Medis
MEDICAL IMAGING

Medis Suite MRCT 2026

User Manual

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On the Medis website, select “Products” and then the applicable product group. The user documentation can be found on that page.

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Legal Notices

Copyright Notice

Trademark Acknowledgments

Regulatory Information

Intended Use

Medis Suite MRCT is a software intended to be used for the visualization and analysis of MR and CT images of the heart and blood vessels.

Medis Suite MRCT is intended to support the following visualization functionalities:

- cine loop and 2D review
- double oblique review
- 3D review by means of MIP and volume rendering
- 3D reformatting
- performing caliper measurements

Medis Suite MRCT is also intended to support the following analyses:

- cardiac function quantification
- MR velocity-encoded flow quantification
- anatomy and tissue segmentation
- signal intensity analysis for the myocardium and infarct sizing
- MR parametric maps (such as T1, T2, T2* relaxation)

Medis Suite MRCT is also intended to be used for:

- quantification of T2* results in MR images that can be used to characterize iron loading in the heart and the liver
- MR velocity-encoded flow quantification of cerebral spinal fluid

These analyses are based on contours that are either manually drawn by the clinician or trained medical technician who is operating the software, or automatically detected by the software and subsequently presented for review and manual editing. The results obtained are displayed on top of the images and provided in reports.

The analysis results obtained with Medis Suite MRCT are intended for use by cardiologists and radiologists to support clinical decisions concerning the heart and vessels.

Indications for Use

Medis Suite MRCT is indicated for use in clinical settings where more reproducible than manually derived quantified results are needed to support the visualization and analysis of MR and CT images of the heart and blood vessels for use on individual patients with cardiovascular disease. Further, Medis Suite MRCT allows the quantification of T2* in MR images of the heart and the liver. Finally, Medis Suite MRCT can be used for the quantification of cerebral spinal fluid in MR velocity-encoded flow images.

When the quantified results provided by Medis Suite MRCT are used in a clinical setting on MR and CT images of an individual patient, they can be used to support the clinical decision making for the diagnosis of the patient. In this case, the results are explicitly not to be regarded as the sole, irrefutable basis for clinical diagnosis, and they are only intended for use by the responsible clinicians.

Limitations

Currently no limitations have been specified for Medis Suite MRCT 2026.

WARNINGS

Medis Suite MRCT must be used by cardiologists, radiologists, or trained technicians who are qualified to perform cardiac analysis. If the analysis results are used to reach a diagnosis, the results must be interpreted by a qualified medical professional. In clinical practice Medis Suite MRCT should not be used for purposes other than those indicated in the section Intended Use.

Users must have sufficient proficiency in the language of the user manual, read the user manual, and become familiar with Medis Suite MRCT to be able to obtain reliable analysis results.

Note on Monitor Aspect Ratio and Resolution

The shapes of objects and calipers displayed may get slightly distorted when the resolution is set to an aspect ratio different than the monitor's physical aspect ratio. This distortion does **NOT** affect the accuracy of measurements or analyses. To avoid distortion, set the resolution of the monitor to an aspect ratio equal to the physical aspect ratio. LCD monitors typically operate best at their native resolution. Microsoft Windows recommends a resolution when it has sufficient information to do so.

European Regulations

CE 0476	Medis Suite MRCT is qualified as a class IIa medical device. It complies with the requirements of the Dutch Medical Devices Decree (Besluit Medische Hulpmiddelen, Stb. 243/1995) and the European Medical Device Directive 93/42/EEC.

Medis Suite MRCT is registered as a medical device (class II) by the MoH in Turkey.

The ECV module has not been cleared for clinical use in Europe.

Middle East

Medis Suite MRCT complies with the requirements of MDMA and has been licensed in Saudi-Arabia as a Class II medical device.

North American Regulations

Medis Suite MRCT has been cleared for market in the United States by the FDA (Food and Drug Administration) under the provisions of Section 510(k) of the Food, Drug, and Cosmetic Act.

Caution

Federal law restricts this device to sale by or on the order of a physician.

South American Regulations

Medis Suite MRCT complies with the requirements of ANVISA and has been licensed in Brazil as a Class II medical device.

Asia-Pacific Regulations

Medis Suite MRCT complies with the requirements of the Australian Therapeutic Goods Administration and has been licensed as a Class IIa medical device.

Medis Suite MRCT complies with the requirements of the Japanese Pharmaceutical and Medical Device Law and has been licensed as a Class II medical device. The QFlow 4D, QStrain and ECV modules have not been cleared for clinical use in Japan.

Medis Suite MRCT complies with the requirements of the South Korean Medical Device Act and has been licensed as a Class II medical device.

Medis Suite MRCT complies with the requirements of AKL and has been licensed in Indonesia as a Class II medical device.

Conventions Used

The following conventions are used throughout this manual to indicate mouse and keyboard actions and to refer to elements in the user interface.

Mouse

Click	Press and release the primary mouse button. If you are left-handed, you may have set the right mouse button as your primary mouse button.
Right-click	Press and release the secondary mouse button. If you are left-handed, you may have set the left mouse button as your secondary mouse button.
Middle-click	Press and release the wheel button or the middle mouse button. If you have a two-button mouse, press and release the left and the right mouse button simultaneously.
Double-click	Press and release the primary mouse button twice.
LMB, MMB, RMB	Left Mouse Button (LMB), Middle Mouse Button (MMB), and Right Mouse Button (RMB).

Keyboard

SHIFT/CTRL+click	Press and hold down the SHIFT or CTRL key on your keyboard while you click a button or object.
CTRL+O	Press and hold down the CTRL key on your keyboard while you press O, then release both keys. This example opens the dialog window for opening a study.

Typographical Conventions

On the **Display** tab, select the **Hide all drawings** option.	Names of buttons, fields, menus, menu options, and tab names are capitalized and in bold.
View > Movie	A sequence of menu options that you select to perform a specific task, is indicated by angular brackets.
`mass.ini`	Text that you type or that appears on the screen, such as file names and file locations, is displayed in `Courier New`.

Symbols Used

	**Reference**. Points to related documentation or to related sections in the document that may be relevant in your situation.
	**Tip**. Provides helpful information or an alternative working method.
	**Note**. Brings additional information to your attention.

Caution. Tells you to be careful when performing a task.

Warning. Warns you for a potentially dangerous situation in the image representation or analysis, which may lead to incorrect results. You are advised to follow the instructions to avoid this.

Table of Contents

1 About Medis Suite MRCT

Medis Suite MRCT is Medis' software solution for the analysis of cardiac MRI and CT studies. It consists of a number of applications (apps) with specific functions: QMass, QFlow, QFlow 4D, 3DView and QStrain.

Please be aware that certain applications (or sub parts) might not be available in particular jurisdictions (see Section on Regulatory Information for information on this) or due to restrictions in the license configuration.

Its automatic contour detection enables you to perform quantitative analyses quickly and accurately. Medis Suite MRCT features MRI visualization and quantification tools for function analysis including ventricular function analysis, strain analysis, and inward displacement analysis. Next to that tissue characterization quantification tools for infarct size analysis (referred to as Delayed Signal Intensity or DSI analysis), T2w analysis, Combined T2w-DSI, first-pass perfusion analysis (referred to as time-signal intensity or TSI analysis), stress level function analysis (referred to as comparison analysis), T1 analysis, T2/T2* analysis. Further, applications for Flow analysis, including 2D flow analysis and 4D flow analysis which enables the 3D visualization and 2D quantification of 4D flow MR studies.

Medis Suite MRCT also features CT visualization and quantification tools to either reformat Computed Tomography Angiography (CTA) data, perform functional and strain analysis on that data or to perform calliper measurements on the 2D visualization.

Medis Suite MRCT must be used by qualified medical personnel or trained technicians. If the analysis results are used to reach a diagnosis, the results must be interpreted by a qualified medical professional. Medis Suite MRCT should not be used for purposes other than those indicated in the section Intended Use.

Medis Suite MRCT cannot perform the following analyses on CT reformatted data; infarct size tissue analysis, T2w analysis, perfusion analysis, T1 analysis, T2 analysis, and T2* analysis.

Automatically and manually created contours can lead to incorrect results. Make sure to review them and correct if necessary.

2 System Requirements

2.1 Hardware

Medis Suite MRCT:

- A 64 bit processor
- 8 GB RAM
- 10 GB free disk space after the software is installed
- A monitor with a screen resolution of 1.3 Megapixels (e.g. 1280 x 1024 pixel for a display ratio 4:3, 1600 x 900 pixels for display ratio 16:9)

Sentinel license server:

- A 32 or 64 bit processor
- 4 GB RAM
- 5 GB of available hard disk space

NOTES:

- All hardware must be compliant with the operating system.
- The requirement for the disk space does not take storage space for image data into account. If you want to store images on the local machine, make sure that sufficient disk space is available. Also note that client machines will cache image data from the server temporarily on the local machine.
- To view image data a dedicated graphics card supporting OpenGL and at least 512 MB memory is recommended.
- To connect your workstation with other machines in the network (e.g. a client-server configuration, or receive and send images to a remote DICOM node) a network connection will be required. A network interface card supporting at least 100 mbps is recommended.
- For the license server, a workstation with a fixed IP address or a reserved IP address in the DNS server is recommended.

2.2 Operating System

Medis Suite MRCT:

- Microsoft Windows 10, 64-bit
- Microsoft Windows 11, 64-bit
- Microsoft Windows Server 2019, 64-bit
- Microsoft Windows Server 2022, 64-bit
- Microsoft Windows Server 2025, 64-bit

Sentinel license server:

- Microsoft Windows 10, 64-bit
- Microsoft Windows 11, 64-bit
- Microsoft Windows Server 2019, 64-bit
- Microsoft Windows Server 2022, 64-bit
- Microsoft Windows Server 2025, 64-bit

3 Support

Medis is committed to offering high-quality products and services. If you have questions about the software or if you would like to make suggestions for improvements in the software or the documentation, please contact the Medis helpdesk.

If you contact the Medis helpdesk by e-mail, mention the name of the software and the version number in the subject field.

To look up the version number of your software, select the application menu by clicking  in the upper right corner of the Medis Suite window, and then **Help > About….**

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4 Medis Suite

To start Medis Suite, double-click the **Medis Suite** icon on the desktop, or select **Medis Suite** from the Windows start menu.

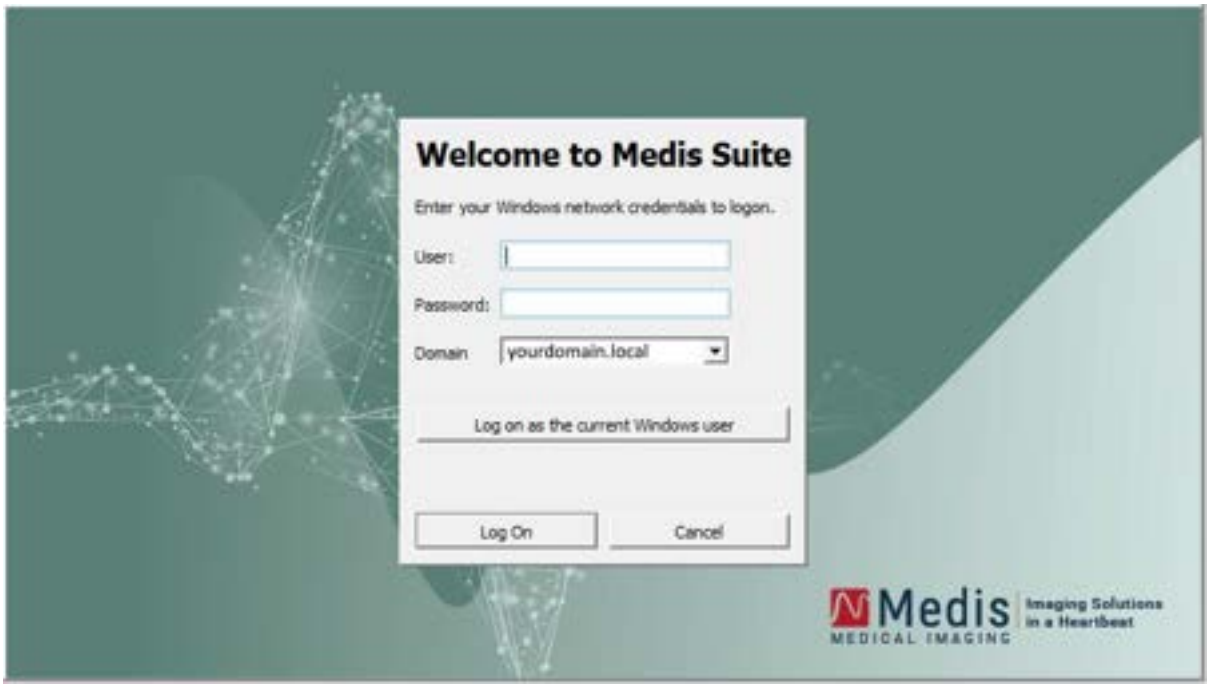
Medis Suite provides its graphical user interface in the following languages: English, German, Spanish, Italian, French, Japanese, and Portuguese.

The active language can be set in the Medis Suite options dialog (click > **Tools > Options,** and select the **General** tab). If the language of your Windows operating system is supported by Medis Suite, it will be activated automatically on the first startup.

After Medis Suite has been installed on a computer system, it must be configured with the appropriate **licenses**, and the **'post install test'** must be executed, to ensure that the system is installed and configured properly and will provide you with accurate clinical results. For more information on how to configure the licenses and how to execute the post install test, refer to the Installation Manual. Without a valid license and a successfully executed post install test, it will not be possible to load data in Medis Suite.

4.1 Logon to Medis Suite

Dependent on your Medis Suite configuration, you may have to specify your Windows username and password to log on to Medis Suite.



If the user logon to Medis Suite is enabled, and you logon to Medis Suite as a different user than the one that is logged into the Window system, be aware that mapped network drives that are available to the Windows user are not available in Medis Suite. You will not be able to import or export data from those mapped network locations.

If user logon to Medis Suite is disabled, to prevent unauthorized access to Medis Suite the Windows operating system must be configured such that no unauthorized logon to Windows can be achieved.

To prevent unauthorized access to Medis Suite, lock the Windows system or close Medis Suite when you leave the computer system. Both Windows and Medis Suite provide configuration options to lock or close automatically when they are not actively used.

While Medis Suite is running, it will use computer resources such as a license and computer memory that will thereby no longer be available for other users. To free resources and make them available for others, close Medis Suite when you are not using it. Medis Suite provides configuration options to close automatically when it is not actively used.

4.2 Role Based Access Control

Medis Suite offers 'role based access control' to some of its functionalities. Specific functionality of Medis Suite may be accessible or inaccessible for individual users that logged on to Medis Suite. Role based access control is configured by your system administrator.

The following functionalities may or may not be available for you, dependent on your role:

- General (startup, view, analyze),
- Access to advanced options,
- Import data into a repository,
- Export data from a repository,
- Delete data from a repository,
- Anonymize data from a repository,
- Export report and results,
- View and export pay per use voucher details.
- Access to shared repositories.

4.3 Licenses and Pay-Per-Use Vouchers

Your workstation needs access to licenses and/or pay-per-use vouchers in order to work with Medis Suite and the installed apps. The availability of specific application functionality may be dependent on the available licenses and/or pay-per-use vouchers.

For an overview of your current license configuration, click  > **Tools > Show available licenses…**. Select a license or a pay-per-use voucher from the overview to review its details. This includes license expiration date, other users that have claimed a license, or an overview of claimed pay-per-use tokens.

To refresh the overview of available licenses and pay per use vouchers, click  . To start the CMS License Manager application, click  . To save an overview of your pay per use vouchers, click  .

The overview of claimed pay-per-use tokens can be filtered to only show the tokens that have been claimed during a certain time period, or by specific users. To filter by time, use the available dropdown box to set a predefined date range (e.g. "Last month") or specify a custom date range. To filter by user use the available dropdown box and select the users that you want to include or exclude in the filter. To export the filtered list of claimed pay-per-use tokens, click  .

Changes to the license configuration (including installation of new licenses or pay-per-use vouchers) can only be made from the CMS License Manager application. Please contact your system administrator for additional information.

Medis Suite will show a warning when your Medis Suite license is about to expire (30 days by default) or when any of your pay-per-use vouchers is getting close to be fully redeemed (30 tokens by default). The warning thresholds can be set in the Medis Suite options.

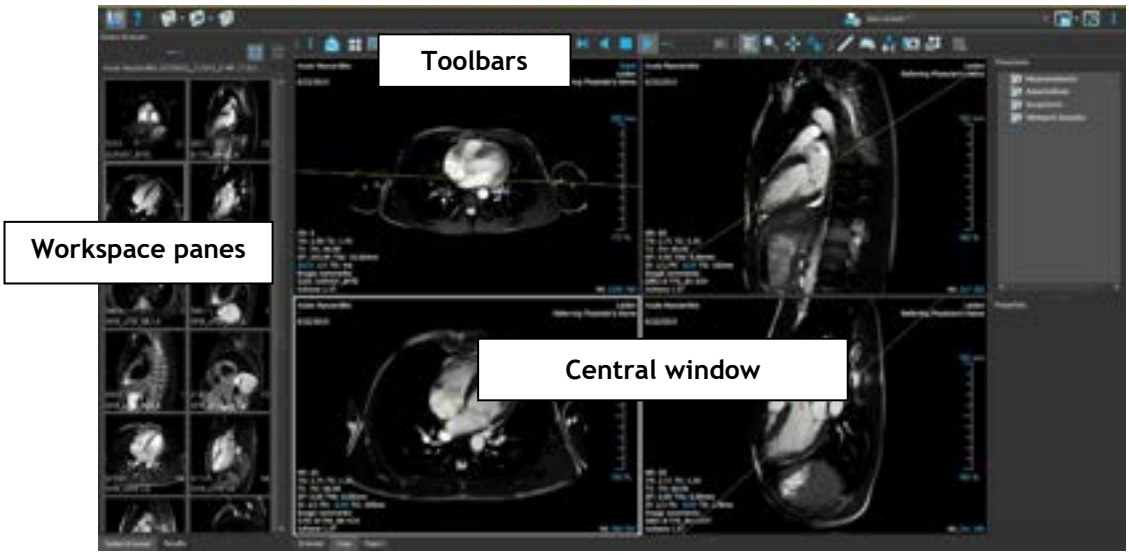
4.4 Medis Suite Workspace

This chapter covers the following topics:

- Overview
- Toolbars
- Workspace panes
- Central window

4.4.1 Overview

The main workspace of Medis Suite consists of toolbars, several workspace panes, and the central window area.



You can customize the main workspace by hiding or moving the workspace panes and toolbars. Any changes that you make to the main workspace are saved for each Windows user.

The central window area holds the **Browser**, **View** and **Report** tabs that are provided by Medis Suite. Next to that, the central window is the area where integrated Medis Suite applications will be displayed after launching them.

4.4.2 Medis Suite

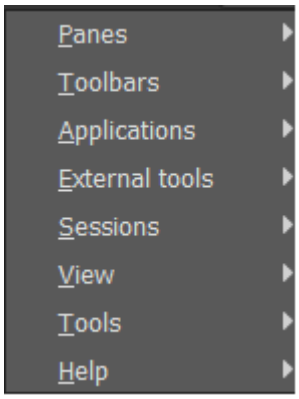
Menu

The menu contains commands to activate the functionality that you need when you are working with Medis Suite.

To make the menu visible:

- Click on the menu icon  in the **Main** toolbar of Medis Suite.

The menu commands are organized into seven main menus: **Panes**, **Toolbars**, **Applications**, **Sessions, View, Tools,** and **Help**. For some of the commands, tool buttons are available in the toolbars as shortcuts.

Menu	Command	Function
	Panes	Show or hide a workspace pane
	Toolbars	Show or hide a toolbar
	Applications	Start one of the Medis Suite apps
	External tools	Start one of external tools
	Sessions	Save or reset a Medis Suite session
	View	Change the appearance of Medis Suite
	Tools	Access to options and tools
	Help	Access to user documentation and information about Medis Suite and all installed Medis Suite apps

Toolbars

The icons in the toolbars are shortcuts to frequently used menu commands. You can move toolbars to another part of the main window. You can also show or hide toolbars.

To move a toolbar

- Click on the double-bar grip handle  of the toolbar and drag it.

  You can now move the toolbar to any location on the sides of the main window. Simply click and drag the toolbar to its new position. The position of the toolbar is saved for a next session when you close the application.

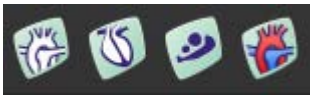
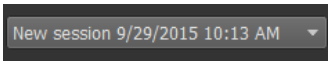
To show or hide a toolbar

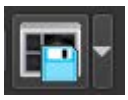
1. Select  **> Toolbars**.
2. Select a check box to show the toolbar, clear a check box to hide the toolbar.

To reset the toolbar layout

- Select  **> View > Reset layout**, or press F12.

The state of the toolbars is saved when you close the application.

Icon	Function
General Toolbar	
	Show or hide the Medis Suite workspace panes
	Show user documents of Medis Suite and installed apps
Applications Toolbar	
The applications toolbar shows buttons for all apps that are installed for advanced image analysis and/or your available licenses. Examples of apps include 3D View, QMass, QFlow, QFlow 4D, QStrain, QAngio XA and QAngio XA 3D. Some apps may provide multiple buttons in the toolbar, one for each supported analysis.  	
External tools Toolbar	
The external tools toolbar will show the icons of the external tools that are configured in the Medis Suite options.	
Main Toolbar	
	Close patient/study
	Select one of the available sessions

Icon	Function
	Save / Save as of the active session
	Reset session
	Open the menu

Workspace Panes

By default, the workspace displays two panes on the left of the application area; the **Series Browser** pane and the **Results** pane.

You can show or hide panes, dock panes, combine panes into one tabbed panel and remove panes from a panel.

To show or hide a pane

- Select  **> Panes**, and select a pane to show it. Clear its check box to hide it.

To show or hide all panes

- Click  in the **General** toolbar, or press F11 to show or hide all panes.

To dock a pane

1. Click and drag the title bar of the pane.
2. Move the pane to the sides of the main window to select one of the dock areas.

   As the pane approaches a dock area, the area is highlighted with a dotted line. The pane can be combined with another pane or inserted separately.
3. When the dock area of your choice appears highlighted, release the mouse button.

   This docks the pane into the selected position.

To combine panes into one tabbed panel

- Click and drag the title bar of the pane to the title bar of the pane with which you want to combine it.

  This creates a tabbed panel.

To remove panes from a panel

- Click and drag the title bar of the pane away from the panel.

To reset the panel layout

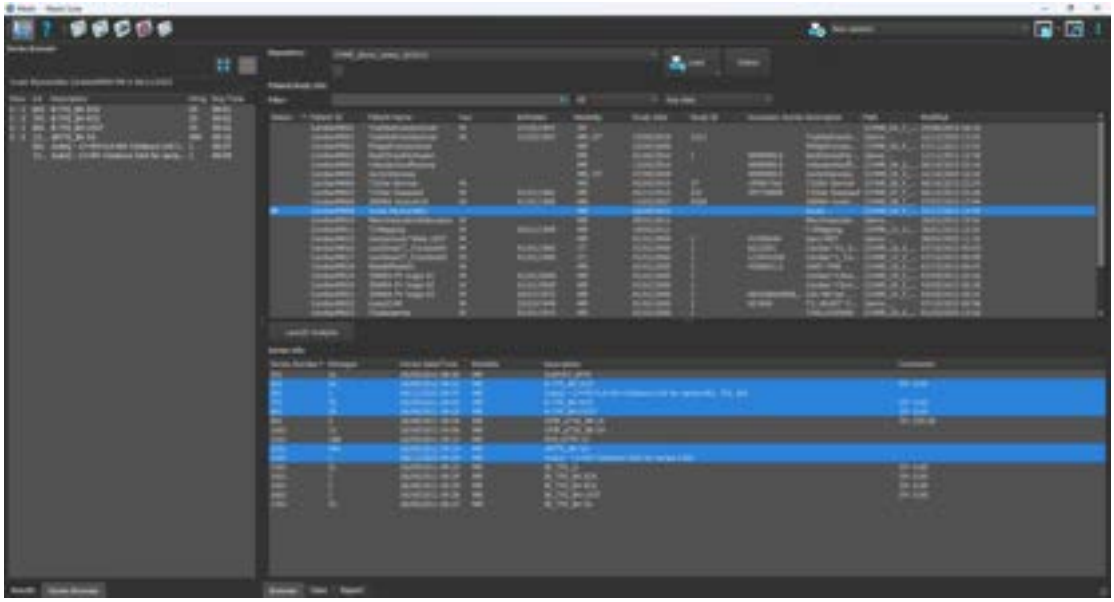
- Select  **> View > Reset layout**, or press F12.

Patient/Study – Series Info Panes

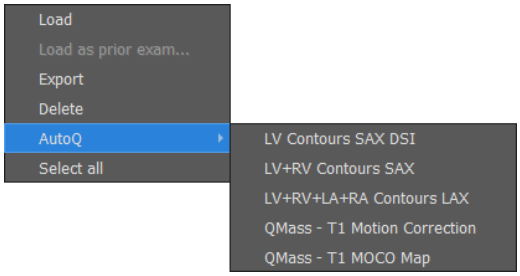
The **Patient/Study Info** pane shows an overview of the patients in the active repository within Medis Suite.

The **Series Info** pane shows an overview and detailed information of the series that belong to the active Patient/Study.

The **Info panes** show the data as combined in DICOM. The **Series Browser pane** shows the data after loading and sorting into Medis Suite.



When selecting and activating the patient-study in the Patient/Study Info, the patient is loaded in Medis Suite with all data or, when sessions are available for that Patient/Study, the last stored session will be loaded.



In the Series Info pane, the user can select and load data into Medis Suite via Drag 'N Drop or via right mouse button.

It is possible to delete data or initiate automatic contour detection on the selected data, using the context menu which is accessible via the right mouse button. It is also possible to delete data or initiate automatic contour detection on the selected data.

The progress of the contour detection can be seen in the **Status dialog**.

When the contour detection has finished the AutoQ session file will be added to the study and will be visible in the Series Info pane.

Workflows

Workflows enable starting a predefined group of applications with automatically pre-loaded data. The workflow button(s) are located between Patient/Study Info and the Series Info.

The workflow button "**Launch Analysis**", will start functional analysis applications and preload each application with corresponding data, if the data is available. The following steps will occur in Medis Suite.

- QMass will be loaded with short axis and long axis data and if available a corresponding AutoQ session file.
    - The functional short axis and long axis analysis will be started. This will result in short axis and long axis functional results in the report.
- QStrain will be loaded with short axis and long axis data and if available a corresponding AutoQ session file.
    - The strain short and long axis analysis will be started. This will result in strain short and long axis results in the report.
- QFlow will be loaded with flow data.
- The series data required for each type of analysis will be loaded in Medis Suite and shown in the Medis Suite Viewer.

Applications that have no corresponding series data will be automatically closed.

Support for custom workflows can be requested at Medis customer support.

Series Browser Pane

The **Series Browser** pane shows an overview and detailed information of the series that are loaded in Medis Suite.

The **Series Browser** pane is automatically activated when new or additional data is loaded into Medis Suite.

The **Series Browser** can present all series in image view and text view.

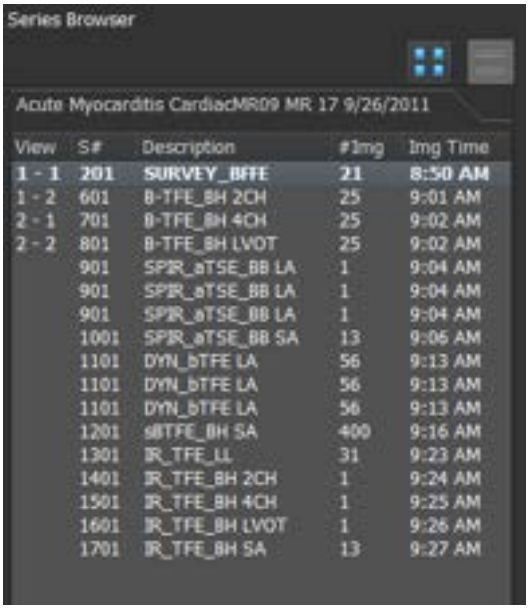
- The image view presents an overview of all series in an icon list. The overlay of each icon displays the following information:
    - The series number (e.g. S201)
    - The series description (e.g. SERVEY_BFFE)
    - The number of images contained in the series (e.g. 21)
    - The viewport in which the series is displayed (e.g. 1-2, row 1 and column 2)

When the View tab is active, the series displayed in the active viewport is highlighted with a white border. This highlight is not visible when the browser, report, or an app is active.

- The text view presents an overview of all series in a text list. Each item in the lists displays the following information:

    - The viewport number displaying the series (e.g. 1-2, row 1 and column 2)
    - The series number (e.g. 201)
    - For MR and CT series: The series description (e.g. SURVEY_BFFE)
    - For XA series: The acquisition angles (e.g. RAO 15, CRA 33)
    - The number of images contained in the series (e.g. 21)
    - The date and/or time of the acquisition (e.g. 8:50 AM)

  When the View tab is active, the series displayed in the active viewport is highlighted in bold text. This highlight is not visible when the browser, report, or an app is active.



If a series is displayed in multiple viewports, the first viewport number is displayed in the series browser, and appended with a '+' character, e.g. '1-2+'.

To activate the image view

- Click the image view icon on the **Series Browser** pane

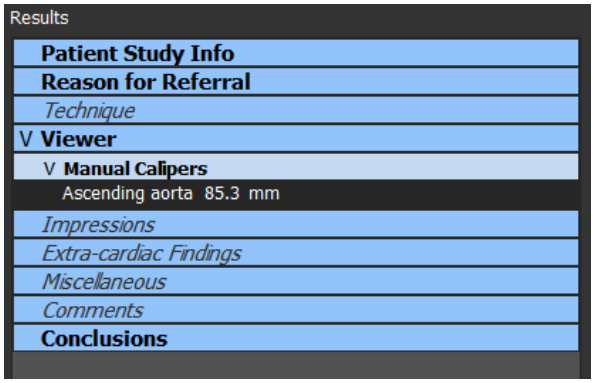
To activate the text view

- Click the text view icon on the **Series Browser** pane

Results Pane

The **Results** pane shows all results that are available for the current session of the current study. The results are gathered from the Medis Suite viewer and the running Medis Suite apps.

When Medis Suite apps are closed, their accompanying results will be removed from the Medis Suite **Results** pane and the report.



All Medis Suite results are grouped into paragraphs and sections. You can collapse and expand the sections and paragraphs of the tree by clicking “v” or “>” in the top-level nodes.

You can set the visibility of the results in the Medis Suite report from the **Results** pane.

To show or hide a result from the report

- Click on the name or any of the values of the result to toggle its visibility.

To show or hide a paragraph with all contained results from the report

- Click on the name of the paragraph to toggle its visibility.

To show or hide a section with all contained paragraphs and results from the report

- Click on the name of the section to toggle its visibility.

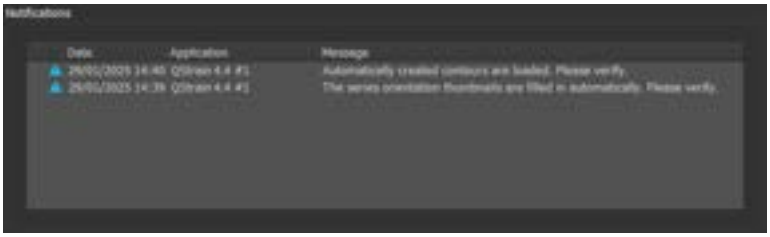
Sections, paragraphs and results that are hidden in the report, are displayed in the **Results** pane with a grayed out and italic font.

The Results pane is automatically activated when you activate the report.

Notifications

Notifications from analysis that could impact the results will be shown on the bottom right of Medis Suite. They will disappear within a few seconds. The blue notification indicator indicates that there are () or are not () notifications that have not been visited in the Status dialog.

