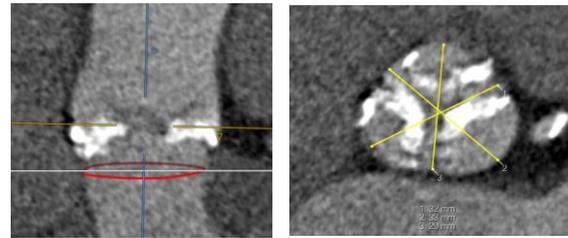
1.  Activate the *Rotate around the Annulus* button and drag the cross hairs until it cuts the coronary cusp and the ostium is displayed in the double oblique window . Display the ostium in the *Double-Oblique* frame.
2.  Pick up the *Ostium Height* measurement tool
3. Drop a point at the height of the otium with a left mouse click. A line measurement perpendicular to the annulus plane will be performed automatically



4.  *Add to Report*: Select frame and measurements and provide comments and annotations (s.b)

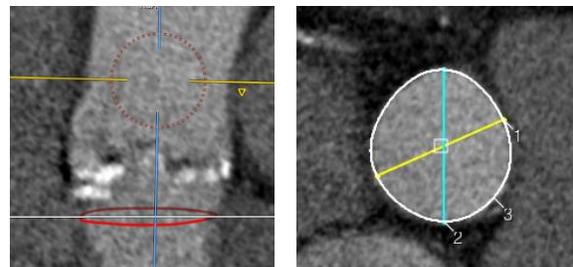
19.3.1.2 How to measure the sinus of valsalva

1. In the oblique axial image display the sinus
2. Pick up the line contour to measure the diameter (push the left mouse button, drag and release)
3. *Add to Report*: Select frame and measurements and provide annotations (s.b)



19.3.1.3 How to measure the sino-tubular junction

1. Display the junction in the oblique long axis images
2. Measure the diameter
3. *Add to Report*: Select frame and measurements and provide annotations (s.b)



19.3.1.4 How to report calcification and additional findings

Calcification is associated with a 3-fold increase in vascular complication. Report if calcification is circumferential or nearly circumferential and/or located at vessel bifurcations along the access path
 If a native data set is available a calcium score can be assessed in the *Calcium Scoring Module*.
 In addition, the left ventricle should be evaluated for the presence of thrombi.

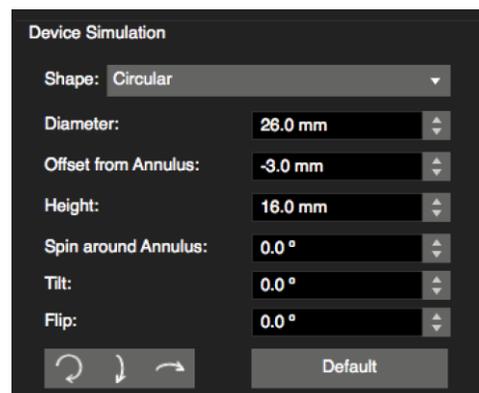
19.3.1.5 How to simulate a device

19.3.2 Device Simulation:

-  The device simulating buttons open a menu:

Circular

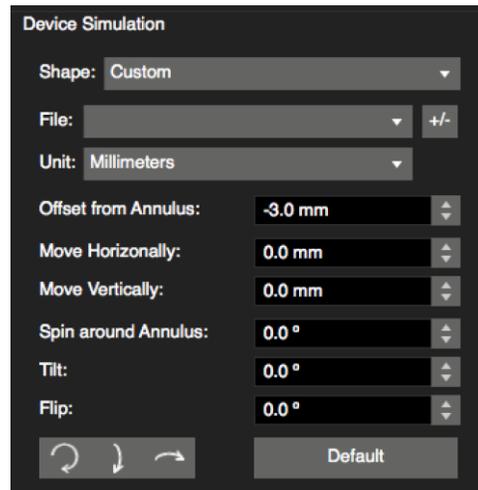
- Change the shape
- Change the diameter and/or height of the device
- Shift it up or down by setting an off-set
- Tilt and/or flip it by a defined degree
- Spin it around the annulus



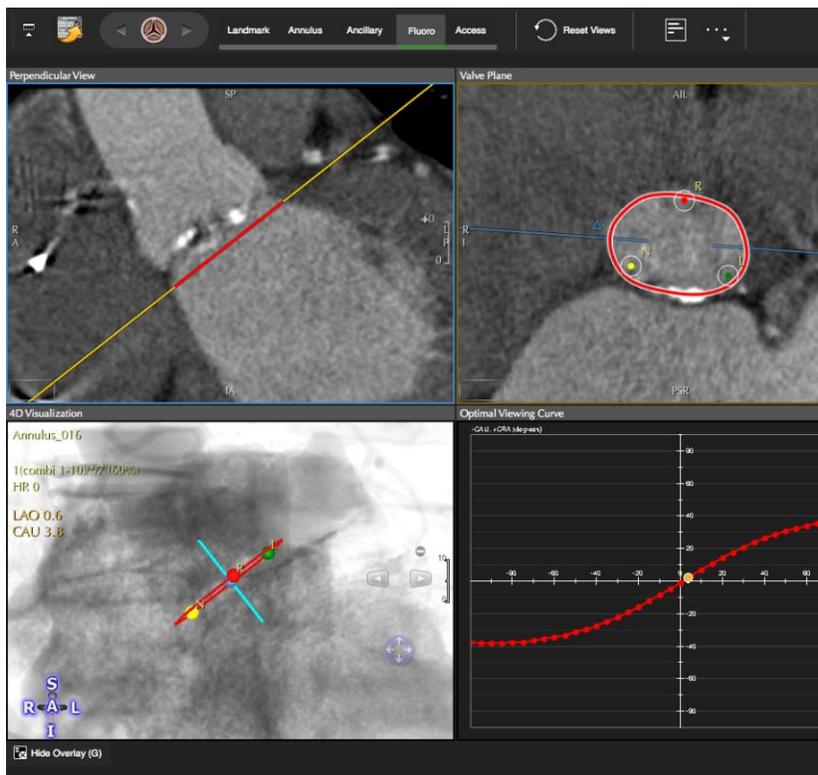
Custom

additional options are:

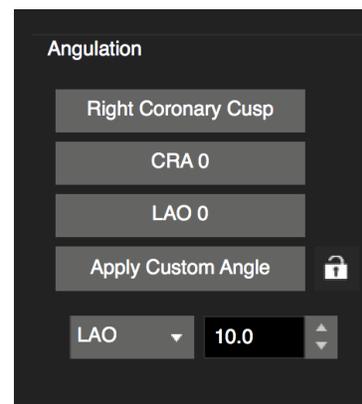
- add a file with vendor specific devices
- change units from metric to imperial



19.4 Fluoro page

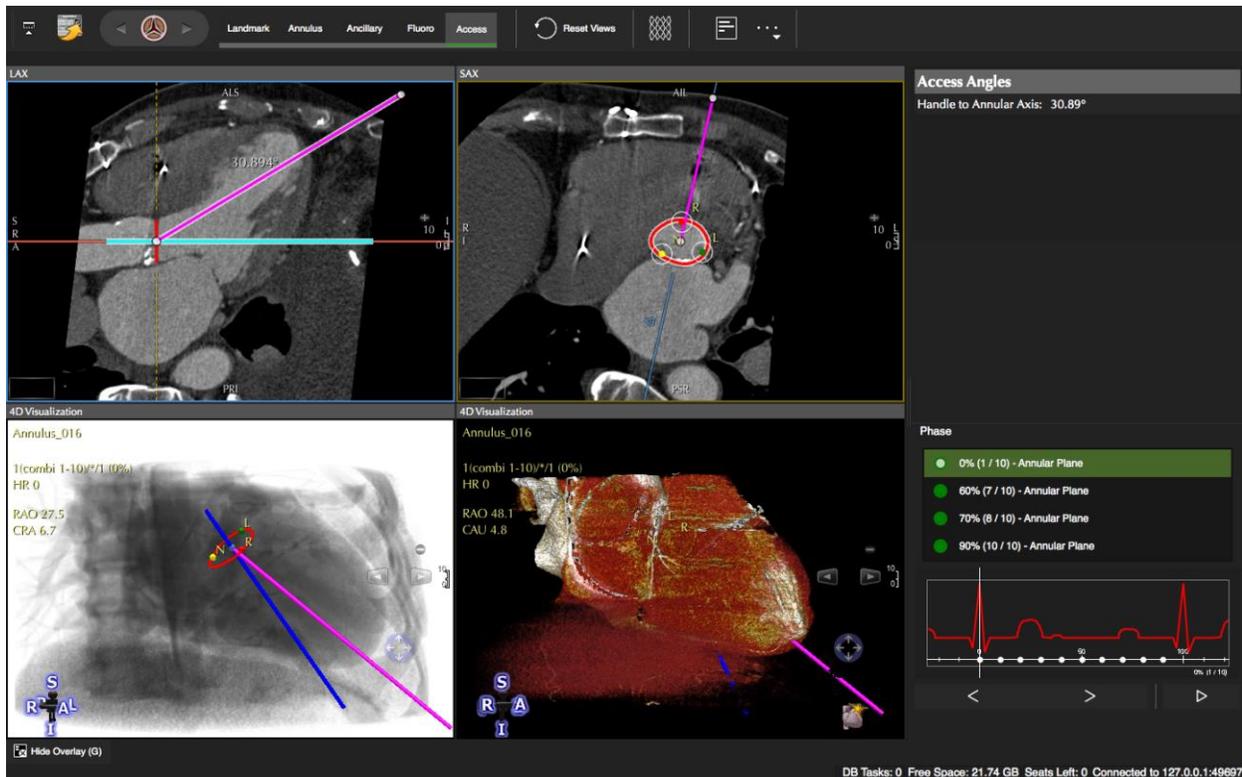


19.4.1.1 How to identify angulation for fluoroscopy



1. Scrolling along the optimal viewing curve allows to display the angles in the synchronized 4D and MPR viewers.
2. There are preset angles that will be reported
3. Add custom angles by opening the lock angles in the angulation pane.

19.5 Access page



If a trans-apical access route is planned, the position of the LV apex relative to the chest wall and alignment of the LV axis with LV outflow tract (OT) orientation should be assessed and recorded.

In the long axis double oblique view drag the yellow dot along the preferred access.

19.6 References

1. Achenbach et al. SCCT expert consensus document on computed tomography imaging before transcatheter aortic valve implantation (TAVI)/transcatheter aortic valve replacement (TAVR) . Journal of Cardiovascular Computed Tomography (2012) 6, 366–380.
2. Achenbach S, Schuhbäck A, Min JK, Leipsic J. Determination of the Aortic Annulus Plane in CT Imaging—A Step-by-Step Approach. JCMG. Journal of the American College of Cardiology; 2013 Feb 1;6(2):275–8.

³Jabbour A, Ismail TF, Moat N, et al. Multimodality Imaging in Transcatheter Aortic Valve Implantation and Post-Procedural Aortic Regurgitation: Comparison Among Cardiovascular Magnetic Resonance, Cardiac Computed Tomography, and Echocardiography. *J Am Coll Cardiol*. 2011;58(21):2165-2173. doi:10.1016/j.jacc.2011.09.010.

⁴Jeroen J. Bax et al. Open issues in transcatheter aortic valve implantation. Part 1: patient selection and treatment strategy for transcatheter aortic valve implantation. 1,* . *Eur Heart J* (2014) 35 (38: 2627 - 22638

⁵Holmes DR, Jr., Mack MJ, Kaul S, et al. 2012 ACCF/AATS/SCAI/STS Expert Consensus Document on Transcatheter Aortic Valve Replacement. *J Am Coll Cardiol*. 2012;59(13):1200-1254. doi:10.1016/j.jacc.2012.01.001.

20 LV/RV Function Modules

20.1 Bi/Triplanar Module	134
20.1.1 LV Function Analysis	135
How to do bi-triplanar LV function and volume analysis	135
20.1.2 Atrial Volumetry	136
How to do atrial volumetry in one or two planes	136
20.2 Multiple Long LAX Module	137
How to do LV function with multiple radial long axis	138
20.2.1 Ventricular volume/mass over time	140
20.3 Short 3D Module	141
20.3.1 Short 3D Interface	141
20.3.1.1 Customize the interface:	142
20.3.1.2 Thumbnail Grid	142
20.3.2 Global LV function and volume analysis	143
How to do LV segmentation	143
20.3.2.1 Automatic Segmentation	144
How to do automatic LV segmentation	144
20.3.2.2 Manual Definition of Systole and/or Diastole for LV and/or RV	145
How to manually define systole and diastole	145
20.3.2.3 Mitral Valve Plane Correction	146
20.3.2.4 Exclude Atrial Volume	146
20.3.2.5 Papillary Muscles	146
20.3.2.6 Ventricular Volume/Mass Over Time	147
20.3.3 Regional Wall Analysis	148
How to do wall motion analysis	148
20.3.4 RV function and volume analysis	150
How to do manual RV segmentation	151
How to do automatic RV segmentation	152
20.3.5 Atrial volumetry	153
How to do atrial volumetry in short or long axis orientation	153

The following approaches are available:

Left ventricle:

- ⦿ 2-chamber, 4-chamber and short axis view. (see Module *Bi/triplanar LAX*)
- ⦿ Multiple radial long axis planes. (see Module *Multiple Long LAX*)
- ⦿ Parallel SAX stack (see *Module Short 3D*)

Right ventricle:

- ⦿ Parallel SAX stack (see *Module Short 3D*)
- ⦿ Parallel LAX stack (see *Module Short 3D*)

Atria:

- ⦿ Bi/Triplanar : (see Module *Bi/triplanar LAX*)
- ⦿ Parallel LAX stack (see *Module Short 3D*)

20.1 Bi/Triplanar Module

Intended use:

- ⦿ LV function analysis biplanar in 2CV and 4CV or triplanar by adding a short axis view.
- ⦿ Atrial volumetry in one or 2 planes

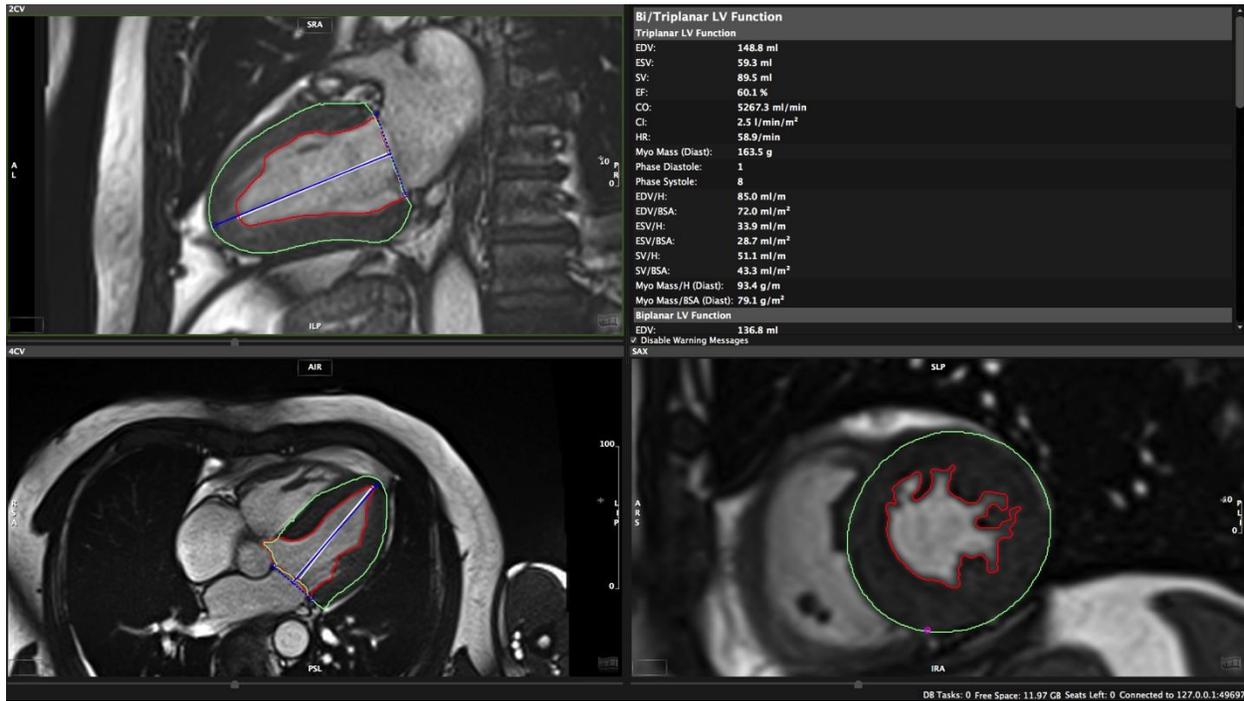
WARNING: Bi/Triplanar

For the calculations, the diastolic and systolic phase are assumed to be in the same phase of the cardiac cycle in all three views. The volume calculation is done per phase. The smallest volume is assumed to be the systolic volume and the largest volume is assumed to be the diastolic volume. In case a volume can be calculated for one phase only, ESV and EDV will be displayed as equal and no calculations will be performed for derived parameters such as ejection fraction.

Endocardial contours must always be on the inside of the epicardial contour, cmr⁴² does not check for that.

Calculations in cmr⁴² are performed based on the current state of contour definition and image selection. For every change the calculations are updated immediately. It is the responsibility of the user to decide whether the stage of contour definitions reflects the intended measurement task before releasing final results.

20.1.1 LV Function Analysis



How to do bi-triplanar LV function and volume analysis

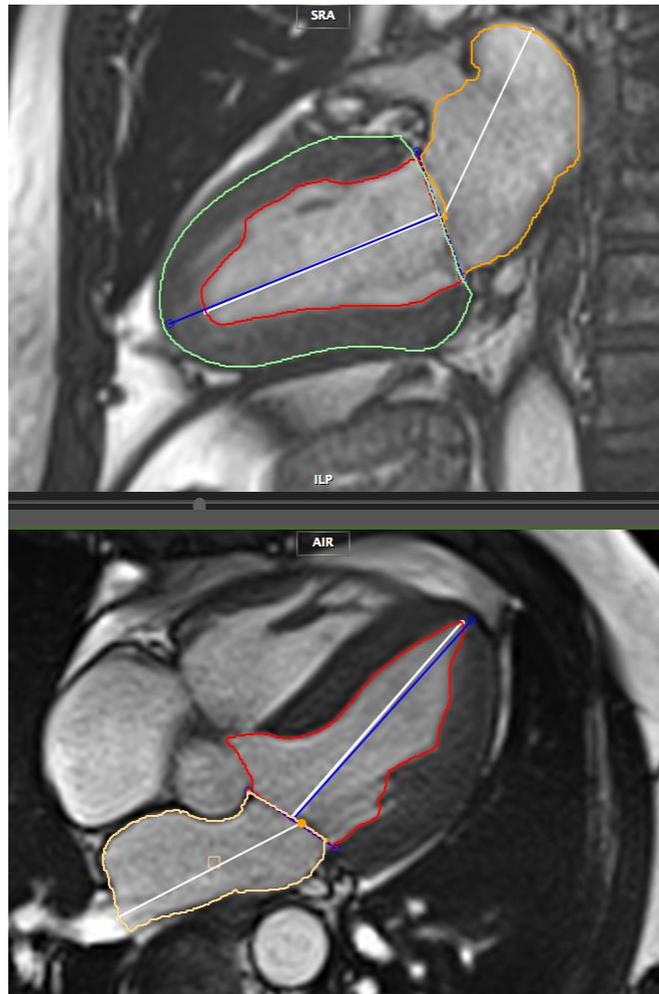
1. Drag and drop the series (2CV, 4CV, SAX) from the thumbnail panel into their respective frames and adjust viewer properties
2. Select the slice and phase by using the navigation buttons or the arrow keys on your keyboard
3.  **Automatic endocardial edge detection** requires the definition of the LV extent:
 - pick up the *LAX LV Extent* tool and set two points defining the mitral valve plane, and a third point in the apex to define the length of the ventricle.
 - As soon as the apex point has been set, the endocardial contour will be detected automatically. Correct if necessary.
4. Draw an epicardial contour
5.  **Propagate endo- and epicardial contours:** Click on the *Segment Myocardial Contours LAX in Slice* button.
6. Repeat for both phases
7. Add analysis to Report  .

20.1.2 Atrial Volumetry

How to do atrial volumetry in one or two planes

Mono or bi-plane area-length method

1.  You have to define ventricular end-systole first, using *the LV extent contour* button.
2.  Next, select the *Left* or *Right Atrium Contour* button and delineate the atrium: start at the valve, trace the atrial the border and finish at the valve plane.
3. The valve plane will be determined automatically. The yellow dot in the valve plane can be dragged to adjust the contour for the shape of the valve.
4. Add analysis to Report  .



Trouble Shooting

Despite drawn contours there are no results calculated:
Systole has not been determined (see step 1. above)!

20.2 Multiple Long LAX Module

Intended use: LV function volume and mass analysis.

WARNING: Multiple Long

The input for multiple long calculations requires a multi-slice series with long axis slices that are acquired along a central rotation axis. *cmr*⁴² and *cvi*⁴² check for the presence of these requirements, although it allows some variance to avoid small aberrations being rejected from the analysis. It is the responsibility of the user to verify the cutting line of the slices and decide whether the variance in the rotation axis is acceptable.

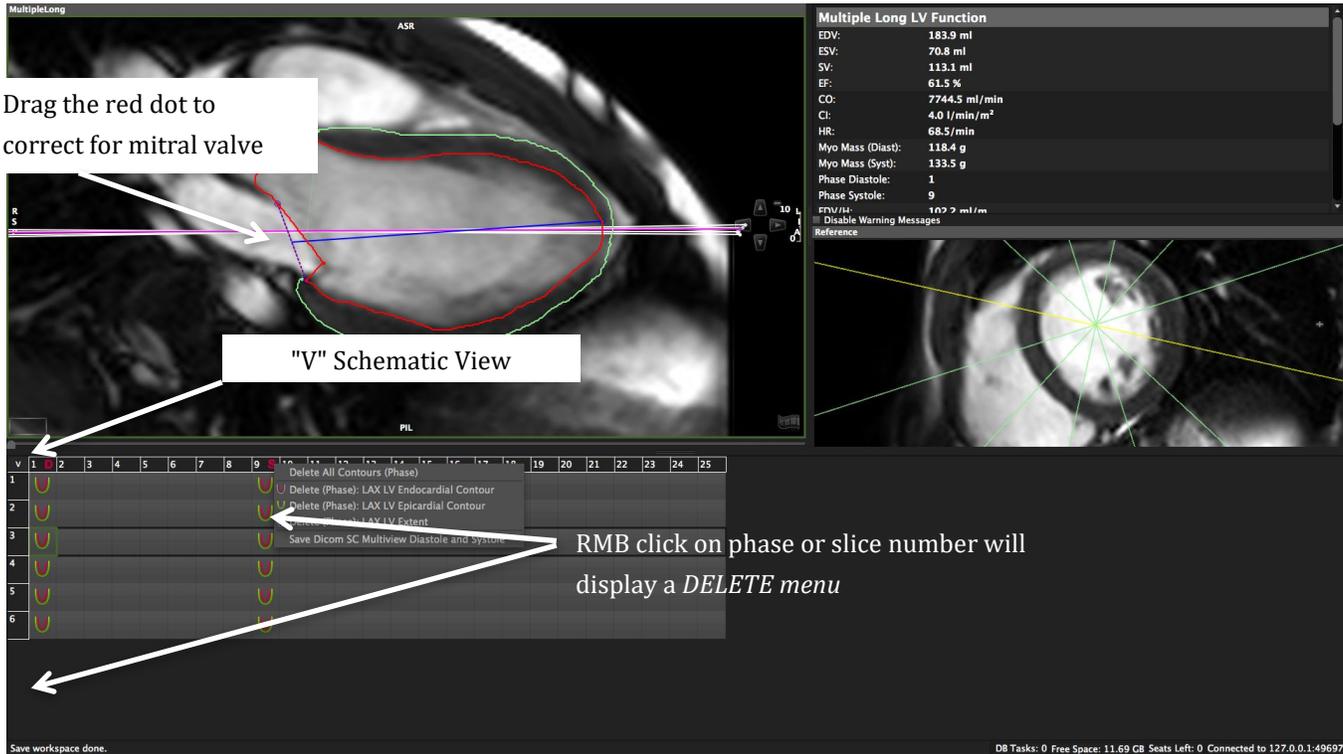
Depending on the shape of the left ventricle the method in use might not be suitable for all evaluations (e.g. severe regional wall motion abnormalities), it is the user's responsibility to verify the suitability of the selected method.

