 USER MANUAL

cvi^{42} / cmr^{42} / ct^{42}
Version 5.5
cvi\textsuperscript{42}
cmr\textsuperscript{42}
ct\textsuperscript{42}

**USER MANUAL**

*November 30, 2016*
Regulatory Information

Manufactured by

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Australia:
ARTG Certificate No.: 177785
Sponsor: Market Access Australia Pty Lt
PO Box 1019,
WAHROONGA, NSW, 2076

European Union

cmr4² only

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

EU Authorized Representative
Philipp Barckow Dipl. MedInf.
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14163 Berlin
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Canada
cmr4² Health Canada device license #: 78347
t² Health Canada device license #: 87520
cvi42 Health Canada device license #: 93385

United States of America
cmr4²: US FDA 510K number: K082628
t²: US FDA 510K number: K111373
cvi42: US FDA 510K number: K141480

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™cmr4² Medical Image Post Processing Software for Cardiac Magnetic Resonance is a registered trademark of Circle Cardiovascular Imaging Inc.

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1 About

1.1 System Requirements

1.1.1 cvi42 Standalone and Client System Requirements\(^1\) v5.5

<table>
<thead>
<tr>
<th>Requirement</th>
<th>Minimum Requirements</th>
<th>Recommended Requirements</th>
</tr>
</thead>
<tbody>
<tr>
<td>Operating System</td>
<td>Windows 7 64-bit/</td>
<td>Windows 10 64-bit/</td>
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<td></td>
<td>Mac OS X 10.9</td>
<td>Mac OS X 10.11</td>
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<td>100BaseT</td>
<td>1000BaseT</td>
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<tr>
<td>Network (WAN) for client</td>
<td>10Mbps Downstream</td>
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<tr>
<td></td>
<td>2.5Mbps Upstream</td>
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<tr>
<td>Display</td>
<td>1280x800 Resolution at 24-bit color</td>
<td>1920x1080 Resolution or higher(^3)</td>
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<tr>
<td>Processor</td>
<td>Intel Core 2 Duo at 2.2 GHz</td>
<td>Intel i7 2.2 GHz or greater</td>
</tr>
<tr>
<td>Video Card</td>
<td>nVidia or AMD Dedicated GPU</td>
<td>nVidia Dedicated GPU</td>
</tr>
<tr>
<td>MR</td>
<td>4 GB</td>
<td>8 GB</td>
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<tr>
<td>CT</td>
<td>8 GB</td>
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<tr>
<td>MR</td>
<td>1 GB</td>
<td>2 GB</td>
</tr>
<tr>
<td>CT</td>
<td>1 GB</td>
<td>4 GB</td>
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</table>

Systems without dedicated graphics\(^4\)

<table>
<thead>
<tr>
<th>Processor / Graphics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Intel i7 with HD 3000 integrated Graphics(^5)</td>
</tr>
</tbody>
</table>

\(^1\) 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.
### 1.1.2 cvi Enterprise Server System Requirements v5.5

<table>
<thead>
<tr>
<th>Requirement</th>
<th>Minimum Requirements</th>
<th>Recommended Requirements</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Operating System</strong></td>
<td>Windows Server 2008 R2</td>
<td>Windows Server 2012 R2</td>
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<tr>
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<td>Mac OS X 10.9</td>
<td>Mac OS X 10.11</td>
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<tr>
<td><strong>Network (LAN)</strong></td>
<td>100BaseT</td>
<td>1000BaseT</td>
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<tr>
<td><strong>Network (WAN)</strong></td>
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<td>1000Mbps Upstream</td>
</tr>
<tr>
<td><strong>for server</strong></td>
<td>5Mbps Downstream</td>
<td>100Mbps Downstream</td>
</tr>
<tr>
<td><strong>Display</strong></td>
<td>24-bit color</td>
<td>24-bit color</td>
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<tr>
<td><strong>Processor</strong></td>
<td>Intel Core 2 Duo at 2.2 GHz</td>
<td>Intel i7/Xeon 2.2 GHz or greater</td>
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<tr>
<td><strong>System RAM</strong></td>
<td>4 GB (MR or CT)</td>
<td>4 GB (MR) or 8 GB (CT)</td>
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<tr>
<td><strong>Storage space</strong></td>
<td>1 TB Hard Drive&lt;sup&gt;6&lt;/sup&gt;</td>
<td>2 TB RAID 1+0, 5,6, or SAN&lt;sup&gt;6&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

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

### 1.1.3 cmr Standalone and Client System Requirements<sup>1</sup> v5.5

<table>
<thead>
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<th>Requirement</th>
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<th>Recommended Requirements</th>
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<tbody>
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<td>Windows 10 64-bit&lt;sup&gt;2&lt;/sup&gt; or</td>
</tr>
<tr>
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<td><strong>for client</strong></td>
<td>2.5Mbps Upstream</td>
<td>100Mbps Upstream</td>
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<td><strong>Display</strong></td>
<td>1280x800 Resolution at 24-bit color</td>
<td>1920x1080 Resolution or higher&lt;sup&gt;3&lt;/sup&gt;</td>
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<td><strong>Video RAM</strong></td>
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</tr>
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</table>

**Systems without dedicated graphics<sup>4</sup>**

| **Processor / Graphics**  | Intel i7 with HD 3000 integrated Graphics<sup>5</sup> |

<sup>1</sup> 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.

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

<sup>5</sup> Intel HD 520/530 Video (Skylake) with Windows 10 not supported (with current drivers as of Feb 5, 2016)
### cmr⁴² Enterprise Server System Requirements v5.5

<table>
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<tr>
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<td>4 GB</td>
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<td><strong>Storage space</strong></td>
<td>1 TB Hard Drive⁶</td>
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### ct42 Standalone and Client System Requirements v5.5

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1.2 Regulatory Information

<table>
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<th>CVI 42</th>
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<td>Pending</td>
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1.3 Basic Components and Indication for Use

cvi® 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 lenght)

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

Module: *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
 ABOUT

Module: Calcium Scoring (cvi^42 and ct^42 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. cvi^42 /cmr^42 is a software application that can be used as a stand-alone product or in a networked environment.

The target population for the cvi^42 /cmr^42 is not restricted, however the image acquisition by a cardiac magnetic resonance scanner may limit the use of the device for certain sectors of 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 cvi^42/cm^r^42, intended to be used only for scientific research is available upon request.
*Analysis of Computed Tomography (CT) images is not available in Europe for clinical purpose. A non-diagnostic version intended to be used only for scientific research is available upon request.**
1.4 Measurement Accuracy

All the measurements in the software application are direct transfer of the original DICOM data acquired as a result of image acquisition process. The expected error for the on-screen measurements will be limited to sub pixel matrix size, which divides up each pixel of the input image into a set of sub pixels, i.e.

![Original Pixel](image1) ![4 x 4 sub pixel matrix](image2)

Depending on the original pixel dimensions and the number of sub pixels used, the accuracy of our measurements will be limited to each sub pixel dimension.

For example, given an original CT or MR image with an isotropic pixel dimension of 0.4 mm and a sub pixel matrix size of 4 x 4, the length (min/max/average diameter) accuracy will be limited to ±0.05 mm. The accuracy for area and volume will be dependent on the size and complexity of shape, in addition to the sub pixel matrix size. For example, a 4 pixel diameter circle with isotropic pixel dimension of 0.4 mm and 1 x 1 sub pixel matrix will have an accuracy of ±0.96 mm².

![Example Image](image3)

1.5 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
<table>
<thead>
<tr>
<th>Term</th>
<th>Description</th>
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</tr>
<tr>
<td>RMB</td>
<td>Right mouse button</td>
</tr>
<tr>
<td>rc</td>
<td>Right click</td>
</tr>
<tr>
<td>ROI</td>
<td>Region of interest</td>
</tr>
<tr>
<td>TC</td>
<td>Tissue Characterization</td>
</tr>
<tr>
<td>SAX</td>
<td>Short axis</td>
</tr>
</tbody>
</table>
2 Getting Started

2.1 Installation

Running cvi or cmr on a local server

- Download from the website
- Run installer application
- Open the client (cvi or cmr)
- Client Login

Connect to the local server. You will find the server.app (Mac) or server.exe (Windows) in the same folder as the cvi 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: password

The first time you run cvi or cmr to your local server and/or if you move or rename the path to the server, you may be asked to locate the cvi 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

![Request license 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:
Manually remove the license files / lines that are superseded by the newly installed license
Restart the server

2.3 Load Images

Click on the Import Images button and select the image file on the local system, the network or CD/DVD.
After the import is completed, the study will be added to the Main DB tab.
One LMB click loads the study in the preview window. Double LMB click opens the study in the Series Overview.
From here choose your series and drag it in the analysis module.

2.4 Analysis

Before starting the evaluation, make sure all patient data required to calculate relevant values are present.
You can review the data in the Patient Data module.
In most cases analysis requires the definition of the heart contour or a region of interest (ROI). Therefore cmr^42 and cvi^42 provide different sets of contouring tools, to be found in the top toolbar.

- Hovering with the mouse over the tools will provide a description.
- A LMB click selects the tool.

- Icons with a star perform semiautomatic contour detection
- Icons with a little arrow provide additional options.
- To deselect tools either pick a different tool or with the LMB click somewhere in the background of the analysis window.
- In most cases, when there is a long axis reference image, you are required to determine your analysis range.
  Select the tool in the left bottom corner of the reference window and with two clicks you define the mitral valve plane, placing a third point in the apex determines the length of the LV.

2.4.1 Recommended Contouring Options

2.4.1.1 Semiautomatic Endo and Epicardial Contours for Phases or an Entire Stack in SAX

- Draw LAX LV Extent (see above)

Draw an endo- and epicardial reference contour
GETTING STARTED

a) Program your button to detect a **phase**: Open drop down menu, drag the cursor to the desired function (*Detect Epi/Endo Contours current Phase*) and release LMB. To perform the detection, click the button again. Correct contours: select contour with a double click and redraw

or

b) Program your button to perform "stack detection": Open drop down menu, drag the cursor to *Detect Epi/Endo Contours Stack*, release LMB. The detection mode has now changed, indicated by the two arrows (in reference to the grid pointing in phase and slice direction). LMB click will perform the detection.

2.4.1.2 Manually Drawn Endocardial Contours and/or Contour Correction

- **Activate Threshold Contours mode**

- **Pick the endocardial contour tool**;

  Move the cursor into the LV cavity, press LMB and drag up/down and left/right, to find the best match with the endocardial border.

  When you are done, click Freehand Draw Contours

2.4.1.3 Manually Drawn Epicardial Contours

- **First activate Click Draw Contours**

- **Next, select epicardial contour and with the LMB**

  Place points along the epicardial border

  A double click completes the contour.