In the status dialog all sent notifications during the lifetime of the Medis Suite instance will be collected.



Only notifications that could impact the results are shown.

4.4.3 Browser

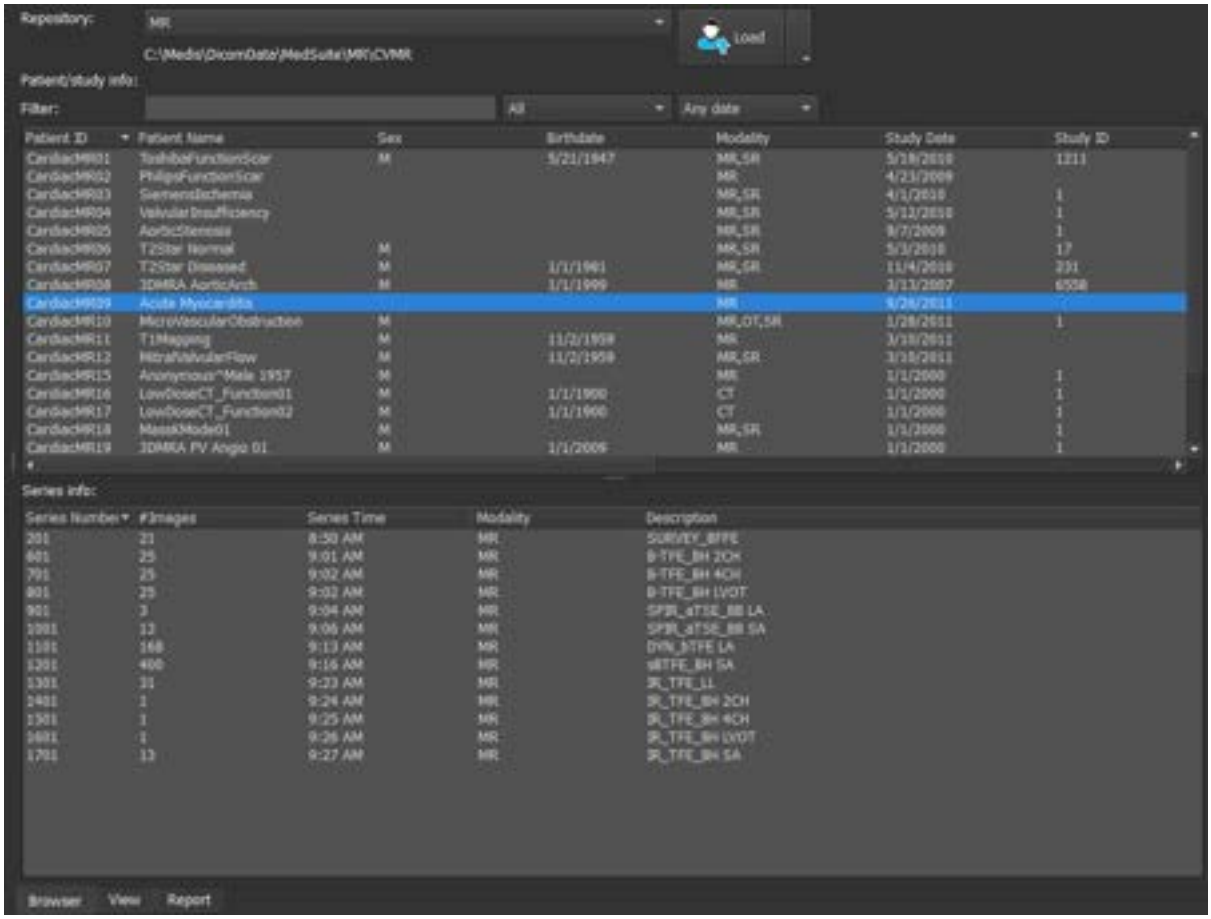
The **Browser** tab in the central window of Medis Suite provides functionality to import, view, filter, load, export, delete, and anonymize data.

Any data that you would like to process must be contained in a Medis Suite **Repository**. Local repositories are located on your local machine or network drive. Shared repositories are managed through a Medis Suite server. You can have one or multiple repositories to work with. All configured repositories are listed in the Repository drop down in the Browser.

The visibility of and access to each available Medis Suite repository can be allowed or blocked (role based access control) by your system administrator.

Export, delete, and anonymize data from a repository is functionality that can be allowed or blocked (role based access control) by your system administrator.

The Medis Suite repositories are not intended to be used for long term storage or archival of your data. Make sure that the image data, as well as the Medis Suite sessions and results are persistently stored and archived on another location, such as your PACS or VNA.



Repository configuration

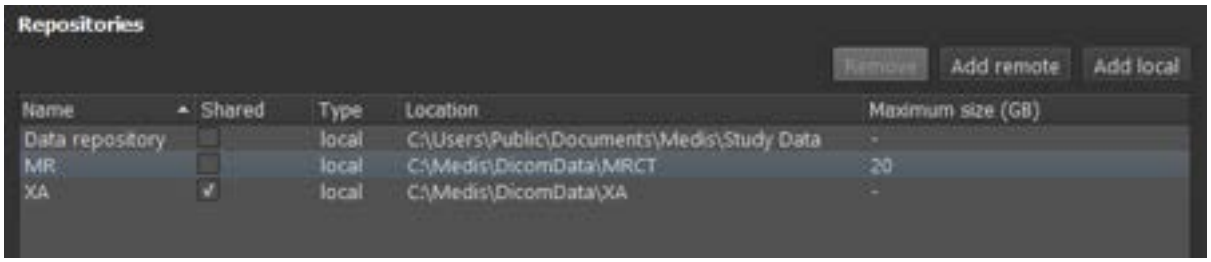
To configure the Medis Suite repositories:

- Click on the dropdown icon next to the Load button  in the Browser, and select **Configure…** This will open the Options dialog in the Repository section.
- Configure an existing repository, or add a local or remote repository.

or

- Click  > Tools > Options (or Server options for a server configuration) and choose Repository.
- Configure an existing repository, or add a local or remote repository.

Local Repository Configurations



To add a local repository:

- Click Add local to add a new repository. Click in the Location field and select "Browse…" to select the root folder of your data repository. Double click in the Name field to edit the repository name.

By default, there is no size limit on a repository, which is depicted by "-". A size limit can be configured for local repositories. If enabled, Medis Suite will clean up the repository every night by deleting the DICOM data that has not been used for the longest amount of time; recently accessed studies will remain in the repository. The cleanup will delete study by study from the repository, until the repository size meets the defined criteria. Only images will be removed, the Medis Suite sessions and results will never be cleaned and will always remain available in the repository.

To define a size restriction of a repository in gigabytes:

- Click on the field "Maximum size (GB)" and enter the number of gigabytes.

Shared Repository Configurations

When Medis Suite is installed in a client-server configuration, repositories can be shared between workstations.

On a client machine, in order to share a local repository, or to connect with shared repositories from other machines, Medis Suite must be connected to a Medis Suite server.

To connect to a Medis Suite server:

- Enter the computer name or IP address of the system that hosts the Medis Suite server.
- Test the connection by clicking the Test services button.
- Select the "Apply" button.

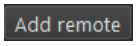
Your local repositories can now be shared with other Medis Suite workstations.

To share a local repository:

- Select the check-box in the “Shared” column of the repository list.

You can connect with remote repositories that are shared from other Medis Suite workstations.

To add a remote repository:

- Click 

to add a new repository.
- Click in the Location field and choose a repository from the list of shared repositories.

Selecting a Repository

To change the active Medis Suite repository:

- Open the Browser pane and open the repository dropdown box to see all configured repositories.
- Click on the name of the repository to activate it. For local repositories, the folder that is associated with the repository will be displayed directly underneath the dropdown box.

The Medis Suite repositories are defined and available for all users on the computer system. Which repository is activated is saved for each individual Windows user.

Import Data into Repository

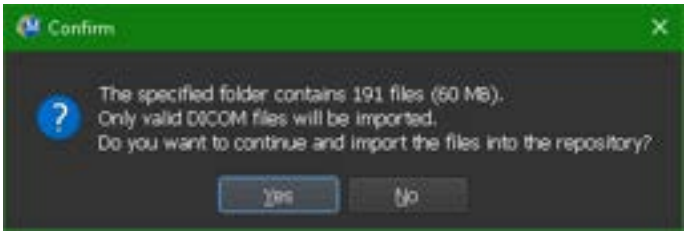
Data can be imported into the Medis Suite repository directly from the Browser. This is especially useful to import data from CD, DVD, USB, or any folder on your computer or network.

Importing data into a repository is functionality that can be allowed or blocked (role based access control) by your system administrator.

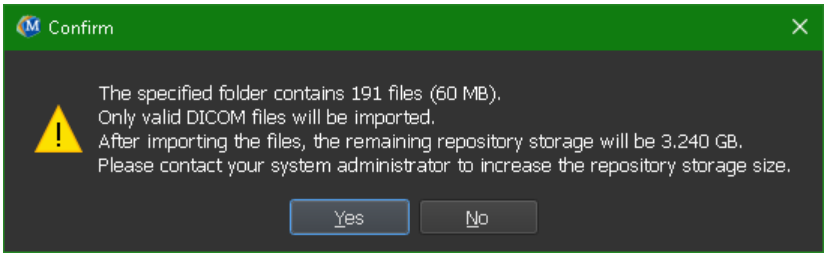
Medis Suite will automatically keep track of all files that are in your repository folders, if they are imported by Medis Suite, received by the Medis Suite DICOM connectivity module, or removed from the Browser.

To import data into the Medis Suite repositories:

- Click on the dropdown icon next to the Load button  in the Browser and select **Import…**.
- Browse to the folder you would like to import and click **Select Folder**.
- The folder and any sub-folders will be scanned to determine the number of files and the size of the data set to be imported.
- A confirmation dialog box showing the number of files and the dataset size will be displayed. The contents of this dialog box will depend on the available resources. If there is sufficient disc space available for the repository:



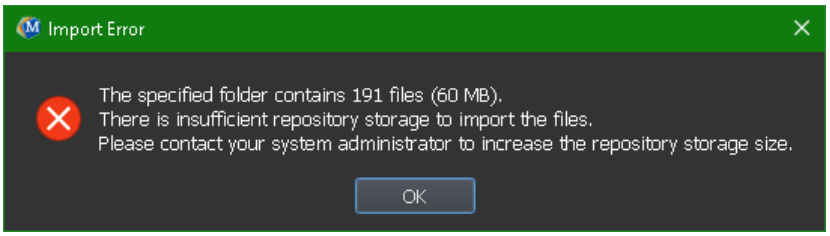
If the disk space is low, i.e. less than 10GB, but not yet critical:



In either case

  - If **No** is selected, then no further action will be taken, and you will be returned to the Browser.
  - If **Yes** is selected, then the dataset will be scanned, to identify valid[1] DICOM files. Only these files will be imported into the repository.

- If there are insufficient resources available for the import, the following dialog will be displayed:



In order to proceed with the import, extra storage must be made available.

[1] A valid DICOM file is a DICOM file that has a valid study instance UID.

- During the import, a series of messages will appear in the message box indicating the current state of the import. On completion, the number of files that were imported and ignored will be displayed:

Files that are copied into or deleted from the repository folder, for example, by using the Windows Explorer, are **not** automatically detected by Medis Suite; a rescan of the repository is required to process such repository modifications.

Rescan Repository

To rescan the files in a Medis Suite repository:

- Click on the dropdown icon next to the Load button  in the Browser and select **Rescan**. This will identify newly added or removed files.

Or,

- Press **F5** with the Browser window active. This will identify newly added or removed files.

Or,

- Press Ctrl+**F5** with the Browser window active. This will rebuild the repository.

Note: If the active repository is a remote repository, Ctrl+F5 will rebuild the repository on the remote machine. For very large repositories this operation can take considerable time and it is therefore not recommended. Only 'rebuild' the repository to fix inconsistency errors in your repository that cannot be handled by a 'rescan'.

AutoQ

Some of the Medis Suite apps provide preprocessing functionality, which is referred to as AutoQ algorithms. The AutoQ algorithms can be started manually, or automatically when data arrives in the repository.

To launch an AutoQ algorithms manually:

- Select one or multiple series in the browser.

- Right-click the selection.
- From the context menu, activate the AutoQ submenu, and the AutoQ algorithm of your choice.

The AutoQ algorithm will be started and preprocessing on the selected series will be performed as a background process without any user input. In the meantime, you can continue to work with Medis Suite.

Progress and status messages of the AutoQ algorithm will be presented in a separate tab which can be accessed by clicking on the AutoQ status button in the browser. An icon  is also shown in the status column of the browser to indicate that the AutoQ algorithm is in progress. When completed, any output of the AutoQ algorithm will be added to the series list, and can be loaded into Medis Suite.

AutoQ algorithm can be connected with rule definitions that will check new data that arrives in your repository. If the data complies to the rule definitions (e.g. 'has the data an MR short axes cine series?') the corresponding AutoQ module will be started automatically.

Medis suite itself does not provide AutoQ algorithms, they are only installed with specific apps.

Automatic startup of AutoQ algorithms is disabled by default, and can be enabled for each repository in the Medis Suite options.

If your computer is connected with a repository coordinator (referred to as the server), Medis Suite will connect with the server to provide you access to the AutoQ algorithms that are installed on that computer. When you activate the AutoQ algorithms available on the server, it will be executed there, and it will not consume resources (CPU or memory) on your local system. For AutoQ modules from the server to show up in your browser, they should also be installed on your local system.

If you don't see the AutoQ button in the browser or the AutoQ submenu in the context menu, there are no Apps installed that provide AutoQ algorithms.

Anonymization

The data contained in the Medis Suite repository can be anonymized and exported from the patient study browser.

Anonymization data from a repository is functionality that can be allowed or blocked (role based access control) by your system administrator.

To anonymize and export a patient study:

- Select one patient study in the browser.
- Right-click the selection.
- From the context menu, select Anonymize.
- Specify the desired new value for Patient Name and Patient ID.
- Set the option to export to folder, or to repository.

  When exporting to a folder, set target path for the exported anonymized data. Medis Suite will create a new sub folder in this target path with the new patient name and patient ID, to export the output files. Optionally, Medis Suite can create a zip file with all anonymized data.

  When exporting to a repository, select the repository to export to, and specify a directory name that will be used in the repository to store the anonymized files.
- Select Start to anonymize and export the data.

Anonymization will always include all data from the selected study, it is not possible to anonymize a subset of the data.

All DICOM Secondary Capture images of reports and snapshots will be excluded from the anonymization and export process, as they are likely to contain burned-in patient information.

The Medis Suite session data will be included in the anonymization process. However, snapshots and viewport layouts will be removed from the session data, as they are likely to contain burned-in patient information. Results provided by apps will only remain in the Medis Suite session data if the app can anonymize the results. In other cases, the results will be removed from the session.

Loading a Patient

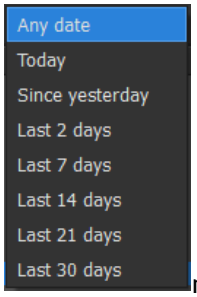
To search for a specific patient or study:

- Edit the Patient/Study info filter by entering the filter text.
- 

The Patient / Study list contents will be updated while you type.

- To filter out any specific patient or study properties, click the filter combo box (default selection: **All**) and select the column on which you would like to filter. Filter text can be cleared by clicking the blue 'X' button.

- To filter out studies on a specific date, click the study date box (default selection: **Any date)** and select the study date on which you would like to filter.



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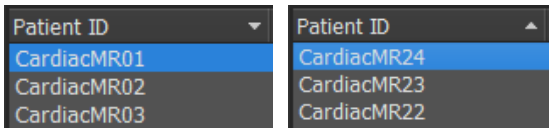
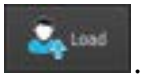
- To sort the patient / studies entries in the list, click on the header to sort in ascending (a to z) order. Click the header again to sort in descending (z to a) order.



To load a patient / study in Medis Suite:

- Select one patient / study entry in the list and click 

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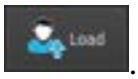
Or,

- Double click on a patient / study entry in the list.

Medis Suite can only load data of one single patient / study. Loading a new patient / study will automatically unload any previously loaded patient / study.

To load one or multiple series from a patient / study in Medis Suite:

- Select one patient / study entry in the patient / study list.
- Select one or more series in the series list
- Click 

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Or,

- Select one patient / study entry in the patient / study list.
- Double click on one or more series in the series list.

The image files that are part of a patient / study can be exported, deleted, or anonymized. To start, right click on the appropriate entry in the patient / study list, and select the Export, Delete, or Anonymize menu item.

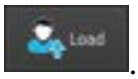
The export, delete and anonymize data from a repository is functionality that can be allowed or blocked (role based access control) by your system administrator.

Loading Prior Exams

To load prior exams of either the same or multiple patients, each prior exam is opened in a new instance of Medis Suite.

To load a Prior Exam in Medis Suite:

From the Browser, load the first study.

- Select a patient / study entry in the patient / study list.
- Select one or more series in the series list
- Click 

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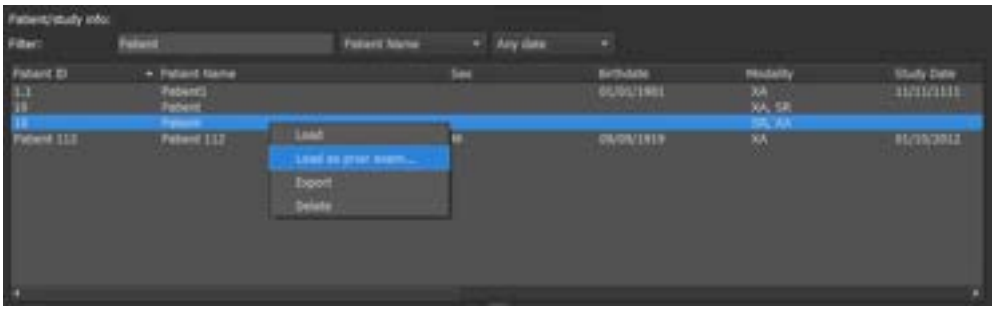
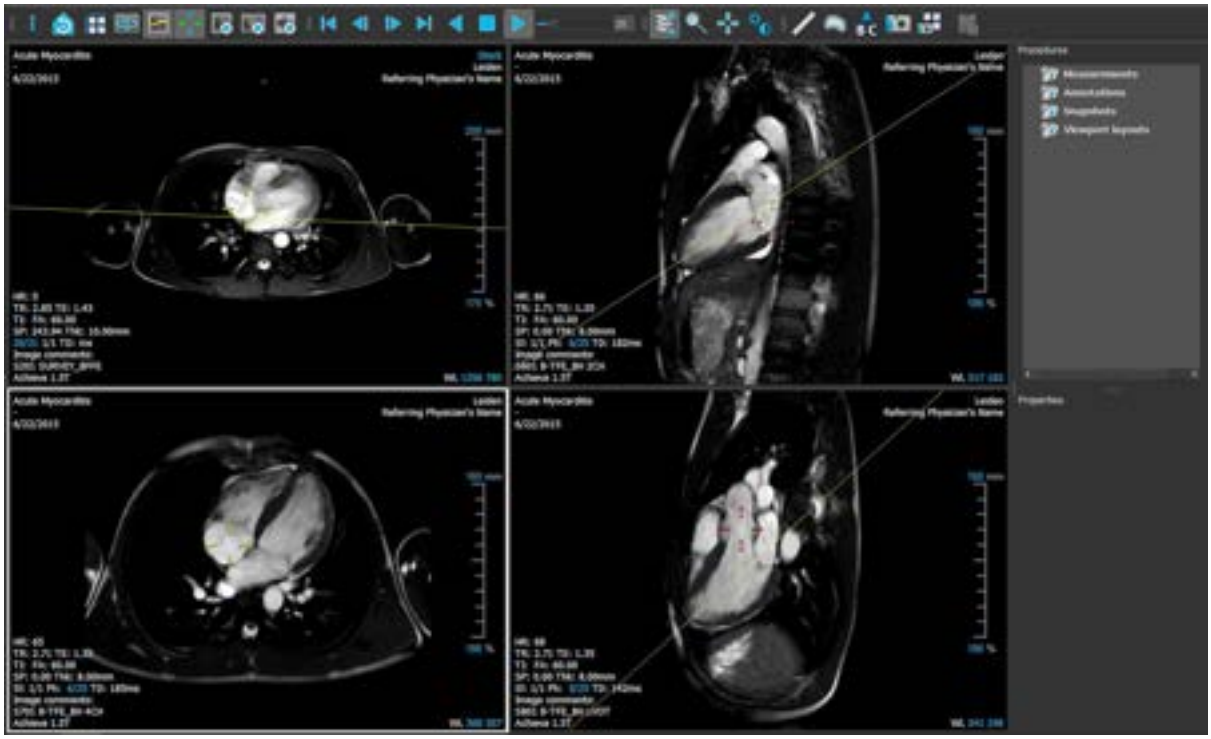
Load the next study as a Prior Exam. (This step can be repeated for multiple studies).

- Select the second / study entry in the patient / study list.
- Right-click and select “Load as Prior Exam...”



4.4.4 View

The **View** tab in the central window of Medis Suite provides the viewing functionality.



You can customize the viewer workspace by hiding or moving the workspace panes and toolbars. Any changes that you make to the viewer workspace are saved for each Windows user.

Menu

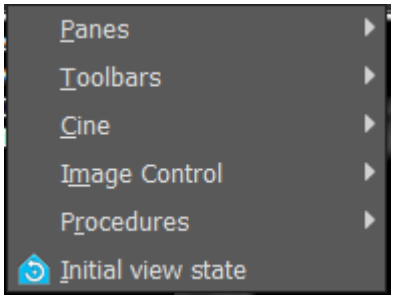
The menu contains commands to activate the functionality that you need when you are working with the viewer.

To make the menu visible:

- Click on the menu icon  in the **General** toolbar of the viewer.

The menu commands are organized into five main menus: **Panes**, **Toolbars**, **Cine**, **Image Control,** and **Procedures**, and one menu command: **Initial view state**. For some of these commands, tool buttons are available in the toolbars as shortcuts.

Menu commands may be grayed out when you are performing a procedure, such as a distance measurement. You can make the menu commands active by canceling or finishing the procedure.

Menu	Command	Description
	Panes	Show or hide a workspace pane
	Toolbars	Show or hide a toolbar
	Cine	Control the time point selection
	Image Control	Set the image control
	Procedures	Start a new procedure
	Initial View State	Reset the view state (F12)

Toolbars

You can move toolbars to another part of the main window. You can also show or hide toolbars.

To move a toolbar

- Click on the double-bar grip handle  of the toolbar and drag it.

  You can now move the toolbar to any location on the sides of the main window. Simply click and drag the toolbar to its new position. The position of the toolbar is saved when you close the application.

To show or hide a toolbar

1. Click on the menu icon  in the **General** toolbar of the viewer and select **Toolbars**.
2. Select a check box to show the toolbar, clear a check box to hide the toolbar.

Or,

1. Right-click in the toolbar area. This opens a context menu.
2. Select a check box to show the toolbar, clear a check box to hide the toolbar.

The state of the toolbars is saved when you close the application.

Icon	Function
General Toolbar	
	Show the menu
	Go to the initial view state, reset zoom \ pan \ window width \ window level
	Select the viewport layout
	Select synchronization mode
	Enable / disable cross reference line
	Enable / disable cross reference cursor
	Close active viewport
	Close all viewports
	Toggle the visibility of the image overlay
Cine Toolbar	
	Go to the first time point
	Go to the previous time point
	Go to the next time point
	Go to the last time point

Icon	Function
	Play a cine in a backward direction
	Stop the cine
	Play a cine in a forward direction
	Set the cine playback speed
Mouse Controls Toolbar	
	Stack
	Cine
	Zoom
	Pan
	Window width and window level
Procedures Toolbar	
	Calibrate the selected XA image
	Create a distance measurement
	Create an area measurement
	Create a text annotation

Icon	Function
	Create a snapshot of the active viewport
	Create a viewport layout snapshot
	Copy all measurement results to the clipboard

Workspace Panes

By default, the workspace displays two panes to the right of the viewer; **Procedures** and **Properties**.

You can show or hide panes, dock panes, combine panes into one tabbed panel and remove panes from a panel.

To show or hide a pane

- Click on the menu icon  in the **General** toolbar of the viewer, select **Panes**, and select a pane to show it. Clear its check box to hide it.

To dock a pane

1. Click and drag the title bar of the pane.
2. Move the pane to the sides of the viewer window to select one of the dock areas.

   As the pane approaches a dock area, the area is highlighted with a dotted line. The pane can be combined with another pane or inserted separately.
3. When the dock area of your choice appears highlighted, release the mouse button.

   This docks the pane into the selected position.

To combine panes into one tabbed panel

- Click and drag the title bar of the pane to the title bar of the pane with which you want to combine it.

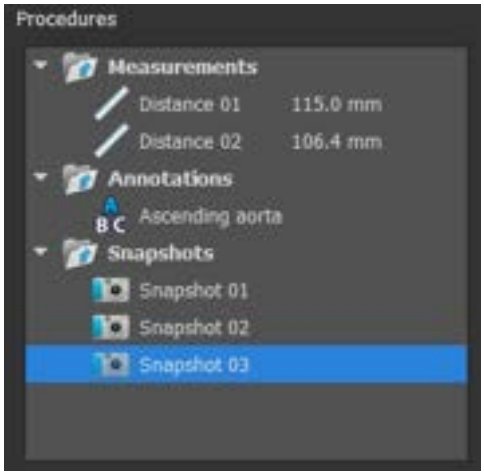
  This creates a tabbed panel.

To remove panes from a panel

- Click and drag the title bar of the pane away from the panel.

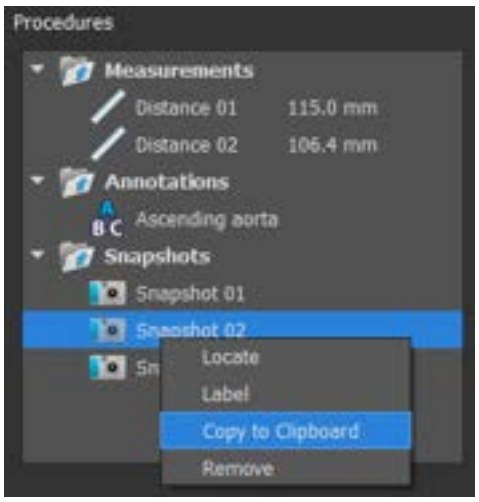
Procedures Pane

The **Procedures** pane lists the different procedures, such as, measurements, annotations and snapshots that are performed on the series that is loaded in the viewport.



You can collapse and expand the branches of the tree by double-clicking the top-level nodes.

You can right-click a procedure to perform actions on the procedure. Depending on the type of procedure, you will get a context menu with several options.



Locate: The image at which the procedure was originally performed will be activated.

Locate may be grayed out. You can make this menu item active by canceling or finishing the active procedure.

Label: Change the label of the selected procedure.

Copy to Clipboard: The annotation label, distance measurement and value, area measurement and values, or the snapshot image is copied to the clipboard.

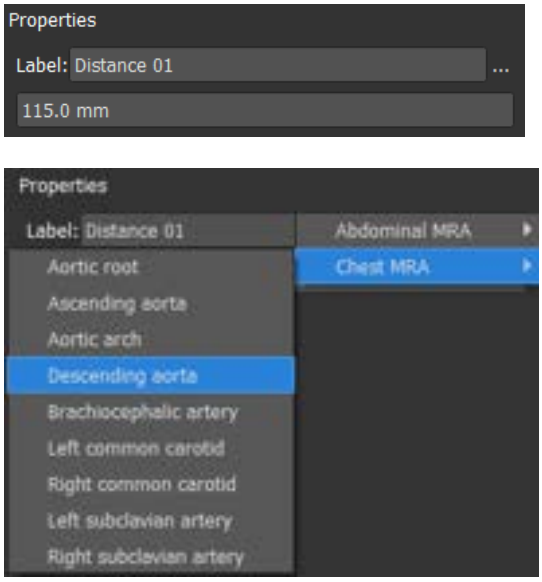
Remove: The procedure is deleted.

Properties Pane

The **Properties** pane shows the properties of the selected procedure.

To modify a Label

1. On the **Procedures** pane, select the procedure (E.g. A measurement procedure).
2. On the **Properties** pane, click the ellipsis ... on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.



Or,

1. On the **Procedures** pane, right-click on the procedure and select **Label**.
2. Select a predefined label, or type a custom label and press Enter.

The predefined labels provided by Medis Suite are dependent on the modality of the active image data.

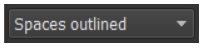
Working with the Medis Suite viewer is explained in more detail in chapter 4.5.

4.4.5 Report

The **Report** tab in the central window of Medis Suite provides the reporting functionality.

Toolbars

The positions and visibility of the toolbars in the **Report** tab are fixed.

Icon	Function
Report Toolbar	
	Show the graphical report
	Show the textual report
	Set the separator of the textual report output The separator selection is only active when the textual report is active.
	Clear the report by hiding all results

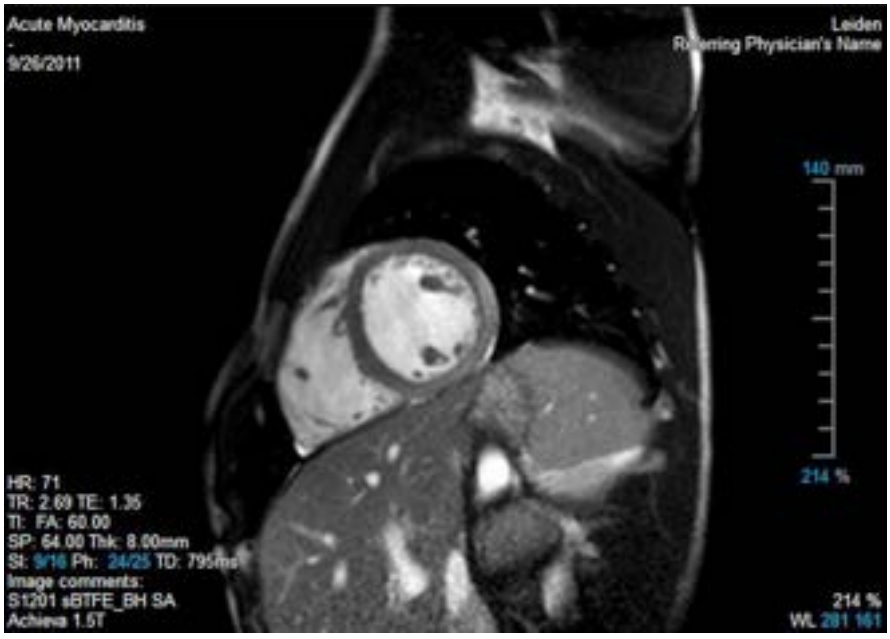
Icon	Function
Export Toolbar	
	Select all exportable results
	Deselect all exportable results
	Export the selected exportable results

More detailed information on working with the report and the export of results is given in chapters 4.8.4 and 4.10.

4.5 Viewing

4.5.1 Viewport

The image viewport displays all images that are contained in the currently loaded series.



The image overlay displays detailed information about the patient, the hospital, the image acquisition information, and the display settings.

When a series is “Lossy”, “Derived”, or “Resampled” this will be indicated as a warning in the image overlay at the bottom right corner of the viewport.

To adjust the visibility of the image overlay

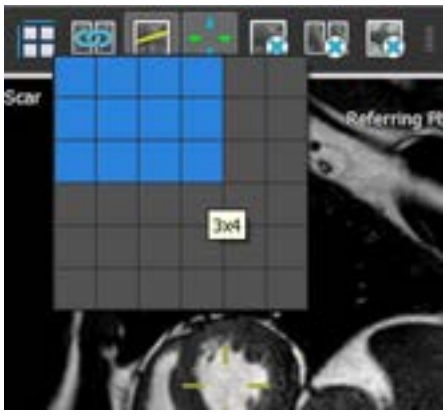
- Click  in the general toolbar.
- All image overlays will be hidden on the first click. Subsequent clicks will display the image warnings, display settings, image acquisition information, hospital information and patient information.