Endocardial contours must always be within (i.e. on the luminal side of) the epicardial contour, *cmr*⁴² does not check for that.

The volume calculation is performed for every phase. The smallest volume is assumed to be the systolic volume and the largest volume is assumed to be the diastolic volume. If the volume can only be calculated for one phase, ESV and EDV will be displayed as equal and no further calculations are done.

Missing contours are interpolated, if possible.

Calculations are performed based on the current state of contour definition and image selections. For every change in this state the calculations are updated immediately. It is the responsibility of the user to verify that the contours reflect the desired measurements before releasing final results.



How to do LV function with multiple radial long axis

1. Drag the radial long axis series from the thumbnail panel into the respective frame and adjust viewer properties. A perpendicular short axis cine series (if available) will automatically be displayed in the reference window. The currently active slice is highlighted in yellow.
2. For a better orientation **switch to a schematic view** of the study display grid: Clicking on the “V” in the left top corner switches to a schematic view to help you find the right slice and phase
3. Select the slice and phase by using the navigation buttons or the arrow keys on your keyboard. Start and stop a cine loop by clicking on the film icon.
4. Endocardial Contour:



Start with the definition of the LV extent:

Pick up the LAX LV Extent tool and set two points defining the mitral valve plane and a third point in the apex to define the length of the ventricle.

As soon as the apex point has been set, the endocardial contour will be detected automatically. Correct if necessary.

5. Draw an epicardial contour  manually or  Semiautomatic



6. To forward a contour use the toolbar button *Segment Myocardial Contours LAX in Slice* button.

•

7. Repeat for all slices

Systole and diastole will be indicated by the letters "S" and "D" next to the phase number in the grid.



8. Contour adjustment:

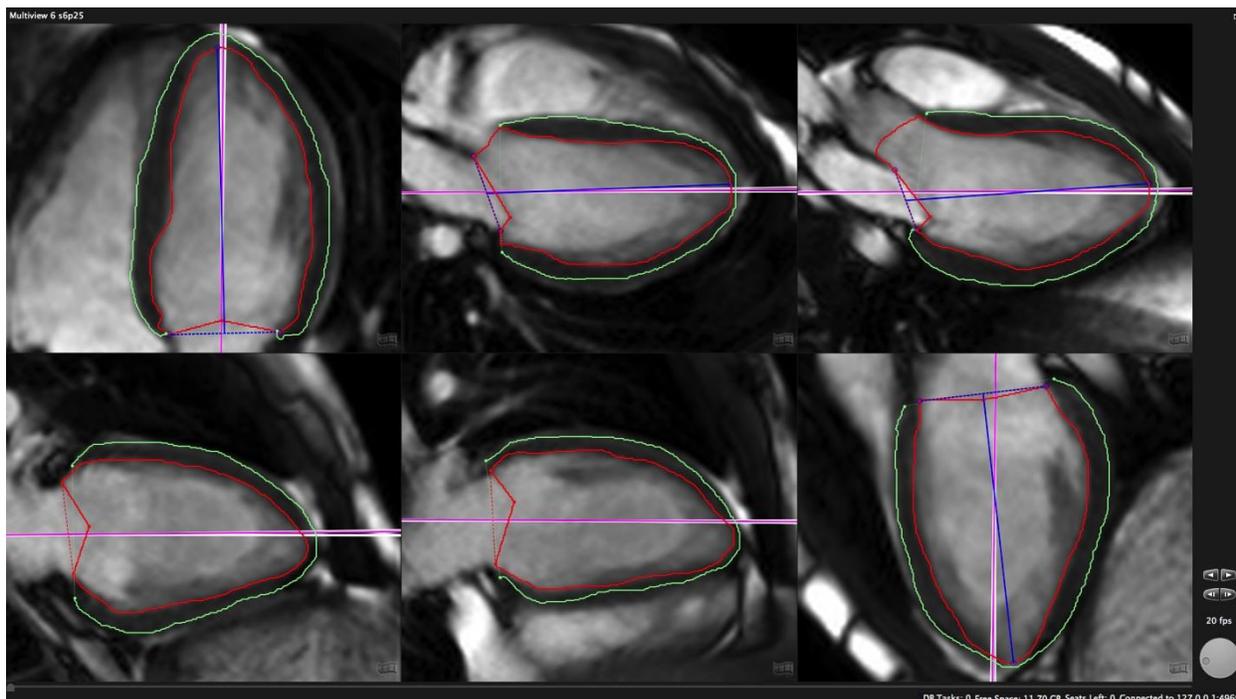
Scroll through the phases and slices and correct where required.

- If necessary correct for the angulation of the mitral valve plane by clicking and dragging the red dot to adjust it to the mitral valve.
- Using the tab-key allows to switch between contours.
- The shift-key hides contours and allows to check borders.
- A click in the grid on the slice-number column or the phase-number row opens a delete menu



9. Add analysis to Report

•



Warning messages:

A warning message will be displayed in the results frame (and the exported reports) when:

- only one phase has been evaluated,
- the number of evaluated slices differs between systole and diastole
- less than 3 slices are used for calculations
-

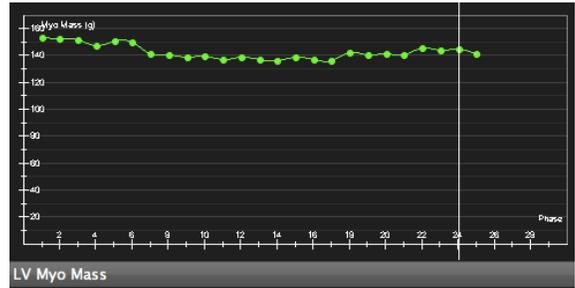
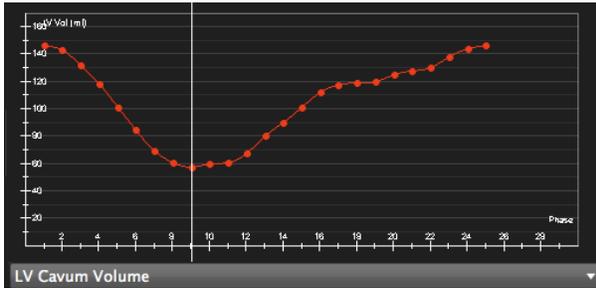
Note:

It is at the user's discretion to disregard warning messages by checking the box underneath the analysis report window, next to Disable Warning Message. As soon as there are alterations to the analysis the warnings will be re-activated

20.2.1 Ventricular volume/mass over time



Define endocardial and epicardial contours in all phases and slices and click *LV volume curve*



Peak Ejection and Filling Rate and Peak Wall Thickness can be found in the scientific report

Peak Ejection Rate (ml/s): 654
Peak Filling Rate (ml/s): 613

20.3 Short 3D Module

Intended use:

Using the disc-summation technique this module is able to analyze a stack of parallel images in long or short axis orientations

- Global and regional LV function and volume analysis
- Global RV function analysis
- Atrial volumetry

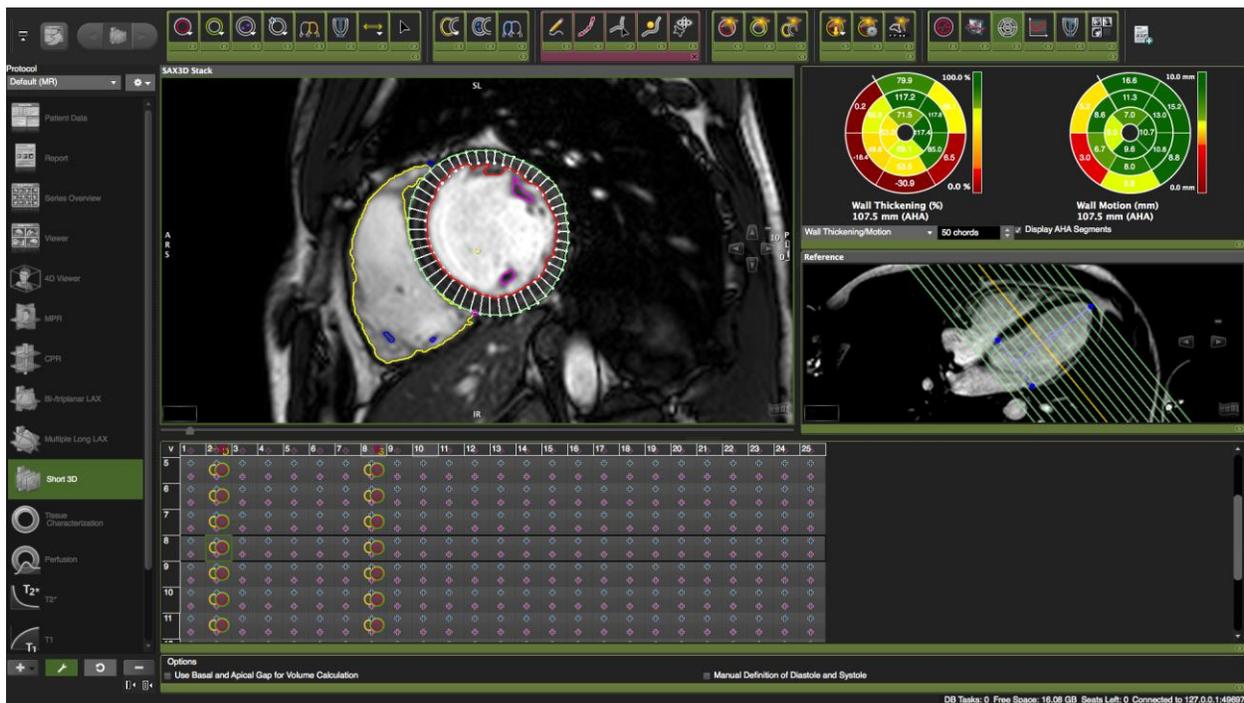
WARNING: SA 3D

The volume calculation is done for phases. The smallest volume is assumed to be in systole and the largest volume is assumed to represent diastole. In case a volume can only be calculated in one phase, ESV and EDV will be displayed as equal and no further calculations are done.

Missing contours are interpolated, if possible.

Calculations are performed based on the current state of contour definition and image selections. For every change in this state the calculations are updated immediately. It is the responsibility of the user

20.3.1 Short 3D Interface



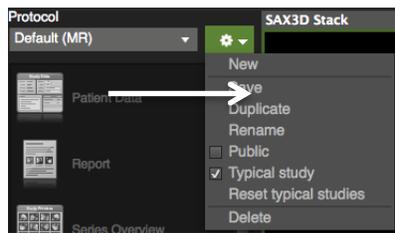
20.3.1.1 Customize the interface:

The module is quite comprehensive and sections that are not part of your clinical routine can easily be hidden in the interface.

In the protocol pane click on wrench "Edit Protocol".

Here is what you can customize:

- View ports like the thumbnail grid or reference viewer
- Tool sets or buttons for e.g. RV volumetry or the features for extended LV function analysis (*View Regional Function, View LV volume curve*)
- *Options* menu, offering the following feature
 - *Manually define diastole and systole.*
 - *Use Basal and Apical Gap for Volume Calculation:* This applies to a stack with a defined gap. Checked, the software will add half of the gap to the slice thickness of apical and basal slice

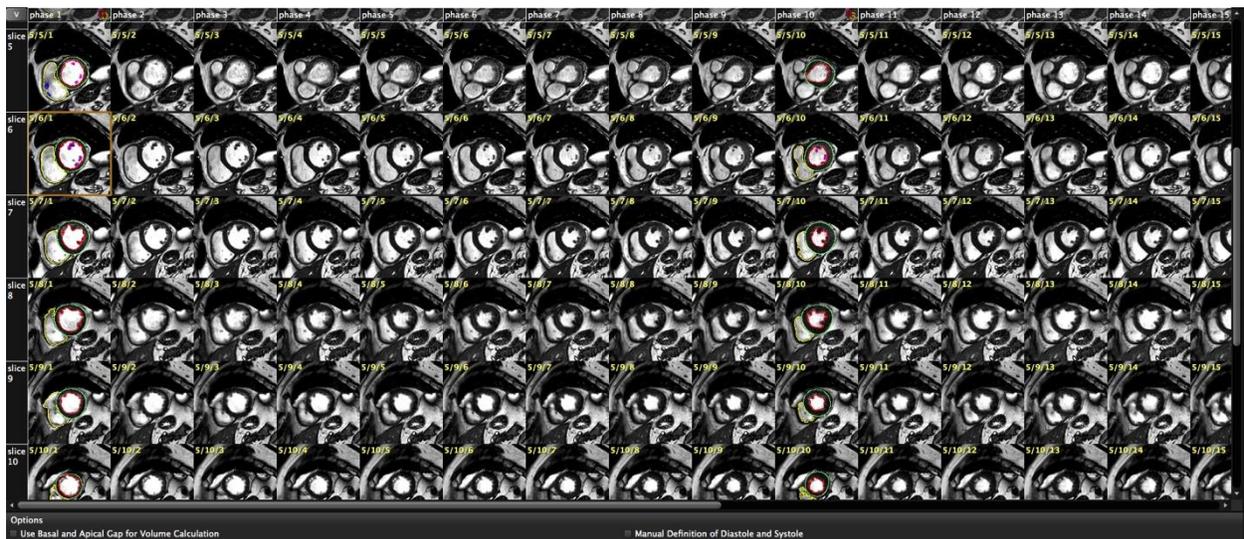


Save your settings

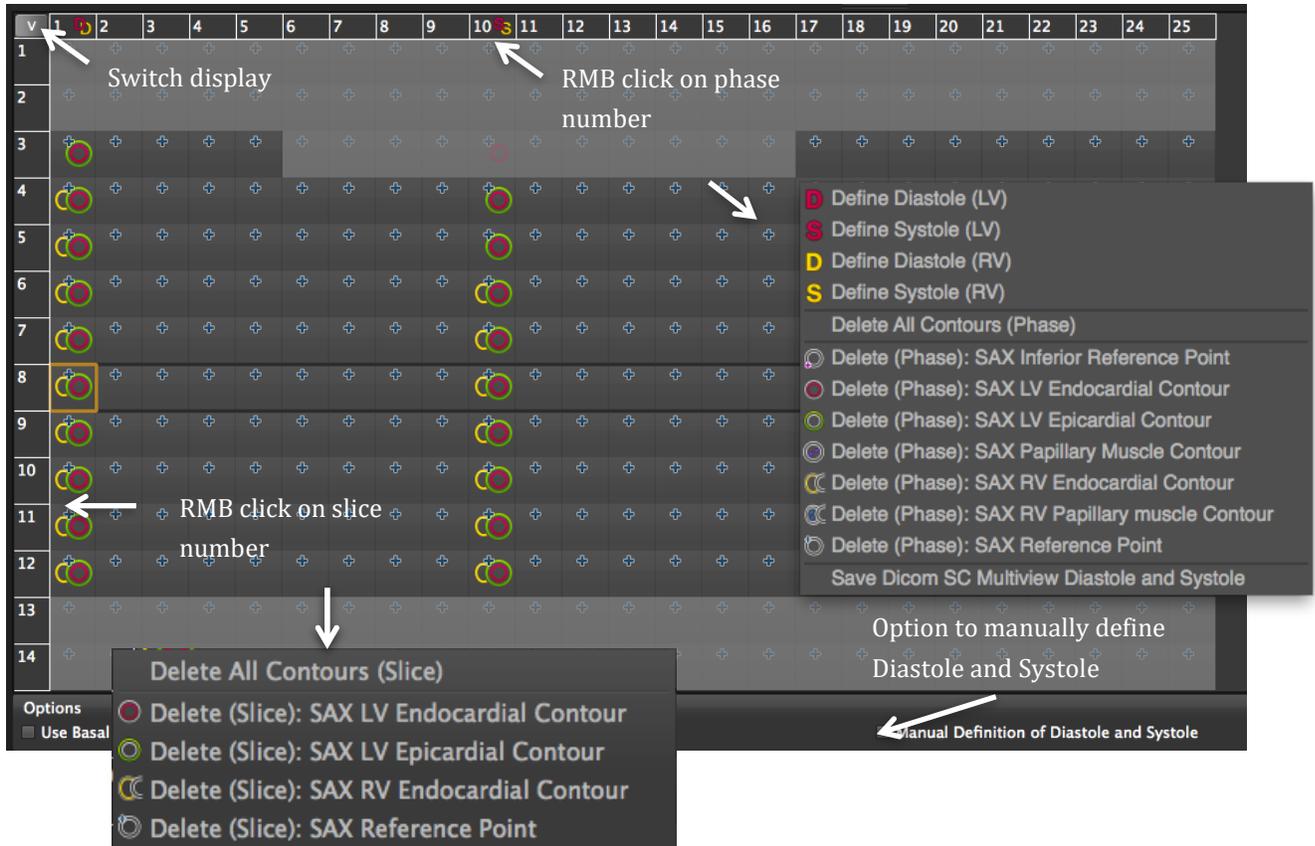
The protocol pane and the thumbnail panel can be hidden by clicking on the icon on the left  and  right bottom corner. They can still be accessed by hovering the mouse over the very left and right frame border.

20.3.1.2 Thumbnail Grid

The thumbnail grid represents images of all slices and phases that are contained in a parallel stack.



Optionally, the display can be changed to a schematic view click the "V"



- ⦿ Right mouse button click on a phase number opens a menu
 - to delete contours
 - to manually define systole and diastole. That requires to check the respective box in the option menu
 - to save a secondary DICOM capture of systole and diastole
- ⦿ Right mouse button click on a slice number or a table cell will open a *Delete* menu for the respective slice or image.

20.3.2 Global LV function and volume analysis

How to do LV segmentation

1. Drag short axis series into the analysis frame.

A perpendicular long axis cine series (if available) will be automatically displayed in the reference window, highlighting the selected slice in yellow. Starting version 5.3.0, an uneven phase count will be accepted.

2. Scroll through the phases and identify diastole and systole
3. For border delineation select a contouring tool  ,  as well as a contouring mode   or use the semi-automatic options for endo  and epicard.  (please refer to the chapter *Contouring Drawing and Labeling*)
4. Switching to a schematic view in the thumbnail grid (click on the “v”), provides a better overview of existing contours. In addition it allows for deleting certain contours (RMB click). Current images are framed in green.
5. To move to the next slice, use the on-screen navigation buttons or the arrow keys on your keyboard, or click on the respective image in the grid.
6. Repeat for all applicable slices

20.3.2.1 Automatic Segmentation

Specific to the Short 3D module is the automatic contour detection that will perform a contour detection for a group of images.

How to do automatic LV segmentation

1. Centre your LV, so that the yellow target point is in the middle of the left ventricle.
2.  Program the automatic contour detection button: The button is located in the top toolbar. It can be programmed to perform edge detection for multiple slices/phases or the entire stack at once.

A RMB click opens a menu:



Detect endo, epi or both contours for the current phase



Detect endo, epi or both contours for the current slice



Detect endo, epi or both contours for the entire stack

Drag the mouse to the desired option and release the button.

The image of the icon will change according to the selected function.

3. Define your analysis range:

If your stack has slices beyond the left ventricle, they have to be excluded for the automatic LV segmentation.

In the reference frame, open the pencil box and select the *LAX LV Extent* contour.

Using the navigation buttons, select end-systole.

The *LAX LV Extent* contour tool allows to set 3 points (= 3 LMB clicks):

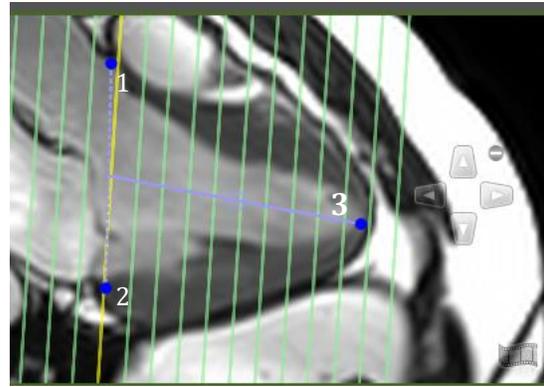
The first two points define the mitral valve plane and the third point has to be placed at the apex (sub-epicardial). Make sure the blue base line is in close proximity to the first, basal slice.

Slices/images that will be excluded from analysis are highlighted in grey in the thumbnail grid (see image above)

Repeat for end-diastole.



Alternatively, use the *Forward the LAX range contour* (top toolbar). This will propagate the slice selection to all phases. Start the cine loop to check the registration. To correct, double-click on the blue t-bar and adjust the points



4. Draw a reference contour for diastole and systole: Before you click the automated edge detection it is recommended to provide a reference contour for the endo- and epicardial borders in a mid-ventricular slice.

5. Trigger edge detection: LMB click on the automatic contour detection button will trigger the edge detection

The software will pick the the phase with the largest (diastole) and the smallest volume (systole) and mark them with the letters "S" and "D" next to the phase number in the grid.

20.3.2.2 Manual Definition of Systole and/or Diastole for LV and/or RV

In case you would like to change the automatically detected phase for systole and diastole (largest and smallest LV volume) you can do the following:

How to manually define systole and diastole

1. In the Option menu, check Manual Definition of Diastole and Systole
2. If you can't see an Option menu, click the wrench in the protocol pane and switch on the display.
3. Select the phase, then RMB click on the phase-number
4. LMB click on Systole/Diastole to overwrite the automatic selection

Note: The setting for *Manual Definition of Diastole and Systole* will be remembered and **no calculation will be processed unless you manually define diastole and systole**. If this is not intended for all your analyses, uncheck this option after you are done!

20.3.2.3 Mitral Valve Plane Correction

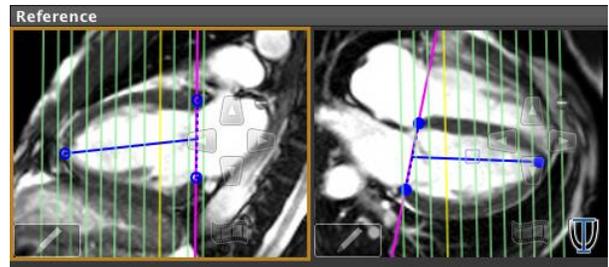
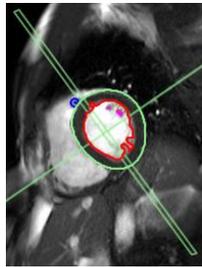
- ① **Visually:** Identify the most basal slice of the left ventricle and/or the outflow tract:
Start cine by clicking on the film icon in the analysis window and **watch cine in the reference window** (carefully control the slice position in systole to avoid accidental inclusion of left atrial volume).

- ①  **Mitral valve plane correction** button: LMB Click on the icon will display two more reference windows.



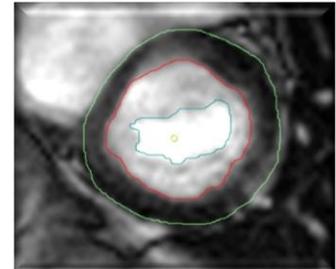
Using the Cross-Reference display, define the plane in two orthogonal orientations.

A correction will automatically be calculated.



20.3.2.4 Exclude Atrial Volume

- ①  Use the exclude area tool to exclude atrial volume in mitral plane.



20.3.2.5 Papillary Muscles

By default, the automatic contour detection will include papillary muscles in mass calculations and exclude them from the lumen.

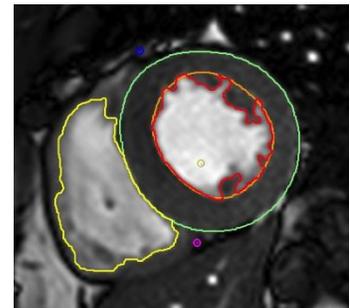
- ① Exclude Papillary Muscles

- Per Image:



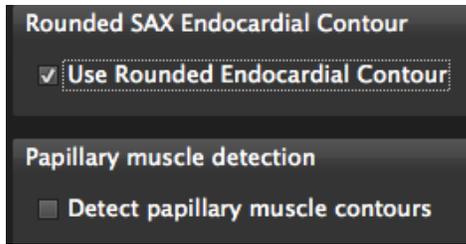
To exclude papillaries and trabecular structures **in the current image** use the *Exclude Papillars* tool.