  When you are done, click the pencil again to leave the mode
3  Set Up

3.1 How to Define a Protocol

3.2 Protocol Examples

3.3 Customize Tools and Working Modules

The definition of protocols allows for setting up a workflow according to standardized image acquisition protocols. This can be done for several clinical indications and they can be named accordingly.

Once this has been done you can hide the protocol list (Display on Mouse Hovering) and switch to the next module with the arrows located on the top left corner.

In addition to being faster, it provides guidance for inexperienced user.

3.1 How to Define a Protocol

- **Generate a new protocol:**
  1. Open the drop-down menu next to Protocol selection.
  2. Choose New and type in the protocol name. Hitting the return key will enter the new name and clear the list.
  3. Go to Add and select your modules.

- **Rearrange modules** via drag and drop

- **Rename a module** with a double LMB click on the name (e.g. change "Tissue Characterization" into "Infarct")

- **Delete a module** with the Delete button (bottom right)

- Tip for setting up multiple protocols at once: Save some time by duplicating and renaming lists. Go to the menu click Duplicate, Next Rename. Type in a new name and click enter-key,
SET UP & CUSTOMIZATION

Add, delete, rearrange or rename modules.

- **Publish your protocol:** Mark protocols that shall be visible to other users on the same server as "Public"

- **Automate protocol selection:** If you are using standardized image acquisition protocols, you can link your cvi42 protocol to the scanning protocol. Open a standard e.g. AMI sequence, set up a post-processing protocol, open the menu and choose "typical". The next time you open an AMI sequence that exact protocol with all the defined presets will pop up.

- **Reset typical studies:** This removes all recorded study characteristics for the respective protocol and allows to start selecting typical studies from scratch.

### 3.2 Protocol Examples

**Myocardial Perfusion and Viability**

- Series Overview
- Viewer
- Patient Data
- Short 3D
- Perfusion
- Tissue Characterization

**C-M-P: Cardiomyopathy/Myocarditis/Pericardium:**

- Series Overview
- Patient Data
- Viewer
- Short 3D or Multiple Long LAX
- Tissue characterization

**Valvular**

- Series Overview
- Viewer
- Patient Data
- Short 3D or Multiple Long LAX
- Flow
3.3 Customise 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 e.g. greyzone analysis.

The following modules don’t 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. Everything that is now highlighted in green and has a little circular off button in the right lower corner of the frame can be turned on or off. You can hide single buttons or entire groups of buttons. They will be hidden in all your protocols
4. Hovering with the mouse over the buttons will display a tool tip
5. De-activated functionality is highlighted by a purple frame
6. To reactivate click on the X
7. To return to default click
8. Save your selection by clicking the wrench again.

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

will be available in the Context Menu, when disabled in the Protocol.
4 Working with Multiple Monitors

4.1 Set up your displays

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

4.2 Activate multiple screen functionality

In cvi, go to the Preferences>Appearance >Startup View and check Use Multiple screens click ok
Quit cvi 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

![Main screen and Patient List module](image1)

- **Patient List** module icon in the top tool bar

![Main screen and Second screen](image2)

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
  5.1.1 Viewer Overlays, Annotations
  5.1.2 Sequence Parameter

5.2 Image Editing, Viewer Controls
  5.2.1 Panning
  5.2.2 Windowing
  5.2.3 Main Viewer Controls Table
  5.2.4 Shortcut and modifier keys
  5.2.5 Context Menu Table

5.3 Additional Viewing
  5.3.1 Floating Viewer
  5.3.2 Reference Viewer
  5.3.3 4D Visualization Viewer
    5.3.3.1 Mesh Model Options

5.4 Compare Two Studies

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.

More parameters are available in Image Database/Extended View

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 Image Editing, Viewer Controls

5.2.1 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.

5.2.2 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:

```
Add Current Window
Remove Windows
Current Window Default
Reset Default Window
Reset All Default Windows
```

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%).

### 5.2.3 Main Viewer Controls Table

<table>
<thead>
<tr>
<th>ICON</th>
<th>FUNCTION</th>
<th>MOUSECLICKS</th>
<th>ALTERNATIVE</th>
</tr>
</thead>
<tbody>
<tr>
<td><img src="image" alt="Windowing Icon" /></td>
<td>Windowing</td>
<td>Window: push mouse wheel and drag</td>
<td>Windowing presets: keyboard keys 1-2-3-0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Auto adjust: double click MMB</td>
<td>Windowing presets: context menu</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Holding shift-key+LMB and drag</td>
<td>Define your own preset via <em>Edit</em> in the context menu</td>
</tr>
<tr>
<td><img src="image" alt="Panning Icon" /></td>
<td>Panning</td>
<td>Hold LMB down and pan</td>
<td></td>
</tr>
<tr>
<td><img src="image" alt="Zooming Icon" /></td>
<td>Zooming</td>
<td>Scroll mouse wheel</td>
<td>Move cursor to the right frame border until symbol appears; LMB drag up/down</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Context menu: Image/Auto adjust Zoom</td>
</tr>
<tr>
<td><img src="image" alt="Cine Mode Icon" /></td>
<td>Cine mode</td>
<td>LMB click</td>
<td></td>
</tr>
<tr>
<td><img src="image" alt="Navigation Icon" /></td>
<td>Navigation</td>
<td>Open on-screen navigation buttons</td>
<td></td>
</tr>
</tbody>
</table>
| ![Scroll Through Phases/Slices and Series Icon](image) | 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        |
### Shortcut and modifier keys

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

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

<table>
<thead>
<tr>
<th>CONTEXT MENU</th>
<th>COMMAND</th>
<th>DESCRIPTION</th>
</tr>
</thead>
<tbody>
<tr>
<td>Undo</td>
<td>⌃Z</td>
<td>Deletes last action e.g. last drawn contour</td>
</tr>
<tr>
<td>Redo</td>
<td>⌃Y</td>
<td>Retrieves deleted action</td>
</tr>
<tr>
<td>Copy Contour</td>
<td>⌃C</td>
<td>Copies a selected contour</td>
</tr>
<tr>
<td>Paste Contour(s)</td>
<td>⌃V</td>
<td>Pastes previously copied contours</td>
</tr>
<tr>
<td>Delete Contour</td>
<td>⌃X</td>
<td>Deletes a selected contour (double click)</td>
</tr>
<tr>
<td>Copy/Forward</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Copy All Contours</td>
<td>⌃A</td>
<td>Copies all contours that are drawn on the selected image</td>
</tr>
<tr>
<td>Forward Contour (Slice)</td>
<td>⌃F</td>
<td>Forwards a selected contours across all phases</td>
</tr>
<tr>
<td>Forward All Contours (Slice)</td>
<td>⌃E</td>
<td>Forwards all contours of a selected slice across all phases</td>
</tr>
<tr>
<td>Delete</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Delete All Contours</td>
<td>⌃⌫</td>
<td>Deletes all contours in the active frame</td>
</tr>
<tr>
<td>Delete Contour (Slice)</td>
<td>⌃D</td>
<td>Deletes a selected contour in all phases per slice</td>
</tr>
<tr>
<td>Deletes All Contours (Slice)</td>
<td>⌃M</td>
<td>Deletes all contours in one slice across all phases</td>
</tr>
<tr>
<td>Delete Contour (Phase)</td>
<td>⌃O</td>
<td>Deletes a contour in all slices of a selected phase</td>
</tr>
<tr>
<td>Delete All Contours (Phase)</td>
<td>⌃P</td>
<td>Deletes all contours in all slices of a selected phase</td>
</tr>
<tr>
<td>Delete Contour (Series)</td>
<td>⌃O</td>
<td>Deletes a selected contour within a series</td>
</tr>
<tr>
<td>Delete All Contours (Series)</td>
<td>⌃P</td>
<td>Deletes all contours of the selected series</td>
</tr>
<tr>
<td>Contours</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Smooth Contour</td>
<td>⌃S</td>
<td>Smoothes a shivery contour</td>
</tr>
<tr>
<td>Round Contour</td>
<td>⌃L</td>
<td>Contour will assume a round shape</td>
</tr>
<tr>
<td>Derive Cardiac Contours</td>
<td>⌃L</td>
<td>Existing contours in short axis can be retrieved in other series</td>
</tr>
<tr>
<td>Derive Cardiac Contours Phase</td>
<td>⌃L</td>
<td>Existing contours in short axis can be derived for an entire phase</td>
</tr>
<tr>
<td>Forms - Tools for planimetry</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Freehand</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Line</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Box</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Circle</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Annotate</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Annotation Text</td>
<td></td>
<td>Type in text</td>
</tr>
<tr>
<td>Annotation Arrow</td>
<td></td>
<td>Point out a structure with an arrow</td>
</tr>
<tr>
<td>VIEWER CONTROLS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>-----------------</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Annotation Arrowhead</strong></td>
<td>Point out a structure with an arrowhead</td>
<td></td>
</tr>
<tr>
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<td>Point out a structure by encircling it</td>
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<tr>
<td><strong>Display Contours</strong></td>
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<td><strong>Display Text Annotations</strong></td>
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<td><strong>Edit</strong></td>
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<tr>
<td>Add Current Window</td>
<td>Adds a custom window preset to the menu</td>
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<td>Allows to remove one or all custom presets</td>
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<td>Current Window Default</td>
<td>Sets the window as a default for the chosen image type</td>
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<td>If there are multiple defaults they will be reset</td>
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<td><strong>Export As</strong></td>
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<tr>
<td>Export Image</td>
<td>Opens a window that allows the user to save the active frame to a different location</td>
<td></td>
</tr>
<tr>
<td>Export Image Multiview</td>
<td>Exports the images in a multiview format and displays them all at once side-by-side</td>
<td></td>
</tr>
<tr>
<td>Copy Image To Clipboard</td>
<td>Copies the image and allows the user to paste it into any other application</td>
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<tr>
<td>Export Cine Current Slice</td>
<td>Exports the cine of a selected slice to a new file as AVI movie</td>
<td></td>
</tr>
<tr>
<td>Export Movie All Slices Multi View</td>
<td>Exports all slices and phases of a selected cine as one movie file (AVI)</td>
<td></td>
</tr>
<tr>
<td><strong>VIEWER CONTROLS</strong></td>
<td></td>
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<tr>
<td>---------------------</td>
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<tr>
<td><strong>Export Movie All Slices Stacked</strong></td>
<td>Separates the slices of a cine and exports them as a sequential stack of movie files (AVI)</td>
<td></td>
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<tr>
<td><strong>Add Current Series To Case Review</strong></td>
<td>Adds a complete series to the case review in the Patient-Data module</td>
<td></td>
</tr>
<tr>
<td><strong>AddFrameToReport</strong></td>
<td>Adds the active frame to the report</td>
<td></td>
</tr>
</tbody>
</table>

### 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 grayscale (negative image) |
| **Display Overlay** | Displays existing color-coded overlays e.g. LE |
| **Display Cursor Signal Intensity** | Display of SI in accordance 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

| **Clear Frame** | Removes image from frame |

### Show DICOM Dump

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

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

### 5.3 Additional Viewing

#### 5.3.1 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.

- **Provides a cross reference**

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.