The visibility of the image overlay will always be restored on loading a new patient.

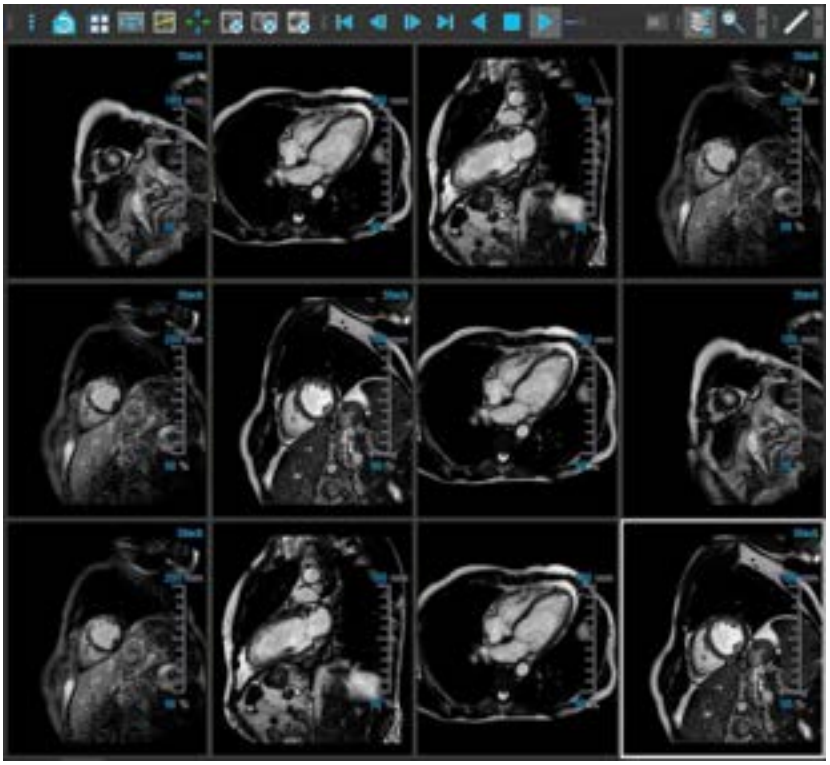
4.5.2 Viewport layout

To adjust the viewport layout

- Click  in the general toolbar. A table of rows and columns will appear.
- Drag the mouse to determine the number of viewport rows and columns.



- The viewport layout will be applied.



To clear a series from a viewport

- Select the viewport.
- Click  in the general toolbar.

To clear all series from all viewports

- Click  in the general toolbar.

To enable or disable overlays in all viewports

- Click  in the general toolbar, or press the Tab key. This will toggle off all overlays.
- Continue to click  or press the Tab key to enable each sub-set of overlays.

4.5.3 Loading Series

Series can be loaded in the viewport from the **Series Browser**.

To load series in the viewport

1. Click an item in the image view or text view of the **Series Browser** to select it.
2. Click and drag the selected series from the **Series Browser** to the viewport.

   This will load the series into the viewport. When multiple slices are contained in the series, the middle slice is displayed by default. When multiple time points are contained in the series, the first time point is displayed by default. The **Series Browser** highlights the displayed series with a white border around the icon in the image view, or bold text in the text view.
3. Double click an item in the image view or text view of the **Series Browser** to select it.

To review all series in the active study

1. Press **Page Down** on your keyboard to load the next series into the viewport
2. Press **Page Up** on your keyboard to load the previous series into the viewport

4.5.4 Navigation

You can move forward or backward through the slices and time points in the series in several ways.

To move forward or backward through slices

Moving through slices can be done by using keys:

- Press arrow up or down to move to the previous or next slice.

Or,

- Press HOME or END to move to the first or last slice.

Moving through slices can be done by using interactive graphics:

- Click or right-click the interactive graphics for slice (‘Sl’) on the viewport to move to the first or last slice.

To move forward or backward through time points

Moving through time points can be done by using buttons:

- Click  or  on the Viewing toolbar to move to the previous or next time point.

Or,

- Click  or  on the Viewing toolbar to play a cine through the time points in backward or forward direction. Click  to stop the cine.

Or,

- Click  or  on the Viewing toolbar to move to the first or last time point.

Moving through time points can be done by using keys:

- Press the left or right arrow key to move to the previous or next time point.

Or,

- Press CTRL + left arrow, CTRL + right arrow to play a cine through the time points in backward or forward direction. Press Esc to stop the cine.

Or,

- Press HOME or END to move to the first or last slice time point.

Moving through time points can be done by using interactive graphics:

- Click the interactive graphics for phase ('Ph') on the viewports to move to the next time point.

Or,

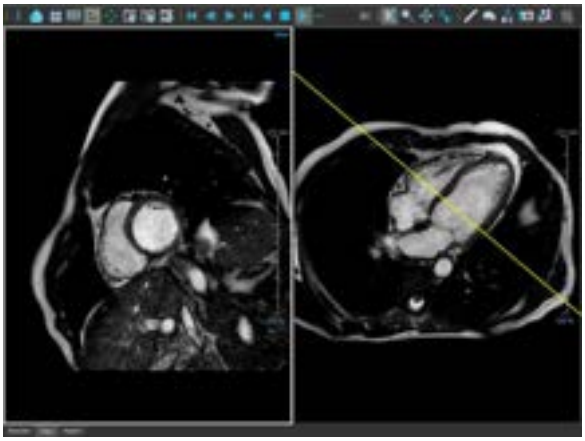
- Right-click the interactive graphics for phase ('Ph') and enter the desired number of the time point.

4.5.5 Cross Referencing

The scanline  and cross hair  tools enable the user to visually relate the active image and image position with that of the different series loaded in other viewports. Cross Referencing is visible when multiple related series are loaded.

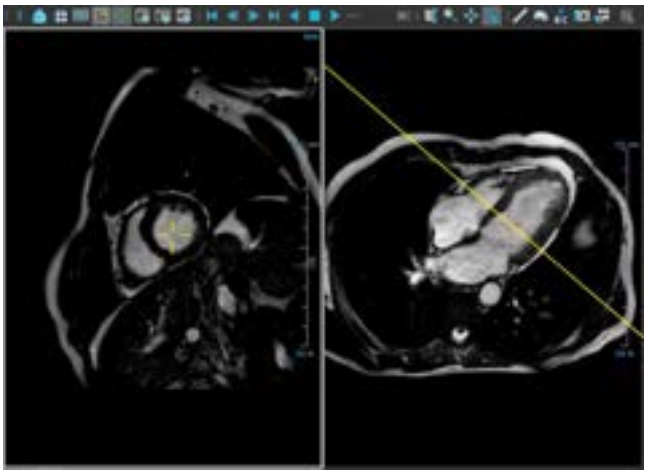
To enable/disable the scanlines

- Click  in the general toolbar to enable or disable scanlines.



To enable/disable the cross hairs

- Click  in the general toolbar to enable or disable cross hair



A cross hair reference of the same color implies there is an exact or nearby position cross reference. A different color cross hair indicates the position is out of range of the cross hair in the active image.

4.5.6 Mouse Controls

Stacking / Cine

You can move through the slices and time points using **Stacking** (MR and CT images) or **Cine** (XA images) when you see the stack cursor  .

To activate the stacking or cine mouse control

- Click  or  in the mouse controls toolbar.

Or,

- Select **Stacking** or **Cine** from the viewport context menu.

To stack forward or backward through slices (MR and CT images)

- Scroll the mouse wheel to stack through the slices.

Or,

- Click and drag the mouse forward and backward to stack through the slices.

With either technique, if scrolling reaches either end it will stop at the first or last slice.

The current slice number is displayed on the scale overlay graphics in the viewport ('Sl').

To stack or cine forward or backward through time points (MR, CT, and XA Images)

- Scroll the mouse wheel to stack through the time points (only in a single slice series).

  If scrolling reaches either end of the time points, it will stop at the first or last time point.

Or,

- Click and drag the mouse left and right or down and up to scroll through the time points.

  If dragging reaches either end of the time points, it will loop to the first or last time point and continue stacking.

The current time point number is displayed on the scale overlay graphics in the viewport ('Ph' or 'Frame').

Zooming

You can zoom in and out of the viewport using **Zooming** when you see the magnify cursor  .

To activate the zooming mouse control

- Click  in the mouse controls toolbar.

Or,

- Select **Zooming** from the viewport context menu.

To zoom in and out

- Click and drag the mouse forward and backward to zoom in and out.

Or,

- Click and drag on the interactive labels of the scale overlay graphics.

The current zoom factor is displayed on the scale overlay graphics in the viewport. The value above the scale is the physical size of the scale. The number below the scale indicates the relative zoom: 100% means one display pixel equals one acquisition voxel.

Panning

You can move the image within the viewport left, right, up and down using **Panning** when you see the hand cursor .

To activate the panning mouse control

- Click  in the mouse controls toolbar.

Or,

- Select **Panning** from the viewport context menu.

To pan the image

- Click and drag the mouse in any direction.

Or,

- Middle-click and drag the mouse in any direction.

Window Width and Level

You can adjust the window width and level (WWL) when you see the WWL cursor .

To activate the window/level mouse control

- Click  in the mouse controls toolbar.

Or,

- Select **Window/Level** from the viewport context menu.

To adjust the window width and level

- Click and drag
  - Right or left to increase or decrease the width.
  - Down or up to increase or decrease the level.

Or,

- Right-click and drag
  - Right or left to increase or decrease the width.
  - Down or up to increase or decrease the level.

Or,

- Click on the window width or level interactive graphics and drag up or down to increase or decrease the window width or level.

Or,

- Right-click on the window width or level interactive graphics and enter the desires values.

The current window width and level values are displayed in the lower-right overlay graphics in the viewport.

Image Inversion

You can invert the image view, i.e. turn blacks to whites and whites to blacks from the “Invert image” option in viewport context menu.

Initial View State

To reset the zooming, panning and window width and level settings to the initial view state

- Click  to reset the zooming, panning and window width and level.

4.6 Calibration of XA Images

XA images may be accompanied by isocenter calibration information that allows Medis Suite to automatically calibrate the image data. If this information is not available or if the object to be measured is not in the isocenter, the images must be manually calibrated before measurements can be done on the images. Medis Suite supports isocenter calibration, catheter calibration, line calibration, manual calibration, sphere/circle calibration, or can take over calibration values from another acquisition.

The calibration of an XA image is automatically taken over and applied in Medis Suite and all running apps that have analyzed the same XA image.

Errors in the calibration of an XA image can enlarge the subsequent measurement error. Therefore, the calibration procedure and the accuracy of its result have been topics of validation studies [1,2,3,4]. Using manual caliper measurements is superior to visual inspection (but inferior to stenosis analysis with automated edge detection methods) [5,6,7,8].

4.6.1 Performing Calibrations

To start a calibration

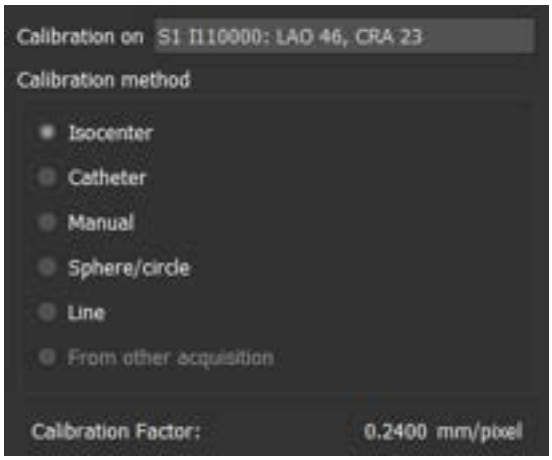
1. Select the viewport to calibrate.
2. Click  in the toolbar, or select  > **Procedures > Calibration**.
3. Select the calibration method and fill in the necessary information (see below).
4. Click **Done** to finish and apply the calibration factor to the XA acquisition.

This adds the calibration to the Calibrations list in the **Procedures** pane. At any time while the calibration is still active you can press Esc to cancel the calibration.

Isocenter Calibration

If isocenter data is available for the image, the default calibration method is Isocenter. No further actions are required to use isocenter calibration.

The isocenter calibration factor is only valid for measurements at the level of the isocenter.



Catheter Calibration

You can use the known diameter of a catheter to calculate the calibration factor that is required for performing accurate measurements and analyses.

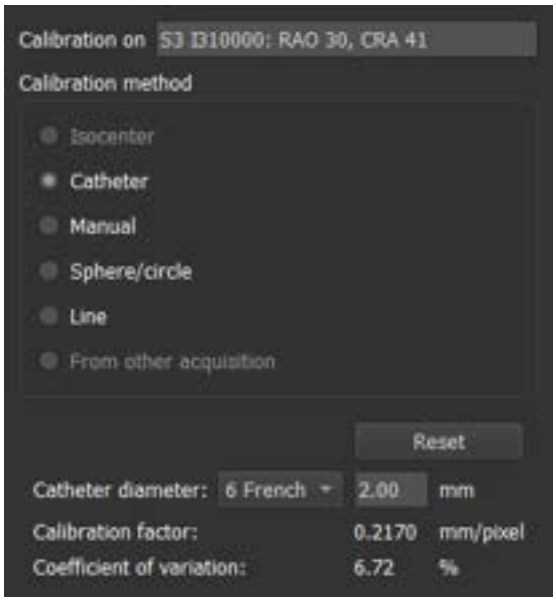
The following selection criteria apply to catheter calibration:

- The frame that shows the catheter must be acquired with the same image intensifier size and angulation/rotation as the frame in which measurements or analyses are to be performed.
- The catheter must be shown with a minimum of motion.
- The catheter must be contrast-filled, clearly visible, and with a minimum overlap of contrast agent in the aorta.
- The catheter must be in the same plane as the measurements or analyses to be performed.

- The part of the catheter shown must be more than 5 times the diameter to ensure accuracy.

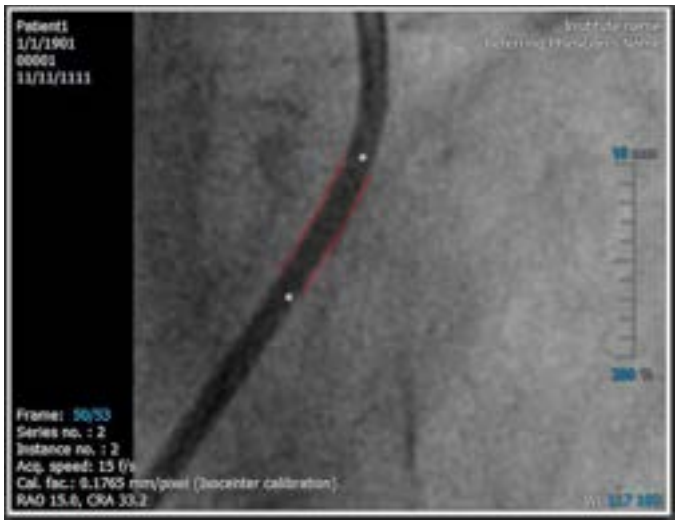
To perform catheter calibration

1. Select **Catheter** as the Calibration method.



2. In the viewport, make sure to select the image that best meets the selection criteria for catheter calibration.

3. Click in the image to specify the proximal point of the catheter, and then click to specify the distal point.



4. Verify that the catheter contours are correct.

5. Under **Catheter Diameter**, specify the known catheter size by selecting the size in French or typing the size in mm.

You can change the default catheter size. Click on the menu icon  in the **General** toolbar of the viewer, select >**Tools > Options…** and then select **Calibration** under **Viewer**.

The calculated calibration factor and the coefficient of variation are shown. The coefficient of variation is an indication for the reliability of the calibration. You are warned if the variation coefficient exceeds the 8% threshold. When you get this warning, select a longer or straighter catheter segment.

6. Click **Done** to finish and apply the calibration.

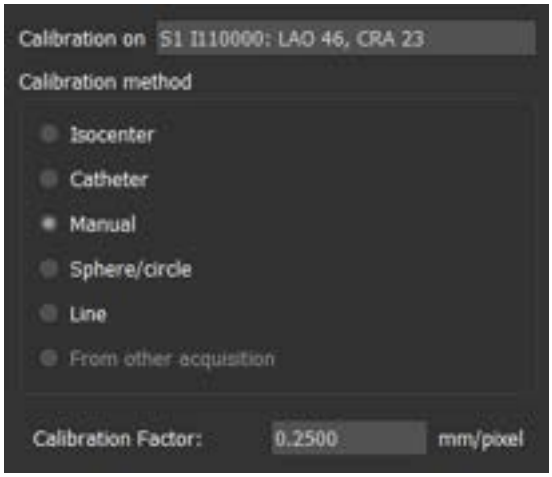
Manual Calibration

If the image or image run does not include a calibration device, you can resort to specifying the calibration factor manually.

Results obtained from images that have manual calibration applied are less reliable than results obtained from images calibrated using a calibration device.

To perform manual calibration

1. Select **Manual** as the Calibration method



2. Under **Calibration factor**, type the known calibration factor. Click outside the edit box or press Enter.

3. Click **Done** to finish and apply the calibration.

Sphere / Circle Calibration

You can use the known diameter of a circular or spherical object to calculate the calibration factor that is required for performing accurate measurements and analyses.

The following selection criteria apply to calibration based on circular objects, such as coins or spherical objects, such as billiard balls:

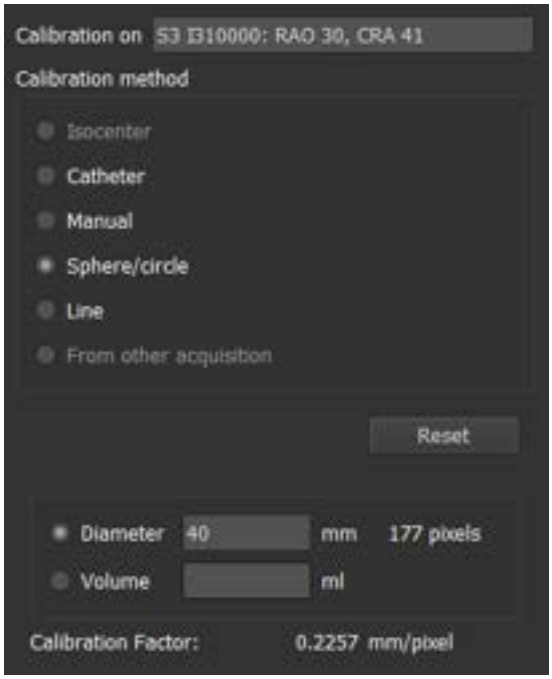
- The frame that shows the circular or spherical object must be acquired with the same image intensifier size and angulation/rotation angles as the frame in which the measurements or analyses will be performed.

- The circular object must be shown with a minimum of motion.

- The frame that shows the circular or spherical object must be acquired at the same height - being with the same distance to the image intensifier- as the object on which the measurements or analyses will be performed.

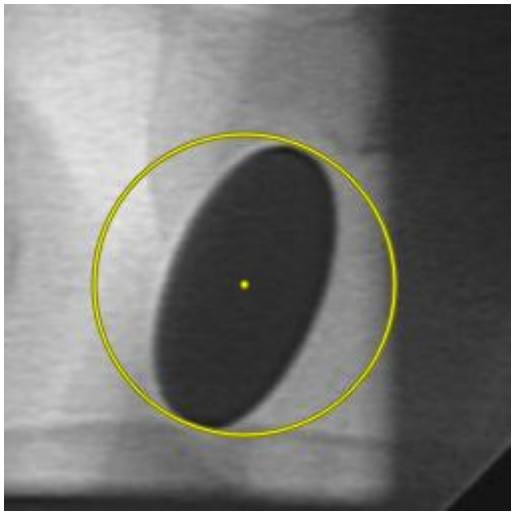
To perform sphere/circle calibration

1. Select **Sphere/circle** as the Calibration method.



2. In the viewport, make sure to select the image that best meets the selection criteria for sphere/circle calibration.

3. Click in the image to specify the center of the circle/sphere and then drag to specify the diameter.



4. Under **Enter the diameter or volume**, select whether you will be specifying the **Diameter** or the **Volume**.

5. Type the diameter in mm or the volume in ml. Click outside the edit box or press Enter.

You can change the default circle diameter or sphere volume. Click on the menu icon in the **General** toolbar of the viewer, select **Tools > Options…** and then select **Calibration** under **Viewer**.

The calculated calibration factor is shown.

6. Click **Done** to finish and apply the calibration.

Line Calibration

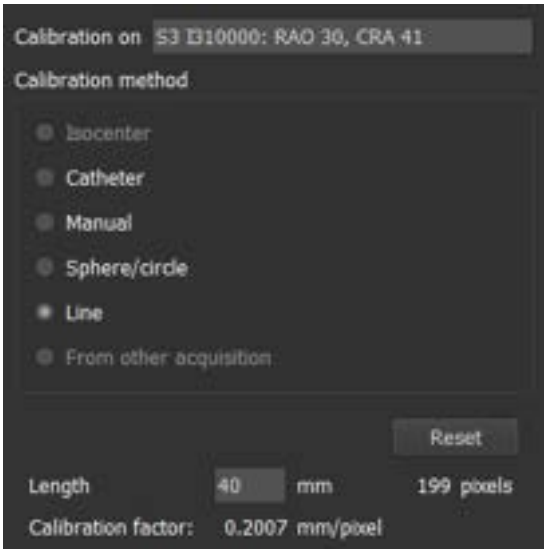
You can use the known length of an object (typically a ruler) to calculate the calibration factor that is required for performing accurate measurements and analyses.

The following selection criteria apply to line calibration:

- The frame that shows the calibration object must be acquired with the same image intensifier size and angulation/rotation angles as the frame in which the measurements or analyses will be performed.
- The object must be shown with a minimum of motion.
- The frame that shows the object must be acquired at the same height -being with the same distance to the image intensifier- as the object on which the measurements or analyses will be performed.
- The part of the object of which the distance is measured should be parallel with the image intensifier.

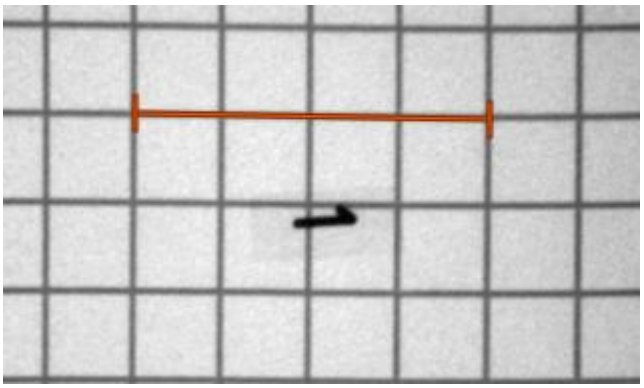
To perform line calibration

1. Select **Line** as the Calibration method.



2. In the viewport, make sure to select the image that best meets the selection criteria for line calibration.

3. Click in the image to specify start point and then drag to specify the end point.



4. Under **Enter the line length**, type the distance in mm. Click outside the edit box or press Enter.

You can change the default line length. Click on the menu icon  in the **General** toolbar of the viewer, select **Tools > Options…** and then select **Calibration** under **Viewer**.

The calculated calibration factor is shown.

5. Click **Done** to finish and apply the calibration.

Calibration from Other Acquisition

If the image or image run does not include a calibration device, you can resort to using the calibration factor of a similar image of the same study that was calibrated using a calibration device.

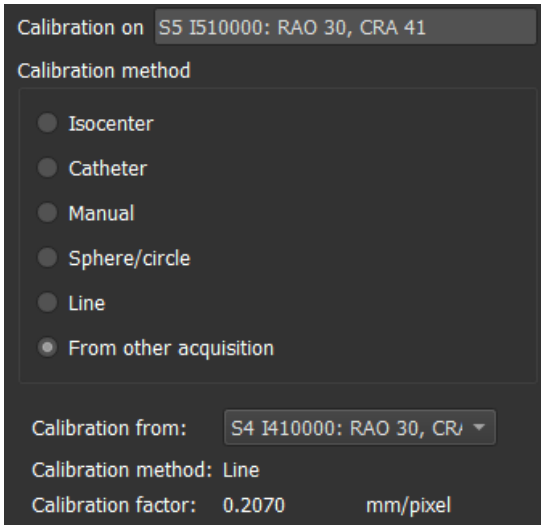
You must make sure that both image runs were obtained using the same acquisition settings and that the measurements or analyses are in the same plane as the calibration device on which the original calibration was performed.

To perform calibration from other acquisition

1. Make sure that a catheter, line, sphere/circle or manual calibration is performed on one of the other images of the same study.
2. Select **From other acquisition** as the Calibration method.

You can only select '**From other acquisition**' if a catheter, line, sphere/circle or manual calibration is performed in one of the other acquisitions of this study. If no other calibration is available, the radio button will be disabled.

3. Select the other acquisition from the list with series and instance numbers and acquisition angles.



The calibration method and calibration factor of the other acquisition are shown. You are warned if the acquisition time, image intensifier size, magnification or acquisition angles differ too much from the other acquisition.

4. Click **Done** to finish and apply the calibration.

If the calibration in the other acquisition is modified, the calibration factor in the dependent image will also be updated. The calibration in the other acquisition cannot be changed to anything else than catheter, line, sphere/circle or manual.

4.6.2 Editing Calibrations

You can modify a calibration that was performed previously.

To edit a calibration

On the **Procedures** pane, right-click the calibration and select Edit from the menu.

Or,

While the viewport that contains the calibrated image is active, click  in the toolbar.

It is not possible to delete a calibration. However, if isocenter data is available for the image, you can edit the calibration and select Isocenter as the method to reset the default calibration.

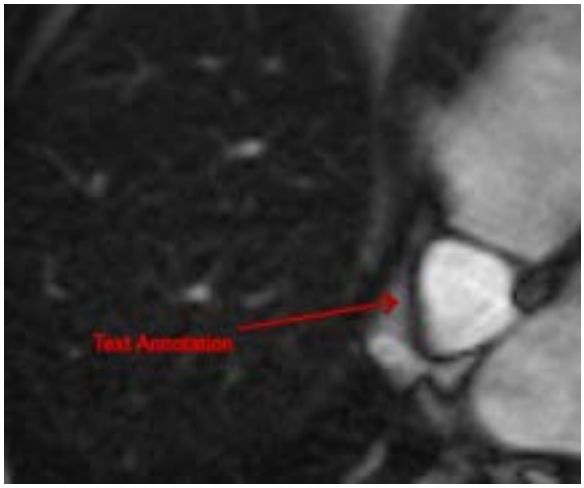
4.7 Procedures

Medis Suite supports the following procedures:

- Annotations,
- Distance measurements,
- Area measurements,
- Snapshots,
- Viewport layout snapshots.

4.7.1 Annotations

You can add annotations to a viewport to mark it for analysis or to draw attention to specific details. Annotations are displayed in the viewport. All annotations of the active series are listed on the **Procedures** pane of the viewer.



When you navigate to another series, slice or time point, your annotation is no longer displayed in the viewport. This is because the point to which the annotation refers does not lie on the currently visible image. To see your annotation again, right-click on the annotation on the **Procedures** pane and select **Locate**; or double-click on the annotation on the **Procedures** pane.

Creating Annotations

To create an annotation

1. Click  in the toolbar, or select  > **Procedures** > **Text Annotation**.
2. Click and drag in the image to draw the annotation arrow.
3. Select a predefined label, or type a custom label and press Enter.
4. Click and drag the arrowhead or the text to adjust the exact location of the image that you want to mark.
5. Click outside the annotation. The graphic changes to white indicating it has left edit mode.

This adds the annotation to the Annotations list in the **Procedures** pane. At any time while the annotation is still active you can press Esc to remove the annotation.

Editing Annotations

You can modify the text and location of annotations that were added previously.

To edit annotation text

1. On the **Procedures** pane, select the procedure.
2. On the **Properties** pane, click the ellipsis  on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.

Or,

1. On the **Procedures** pane, right-click on the procedure and select **Label**.
2. Select a predefined label, or type a custom label and press Enter.

To edit the annotation location

1. Click the annotation graphic.
2. Click and drag the arrowhead or the text to adjust the exact location of the image that you want to mark.

Deleting Annotations

You can delete any annotation that was added to a viewport.

To delete an annotation

- Click the annotation graphic and press Delete.

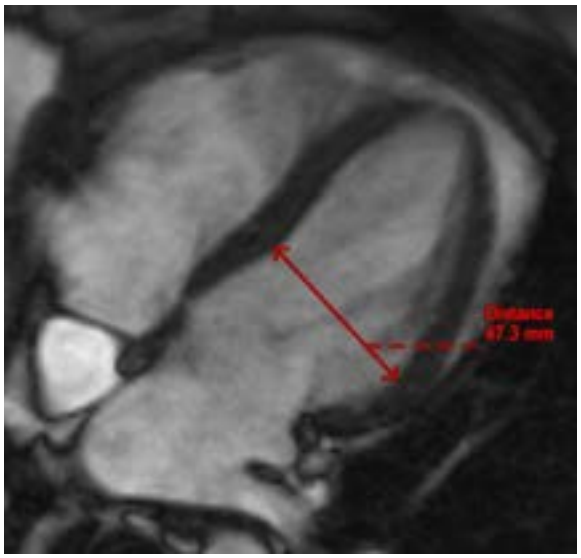
Or,

1. Select the annotation in the Annotations list in the **Procedures** pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the annotation.

4.7.2 Distance Measurements

You can measure the distance from one point to another. When you have measured a distance, you can modify the annotation and the end points of the measurement. All distance measurements of the active series are listed on the **Procedures** pane of the viewer. All distance measurements of the active session are listed on the **Results** pane of Medis Suite.



When you navigate to another series, slice or time point, your distance measurement may not be displayed on the viewport. This is because the points between which you measured do not lie on the currently visible image. To see your measurement again, right-click on the measurement on the **Procedures** pane and select **Locate**; or double-click on the measurement on the **Procedures** pane.

Creating Distance Measurements

To measure a distance

1. Click  in the toolbar, or press the D key, or select  > **Procedures > Distance Measurement**.
2. Click and drag in the image from the start point of the measurement to the end point.
3. Select a predefined label, or type a custom label and press Enter.
4. Click and drag either arrowhead or the text to adjust the points of the image between which you want to measure.

5. Click outside the measurement. The graphic changes to white indicating it has left edit mode.

This adds the measurement to the Measurement list in the **Procedures** pane. At any time while the measurement is still active you can press Esc to remove the measurement.

Editing Distance Measurements

You can modify the text and location of distance measurements that were added previously.

To edit distance measurement text

1. On the **Procedures** pane, select the distance measurement.
2. On the **Properties** pane, click the ellipsis  on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.

Or,

1. On the **Procedures** pane, right-click on the distance measurement and select **Label**.
2. Select a predefined label, or type a custom label and press Enter.

To edit distance measurement end points

1. Click the distance measurement graphic.
2. Click and drag either arrowhead to adjust the points in the image between which you want to measure.

Copying Distance Measurements

You can copy the result values of a distance measurement to the clipboard as textual output.

To copy a distance measurement

- On the **Procedures** pane, right-click on the distance measurement and select **Copy to Clipboard**.

The distance measurement label and value are copied to the clipboard.

Deleting Distance Measurements

You can delete any distance measurement that was added to a viewport.

To delete a distance measurement

- Click the distance measurement graphic and press Delete.