An orange contour displays the endocardial contour without papillars.



- For all Images:

Change your settings to exclude papillary and trabecular structures



In the *Preferences/Contour* menu:

1. Check "Use Rounded Endocardial Contour". Using automated edge detection, the software will apply a rounded contour, cutting off trabecular structures and/or papillaries.
2. De-select *Detect papillary muscle contours* to turn off the detection of papillaries within the LV lumen (pink contour)

② Include Papillary Muscles

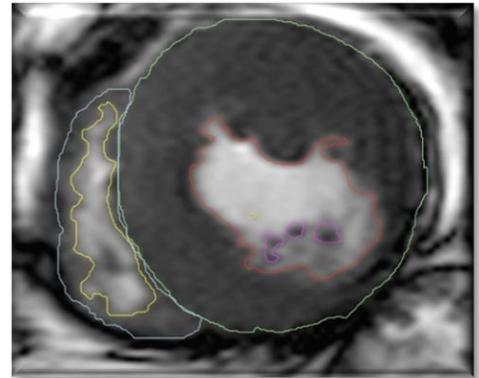
-  Manually in each image

To include papillary muscles in the current image use the SA papillary muscle contour tool. The LV mass calculations will add them to the mass and subtract them from LV volume.

A warning line in red will be added to your report in case less than 3 slices have been used for calculating the volume of the papillary muscles.

- For all images using automated (and thresholding) segmentation methods

To include papillary muscles, not connected to the compact wall, go to the *Preferences/Contour* and check *Detect papillary muscle contours*.

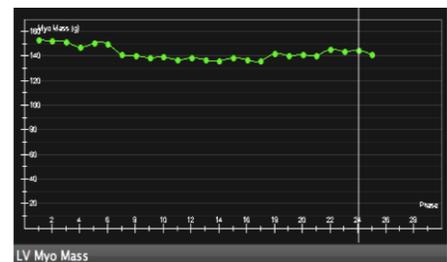
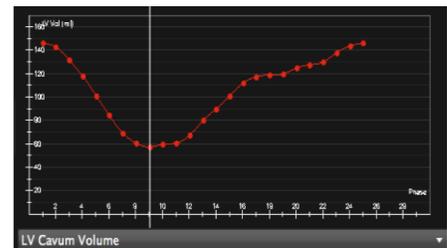


20.3.2.6 Ventricular Volume/Mass Over Time

If you have endocardial and epicardial contours in all phases, you have the option to view a LV volume curve.



- ② A click on the volume curve button will display a graph next to the study display frame.
- ② A warning message will be displayed in the results frame (and the exported reports) if:
 - only one phase was evaluated,



- the number of evaluated slices differs between systole and diastole, or
 - less than 3 slices are used for calculations.
 -
- Ⓒ Peak Ejection Rate and Filling Rate and Peak wall thickness will be reported in the Scientific Report (Report Module)

20.3.3 Regional Wall Analysis

Myocardial thinning and wall motion abnormalities are important indicator for suspected impaired function. (myocardium < 4 mm is unlikely to be viable).

Peak diastolic wall thickness will be reported in the scientific report

How to do wall motion analysis

1. **Define the analysis range:** Define length of anatomical long axis using the *LA LV Extent Contour* button. (see above)



The purpose of this contour is

- a.) to select the slices that shall be included into the analysis and
- b.) to assure displayed polar maps reflect the entire left ventricle. Polar Maps will display a grey ring if
 - slices do not cover the entire ventricle or
 - the gap between slices is too large for interpolation
 - there are missing contours in existing slices

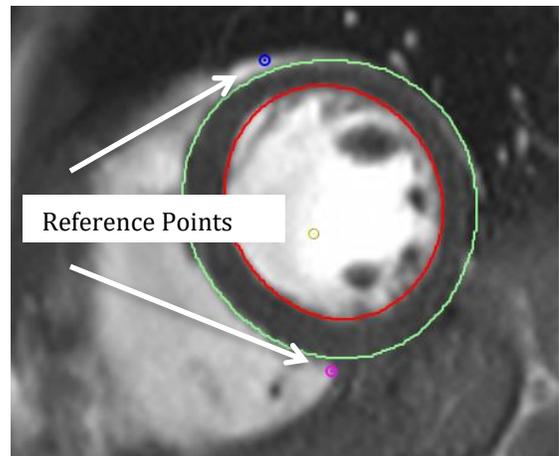
2.  **Define reference points for the segmentation:** In the analysis window select a mid-ventricular slice and set the points at the anterior and inferior insertion of the RV.

The two reference points define the septum, whereas the septal part will be accounted as one third of the total circumference.

The points will automatically be forwarded.

Note: The segmentation points don't have to be adjusted in the remaining images.

To move the point within the image, grab and shift it.
To re-do the entire phase or stack, delete the point (Context menu: *Delete.../DeleteContour Series*) and



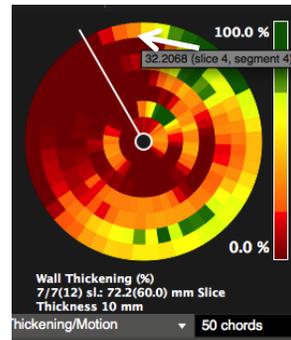
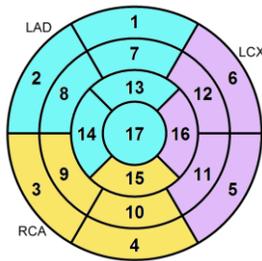
reposition.



3. **Display Polar Map:** To view the polar maps click the *View Regional Function* button

Define Segmentation:

- Chords: Range between 2 and 100 chords. (segments will be counted clockwise)
- AHA segmentation: Volumes per AHA segment will be reported in the *Scientific Report*



- AHA segments and corresponding territories (segments are defined counter-clockwise)

Using chords, segments are defined clockwise. Hovering over the segment will display the respective value (they are reported in the scientific report).

Choose the value you would like to display in a Polar Map

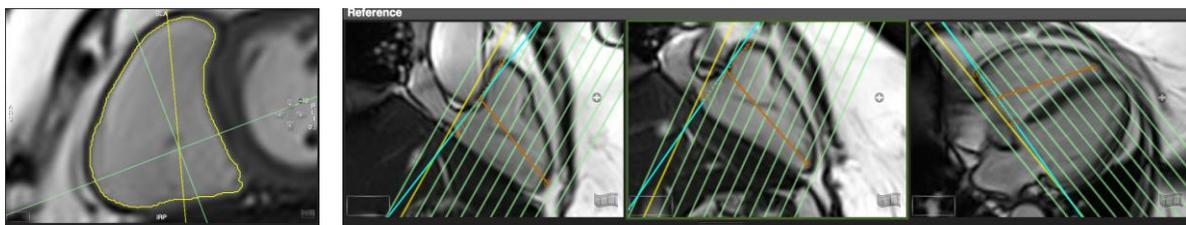
- Wall Thickening
 - Wall Motion
 - Wall Thickness for Diastole and Systole
 - **Note:** max. wall thickness is reported in the scientific report
4. LMB Click on the polar map will synchronize 4D Visualization and display the parameter
 5. RMB click allows to export the polar map

How to do manual RV segmentation

1. Verify that the right ventricle is in the center of the frame by panning the image, so that the **yellow seed point is in the center of the RV.**
2. To determine the tricuspid valve plane open the 3 reference viewer and drag the applicable images into the frames.



Mitral/Tricuspid Valve Plane Correction on/off



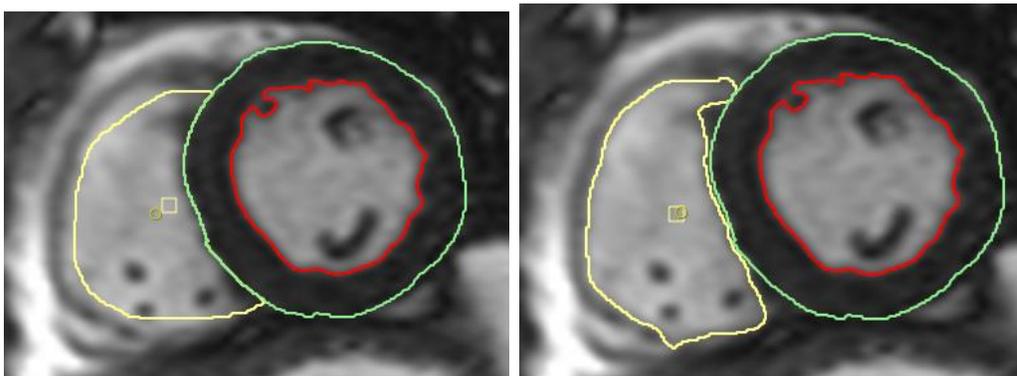
3. Select the *LAX RV Extent* tool and define the plane as well as the length of the RV.



4. Turn on the cross-reference lines for better orientation. Clicking one of the reference windows will highlight the respective plane in yellow in the analysis viewer. Vice versa, the slices will be highlighted in yellow in the reference viewer.
5. Select phase and images for evaluation using the navigation buttons or run the cine by clicking on the film icon.

To be able to view a cine during evaluation, use the floating viewer (see chapter 6)

6. Contours can be drawn and or corrected freehand (default) or by using a specific drawing mode e.g. *Click-Draw* mode or *Threshold Segmentation* (preferred if you have good contrast) mode

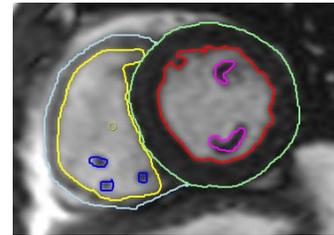
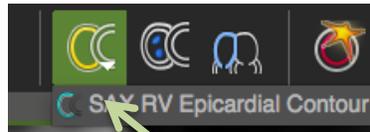


- Exclude papillary muscles from the volume: go to *Preferences>Contours> Detect Papillary Muscle Contours*. This setting will affect all automatic and semiautomatic edge detection.



To include papillaries for each image individually, use RV Papillary muscle Contour.

- For mass calculation, draw an epicardial RV contour: You will find the contour button for the *RV epicardial contour* by clicking on the white arrow.



- Repeat for all slices you want to include in the analysis.

- Add analysis to Report 

Note: Make sure to always use the same technique, either in or exclude papillaries and/or delineate trabecle. Left and right SV should match! Follow-up results done with a different contouring technique can mimic deterioration!

How to do automatic RV segmentation

- Verify that the right ventricle is in the center of the frame by panning the image, so that the **yellow seed point is in the center of the RV**.
- For automatic endocardial RV detection, make sure you have defined the tricuspid valve plane in systole and diastole
- Set the automatic RV contour detection button to the desired option:



- Provide a reference contour in systole and diastole.
- Release the button to run the contour detection.
- Click *space-bar* key on your keyboard to get a multi-view display

7. Click *RV volume curve* for a time resolved volume analysis
8. Double-click a contour for correction. Do a right mouse-click to open a contextual contour menu.
9. Click the *Add to Report* button

20.3.4 Atrial volumetry

How to do atrial volumetry in short or long axis orientation

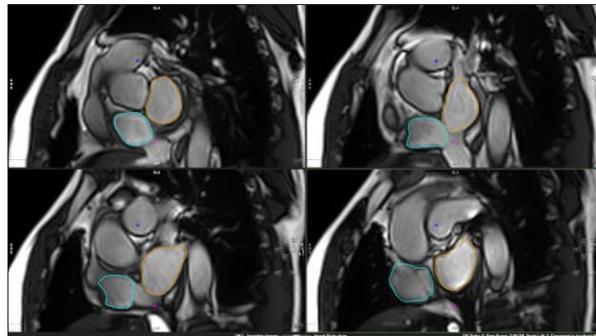
1. Drag a stack of parallel images, long or short axis, into the analysis frame.

The atrial volumes will be reported for LV systole and diastole and therefore require the definition for the LV endsystolic and enddiastolic phase.

If there is no LV analysis applicable, you can manually define the phases. Please refer to the chapter "Manual Definition of Systole and/or Diastole for LV and/or RV".

2.  Click on the *SAX Left Atrium Contour* tool to trace the border of the left atrium.
3.  use the *SAX right Atrium Contour* tool for the right atrium.

The software will report ESV, and EDV for the right and left atrium



21 Tissue Characterization Module**

21.1 Global Late Enhancement and T2 Imaging	155
21.1.1 Analysis of LGE and T2 Images	156
21.1.1.1 Customizing the Module to Your Needs	156
How to do scar and edema analysis in ischemic disease	156
21.1.1.2 Myocardial Reference and Threshold Settings	157
How to do edema analysis in non-ischemic disease	160
21.1.2 Tip :How to improve image quality in T2 images:	160
21.1.2.1 Areas with 'No Reflow' (Add Myocardium to the Enhanced Volume)	161
21.1.2.2 Greyzone Analysis.....	161
21.1.2.3 Salvaged Area at Risk	162
21.2 Regional LGE and T2 analysis and assessment of transmural	162
How to do segmental scar and edema analysis	163
How to assess transmurality	163
How to display a greyzone polar map	164
21.2.1 Analysis of Phase Sensitive Sequences (PSIR).....	165
21.3 Early Enhancement Analysis	165
How to do contour definition in Early Enhancement images	165
21.3.1 Tip - How to improve the image quality in EGE images	166

cmr⁴² and cvi⁴² provide four adjustable viewer frames for determining various tissue characteristics by CMR methods (Late Gd Enhancement=LGE; T2-weighted CMR; Early Gd Enhancement=EGE).

The viewer layout is customizable, depending on your protocol (please refer to the chapter “*Set Up/Customize Tools and Working Modules*”)

21.1 Global Late Enhancement and T2 Imaging

LGE is a T1 sensitive imaging technique that depicts contrast agent that diffuses freely in interstitial space. The distribution volume of contrast agent in damaged or dead tissue, around 10 min after application, is increased in acute and chronic MI, as well as in areas of fibrosis due to other pathology such as myocarditis or cardiomyopathy.

T2 weighted, black blood images have a strong fluid weighting, with no signal from the blood. This method has become established to diagnose edema that occurs in inflammatory conditions, such as myocarditis or acute myocardial infarction.

Next to cine and stress perfusion imaging, LGE and T2 imaging are the most important methods for the assessment of viability

Imaging starts around 10 min after contrast application.

Postprocessing for the analysis of **LGE and T2 weighted images** include:

- ⦿ The definition of endo- and epicardial borders,
- ⦿ The definition of healthy myocardium as an area of reference
- ⦿ The definition of a threshold to depict signal enhancement
- ⦿ The definition of microvascular obstruction
- ⦿ Setting a threshold for peri- infarct “greyzones” .
- ⦿ Segmentation to generate a Polar Map View

21.1.1 Analysis of LGE and T2 Images

21.1.1.1 Customizing the Module to Your Needs



The module allows assessment of multiple tissue characteristics. Not all of them are used in the clinical routine.

Here is what you can customize:

1. Turn on/off view ports
2. Select tool sets or buttons
3. Select additional analysis such as greyzone
4. Turn on/off an option menu
5. Set your preferred threshold algorithm



How to do scar and edema analysis in ischemic disease

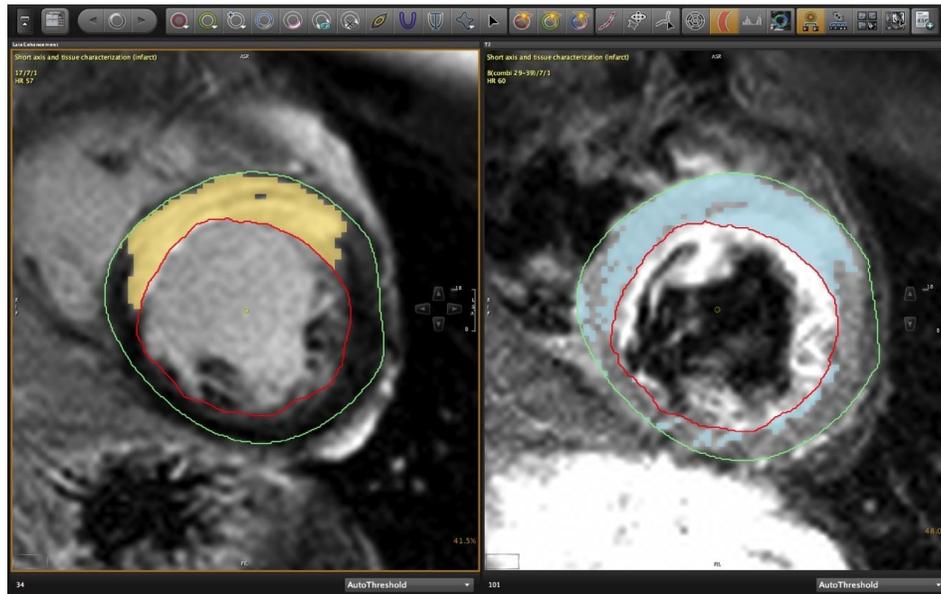
1. Drag and drop series into the frames marked "Late Enhancement" and "T2" respectively.
2. **Derive** existing contours via *Context Menu/Contours/Derive Cardiac Contours*. Correct if needed. If no contours are present, synchronize contour drawing, and draw endocardial and epicardial contours for each slice



Synchronize Contours (button in the top toolbar): Provided that T2 and LGE images have the same slice location contours will automatically be copied to the other frame. You can refresh the contour synchronization by altering the contour slightly.

3. Choose a threshold algorithm and define a reference if needed. (see below for more detail 21.1.1.3).
4.  Toggle the *Overlay Display* to display a color overlay for scar and edema. (For T2 ratio please see below 21.1.1.4)
5.  Use the *Exclude Enhancement* contour in case of e.g. artifacts.
6.  Quantify MVO (see below for more information)
7.  Click on Display Result to view the analysis
8. Add measurements to report by clicking the Add to Report button .

In the *Preferences/Reporting* menu, you can choose if you would like to display (default) or hide the threshold contours on your report images.



LGE and T2 weighted image: Contours are synchronized; Color overlay depicts scar

21.1.1.2 Myocardial Reference and Threshold Settings

Except for choosing *Autothreshold*, or the *Manual* settings, where you use the histogram to determine the threshold, you have to draw a myocardial reference ROI in every slice.

The threshold will automatically be applied to all slices, except for the *Manual per Slice* setting.

- ⦿ Preferred thresholds for LGE are
 - Infarct 5 SD over remote myocardium
 - Inflammatory diseases 2-3 SD over remote myocardium
 - Hypertrophic CM 6SD over remote myocardium
- ⦿ Preferred threshold for T2 imaging:
 - 2 SD over remote myocardium
- ⦿ Preferred threshold for Greyzone analysis:
 - 2-3 SD over remote myocardium (SD for the greyzone has to be below the SD for fibrosis)

Drop Down Menu options are:

- mean +2 to +10 x SD
- mean -2 to -10 x SD
- FullWidthHalfMax
- AutoThreshold
- Manual per Slice: threshold will be set manually, using the histogram for each slice separately
- Manual
- Enhancement ROI

To enable more threshold options, go to the *Option* menu at the bottom of your screen.

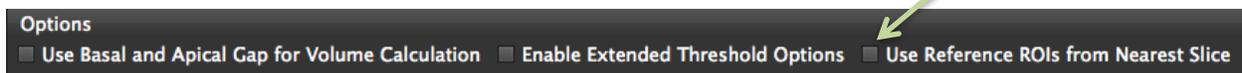
- ⦿ Automatic thresholding:
Autothreshold does not require to define an area of reference, this will be done automatically. It uses the OTSU algorithm. This algorithm finds the point that best differentiates remote from enhanced myocardium.

- ⦿ Standard Deviations
 The drop Down Menu provides SD from +2 to 5 (+10 in the extended Option) and -2 to -5 (-10)



From the toolbar select either the SAX Myocardial Reference tool and define a region of visually healthy myocardium or

You can use your defined myocardial reference for all slices by checking *Use Reference ROIs from Nearest Slice* in the option menu.



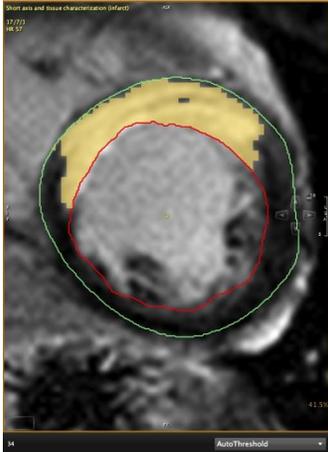
use the *Segment Reference ROIs* button to automatically detect remote and enhanced myocardium

Note:

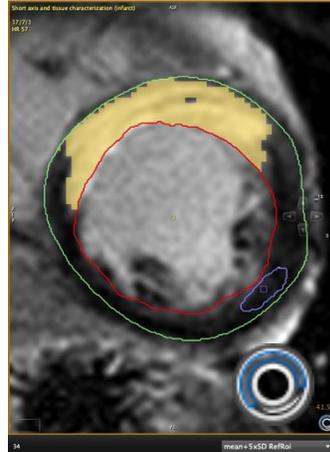
Using the *Segment Reference ROI* button will provide 2 contours:

blue = is the myocardial reference, when you are working with a defined threshold.

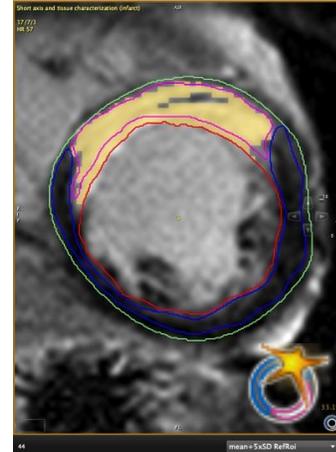
pink = is the myocardial reference, when you are working with the *Full Width Half Max*, which requires a reference in the enhanced area. This does **not** segment **scar**



Autothreshold

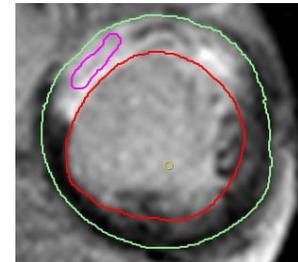


mean+5xSD,



mean+5xSD,

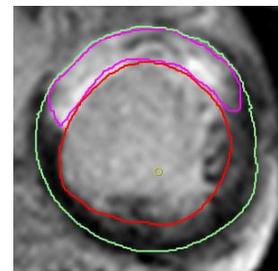
- 
FullWidthHalfMax requires to define a ROI within the brightest area of the enhanced myocardium.



- 
 For **Manual** threshold settings toggle the *Histogram Display* (toolbar) and move the slider. The threshold to best differentiate remote from enhanced myocardium lies between the bell-curves of the lowest and highest signalintensities



- Manual per Slice** setting requires to set the threshold for each slice separately



- ① **Enhancement ROI:** This contour allows to directly delineate the enhancement on the base of visual assessment.



Use the *SAX Enhanced Area Reference* contour tool and trace the enhancement in every slice.

How to do edema analysis in non-ischemic disease

In non-ischemic heart disease edema as well as scarring does not adhere to perfusion territories and will be found in a more diffuse pattern. In this case, a skeletal muscle reference will be defined outside the heart muscle (e.g. m. serratus anterior) instead the myocardial reference and a T2 ration will be calculated.

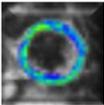


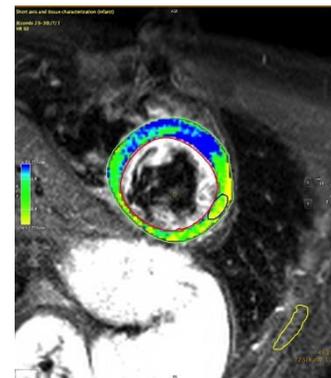
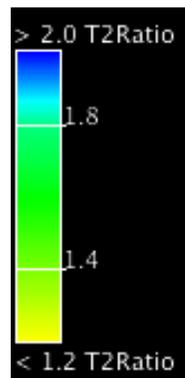
1. Select the Skeletal Muscle Contour tool and draw a contour within skeletal muscle. The global signal intensity ratio will be quantified by dividing the myocardial signal intensity by that of the skeletal muscle, with a **ratio value of > 2 is typically indicating edema.**

The percentage as well as the SI ratio will be reported on the right bottom corner of the frame.