5.3.2 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.
5.3.3 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.

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<tr>
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<th>SHORTCUT</th>
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<td>Display Volume Frame</td>
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<td>Export Image</td>
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<td>Save Rotation Images</td>
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### Mesh Model Options

<table>
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<th>MESH MODEL Options</th>
<th>Description</th>
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<tr>
<td><img src="Image" alt="Short 3D Model" /> <img src="Image" alt="Tissue Char. (Late Enh.) Model" /> <img src="Image" alt="Tissue Char. (T2) Model" /> <img src="Image" alt="Perfusion (Rest) Model" /> <img src="Image" alt="Display Mesh Model" /></td>
<td>Choose a set of contours to create a 3D Model</td>
</tr>
<tr>
<td><img src="Image" alt="Wall Thickening" /> <img src="Image" alt="Wall Motion" /> <img src="Image" alt="Wall Thickness Diastole" /> <img src="Image" alt="Wall Thickness Systole" /> <img src="Image" alt="Apply Polarmap Color" /></td>
<td>Choose the analysis to visualize, or simply click on the corresponding polar map</td>
</tr>
</tbody>
</table>
| ![Show Endocardium](Image) ![Show Epicardium](Image) ![Show RV](Image) ![Show Slice Highlight](Image) | Choose which contour to display  
D - on/off endocardial contour  
E - on/off endocardial contour |
| ![Endocardium Wireframe](Image) ![Epicardium Wireframe](Image) | Switch to a wireframe display  
Q - on/off endo wireframe  
W - on/off epi wireframe |
| ![Tissue Char. (Late Enh.) Volume](Image) ![Tissue Char. (T2) Volume](Image) ![Display Volume](Image) | Display color overlay for LGdE and T2 |
| ![Image Plane](Image) ![Image Plane 2](Image) ![Image Plane 3](Image) ![Unload Selected Plane](Image) ![Unload All Planes](Image) ![Display Image Planes](Image) | 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](Image) | Click to pan the model |
5.4 Compare Two Studies

cvi\(^2\) and cmr\(^2\) allow for the comparison of two studies side by side, even of two different modalities.

Load the first study (double-click)
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)
In the Series Overview Module, both studies will be shown side by side.
In the Viewer Module click on the Primary Study tab above the thumbnails and select your images for viewing
Go to the Secondary Study tab and make your selection. Images from the secondary study are highlighted with an thicker frame
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

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POST-PROCESSING

- 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 angle 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;
- for 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)

Start with selecting the contouring mode,

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 an 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 cmr$^{42}$ and cvi$^{42}$ (Clinical Report)

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<td></td>
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<tr>
<td>LV EDV</td>
<td>(ml)</td>
<td>End diastolic volume</td>
</tr>
<tr>
<td>LV ESV</td>
<td>(ml)</td>
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</tr>
<tr>
<td>LV SV</td>
<td>(ml)</td>
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<td>LV EF</td>
<td>(%)</td>
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</tr>
<tr>
<td>LV EDV/H</td>
<td>(ml/cm)</td>
<td>End diastolic volume, indexed to height</td>
</tr>
<tr>
<td>LV ESV/H</td>
<td>(ml/cm)</td>
<td>End systolic volume, indexed to height</td>
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<tr>
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<td>(ml/cm)</td>
<td>Stroke volume, indexed to height</td>
</tr>
<tr>
<td>LV EDV/BSA</td>
<td>(ml/m²)</td>
<td>End diastolic volume indexed to body surface area</td>
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<tr>
<td>LV ESV/BSA</td>
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<td>LV MyoMass/H (syst)</td>
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<td>LV MyoMass/BSA (diast)</td>
<td>(g/m²)</td>
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<td>LV MyoMass/BSA (syst)</td>
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<td>Requires contours in all slices and phases</td>
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<tr>
<td>Peak Filling Rate (scientific report)</td>
<td>(ml/s)</td>
<td>Requires contours in all slices and phases</td>
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<td>RV EDV</td>
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<td>End diastolic volume</td>
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<tr>
<td>RV ESV</td>
<td>(ml)</td>
<td>End systolic volume</td>
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<tr>
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<tr>
<td>RV EDV/H</td>
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<td>End diastolic volume, indexed to height</td>
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</tbody>
</table>

7.3 Atrial Volumetry

<table>
<thead>
<tr>
<th>Name</th>
<th>Units</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>EDV (left and right atrium)</td>
<td>(ml)</td>
<td>Disc summation (Short 3D Module) and area lenght technique (Bi-, Tri-Planar Module)</td>
</tr>
<tr>
<td>ESV (left and right atrium)</td>
<td>(ml)</td>
<td></td>
</tr>
</tbody>
</table>

7.4 Late Gadolinium Enhancement

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

7.5 T2 Signal Intensity Analysis

<table>
<thead>
<tr>
<th>Name</th>
<th>Units</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Myocardial Volume</td>
<td>(ml)</td>
<td>Myocardial volume</td>
</tr>
<tr>
<td>Myocardial Mass</td>
<td>(g)</td>
<td>Myocardial mass (g)</td>
</tr>
<tr>
<td>Total Enhanced Volume</td>
<td>(ml)</td>
<td>Total enhanced volume</td>
</tr>
<tr>
<td>Total Enhanced Mass</td>
<td>(mg)</td>
<td>Total enhanced mass</td>
</tr>
<tr>
<td>No Reflow Volume</td>
<td>(ml)</td>
<td>No reflow volume</td>
</tr>
<tr>
<td>No Reflow Mass</td>
<td>(g)</td>
<td>No reflow mass</td>
</tr>
<tr>
<td>Enhanced Volume/Mass (relative)</td>
<td>(%)</td>
<td>Enhanced volume related to myocardial mass</td>
</tr>
<tr>
<td>Salvaged area at risk</td>
<td>(ml)</td>
<td></td>
</tr>
<tr>
<td>Manually excluded Volume</td>
<td>(ml)</td>
<td></td>
</tr>
<tr>
<td>Manually excluded Volume/Mass (rel)</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>-----------------------------------</td>
<td>-----</td>
<td></td>
</tr>
<tr>
<td>T2 Signal Intensity Ratio</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total Ratio</td>
<td>SI myocardium/SI skeletal muscle</td>
<td></td>
</tr>
<tr>
<td><strong>Per slice:</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T2 SI Ratio</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Myocardial SI + SD</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Skeletal Muscle SI + SD</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### 7.6 T1 Early Gd Enhancement

<table>
<thead>
<tr>
<th>Myocardial Early Enhancement</th>
<th>(%)</th>
<th>Mean SI and standard deviation in T1</th>
</tr>
</thead>
<tbody>
<tr>
<td>EGER</td>
<td>Early Gadolinium Enhancement ratio: myocardial enhancement/skeletal muscle enhancement</td>
<td></td>
</tr>
<tr>
<td><strong>Per slice, pre and post CA</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EGER</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Myocardial Enhancement</td>
<td>(%)</td>
<td>Myocardial SI enhancement</td>
</tr>
<tr>
<td>Myocardial SI + SD</td>
<td>Myocardial SI + standard deviation</td>
<td></td>
</tr>
<tr>
<td>Skeletal Muscle SI + SD</td>
<td>Skeletal muscle SI + standard deviation</td>
<td></td>
</tr>
</tbody>
</table>

### 7.7 Perfusion

**For Rest and Stress:**
- 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)
- Myocardial Perfusion Reserve Index (MPRI)
  - (PI (stress)/PI (rest))

### 7.8 T2*

- T2* Relaxation time (m/s)
- R² value
  - Estimation of accuracy (coefficient of determination)

### 7.9 T2 mapping

- Global and Regional Segmental T₂ time (ms)
- R² value
  - Estimation of accuracy (coefficient of determination)

### 7.10 T1 mapping

- Global and regional and segmental T₁ time (ms)
- R² value
  - Estimation of accuracy (coefficient of determination)
- ECV per slice and segment (%)
### 7.11 Flow Analysis

<table>
<thead>
<tr>
<th>Metric</th>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Forward Volume (TFV)</td>
<td>ml</td>
<td>positive + negative velocities = positive value (above x-axis)</td>
</tr>
<tr>
<td>Total Backward Volume (TBV)</td>
<td>ml</td>
<td>positive + negative velocities = negative value (below x-axis)</td>
</tr>
<tr>
<td>Total Volume</td>
<td>ml</td>
<td>TFV + TBV</td>
</tr>
<tr>
<td>Net positive Volume</td>
<td>ml</td>
<td>only positive velocities (above x-axis)</td>
</tr>
<tr>
<td>Net Negative Volume</td>
<td>ml</td>
<td>only negative velocities (below x-axis)</td>
</tr>
<tr>
<td>Regurgitation Fraction</td>
<td>%</td>
<td></td>
</tr>
<tr>
<td>Volume/min</td>
<td>ml/min</td>
<td></td>
</tr>
<tr>
<td>Volume/min effective</td>
<td>ml/min</td>
<td></td>
</tr>
<tr>
<td>Heart rate</td>
<td>bpm</td>
<td></td>
</tr>
<tr>
<td>Maximum pressure gradient</td>
<td>mmHg</td>
<td></td>
</tr>
<tr>
<td>Mean pressure gradient</td>
<td>mmHg</td>
<td></td>
</tr>
<tr>
<td>Maximum velocity</td>
<td>cm/s</td>
<td></td>
</tr>
<tr>
<td>Maximum mean velocity</td>
<td>cm/s</td>
<td>The phase with the maximum velocity out of all calculated mean (per phase) velocities</td>
</tr>
<tr>
<td>Minimum velocity</td>
<td>cm/s</td>
<td></td>
</tr>
<tr>
<td>Maximum Flow</td>
<td>ml/s</td>
<td></td>
</tr>
<tr>
<td>Minimum Flow</td>
<td>ml/s</td>
<td></td>
</tr>
<tr>
<td>Inside Ruler Volume</td>
<td>ml</td>
<td></td>
</tr>
<tr>
<td>Outside Ruler Volume</td>
<td>ml</td>
<td></td>
</tr>
</tbody>
</table>