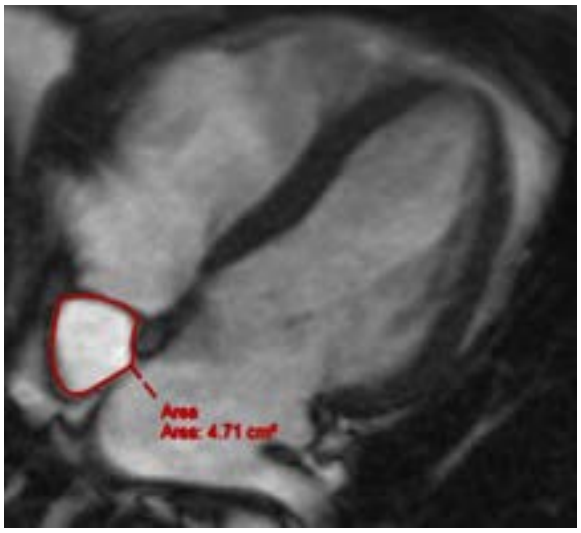
Or,

1. Select the distance measurement in the Measurements list on the **Procedures** pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the distance measurement.

4.7.3 Area Measurements

You use the area measurement tool to draw and measure 2D areas. When you have measured an area, you can modify the area contour or annotation. All area measurements of the active series are listed on the **Procedures** pane of the viewer. All area measurements of the active session are listed on the **Results** pane of Medis Suite.



When you navigate to another series, slice or time point, your area measurement may not be displayed on the viewport. This is because the image on which you measured the area is not the same as the currently visible image. To see your measurement again, right-click on the measurement on the **Procedures** pane and select **Locate**; or double-click on the measurement on the **Procedures** pane.

Creating Area Measurements

To measure an area

1. Click  in the toolbar, or press the A key, or select  > **Procedures > Area Measurement** in the menu.
2. Click and drag to draw the area. The contour is automatically closed when you release the mouse button.
3. Modify the contour as necessary (see Editing Area Measurements below).
4. In the **Properties** pane, select the check boxes to include **Area**, **Circumference, or Signal Intensity (SI)** measurements in the image overlay.

5. Click outside the contour. The graphic changes to white indicating it has left edit mode.

This adds the measurement to the Measurement list in the **Procedures** pane. At any time while the measurement is still active you can press Esc to remove the measurement.

Editing Area Measurements

To modify the contour

1. Click the contour to make it active.
2. Near the existing contour click and drag an altered contour. The alteration will be combined with the original.

   Or,

1. Right-click on the contour and drag it, using the rubber-band tool  .
2. Click outside the contour. The graphic changes to white indicating it is no longer in edit mode.

Copying Area Measurements

You can copy the result values of an area measurement to the clipboard as textual output.

To copy an area measurement

- On the **Procedures** pane, right-click on the area measurement and select **Copy to Clipboard**.

The area measurement label and value(s) are copied to the clipboard.

Deleting Area Measurements

You can delete any area measurement that was added to a viewport.

To delete an area measurement

- Click the area measurement graphic and press Delete.

Or,

1. Select the area measurement in the Measurements list on the **Procedures** pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the area measurement.

4.7.4 Snapshots

You can save snapshots as evidence of a diagnosis. Snapshots are displayed on the **Properties** pane, and are listed on the **Procedures** pane. When a snapshot is created, you can modify the name at any time.

When you navigate to another series, slice or time point, the annotations and measurements shown in the snapshot may not be displayed on the viewport. This is because the points at which the annotations and measurements were created do not lie on the currently visible image. To return to the same slice where a snapshot was created, right-click on the snapshot on the **Procedures** pane and select **Locate**; or double-click on the snapshot on the **Procedures** pane.

Creating Snapshots

You can create a snapshot of the current state of the viewport.

To save a snapshot

1. Click  in the toolbar, or press the S key, or select  > **Procedures > Snapshot**.
2. On the **Properties** pane, click the ellipsis  on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.

Deleting Snapshots

You can delete any snapshot that was created.

To delete a snapshot

1. Select the snapshot in the Snapshots list on the **Procedures** pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the snapshot.

4.7.5 Viewport Layout Snapshots

You can save and restore the layout and state of all viewports by creating a viewport layout snapshot. The snapshots are displayed on the **Properties** pane, and are listed on the **Procedures** pane. When a viewport layout snapshot is created, you can modify the name at any time.

Creating Viewport Layout Snapshots

You can create a snapshot of the current viewport layout.

To save a viewport layout snapshot

1. Click  in the toolbar, or select  > **Procedures > Viewport Layout**.
2. On the **Properties** pane, click the ellipsis  on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.

Deleting a Viewport Layout Snapshot

You can delete a snapshot of a viewport layout.

To delete a snapshot of a viewport layout

1. Select the viewport layout snapshot in the Viewport layouts list on the **Procedures** pane.

Press Delete on your keyboard or right-click and select **Remove**.

This deletes the snapshot.

4.8 Medis Suite Apps and External Tools

Where Medis Suite procedures provide basic image analysis and results, for advanced image analysis and additional results Medis Suite integrates dedicated applications, or 'apps'.

The clinical apps that are available in Medis Suite include QMass, QFlow, 3D View, QTavi, QAngio XA, QAngio XA 3D. Additional apps are released on a regular basis, visit the Medis website to learn more about our products.

Medis Suite also supports apps for research use and/or investigation use only. These apps can be recognized by a purple color of the graphical user interface. Results of the research apps that are included in the Medis Suite report will be marked to be for research use and/or investigational use only.

 Results from research apps should not be used for clinical decision making.

4.8.1 Starting a Medis Suite App

To start a Medis Suite app

- Click on the app icon in the **Applications** toolbar.

  This will start the app without loading any series.

Or,

1. Right-click in the image viewport.

2. From the context menu, select the app name.

   This will start the app, and load the series visible in the viewport into the app.

Or,

1. Select the series you want to load into the app in the **Series Browser**.

   Multiple series can be selected by holding the SHIFT or CTRL key.

2. Right-click on one of the selected series in the **Series Browser**.
3. From the context menu, select the app name.

   This will start the app, and load all selected series into the app.

Or,

1. Select the series you want to load into the app in the **Series Browser**.

   Multiple series can be selected by holding the SHIFT or CTRL key.

2. Click and drag the selected series onto the app icon in the **Applications** toolbar.

   This will start the app, and load all selected series into the app.

When the Medis Suite app is started, it will be displayed on a new tab in the central window area of Medis Suite. The launched apps will be displayed after the **View** tab and before the **Reporting** tab in the order they were started.

Multiple instances of Medis Suite apps can be started. They will be running next to each other and can be identified by a sequence number '#1', "#2', etc.

Multiple versions of an app can be installed, for example QMass version 8.0 and version 8.1. You can configure how Medis Suite handles multiple app versions when reloading data from a session. Click  in the main Medis Suite toolbar, select Tools, Options and the select the **General** tab.

Results from the Medis Suite apps will be visible in the **Results** pane of Medis Suite automatically or by actively pushing results from the apps to Medis Suite. Refer to the user manuals of the Medis Suite apps for more detailed information.

4.8.2 Loading Series into Medis Suite Apps

You can load series into Medis Suite apps that were already running, appending or replacing data that was already loaded.

To load series into Running Medis Suite apps

1. Click on the tab that holds the running Medis Suite app in the central window of Medis Suite

2. Select the series you want to load into the Medis Suite app in the **Series Browser**.

   Multiple series can be selected by holding the SHIFT or CTRL key.

3. Double-click one of the selected series, or click one of the selected series and drag the selection onto the running Medis Suite app.

   The series will be loaded by the Medis Suite app and the first series will be activated.

Press SHIFT during dragging to add the data to the running Medis Suite app without modifying the app's series selection.

Press CTRL during dragging to unload previously loaded series from the Medis Suite app, and load the new series.

4.8.3 Closing a Medis Suite App

To close a Medis Suite app

- Click the 'X' on the tab that holds the running instance of the app.

When Medis Suite apps are closed, their accompanying results will be removed from the Medis Suite **Results** pane and the report.

When you switch to another patient or study in the **Browser**, all running Medis Suite apps will be closed.

4.8.4 External Tools

Medis Suite can be configured to launch 3rd party tools, for example to parse and process the results available in Medis Suite. External tools will not run embedded in the Medis Suite window on a tab, but will be launched to run independent from the Medis Suite environment.

Before Medis Suite will launch an external tool, it can export sessions, reports, results, snapshots and movies that you can be used as input for the external tool.

To start an external tool

- Click on the external tool icon in the **external tools** toolbar.

Configuration of the external tools is performed through the "External tools" tab of Medis Suite options dialog. The configuration includes the location of the external tool, the icon to

be displayed in the external tools toolbar or menu, optional command line parameters, the startup and shutdown properties, as well as the pre-launch export options.

Errors in the configuration of external tools or misuse of external tools can lead to unexpected results, such as data loss. Carefully verify that the proper information is exchanged between Medis Suite and the external tool.

Medis Suite provides an external tool template to export results into the CMR-COOP database. To use this external tool, you will require a CMR-COOP account and have to download the accompanying external tool from the CMR-COOP website and install it on your local system.

4.9 Reporting

All results available in Medis Suite, either from the Medis Suite viewer or from any of the running Medis Suite apps, within the active session of the active study can be used to generate a combined report.

Next to the results from the Medis Suite viewer and the Medis Suite apps, the following sections can be included in the report:

- Patient Study Info
- Reason for Referral
- Technique
- Impressions
- Extra-cardiac Findings
- Miscellaneous
- Comments
- Conclusions

Report Customization

Reports in Medis Suite can be customized using templates. Administrators can create report templates that define which sections, procedures, and result items are included, excluded, expanded, or collapsed. The order of sections can also be configured.

- Each template consists of a list of sections.
- Each section contains a list of procedures.
- Sections, procedures, and result items can be enabled or disabled.
- Sections and procedures can be set to collapsed or expanded.

Users can select a template to generate reports tailored to their clinical or institutional requirements.

4.9.1 Create a Report

You can create a Medis Suite report from the **Results** pane, by showing or hiding results, paragraphs or sections from the report.

To show or hide a result from the report

- Click on the result name or any of the result values to toggle the visibility.

To show or hide a paragraph with all contained results from the report

- Click on the paragraph name to toggle the visibility.

To show or hide a section with all contained paragraphs and results from the report

- Click on the section name to toggle the visibility.

To hide all results from the report

- Click  in the toolbar.

To print the report

- Click  in the toolbar.
- Select the target printer and click OK.

Sections, paragraphs and results that are hidden in the report, are displayed in the **Results** pane with a grayed out and italic font.

The **Results** pane is automatically activated when you activate the report.

Your organization name and logo can be configured in the Medis Suite options. To open the options dialog, click  in the **Main** Medis Suite toolbar, and select Tools, Options.

4.9.2 Modify a Report

You can modify the following sections from the report:

- Reason for Referral
- Technique
- Impressions
- Extra-cardiac Findings
- Miscellaneous
- Comments
- Conclusions

To modify an editable section from the report

1. Make sure the editable section is visible in the report.

   If the section is not visible yet, click on the section name to show it.

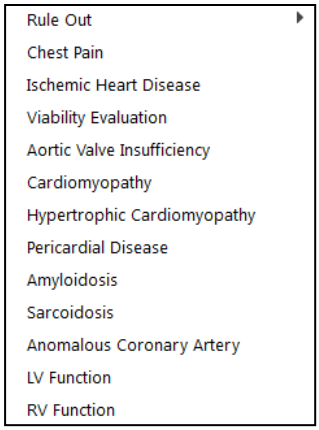
2. Click Edit.

3. Modify the section data by:

   - Remove, modify or add text using the keyboard.

   Or,

- Click Labels to open a list of predefined labels and select one of the labels.



  By default, the label will be appended at the end of the text in the edit box. To insert the label at another location, select that location with your mouse first.

4. Click OK to close the edit box.

4.9.3 Textual Report

By default Medis Suite will show the report in a graphical layout. In addition, you can generate a textual report to allow copy-and-paste of results from Medis Suite to another application.

To open the textual report

- Select  from the report toolbar

The textual report only includes the results that are visible in the graphical report. To change the report content, modify the selections in the **Results** pane.

To copy results from the textual report

1. Press CTRL+A or select **Select All** from the context menu.
2. Press CTRL+C or select **Copy** from the context menu.

   The entire textual report content is copied to the clipboard.

Or,

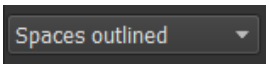
1. Select a part of the textual report content.

2. Press CTRL+C or select **Copy** from the context menu.

   The selection is copied to the clipboard.

You can paste the information to, for example, another report or spreadsheet with CTRL+V. It may be required to change the outlining of the textual report content to get a proper result.

To change the outlining of the textual report content

- Select 

from the report toolbar and select one of the available outline options:
  - Spaces outlined
  - Space separated
  - Tab separated

To paste results into a Microsoft Excel workbook, use the **Tab separated** outlining, and past the results as text with the **Paste special** command of Microsoft Excel.

To reopen the graphical report

- Select  from the report toolbar.

To show or hide a result from the report

- Click on the result name or any of the result values to toggle the visibility.

To show or hide a paragraph with all contained results from the report

- Click on the paragraph name to toggle the visibility.

To show or hide a section with all contained paragraphs and results from the report

- Click on the section name to toggle the visibility.

To hide all results from the report

- Click  in the toolbar.

To print the report

- Click  in the toolbar.
- Select the target printer and click OK.

Sections, paragraphs and results that are hidden in the report, are displayed in the **Results** pane with a grayed out and italic font.

The **Results** pane is automatically activated when you activate the report.

Your organization name and logo can be configured in the Medis Suite options. To open the options dialog, click  in the **Main** Medis Suite toolbar, and select Tools, Options.

4.9.4 Reporting Customization

Administrators can create and manage multiple report templates, defining the visibility and order of sections, and the visibility of procedures and individual results. Users can select from a list of templates to generate customized reports with content and layout based on the selected template.

Report templates can be managed in Medis Suite under **Tools > Options > Reporting > Templates**. The system default report template is labelled "System Default".

Accessing Report Template Tools

To access all report template tools:

- In the main Medis Suite toolbar, click Tools, then select **Options > Reporting > Templates**.

Managing Report Templates

To create a report template:

- Click  and enter a name in the **Template Name** field.
- Check **Set as Default** if the template should be automatically selected when Medis Suite starts.

A session will not automatically apply the default selected template.

To delete a report template:

- Select the template and click  (Delete).

To reset a report template to its default state:

- Select the template and click  (Reset).

To copy a report template:

- Select the template and click  (Copy).

Customizing Section Order

To set the order of sections in a report template:

- Use the  controls in the **Sections** column to move sections up or down.

Selecting a Report Template

To select a report template during reporting:

- Use the dropdown menu above the **Findings** section to choose from the available templates.

4.10 Exporting

From the Report tab you can export reports and results.

The export of the report and results is functionality that can be allowed or blocked (role based access control) by your system administrator.

The following items are available for export from Medis Suite:

- Report
- Snapshots
- Values

In addition, the Medis Suite apps can add items to the export list, for example:

- Images
- Snapshots
- Movies
- Values

The report, snapshots, images, and movies are displayed as a thumbnail in the export list on the Report tab.

4.10.1 Select Results for Export

You can select the report, snapshots, images, and movies from the export list to mark them for export.

To include or exclude results for export

- Click on a thumbnail image to include or exclude the result for export

Or,

- Click  to include all results for export.

Or,

- Click  to exclude all results for export.

Results that are included for export have a thumbnail that is visible in normal colors and is highlighted with a white border. Results that are excluded for export have a thumbnail that is grayed out and has no border.

4.10.2 Export Results

You can export all selected results in DICOM format to your repository or PACS for future review or reference.

The export targets and formats of the results can be set in the Medis Suite options.

To export results

- Click  to export the selected results.

4.10.3 Export to Common Image Format

Results can also be exported in common image formats.

To export a single result into a common image format:

- Right click on the result to export, and select Export…
- In the Export dialog, select the output format, specify a filename, and click OK.

To export a group of results into a common image format:

- Select or deselect the results in the group you would like to export.
- Right click on the header of the result group, and select Export selected…
- In the Export dialog, select the output format, specify a filename, and click OK.

4.11 Sessions

Status information of Medis Suite can be saved. The session can be reloaded to continue or review the image analyses performed by Medis Suite.

Medis Suite sessions contain the following information:

- The running Medis Suite apps.
- All results from Medis Suite and the running Medis Suite apps.
- The visibility status of all results in the report.
- Information added to the editable sections in the report.

If supported by the Medis Suite apps, sessions can also contain the following information:

- The series loaded by the Medis Suite app.
- Analysis settings and results (such as contours) created by the Medis Suite app.

4.11.1 Working with Sessions

Medis Suite can maintain multiple sessions for each study, but only a single session can be active at a time. All sessions can be accessed through the session combo-box in the Main toolbar.

After loading a study, Medis Suite will automatically create a new session that is identified by the date and time on which the session was created, and your name.

You can save sessions and create new sessions. Once loaded into Medis Suite, sessions cannot be removed.

A session is marked as modified whenever results are changed, the report content is changed, or Medis Suite apps are started or stopped. A modified session can be identified by an "*" displayed in the name.

To save a Medis Suite session

- Select  from the Main toolbar and click Save session

  The name of the session is updated to indicate that it is saved.

Or,

- Select  from the Main toolbar and click Save session as…

  Specify the name of the session and click OK.

  The name of the session is updated to indicate that it is saved.

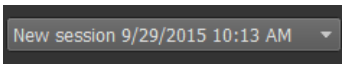
Once a session is saved, its contents cannot be overwritten or modified by Medis Suite.

To reset a Medis Suite session

- Select  from the Main toolbar.

  A new session is created.

To select a Medis Suite session

- Open the session combobox in the Main toolbar 

and select the Medis Suite session.

When you switch or reset a session, all open Medis Suite apps will be closed and their results will be removed from Medis Suite. The Medis Suite apps that were contained in the newly activated session will be started and their results will be loaded in Medis Suite.

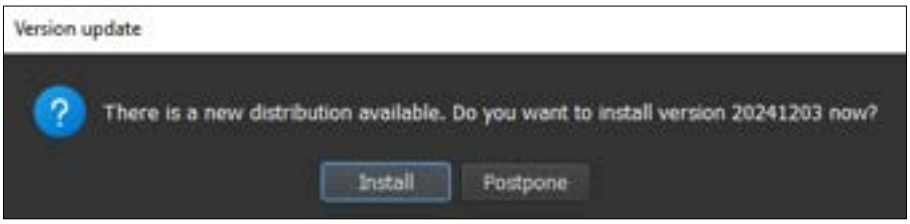
Before Medis Suite closes a modified session, you will be asked if you want to save the session.

4.12 Client-Server Software Updates

In a Client-Server system setup, software updates for Medis Suite can be deployed from the server to the clients.

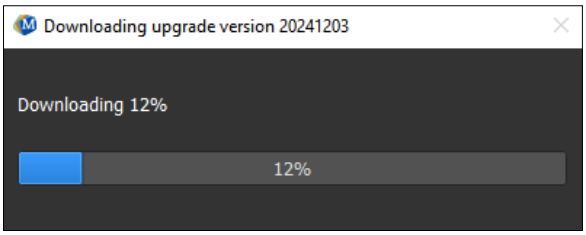
An upgrade of a Medis Suite distribution, is started by upgrading the server installation of Medis Suite manually. Once the server is upgraded the client can be upgraded.

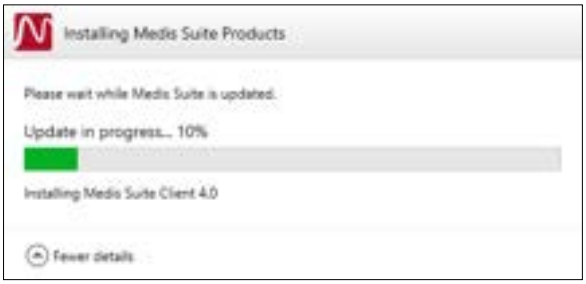
On a client machine, when Medis Suite is started, a query will be sent to the server for a software update. In case of an available software update Medis Suite, on the client, will ask the user whether to upgrade immediately, or to postpone the software update.



On the client, the update consists of the following steps:

- A download of the software from the server takes place.
- A progress / status dialog will be shown.
- The active Medis Suite will be closed.
- The software will be updated.
- When finished the dialog shows the result.
- Medis Suite will be started.

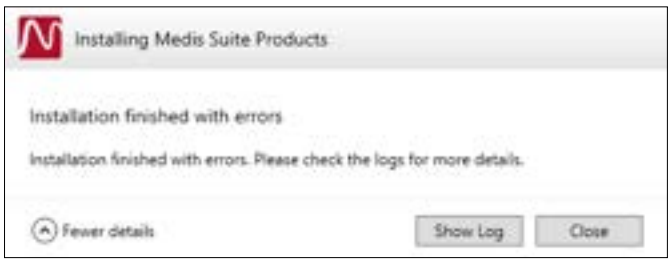




After the distribution update Medis Suite will automatically start. It is advised to directly perform the Post Install Test from the Tools menu.

In case of errors during the update the status dialog will show the following information:

- The error that occurred.
- The path to the location of the logfiles of the software update process.



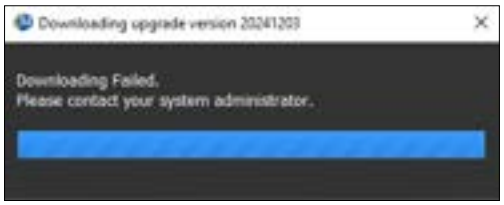
Medis Suite installed in standalone mode does not support automatic updates.

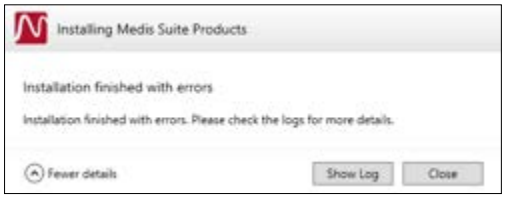
4.12.1 Options

Client-Server options can be enabled or disabled from both the server side as for the client side. The default for Client and Server is enabled. The setting can be changed on the Options -> Services page.

4.12.2 Troubleshooting software updates

During a software update process a failure of the software update will be notified to the user via the progress and status dialog.





The path to the logging of the software update process is displayed on the dialog. The generic path is: "C:\ProgramData\Medis\Deployment\Logs\". For each update process there is a specific folder with logs. The logfile folder name is in the format of: Log_YYYYMMDD_HHMMSS (eg. Log_20240709_171412).

4.13 DICOM Connectivity

Medis Suite supports the following DICOM services:

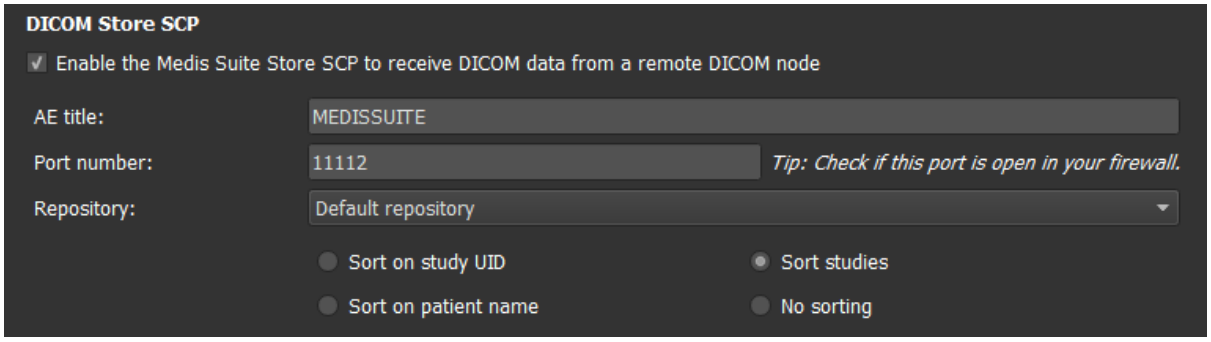
- Echo SCU to test the DICOM connection with a remote DICOM node, such as a PACS.
- Store SCP to receive data from a remote DICOM node, such as a PACS;
- Store SCU to send data to a remote DICOM node, such as a PACS;
- Find SCU and Move SCU to query and retrieve data from a remote DICOM node, such as a PACS.

In order to create an efficient setup with DICOM connectivity, you can share the DICOM connectivity service on the Medis Suite server machine with one or more Medis Suite client machines.

To configure the DICOM connectivity of the Medis Suite server

- Go to the machine that acts as a Medis Suite server and start Medis Suite.
- Click  in the **Main** Medis Suite toolbar, select Tools, Options and select the DICOM connectivity tab.

To enable the Store SCP:



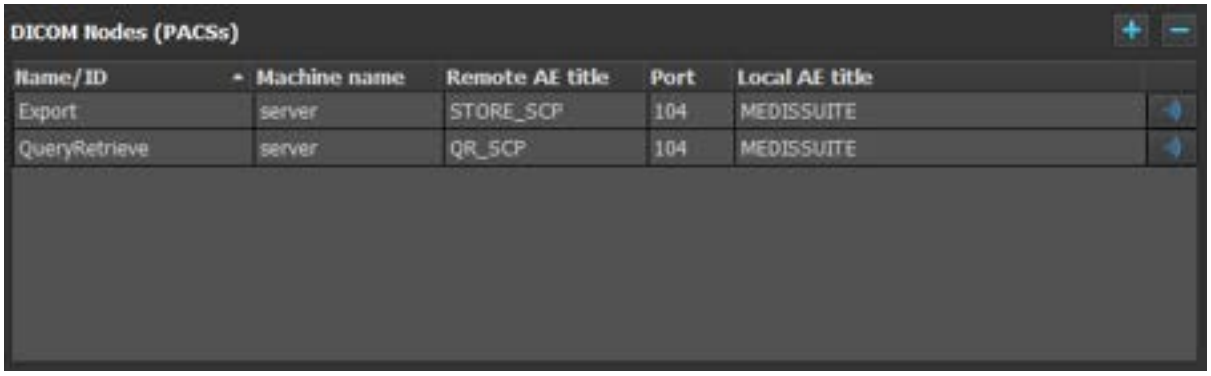
- Select the check box “Enable the Medis Suite Store SCP…”
- Set the appropriate AE title and port number for the Store SCP of Medis Suite.

The default settings are MEDISSUITE and port number ‘11112’.

- Select the repository to store received data.

In order to establish a successful connection, make sure to register the Medis Suite Store SCP with its AE title and port number on the PACS as a destination DICOM node.

To enable the Store SCU:



- Click  to add a new DICOM node.
- Set the appropriate Remote AE title, port number, and machine name of the SCP on the PACS, and enter an appropriate node name.
- Click  to test the newly defined DICOM node.
- Select the newly defined DICOM node from the dropdown list of Export nodes.

To enable the Find SCU and Move SCU to enable Query and Retrieve:

- Click  to add a new DICOM node.

- Set the appropriate Remote AE title, port number, and machine name of the SCP on the PACS, and enter an appropriate node name.
- Click  to test the newly defined DICOM node.
- Select the newly defined DICOM node from the dropdown list of Query/Retrieve nodes.

To configure the DICOM connectivity of the Medis Suite client

- Go to the machines that act as a Medis Suite client and start Medis Suite.
- Click  in the **Main** Medis Suite toolbar, select Tools > Options, and select the Services tab.
- Enter the machine name or IP address of your Medis Suite server.

- Click 'Test services' to verify the connection with your Medis Suite server.
- The Medis Suite client machine will now be able to use the DICOM connectivity functionality from the Medis Suite server.

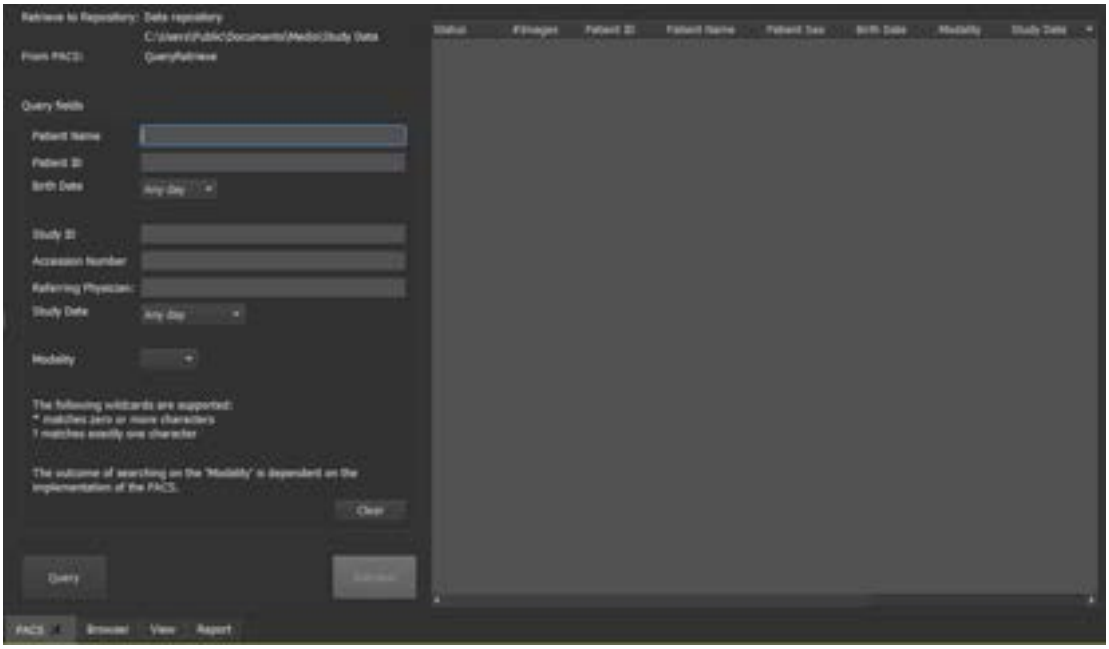
4.14Query / Retrieve from PACS

Medis Suite supports both Query and Retrieve from a predefined PACS.

To query and retrieve from a PACS

- Open the Browser tab, and click 

. The PACS tab will be opened.

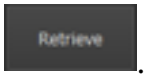


The PACS button will only be visible and enabled when a DICOM node is configured for DICOM Query and Retrieve.

Query a PACS

- Using the Query fields to define the search criteria.
- Click  .
- Matching patient and study information will be displayed in the list.

Retrieve from PACS

- Select an item from the list of patient and study information.
- Click  .
- The patient/study will be retrieved and appended to the repository.
- Go to the Browser tab to confirm that the patient data is appended to the repository, and load the data into the Viewer.

Clear results

- Click Clear and the previous queried results will be cleared.

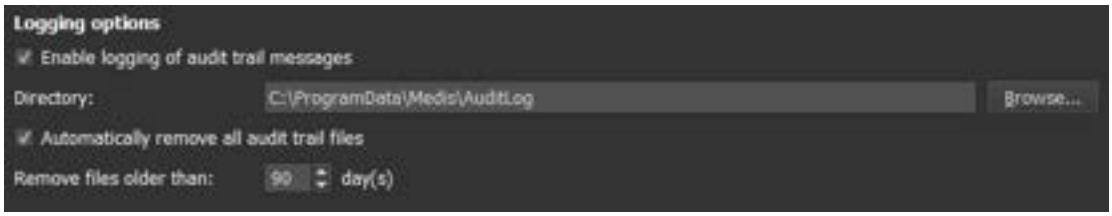
4.15 Audit Trail

Medis Suite supports audit trailing functionality to maintain a log of relevant actions performed by Medis Suite or any of the integrated apps.

In order to create an efficient setup with audit trailing, you can share the audit trailing service on the Medis Suite server machine with several Medis Suite client machines.

To configure the audit trailing of the Medis Suite server

- Go to the machine that acts as a Medis Suite server and start Medis Suite.
- Click in the **Main** Medis Suite toolbar, select Tools, Options, and select the Audit Trail tab.



- Select the check box “Enable logging of audit trial messages”
- Edit the directory where the audit trail must be stored.
- Enable or disable the auto cleanup of audit trail files.

If you want Medis Suite to store data on a network drive, the Medis Suite Audit trail Windows service will require additional privileges that must be configured by your system administrator. Also, make sure to use the UNC network folder path (e.g. “\\machine\foldername”) instead of a drive mapping (e.g. “N:\foldername”).