Tip to verify skeletal reference position

An image acquired with an SSFP sequence or T1-weighted image may be used to verify the correct position of the contour within the skeletal muscle. You can drag and drop such an image into the floating frame.

2.  Activate the *T2 Ratio Overlay*.
The color will depict a ratio between 1.2 (yellow/green transition) and 2.0 (green/blue transition)



3. Repeat for all slices.

21.1.2 Tip :How to improve image quality in T2 images:

- Slice thickness ≥ 12 mm
- Use the body coil to reduce the signal gradient of surface coils (underestimation of inferolateral and overestimation of anteroseptal signal)
- Effective TR > 2 sec (if the HR is >60bpm consider 3 RR intervals)
- TE 60-70 ms
- Consider beta-blockers if arrhythmia or tachycardia

WARNING: Automatic Contour Detection

The expected input for the volume calculation in this module is a series containing parallel slice in the short axis direction.

Endocardial contours must always be inside the epicardial contour. cmr⁴² and cvi⁴² do not check for that.

In case of missing contours in one slice linear interpolation is done if possible.

Module calculations in cmr⁴² are in generally done based on the current state of contour definition and image selections. For every change in this state, the calculations are updated immediately. It is the responsibility of the user to decide whether the stage of contour definitions reflects the desired measurement task before releasing final results.

21.1.2.1 Areas with 'No Reflow' (Add Myocardium to the Enhanced Volume)

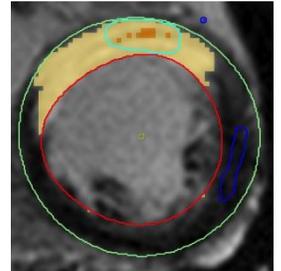


To quantify a 'No Reflow Area' (depicting MVO - micro vascular obstruction), use the *No Reflow Contour* button.

The no-reflow areaThe contour doesn't have to be exact, roughly draw a contour around the region with low signal. Within the contour, (only) the areas with low SI will be added to the late enhancement region.

Trouble-shooting: No-reflow area is not added to the calculation.

The reason might be that either there is no-reflow or you choose the manual thresholding and your threshold is set to "0".



21.1.2.2 Greyzone Analysis

Infarct border regions reflect a mixture of fibrosis and viable myocardium and has been associated with increased susceptibility to ventricular arrhythmias.

Greyzone Analysis calculates the volume/area of the peri-infarct area with intermediate signal intensity providing the following threshold options:

- Threshold: $2 \times \text{SD} + \text{mean SI}$ to $5 \times \text{SD} + \text{mean SI}$ of remote myocardial area
- Threshold: 10% max SI to 40% max SI of enhanced myocardial area
- Threshold: peak SI of remote myocardial area

The grey zone will automatically be displayed in a color overlay

The upper threshold is given by the threshold for the core region.

Note: Areas within MVO that have the same SI as the **greyzone** will be displayed as such.

21.1.2.3 Salvaged Area at Risk

The salvaged area of risk will be measured as therapy control after intervention. Using the results of LGE and T2 segmentation, calculation will be done automatically by subtracting scar from edema volumes.



You will find the quantified area at risk in the result pane (click on the *Display Result* button).

Note:

It will **not** be calculated in case

- slice locations are not matching
- number of slices are not matching
- there is a difference of myocardial volumes > 10%

Late Enhancement

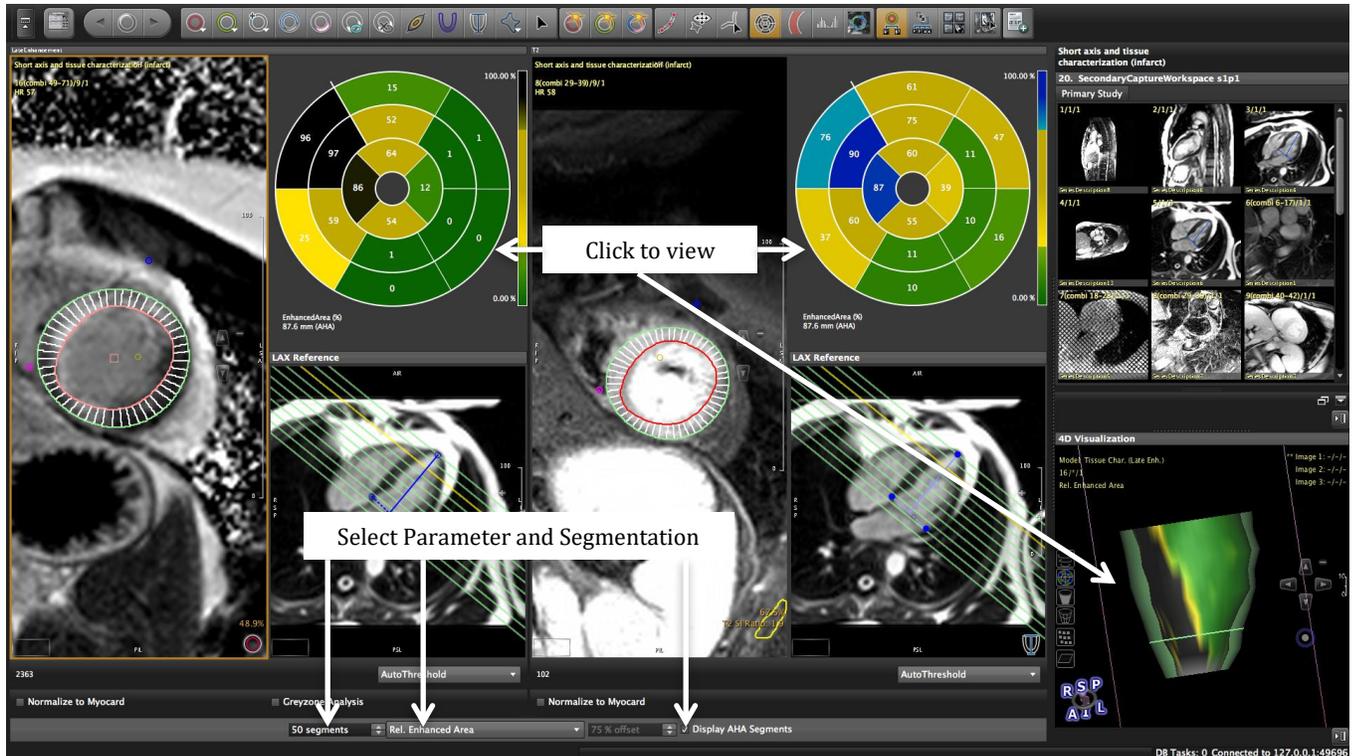
Late Enhancement

FullWidthHalfMax

MyocardialVolume: 109.8 ml
 MyocardialMass: 115.3 g
 TotalEnhVolume: 28.1 ml
 NoReflowVolume: 0.0 ml
 NoReflowMass: 0.0 g
 ManuallyExcludedVolume: 0.0 ml
 ManuallyExcluded: 0.0 g
 EnhancedVolume/Mass (rel): 25.6 %

Salvaged Area at Risk: -28.1 ml

21.2 Regional LGE and T2 analysis and assessment of transmuralty



Toggle Polar Map  button.

How to do segmental scar and edema analysis

1.  Set **Segmentation points**: Position at the anterior and inferior insertion point of the RV ventricle in a mid-ventricular slice. It will automatically be forwarded to all other slices and phases. To move the point within the image, grab and move it. To redo the entire stack, delete and re-draw the point.

2. Define length of anatomical long axis using the *LAX Extent* contour button  .

The purpose of this contour is to

- a) select the slices that shall be included into the analysis
- b) ensure displayed polar maps reflect the entire left ventricle

In end-systole draw a line between the mitral valve plane and the left ventricular apex. Slices beyond the range will not be included in the Polar Maps.

Segments will be greyed out in case

- slices don't cover the entire ventricle
 - the gap between slices is too big for interpolation
 - there is input missing for that particular slices (check contours, reference ROIs, segmentation points)
 -
3. Select Parameter from Drop Down Menu
 - Relative Enhanced Area*: The enhanced area can be divided into a user-defined number of segments (range 3-100).
AHA segment model can be applied by checking the "*Display AHA Segments*" box. The result is displayed as the ratio non-enhanced/enhanced area

How to assess transmuralty

1. Repeat step 1-2
2. Select one of the following from the drop down list
 - *Maximum Transmuralty*: the maximal transmural extent of segments with late enhancement will be calculated for 100 segments only (it will not be reported in an AHA-segmentation display since segments are too large and averaged percentages would not provide an accurate picture)
3. To view a percentage transmuralty select one of the display options below and set the transmuralty percentage using the arrow keys to the right.
 - Transmuralty offset

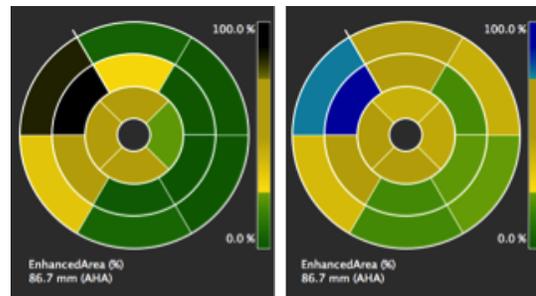
Enable Extended Options

- *Maximum Transmurality (endo)*: Filters for segments where, late enhancement originates sub-endocardial.
- *Transmurality (endo) offset*: applying an offset of e.g. 75% (default) will display all segments that have a transmuralty >75% in black, and segments with a transmuralty <75% in green

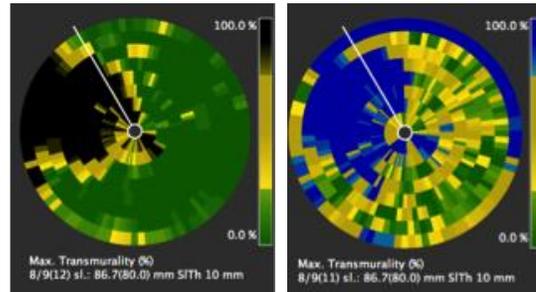
How to display a greyzone polar map

1. Repeat step 1-2
2. Select *Relative Greyzone* from the menu (make sure you have defined a threshold for the greyzone and activated the analysis option)

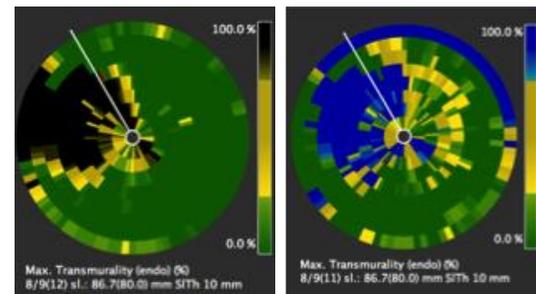
Enhanced Area



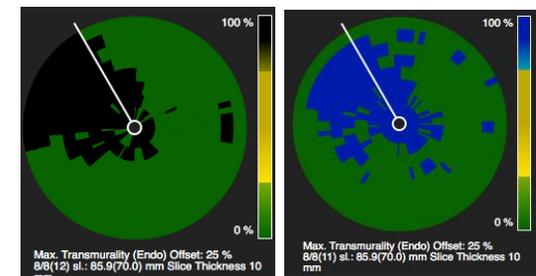
Maximum Transmurality



Maximum Transmurality (endo)



25% Transmurality (offset)



21.2.1 Analysis of Phase Sensitive Sequences (PSIR)

Phase-sensitive image reconstruction results in reduced need for precise choice of TI and more consistent image quality. But there are less greyscale values and results might differ between magnitude and psir.

McAlindon E, Pufulete M, Lawton C, Angelini GD, Bucciarelli-Ducci C. Quantification of infarct size and myocardium at risk: evaluation of different techniques and its implications. European heart journal cardiovascular Imaging. 2015;16(7):738–746.

In phase sensitive images the histogram is shifted towards higher signal intensities. For proper analysis the SI have to be *normalized to the Myocardium*.

If the Checkbox is not available, go to *Edit* in your protocol pane and click on the little “x” on the right.



21.3 Early Enhancement Analysis

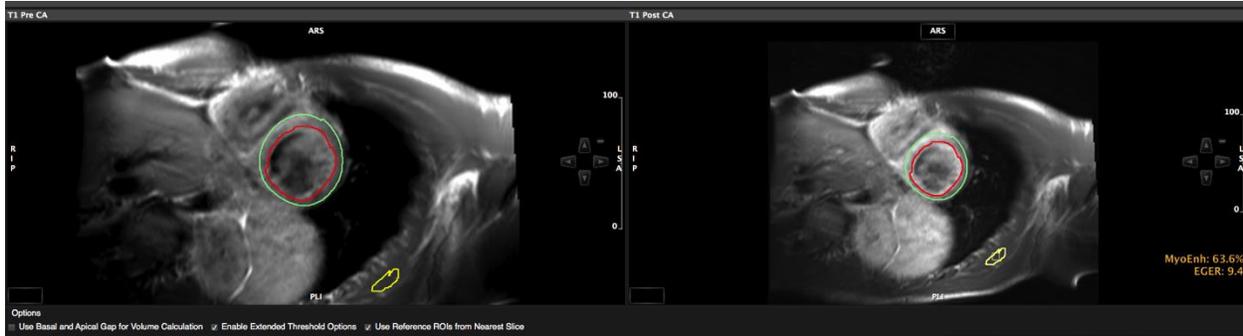
The early enhancement method uses T1 weighted images where image acquisition starts immediately after contrast application

Indications for *Early Enhancement Imaging* amongst others are

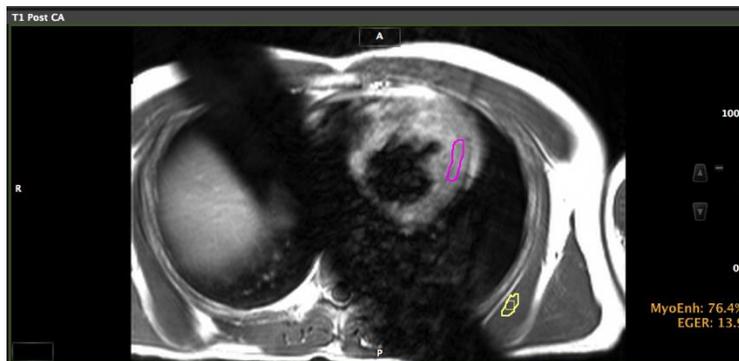
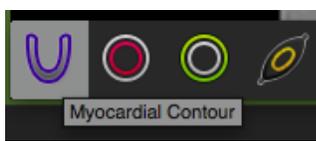
- Inflammation (hyperemia)
- Microvascular Obstruction
- Intracardiac Thrombus

How to do contour definition in Early Enhancement images

1. Draw endocardial and epicardial contours in T1 pre and post contrast images.
2. Define a skeletal reference
3. Repeat for all slices.



In case of bad image quality, you can still assess the Early Gadolinium Enhancement Ratio (EGER) by using the *Myocardial Contour* tool



4. To View analysis results click the Display Result button

The enhancement is positive if there is

- A global signal intensity ratio (EGER) of myocardium over skeletal muscle of > 4
- or
- An absolute myocardial enhancement > 45% , (independent of the skeletal muscle)
 $(SI(\text{nach Gd}) - SI(\text{vor Gd})) / SI(\text{vor Gd}) \times 100$



5. Add measurements to report using the *Add to Report* button

21.3.1 Tip - How to improve the image quality in EGE images

- Slice thickness $\geq 10\text{mm}$
- Axial orientation often provides better image quality than short axis
- Non-breath hold, emphasize regular breathing
- Start 10-20 seconds after contrast injection
- Acquisition time between 2 and 3 min

Lake Louise Criteria Criteria for Cardiovascular MR in Suspected Myocarditis

In the setting of clinically suspected myocarditis^a, CMR findings are consistent with myocardial inflammation, if at least two of the following criteria are present:

1. Regional or global myocardial SI increase in T2-weighted images^b.
2. Increased global myocardial early gadolinium enhancement ratio between myocardium and skeletal muscle in gadolinium-enhanced T1-weighted images^c.
3. There is at least one focal lesion with non-ischemic regional distribution in IR-prepared gadolinium-enhanced T1-weighted images ("late gadolinium enhancement")^d.

A CMR study is consistent with myocyte injury and/or scar caused by myocardial inflammation, if

- criterion 3 is present.

A repeat CMR study between 1 and 2 weeks after the initial CMR study is recommended, if

- none of the criteria are present, but the onset of symptoms has been very recent and there is strong clinical evidence for myocardial inflammation.
- one of the criteria is present.

The presence of LV dysfunction or pericardial effusion provides additional, supportive evidence for myocarditis.

^a: The clinical suspicion for active myocarditis should be based on the criteria listed in table 5.

^b: Images should be obtained using a body coil or a surface coil with an effective surface coil intensity correction algorithm; global signal intensity increase has to be quantified by an signal intensity ratio of myocardium over skeletal muscle of ≥ 2.0 . If the edema is more subendocardial or transmural in combination with a co-localized ischemic (including the subendocardial layer) pattern of late gadolinium enhancement, acute myocardial infarction is more likely and should be reported.

^c: Images should be obtained using a body coil or a surface coil with an effective surface coil intensity correction algorithm; a global signal intensity enhancement ratio of myocardium over skeletal muscle of ≥ 4.0 or an absolute myocardial enhancement of $\geq 45\%$ is consistent with myocarditis.

^d: Images should be obtained at least 5 minutes after gadolinium injection; foci typically exclude the subendocardial layer, are often multi-focal, and involve the subepicardium. If the late gadolinium enhancement pattern clearly indicates myocardial infarction and is co-localized with a transmural regional edema, acute myocardial infarction is more likely and should be reported.

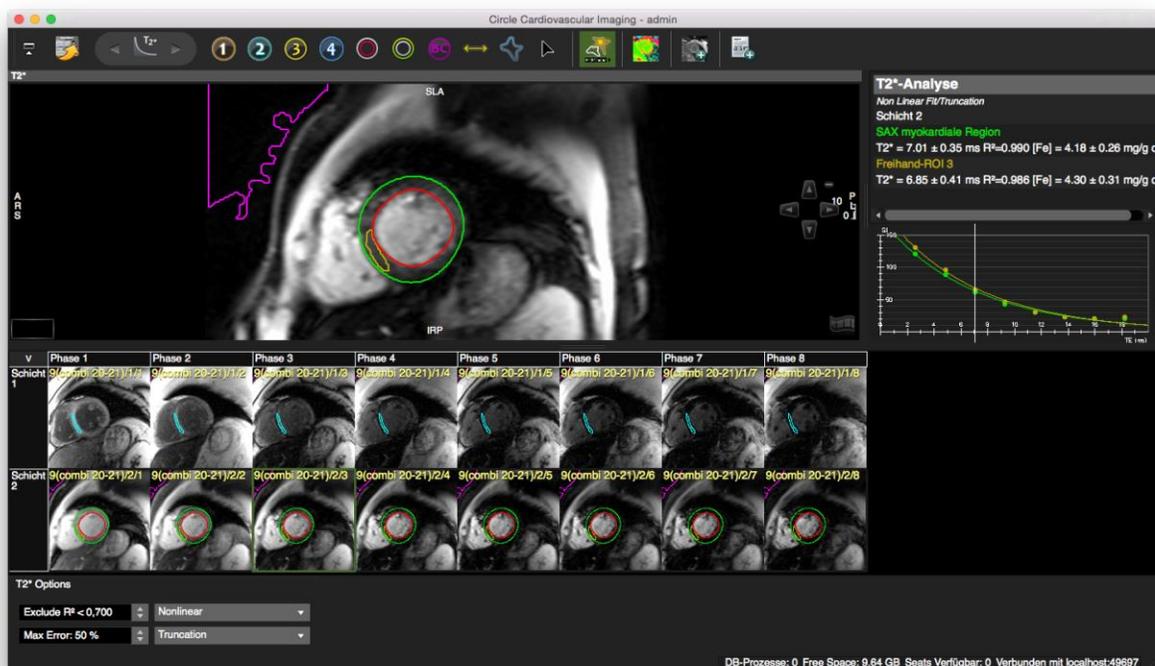
22 T2* Module

22.1 Assessment of T2* Times	168
22.1.1.1 Customizing the module to your needs	169
How to do T2* Analysis	169
22.1.2 Options Menu	170

Intended use:

Cardiac involvement in siderotic cardiomyopathies can cause arrhythmia and/or congestive heart failure and indicates a poor prognosis. The module allows for the analysis of T2* values for disease monitoring and guiding chelation therapy

22.1 Assessment of T2* Times



22.1.1.1 Customizing the module to your needs

To adapt the module to your requirements click the wrench (*Edit protocol*) in the Protocol pane. Here is what you can customize:

- Tool sets
- Color map options
- Decay curve settings

After customization save your settings!

How to do T2* Analysis

1.  For global T2* times, draw an endocardial and an epicardial contour for the assessment of global T2* values

2.  Draw a ROI contour in the septal wall for regional T2* values

3.  Forward contours to other images within the series.

Check contour in every image and correct if necessary (turn off the *Forward Contours* button)

T2* values will immediately be displayed, as well as the absolute iron content (1.5 Tesla only).

Normal : 52+16 ms

Reduced : cutoff: 20 ms

Severe : <10 ms

T2*-Analyse	
Non Linear Fit/Truncation	
Schicht 2	
SAX myokardiale Region	
T2* = 7.01 ± 0.35 ms R ² =0.990	[Fe] = 4.18 ± 0.26 mg/g d
Freihand-ROI 3	
T2* = 6.85 ± 0.41 ms R ² =0.986	[Fe] = 4.30 ± 0.31 mg/g d

Anderson LJ, Holden S, Davies B, Prescott E, Charrier CC, Bunce NH, Firmin DN, Wonke B, Porter J, Walker JM, Pennell DJ. Cardiovascular: T2-star (T2*) magnetic resonance for the early diagnosis of myocardial iron overload. *Eur Heart J* 2001;22:2171–2179.

4. T2* decay curves will immediately be displayed, choose a fitting algorithm (non linear=default) from the context menu.

T2/T2*	Color
0 - 10	Dark red
0 – 25 ms	Red
25 – 40 ms	Yellow
40 – 55 ms	Green

55 - 80 ms	Blue
80 ms and above	Blue

5. Toggle color map on



Choosing a lower threshold for the R2 and a higher error tolerance for T2* will include more pixel into the colormap.

6. Create DICOM Map



Optional map output for pixelwise fitting in grayscale. In addition to the grayscale map a R2 map will be created. You will find both maps combined in one series. The will be appended to your thumbnails.

*Reference: Taigang He, Peter D. Gatehouse, Paul Kirk, Raad H. Mohiaddin, Dudley J. Pennell and David N. Firmin Myocardial T*2 Measurement in Iron-Overloaded Thalassemia: An Ex Vivo Study to Investigate Optimal Methods of Quantification Magnetic Resonance in Medicine 60:350–356 (2008)*

22.1.2 Options Menu

⊙ Error Threshold Options

- *Exclude R²*: The coefficient of determination indicates the strength of the correlation between the curve fitting logarithm and the data points (default is 0.7). R² should be > 0.99
- *Max Error*: Adjusting the error tolerance changes the allowed maximum error of the T2* times, for which the result of the fitting should be displayed (default 100%) When the T2* map is generated, any pixels that have higher than the allowed accuracy, or higher than the error threshold selected, will be set to a value of zero.
-

⊙ Fitting Options

- Nonlinear (default)
- Linear
- Linear Weighted
-

⊙ Fitting Correction methods

- *Truncation (default)*: Uses the mean value of the background noise (purple contour) as a reference and truncates all data below that value. The truncation model was shown to produce more reproducible and accurate T*2 measurements.
- *Baseline subtraction*: noise is directly subtracted from each echo time image.
- *Three parameter fit*: an offset is added to the curve fitting equation to account for noise and artifacts.