### Comparison of two flow studies (Qp/Qs)

<table>
<thead>
<tr>
<th>Metric</th>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Difference total volume (Flow 1-Flow 2)</td>
<td>ml</td>
<td></td>
</tr>
<tr>
<td>Difference volume/min (Flow 1-Flow 2)</td>
<td>ml/min</td>
<td></td>
</tr>
<tr>
<td>Ratio Total Volume (Flow1/Flow2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ratio Total Volume (Flow2/Flow1)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ratio vol/min (Flow1/Flow2)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ratio vol/min (Flow2/Flow1)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### 7.12 Auto Plaque

<table>
<thead>
<tr>
<th>Metric</th>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>NCP Volume</td>
<td>(mm³)</td>
<td></td>
</tr>
<tr>
<td>CP volume</td>
<td>(mm³)</td>
<td></td>
</tr>
<tr>
<td>Total Plaque Volume</td>
<td>(mm³)</td>
<td></td>
</tr>
<tr>
<td>Low-density NCP Volume</td>
<td>(mm³)</td>
<td></td>
</tr>
<tr>
<td>NCP Perc</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>Low-density NCP Perc.</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>NCP Burden</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>CP Burden</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>Total Plaque Burden</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>Low-density NCP Burden</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>Parameter</td>
<td>Unit</td>
<td></td>
</tr>
<tr>
<td>-----------------------------------</td>
<td>--------</td>
<td></td>
</tr>
<tr>
<td>Dm Stenosis (Vessel Taper)</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>Minimal Luminal Area</td>
<td>(mm³)</td>
<td></td>
</tr>
<tr>
<td>Mean Ref. Dist. Stenosis</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>Area Stenosis</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>Remodeling Index</td>
<td>(FU)</td>
<td></td>
</tr>
<tr>
<td>Contrast Density Drop</td>
<td>(%)</td>
<td></td>
</tr>
<tr>
<td>NCP X-sections</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CP X-sections</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total X-sections</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Plaque lenth</td>
<td>(mm)</td>
<td></td>
</tr>
<tr>
<td>Proximal Dm.</td>
<td>(mm)</td>
<td></td>
</tr>
<tr>
<td>Distal Dm.</td>
<td>(mm)</td>
<td></td>
</tr>
<tr>
<td>Max. Stenosis Dm.</td>
<td>(mm)</td>
<td></td>
</tr>
<tr>
<td>NCP Threshold</td>
<td>(HU)</td>
<td></td>
</tr>
<tr>
<td>Peak Threshold</td>
<td>(HU)</td>
<td></td>
</tr>
<tr>
<td>CP Threshold</td>
<td>(HU)</td>
<td></td>
</tr>
</tbody>
</table>
8 Patient List

8.1 Study List
  8.1.1 Series List
  8.1.2 Image List
8.2 Study Import
8.3 Study Filter
8.4 Study Export
8.5 Delete Study or Series
8.6 Sort your Studies by Applying a Tag
8.7 Anonymize Studies
8.8 "View" Buttons
8.9 Rebuild Database
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 XYX (DICOM Node)
  - Log...

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

*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.

8.1.1 Series List

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.

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

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

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.

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.

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

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:
  cmr^42 and cvi^42 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 cmr^42 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 magifying 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.

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

Click on the respective server button on the bottom right, underneath the thumbnails.

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 nodes 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
- RMC 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
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):
   - McCarthy - Snow Trial 2014-001
   - Mayer - Snow Trial 2014-002...

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/Pseudanonymization of DICOM data sets removes all data that are selected. In addition to the DICOM information, `cmr^42` 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

- *I hope it ed View*: 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

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  9.2.1  Enter Patient Related Comments ............................................................... 63
  9.2.2  Create a Case Review Presentation ............................................................. 63
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.

Select an Image for Case Review: Select your image for review via context menu Add Current Series to Case Review or ⌘R.

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.

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

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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.

The command in the Context Menu allows adding additional images.

To review report additions, navigate to the Report module.

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

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

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

To remove warning messages from the report, go back to the analysis module and check the box in the report window:
10.2 Review the Scientific Report

For scientific purposes, cvi/cmr\textsuperscript{42} 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

![Image of 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/cmr\textsuperscript{42} 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.
10.4 Customize the Header and Generate Canned Text

cmr\textsuperscript{42}/cv\textsuperscript{i42} provides the option to customize the header and to define 'pre-canned' text modules.
10.4.1 Writing the Text File

Create a text file (see example below)
Save it with the suffix ".conf"
Copy the file (e.g. "cmr42ReportText.conf") into the Documents/cvi42 (or cmr42) folder
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
Type [InstitutionName] in rectangular brackets in the first line
Next line will be your free text: Institution name and address
[/InstitutionName] ends the command

◉ Standard phrases (example):
Type [LV function] in rectangular brackets in the first line
Next line will be your free text: e.g. Left ventricle not enlarged, no hypertrophy
[/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/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 hypokinesis
Impaired LV function with basal/midventricular/apical anterior/lateral/posterior/inferior/septal/anteroseptal hypokinesis
Severely impaired LV function with global hypokinesis

[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.

![Save options](image)

10.5.1  Save and Export the Clinical Report

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

- 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 .............................................................. 73
11.2 Features .................................................................................................. 73
   How to open a series in one of the analysis module ...................................... 74
   How to use a multiview window as an add-on viewer in other modules .......... 74
11.3 Series Composer ..................................................................................... 76
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 have to 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 navigation 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**

Select the series
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”**).
SERIES OVERVIEW MODULE

- grab the window
- detach
- scroll to the next phase or series
- play cine and change frame rate
- resize window
11.3 Series Composer

The Series composer allows to generate new manually composed series.

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 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.

For sequence information (e.g. trigger time or slice location) hover over an image.

In the Composer select the phase/slice or series and use the context menu to remove, insert or sort images.

Click Apply to assemble the newly composed series. The lower window provides a showcase for newly composed series.

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))
Plausibility check: cmr/cvi 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:
  1. same number of phases in each slice
  2. parallel slices or slices with a central rotation axis
  3. for parallel stacks:
     4. equal slice distances,
     5. sort order from basal to apical.
  6. 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

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12.2 Optimize Image Viewing.................................................................................. 79
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

- Display...
  - ClearFrame
  - Localizer...
    - DisplayLocalizer
    - DisplayLocalizerCutLine
    - DisplayLocalizerBox
    - DisplayCurrentLocalizerBox
  - Histogram...
  - Other...
    - DisplayImageHistogram
    - DisplayContourHistogram
    - DisplayPosTags
    - DisplayScale
    - DisplayWindow
    - DisplayCineTags
13 4D Viewer

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  13.1.1 4D Viewer Control Features (Table) ................................................................................. 83
  13.1.2 How to use the measurement option .................................................................................. 86
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    How to use clipping and cropping ............................................................................................. 89
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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)

<table>
<thead>
<tr>
<th>4D VIEWER SPECIFIC COMMANDS</th>
<th>SYMBOL</th>
<th>WINDOWS</th>
<th>MAC</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>High Quality</strong> (bottom left)</td>
<td><img src="image" alt="Symbol" /></td>
<td>H</td>
<td>H</td>
</tr>
<tr>
<td>Applying a shorter sampling distance while ray casting allows for capturing finer details within the volumetric data.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Spin</strong></td>
<td><img src="image" alt="Symbol" /></td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>control speed with the fps wheel in the top tool bar</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Windowing</strong></td>
<td><img src="image" alt="Symbol" /></td>
<td>+/-</td>
<td>+/-</td>
</tr>
<tr>
<td>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</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Zooming</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Use the mouse wheel to zoom in (scroll down) or out (scroll up)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Phase/Slice Navigation</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Open the navigation bar to use the on screen widgets</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Panning</strong></td>
<td><img src="image" alt="Symbol" /></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Move the cursor over the icon and drag</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Rotation</strong></td>
<td><img src="image" alt="Symbol" /></td>
<td>(S)</td>
<td>(S)</td>
</tr>
<tr>
<td>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.</td>
<td>(I)</td>
<td>(I)</td>
<td></td>
</tr>
<tr>
<td>(P)</td>
<td>(A)</td>
<td>(A)</td>
<td></td>
</tr>
<tr>
<td>(L)</td>
<td>(P)</td>
<td>(L)</td>
<td></td>
</tr>
<tr>
<td>(R)</td>
<td>(R)</td>
<td>(R)</td>
<td></td>
</tr>
<tr>
<td><strong>Aspect</strong></td>
<td><img src="image" alt="Symbol" /></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Navigator: clicking on the navigator in the bottom left corner switches to different aspects</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Segmentation</strong> (see below <em>How to do</em>)</td>
<td><img src="image" alt="Symbol" /></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### 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.

<table>
<thead>
<tr>
<th>Freehand Cut</th>
<th>Axial</th>
<th>Cylindrical</th>
<th>View</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ctrl+D</td>
<td>Shift+Ctrl+D</td>
<td>⌘D</td>
<td></td>
</tr>
</tbody>
</table>

**Freehand Crop**

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 *Free hand* drawing and *Click-Draw*.

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

**Clipping options (axial/cylindrical)**
### Context Menu 4D View Ports

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

Select the *Region of Interest*

Select one of 4 options

<table>
<thead>
<tr>
<th><strong>ROI-Heart:</strong></th>
<th><img src="image" alt="Heart" /></th>
</tr>
</thead>
<tbody>
<tr>
<td>The heart will be segmented automatically</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>ROI - User defined:</strong></th>
<th><img src="image" alt="Cutaway View" /></th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Activate the <em>Cutaway</em> button (former <em>View Clip</em>)</td>
<td></td>
</tr>
<tr>
<td>2. Activate the <em>3D Region Grow Clip</em></td>
<td></td>
</tr>
<tr>
<td>3. Point the cursor in the middle of your ROI and drag</td>
<td></td>
</tr>
<tr>
<td>4. When you are done, go to the clipping pane and click <em>Keep</em></td>
<td></td>
</tr>
<tr>
<td>5. Turn off the grow button</td>
<td></td>
</tr>
<tr>
<td>6. Optionally, add a background: <em>Context menu &gt; Rendering &gt; Background</em></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>ROI-LV</strong></th>
<th><img src="image" alt="LV" /></th>
</tr>
</thead>
<tbody>
<tr>
<td>Repeat steps 1-6</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>No Region of Interest</th>
<th><img src="image" alt="Original Volume" /></th>
</tr>
</thead>
<tbody>
<tr>
<td>Will display the original volume</td>
<td></td>
</tr>
</tbody>
</table>
13.1.5 Manual Segmentation

The toolbar offers cutting, cropping, and growing tools.