To configure the audit trailing of the Medis Suite client

- Go to the machines that act as a Medis Suite client and start Medis Suite.
- Click in the **Main** Medis Suite toolbar, select Tools > Options, and select the Services tab.
- Enter the machine name or IP address of your Medis Suite server.

- Click ‘Test services’ to verify the connection with your Medis Suite server.
- The Medis Suite client machine will now be able to use the audit trail functionality from the Medis Suite server.

4.16 Troubleshooting

Menu commands or toolbar buttons are disabled

Menu commands or toolbar buttons may be grayed out when you are performing a procedure, such as a distance measurement. You can make them active again by canceling or finishing the procedure.

Annotation or measurement is not visible

When you navigate to another location in the volume, your annotation or measurement may not be displayed on the viewport. This is because the point to which the result refers does not lie on the currently visible slice. To see your result again, right-click on the result on the Procedures pane and select **Locate**; or click on the result on the Procedures pane.

4.17 Literature

1. Koning G, van der Zwet PM, von Land CD, Reiber JHC. Angiographic assessment of dimensions of 6F and 7F Mallinckrodt Softouch coronary contrast catheters from digital and cine arteriograms. Int J Card Imaging. 1992; 8(2):153-61. PubMed PMID: 1629641.
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3. Ito S, Kinoshita K, Endo A, Nakamura M, Muramatsu T. Impact of catheter size on reliability of quantitative coronary angiographic measurements (comparison of 4Fr and 6Fr catheters). Heart and vessels, 2016, Springer.
4. Sanmartin M, Goicolea J, Castellanos R, Bravo M, Ocaranza R, Cuevas D, Mantilla R, Ruiz-Salmeron R. Validation of 4 French catheters for quantitative coronary analysis: in vivo variability assessment using 6 French guiding catheters as reference scaling devices. Journal of Invasive Cardiology, 2004 Mar;16(3):113-6. PMID: 15152158.
5. Md, D.K., Lythall Bs, D.A.,.M., Cooper, I.C., Ba, A.C. and Webb-Peploe, M.M. (1988), Assessment, of coronary angioplasty: Comparison of visual assessment, hand-held caliper measurement and automated digital quantitation. Cathet. Cardiovasc. Diagn., 15: 237-242.
6. Maarten AG, Merkx MAG , Bescós JO, Geerts L, Bosboom EMH, van de Vosse FN, Breeuwer M. Accuracy and precision of vessel area assessment: Manual versus automatic lumen delineation based on full-width at half-maximum. J Magn Reson Imaging. 2012 Nov;36(5):1186-93. PMID: 22826150.
7. Koning, G, Reiber JHC, von Land CD. Advantages and limitations of two software calipers in quantitative coronary arteriography. Int J Cardiac Imag 7, 15–30 (1991).

8. Bruschke AVG, Buis B. Quantitative angiography. Current Opinion in Cardiology, November-December 1988 - Volume 3 - Issue 6 - p 881-886.

4.18 Shortcut Keys

When you are working with Medis Suite, you can use several combinations of keys on your keyboard and mouse actions to quickly perform the following tasks.

Medis Suite and apps may use the same shortcut key for different functionalities. Which application handles your shortcut key is dependent on which application has 'focus'.

Press	To
Layout	
F10	Maximize or restore the active image viewport
F11	Show or hide the workspace window panes
F12	Reset toolbar and workspace window pane layout
Image control	
Middle-click and drag, or Ctrl and drag	Pan
Ctrl+Shift and drag	Zoom
Alt+Shift and drag	Stack
Ctrl+I	Invert image
Procedures	
D	Create a distance measurement

Press	To
A	Create an area measurement
H	Hide the graphics in the image viewport
S, or CTRL+SPACE	Create a snapshot
Esc	Stop editing the procedure
Delete	Delete the currently selected procedure
SHIFT+Delete	Delete all procedures
Navigation Controls	
HOME	Display the first time point
END	Display the last time point
Arrow up	Display the previous slice
Arrow down	Display the next slice
Arrow left	Display the previous time point
Arrow right	Display the next time point
CTRL+arrow left	Play cine backward
CTRL+arrow right	Play cine forward
Esc	Stop playing cine
Page Up	Display the previous series

Press	To
Page Down	Display the next series

5 3D View

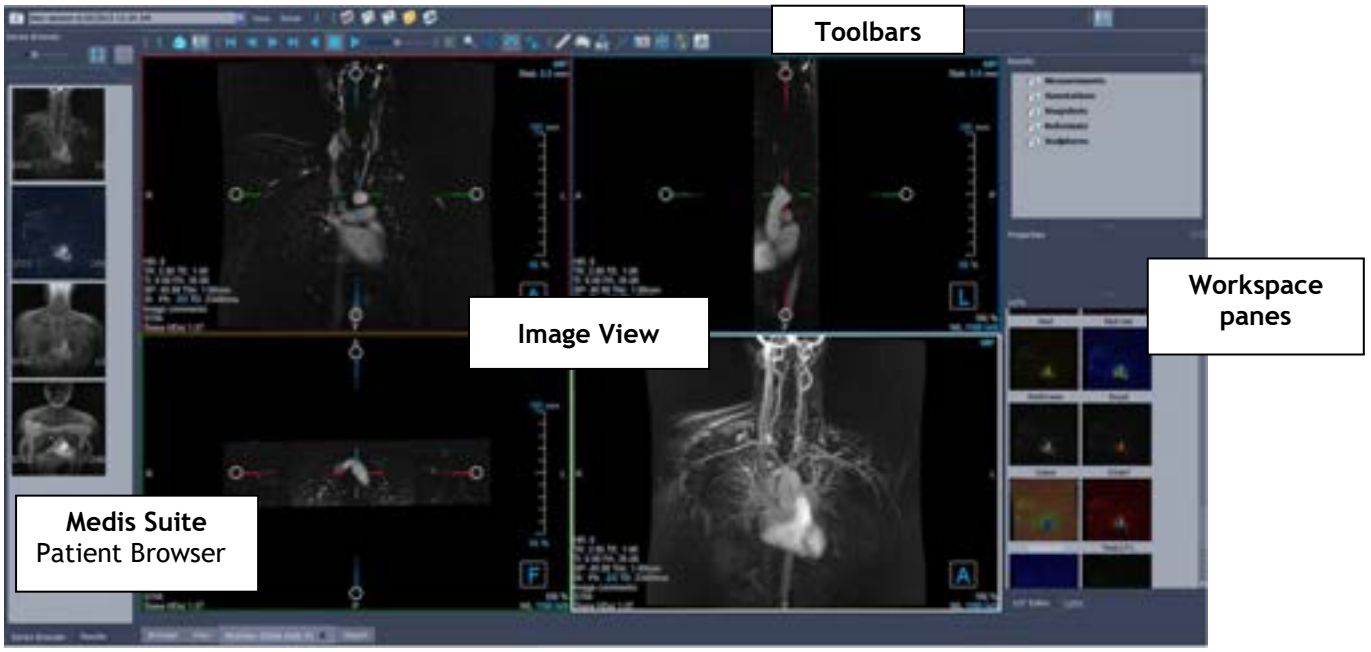
5.1 The 3D View Workspace

This chapter covers the following topics:

- overview
- toolbars
- workspace panes
- image view

5.1.1 Overview

The main workspace consists of toolbars, multiple workspace panes, and the image view.

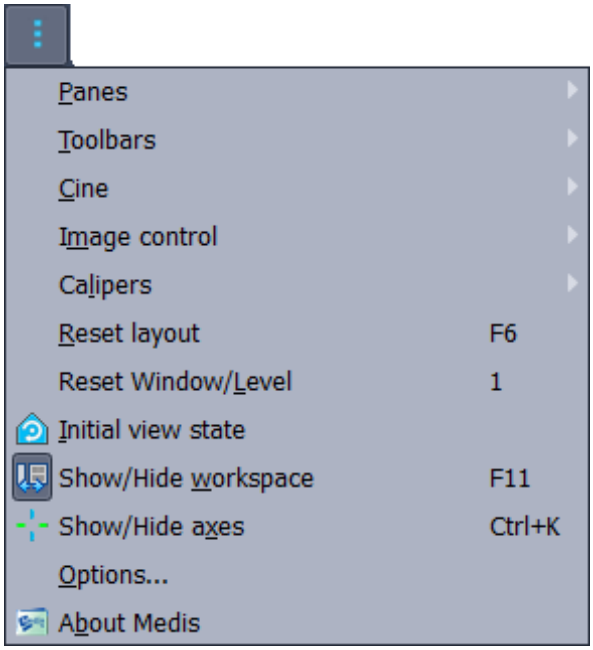


You can customize the main workspace by hiding or moving the workspace panes and toolbars. Any changes that you make to the main workspace are saved on a per user basis for future sessions.

5.1.2 Menu

The menu button  contains all of the main functionality that you need when you are working with 3D View. These main commands are organized as follows: **Panes**, **Toolbars**, **Cine**, **Image Control** and **Calipers**. For some of these commands, tool buttons are available in the toolbars as shortcuts.

Menu commands may be grayed out when you are performing a procedure, such as a radial reformat. You can make the menu commands active by canceling or finishing the procedure.

Menu item: View	Option	Description
	Panes >	Show / hide panes (patient, results)
	Toolbars >	Show / hide toolbars
	Cine >	Show different time points
	Image Control >	Zoom, panning, swivel and stacking.
	Calipers >	Add measurements, annotations, sculpture and reformats.
	Reset layout	Reset the window and toolbar layout
	Reset Window/Level	Reset the Window/Level
	Initial View State	Return to volume in original state
	Show/Hide Workspace	Show/hide workspace panes
	Show/Hide axes	Show/hide the axes
	Options…	Open dialog for general options
	About Medis	About box

5.1.3 Toolbars

The icons in the toolbars are shortcuts to frequently used menu options. You can make toolbars float and move them to another part of the main window. You can also show or hide toolbars.

To make a toolbar float

- Click on the double-bar grip handle of the toolbar and drag it.

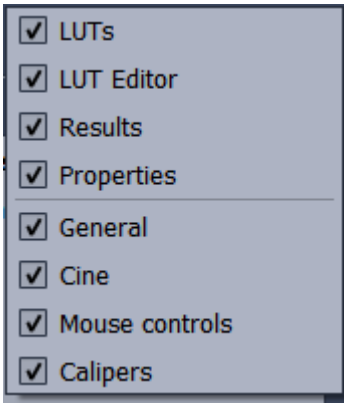
  You can now move the toolbar to any location in the main window or outside of the application. Simply click and drag the toolbar to its new position. The position of the toolbar is saved for a next session when you close the application.

To show or hide a toolbar

Select the toolbars menu by right clicking any space in the toolbar. This context menu will appear

1. Select the toolbutton  and **Toolbars**.
2. Select a check box to show the toolbar, clear a check box to hide the toolbar.

Or,



1. Right-click in the toolbar area. This opens a context menu.
2. Select a check box to show the toolbar, clear a check box to hide the toolbar.

The state of the toolbars is saved on a per user basis for future sessions when you close the application.

Icon	Function
General Toolbar	
	Go to the initial view state
	Show or hide the workspace
	Show or hide the axes
Movie Toolbar	
	Go to the previous time point
	Go to the next time point
	Set to the first time point
	Set to the last time point

Icon	Function
	Stop the movie
	Play the movie forward
	Play the movie backward
	Moderate the speed of the movie.
Results Toolbar	
	Create a distance measurement
	Create an area measurement
	Create an annotation
	Create a double distance measurement
	Create a snapshot
	Create a reformat
	Create a radial reformat
	Create a sculpture
	Copy all measurement information to clipboard
Image Control Toolbar	
	Scroll through the images
	Zooming
	Panning
	Swivel
	Alter Window width and Window Level

5.1.4Workspace Panes

By default, the workspace displays the following panes to the right of the image view.

- LUTs
- LUT Editor
- Results
- Properties

You can show or hide panes, make panes float, dock panes, combine panes into one tabbed panel and remove panes from a panel.

To show or hide a pane

- Select the button  and choose **Panes**, and select a pane to show it. Clear its check box to hide it.

To show or hide all panes

- Click  in the toolbar, or press F11 to show or hide all panes.

To make a pane float

- Click and drag the title bar of the pane over the area of your screen to which you want to move it.

To dock a pane

- Double-click the title bar to move a pane back to its original docked position.

Or,

1. Click and drag the title bar of the pane to the left or right side of the workspace as shown in the picture on page 80.
2. Move the pane up or down to select one of the anchor areas available.

   As the pane approaches an anchor area, the area is highlighted with a dotted line. The pane can be combined with another pane or inserted separately.
3. When the anchor area of your choice appears highlighted, release the mouse button.

   This moves the pane to the selected position.

To combine panes into one tabbed panel

- Click and drag the title bar of the pane to the title bar of the pane with which you want to combine it.

  This creates a panel. You can dock all panes into a panel.

To remove panes from a panel

- Click and drag the title bar of the pane away from the panel.

To reset the panel layout

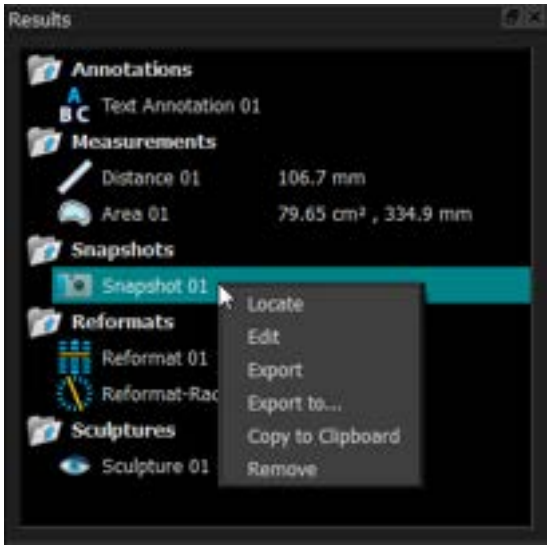
- Select the button  and choose **View > Reset Layout** from the menu, or press F6.

Results Pane

The Results pane lists the results of actions performed on the volume: annotations, measurements, snapshots, reformats and sculptures.

You can collapse and expand the branches of the tree by double-clicking the top-level nodes.

You can right-click a result to perform actions on the result. Depending on the type of result, you will get a context menu with several options.



Locate: The volume is rotated to the orientation at which the result was originally performed.

Locate may be grayed out. You can make this menu item active by canceling or finishing the active procedure.

Edit: The Properties pane is activated. You can modify the properties.

Save: The result is saved to the system. Results that are saved (as opposed to exported) can be loaded back into Medis Suite.

This option is only available for systems where 3D View is integrated.

Export: The result is exported to the system. Results that are exported (as opposed to saved) cannot be loaded back into 3D View.

This option is only available for systems where 3D View is integrated.

Export to…: You are prompted to select a file path, after which the snapshot is exported to disk.

Copy to Clipboard: The result label and value (if applicable) are copied to the clipboard.

Remove: The result is deleted.

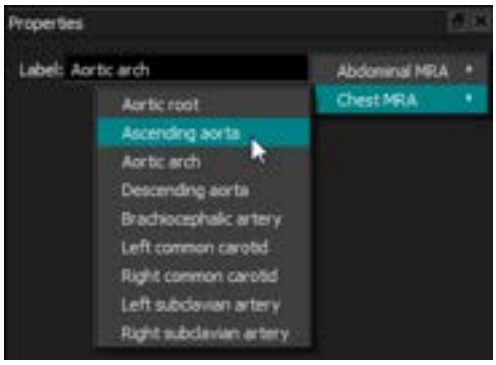
Properties Pane

The Properties pane shows the properties of the selected result. You can always modify the Label, but you must activate a reformat or sculpture to view or modify their other properties.

To modify a Label

1. On the Results pane, select the result.

2. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.



Or (annotations, measurements and snapshots only),

1. On the Results pane, right-click on the result and select **Edit**.
2. Select a predefined label, or type a custom label and press Enter.

To modify the other properties of a reformat or sculpture

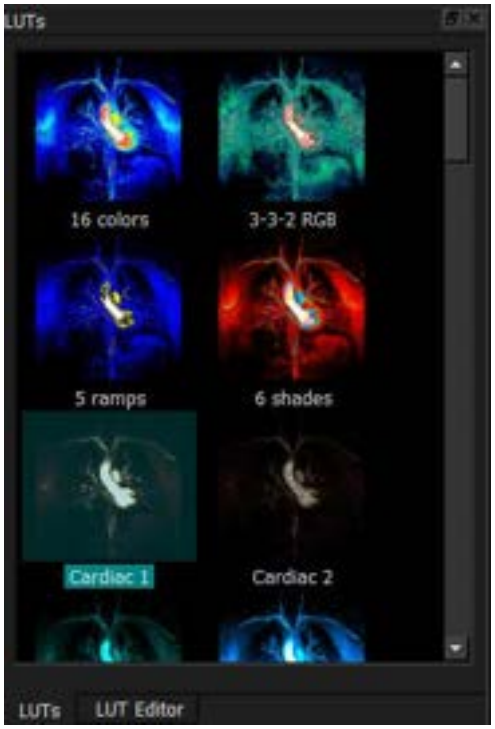
1. On the Results pane, right-click on the reformat or sculpture and select **Edit**.
2. On the Properties pane, modify the properties.

LUTs

LookUp Tables (LUTs) are used to enhance visualization in the 3DVR view. Rather than grey-scale values shown relative to a window and level, the grey-scale is mapped to a more general color scheme, which can help to visualize the data with the volume rendering (3DVR) view. For MR data, there is no canonical scale, and the LUT uses the window and level from the double oblique view as a default value. For CT data, Hounsfield units provide a canonical scale, and the LUT will use a predefined window and level, in Hounsfield units, if available.

LUTs Pane

The LUTs pane displays the available LUTs as thumbnails of the volume rendering (3DVR) view. Use the LUTs pane to select another LUT to apply to the 3DVR view. If CT data is loaded, and one of the LUTs Cardiac 1-4 is selected, it will use a predefined window and level.



The LUTs pane has a context menu, which you can access by right-clicking on a thumbnail. From the context menu, you can set the selected LUT as the default, save the selected LUT with a new name, or, if the LUT is not one of the standard LUTs, delete the selected LUT.

To set the selected LUT as the default

- Right-click on the desired LUT and select **Set As Default**.

The default LUT is the LUT first used when 3D View starts.

To save the selected LUT with a new name

1. Right-click on the desired LUT and select **Save As…**
2. Type the name of the new LUT and click OK.

To delete the selected LUT

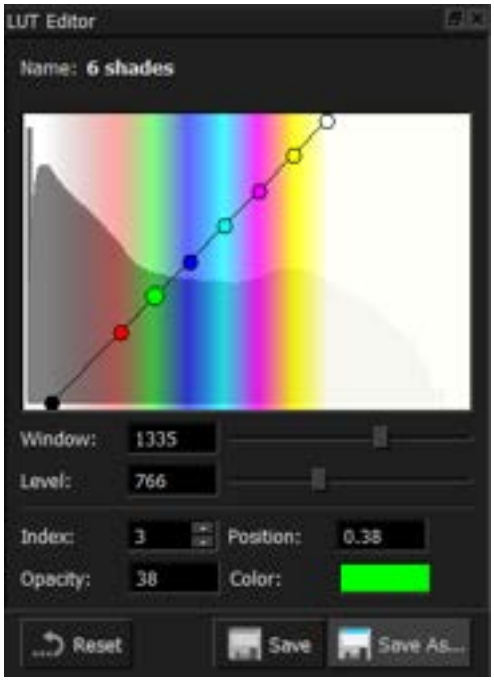
- Right-click on the desired LUT and select **Delete**.

Or,

- Click on the desired LUT and press the Delete key.

LUT Editor Pane

You can create a new LUT, or modify an existing one, on the LUT Editor pane.



To aid in creating a LUT, a histogram is shown in grey in the chart on the LUT Editor pane. This indicates how many voxels in the original image occur for each grey-scale value. You may choose to display the grey values in a certain range with a specific color.

To create a LUT, you define any number of points, each with its own position, color and opacity.

To create a new point

- Click anywhere on the chart (except on a point).

To delete a point

- Click on the point and press the Delete key.

Or,

- Select the point, then right-click on the chart and select **Delete Active Point**.

To change the color of a point

- Click on the **Color** field to open the color picker.

The transition between neighboring colors is smoothed.

The position ranges from 0.0 to 1.0, and the opacity ranges from 0 to 100.

3D View is delivered with a set of predefined LUTs which may be modified, but not saved.

To return a predefined LUT to its default settings

- Click the **Reset** button.

To save a modified LUT with a new name

- Click the **Save As…** button.

Changes to a predefined LUT are reverted with the **Save As…** action, and when 3D View is restarted.

To save changes to a custom LUT

- Click the **Save** button.

The Save button is only enabled once you have created your own LUT with **Save As…**, and then modified the custom LUT.

It is common to define a LUT with an ascending opacity, i.e. the larger the grey value, the larger the opacity.

To reset the LUT to a ramp

- Right-click on the chart and select **Reset to Ramp**.

A LUT is created with two points with ascending opacity.

The **Window** is the range of grey scales displayed. Voxels with grey scales outside that range are mapped to the nearest color in the LUT. The **Level** is the grey scale at the center of the **Window**. Thus, you can adjust the **Window** and **Level** to quickly include a select range of grey scale values.

Saving a LUT while CT data is loaded will cause the current **Window** and **Level** to be saved. They will then be taken as the default values if the LUT is used with CT data in the future. If the LUT is used with MR data, it will simply reuse the current **Window** and **Level**.

5.1.5 Image View

The Image View displays the currently loaded volume 2x2 in several different representations.

By default, the images in the Image View display a number of patient details and volume information. You can show or hide these overlays from the image.

To show or hide the patient or volume information

- Select the button  and choose **> Options**, select **Hangings**, and select or deselect **Show patient information**.

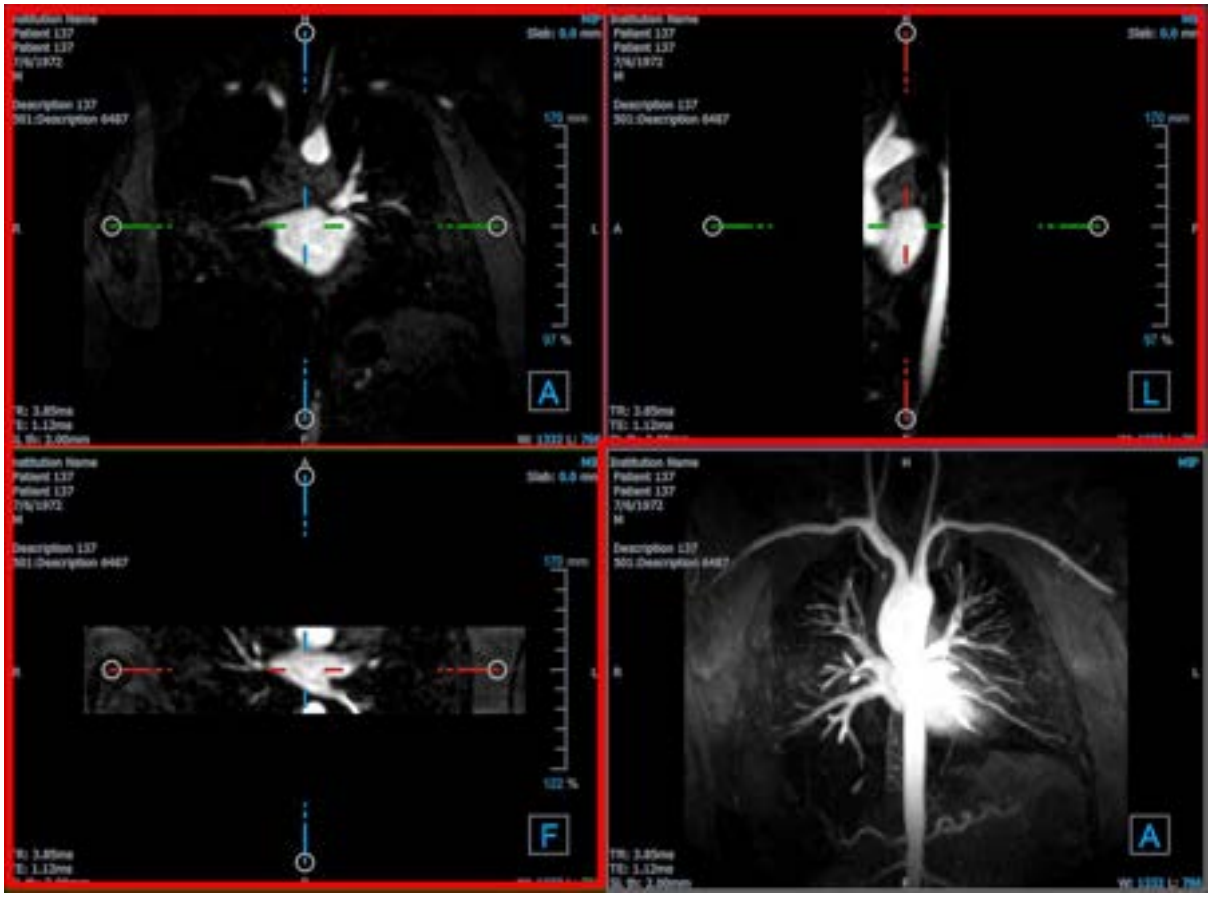
To temporarily hide all overlay graphics

- Hold down the ALT key and the right mouse button.

You can enlarge one of the viewports by double clicking on it.

Double-Oblique View

The three viewports highlighted below, collectively called the “double oblique” view (DOV), are always displayed. They show the volume from three perpendicular points of view.



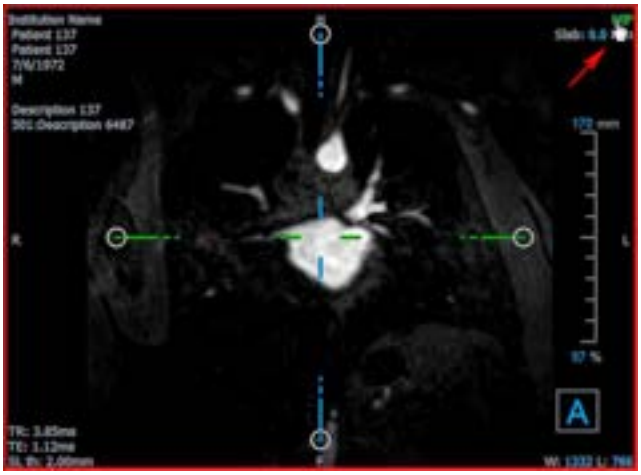
Slabs

Each double-oblique image is a maximum intensity projection (MIP), minimum intensity projection (MinIP) or Average image from a slice through the volume, called a slab. The slab thickness is displayed in the upper-right corner of each double-oblique viewport.

You can change the projection method performed on each slab among MIP, MinIP and Average. The MIP displays the maximum voxel value through the slab, the MinIP displays the minimum voxel value through the slab, and the Average displays the average voxel value through the slab.

To toggle among MIP, MinIP and Average

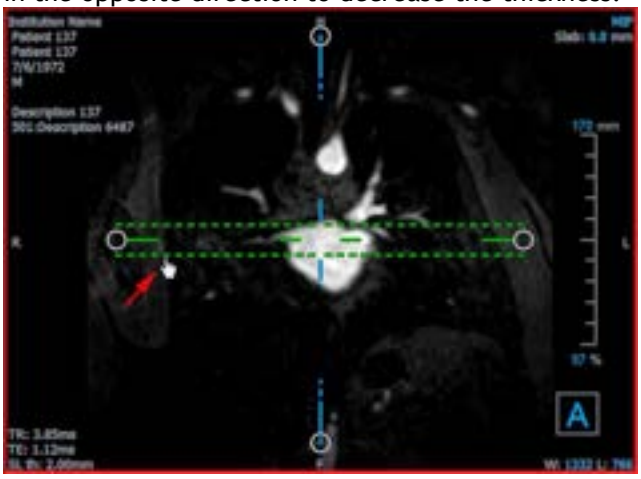
Click the overlay graphic in a double-oblique viewport.



You can change the thickness of the slab from which each double-oblique image is generated.

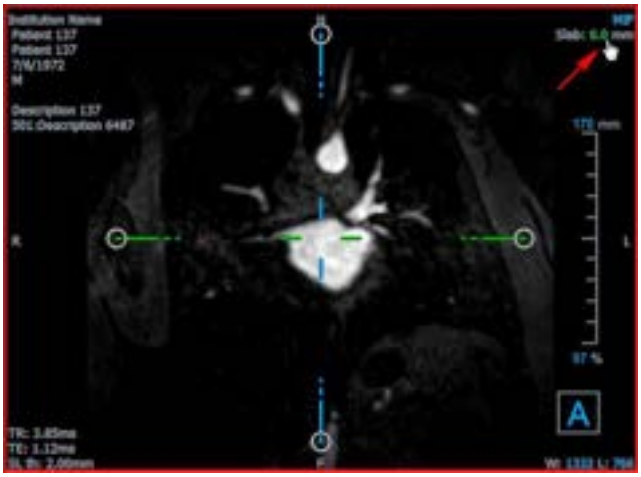
To change the double-oblique slab thickness

- Click the dashed segment of one axis and drag up or left to increase the slab thickness, or in the opposite direction to decrease the thickness.



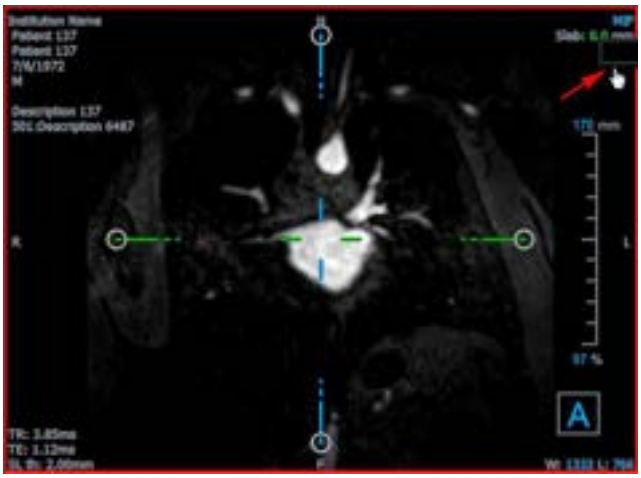
Or,

- Click the Slab interactive overlay graphics and drag up or down to increase or decrease the thickness.



Or,

- Right-click the Slab interactive overlay graphics and type a specific value into the entry field.



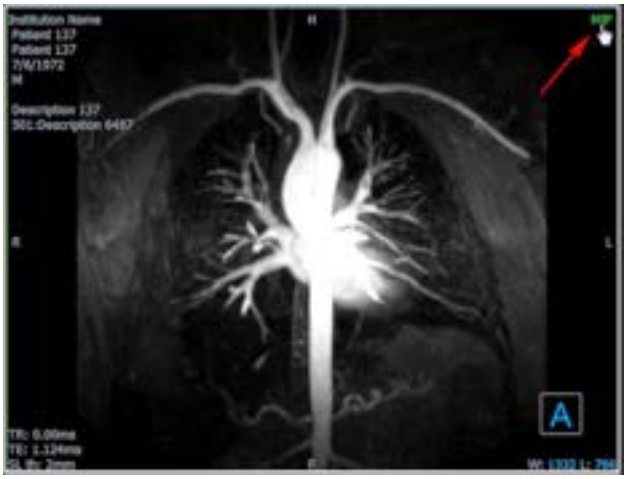
MIP, 3DVR and Stack Views

You can toggle the lower-right viewport among several different representations. By default the maximum intensity projection (MIP) of the entire volume is displayed. You can change the lower-right viewport to the volume rendering (3DVR) view or, when a reformat has been performed, to the Stack view.

The MIP and 3DVR views are enabled by default with the option,  and choose **> Options > Hangings > DoubleOblique > Enable hardware rendering**. If this option is unchecked, the MIP, 3DVR and LUT thumbnails will not be generated.