23 T2 Mapping

23.1	T2 Measurements	173
	How to do a T2 analysis	173
23.1.1	T2 Options menu	173
23.1.2	Motion Correction.....	174
	How to apply a motion correction to T2 series	174
23.2	T2 Map	175
	How to analyze T2 maps	175

T2 mapping quantifies T2 of tissue, which directly reflects free water content and thus is a very accurate tool for identifying myocardial edema, overcoming limitations of standard T2-weighted imaging (susceptibility to motion artifacts, inconsistent image quality among scanner models).

The module consists of two pages

- ① T2 Measurements: that allow for the assessment of T2 times
- ① T2 Map: and the analysis of a T2 map.

23.1 T2 Measurements



How to do a T2 analysis

1.  Segment the myocardium for global T2* values. Forward the contours via context menu.
2.  Select one of the ROI contours for the assessment of a specific region of interest. The ROI can be forwarded with the *Forward contour* button .
3. Global and regional T2 times will be calculated immediately.
4. The decay curve will be displayed. A right mouse click in the graph allows to change the display or to export the graph
5.  Add calculations to your report.

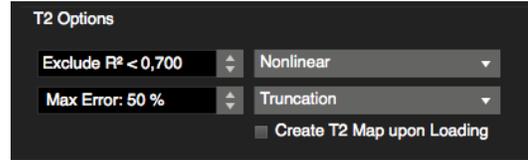
23.1.1 T2 Options menu

-  Error Threshold Options

- *Exclude R²*: The coefficient of determination indicates the strength of the correlation between the curve fitting logarithm and the data points (default is 0.7). R² should be > 0.99
- *Max Error*: Adjusting the error tolerance changes the allowed maximum error of the T2 times, for which the result of the fitting should be displayed (default 100%) When the T2 map is generated, any pixels that have higher than the allowed accuracy, or higher than the error threshold selected, will be set to a value of zero.

⦿ Fitting Options

- Nonlinear (default)
- Linear
- Linear Weighted



⦿ Fitting Correction methods

- *Truncation (default)*: Uses the mean value of the background noise (purple contour) as a reference and truncates all data below that value.
- *Baseline subtraction*: Noise is directly subtracted from each echo time image.
- *Offset*: An offset is added to the curve fitting equation to account for noise and artifacts.

⦿ **Create T2 map upon loading**: Automate DICOM map generation by checking the box for *Create map upon loading*. Save this step to your protocol.



23.1.2 Motion Correction

How to apply a motion correction to T2 series

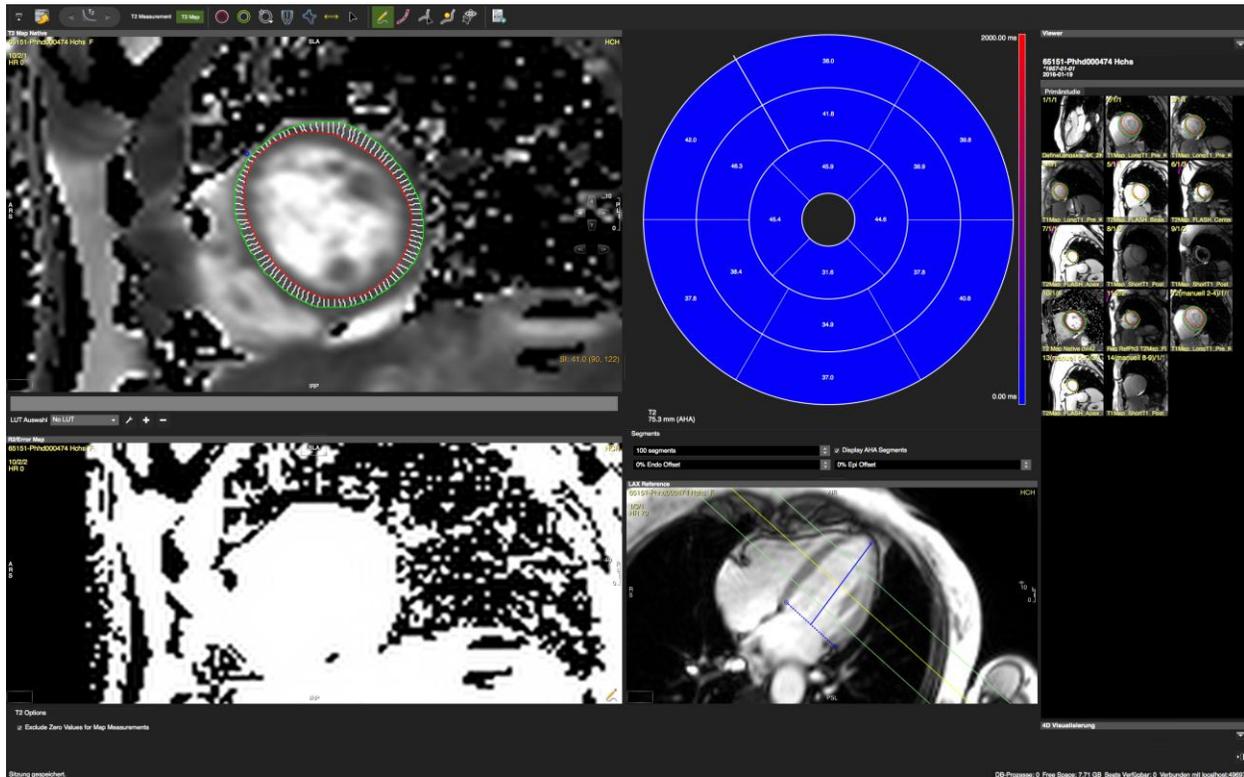
1. Make sure you have endo- and epicardial contours in all images.
2. After forwarding, correct contours.
3.  Set the Segmentation point.
4. Select the image with the best contrast and enter the phase that you would like to use for the registration.



5.  Click the registration button: The new series will be created and automatically loaded into the respective frames. You will find the new series in the thumbnail panel under “Reg NativePh# .[original series description]”. The contours of the reference phase will be forwarded to all registered images.
6. If you decide to use a different phase for registration, reload the original series and repeat steps 1-4.

Note: The registration works for points that are on or inside the contours; the image outside of the contours may appear warped or distorted after registration. This is expected, and users should not use any outer regions for analysis.

23.2 T2 Map



The module consists of 2 viewports: the upper one for the T2 map, the lower one for the R² map.

To the right you will find the polar map and the window for the long axis reference.

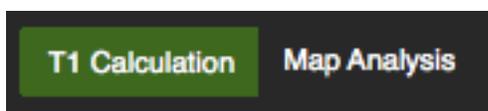
How to analyze T2 maps

1. Drag and drop the map from the thumbnail panel into the respective window.
2. Drag a long axis reference into the reference window and define the extent of the left ventricle: Set 3 points. Two define the base, one defines the apex and define the long axis extent.
3. Derive existing contours from the T2 measurement via context menu > *Derive Contours Phase*. Alternatively, draw new contours.
4. Set a segmentation reference point.
5. To add the polar map to report⁴² export the image via context menu and import into report. ⁴²
6. The values can be found in the scientific report

24 T1 Mapping and ECV quantification

24.1 T1 Calculation (Native and Post contrast)	177
Page Features	177
How to apply T1 fitting to various sequences	177
How to do global or regional myocardial T1 analysis	178
How to create a map	179
How to utilize T1* Maps	180
24.2 Motion Correction for Map Generation	180
How to do feature/contour based registration:	180
How to do Intensity Based Registration	181
24.3 T1 Map Analysis	182
Page Features	182
How to analyse the T1 maps	182
24.4 ECV and lambda quantification (λ)	184
How to do segmental ECV and lambda quantification	185
24.5 T1 mapping Troubleshooting	186

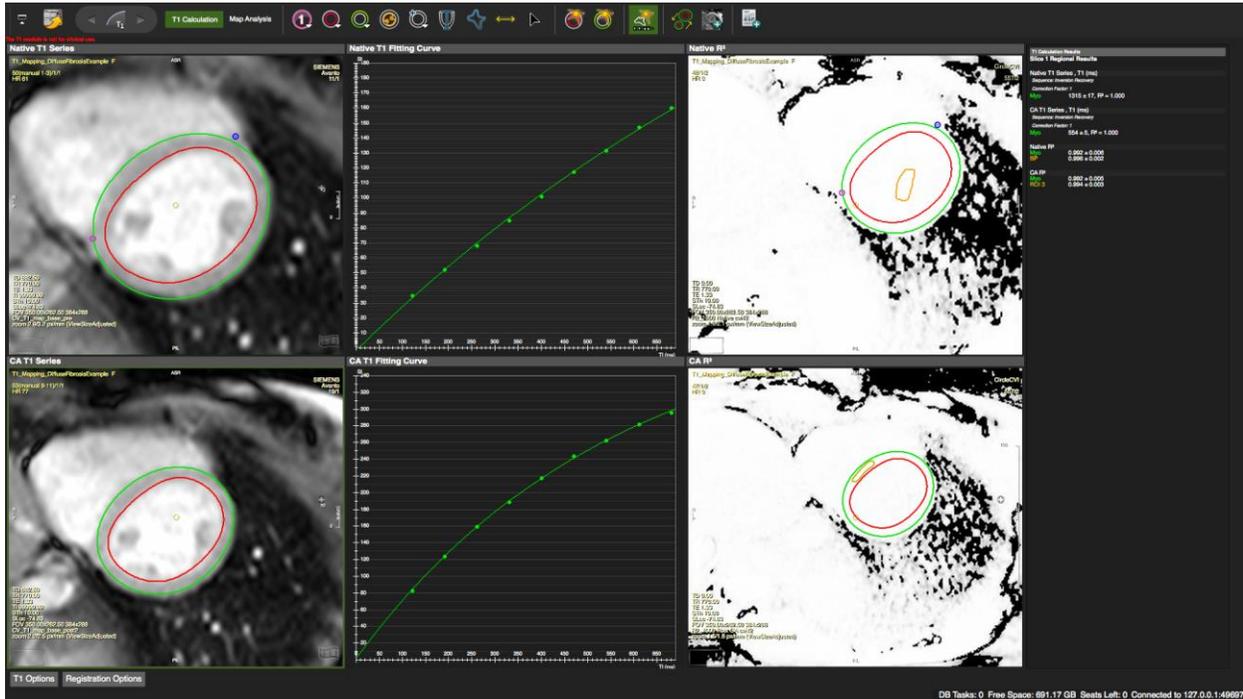
Module layout



Analysis options are organized in 2 pages

- ⦿ *T1 Calculation*: Calculates T1 values and recovery curves for drawn/generated myocardial, bloodpool, and user contours.
- ⦿ *Map Analysis*: Allows for regional analysis and display of T1, ECV, and Lambda maps.

24.1 T1 Calculation (Native and Post Contrast)



Page Features

- Calculation of global T1 times for drawn/generated myocardial, bloodpool and user contours
- Motion Correction
- T1 Map Generation
- Evaluation of recovery curve and R² map

How to apply T1 fitting to various sequences

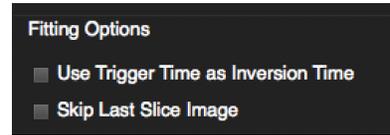
1. Go to the T1 Options on the bottom left on your screen.
2. Select the sequence.
3. Select the series from the thumbnail panel. Hovering over the thumbnail will provide a series description. Drag it into the analysis window.



4. If the series is rejected, check the following:

-
- **Siemens:** The last image of the series is a scanner generated map and should not be used in the fitting.

cvi⁴² solution: In the *T1 Options* menu, check the box for *Skip Last Slice Image*



-
- **Philips:** In the DICOM header the 'Inversion Time' is encoded in the field for the 'Trigger Time'.

cvi⁴² solution: In the option menu, check the box for *Use Trigger Time as Inversion Time*

-
- During anonymization the information for TI has been stripped and you get a warning message "TI times are equal." Go to the patient list module and in the *Extended View* check if the information for the TI can be found under either *TI* or *Image Comments (Siemens)*. If possible, try to re-anonymize the data in cvi⁴², preserving the TI information.

Note: Some recent **Siemens** sequences use a correction or scaling factor for the calculation of T1 times. In this case, there might be a deviation between Siemens and cvi⁴² calculated T1 times.

The scaling factor can be found in your Siemens documentation; otherwise consult your Siemens representative. In the *T1 Options* menu (where you selected the sequence) you can enter the correction factor. This will eliminate any deviation. Alternatively, use Siemens-generated T1 maps.

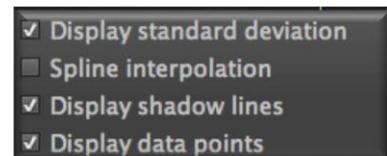
How to do global or regional myocardial T1 analysis

1.  For global T1 values, draw endocardial and an epicardial contours. Forward the contours via context menu *Forward All Contours Slice* (short-cut: /ctrl E)

2.  For regional analysis, select one of the ROI contours. This contour can be forwarded via toolbar button 

3. Repeat for all slices.

4. The T₁ recovery curve will be presented in the frame to the right. Right clicking on the graph opens a context menu to configure the display options for the curve.



5. You can adjust the error and noise limit thresholds, and other curve fitting options in the *T1 Options* menu

6. Myocardial, blood pool, and regional T₁ relaxation times and R²-values will be shown in the reporting pane.

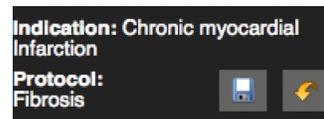
How to create a map

1. It is recommended to perform a contour registration before map generation (see below).



2. Click the button in the toolbar. Generated T₁ maps, R² maps, and T₁* maps (if relevant) will be automatically loaded into their respective frames* and contours are forwarded to the maps.
3. Generated T₁ maps, R² maps, and T₁* maps (if applicable, see below) will be automatically loaded into their respective frames and contours are forwarded to the maps.

4. Automate DICOM map generation: In the T₁ Options menu, check the box for *Create map upon loading* and, if you have admin rights, save this step to your protocol.



5. For the post-contrast series, contours can be derived via context menu: The command *Derive Contours>Derive Contours Cardiac Phase*, will derive previously drawn contours for all slices.



6. Add evaluation (images, values and graph) to the report
7. Go to Map Analysis

Note: No maps will be calculated if slice locations do not match

How to utilize T1* Maps

T1* maps can be used for selecting blood pool T1 for ECV calculation. The frames are not displayed by default.

1. Click on the wrench in the workflow pane
2. Click on the purple bar at the bottom at the frame.
3. Click the wrench again
4. If you have admin rights, save the setting to your protocol.
5. T1* maps will be automatically extracted from Molli, shMolli and Molli Oxford sequences and will be loaded into the respective frame

Bhuva AN, Treibel TA, Bulluck H, Simpson J, Manisty C, Moon J. Precision and reproducibility of blood T1 estimation: implications of T1 star on ECV calculation. J Cardiovasc Magn Reson. BioMed Central Ltd; 2015 Feb 3;17(Suppl 1):P4.

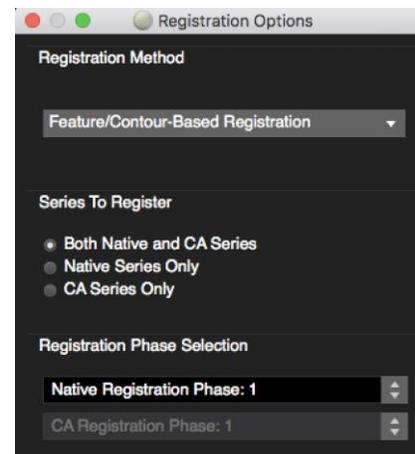
24.2 Motion Correction for Map Generation

Intensity-based registration is to be used with already motion corrected images and will register between pre- and post-contrast series. If you don't have motion corrected series, move to *Feature-based* registration.

How to do feature/contour based registration:

This registration can be used on motion and non-motion corrected series. It registers every phase in one of, or both of, the native and post-contrast series to a chosen reference image. Registration methods and phases can be selected in the *Registration Options* menu.

1. Select an option:
 - *Native or CA series only*: Images will be registered to a selected image in the native or the CA series respectively.
 - *Both Native and CA Series* registers all images (pre- and post-contrast) to a selected image in the native series.
2. In the *Registration Options* enter the chosen registration phase(s).
3. Make sure you have accurately drawn the endo- and epicardial contours, as well as a segmentation point (*i.e.*, the features) in all the images, for all slices, for pre- and/or post-contrast series to be registered. Due to motion, contours across the phases may not be exactly the same.
4. Correct contours where necessary.
5. Ensure to have contours and a segmentation points in all images and slices.



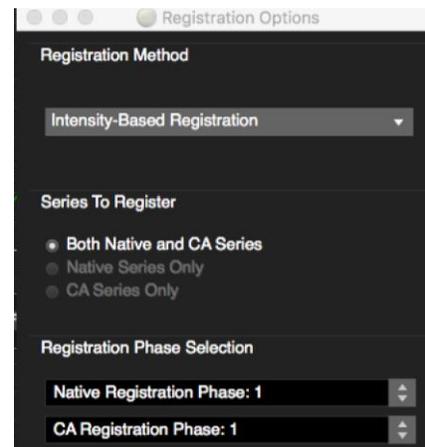
6.  Click the registration button: The new registered series will be created and automatically loaded into the respective frames, and can also be found in the thumbnail pane. The new series description will be prefixed with “Reg NativePh# [original series description].” The contours of the reference phase will be forwarded to all registered images.
7. To use a different phase for registration, or to redo the registration, reload the original series into the T1 Series pane and repeat steps 1-7.

Note: The registration works for pixels that are on or inside the contours; the image data outside of the contours may appear warped or distorted after registration. This is expected, and users should not use any outer regions for analysis.

How to do Intensity Based Registration

Intensity based Registration option will register between native and CA series only, i.e. not within native or CA series. This option should only be used for motion corrected images.

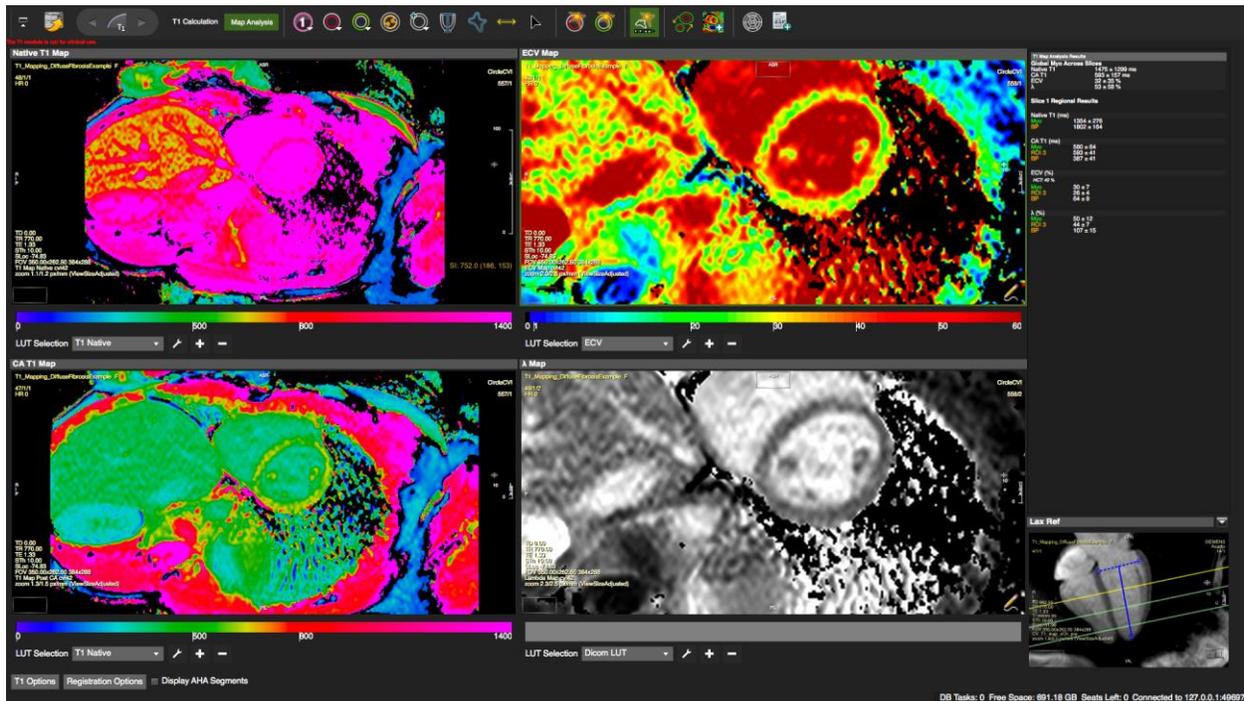
1. Drag the motion corrected series into the respective viewer frames: T1 Native/T1 CA Series.
2. Although the algorithm does not require any contours, it is recommended to draw contours on the chosen reference phase for a visual evaluation of the registration performance.
3. Choose a phase that has good contrast between endo- and epicardial contours, as well as between surrounding tissues in both the native and post contrast series. Avoid images with bright intensities in the outer regions (areas of fat, air regions, etc.).
4. In the *Registration Options* enter the chosen registration phases:
 - Select a native phase (*Native Registration Phase*) to be the reference phase.
 - Select *CA Registration Phase*, to be registered with the reference phase.



5.  Click the registration button.
6. The registration registers the CA Series to the Native Series. As the series are already motion corrected - and it is assumed that the native series aligns well throughout the phases - only one new series distinguish the registration phases that were selected as follows: “Reg NativePh# CaPh# [original series description].”
7. Contours drawn on the Native Registration Phase will be forwarded to the newly registered CA series, and should correspond with the registered image’s endo/epi cardial borders.

If contours do not match well, or if the endo/epi contours have an abnormal shape, try the registration again using another Native and/or CA registration phase. Reload the original series before applying image registration again.

24.3 T1 Map Analysis



Page Features

- Evaluation of cvi⁴² or inline maps.
- Generation of look up tables (LUT)
- Pre- and post-contrast image registration
- ECV and lambda map calculation
- Some vendors append inline T1 maps to their series. To analyse inline maps, load the series into the *Series Overview>Composer* and isolate the map.

How to analyse the T1 maps

1. Make sure segmentation in all slice is complete. Depending on your workflow requirements are:
 - endo-epi contours for global and segmental myocardial T1 analysis
 - Anterior (and optionally an inferior) segmentation reference point and LAX -extent contour for polar map generation
 - Blood pool contour for ECV map generation

2. Display or create a color map: Select from the drop down menu. DICOM maps have to be enabled in the *Preferences>Viewer> DICOM LUT* in order to be displayed. For instructions on how to create a LUT, see below



3. Display polar maps: Click the *Display Polarmap* button in the tool bar. The number of segments can be customized in the *T1 Options*. Alternatively switch to *Display AHA segments* (bottom right, next to T1 Options)



4. The mean values for generated contours in the current slice, and the global myocardial value across slices, will be displayed in the screen report.
5. Repeat for post-contrast maps.



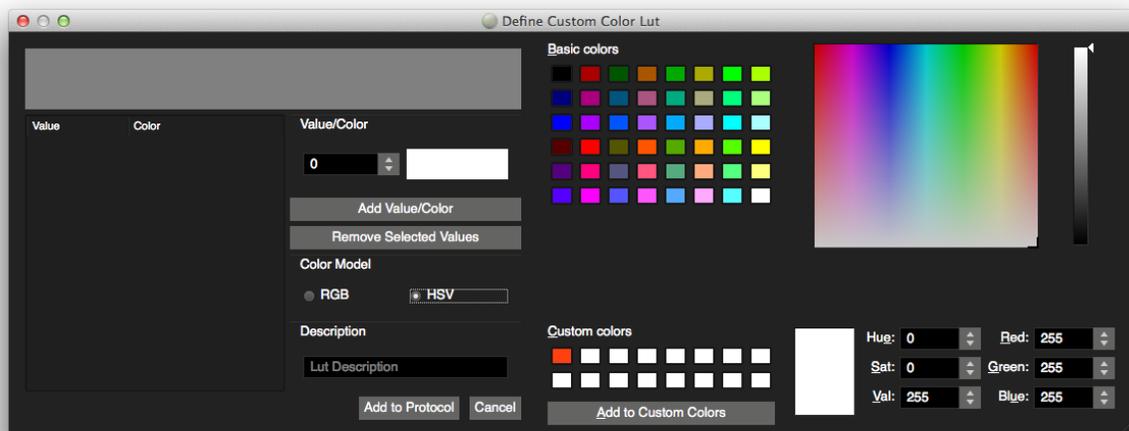
6. Add to report

How to customize the color look up table

The LUT Selection menu offers a DICOM LUT (if present) as well as a predefined T1 Native map.