**How to use clipping and cropping**

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

- **Cut**: Drag the mouse cursor to encircle structures you would like to remove
- **Crop**: Drag the mouse cursor to encircle things you would like to keep

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.

In DVR create an image that you would like to use as background MIP via auto-segmentation, growing, clipping or cutting.

Save the segmentation by clicking *Set as Background Mask* in the DVR drop down menu.

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.

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)

Continue segmentation and click Add

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**: cmr\(^{42}\) and cvi\(^{42}\) 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.
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

- **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 cmr/cvi).

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
14.1.1 Layout
14.1.2 Phase Indicator
14.1.3 Toolbar
14.1.4 MPR Control feature
14.1.5 MPR Viewer Controls
14.1.6 Reporting and saving of image captures and measurements
   How to save, restore and clear images/measurements
   How to add multiple MPR frame sets to the report
   How to generate a short axis stack and a long axis reference:
14.1.6.1 The context menu options

14.2 "Navigation" tab
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:

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)
- Sagital 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
14.1.2 Phase Indicator

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

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:** 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 rotation 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.
MULTIPLE PLANAR REFORMATTING (MPR)

- **Panning** the MPR centre:
  Moving the center point will move the entire image plane through the 3D data

![Figure 4: Panning the MPR center](image)

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

- **Adjust the Slab-Thickness:**

  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

![Figure showing slab thickness](image)

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.

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.
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

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| Enlarge View          | Click space bar                   |

14.1.6 Reporting and saving of image captures and measurements

**How to set up categories and respective measurement lists**

- Open the menu and choose 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*.
- To remove an item, select and click the trash can.
- Lock the list when you are done.
- *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**

Select the item in the group you are about to measure.

Use the measurement tools in the toolbox of the respective MPR viewport and perform a measurement. To enlarge the image click *spacebar*.

If you wish you can label a contour in the image for future reference via *context menu/contour labels*.

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

Clear all images/measurements

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

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

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

Save a Layout View to the report

**How to add multiple MPR frame sets 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 (Multi Frame)* 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.

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

- Click *LV* automatically creates a 4 CV, 2 CV and SAO orientation.
- Double click the view port to change to the desired reference slice
- Select the *Slice Thickness* (e.g. 7 mm) and *Gap* (e.g. 3 mm)
- Set *Forward/Backward* slices and make sure to cover the entire LV.
- Check *With Ref. Images* to generate a reference image in LAO

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/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)

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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

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

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

*Trace Vessel* will segment the artery
To extract the centerline place a start and endpoint:
The system will automatically set a starting point at the proximal end of the segment.
*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.

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](image.png)

## 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

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

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

Move to the stenosis image. The contour should be generate automatically if the *Auto Vessel Lumen Contour* is still active (green).
To adjust the threshold, click the green contour label. It will open up a slider that allows to adjust the contour.

Stenosis measurements will be filled in automatically.

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.

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

In the reference viewer, click the *Endoluminal view.*

To move slowly through the vessel, drag the stenosis marker in the CPR viewer.

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.

The context menu offers, viewing, rendering, saving, export and more options.
15.4.1.4 How to perform Plaque Analysis

Load the study into the Vessel module.

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

Click on auto plaque.

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

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

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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 viewers
- Define a vessel (see above)

#### 16.1.2 Region Growing Page
Alternatively, trace a centerline via region growing. 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

- Grow the vessel by dragging on the 3D surface
- Click Clear to deleted the tracing
- Click Trace vessel, to extract the vessel

To add more segments click Grow. 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

17.2 Centerline Page
  17.2.1.1 How to generate a centerline
  17.2.1.2 How to assess calcifications

17.3 Curved MPR

17.4 Cross Section
  17.4.1.1 How to analyze the vessel
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

Trace a centreline via *Region Growing*

Activating the button...

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

A warning message will pop up if the system is not able to segment the vessels
Try to grow the vessels manually:

Point the cursor in the vessel. A black dot will appear as soon as the system detects a traceable structure. 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.

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

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

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

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

*Done* will bring you back to the centerline.

(clip off) For the reference image you have the choice to see the entire volume or (clip 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
- Turtuosity

17.4.1.1 How to analyze the vessel

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

Adjust the threshold if necessary

Add to report
18 Calcium Scoring

18.1 Toolbar

How to do Calcium Scoring
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).

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.
19 Aortic Valve

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**Intended Use**

cvi® – The Aortic Valve module 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
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 \(D_{49}\). 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

In case you have a multiphase data set, start with selecting the appropriate phase.

Display the annulus plane in the Annulus view port.

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.

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 Imaging.²

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

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19.2.1.1 How to analyze the aortic annulus

Measurements will be performed in the annulus view frame.

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

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

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 (mm$^2$, cm$^2$)

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

Click to edit the perimeter

19.2.1.2 How to save and report images and measurements

Save a stack of images as a secondary DICOM capture

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 future 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.

Save the Layout view.
19.3 Ancillary Page

19.3.1.1 How to measure the ostium height

ileged

 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**.

1. Pick up the **Ostium Height** measurement tool

 Drop a point at the height of the ostium with a left mouse click. A line measurement perpendicular to the annulus plane will be performed automatically.

2. 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

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

19.3.1.3  How to measure the sino-tubular junction

Display the junction in the oblique long axis images
Measure the diameter
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

Scrolling along the optimal viewing curve allows to display the angles in the synchronized 4D and MPR viewers.

There are preset angles that will be reported.

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


20 LV/RV Function Modules

20.1 Bi/Triplanar Module

20.1.1 LV Function Analysis
   How to do bi-triplanar LV function and volume analysis

20.1.2 Atrial Volumetry
   How to do atrial volumetry in one or two planes

20.2 Multiple Long LAX Module
   How to do LV function with multiple radial long axis

20.2.1 Ventricular volume/mass over time

20.3 Short 3D Module

20.3.1 Short 3D Interface
   20.3.1.1 Customize the interface:
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20.3.2 Global LV function and volume analysis
   How to do LV segmentation
   20.3.2.1 Automatic Segmentation
   How to do automatic LV segmentation
   20.3.2.2 Manual Definition of Systole and/or Diastole for LV and/or RV
   How to manually define systole and diastole
   20.3.2.3 Mitral Valve Plane Correction
   20.3.2.4 Exclude Atrial Volume
   20.3.2.5 Papillary Muscles
   20.3.2.6 Ventricular Volume/Mass Over Time

20.3.3 Regional Wall Analysis
   How to do wall motion analysis

20.3.4 RV function and volume analysis
   How to do manual RV segmentation
   How to do automatic RV segmentation

20.3.5 Atrial volumetry
   How to do atrial volumetry in short or long axis orientation
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

Drag and drop the series (2CV, 4CV, SAX) from the thumbnail panel into their respective frames and adjust viewer properties.

Select the slice and phase by using the navigation buttons or the arrow keys on your keyboard.

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.

Draw an epicardial contour

Propagate endo- and epicardial contours: Click on the Segment Myocardial Contours LAX in Slice button.

Repeat for both phases.

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

You have to define ventricular end-systole first, using the LV extent contour button.

Next, select the Left or Right Atrium Contour button and delineate the atrium: start at the valve, trace the atrial border and finish at the valve plane. 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.

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\(^4\) and cvi\(^4\) 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\(^4\) 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

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.

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

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.

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.

Draw an epicardial contour manually or Semiautomatic
LV FUNCTION ANALYSIS – MULTIPLE LONG MODULE

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

Repeat for all slices

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

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

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
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 to verify that the contours reflect the desired measurements before releasing final results.

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**

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.
Scroll through the phases and identify diastole and systole

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*)

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.

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.

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**

Centre your LV, so that the yellow target point is in the middle of the left ventricle.

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.
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 \textit{LAX LV Extent} contour.
  - Using the navigation buttons, select end-systole.
  - The \textit{LAX LV Extent} contour tool allows to set 3 points \textit{(= 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 \textit{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.

\textbf{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.

\textbf{Trigger edge detection}: LMB click on the automatic contour detection button will trigger the edge detection. The software will pick 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.

\textbf{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:

\textbf{How to manually define systole and diastole}

In the Option menu, check Manual Definition of Diastole and Systole.

If you can't see an Option menu, click the wrench in the protocol pane and switch on the display.

Select the phase, then RMB click on the phase-number

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

- **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).

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

  ![Mitral Valve Plane Correction](image)

  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

- **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.

- **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:

Check "Use Rounded Endocardial Contour". Using automated edge detection, the software will apply a rounded contour, cutting off trabecular structures and/or papillaries.

De-select Detect papillary muscle contours to turn off the detection of papillaries within the LV lumen (pink contour)

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.

- A click on the volume curve button will display a graph next to the study display frame.

- 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

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
     o slices do not cover the entire ventricle or
     o the gap between slices is too large for interpolation
     o there are missing contours in existing slices

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.
**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

LMB Click on the polar map will synchronize 4D Visualization and display the parameter

RMB click allows to export the polar map
20.3.4 RV function and volume analysis
How to do manual 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.

To determine the tricuspid valve plane open the 3 reference viewer and drag the applicable images into the frames.

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

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.

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)

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
Click *RV volume curve* for a time resolved volume analysis

Double-click a contour for correction. Do a right mouse-click to open a contextual contour menu.

Click the *Add to Report* button

20.3.5 Atrial volumetry

**How to do atrial volumetry in short or long axis orientation**

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".

Click on the *SAX Left Atrium Contour* tool to trace the border of the left atrium.

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**

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TISSUE CHARACTERIZATION

cmr$^{42}$ and cvi$^{42}$ 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 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 microvasular 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:

- Turn on/off view ports
- Select tool sets or buttons
- Select additional analysis such as greyzone
- Turn on/off an option menu
- Set your preferred threshold algorithm

**How to do scar and edema analysis in ischemic disease**

Drag and drop series into the frames marked “Late Enhancement” and “T2” respectively.

**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.
Choose a threshold algorithm and define a reference if needed. (see below for more detail 21.1.1.3).

- Toggle the Overlay Display to display a color overlay for scar and edema. (For T2 ratio please see below 21.1.1.4)

- Use the Exclude Enhancement contour in case of e.g. artifacts.

- Quantify MVO (see below for more information)

- Click on Display Result to view the analysis

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.

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.

**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 signal intensities.
Manual per Slice setting requires to set the threshold for each slice separately.

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.

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.

Activate the T2 Ratio Overlay.

The color will depict a ratio between 1.2 (yellow/green transition) and 2.0 (green/blue transition)

Repeat for all slices.