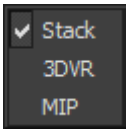
To toggle among MIP, 3DVR and Stack views

- Click the overlay graphic in the lower-right viewport.



Or,

- Right-click the overlay graphic in the lower-right viewport and select the view from the context menu.

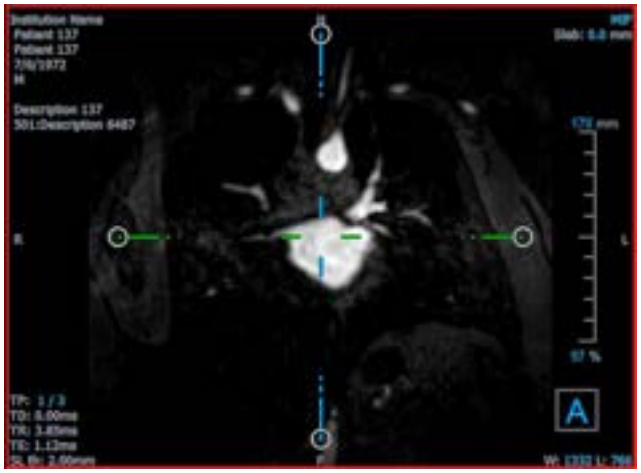


Or,

1. Click the lower-right viewport to select it.
2. Successively press the space bar or the backspace key.

Multi-Time Point Image View

You can display images with multiple time points. When such an image is loaded, additional overlay graphics are displayed.



TP: The time point / Total number of time points

TD: Trigger delay

You can move forward or backward in time in several ways.

To move forward or backward in time

- Click  or  on the Viewing toolbar to move to the previous or next time point.

Or,

- Activate the stacking tool  in the mouse controls toolbar and click and drag the mouse left and right to scroll through the time points.

Or,

- Press the left or right arrow key to move to the previous or next time point.

Or,

- Click the TP interactive graphics on one of the viewports to move to the next time point.

Or,

- Right-click the TP interactive graphics and enter the desired number of the time point.

Or,

- Select  and choose **Cine > Previous Time Point** or **View > Next Time Point**.

5.2 Image Navigation

This chapter describes how you can move around inside the volume to focus on what is most interesting.

To return the volume to its initial state

- Click  in the toolbar, or select  and choose **Initial View State**.

5.2.1 Double-Oblique View

The three viewports that make up the double-oblique view (DOV) show the volume from three perpendicular perspectives. Each perspective shows a slice at a specific depth with a certain thickness.

The orientation for each viewport is indicated by the orientation cube in the lower right. Rotating one viewport has the effect of moving a camera's perspective. As you rotate the volume, the orientation cube rotates, too. The letters on the cube indicate position:

 Anterior  Posterior  Head

Feet

Left

Right

Right-click on the orientation cube to select and rotate to one of the six primary orientations, the **Original** orientation produced while scanning, or **Reset** to the default orientation when 3D View first started.

The axes shown on each viewport also indicate orientation. Each color axis appears on two viewports, forming a plane: red, green and blue.

To show or hide the axes

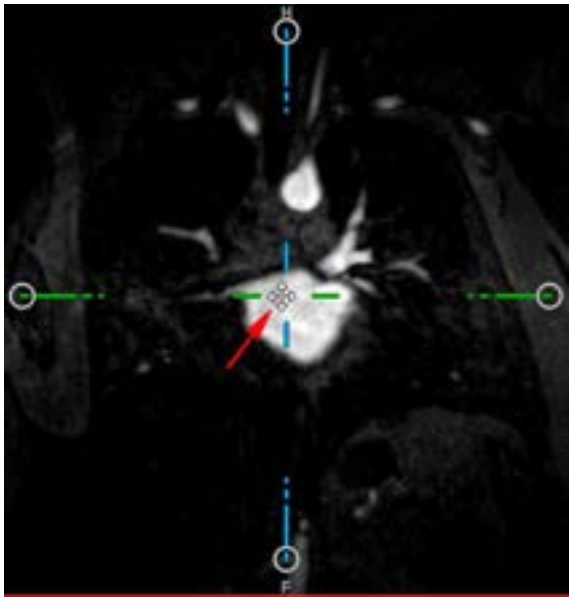
- Click in the toolbar, or press CTRL+K, or select and choose **Show/Hide Axes** in the menu.

You can navigate through the volume in many different ways. The primary method of navigation is to click and drag the axes, or rotate the axes. The axes are re-centered in the viewport after translating them.

To center the image at a new location

1. Move the mouse to the axes center. The mouse cursor changes to the Move cursor .
2. Click and drag the axes to the desired location.

   By default, the axes are re-centered in that viewport. To disable auto-centering, select and **Options > Hangings > DoubleOblique.** Deselect **Enable auto center**.

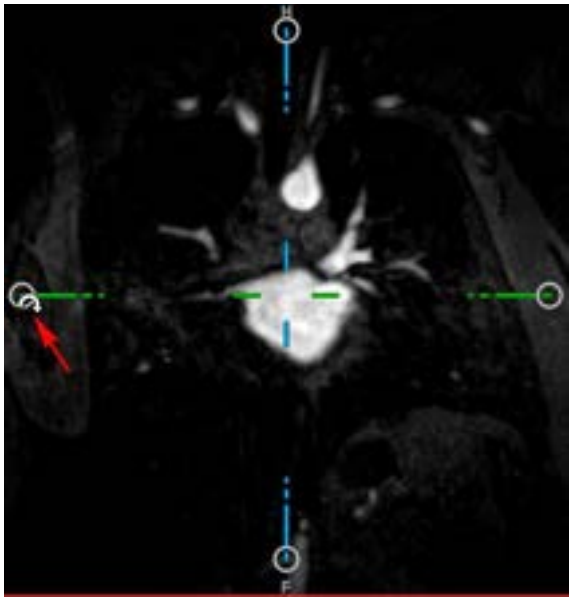


To drag the axes vertically, press the Ctrl key after pressing the mouse key, then drag.

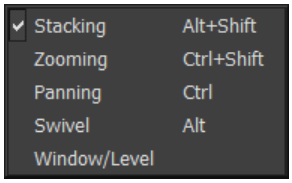
To drag the axes horizontally, press the SHIFT key after pressing the mouse key, then drag.

To rotate the image about the center of the axes

1. Move the mouse to a circular grip at the end of one axis. The mouse cursor changes to the Rotate cursor .
2. Click and drag the axes to the desired angle.



You can also select from one of several navigation methods on the left mouse button. Each method is available from the context menu of the double-oblique viewport. The selection in the context menu defines what the click-and-drag mouse function does.



The default action of the left mouse button can be changed with the option , select and **Options > Hangings > DoubleOblique.** Modify **Left Mouse Button Default Action > DOV**.

Stacking

You can move into and out of the viewport slices using **Stacking** when you see the Stack cursor .

To move in and out

- Scroll the mouse wheel.

Or,

- Press and hold ALT+SHIFT, then click and drag the mouse up and down.

Or,

1. Select **Stacking** from the context menu.

2. Click and drag the mouse forward and backward to scroll through the slices.

With either technique, if scrolling reaches either end it will stop at the first or last slice.

Zooming

You can zoom in and out of the viewport using **Zooming** when you see the Magnify cursor .

To zoom in and out

- Press and hold the CTRL key while turning the mouse wheel.

Or,

- Press and hold SHIFT+CTRL, then click and drag the mouse up and down.

Or,

- Click and drag on the interactive labels of the scale overlay graphics.

Or,

- Click on the interactive labels of the scale overlay graphics to zoom in.
  Right-click on the interactive labels to zoom out.

Or,

1. Select **Zooming** from the context menu.
2. Click and drag the mouse forward and backward to zoom in and out.

The current zoom factor is displayed on the scale overlay graphics in each viewport. The value above the scale is the physical size of the scale. The number below the scale indicates the relative zoom: 100% means one display pixel equals one acquisition voxel.

Panning

You can move the image within the viewport left, right, up and down using **Panning** when you see the Hand cursor .

To pan the image

- Press and hold the CTRL key, then click and drag the mouse in any direction.

Or,

- Middle-click and drag the mouse in any direction.

Or,

1. Select **Panning** from the context menu.
2. Click and drag the mouse in any direction.

Swivel

You can rotate the volume about the axes using **Swivel** when you see the Rotate cursor  .

To swivel about an axis

- Press and hold the ALT key, then click and drag the mouse in any direction.

Or,

1. Select **Swivel** from the context menu.
2. Click and drag the mouse in any direction.

The volume rotates around the axis (red, green or blue) perpendicular to the direction of mouse movement.

Window Width and Level

You can adjust the window width and level (WWL) when you see the WWL cursor  .

To adjust the window width and level

- Right-click and drag
  - Right or left to increase or decrease the width.
  - Up or down to increase or decrease the level.

Or,

- Click on the window width or level interactive graphics and drag up or down to increase or decrease the window width or level.

Or,

- Right-click on the window width or level interactive graphics and enter the desires values.

Or,

1. Select **Window/Level** from the context menu
2. Click and drag
   - Right or left to increase or decrease the width.
   - Up or down to increase or decrease the level.

 The current window width and level are displayed in the lower-right overlay graphics in each viewport.

 **To reset the window width and level**

- Press the 1 key.

Or,

- Click the middle mouse button on the window width and level interactive graphics.

Different window width and level values are maintained for the double-oblique view, MIP view and 3DVR view.

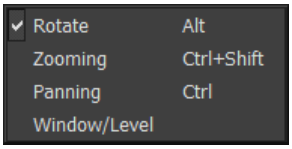
5.2.2 MIP, 3DVR and Stack Views

You can view the maximum intensity projection (MIP), volume rendering (3DVR) and Stack views in the lower-right viewport as explained in section 0.

The MIP and 3DVR views are enabled by default with the  and **Options > Hangings > DoubleOblique > Enable hardware rendering**. If this option is unchecked, the MIP, 3DVR and LUT thumbnails will not be generated.

You can select from one of several navigation methods on the left mouse button. Each method is available from the context menu of the lower-right viewport. The selection in the context menu defines what the click and drag mouse function does.

Stack



MIP and 3DVR

The default action of the left mouse button can be changed with the option  and **Options > Hangings > DoubleOblique > Left Mouse Button Default Action > Stack** or **MIP and VR**.

Rotate

You can rotate the volume rendering in 3D space using **Rotate** when you see the Rotate cursor  .

To rotate

- Press and hold the ALT key, then click and drag the mouse in any direction.

Or,

1. Select **Rotate** from the context menu.
2. Click and drag the mouse in any direction.

The volume rotates around the axis perpendicular to the direction of mouse movement.

Zooming

You can zoom in and out of the viewport using **Zooming** when you see the Magnify cursor  .

To zoom in and out

- Press and hold the CTRL key while turning the mouse wheel.

Or,

- Press and hold SHIFT+CTRL, then click and drag the mouse up and down.

Or,

- (Stack only) Click and drag on the interactive labels of the scale overlay graphics.

Or,

- (Stack only) Click on the interactive labels of the scale overlay graphics to zoom in. Right-click on the interactive labels to zoom out.

Or,

1. Select **Zooming** from the context menu.
2. Click and drag the mouse forward and backward to zoom in and out.

 The current zoom factor is displayed on the scale overlay graphics in the Stack viewport. The value above the scale is the physical size of the scale. The number below the scale indicates the relative zoom: 100% means one vertical display pixel equals one acquisition voxel.

 You can reset the zoom factor to 100% by clicking the middle mouse button over the zoom interactive graphics.

Panning

You can move the image within the viewport left, right, up and down using **Panning** when you see the Hand cursor  .

To pan the image

- Press and hold the CTRL key, then click and drag the mouse in any direction.

Or,

- Middle-click and drag the mouse in any direction.

Or,

1. Select **Panning** from the context menu.
2. Click and drag the mouse in any direction.

Window Width and Level

You can adjust the window width and level (WWL) in two ways when you see the WWL cursor  .

To adjust the window width and level

- Right-click and drag
    - Right or left to increase or decrease the width.
    - Up or down to increase or decrease the level.

Or,

1. Select **Window/Level** from the context menu
2. Click and drag
    - Right or left to increase or decrease the width.
    - Up or down to increase or decrease the level.

The current window width and level are displayed in the lower-right overlay graphics.

The 3DVR window width and level can also be adjusted on the LUT Editor.

You can reset the window width and level by pressing the 1 key.

Different window width and level values are maintained for the double-oblique view, MIP view and 3DVR view.

5.3 Results

Results are the work products that you can produce with 3D View. In this application the results you can create include:

- Annotations,
- Distance measurements,
- Area measurements,
- Double distance measurements,
- Snapshots,
- Sculptures to remove extraneous information,
- Reformats in a rectangular format,
- Reformats in a radial format, and
- You can save all the results by various means.

3D View is delivered with a default set of predefined result labels. The predefined labels can be modified in the file Q3DViewProcedureLabels.xml found in your application data folder.

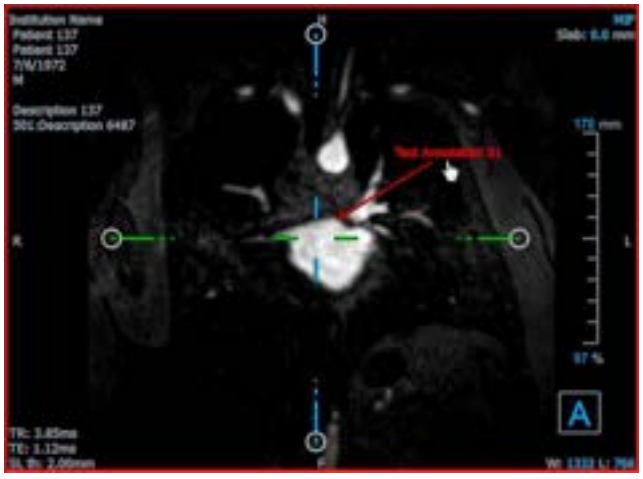
5.3.1 Annotations

This chapter covers adding, editing and deleting annotations.

You can change the default text label, graphics color, and arrowhead style by selecting  and **Options > Results > Text annotation**. The new graphics color and arrowhead style are applied to existing annotations.

Adding Annotations

You can add annotations to a viewport to mark it for analysis or to draw attention to specific details. Annotations are displayed in the Image View, and listed on the Results pane.



When you navigate to another location in the volume, your annotation may not be displayed on the double-oblique viewport. This is because the point to which the annotation refers does not lie on the currently visible slice. To see your annotation again, right-click on the annotation on the Results pane and select **Locate**; or double click on the annotation on the Results pane.

To add an annotation

1. Click  in the toolbar, or select **Results > Text Annotation** in the menu.
2. Click and drag in the image to draw the arrow.
3. Select a predefined label, or type a custom label and press Enter.
4. Click and drag the arrowhead or the text to adjust the exact location of the image that you want to mark.
5. Click outside the annotation. The graphic changes to white indicating it has left edit mode.

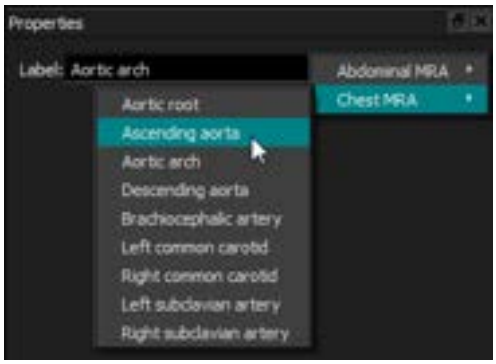
This adds the annotation to the Annotations list in the Results pane. At any time while the annotation is still active you can press Esc to remove the annotation.

Editing Annotations

You can modify the text and location of annotations that were added previously.

To edit annotation text

1. On the Results pane, select the result.
2. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.



Or,

1. On the Results pane, right-click on the result and select **Edit**.
2. Select a predefined label, or type a custom label and press Enter.

To edit the annotation location

1. Click the annotation graphic.
2. Click and drag the arrowhead or the text to adjust the exact location of the image that you want to mark.

Deleting Annotations

You can delete any annotation that was added to a viewport.

To delete an annotation

- Click the annotation graphic and press Delete.

Or,

1. Select the annotation in the Annotations list in the Results pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the annotation.

5.3.2 Measurements

This section covers the following topics:

- Creating, editing and deleting distance measurements
- Creating, editing and deleting area measurements, and
- Creating, editing and deleting double distance measurements.

Distance Measurements

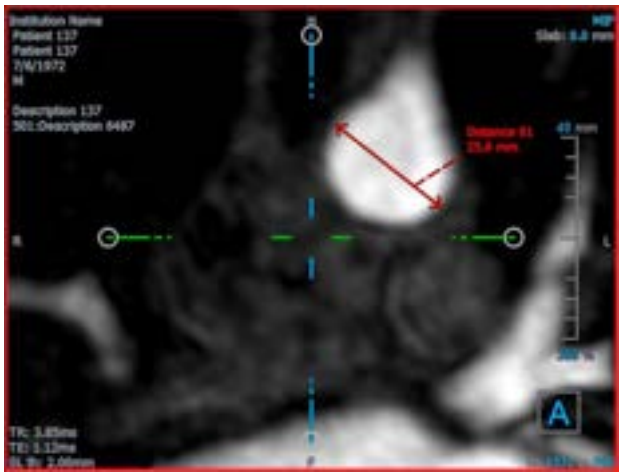
You can measure the distance from one point to another. When you have measured a distance, you can modify the annotation and the end points of the measurement.

You can change the default text label, graphics color, and arrowhead style by selecting  and **Options > Results > Distance measurement**. The new graphics color and arrowhead style are applied to existing double distance measurements.

 When you navigate to another location in the volume, your measurement may not be displayed on the double-oblique viewport. This is because the points between which you measured do not lie on the currently visible slice. To see your measurement again, right-click on the measurement on the Results pane and select **Locate**; or double click on the measurement on the Results pane.

Creating Distance Measurements

You can add distance measurements to a viewport for analysis. Distance measurements are displayed in the Image View, and listed on the Results pane.



To measure a distance

1. Click  in the toolbar, or press the D key, or select **Results > Distance Measurement** in the menu.
2. Click and drag in the image from the start point of the measurement to the end point.
3. Select a predefined label, or type a custom label and press Enter.
4. Click and drag either arrowhead or the text to adjust the points of the image between which you want to measure.
5. Click outside the measurement. The graphic changes to white indicating it has left edit mode.

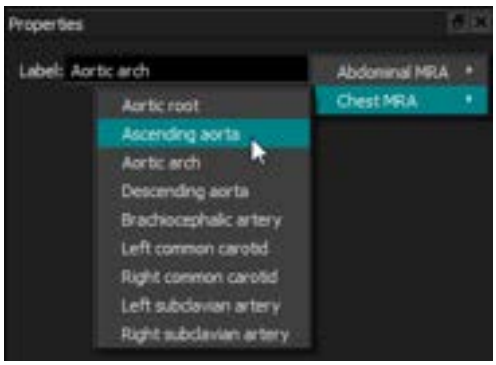
This adds the measurement to the Measurement list in the Results pane. At any time while the measurement is still active you can press Esc to remove the measurement.

Editing Distance Measurements

You can modify the text and location of distance measurements that were added previously.

To edit distance measurement text

1. On the Results pane, select the result.
2. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.



Or,

1. On the Results pane, right-click on the result and select **Edit**.
2. Select a predefined label, or type a custom label and press Enter.

To edit distance measurement end points

1. Click the distance measurement graphic.
2. Click and drag either arrowhead to adjust the points in the image between which you want to measure.

Copying Distance Measurements

You can copy a distance measurement to the clipboard.

To copy a distance measurement

- On the Results pane, right-click on the result and select **Copy to Clipboard**.

The result label and value are copied to the clipboard.

Deleting Distance Measurements

You can delete any distance measurement that was added to a viewport.

To delete a distance measurement

- Click the distance measurement graphic and press Delete.

Or,

1. Select the distance measurement in the Measurements list on the Results pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the distance measurement.

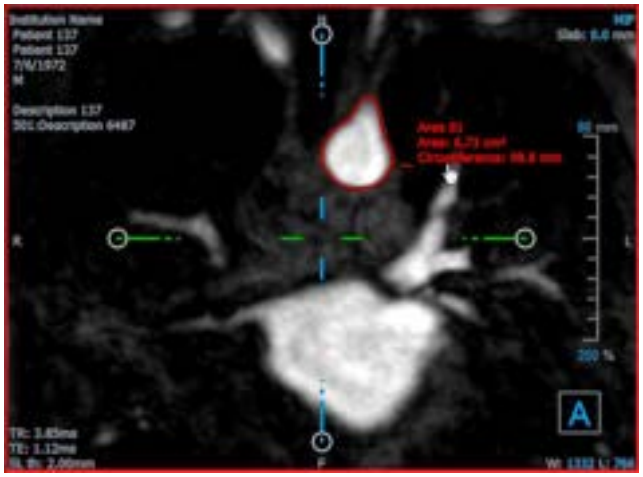
Area Measurements

You use the area measurement tool to draw and measure 2D areas. When you have measured an area, you can modify the area contour or annotation.

You can change the default text label, graphics color, and which measurements are displayed by selecting  and **Options > Results > Area measurement**. The new graphics color is applied to existing area measurements.

When you navigate to another location in the volume, your measurement may not be displayed on the double-oblique viewport. This is because the 2D plane on which you measured the area is not coplanar with the currently visible slice. To see your measurement again, right-click on the measurement on the Results pane and select **Locate**; or double click on the measurement on the Results pane.

Creating Area Measurements



To measure an area

1. Click  in the toolbar, or press the A key, or select **Results > Area Measurement** in the menu.

2. Click and drag to draw the area. The contour is automatically closed when you release the mouse button.

3. Modify the contour as necessary (see Editing Area Measurements below).

4. In the Properties pane, check **Area** or **Circumference** to display either or both measurements.

5. Click outside the contour. The graphic changes to white indicating it has left edit mode.

This adds the measurement to the Measurement list in the Results pane. At any time while the measurement is still active you can press Esc to remove the measurement.

Editing Area Measurements

To modify the contour

1. Click the contour to make it active.
2. Near the existing contour click and drag an altered contour. The alteration will be combined with the original.

   Or,

   Right-click on the contour and drag it, using the rubber-band tool  .

3. Click outside the contour. The graphic changes to white indicating it is no longer in edit mode.

Copying Area Measurements

You can copy an area measurement to the clipboard.

To copy an area measurement

- On the Results pane, right-click on the result and select **Copy to Clipboard**.

The result label and value(s) are copied to the clipboard.

Deleting Area Measurements

You can delete any area measurement that was added to a viewport.

To delete an area measurement

- Click the area measurement graphic and press Delete.

Or,

1. Select the area measurement in the Measurements list on the Results pane.

2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the area measurement.

Double Distance Measurements

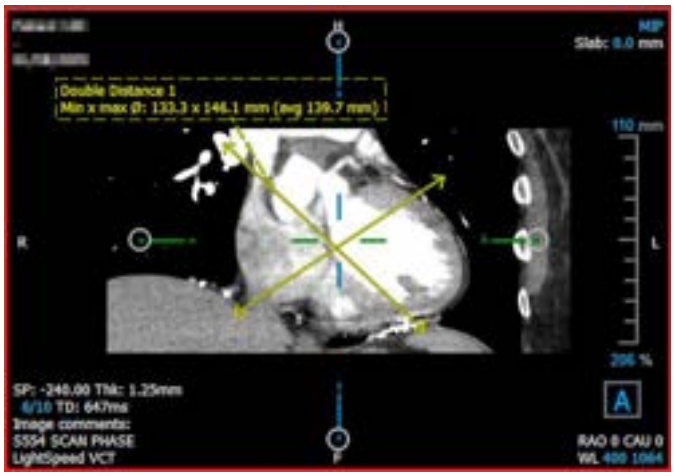
You use the double distance measurement tool to draw and measure two related distances. When you have measured a double distance, you can modify the annotation and the end points of the measurement.

You can change the default text label, graphics color for active and inactive status, and arrowhead style by selecting  and **Options > Results > Double Distance measurement**. The new graphics color and arrowhead style are applied to existing distance measurements.

When you navigate to another location in the volume, your measurement may not be displayed on the double-oblique viewport. This is because the points between which you measured do not lie on the currently visible slice. To see your measurement again, right-click on the measurement on the Results pane and select **Locate**.

Creating Double Distance Measurements

You can add double distance measurements to a viewport for analysis. Double Distance measurements are displayed in the Image View, and listed on the Results pane.



To measure a double distance

1. Click  icon in the toolbar, or press the R key, or select **Results > Distance Measurement** in the menu.

2. In the same way than for the Distance measurement, click and drag in the image twice to create the two measurements.

3. Select a predefined label, or type a custom label and press Enter.

4. Click and drag any of the following elements to suit your needs:

- Arrow heads
- Measurement lines' bodies
- Text

5. Click outside the measurement. The graphic changes to inactive indicating it has left edit mode.

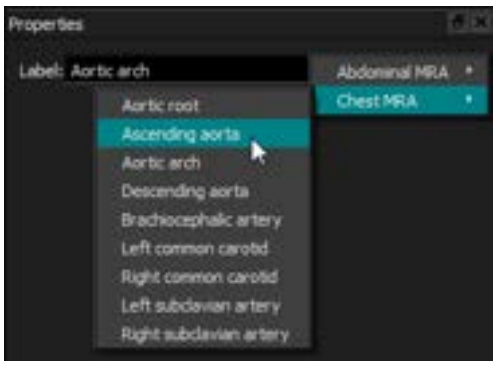
This adds the measurement to the Measurement list in the Results pane. At any time while the measurement is still active you can press Esc to remove the measurement.

Editing Double Distance Measurements

You can modify the text and location of the double distance measurements that were added previously.

To edit double distance measurement text

1. On the Results pane, select the result.
2. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.



Or,

1. On the Results pane, right-click on the result and select **Edit**.
2. Select a predefined label, or type a custom label and press Enter.

To edit double distance measurement end points

1. Click the double distance measurement graphic.
2. Click and drag any arrow head to adjust the points in the image between which you want to measure.

Copying Double Distance Measurements

You can copy a double distance measurement to the clipboard.

To copy a double distance measurement

- On the Results pane, right-click on the result and select **Copy to Clipboard**.

The result label and values are copied to the clipboard.

Deleting Double Distance Measurements

You can delete any double distance measurement that was added to a viewport.

To delete a double distance measurement

- Click the double distance measurement graphic and press Delete.

Or,

1. Select the double distance measurement in the Measurements list on the Results pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the double distance measurement.

5.3.3 Snapshots

You can save snapshots as evidence of a diagnosis. Snapshots are displayed on the Properties pane, and are listed on the Results pane. When a snapshot is created, you can modify the name at any time. A snapshot can be exported as described in section 0.

You can change the default text label by selecting  and **Options > Results > Snapshot**.

A snapshot contains by default all graphics elements but no text. You can also include all text for future snapshots by checking the option  and **Options > Results > Snapshot > Include overlay text**.

 When you navigate to another location in the volume, the annotations and measurements shown in the snapshot may not be displayed on the double-oblique viewport. This is because the points at which the annotations and measurements were created do not lie on the currently visible slice. To return to the same slice where a snapshot was created, right-click on the snapshot on the Results pane and select **Locate**; or double click on the snapshot on the Results pane.

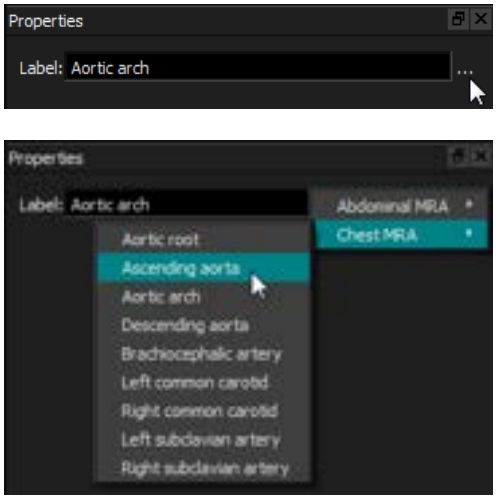
Creating Snapshots

You can create a snapshot of the current state of any viewport.

To save a snapshot

1. Click  in the toolbar, or press the S key, or select **Results > Snapshot** in the menu.
2. Click the viewport that you want to save as a snapshot.

3. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.



Deleting Snapshots

You can delete any snapshot that was created.

To delete a snapshot

1. Select the snapshot in the Snapshots list on the Results pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the snapshot.

5.3.4 Sculpting

You can remove extraneous information from the volume using sculpting. This can help draw attention to the subject of interest. Once created, you can later modify a sculpture. Sculptures are usually saved as part of a reformat.

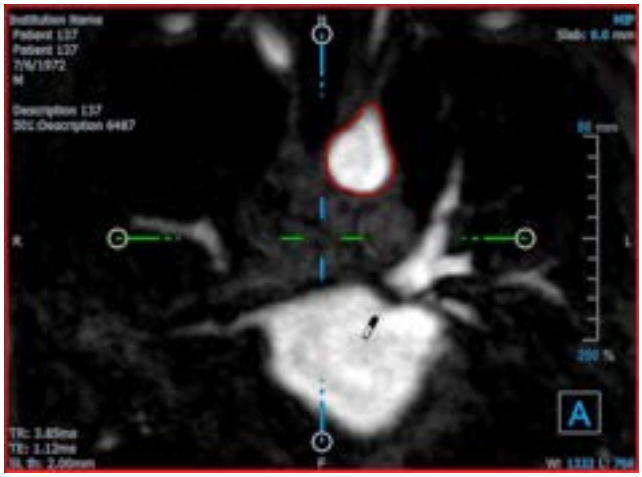
You can change the default text label by selecting  and **Options > Results > Sculpture**.

Creating Sculptures

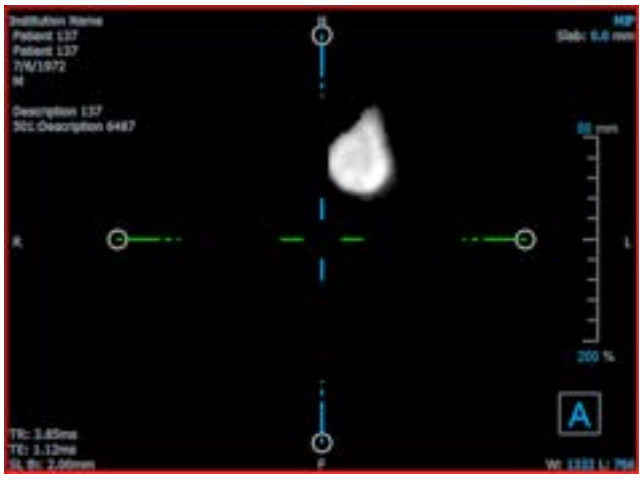
Sculpting is done by drawing a 2D contour which is then projected through the volume. Thus, it can be useful to first orient the volume strategically before drawing the contour. You can then remove (or restore) the voxels inside or outside the contour.

Original

(with sculpture contour)



Sculpted



To create a sculpture

1. Click  in the toolbar, or select **Results > Sculpture** in the menu.
2. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.
3. Click and drag to draw the contour. The contour is automatically closed when you release the mouse button.

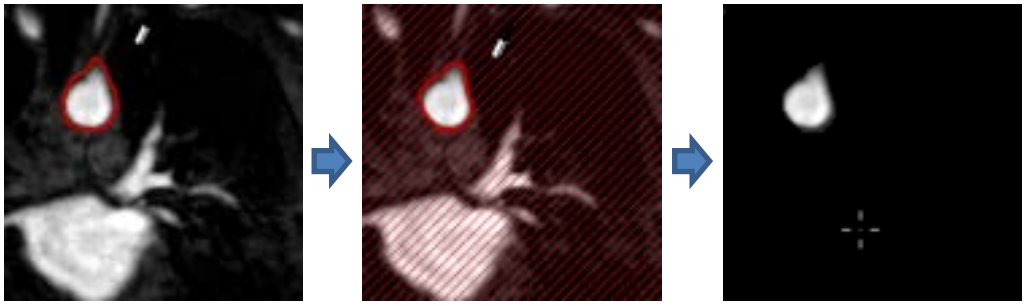
   Anytime a contour is active, you can delete it by pressing the Delete key.
4. Modify the contour as necessary.