To create a table that better highlights specific or out-of range T1 values, based on your own data, for different field strengths or sequences, you have the option to create several custom color look-up tables.

1. Click the (+) or (-) to add/delete a color table. Click the wrench to alter an existing table.



2. To assign a color to a T1 value, start with typing a value (T1 time) in the box.
3. Choose a color model: RGB or HSV (**R**ed-**G**reen-**B**lue table, or a cylindrical-coordinate color point representation, called **H**ue-**S**aturation-**V**alue look-up-table.)
4. Select a color from an existing palette.

5. To define a custom colors, click on a the white box under *Custom Color*. Select a color and click *Add to Custom Color*. Adjust the selection with the options to the right (for HSV the *Hue* is limited to 255).
6. To apply the color to the value click *Add Value/Color*.
7. Repeat for all values to display.
8. To remove a color from a value, select from the table on the left and click *Remove Selected Value*.
9. When finished, provide a description to the LUT.
10. Add the LUT to the protocol.
11. Save the protocol if desired to use the LUT for all future series.



12.  Add evaluation (images, values and graph) to the report

Note:

For encoding purposes, HSV values are expressed in values ranging from 0-255 instead of percentages (0-100%) or degrees (0-359°). Therefore, when trying to translate HSV to RGB using a color conversion app the values might be different

24.4 ECV and lambda quantification (λ)

ECV is a measure of interstitial space that is derived from the partition coefficient, reflecting the distribution of contrast agent between blood and myocardium, corrected for the hematocrit (minus volume fraction of erythrocytes).

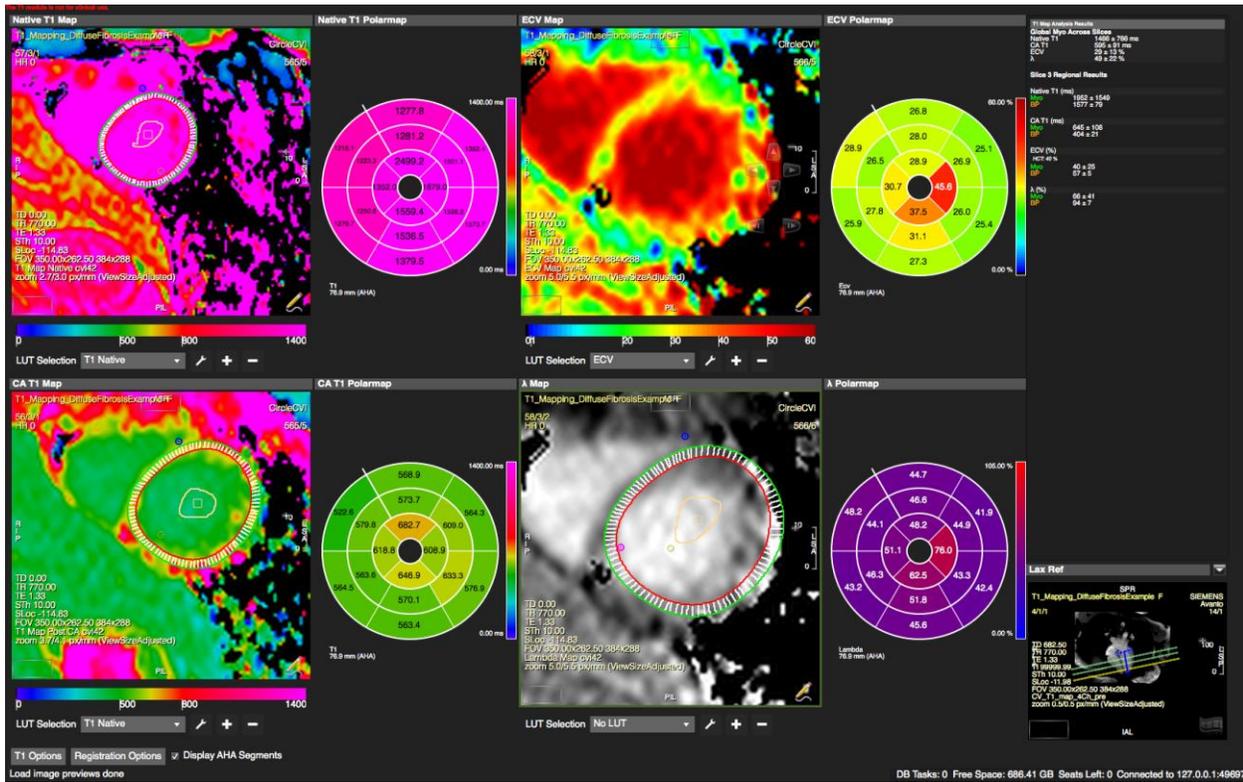
Partition Coefficient : $\lambda = \Delta R1_{\text{myocardium}} / \Delta R1_{\text{blood}}$ (where $R1=1/T1$)

$ECV = \lambda * (1 - \text{hematocrit})$

An accurate estimation of ECV requires contrast equilibrium between blood and myocardium and must be achieved prior to image acquisition (aprox. 8.5 minutes post contrast injection*).

**Lee JJ, Liu S, Nacif MS, et al. Myocardial T1 and extracellular volume fraction mapping at 3 tesla. J Cardiovasc Magn Reson 2011;13:75.*

How to do segmental ECV and lambda quantification



1. It is recommended to perform a contour registration before ECV map generation.
2. Make sure you have endo and epicardial contours, segmentation points and a blood-pool contour in all slices in both *T1 map. Native* and *T1Map CA*. The blood pool contour can be drawn either in the T1 or the T1* map (see above).



3. Perform a registration (see above) if images were not already registered before T1 map creation.
4. Enter the hematocrit for the ECV quantification in the *T1 Options*



5. Generate an ECV and lambda map.

Note: No map will be generate if slice locations do not match.

6. For a polar map display, make sure you have defined the long axis extent in the reference frame.



7. Add evaluation (images, values and graph) to the report

24.5 T1 mapping Troubleshooting

- ⦿ The dataset can not be loaded
 1. Check in the T1 *Option* menu to ensure the correct sequence. Is selected
 2. For some sequences, the trigger time is entered in the inversion time field (e.g. some Philips or Siemens sequences). Check *Use Trigger Time as Inversion time*
 3. If a map is appended to the series, it can't be loaded. Check *Skip Last Slice Image*
 -
- ⦿ There is a grey ring in the polar map:
 1. Check that you have contours and a segmental reference point in each slice
 2. Check that you have defined the LV extent.
 3. Check if the slices truly cover the entire LV or the anticipated region: e.g. first slice is too far away from the mitral valve plane to actually reflect the base.
- ⦿ No ECV map output: check that you have a blood-pool contour defined in the native and post-CA map and in every slice

Reference Paper:

Moon JC, Messroghli DR, Kellman P, Piechnik SK, Robson MD, Ugander M, Gatehouse PD, Arai AE, Friedrich MG, Neubauer S, Schulz-Menger J, Schelbert EB. Myocardial T1 mapping and extracellular volume quantification: a Society for Cardiovascular Magnetic Resonance (SCMR) and CMR Working Group of the European Society of Cardiology consensus statement. *J Cardiovasc Magn Reson.* 2013 Oct 14;15(1):92. doi: 10.1186/1532-429X-15-9

C. Jellis and D. Kwon. Myocardial T1 mapping: modalities and clinical applications. *Cardiovascular Diagnosis and Therapy.*

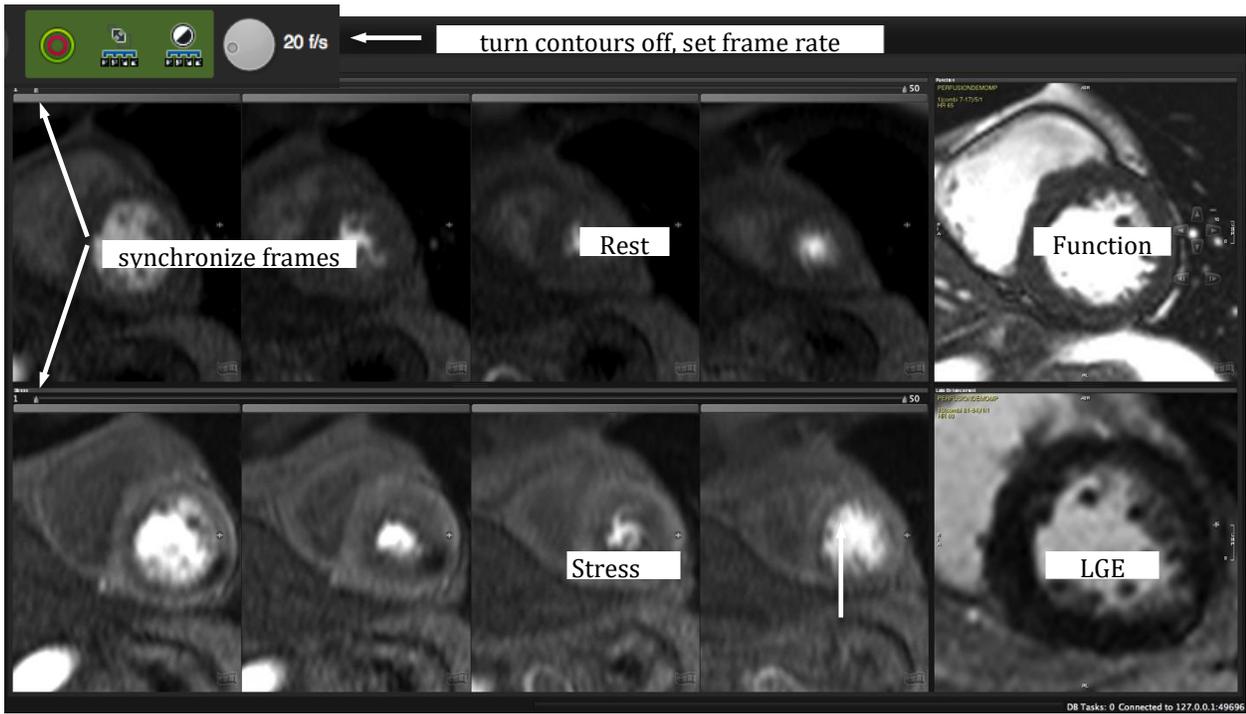
25 First Pass Perfusion Module

25.1 "Multi View" Compare Rest and Stress Perfusion	188
How to do a visual perfusion analysis	189
25.2 "Edit Contour", semi quantitative analysis	189
How to do Semi-Quantitative Perfusion Analysis	190
25.2.1 Option Menu.....	192
How to analyze the perfusion curves	192
25.3 "Analysis", segmental analysis	194
How to do a regional perfusion analysis	194
25.3.1 Perfusion Analysis Troubleshooting.....	195

The Perfusion module consists of 3 pages

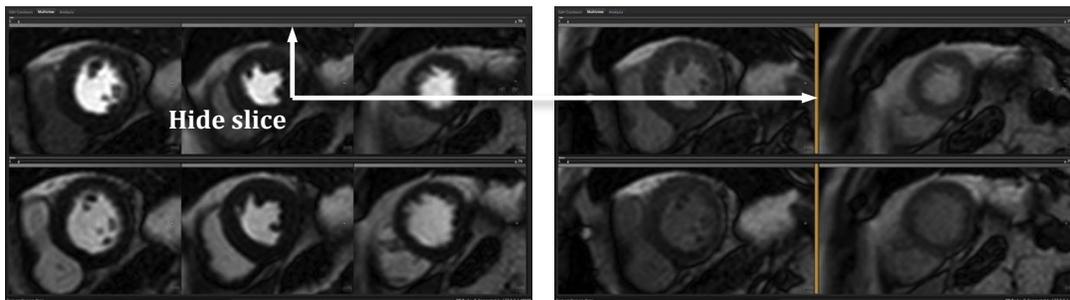
- Multi View: Compare rest and stress perfusion with scar images and wall motion kinetics
- Edit Contour: Semi-quantitative analysis
- Analysis: Polar Maps

25.1 "Multi View" Compare Rest and Stress Perfusion



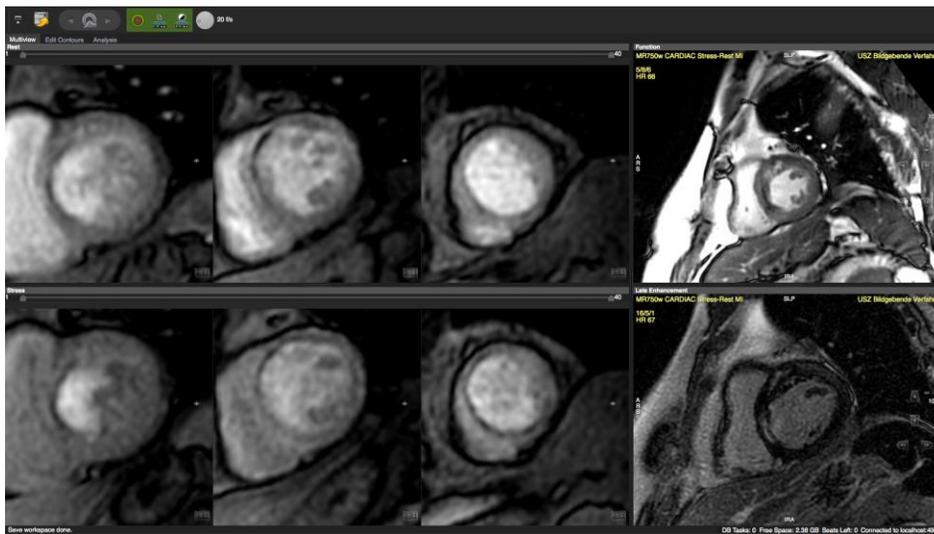
Visual Analysis of Rest and Stress Series

To hide a slice, click the grey bar above the slice.

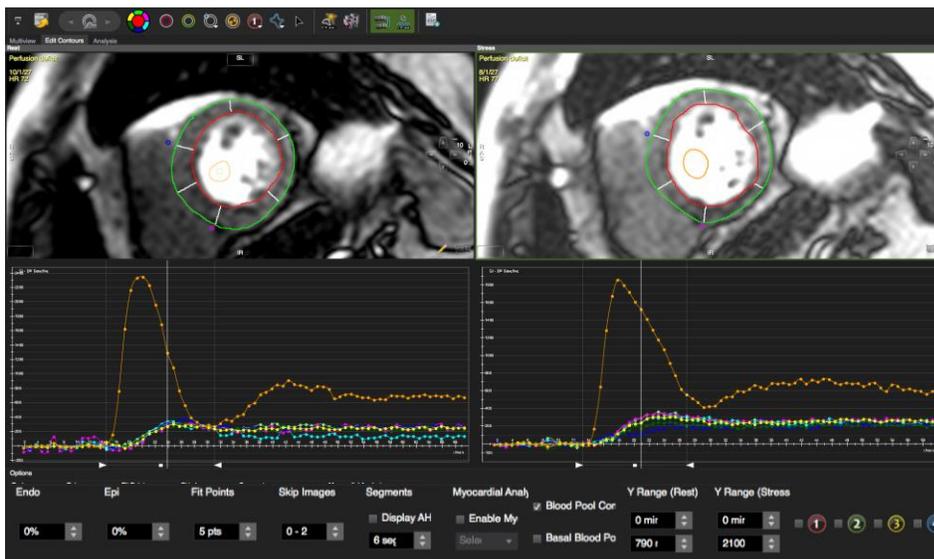


How to do a visual perfusion analysis

1. Adjust window and zoom for rest and stress series.
2. To set the frame rate use the wheel in the toolbar
3. Turn existing contours off (toolbar button)
4. Synchronize the frames for rest and stress by using the slider
 - If applicable drag Late Enhancement and Function images into their respective frames for comparison
5. Add the *Floating Viewer* for more viewing options



25.2 "Edit Contour", semi quantitative analysis



To adapt the module to your requirements click the *wrench* button in the *protocol* pane.

- ⦿ Select specific buttons and tool sets
- ⦿ Switch on/off the *Option menu* (see below)

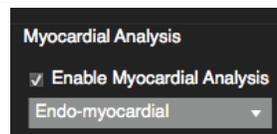
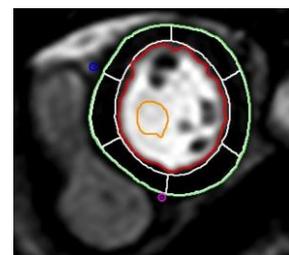
How to do Semi-Quantitative Perfusion Analysis

1. Drag the appropriate series in the *Rest* and *Stress* frame and adjust viewer properties.
2. Select a phase with good contrast and draw endo- and epicardial contours
3. Draw endo- and epicardial contours. To copy and paste contours from rest to stress series via context menu
 -
4.  Draw a *Blood Pool* contour, (input function) in the brightest, most homogeneous area of the blood pool.

Bloodpool Contour
 Basal Bloodpool Contour
5. Check *Use Bloodpool Contour* in the *Options* (underneath the graph). In case the option *Search for Basal Bloodpool Contour* is checked, the software will only use the most basal blood pool contour for calculation purposes.


6.  Set the anterior and inferior segmentation reference points at the insertion of the RV to the epicardial border of the LV.
7.  Contour Propagation: Forward all contours, including blood pool contour and segmentation point to the remaining phases.
8.  **Check and adjust contours** for each phase within the analysis range. Use the align contour button to correct for breathing motion

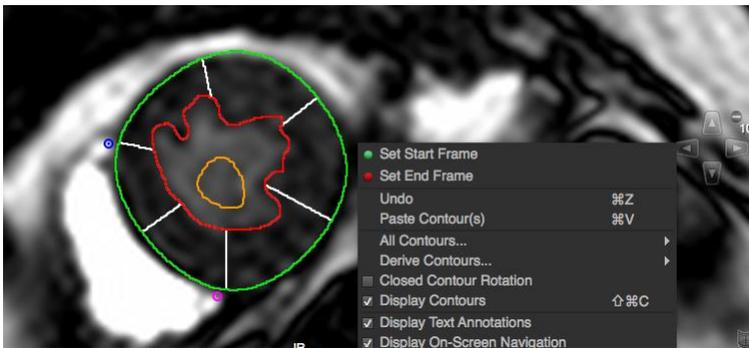
To manually shift all contours at once: press and hold the *command* (\mathbb{H}) key and shift the contours with the LMB.
9. Choose AHA segmentation or a number of custom segments per slice or from the *Options/Segments* menu (see below).
10. Optionally apply an Offset:



Endo: Modifies the region for evaluation by moving the endocardial border contour towards the epicardial border (0 - 50%)

Epi: Modifies the region for evaluation by moving the epicardial border towards the endocardial border. (range 0 - 50%)

11. Analysis of myocardial layers: Use the menu in the *Options* to generate curves of endo-, mid-, and epicardial layers.
12. Define the analysis range (contrast inflow during first pass) by moving the left and right slider at the bottom of the graph, or by using the context menu while scrolling through the phases. This will also limit the frames in the 'Multi View' to the defined range.



13. Apply baseline correction via context menu (RMC in the graph)
14. For a special region of interest, there are 4 additional contours in the top tool bar. To view the curve, check the respective ROI in the *Option* menu



15.  Repeat for all slices and add results to the report

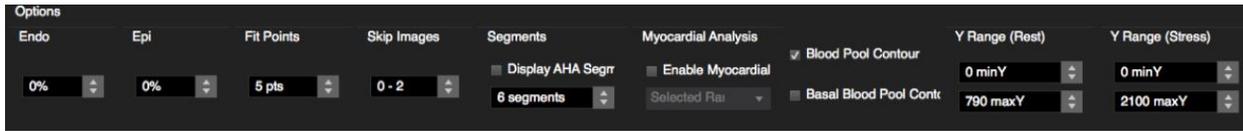
The following will be added to the clinical report:

- the calculated values for each segment and each slice,
- the polar maps as specified below
- the first phase frame of each slice as a sample image.

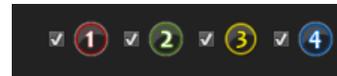
The following will be added to the *scientific* report:

- the calculated values for each slice and each segment,
- for each slice, each segment, and each phase: the average, maximum, minimum, and median signal intensity, the standard deviation thereof, and the area of the region (segment or cavum).

25.2.1 Option Menu

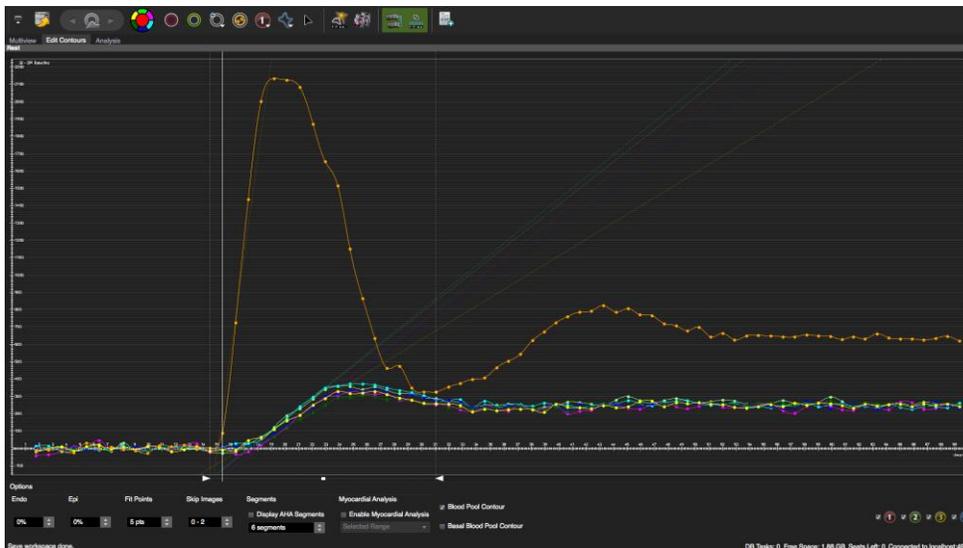


- *Endo/Epi*: Exclude sub-endocardial and/or sub-epicardial layers
- *Fit points*: Choose the number of points that will define the slope
- *Skip Images*: you can exclude images from the from baseline
- *Segments*: Choose between custom segments (up to 100) or AHA segmentation
- *Myocardial Analysis*: allows to analyze endo-, mid- and epicardial layers separately
- *Blood Pool contour*: Checked, it requires to define a blood pool contour
- *Y-range*: Allows to change the scale of the graph for a better differentiation of the curves
- *Basal Blood Pool Contour*: The software only uses the most basal blood pool contour
- Check a box to view the perfusion curve of a drwan ROI



How to analyze the perfusion curves

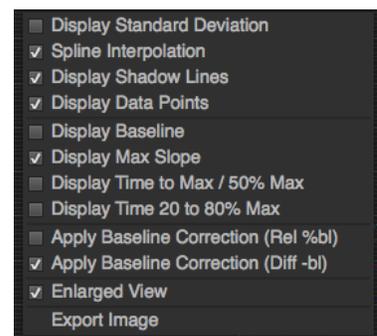
1. Clicking a data point in the perfusion curve will display the respective phase in the viewer
2. To switch to an enlarged view, go to the context menu and check *Enlarged View*



3.  Move the mouse cursor over the icon to view the curve of the respective segment.

4. The context menu offers several display options:

- Display standard deviation.
- Spline interpolation: Smoothes the graph.