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

- Slice thickness ≥ 12mm
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 area is not a constant, roughly draw a contour around the region with low signal. Within the contour, only the areas with low signal 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: $2 \times SD + \text{mean SI}$ to $5 \times SD + \text{mean SI}$ of remote myocardial area

**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.
• 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%
21.2 Regional LGE and T2 analysis and assessment of transmurality

**How to do segmental scar and edema analysis**

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.

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.
TISSUE CHARACTERIZATION

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)

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 transmurality

Repeat step 1-2
Select one of the following from the drop down list
- Maximum Transmurality: 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)

To view a percentage transmurality select one of the display options below and set the transmurality percentage using the arrow keys to the right.
- Transmurality 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 transmurality >75% in black, and segments with a tranmurality <75% in green.

**How to display a greyzone polar map**

Repeat step 1-2

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


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 (hyperemea)
- Microvascular Obstruction
- Intracardiac Thrombus

**How to do contour definition in Early Enhancement images**

Draw endocardial and epicardial contours in T1 pre and post contrast images.

Define a skeletal reference

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.

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

\[
\frac{\text{SI(nach Gd)} - \text{SI(vor Gd)}}{\text{SI(vor Gd)}} \times 100
\]

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 ≥ 10mm
- 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\textsuperscript{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\textsuperscript{b}.
2. Increased global myocardial early gadolinium enhancement ratio between myocardium and skeletal muscle in gadolinium-enhanced T1-weighted images\textsuperscript{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")\textsuperscript{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.

\textsuperscript{a} The clinical suspicion for active myocarditis should be based on the criteria listed in table 5.

\textsuperscript{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.

\textsuperscript{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 ≥45% is consistent with myocarditis.

\textsuperscript{d} Images should be obtained at least 5 minutes after gadolinium injection; focal 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.

Friedrich et al., J Am Coll Cardiol 2009
22 T2* Module

22.1 Assessment of T2* Times

22.1.1 Customizing the module to your needs
22.1.2 How to do T2* Analysis
22.1.2 Options Menu
**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  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**

For global T2* times, draw an endocardial and an epicardial contour for the assessment of global T2* values.
Draw a ROI contour in the septal wall for regional T2* values.

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: $52 \pm 16$ ms
- Reduced: cutoff: 20 ms
- Severe: $<10$ ms


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

<table>
<thead>
<tr>
<th>T2/T2*</th>
<th>Color</th>
</tr>
</thead>
<tbody>
<tr>
<td>0 - 10 ms</td>
<td>Dark red</td>
</tr>
<tr>
<td>0 – 25 ms</td>
<td>Red</td>
</tr>
<tr>
<td>25 – 40 ms</td>
<td>Yellow</td>
</tr>
<tr>
<td>40 – 55 ms</td>
<td>Green</td>
</tr>
<tr>
<td>55 – 80 ms</td>
<td>Blue</td>
</tr>
<tr>
<td>80 ms and above</td>
<td>Blue</td>
</tr>
</tbody>
</table>

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.

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.

22.1.2 Options Menu

○ Error Threshold Options
  • Exclude $R^2$: The coefficient of determination indicates the strength of the correlation between the curve fitting logarithm and the data points (default is 0.7). $R^2$ should be > 0.99
  • Max Error: Adjusting the error tolerance changes the allowed maximum error of the $T^2*$ times, for which the result of the fitting should be displayed (default 100%). When the $T^2*$ 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 $T^*$ 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.
# T2 Mapping

## 21.1 T2 Measurements

How to do a T2 analysis

## 21.1.1 T2 Options menu

How to apply a motion correction to T2 series

## 21.1.2 Motion Correction

How to apply a motion correction to T2 series

## 21.2 T2 Map

How to analyze T2 maps
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
- T2 Measurements: that allow for the assessment of T2 times
- 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.

Global and regional T2 times will be calculated immediately.

The decay curve will be displayed. A right mouse click in the graph allows to change the display or to export the graph.
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). \( R^2 \) 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**

Make sure you have endo- and epicardial contours in all images.

After forwarding, correct contours.

- Set the Segmentation point.

Select the image with the best contrast and enter the phase that you would like to use for the registration.
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. 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**

Drag and drop the map from the thumbnail panel into the respective window.
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. Derive existing contours from the T2 measurement via context menu > Derive Contours Phase. Alternatively, draw new contours.

Set a segmentation reference point.

To add the polar map to report export the image via context menu and import into report. The values can be found in the scientific report.
24 T1 Mapping and ECV quantification

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Note: Due to a lack of standardization, this module is for research only.
24.1 Module layout

Analysis options are organized in pages

- **T1 Native**: T1 values and recovery curve for global and/or regional myocardium
- **T1 CA**: s.a. post contrast
- **T1 Map Native**: T1 and R² maps and a segmental polar map display (1-100 or AHA)
- **T1 CA**: s.a. post contrast
- **ECV/λ**: Polar maps and global/per slice ECV and partition coefficient (λ) quantification.
24.2 T1 Analysis (native and post contrast)

How to load various sequences

Since the algorithm for the calculation of T1 times differs from sequence to sequence, it is important that your data set matches the chosen algorithm.

Choose from the menu at the bottom of the screen

Select the series from the thumbnail panel. Hovering over the thumbnail will provide a series description. Drag it into the analysis window.

If the series is rejected, it could have been due to one of the following reasons:

- The last image of the series actually is a scanner generated map (Siemens). Solution: In the option menu, check the box for Skip Last Slice Image
- In the DICOM header the TI time is encoded in the field for the Trigger Time (Philips). 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, 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. You will find the scaling factor in your Siemens documentation; otherwise consult your Siemens representative. In the Option menu (where you selected the sequence) you can enter the correction factor. This will eliminate any deviation. Alternatively, use Siemens-generated maps.

How to do global or regional T1 analysis

For global T1 values, draw endocardial and an epicardial contours. Forward the contours via context menu Forward All Contours Slice (short-cut: ⌘E/ctrl E)
For regional analysis, select one of the ROI contours. This contour can be forwarded via toolbar button.

Repeat for all slices.

Global, regional T₁ Relaxation times and R²-values will be shown in the result frame.

The T₁ recovery curve will be presented in the frame below.

RBM click in the graph opens a Context Menu

You can adjust the error and threshold and the curve fitting in the options (see options).

Create DICOM map. Make sure you have set $R^2$, Max. Error and the Noise Limit appropriately.

Click the button in the toolbar.

In addition to the grayscale map a $R^2$ map will be created. You will find both maps, combined in one series, appended to your thumbnails.

Automate DICOM map generation: In the option menu, check the box for Create map upon loading and save this step to your protocol.

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.

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

24.3 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.

Feature-based registration registers all images (pre- and post-contrast) to a selected image in the native series. Therefore, it is required to have contours in both the pre- and post-contrast series as well as in all slices.

Go to the respective pages and select the motion correction of your choice.

How to do Intensity Based Registration

Identify motion corrected series in the thumbnail panel.

Drag the series into the respective pages: T1 Native/T1 CA.

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.

Choose a phase that has good contrast between endo- and epicardial contour 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.).

In the Registration Options enter the chosen registration phases:

- Adjust Native Registration Phase for the image selected in the native series to be the reference image.
- Select CA Registration Phase for the image selected in the post contrast series, to be registered with the reference image.

Click the registration button.

The registration registers the CA Series to the Native Series. Because the series are already motion corrected and it is assumed that the native series aligns well throughout the phases - only one new series distinguishes the registration phases that were selected as follows: “Reg NativePh# CaPh# [original series description].”

If contours were drawn on the Native Registration Phase, they will be forwarded to the new registered CA series. If the registration worked well, contours should line up with the new images.

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

How to do Feature Based Registration

This registration can be used on motion and non-motion corrected series. It registers every phase in both the native and post-contrast series to a chosen reference image in the native series.
T1 MAPPING MODULE

Make sure you have accurately drawn the endo- and epicardial contours, as well as a segmentation point in all images, in pre- and post-contrast series. Due to motion, contours across the phases may not be exactly the same.

Correct contours where necessary.

Select a reference image in the native series with the best contrast and enter the phase into *Native Registration Phase*.

Click the registration button: Two new registered 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.

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.

24.4 T1 Map Analysis

You can either create a map in cvi42 or you can use the map that has been created by the scanner software. Some vendors append the map to their series. In this case, you have to remove it in the *Series Overview&gt;Compose* page Module, or you create a new one.
24.4.1 T1* maps

T1* maps will be automatically extracted from Molli, shMolli and Molli Oxford sequences. T1* maps may offer a more accurate estimation of blood pool T1.


How to analyse the T1 map

Drag the map from the thumbnail panel to the analysis window.
Alternatively, you can check the box for Create T1 Map upon loading
In the option menu adjust the Noise Limit
Draw or derive contours for a segmental analysis

Draw a blood-pool contour for ECV or λ maps.
For a color coded display, select a color map from the drop down menu or create your own LUT (see below: How to create a color Look-Up-Table)
For a segmental polar map display, place an anterior and inferior SAX Reference point.
Define the left ventricular extent in the reference window. This is an important feature for quality control and will assure that the segments and slices displayed in the polar map truly reflect the number and location of
slices. In case the slice gap is too large or a slice or contour is missing, the software will display a grey ring. The same will happen if the distance between the first acquired slice and the base is too large to be recognized as - or truly reflect the basal slice.

In the polar map frame, the number of segments per ring can be customized or you can switch to a 16-segment AHA model.

To exclude zero values (non-signals) you can set an off-set by checking Exclude Zero Values for Map Measurements.

Add evaluations (images, values and graph) to the report.
Repeat for post-contrast maps.

**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.

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

To assign a color to a T1 value, start with typing a value (T1 time) in the box.

Choose a color model: RGB or HSV (Red-Green-Blue table, or a cylindrical-coordinate color point representation, called Hue-Saturation-Value look-up-table.)

Select a color from an existing palette.

To define a custom colors, click on a 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).

To apply the color to the value click Add Value/Color.
Repeat for all values that you would like to display.

To remove a color from a value, select from the table on the left and click *Remove Selected Value*.

When you are finished, provide a description to the LUT.

Add the LUT to the protocol.

Save the protocol if you wish to use the LUT for all future series.

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 degree (0-359°). Therefore when trying to translate HSV to RGB using an color conversion app the values might be different.

24.5 ECV and lambda quantification ($\lambda$)

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 : $\lambda = \frac{\Delta R_1_{myocardium}}{\Delta R_1_{blood}}$ (where $R_1=1/T_1$)

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


**How to do segmental ECV and lambda quantification**

Make sure you have 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). Enter the hematocrit for the ECV quantification.

Add an ECV map.

For a polar map display, make sure you have defined the long axis extent in the reference frame of the T1 Map Native and T1 Map CA page.