   - Near the existing contour click and drag an altered contour. The alteration will be combined with the original.

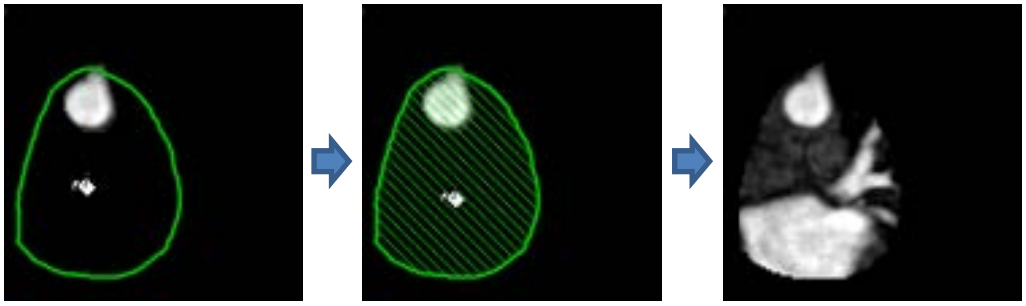
   Or,

   - Right-click on the contour and drag it, using the rubber-band tool .
5. On the Properties pane, select the desired **Action**.

With  **Exclude** selected the mouse cursor changes to an eraser  in the viewport.



With  **Include** selected the mouse cursor changes to a paint bucket  in the viewport.



6. Click inside or outside the contour to perform the selected action.

    Pressing the SHIFT key before the click performs the selected action on the opposite region, inside instead of outside or outside instead of inside.

7. Navigate in the volume as desired.

   - Stacking: Wheel.
   - Zooming: CTRL+wheel.
   - Panning: CTRL+click and drag, or middle-click and drag.
   - Rotate: ALT+click and drag.
   - Window width and level: Right-click and drag.

8. Repeat steps 3 – 7 as necessary.

9. Click **Finish** on the Properties pane.

 While editing a sculpture, you can hide the axes if they get in the way by toggling the **Axes** toolbar button  .

 You can restore the complete volume temporarily.

- If you are editing the sculpture, clear the **Apply sculpture** checkbox on the Properties pane.
- If you are not editing the sculpture, right-click on the sculpture on the Results pane and clear the checkbox next to **Apply**.

You can undo or redo an action by clicking the  or the  button. You can undo all actions by clicking the  button.

Editing Sculptures

You can edit the sculpture label in any state, but to edit the sculpture itself you must enter its edit mode.

To edit sculpture text

1. On the Results pane, select the sculpture.
2. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.

Or,

1. On the Results pane, right-click on the result and select **Edit**.
2. Select a predefined label, or type a custom label and press Enter.

To edit a sculpture

1. On the Results pane, right-click on the result and select **Edit**.
2. Follow the instructions in section 0 beginning at step 3.

Deleting Sculptures

You can delete any sculpture.

To delete a sculpture

1. Select the sculpture in the **Sculptures** list on the Results pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

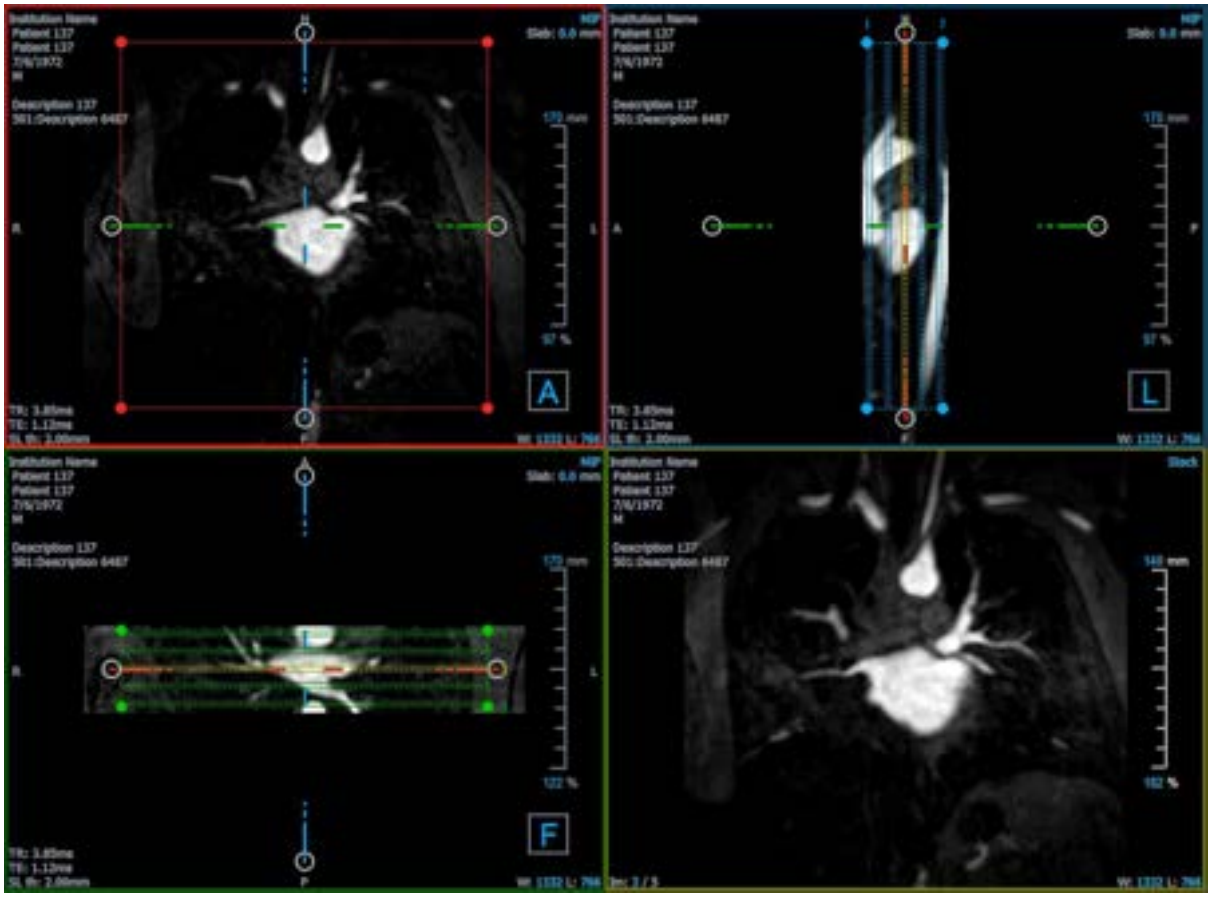
This deletes the sculpture.

5.3.5 Reformatting

You can create a new volume based on a sampling of the existing volume at any affine transformation, such as scaling, rotation, or translation, achieved through the 3D View user interface. You can also create a new volume based on a radial sampling of the existing volume.

Stack Reformatting

A stack reformat is a sampling of the existing volume at the translation, rotation and zoom currently displayed in the double-oblique view. The sampling is stored as a series of slices. The sample spacing is defined as a property of the reformat.



You can change the default properties by selecting  and **Options > Results > Reformat**.

Stack reformats can be saved in DICOM format and reopened in 3D View. Stack reformats can also be saved as a video in AVI format. Videos must be opened with a compatible viewer.

Creating Stack Reformats

You may want to orient the volume before performing a stack reformat. Stack reformats are listed on the Results pane.

To create a stack reformat

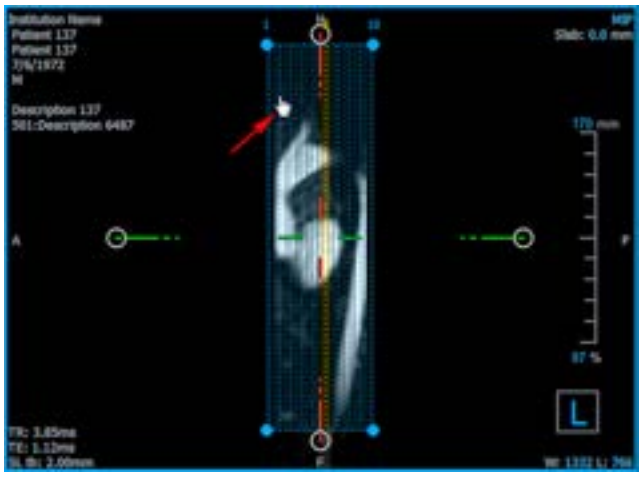
1. Click  in the toolbar, or  and **Calipers > Reformat** in the menu.
2. Click in the viewport that is coplanar to the first slice.
   Overlay graphics appear that indicate the initial geometry of the stack.
   The lower-right viewport switches to the Stack view and shows the reformatted slices.

3. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.
4. Adjust other properties as necessary (see sections 0 and 0). You can also position the overlay graphics with the mouse, or modify the size using the circular grip handles. The currently displayed slice in the Stack view is updated for each change.
5. Click **Finish** on the Properties pane. The remaining slices for the Stack view are calculated.

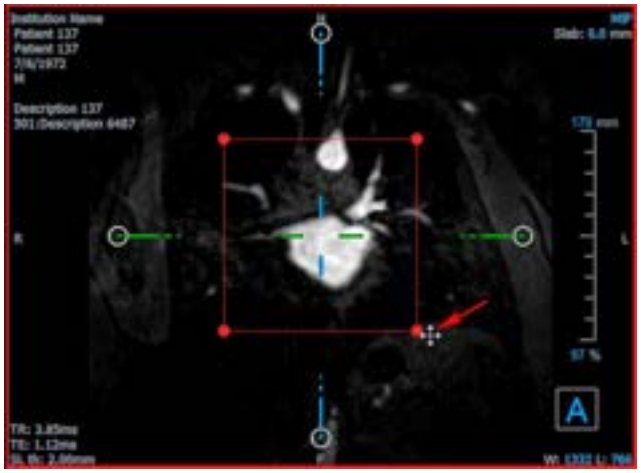
Stack Reformat Interactive Graphics

When a stack reformat is active, you can manipulate the interactive graphics in several ways.

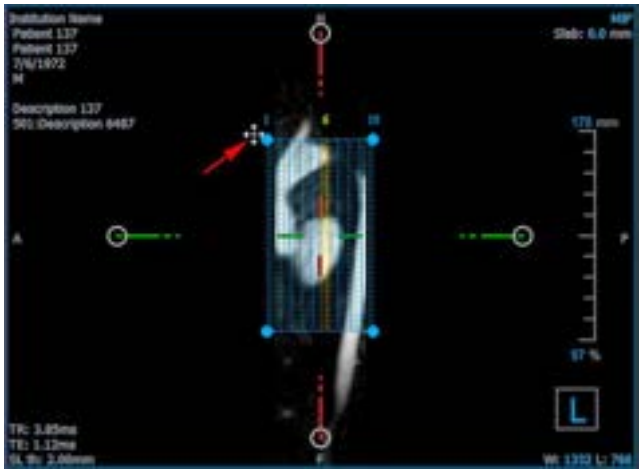
When the Pointing mouse cursor is visible, you can translate the volume on any double-oblique viewport.



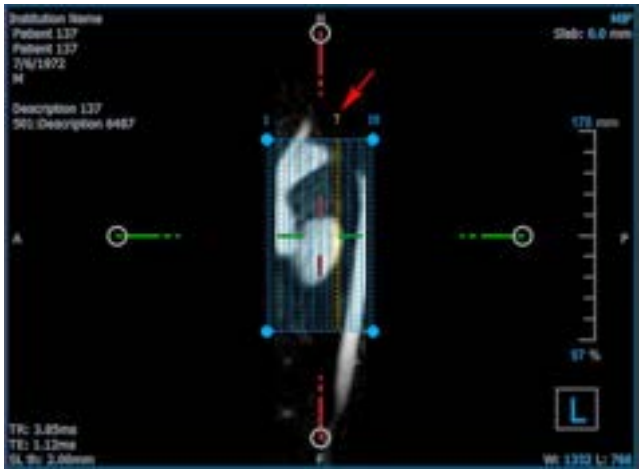
You can adjust the size of each slice on the top view with the circular grip handles.



You can adjust the number of slices on the side view with the circular grip handles.



Using the scroll wheel in the Stack view in the lower-right viewport, you can scroll through the current set of slices. The position of the slice is indicated by the yellow lines and indices in the two side-view double-oblique views.



Stack Reformat Properties

You can edit the properties of a stack reformat while creating it, or afterward by right-clicking on the stack reformat on the Results pane and selecting **Edit**.

Label: The text label for this reformat. Click the ellipsis to choose from a list of predefined labels, or type a custom label.

Method: The method (Stack) used to generate this reformat. This cannot be changed.

Projection method: The projection method (Maximum Intensity (default), Minimum Intensity, or Average Intensity) for this reformat.

Rows x Columns: The number of voxel rows and columns for each slice of the reformat. If **Enable square field of view** is checked, the format is restricted to square slices.

Field of View (mm): Physical size of each slice.

Slice count: Number of slices.

Slice thickness (mm): Physical thickness of each slice. The projection method is performed over this thickness.

Slice gap (mm): Physical distance between slices. A negative value results in overlap between the slices.

Resize mode: The property that changes when you move the circular grip handles of the stack.

Enable square field of view: When checked (default) the field of view is forced to be square. To improve compatibility with other applications, images saved with a non-square field of view are padded to produce a square image.

Show graphics: When checked shows the graphics overlay in the Image View.

Apply to all time points: When checked the reformat is applied for all time points.

Editing Stack Reformats

You can modify the properties of a stack reformat after creating it.

To edit a stack reformat

1. Right-click on the stack reformat on the Results pane and select **Edit**.
2. Modify the properties on the Properties pane as needed.
   Or,
   Click and drag the interactive graphics on the double-oblique view.
3. Click **Finish** on the Properties pane. The remaining slices for the Stack view are calculated.

Deleting Stack Reformats

You can delete any stack reformat that was created.

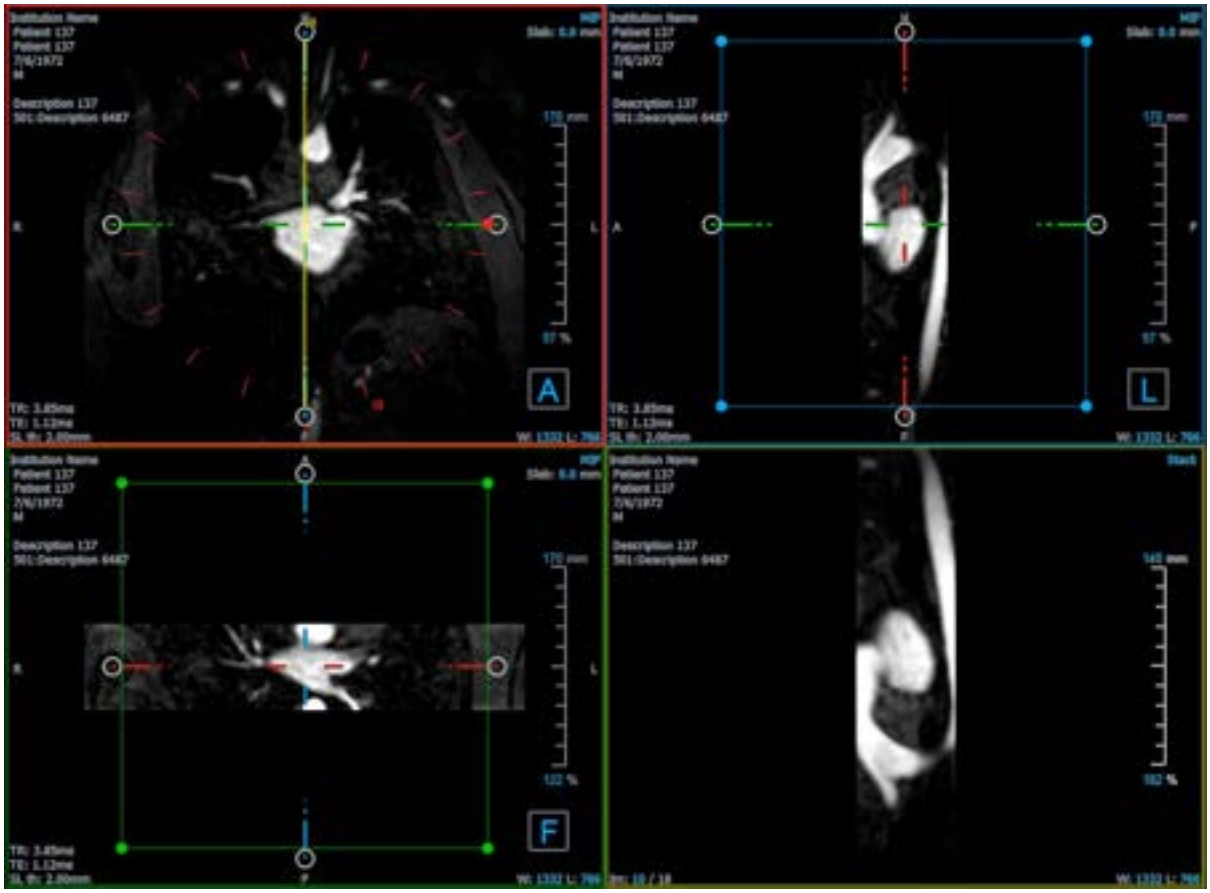
To delete a stack reformat

1. Select the stack reformat in the Reformats list on the Results pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the stack reformat.

Radial Reformatting

A radial reformat is a radial sampling of the existing volume at the translation, rotation and zoom currently displayed in the double-oblique view. The sampling is stored as a series of radially spaced slices. The sample spacing is defined as a property of the reformat.



You can change the default properties by selecting  and **Options > Results > Radial reformat**.

Radial reformats can be exported in DICOM format or as a video in AVI format, but neither can be reopened in 3D View. Videos must be opened with a compatible viewer.

Creating Radial Reformats

You may want to orient the volume before performing a radial reformat. Radial reformats are listed on the Results pane.

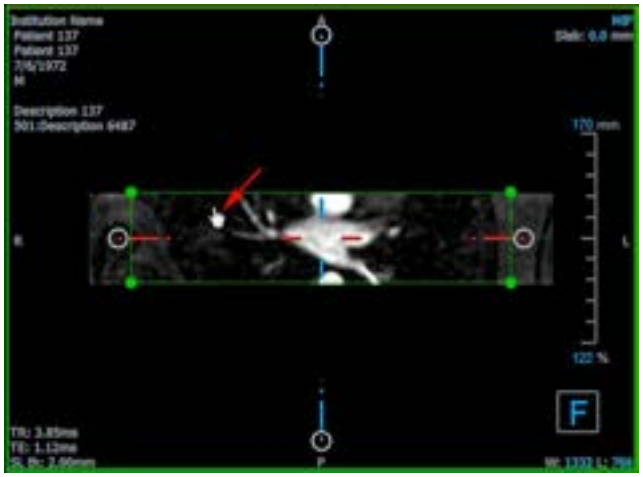
To create a radial reformat

1. Click  in the toolbar, or select  and **Calipers > Reformat-Radial** in the menu.
2. Click in the viewport where you want to view the radial spoke pattern.
   Overlay graphics appear that indicate the initial geometry of the reformat.
   The lower-right viewport switches to the Stack view and shows the reformatted slices.
3. On the Properties pane, click the ellipsis on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.
4. Adjust other properties as necessary (see sections 0 and 0). You can also position the overlay graphics with the mouse, or modify the size using the circular grip handles. The currently displayed slice in the Stack view is updated for each change.
5. Click **Finish** on the Properties pane. The remaining slices for the Stack view are calculated.

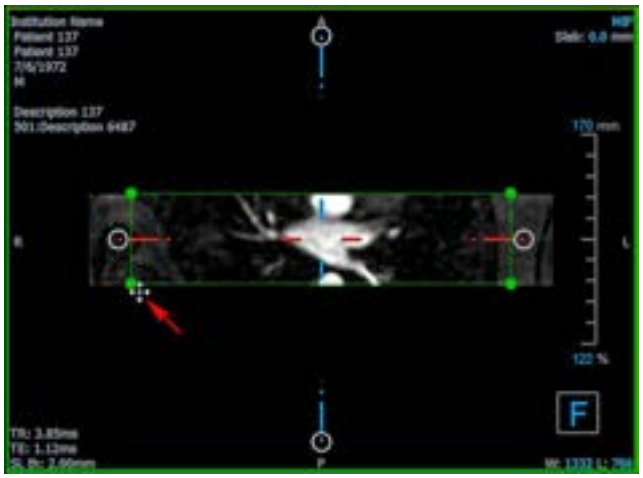
Radial Reformat Interactive Graphics

When a radial reformat is active, you can manipulate the interactive graphics in several ways.

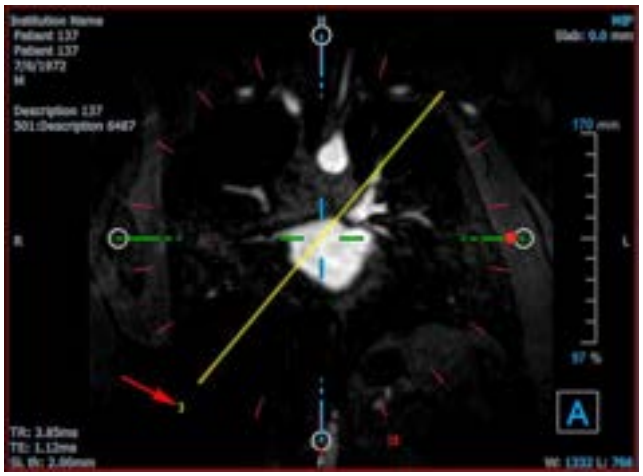
When the Pointing mouse cursor is visible, you can translate the volume on any double-oblique viewport.



You can adjust the size of a slice with the circular grip handles.



Using the scroll wheel in the radial double-oblique view or the Stack view in the lower-right viewport, you can scroll through the current set of slices. The position of the slice is indicated by the yellow line and index in the radial double-oblique view.



Radial Reformat Properties

You can edit the properties of a radial reformat while creating it, or afterward by right-clicking on the radial reformat on the Results pane and selecting **Edit**.

Label: The text label for this reformat. Click the ellipsis to choose from a list of predefined labels, or type a custom label.

Method: The method (Radial) used to generate this reformat. This cannot be changed.

Projection method: The projection method (Maximum Intensity (default), Minimum Intensity, or Average Intensity) for this reformat.

Rows x Columns:	The number of voxel rows and columns for each slice of the reformat. If **Enable square field of view** is checked, the format is restricted to square slices.
Field of View (mm):	Physical size of each slice.
Slice count:	Number of slices. The slices are always equally spaced over 360°.
Slice thickness (mm):	Physical thickness of each slice. The projection method is performed over this thickness.
Enable square field of view:	When checked (default) the field of view is forced to be square. To improve compatibility with other applications, images saved with a non-square field of view are padded to produce a square image.
Show graphics:	When checked shows the graphics overlay in the Image View.
Apply to all time points:	When checked the radial reformat is applied for all time points.

Editing Radial Reformats

You can modify the properties of a radial reformat after creating it.

To edit a radial reformat

1. Right-click on the radial reformat on the Results pane and select **Edit**.
2. Modify the properties on the Properties pane as needed.

   Or,

   Click and drag the interactive graphics on the double-oblique view.
3. Click **Finish** on the Properties pane. The remaining slices for the Stack view are calculated.

Deleting Radial Reformats

You can delete any radial reformat that was created.

To delete a radial reformat

1. Select the radial reformat in the Reformats list on the Results pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the radial reformat.

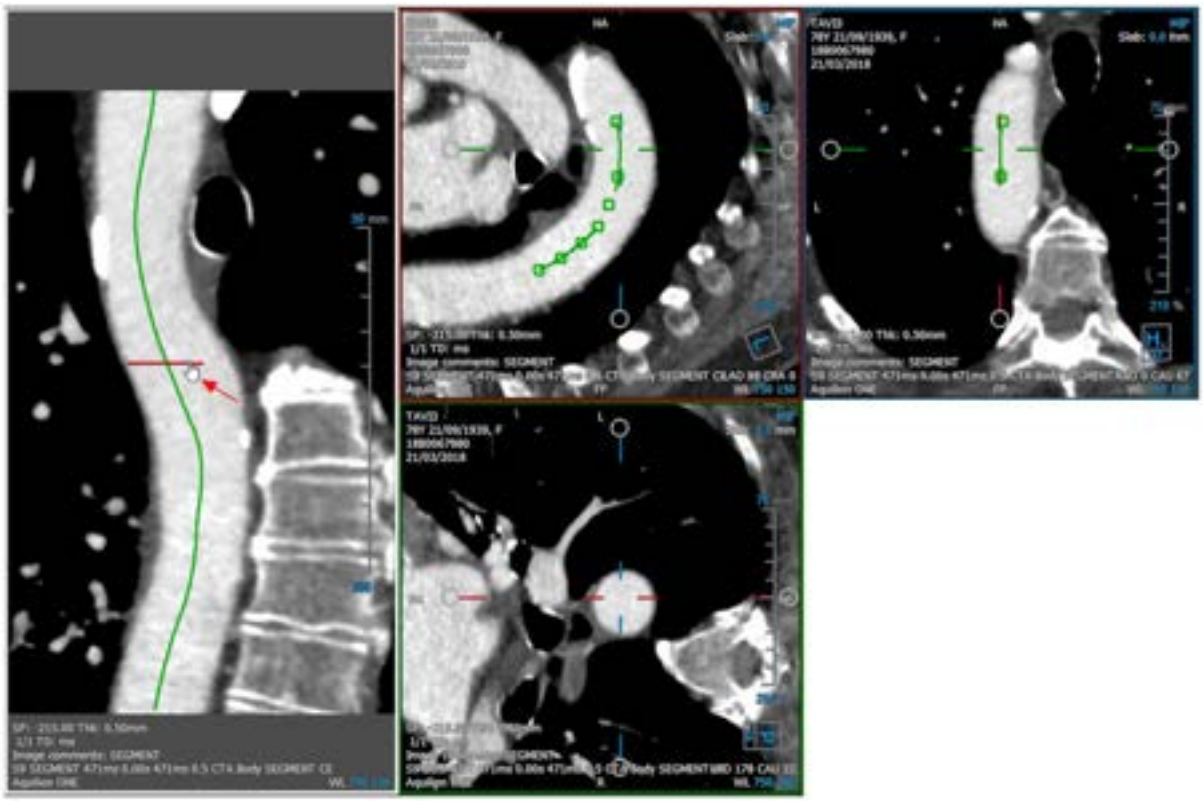
5.3.6 Curved Planar Reformats

You can create a curved planar reformat (CPR) using a set of interaction points clicked on the oblique viewports. This helps in visualizing vascular structures along their path. Multiple reformats can be created to represent and visualize several vessels.

The default text label for each procedure can be changed by selecting  and **Options > Hangings > CPR.**

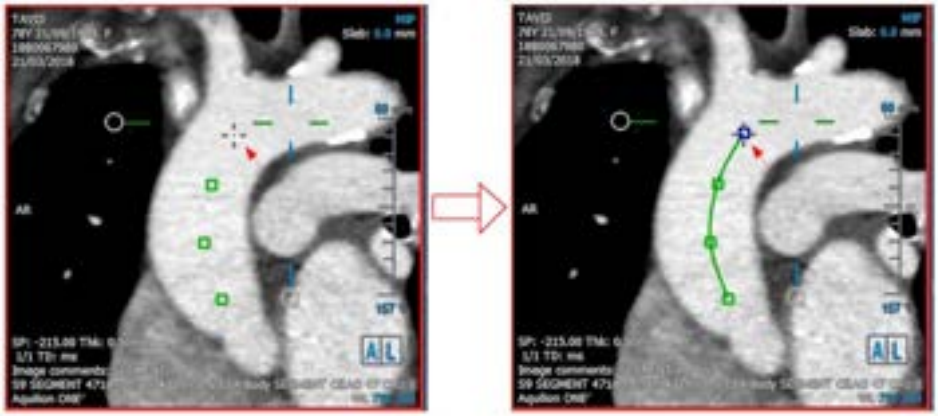
Creating CPRs

CPRs are derived using a set of 3D interaction points clicked by the user. Since such reformats are usually created for a vessel, choose a vessel-of-interest whose anatomy needs to be studied.



To create a path line along the vessel

1. Click (symbol) in the toolbar, or select **Procedures > CPR** in the menu.



2. You can use one of the two techniques below to enter the creation-mode (cross-hair mouse cursor):
   - On the Properties pane, click on Set A Point. The button will change its appearance indicating creation-mode.

   Or,
   - Hold down “C” key. Observe the change in the appearance of Set A Point.

You can start tracing a vessel by clicking on any oblique viewport. Once a minimum of 4 interaction points are clicked, a green path line connecting the points is visible on the viewports.

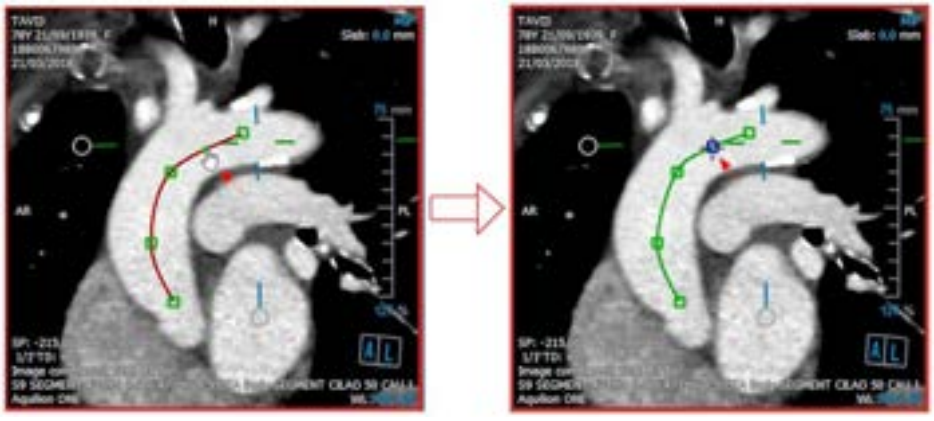
A path line is visible if a minimum of 4 interaction points are clicked. Depending on the plane of the drawn image, the complete (or a part of the) path line is shown.

To edit or delete an existing interaction point

1. You can drag an existing interaction point to a different location. The path line is automatically updated while this is done.
2. You can remove an existing interaction point with a right-click on the point.

To add an intermediate interaction point along the path

1. Hover over the path line using the mouse curser. Once you have reached the preferred location, left-click on the marker ball (green) that indicates the position of the new point.



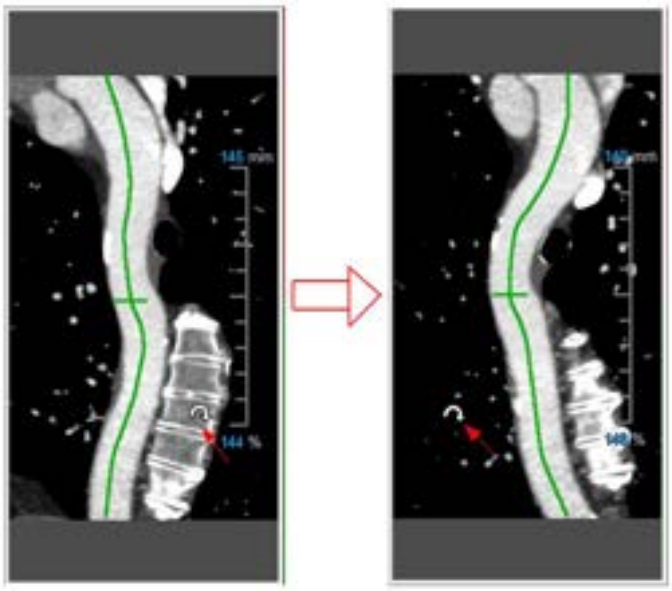
By default, a new interaction point is always appended to the end of the list. To add intermediate interaction points, the path line *should* be visible on the viewport.