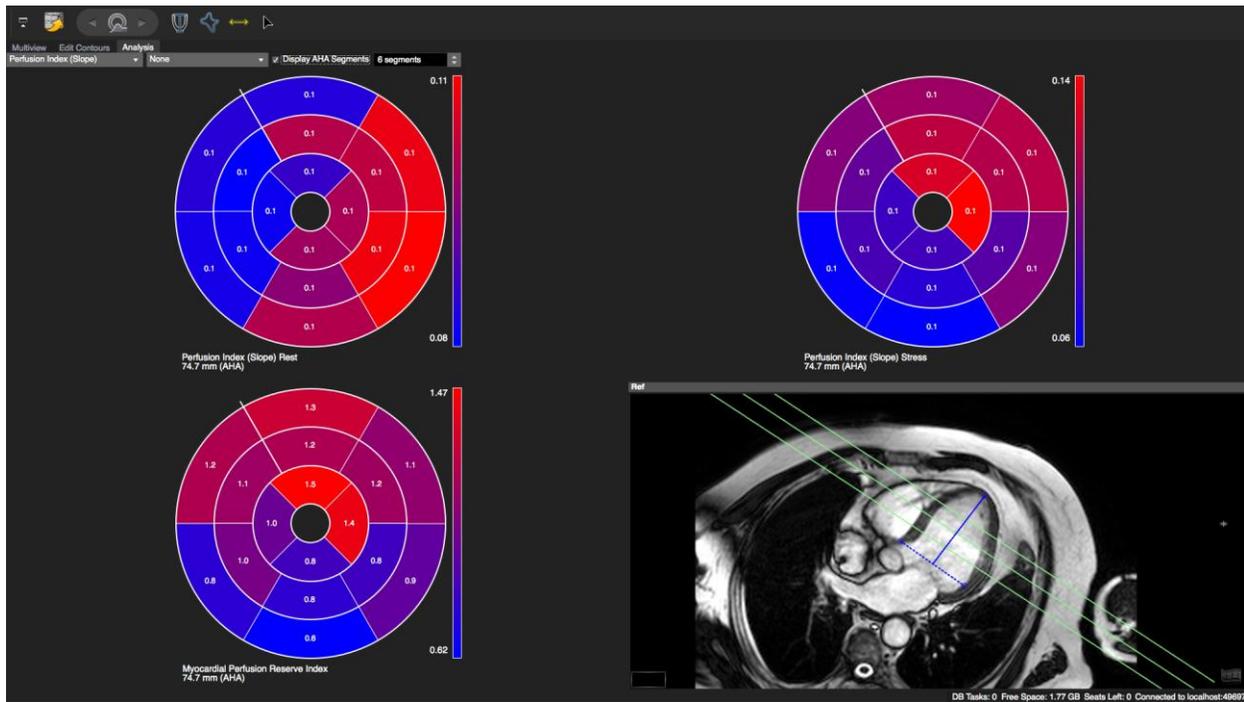


- Display shadow line: A line will indicate the previous line position while modifying the analysis range.
- Display data points.
- Display Baseline: The software calculates and displays a pre-contrast signal intensity baseline (depends on slider setting) for each segment. The Option menu provides a preference that excludes images from the baseline calculation (Skip Images) Display Time to Max/ Time to 50%Max:
- *Maximum slope*: The local slope will be determined from a linear regression fit applied to the adjacent graph points. The number of graph points used can be specified *Option>Fit Points*
- Display for each segment, *SI maximum* and 50% of the maximum
- Display *Time 20 to 80%Max*: This will display the time elapsed between 20 % and 80% of the maximal signal intensity

Note: Lines may not be displayed if the input data does not contain 20, 50 or 80% max criteria for the Perfusion Graph. Try applying a baseline correction.

- *Apply baseline correction (Rel% -bl)*: All SI values are expressed as a percentage of the baseline value. The baseline value is given as the mean SI of all SI values (excluding the first image) before the arrival of the contrast agent in the left ventricle.
- *Apply baseline correction (Diff-bl)*: All SI values are expressed as the difference to the baseline value. The baseline value is given as the mean SI of all SI values (excluding the first image) before the arrival of the contrast agent in the left ventricle
- *Exit the Enlarged View* via context menu (uncheck)

25.3 "Analysis", segmental analysis



How to do a regional perfusion analysis

1. Define length of anatomical long axis using the LAX LV Extent Contour button In end-systole draw a line between the mitral valve plane and the left ventricular apex. Slices beyond the range will not be included in the Polar Maps.

The purpose of this contour is to ensure displayed polar maps reflect the entire left ventricle. cmr/cvi42 will display grey segments in case :

- slices do not cover the entire ventricle
- the gap between slices is too big for interpolation
- there are missing contours in existing slices

2. Select a parameter from the drop down list:

- *Max Slope*: Maximum Signal Intensity increase over time (SI/sec)
- *Time To 50% Max*: Time elapsed between onset of contrast inflow and reaching 50 % of the maximum signal intensity (sec).
- *Time To Max*: Time elapsed between onset of contrast inflow and reaching the maximum signal intensity. (sec)
- *Time 20%to80%*: time elapsed between 20% and 80% of SI maximum
- *MaxSI*: Maximal Signal intensities (SI)
- *Myocardial Perfusion Reserve Index* (dividing the upslopes of the time-intensity curves at stress and rest)

3. Apply a baseline correction

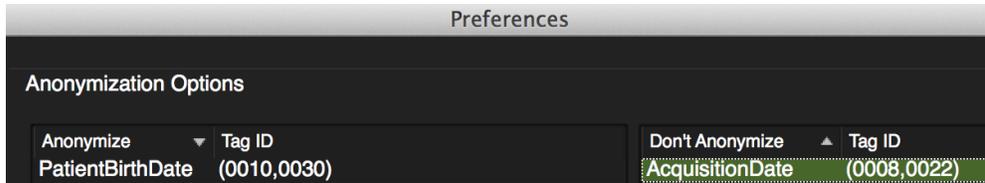
Baseline Difference: $(SI_{corrected} = SI - SI_{baseline})$

Baseline Relation: $(SI_{corrected} = SI / SI_{baseline} * 100)$



25.3.1 Perfusion Analysis Troubleshooting

- In anonymized studies the perfusion curve only has 2 data points: Some vendor sequences the timing information is part of the *Acquisition Date* and should not be removed during anonymization.



- ⦿ The polar map displays grey rings: According to the defined extent of the left ventricle the software was not able to find a true apical or basal slice. Or the slice gap is too large to be interpolated.

26 Flow Module

24.1	Reported values	196
24.2	Flow quantification	197
	How to do a Flow Analysis.....	197
24.3	Comparison of Two Different Flow Series (Qp/QS)	199
	How to assess (Qp/QS)	199
24.4	Invert Results	200
24.5	Sample Size Volume for Maximum and Minimum Velocity Calculation	200
24.6	Flow Profile	200

Flow analysis (Only through plane velocity encoding)

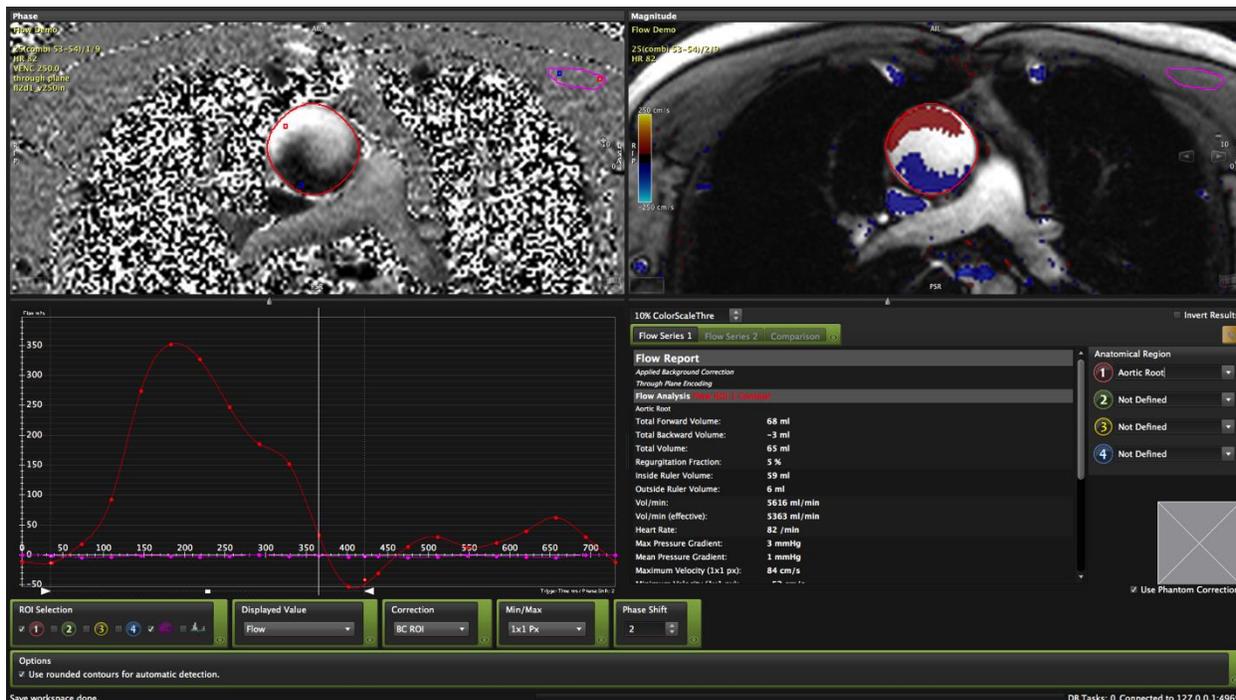
26.1 Reported values

Flow Analysis		
Total Forward Volume (TFV)	ml	positive + negative velocities = positive value (above x-axis)
Total Backward Volume (TBV)	ml	positive + negative velocities = negative value (below x-axis)
Total Volume	ml	TFV + TBV
Net positive Volume	ml	only positive velocities (above x-axis)
Net Negative Volume	ml	only negative velocities (below x-axis)
Regurgitation Fraction	%	ratio between total backward and total forward volume.
Volume/min	ml/min	
Volume/min effective	ml/min	
Heart rate	bpm	
Maximum pressure gradient	mmHg	
Mean pressure gradient	mmHg	
Maximum velocity	cm/s	
Minimum velocity	cm/s	
Maximum Mean velocity	cm/sec	Value of the phase with the highest mean velocity
Maximum Flow	ml/s	
Minimum Flow	ml/s	
Inside Ruler Volume	ml	Using the ruler in the diagram, you can restrict the analysis to a certain range of the cardiac cycle.
Outside Ruler Volume	ml	Volume that is outside the defined range

26.2 Flow quantification

Postprocessing of velocity encoded images requires

- ① Definition of vessel contour in all phases
- ① Application of Background correction



To adapt the module to your requirements, click the *Edit* button in the *protocol* pane.

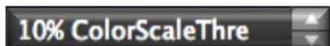
- ① Toggle on/off the option to compare to series
- ① Select display options for the flow curves
- ① Display the *Options* to use rounded contours
- ① Check/uncheck the option to use a phantom correction

How to do a Flow Analysis

1. Drag the *Phase* series into the top left analysis frame, the corresponding *Magnitude* image will be displayed automatically in the right viewer window.



2. For color encoding click on the *Toggle Flow Overlay* button.



To reduce noise, the threshold color overlay can be adjusted; by default it is 15%:

3. Adjust the viewer frame properties and select a reference image with good contrast and some darker pixels.

4.  Define the vessel border, e. g. using the *Threshold Segmentation* mode

5.  Forwarding the contour. The automatic contour detection will grow the contour towards the vessel borders based on the information from all phases. It also forwards the contours to all phases.

6. Correct the contour: Scroll through phases to ensure the contours are correct.

7.  Define the Anatomical Region: Either choose a custom term or pick from the drop down menu, that opens right next to the ROI contour.



8.  Apply Baseline correction:

To incorporate a background correction into your calculations

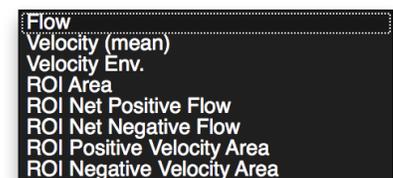
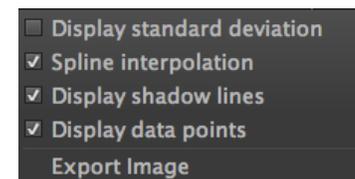
- start by selecting the *Background Correction* button and drawing a BC contour in an area with no flow (turn on the color overlay and run the cine loop to check for flow)
- Forward this contour to all phases with key combination ⌘F (also to be found in the Context menu/Copy Forward...). Do not use the Forward Flow Contour button since it will also grow the contour.
- Apply the Baseline Correction to your measurement by selecting BC ROI from the Correction drop down menu
- To view the BC-curve, check the respective box underneath the graph. All displayed values now incorporate the background correction.



9. **Phantom corrections**, check *Use Phantom Correction* and drag the image into the respective window,

10. Graphical Display

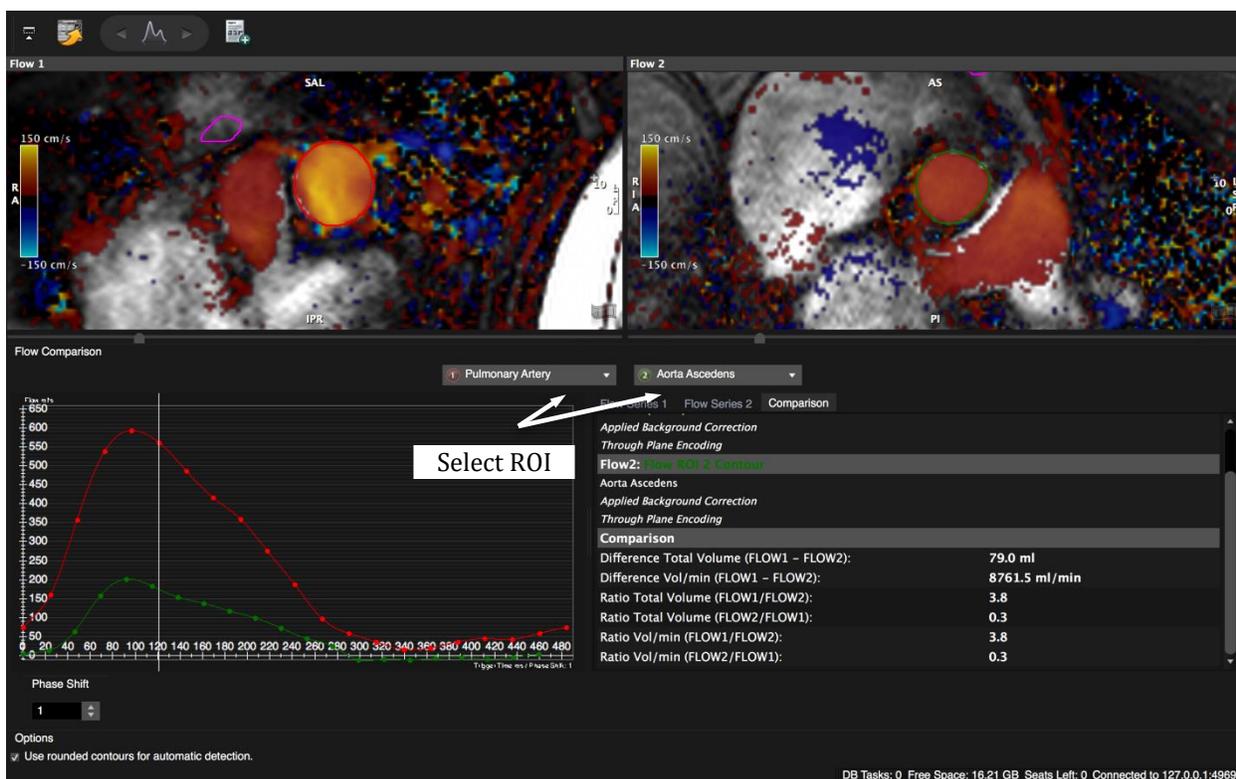
- To view the diagram go to the graph window (lower left hand side) and check the box associated with the ROI.
- A right mouse click in the graph opens a context menu, that offers several display options and an option to export the flow curves.
- Clicking on the menu button '*DisplayedValue*' will open a drop down menu that allows to look at different parameter:
 - *Flow* displays the flow m/s over time within the selected ROI
 - *Velocity (mean)* displays the mean velocity within the selected ROI
 - *Velocity Env.* displays both the maximum velocity and minimum velocity.
 - *ROI Area* displays the area (mm²) of the selected ROI.
 - *ROI Net Positive Flow* forward flow data corrected for inaccuracies caused by turbulent flow within the slice.
 - *ROI Net Negative Flow*
 - *ROI Positive Velocity Area*
 - *ROI Negative Velocity Area*



11. Add to report. Flow assessments of different series have to be added individually to the report.

26.3 Comparison of Two Different Flow Series (Qp/QS)

This function provides an option to perform flow analysis on ROI's of different series and derive values such as flow difference, sum and ratio. Ideal for phantom corrections, to assess shunt volumes and more



How to assess (Qp/QS)

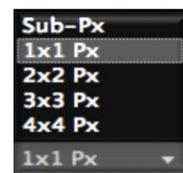
1. Perform analysis of Flow Series 1 and Flow Series 2. Define the Anatomical Region by providing a name to your ROI.
2. For easier reference select 2 different colors, e.g. red ROI1 contour for Series 1 and green ROI2 contour for Series 2.
3. Switch to the Comparison window and select the anatomical regions
4. Add to Report

26.4 Invert Results

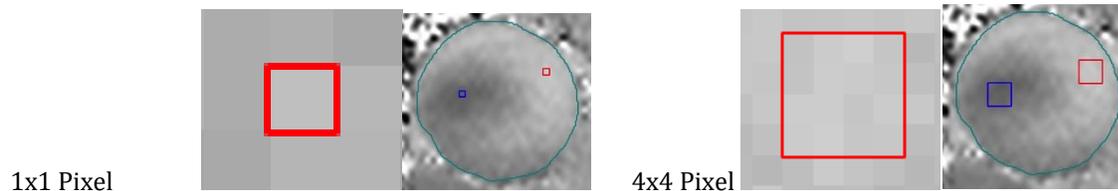
In case of unexpected flow encoding directions, you have the option to invert the input for all calculations (multiplied by -1). Checked it will be used for every report.

26.5 Sample Size Volume for Maximum and Minimum Velocity Calculation

The minimum and maximum velocity calculations are based on an average value of a determined sample volume. The size of the sample volume can be selected with the drop down menu in the lower panel.



Pixel matrix selection: The choices range from sub-pixel up to 4x4 pixel matrices. The size and location is graphically reflected in the phase image, by the red (maximum) and blue (minimum) squares displayed within the selected ROI. The velocity displayed in the graph is the average SI from within the square. Note that as you change the size of the sample volume, the location of the min and max may also change.



26.6 Flow Profile



Select the Flow Line Profile tool and draw a line across the vessel. To view your analysis, check the appropriate box in the ROI Selection menu.

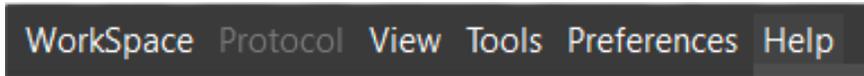
27 Main Menu, Preferences and Configuration

27.1 Preferences	202
27.1.1 Appearance	202
27.1.2 Viewer	203
27.1.3 Image Database	205
27.1.4 Anonymization Settings	205
27.1.5 Series Overview Setting	206
27.1.6 Reporting	206
27.1.7 Settings for Contours, Matrix Size and Standard Deviation	207
27.1.8 4D Viewer	208
27.1.9 Tissue Tracking	209
27.1.10 Workflow	209
27.1.11 Indication Tab	209
27.1.11.1 Disease Cluster/Indication Panel	210
27.1.12 Protocol Tab	211
27.1.13 Network	212
27.1.14 License	213
27.1.15 Server Admin	213
27.1.16 LDAP Admin	214
27.2 Workspace Menu	214
27.3 Protocol	215
27.4 View Menu	215
27.5 Tools	216
27.6 Help	216

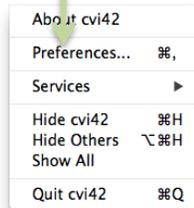
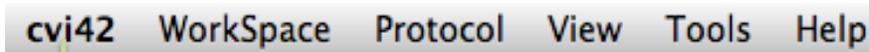
27.1 Preferences

The main menu bar is located at the top of the screen. Here you will find your "Preferences"

PC



MAC



To activate the changes, you have to reload the study

27.1.1 Appearance

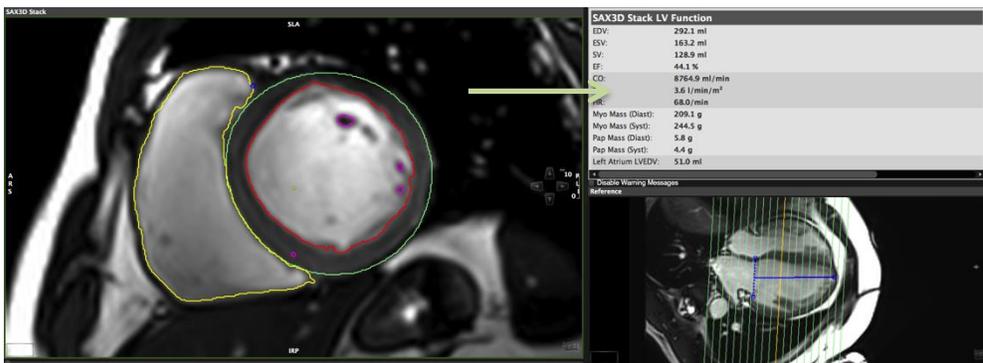
- ⦿ *Font*: Pick the style (default: Lucia Grande). Changes take effect immediately. Applies to text displayed in the viewer, reports and diagrams.
- ⦿ *Apple Options*: Retina Display
- ⦿ *Startup View*: cmr⁴² and cvi42 have the capability to work with several screens for an optimized workflow.
 - *Start Full Screen*: default = turned off
 - *Use Multiple Screens* (default = turned on): Enables the system to work with two screens (see chapter *Set Up*)
 - Select your preferred setting and restart the software. (See chapter 5.3 Working with multiple screens)
- ⦿ *Smart Series Handling*:

The selection of series is based on the DICOM header info. Series that are de-identified, e.g due to anonymization will be excluded.

Images are sorted into:

 - preferred - green checkmark
 - allowed - no tag
 - not allowed - red cross
- ⦿ *Window Frameless (Second Screen)*: default = turned on; text will be omitted

- **Start Module:** Determines the default module that opens upon program start up. Options are:
 - Viewer
 - Series Overview (default)
 - 4D Viewer
 -
- **Patient Data Metric:** applies to Patient Data module(weight and height).
 - Metric Units (*default*)
 - Imperial Units: If changed in the settings to imperial, both units will be shown.
 -
- **Screen Report:** changes to a bright report window background



27.1.2 Viewer

- **Contour Drawing Settings**
 - *Stay in contouring mode:* Double click will not drop a primary selected tool allowing the user to draw a second, third etc. contour.
 - *Exit contour mode:* As soon as the left mouse button is released the tool will quit.
 - **Enable Drawing Mode Pop-up:** Will display a toolbox for drawing modes like Click-Draw or Threshold Segmentation
 - *Use angle within 180 degrees:* The default for angel measurement is 360 degrees and depending on the direction, you set your points (form left to right or vice versa) it will pick the larger or smaller angel. This option checked it will only measure up to 180 degree
 - *Calculate Ellipse Perimeter:* checked the tool will give 2 measurements. The perimeter of the drawn contour and for an elliptical shape
- **Contour Display:** Changes the width of the contourline between 1-2-3 pixels
- **Window/Zoom/Panning Forwarding Policy**
The policies determine if windowing, zooming or panning will be applied to:
 - Series (default)
 - Slice

- Image
- ⊙ Zooming/Panning Settings:
 - *Smart Forwarding policy* (enabled by default): Settings will only be forwarded if images are parallel and/or have the same FOV respectively.
 - In some cases where the images are not parallel, (e.g. multiple long axis series) it doesn't make sense to automatically forward the viewer settings.
 - *Adjust Zoom To View Size*: Adjusts the image size to fit the frame (enabled by default)
- ⊙ Cine Synchronization: Sync by time is the default option
- ⊙ *Cine Preview Mode Enabled*: The option is off by default. If enabled, some image frames may be skipped while playing cines with high frame rate settings on slow machines. If turned on, the setting will be indicated in the viewer frame.
- ⊙ *Default Zoom Factor*: Displays all prospective images by default with the chosen zoom factor
- ⊙ Default Window:

Changes the default window settings given by percentage histogram offset.
E.g. Images are constantly too dark, set the default to a higher value to display brighter images.
The offset ranges from 0-40 %; the default setting is 8%.
The DICOM option will retrieve the window information from the DICOM header.
- ⊙ Mouse Wheel Function:

Changes the wheel functionality from zooming to phase or slice navigation.