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

**Normal Values**


<table>
<thead>
<tr>
<th>MOLLI</th>
<th>1.5 T native (m sec)</th>
<th>1.5 post contrast (m sec)</th>
<th>3T native (m sec)</th>
<th>3T post contrast (m sec)</th>
</tr>
</thead>
<tbody>
<tr>
<td>T1</td>
<td>950 ± 21</td>
<td>415 ± 113</td>
<td>1052 ± 23</td>
<td>421 ± 131</td>
</tr>
<tr>
<td>λ</td>
<td>0.44 ± 0.06</td>
<td>0.44 ± 0.06</td>
<td>0.44 ± 0.07</td>
<td>0.44 ± 0.07</td>
</tr>
<tr>
<td>ECV</td>
<td>0.25 ± 0.04</td>
<td>0.25 ± 0.04</td>
<td>0.26 ± 0.04</td>
<td>0.26 ± 0.04</td>
</tr>
</tbody>
</table>


<table>
<thead>
<tr>
<th>ShMOLLI</th>
<th>1.5 T (msec)</th>
</tr>
</thead>
<tbody>
<tr>
<td>native T1</td>
<td>962 ± 25</td>
</tr>
</tbody>
</table>

**24.6 T1 mapping Troubleshooting**

⚠️ The dataset can not be loaded

Check in the Option menu if you have selected the correct dataset.
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*

If a map is appended to the series, it can’t be loaded. Check *skip last slice image*

- There a grey ring in the polar map:
  Check that you have contours and a segmental reference point in each slice
  Check that you have defined the LV extend
  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

Reference Paper:


C. Jellis and D. Kwon. Myocardial T1 mapping: modalities and clinical applications. *Cardiovascular Diagnosis and Therapy*. 
25 First Pass Perfusion Module

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    How to do a visual perfusion analysis ......................................................................... 200
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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**

Adjust window and zoom for rest and stress series.
To set the frame rate use the wheel in the toolbar
Turn existing contours off (toolbar button)
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
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/or off the Option menu (see below)

**How to do Semi-Quantitative Perfusion Analysis**

Drag the appropriate series in the Rest and Stress frame and adjust viewer properties.
Select a phase with good contrast and draw endo- and epicardial contours
Draw endo- and epicardial contours. To copy and paste contours from rest to stress series via context menu

**Draw a Blood Pool contour, (input function) in the brightest, most homogeneous area of the blood pool.**

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.

Set the anterior and inferior segmentation reference points at the insertion of the RV to the epicardial border of the LV.

Contour Propagation: Forward all contours, including blood pool contour and segmentation point to the remaining phases.

**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 key and shift the contours with the LMB.

Choose AHA segmentation or a number of custom segments per slice or from the Options/Segments menu (see below).

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%)
Analysis of myocardial layers: Use the menu in the *Options* to generate curves of endo-, mid-, and epi-cardial layers.

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.

Apply baseline correction via context menu (RMC in the graph)

For a special region of interest, there are 4 additional contours in the top toolbar. To view the curve, check the respective ROI in the *Option* menu.

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 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 drawn ROI

**How to analyze the perfusion curves**

Clicking a data point in the perfusion curve will display the respective phase in the viewer.

To switch to an enlarged view, go to the context menu and check *Enlarged View*

Move the mouse cursor over the icon to view the curve of the respective segment.

The context menu offers several display options:

- Display standard deviation.
- Spline interpolation: Smooths 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

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

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)

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 *Aquisition 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

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   How to assess (Qp/QS) ...........................................................................................................210
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WARNING: Flow
For the analysis of velocity encoded images the utilization of vendor specific DICOM information is required. If this information is missing or not readable, the particular series will be rejected as a non-valid flow study. Measurements in series of velocity encoded images should only be done in sequences that validated for those measurements. Due to different options for the file encoding of different vendors an initial validation for the used imaging pipeline is strongly recommended.
Flow analysis (Only through plane velocity encoding)

26.1 Reported values

<table>
<thead>
<tr>
<th>Flow Analysis</th>
<th>Unit</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Forward Volume (TFV)</td>
<td>ml</td>
<td>positive + negative velocities = positive value (above x-axis)</td>
</tr>
<tr>
<td>Total Backward Volume (TBV)</td>
<td>ml</td>
<td>positive + negative velocities = negative value (below x-axis)</td>
</tr>
<tr>
<td>Total Volume</td>
<td>ml</td>
<td>TFV + TBV</td>
</tr>
<tr>
<td>Net positive Volume</td>
<td>ml</td>
<td>only positive velocities (above x-axis)</td>
</tr>
<tr>
<td>Net Negative Volume</td>
<td>ml</td>
<td>only negative velocities (below x-axis)</td>
</tr>
<tr>
<td>Regurgitation Fraction</td>
<td>%</td>
<td>ratio between total backward and total forward volume.</td>
</tr>
<tr>
<td>Volume/min</td>
<td>ml/min</td>
<td></td>
</tr>
<tr>
<td>Volume/min effective</td>
<td>ml/min</td>
<td></td>
</tr>
<tr>
<td>Heart rate</td>
<td>bpm</td>
<td></td>
</tr>
<tr>
<td>Maximum pressure gradient</td>
<td>mmHg</td>
<td></td>
</tr>
<tr>
<td>Mean pressure gradient</td>
<td>mmHg</td>
<td></td>
</tr>
<tr>
<td>Maximum velocity</td>
<td>cm/s</td>
<td></td>
</tr>
<tr>
<td>Minimum velocity</td>
<td>cm/s</td>
<td></td>
</tr>
<tr>
<td>Maximum Mean velocity</td>
<td>cm/sec</td>
<td>Value of the phase with the highest mean velocity</td>
</tr>
<tr>
<td>Maximum Flow</td>
<td>ml/s</td>
<td></td>
</tr>
<tr>
<td>Minimum Flow</td>
<td>ml/s</td>
<td></td>
</tr>
<tr>
<td>Inside Ruler Volume</td>
<td>ml</td>
<td>Using the ruler in the diagram, you can restrict the analysis to a certain range of the cardiac cycle.</td>
</tr>
<tr>
<td>Outside Ruler Volume</td>
<td>ml</td>
<td>Volume that is outside the defined range</td>
</tr>
</tbody>
</table>
26.2 Flow quantification

Postprocessing of velocity encoded images requires

- Definition of vessel contour in all phases
- Application of Background correction

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

- Toggel on/off the option to compare to series
- Select display options for the flow curves
- Display the Options to use rounded contours
- Check/uncheck the option to use a phatom correction

How to do a Flow Analysis

Drag the Phase series into the top left analysis frame, the corresponding Magnitude image will be displayed automatically in the right viewer window.

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%:

Adjust the viewer frame properties and select a reference image with good contrast and some darker pixels.

Define the vessel border, e.g. using the Threshold Segmentation mode
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.

Correct the contour: Scroll through phases to ensure the contours are correct.

Define the Anatomical Region: Either choose a custom term or pick from the drop down menu, that opens right next to the ROI contour.

Apply Baseline correction:

- 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.

Phantom corrections, check Use Phantom Correction and drag the image into the respective window,

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
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)

Perform analysis of Flow Series 1 and Flow Series 2. Define the Anatomical Region by providing a name to your ROI.

For easier reference select 2 different colors, e.g. red ROI1 contour for Series 1 and green ROI2 contour for Series 2.

Switch to the Comparison window and select the anatomical regions

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.

![1x1 Pixel](image1) ![4x4 Pixel](image2)

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 Tissue Tracking (Plug-In)

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  25.4.1 How to load and unload selected series .................................................................. 214
25.5 Perform strain analysis .................................................................................................. 214
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  25.14.1 How to display strain and displacement diagrams .................................................. 224

CMR tissue tracking allows for the assessment of left and right ventricular regional function (myocardial deformation) including circumferential, longitudinal, and radial strain/strain rate. In patients with preserved ejection fraction it is suitable to detect subtle systolic and diastolic dysfunction. In addition, it proofed to be useful to evaluate ventricular mechanics in cardiomyopathies and Congenital Heart Disease. In electrophysiology, the method might be considered to better select patients for resynchronization.
27.1 Installation

The module is a separate product and requires its own license.

It runs within the framework of cvi42 version 5 or higher (cvi42 server v5)

In cvi42 (version 5 or higher) go to the Preferences>License and request a new license.

After you have received a license, add the license and restart cvi42.

The module should be visible in the protocol pane. If you don’t see it, go to the bottom of the protocol pane and open the drop-down menu for the module selection by clicking the plus.

27.2 Analysis options and output

27.2.1 Strain analyses

<table>
<thead>
<tr>
<th>Dimension</th>
<th>Orientation</th>
<th>Strain</th>
<th>Display option</th>
</tr>
</thead>
<tbody>
<tr>
<td>2D (LV/RV)</td>
<td>long axis</td>
<td>longitudinal</td>
<td>color overlays (in the image viewer)</td>
</tr>
<tr>
<td></td>
<td>radial</td>
<td></td>
<td>polar maps (LV only)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>diagrams</td>
</tr>
<tr>
<td>2D (LV/RV)</td>
<td>short axis</td>
<td>circumferential</td>
<td>color overlays (in the image viewer)</td>
</tr>
<tr>
<td></td>
<td>radial</td>
<td></td>
<td>polar maps (LV only)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>diagrams</td>
</tr>
<tr>
<td>3D (LV)</td>
<td>short/long axis</td>
<td>circumferential</td>
<td>color overlays (in the 3D visualizer)</td>
</tr>
<tr>
<td></td>
<td>combined</td>
<td>radial</td>
<td>polar maps</td>
</tr>
<tr>
<td></td>
<td></td>
<td>longitudinal</td>
<td>diagrams</td>
</tr>
</tbody>
</table>

27.3 Output

**Diagrams**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>Strain: Radial/Circumferential/Longitudinal (%)</td>
<td>Global myocardium</td>
</tr>
<tr>
<td>Strain Rate: Radial/Circumferential/Longitudinal (%/s)</td>
<td>Per slice:</td>
</tr>
<tr>
<td>Displacement: Radial(mm)/Circumferential(deg)**/Longitudinal (mm)</td>
<td>- Global myocardium</td>
</tr>
<tr>
<td>Velocity: Radial(mm/s)/Circumferential(deg/s)***/Longitudinal (mm/s)</td>
<td>- Endo-/epicardium</td>
</tr>
<tr>
<td>Torsion (twist per unit length): Torsion (deg/cm) and Torsion Rate (deg/(cm *s)) – Global (based on apical and basal slice)</td>
<td>- AHA segments (LV only)</td>
</tr>
</tbody>
</table>

**Note:**

**+**Circumferential displacement is expressed in degrees for 2D algorithm and in mm for 3D algorithm.
+++Circumferential velocity is expressed in degrees/s for 2D algorithm and in mm/s for 3D algorithm.

**Polar maps**
- Peak Radial/Circumferential/Longitudinal Strain
- Elapsed Time to Peak Radial/Circumferential/Longitudinal Strain
- Peak Systolic/Diastolic Radial/Circumferential/Longitudinal Strain Rate
- Peak Radial/Circumferential/Longitudinal Displacement
- Peak Radial/Circumferential/Longitudinal Velocity

**Tables**
- The scientific report provides tables of the above calculated parameter, that can be copy and pasted

**27.4 Series selection and loading**

It is recommended to use SSFP cines with at least 25-30 phases. For 3D analysis short and long axis series have to have the same number of phases. This is not required if you use the LAX as a reference

**27.4.1 How to load and unload selected series**

Drag all applicable series sequentially in the analysis viewer. All slices and images will be displayed in a thumbnail grid underneath the viewer frame. To remove a series, right-click in the thumbnail grid and select *Reset Series* from the pop-up menu.

To switch back to a different loaded series, simply click in the thumbnail grid of the respective series to bring the series into view.

**27.5 Perform strain analysis**

Strain values and all the other associated quantities are defined with respect to the diastolic phase. The software will automatically determine the phase with the largest volume, based on tracking results. The user has the option to define a diastolic phase, using the context menu before running the strain analysis.
27.5.1 How to do LV 2D strain analysis in SAX

In SAX it is recommended to have at least a basal, mid-ventricular and apical slice. For the generation of polar maps an additional orthogonal long axis slice is required.

If you anticipate using an automated contour detection it is best to set the Preferences to rounded contours and de-select the option to Include Papillaries.

Load a short axis stack into the analysis frame.

Next, load a long axis series and use the *LAX LV extend* contour to define the analysis range in the same phase that you will be using for contour definition in SAX.

In the reference phase (most commonly used is end-diastole) define endo- and epicardial contours for all slices that cover the region of interest.

Basal slices in which more than 50% of the blood volume is surrounded by myocardium can be included. The software will account for the basal decent, data points that fall above the mitral valve plane will be excluded from the analysis.
For a regional analysis (polar maps) set two *SAX reference points* at the insertion of the right ventricle.

Select the reference phase by clicking on an image within that phase and click the *Perform Automatic Strain Analysis* button. Strain will be automatically computed in all slices, that contain endo- and epicardial contours.

Click the *2D Results* tab above the polar maps
27.6 How to do LV 2D strain analysis in LAX

It is recommended to have at least 3 LAX slices in total (i.e. one series with at least 3 slices or 3 series with each one slice). And one midventricular short axis slice for the generation of a polar map.

1. Sequentially load all radial long axis series into the viewer.

2. Define endo- and epicardial LAX contours in the reference phase.

3. For the generation of polar maps:
   - Load a short axis slice
   - Draw epicardial and endocardial contours in the SAX image.
   - Place an anterior and inferior RV insertion points for the polar map segmentation.
   - In addition draw a LAX Extent contour in the left ventricle.

4. Select the reference phase by clicking on an image within that phase and click the Perform Automatic Strain Analysis button. Strain will be automatically computed in all slices, that contain endo- and epicardial contours.

5. Show intersection between image planes allows for showing the intersections between the current image plane with the contours from the images orthogonal to the current image plane.
27.7 How to do RV 2D strain analysis in SAX

In SAX it is recommended to have at least a basal, mid-ventricular and apical slice. For a segmental analysis (Basal-Mid-Apical Segmentation strain curves) one additional long axis image is needed.

If you anticipate using an automated contour detection it is best to set the Preferences to rounded contours and de-select the option to Include Papillaries.

1. Load a short axis stack into the analysis frame.

2. In the reference phase define endo- and epicardial contours in all slices that cover the RV.

3. The software will display individual strain curves of existing basal, mid-ventricular and apical slices. To generate the curves:
   - Load a long axis slice of the RV.
   - Select in the same phase that you will be using for contour definition in SAX.
• Define the extend of the RV with the *LAX RV extend* contour tool, so the software can identify and allocate the position of existing short axis slices.

4. Select the reference phase by clicking on an image within that phase and click the *Perform Automatic Strain Analysis* button. Strain will be automatically computed in all slices, that contain endo- and epicardial contours.

5. Click the RV 2D Results tab to view the curves.

27.8 How to do RV 2D strain analysis in LAX

It is recommended to have at least 3 LAX slices in total (i.e one series with at least 3 slices or 3 series with each one slice)

1. Sequentially load all radial long axis series into the viewer

2. Define endo- and epicardial LAX contours. An LV extend contour is not required.

3. Select the reference phase by clicking on an image within that phase and click the *Perform Automatic Strain Analysis* button. Strain will be automatically computed in all slices, that contain endo- and epicardial contours.
4. Select an overlay and click the RV Results (2D) tab to view the curves.

27.9 How to do 3D strain analysis

1. Sequentially load short and long axis cines in the analysis frame.
2. In a LAX cine define the LV extend, which selects slices that will be included into the analysis.
3. Define endo- and epicardial LAX contours.
4. Define endo- and epicardial SAX contours in all slices that that cover the LV. Make sure not to include blood volume.
5. Define the SAX reference point at the insertion of the right ventricle in a SAX
6. Select the reference phase by clicking on an image within that phase and click the Perform Automatic Strain Analysis button. Strain will be automatically computed in all slices, that contain endo- and epicardial contours.
7. Click the 3D Results tab above the polar maps
27.10 Performance check and adjustments

1. Use the overlays to check the performance of myocardial tracking

   **Tracking Display**

   ![Tracking Display](image)

   **Track boundaries**      **Track mesh**      **Track myocardium**

   **Strain Display**

   ![Strain Display](image)

   **Radial**      **Radial**      **Longitudinal**      **Circumferential**

2. The 3D analysis offers an overlay that displays the intersection of the image plane with the tracked surface, they reflect the generated 'contours' by the 3D algorithm

   **Surface Intersection**

   ![Surface Intersection](image)

3. In addition, a menu at the bottom left of the frame allows for showing the intersections between the current image plane with the contours from the images orthogonal to the current image plane (i.e. the user drawn endo- and epicardial contours or the tracked contours by the 2D model).

   The intersection display detects misalignment and/or might serve as an aid to correct a contour.
   Misalignment due to insufficient contour registration will automatically be corrected by the software.
The 3D model displays applicable planes. Epi and endocardial intersection points in the short axis image are displayed in green and red respectively.

4. If you are not satisfied with the strain borders visible in the overlay, try to re-adjust contours or draw contours in a different phase, then re-run the strain analysis.

27.11 4D LV Visualization

27.11.1 How to view a strain cine loop

1. After the strain analysis you can view a cine loop of radial/longitudinal or circumferential strain in the 4D Visualization Viewer.

2. Click the film icon to run the movie. Cines are synchronized with the image viewer.

3. To switch to a different display, select the particular strain display from the Mesh menu. Alternatively click on the respective polar map.

Note: clicking the Polar map will only switch to a different strain display, it will not display static results, such as Peak Strain.
27.12 Regional LV Analysis

27.12.1 How to Display Polar Maps

1. To view polar maps for the different strain analyses, click the 2D or 3D Results tab. 2D Results can be viewed for AHA segments or a defined number (between 6 and 24) of ROIs. To set the number of ROIs per slice, use the drop down menu located underneath the thumbnail panels.

2. Adjust the color map for minimum and maximum strain using the menu located underneath the LAX thumbnail grid.

3. Set the value you would like to display using the drop down menu:
   - Polar maps display the following parameter for radial/longitudinal and circumferential strain
     - Peak Strain (%)
     - Time to Peak Strain (ms)
     - Peak Systolic Strain Rate (1/s) based on maximum
     - Peak Diastolic Strain Rate(1/s) based on maximum
     - Peak Displacement (mm)
     - Peak Velocity (mm/s)

27.13 How to evaluate a single segment

1. To view a specific segment in the 4D viewer check the box for Highlight Segment in 4D Visualization.
2. Double-click a segment in the polar map and view the strain of the selected segment in 4D by clicking the film icon.
3. If your diagram is set to display AHA Segments the diagram of the respective segment will be highlighted automatically.
27.14  Diagrams for Strain, Displacement and Torsion

27.14.1  How to display strain and displacement diagrams

1. Start with selecting a parameter from the drop down list:
2. Choose the region for which you would like to display the parameter:

For ROI of current slice, the number of ROIs can be in-/decreased (minimum is 6, maximum 24) using the menu on the left, located underneath the thumbnail panels.
28 Main Menu, Preferences and Configuration

26.1 Preferences

26.1.1 Appearance

26.1.2 Viewer

26.1.3 Image Database

26.1.4 Anonymization Settings

26.1.5 Series Overview Setting

26.1.6 Reporting

26.1.7 Settings for Contours, Matrix Size and Standard Deviation

26.1.8 4D Viewer

26.1.9 Network

26.1.10 License

26.1.11 Server Admin

26.1.12 LDAP Admin

26.2 Workspace Menu

26.3 Protocol

26.4 View Menu

26.5 Tools

26.6 Help
28.1 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

28.1.1 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**: cmr\textsuperscript{42} 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)

- **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

28.1.2 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 \[\text{Zoom Symbol}\]; 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
Check 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:
Check by default. If this feature is selected it is still possible to retrieve the full menu with a short-cut-key combination ⌘+RMB.
28.1.3 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/cmri42 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.

28.1.4 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.

28.1.5 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
PREFERENCES AND CONFIGURATION

- **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

28.1.6 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

28.1.7 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.
PREFERENCES AND CONFIGURATION

- **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.

28.1.8 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**

- **3D Segmentation (CT images only)**
  Regarding automatic segmentation upon loading you have the choice between heart, coronary tree or left ventricle segmentation.

- **Viewers:**
  - **Enable 4D Mesh Visualization:** When unchecked, no 3D/4D mesh model will be created.
  - **Portrait Layout:** check if preferred

28.1.9 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...
You have to define your own (provider) name = AE title. By default it is “CVI42”. 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.

**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.
Remote DICOM Notes: configure where, who and what to send

28.1.10 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

28.1.11 Server Admin
Allows for configuration of user accounts

28.1.12 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.

### 28.2 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
28.3 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

28.4 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

28.5 Tools

- **Login to server**
- **Disconnect from server**
- **Change Password**

28.6 Help

- **Manual**
- **Video Tutorials**
- **Release Notes**
- **Downloads**
29 Technical Support

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