 - While *Phase Navigation* is enabled the user has the option to zoom by dragging the cursor to the right frame border until the zoom symbol appears ; click on the symbol with the left mouse button, hold and shift up and down.
 - If *Zooming* is selected, the user can switch to *Phase Navigation* temporarily by holding the shift-key while scrolling
 - *Zoom to mouse*: checked it will take the cursor position as a zoom center.
 -
- ⊙ Autosave Workspace:

Customize the interval for automatic workspace saving
- ⊙ DICOM Annotation
 - *Display Additional DICOM Annotations*: When checked it will display DICOM tags (TD,TR, TE....). To activate, reload study!
 - *Display DICOM Annotations in Multiview*: Applies to the multiview layout (tile-display of all slices) that can be entered via spacebar click or by clicking the *Multiview* button in the Viewer Modules

- Ⓒ *Display DICOM LUT*: checked a color look up table defined in the DICOM header will be used for the display in the viewer
- Ⓒ *Floating Viewer*
Checked by default. This functionality synchronizes the slice location of the series loaded into the *Floating Viewer* with the slice location of the series in the main viewer frame. When scrolling through the series, the images in the floating viewer will follow accordingly.
- Ⓒ *Context Menu*:
Checked by default. If this feature is selected it is still possible to retrieve the full menu with a short-cut-key combination ⌘+RMB.

27.1.3 Image Database

- Ⓒ *Export Options*
Write DICOMDIR: Checked, the "Export Images" button in the *Image Database* will export studies in a directory that contains an additional DICOMDIR file.
- Ⓒ *Study Sorting*: allows to accept unordered stacks (Siemens only): cvi⁴² will allow to import stacks that are divided into different series and are unsorted. Slices will be automatically sorted into correct order, thereby preventing consecutive sorting issues with other series.
- Ⓒ *Performance Options*:
 - *Image Cache Size Limit*: Loaded voxel data will be cached in memory. The size of the memory cache is configurable by the user. Default size: 256 MB.
 - In case of performance, options try to increase the cache size.
 - *Smart Image Loading*: cvi⁴²/cmr⁴² uses a smart predictive loading to ensure a smooth image handling for the user. However, in some cases this can cause unstable conditions. When this rare problem occurs, the user can try to turn off the "smart image loading" option.

27.1.4 Anonymization Settings

- Ⓒ *Anonymize Options*: Select the attributes desired to keep during anonymization by dragging them to the right column (*Don't Anonymize*).
Note: In some perfusion sequences the timing information is part of the *Acquisition Date* and you will not be able to display a perfusion curve if this is anonymized.
- Ⓒ *Private Tags*:
When checked, it removes patient **and vendor specific** proprietary data (private DICOM tags). Using the option *Remove Private Tags* will prompt a warning in case velocity encoded images are about to be removed (applies GE and Philips)

⦿ Batch Anonymization:

Allows for anonymizing multiple studies at the same time. Please refer to *Image Database Module /Anonymization*.

27.1.5 Series Overview Setting

Changes apply after reloading.

⦿ *Startup View*:

By default, the Series Overview module displays all images and series comprised in the study.

- *Slide Show*: Presents the study in a slide-show fashion
- *Case Review*: Will only display images that have previously been selected for a case review

⦿ *Study Preview*:

These setting relate to the cine loops and image stacks

- *Auto Start Cine on Mouse Move*: Hovering over cine will automatically run the cine (checked by default)
- *Auto Start All Cine* will start cines as soon as the module is open
- *Show Navigation Buttons* will display on screen buttons to navigate through series, slices, and phases
- *Open Series Selection in Viewer on Double Click*: A double click on an image or a series will display the selection in the *Viewer* module
- *Slide Show*:
- *Show Progress Bar*: Displays a progress bar on the bottom right of the slide frame, indicating the number of current series/total number of series
- *Auto Start Cine*: Cine starts as soon as the slide show mode is entered

27.1.6 Reporting

The Reporting menu relates to the report module and allows defining/changing the settings for DICOM report saving functionality

⦿ *DICOM Export Options*

The *Save DICOM Report* button in the *Report* module by default creates an image of all previously added text reports (analysis).

To add images the following options are provided:

- *Create Additional Images*: Checked it will automatically create and save secondary captures of all polar maps, diagrams, and reference windows.
- *Create Selected Images*: Images that have previously been added to the report will be captured and automatically saved.
- *Create Series Images*: Images with contours will be captured and automatically saved
- *Create Monochrome Images Only*: In order to save memory space images can be saved in black and white.

- *Secondary Capture Image Storage SOP*: Exiting DICOM storage behavior (Multi Frame Secondary Capture SOP class) can be switched to a different class.

⦿ Report Image Export Options

Hides or displays threshold contours in the images added to the report.

⦿ Report Server:

Set the following parameter:

- *Server Type*: report⁴² or generic
- Server URL
- Username
- Password

⦿ Number of Decimals:

Depending on the module, the user can individually choose the number of decimals displayed.

- *Screen*: refers to reporting windows in modules
- *Scientific*: the scientific report
- *Viewer*: refers to values that are displayed on the image in the Viewer

27.1.7 Settings for Contours, Matrix Size and Standard Deviation

⦿ *Sub Pixel Matrix Size*: Changes the spatial resolution of the contour drawing (default: 4x4).

Note:

The higher the resolution, the longer the processing time. With a high resolution and low processing capacity, the system might seem to be unresponsive.

⦿ Signal Intensity Standard Deviation: Changes the sensitivity of the SD calculation.

- Use Sub-pixel Weighted SD (default = checked): The user has the option to determine if the complete pixel or, if checked, a sub-pixel will be counted into the standard deviation. A normal curve of SI distribution is assumed here.
- Use biased SD: Lets the user choose between a normal and biased distribution of Signal Intensities (default = unchecked).
-

⦿ Contour Detection

- *Contour Detection Connect to View* (Reload the study to apply settings):
- Unchecked, a yellow frame will be visible around the area of analysis for contour detection (you may have to zoom out to see it). It is possible to change the frame size by clicking on the frame and dragging the yellow corner dots. Grabbing the center square allows for panning the frame.
- When checked (default), the analysis frame border becomes identical with viewer frame border. To change the area of analysis, the image has to be panned or zoomed.

- *Preserve Manually Drawn Contours*: Contours that have manually been drawn or corrected will not be overwritten by the automatic contour detection
- *Use Contour Detection Dragging*: Applies to the drag contour tool. When checked, the dragging behavior changes and will perform a contour detection while dragging.

⦿ Rounded SAX Endocardial Contour

By applying a rounded endocardial contour when using automated contour detection, papillary muscles and trabecular structures will be cut off, thus excluded from myocardial volume.

⦿ Papillary Muscle Detection

checked, papillary muscles for right and/or left ventricle will be detected and added to the myocardial mass, when using the automated contour detection. Images will display a purple papillary muscle contour within the LV cavity where papillary had been detected.

⦿ SAX chord generation:

By default the centerline method is used to perform segmentation. In some cases, e.g. atypical anatomy, the software is not able to generate chords. By checking the box it is possible to switch to a different approach for segmentation, where the center point will be determined for each slice individually.

27.1.8 4D Viewer

- ⦿ *Voxel Precision* can be changed between 8 and 16 bit. By default, 16 bit precision is being used in order to retain the original data precision. However, if the video memory is limited, 8 bit precision could be selected temporarily to lower the amount of video memory usage.

Note:

In case the original data contains a higher precision than 8 bit and 8 bit precision is selected, the original data is down-sampled to fit the 8 bit memory boundary and some details could be lost.

- ⦿ *Rendering (4D Viewer/MPR Viewer)*: The *Rendering Acceleration* option could be used to speed up rendering during rotation/manipulation/editing. No Acceleration will result in high quality rendering (if the graphics card is fast). Higher settings will decrease rendering quality to achieve faster rendering speed.

- *Use Full Quality Rendering* (requires a fast graphic card)
- *Empty Space Optimization*: if a 3D rendered volume only has a small visible mask or anatomic structure, the rendering algorithm will only load the visible structure into video memory and skip the remaining empty volume. This is designed for performance improvement and speeds up the rendering. Example: If we are only visualizing the coronary arteries in a large volumetric CT with a resolution of 512x512x500, only the coronary artery voxels will be loaded in memory instead of the entire volume since most of the volume is empty.

- Video Memory Saving Mode for Cine Volumes

Viewers:

- *Enable 4D Mesh Visualization*: When unchecked, **no** 3D/4D mesh model will be created.
- Portrait Layout: check if preferred

27.1.9 Tissue Tracking

Choose a coordinate system for the 3D algorithm:

- Use Global Cartesian Coordinate System: : radial direction is perpendicular to Apex-Base line
- Use Local Heart Coordinate System: radial direction is perpendicular to the myocardium.

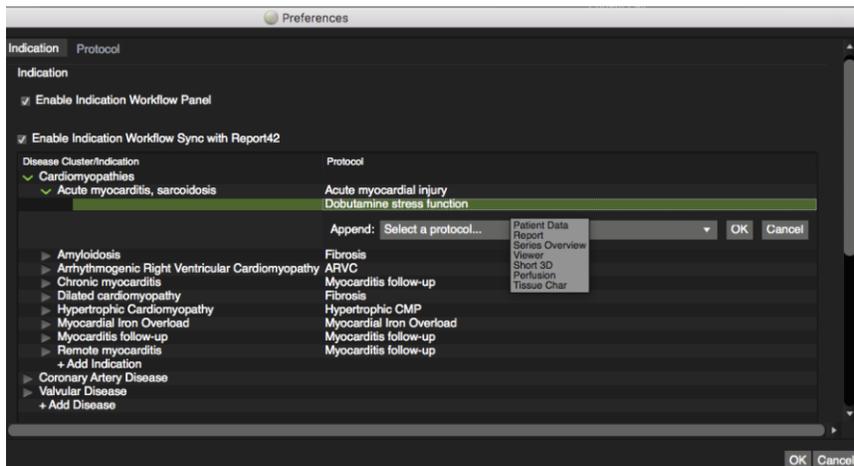
The circumferential and longitudinal directions are defined based on the radial direction.:

Longitudinal direction: perpendicular to radial direction Base

Circumferential direction: perpendicular to radial & long such that R-Lo-C coordinate system is right-handed

27.1.10 Workflow

27.1.11 Indication Tab



Enable Indication Workflow Panel: Enabled by default. Unchecked, cvi⁴² will go back to the old protocol panel.

Enable Indication Workflow Sync with report⁴²: When enabled, this setting will ensure synchronization with r42 v 3.3. i.e. Disease clusters, indications, and protocols (including associated report sections) will be synchronized between cvi⁴² and report⁴².

Note:

For instances where report⁴² is not connected, or the version is 3.2 or below, synchronization is NOT possible and this checkbox is disabled. A notification icon will be displayed and additional information provided on hover.

27.1.11.1 Disease Cluster/Indication Panel

This panel allows Disease Clusters, Indications and Protocols to be displayed (all users) & managed (Admins only).

Administrators can edit as per the below:

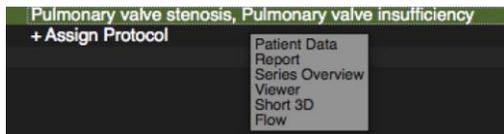
- *Add Disease* allows to create a new workflow



- *Add Indication* to a disease: A left click on a disease cluster will display the associated indications. *Add Indication* allows the user to set up a new indication.



- Assign a protocol to an indication: A left click on an indication will display the associated protocols. Hovering over a protocol will display the modules that are comprised in the respective protocol workflow



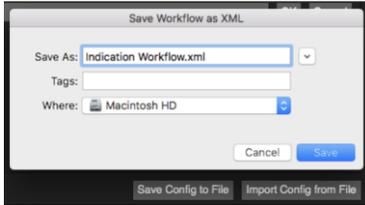
Click *+Assign Protocol* to link a protocol to the indication.

New protocols can be created in the *Protocol Tab* (see below)

- Delete / Rename: A right mouse click on a *Disease Cluster*, *Indication* or *Protocol* allows the user to rename or delete it.

Protocol Export

Protocols can be imported/exported via XML



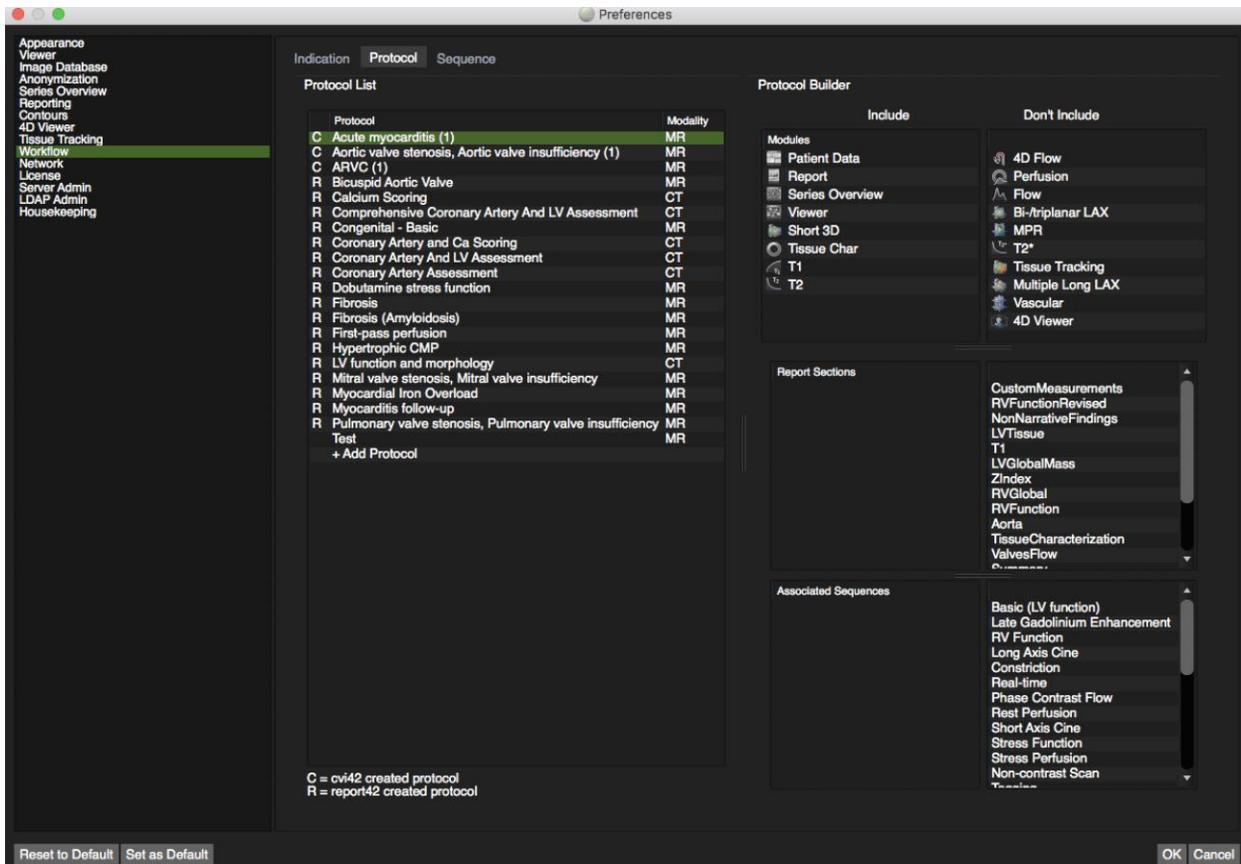
27.1.12 Protocol Tab

1. *Add a Protocol* will prompt you to choose a name and the modality.



2. Next, select the new protocol, which will be clearly indicated, and select the modules to be included with a double-click.

Protocols are labeled *C* if they are a cvi⁴², and *R* if they are a report⁴² created protocol



If report⁴² v3.3 is synchronized any additional new disease clusters/indications/protocols will be imported automatically into report⁴² and vice versa.

Protocols are labeled *C* if they are a cvi⁴², and *R* if they are a report⁴² created protocols.

These disease clusters/indications/protocols with no associated analysis modules and will be identified by a notification icon. Once modules have been assigned, this notification will disappear.



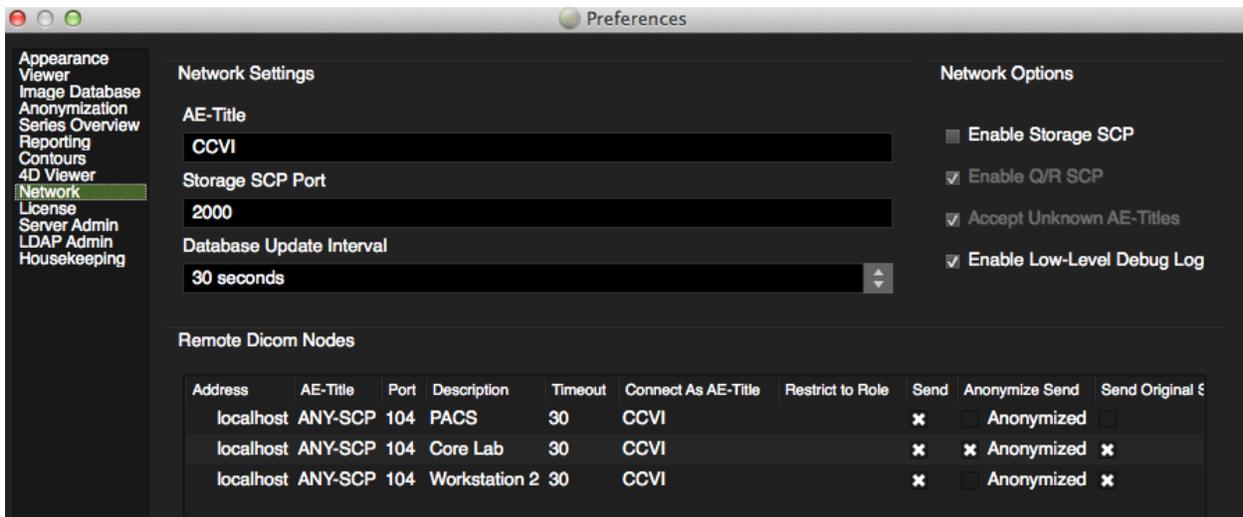
27.1.13 Network

The Network Window Tab allows you to define entities for DICOM communication. In order to connect to another entity, the DICOM communication system needs to know the exact

- AE Title
- IP Address
- Port Number

WARNING: DICOM Networking

The DICOM communication interfaces do not use encryption or user authentication. It is the user's responsibility to use these communications abilities only in a secure environment.



You have to define your own (provider) name = AE title. By default it is "CWI42". This selected name has to be provided to the other entity you wish to communicate with.

⦿ Network Settings

- *AE title*: Define your provider name. By default it is "CVI42". This selected name has to be provided to the other entity you wish to communicate with.
- *Store SCP Port* - A port number has to be defined. Provide that number to the entity you wish to communicate with.
- *Database update interval* - By default every 30 seconds the system updates the image database.
-

⦿ Network Options

- *Enable Storage SCP - Automatic Image Receiving*: Checked: DICOM listener is active and able to receive images automatically.
- *Enable Q/R SCP* - Allows for DICOM Query/Retrieve.
- *Accept Unknown AE Titles* - Allows push from any SCP.
- *Enable Low Level Debug Log* - Turns on Debug logging.

⦿ *Remote DICOM Notes*: configure where, who and what to send

27.1.14 License

(see also Chapter 4.1 Request a License)

⦿ License status:

If the license is valid it notes: x valid licences available.

If the license is expired it notes: No valid license available.

⦿ Available license:

The following information of all available licenses is shown here:

- Product
- Start date
- Expiry date
- Maintenance Expiry
- License holder
- Status
- Count
- Machine ID
- License File

To *Import, Add or Request* a license please refer to Chapter *Request and/or Add License*

27.1.15 Server Admin

Allows for configuration of user accounts

27.1.16 LDAP Admin

⦿ The LDAP Admin Tab allows you to define settings used for connecting on to AD/LDAP server. These settings will allow users to be authenticated against existing AD/LDAP server when logging into cvi⁴².

cvi⁴² needs to know the following information:

1. AD/LDAP server's hostname or IP address
 2. Whether the connection is over TLS/SSL
 3. AD/LDAP's domain
 4. Base distinguish name
 5. Username attribute
 6. Additional criteria (optional)
 - *Primary Server* – A primary server has to be defined. Provide a hostname of the AD/LDAP server for user authentication.
 - *Secondary Server* – This entry is optional, it serves as a backup server to connect when the primary server is unavailable.
 - Use TLS/SSL to connect – If this option is checked, all communication with AD/LDAP server will be performed over TLS/SSL.
 -
- ⦿ Account Info for Initial Bind
- *Username* – This is the field used for entering the username along with a domain of the AD/LDAP server giving administrators the ability to test the AD/LDAP connection. The domain specified here will allow other users logging into cvi⁴² to be authenticated using AD/LDAP.
 - *Password* – User credentials used for testing user authentication against AD/LDAP server.
 - *Anonymous connection: check name* – A button the administrator clicks on to check the authenticity of the given user credentials against the AD/LDAP server.
- ⦿ AD/LDAP Specific Information
- *Base Distinguished Name* – This defines the location (or forest) of the directory to search when performing an AD/LDAP query.
 - *Username Attribute* – A AD/LDAP attribute used when searching for a user on the AD/LDAP server. For example, sAMAccountName is often used when looking up users on Active Directory servers. Or uid for LDAP servers.
 - *Advanced* – Allows you to specify additional criteria to use when searching for a user on the AD/LDAP server. In particular this allows you to specify additional permission a user must have in order to gain access to cvi⁴². For example, a user must be a member of the cvi⁴² group in order to log into cvi⁴².

27.2 Workspace Menu

By default, drawn contours are automatically saved and will be reloaded when the patient study is reopened. In addition, the user has the option to:

- ⦿ *Load Workspace*: Loads a workspace that has been previously stored in a location other than the default location. ("Save Workspace As" option)
- ⦿ *Save Workspace*: Saves a newly created or updated workspace in the default location
- ⦿ *Save Workspace As*: Saves the workspace to a different location
- ⦿ *Load Workspace DICOM*: Loads a workspace that has been previously created as a DICOM Secondary Capture
- ⦿ *Save Workspace DICOM*: Saves the current workspace as a DICOM Secondary Capture and appends it as an image to the series
- ⦿ *Import Workspace*: Imports a workspace from a local file system
- ⦿ *Export Workspace*: Exports a workspace from a local file system
- ⦿ *Reset Workspace*: Deletes all drawn contours in the current patient study
- ⦿ *Close Study*

27.3 Protocol

This menu item lists the default protocol in the protocol pane and all the other protocols that have been generated.

In addition, it is possible to:

- ⦿ *Load Protocols From Server*
- ⦿ *Load Protocols To Server*
- ⦿ *Import protocol definitions from a local XML file*
- ⦿ *Save protocol definitions to a local XML file*

27.4 View Menu

- ⦿ *Full Screen*: Extends or diminishes screen view <command/crl F11>
- ⦿ *Hide Status Bar*: Hides the status bar that displays the progress of an image import
- ⦿ *Show Application Log*: Displays an application log, which might be used for system checks and error logging
- ⦿ *Refresh Study List* <F5>

The software generally tries to refresh the list as necessary, but for times when the list does not seem updated it may be necessary to choose "refresh study list" from the menu.

Examples of when refresh study list may be necessary:

- After importing studies from disk
- After importing studies from PACS
- When expecting studies to be received from scanner
- While user A is currently logged in, and user B has just finished importing a study (and shared it), user A may need to refresh to see it.
- Anytime the study list may look incorrect

27.5 Tools

- ⦿ Login to server
- ⦿ Disconnect from server
- ⦿ Change Password

27.6 Help

The menu comprises the following:

- ⦿ Manual
- ⦿ Release Notes
- ⦿ DICOM Conformance Statement
- ⦿ Software Usage Terms and Conditions
- ⦿ Client Server Installation Guides
- ⦿ Video Tutorials
- ⦿ Downloads

28 Technical Support

For technical questions please contact our team by phone or e-mail:

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