CPR Viewport

You can visualize the stretched CPR image on the vertical viewport. The image is shown once the path line is visible on the oblique viewports. This viewport provides all basic functionalities, such as panning, zooming and the window width/window level modifications.

To rotate the vessel

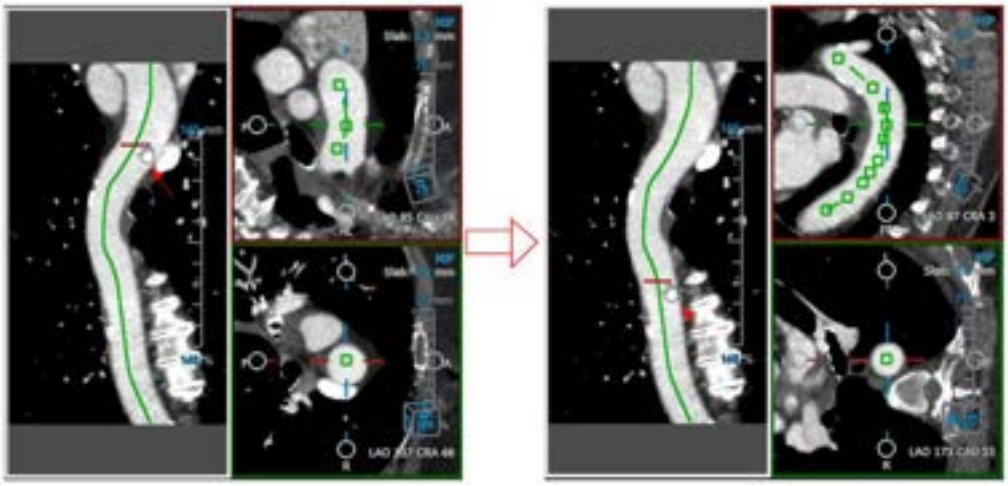
1. Choose the  tool from the Toolbar.
2. While holding the left-mouse button down, move the cursor horizontally along the viewport.



This viewport **does not** support any measurements.

Navigating along the Path Line Overlay

You can axially visualize the contours of the vessel at any location along it by using a position marker tool attached to the path line overlay (green). At a given location along the path line, the 3D position and orientation of the path line can be derived and used to visualize the vessel on the oblique viewports.



To obtain the axial view of the vessel on the oblique viewports

1. In the Properties pane, enable/disable the following options based on their respective outcomes:
   a. If ☑ Synchronize Position is checked, the position of the cross-hair on the oblique viewports will be reset to the current position of the marker tool on the CPR viewport.
   b. If ☑ Synchronize Orientation is checked, the orientation of the image follows the orientation of the path line.
   c. If ☑ Auto-Center Oblique View is checked, the oblique views are auto-centered.
2. Drag the position marker tool along the path line overlay to a location-of-interest.

Both the orientation and auto-center options are unavailable if the position synchronize is **disabled**.

Editing CPRs

You can edit the CPR label in any state, but to edit the created CPR itself you must enter its edit mode.

To edit CPR text

1. On the Results pane, select the CPR.
2. In the Properties pane, type a custom label and press Enter.

Or,

1. On the Results pane, right-click on the results and select **Edit**.
2. Type a custom label and press Enter.

To edit a CPR

1. On the Results pane, right-click on the result and select **Edit**.

Type a custom label and press Enter.

Deleting CPRs

To delete a CPR

1. Select a CPR in the **CPR Procedures** list on the Results pane.
2. Press Delete on your keyboard or right-click and select **Remove**.

This deletes the curved planar reformat.

5.3.7 Export Results

You can export snapshots and reformats. This chapter covers exporting those results to the file system.

Exporting Results to File System

You can save snapshots and reformats to a location on your system or network. For snapshots, the file formats that you can choose from are BMP, DICOM, JPEG, and PNG. For reformats, the file formats that you can choose from are DICOM and AVI.

To save a snapshot to the file system

1. On the Results pane, right-click on a snapshot and select **Export to…**.

   This opens the Export file dialog.

2. Select the location where you want to save the snapshot.

3. Type a name for the file in the **File name** field.

4. Select the file type (BMP, DICOM, JPEG, or PNG) from the **Save as type** drop-down list.

5. Click **Save**.

    You can change the default location to which the files are saved by selecting  and choose **Options > General > Export path**.

To export a reformat to the file system

1. On the Results pane, right-click on a reformat and select **Export to…**.

   This opens the Export file dialog.

2. Select the location where you want to export the reformat.

3. Type a base name for the files in the **File name** field.

   For DICOM file type, this is a base name to which is appended a number per DICOM file.

4. Select the file type from the **Save as type** drop-down list.

- DICOM: The volume is saved as DICOM.
- AVI - stack: Exports all the reformatted slices in the active time point.
- AVI - time resolved: Exports the center slice from all time points.

5. Click **Save**.

You can change the default location to which the files are saved by selecting  and choose **Options > General > Export path**. You can also select whether to create a subfolder automatically.

To send a reformat to the Medis Suite patient browser

1. On the Results pane, right-click on a reformat and select **Send to Medis Suite…**.

The reformat is stored in DICOM and visible within the patient browser located in Medis Suite.

Finishing and saving the session

When you have finished with 3D View, press the save session button on the Medis Suite if you choose to Save any results.

For a detailed description on stopping a Medis Suite session, refer to the Medis Suite Quick Start/User Manual.

5.4 Accuracy of Measurements

QFlow 4D measurements are not intended for a specific clinical purpose and therefore there is no clinical validation, with exception to the length and area measurement calculations, which are validated based on the pixel sizes.

In QFlow 4D all measurements are derived from calculations performed on the loaded DICOM images.

The accuracy of the measurements and calculations exceeds that of the displayed results, by at least one decimal point.

In practice, the image is the limiting factor of the accuracy of measurements. Limiting factors, such as, image resolution both spatial and time-based, image noise, inhomogeneity in the magnetic field and patient determines the accuracy of any given measurement.

Result	Unit	Precision	Accuracy source
Distance measurement	mm	0.1	Not intended for specific clinical measurement.
Area measurement - area	mm^2	0.01	Not intended for specific clinical measurement.
Area measurement - circumference	mm	0.1	Not intended for specific clinical measurement.

Area measurement min and max diameter	mm	0.1	Not intended for specific clinical measurement.

5.5 Troubleshooting

Floating license error after a crash of the software

In a floating license setup, licenses will be returned to the license server when Medis Suite MRCT is closed. In case of an QFlow 4D software crash, the licenses will not be returned and remain locked on the license server. Restarting QFlow 4D will give a warning that the licenses are not available.

To solve this issue, you have to wait at most 2 minutes before you can start the software again. The license server checks every 2 minutes if the claimed licenses are still in use on the client machine. If the licenses are not in use, the license server will release the licenses.

Expiration date not updated after installing non-expiring license

When you install a temporal license with CMS License Manager the license will be given an expiration date. You can see this expiration date in **View available licenses…** in CMS License Manager. When you install a non-expiring license after you installed the temporal license the expiration date is not updated.

To see the correct expiration date of your licenses, you have to delete the expiring license before you install the non-expiring license. You can do this with the following steps:

- Start CMS License Manager (click **Start > All Programs > Medis System Tools > CMS License Manager 2.5**)
- Click **Advanced…**
- Click **Delete licenses…**
- Select all the expiring licenses
- Click **Delete**
- Click **Close**
- Click **Close**
- Click **Install an additional license…**
- Browse to the license file with the non-expiring license
- Make sure all licenses are selected
- Click **Install**
- Click **Close**

You are now able to see the licenses with their correct expiration date in **View available licenses…**

MIP and 3DVR images are black

Some graphics adapters exhibit incompatibility with QFlow 4D by not displaying the MIP, 3DVR and LUT thumbnail images. (If only the 3DVR and LUT thumbnails are black, see below.) In many cases, this is also accompanied by errors related to VTK in CMS Monitor. This may be resolved by having the system administrator update the graphics adapter driver. Otherwise, operation of QFlow 4D using only the double oblique views (DOV) is still possible by disabling the option in  > **Options > Hangings > DoubleOblique > Enable hardware rendering**.

3DVR image is black

Some graphics adapters exhibit incompatibility with QFlow 4D by not displaying the 3DVR and LUT thumbnail images, although the MIP is displayed. In many cases this can be resolved by disabling the option in  > **Options > Hangings > DoubleOblique > Enable hardware shading**.

"Hardware rendering disabled" is displayed on the MIP/3DVR view

If the option in  > **Options > Hangings > DoubleOblique > Enable hardware rendering** is unchecked, the MIP, 3DVR and LUT thumbnails will not be generated.

Custom LUT is not saved as expected

It may appear that your custom LUT is not saved as expected, particularly if you move the first or last point in the LUT; however, note that this is intended behavior. The LUT is displayed in the LUT Editor based on the **Window** and **Level** settings defined in the data set.

Menu commands or toolbar buttons are disabled

Menu commands or toolbar buttons may be grayed out when you are performing a procedure, such as a radial reformat. You can make them active again by canceling or finishing the procedure.

Window width and level are not applied

Different window width and level values are maintained for the double-oblique view, MIP view and 3DVR view.

Annotation or measurement is not visible

When you navigate to another location in the volume, your annotation or measurement may not be displayed on the double-oblique viewport. This is because the point to which the result refers does not lie on the currently visible slice. To see your result again, right-click on the result on the Results pane and select **Locate**; or double click on the result on the Results pane.

The mouse cursor inside a sculpture contour will not change to the eraser or fill icon

A small contour area may not provide enough distance from the edge of the contour area to enable the eraser or fill cursor icon. In this case, move the cursor outside the contour until the desired mouse cursor appears, press the SHIFT key, and then click the mouse button. Pressing the SHIFT key before the click performs the selected action on the opposite region, inside instead of outside or outside instead of inside.

Your issue was not resolved in this troubleshooting section

You may find it useful to run the CMS Monitor diagnostic tool (click **Start > All Programs > Medis System Tools > CMS Monitor 3.5**) and view the messages displayed. If the logged messages do not resolve your problem, click on the **Send** button in CMS Monitor to send relevant information to the Medis help desk. Additional contact information can be found by clicking **Help > About…**

5.6 Shortcut Keys

When you are working with 3D View, you can use several combinations of keys on your keyboard and mouse actions to quickly perform the following tasks.

Press	To
General	
F1	Access the user manual
CTRL+G	Open the Medis website
CTRL+X	Close 3D View
Alt+F4	Close 3D View
Layout	
F6	Reset toolbar and workspace window pane layout
F10	Expand the currently selected viewport.
SPACE	Toggle among MIP, 3DVR and Stack view, with the lower-right viewport selected.
BACKSPACE	Toggle in reverse order among MIP, 3DVR and Stack view, with the lower-right viewport selected.
F11	Show or hide the workspace window panes
Results	
D	Create a distance measurement
A	Create an area measurement
R	Create a double distance measurement

Press	To
S	Create a snapshot
Esc	Stop editing the result
Delete	Delete the currently selected result
SHIFT+Delete	Delete all results
Navigation Controls	
Wheel	Stacking
SHIFT+ALT+click and drag	Stacking
CTRL+Wheel	Zooming
SHIFT+CTRL+click and drag	Zooming
CTRL+click and drag	Panning
Middle-click and drag	Panning and hides graphics
ALT+click and drag	Swivel (double oblique) or rotate (MIP, 3DVR)
Right-click and drag	Window width and level
Viewing Controls	
1	Reset the window width and level
CTRL+K	Show or hide the axes
ALT+right-click	Hide the overlay graphics
Arrow left	Display the previous time point

Press	To
Arrow right	Display the next time point

6 QFlow 4D

6.1 The QFlow 4D Workspace

QFlow 4D is launched from the app toolbar, app context menu, or app pane of Medis Suite, by selecting the QFlow 4D is app icon . Detailed information on how to start an application and how to load series into the application, is described in the Medis Suite user manual.

This chapter covers the following topics:

- Overview
- Menu bar
- Toolbars
- Workspace panes
- Viewing

6.1.1 Overview

The main workspace consists of a menu bar, toolbars, workspace panes and the central window area which is comprised of Double Oblique, 3D-MIP and Velocity image viewports. There are also results and properties panes.

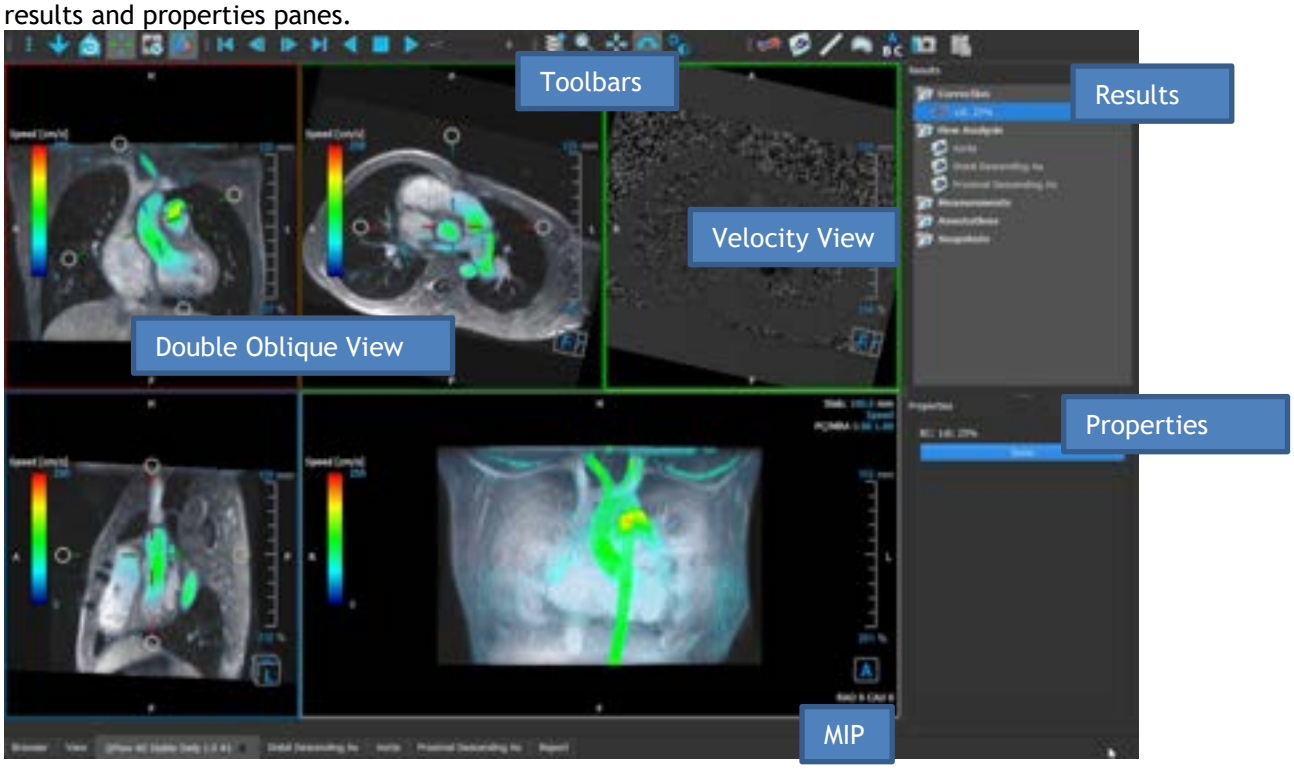


Figure 6-1 : Workspace Overview

You can customize the workspace by hiding, resizing or moving the workspace panes and toolbars. Any changes that you make to the workspace are saved for each individual Windows user.

6.1.2 Menu

The menu contains commands to activate the application functionality.

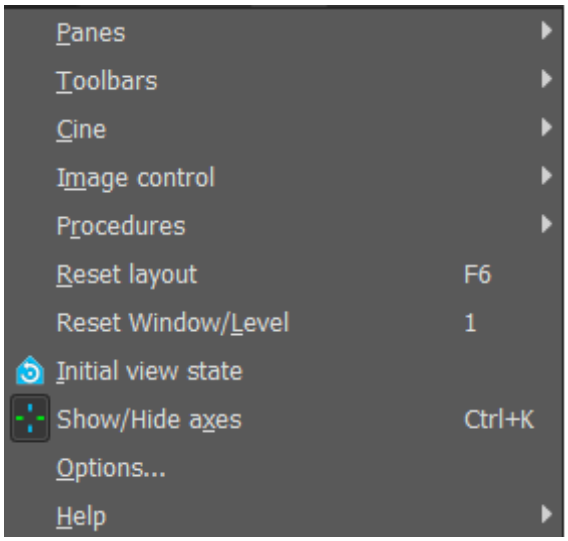
To make the menu visible:

- Select on the menu icon  in the **General** toolbar.

The menu commands are organized into the following main menus; **Panes**, **Toolbars**, **Cine**, **Image Control**, **Procedures** and **Help.**

In addition, there are menu items; **Reset layout, Reset Window/Level, Initial View State, Show/Hide axes** and **Options**. For some of these commands, tool buttons are available in the toolbars as shortcuts.

Menu commands may be grayed out when you are performing a procedure, such as an area measurement. You can make the menu commands active by canceling or finishing the procedure.

Menu	Command	Description
	Panes	Show or hide a workspace pane
	Toolbars	Show or hide a toolbar
	Cine	Control the frame selection
	Image Control	Control the image display
	Procedures	Start a new procedure
	Reset layout	Reset the default layout
	Reset Window/Level	Reset the default window/level
	Initial view state	Reset the view state
	Show/Hide axes	Enable/Disable axes visibility
	Options	Application default settings
	Help	User documentation and About

6.1.3 Toolbars

You can move toolbars to another part of the main window. You can also show or hide toolbars.

To move a toolbar:

- Click on the double-bar grip handle  of the toolbar and drag it.

  You can now move the toolbar to any location on the sides of the main window. Simply click and drag the toolbar to its new position. The position of the toolbar is saved when you close the application.

To show or hide a toolbar:

1. Select  **> Toolbars**.
2. Select a check box to show the toolbar, clear a check box to hide the toolbar.

Or,

1. Right-click in the toolbar area. This opens a context menu.
2. Select a check box to show the toolbar, clear a check box to hide the toolbar.

The state of the toolbars is saved when you close the application.

Icon	Function
General Toolbar	
	Show the menu
	Go to the initial view state, reset zoom \ pan \ window width \ window level
	Verify flow direction.
	Go to the Flow Analysis 3D Layout.
	Go to the 2D View Layout.
	Show and Hide Axes

Icon	Function
	Toggle image text overlay
	Remove background noise on speed overlay
Cine Toolbar	
	Go to the first frame
	Go to the previous frame
	Go to the next frame
	Go to the last frame
	Play a cine in backward direction
	Stop the cine
	Play a cine in forward direction
	Set the cine playback speed
Mouse Controls Toolbar	
	Stack
	Zoom
	Pan
	Window width and window level

Icon	Function
	Swivel (only if the 3D viewport is selected)
Procedures Toolbar	
	Background Correction on data
	Phase Unwrapping on data
	Start a flow analysis
	Start a Mitral Valve flow analysis
	Create a distance measurement
	Create an area measurement
	Create a text annotation
	Create a snapshot
	Copy all measurement results to the clipboard

6.1.4 Workspace Panes

By default, the workspace displays the following panes to the right of the image viewports:

- **Results**
- **Properties**

You can show or hide panes, dock panes, combine panes into one tabbed panel and remove panes from a panel.

To show or hide a pane:

- Select  > **Panes**, and select a hidden pane to show it, or select a visible pane to hide it.

To dock a pane:

1. Click and drag the title bar of the pane.
2. Move the pane to the sides of the viewer window to select one of the dock areas.

   As the pane approaches a dock area, the area is highlighted with a dotted line. The pane can be combined with another pane or inserted separately.
3. When the dock area of your choice appears highlighted, release the mouse button.

   This docks the pane into the selected position.

To combine panes into one tabbed panel:

- Click and drag the title bar of the pane to the title bar of the pane with which you want to combine it.

  This creates a tabbed panel.

To remove panes from a panel:

Click and drag the title bar of the pane away from the panel.

Results Pane

The **Results** pane shows the following in QFlow 4D.

- It shows standard procedures, i.e. measurements, annotations and snapshots performed on the series that is loaded in the viewport.
- It shows the **Background Correction.**
- It shows the list of **Flow Analyses.**

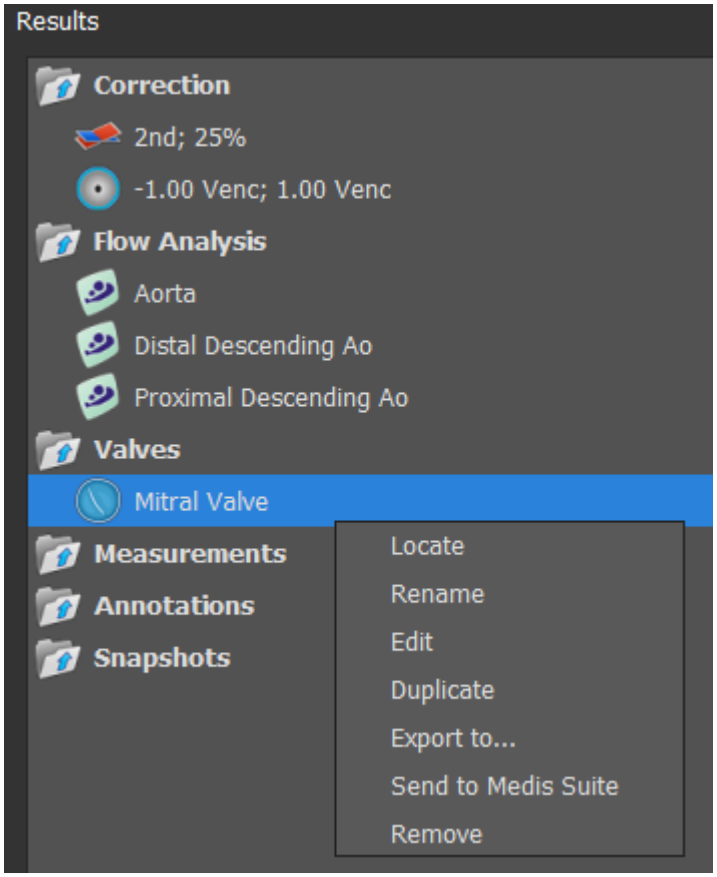


Figure 6-2 Results Pane

You can collapse and expand an item by selecting on the group header.

You can right-click a procedure to perform actions on the procedure. Depending on the type of procedure, you will get a context menu with several options.

Locate:	The image and the image orientation at which the procedure was originally performed will be activated. Locate is automatically enabled for Flow Analysis.
Rename:	Rename the procedure.
Edit	**Edit the procedure**
Duplicate	**Duplicate the procedure**
Export to:	Export the procedure to disk.
Export to Repository:	Export the procedure to a repository.
Remove:	Delete the procedure.

Flow Analysis procedures offer a list of pre-defined labels.

Properties Pane

The **Properties** pane shows the properties of the selected procedure. You can modify QFlow 4D standard procedures, i.e. measurements, annotations or snapshot procedures as well as the Flow Analysis reconstructions.

To modify a label (Measurements, Annotations and Snapshots):

1. On the **Results** pane, select the procedure.
2. On the **Properties** pane, select the ellipsis ... on the right of the **Label** field and select a predefined label, or type a custom label and press Enter.

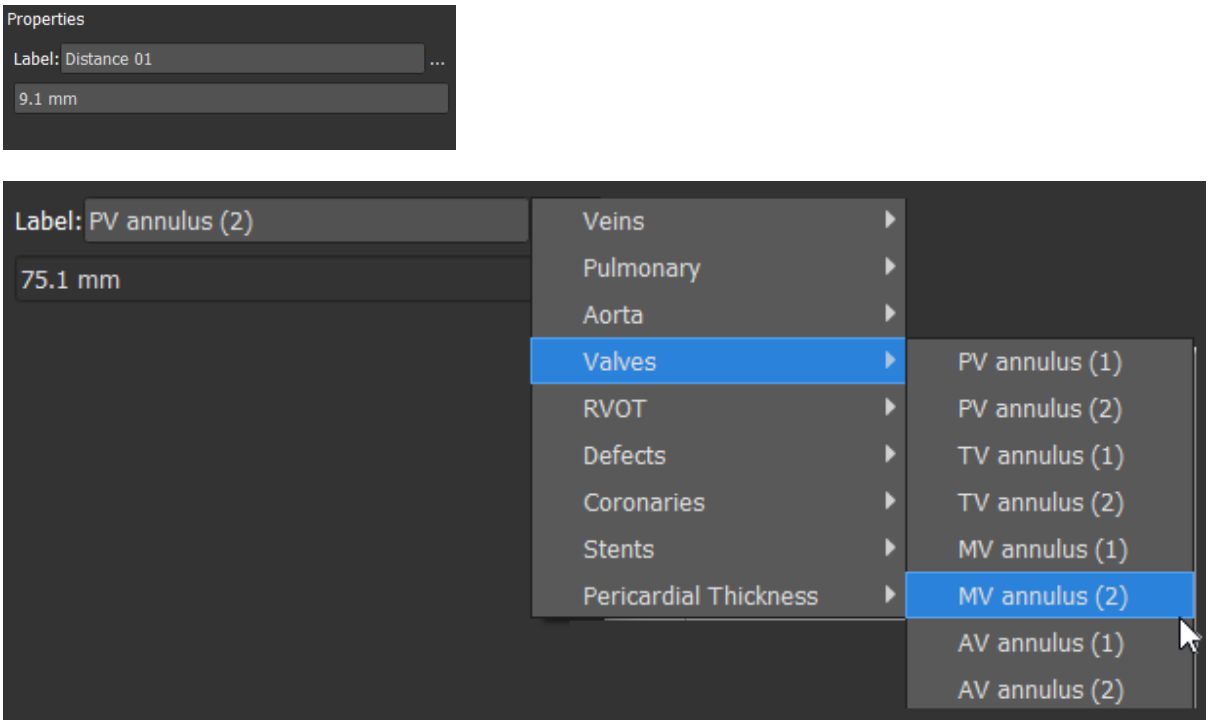


Figure 6-3 Predefined Labels Menu

6.2 Viewing

6.2.1 Loading Series

Series can be loaded into QFlow 4D from the **Series Browser** of Medis Suite. Refer to the Medis Suite user manual for detailed instructions.

A 4D flow MRI dataset consists of time-resolved, three-dimensional series encoded in three velocity directions and a single modulus (or magnitude) series. QFlow 4D, also supports short and long-axis series.

QFlow 4D requires at least one set of 4D flow MRI dataset to begin visualization.

To load series from the Series Browser of Medis Suite

1. Select three sets of 4D flow velocity series and one 4D flow modulus series, in the image or text view of the Medis Suite **Series Browser**.
2. Click and drag the selected items onto any viewport.

Or,

1. Double click an item in the image view or text view of the Medis Suite **Series Browser**.

Or,

1. Select all series in the image or text view of the Medis Suite **Series Browser**.
2. Right-click above the selected series to open a context menu.
   Choose QFlow 4D.

This will load the series into the viewports. By default, a cine will start playing to present all individual image frames.

QFlow 4D only loads MR DICOM series.

6.2.2 Viewports

The viewport text overlay displays detailed information about the patient, the hospital, the image acquisition, and the display settings.

To show or hide the patient and image information:

- Select  **> Options**, **Hangings**.

  Select or deselect **Show patient information** or **Show image information**.

Or

- Use 'O' to toggle through the different modes of hiding the overlay displays.

Or

- Select  in the toolbar, to toggle through the different modes of hiding the overlay displays.

To maximize an image in the viewport:

- Double-click the image.

  This maximizes the viewport, so that it takes up the entire viewport.

  To return to the original viewport layout, double-click the image again.

 Interactive graphics are displayed in blue color 

and allow you to change image or display properties with your mouse.

6.2.3 Viewport Layout

QFlow 4D consists of three independent screen layouts.

- Verification of Flow Direction Layout
- Flow Analysis 3D View Layout
- 2D View Layout

To enable Verification of Flow Direction Layout

Press  to enable Verification of Flow Direction Layout.

To enable Flow Analysis 3D Layout

Press 

to enable Flow Analysis 3D View Layout.

To enable 2D View Layout

Press 

to enable 2D View Layout.

Verification of Flow Direction Layout

This is the layout used for verification of the flow direction.

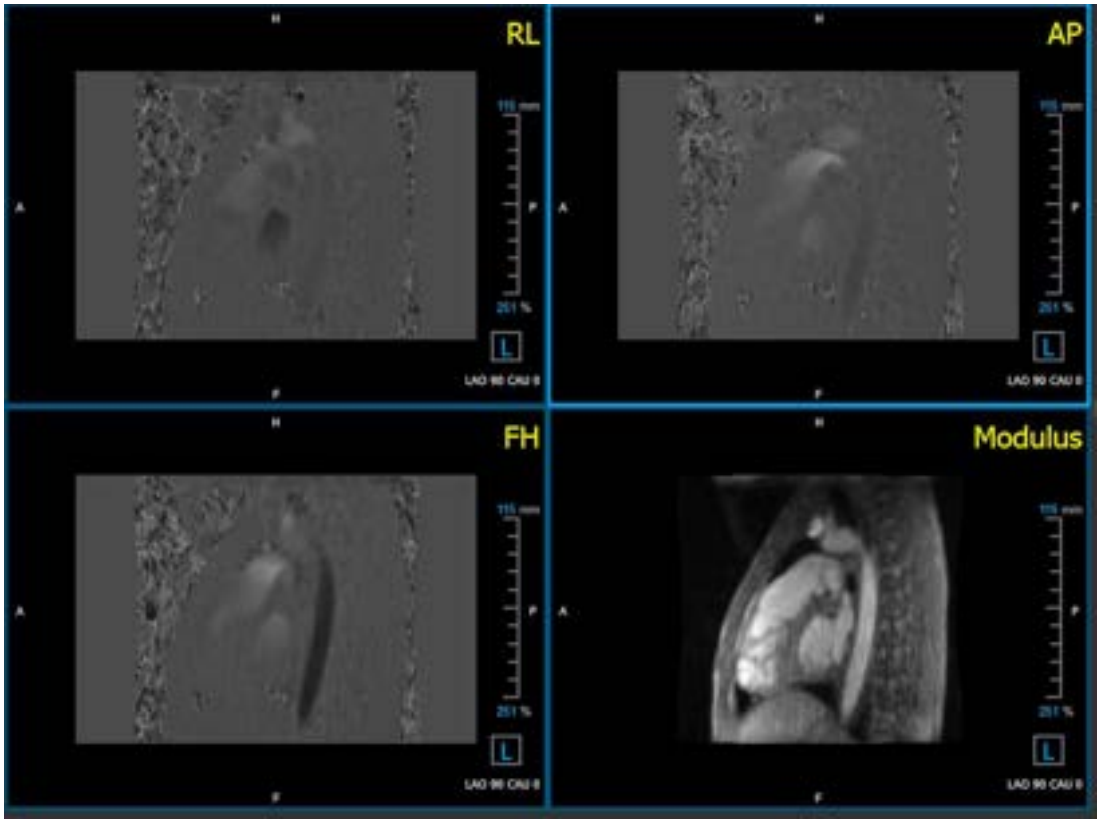


Figure 6-4 Verification Of Flow Direction Layout

Flow Analysis Layout

The primary layout in QFlow 4D consists of five viewports.

1. Three double oblique views
2. 3D View
3. Velocity view

Double Oblique View

The main purpose of the double oblique views is to determine the plane of interest to be used for Flow Analysis in QFlow 4D. The double oblique views show the orthogonal views of the 3D volume.

The double oblique viewports are highlighted in blue in Figure 5 Double Oblique Viewport Layout.

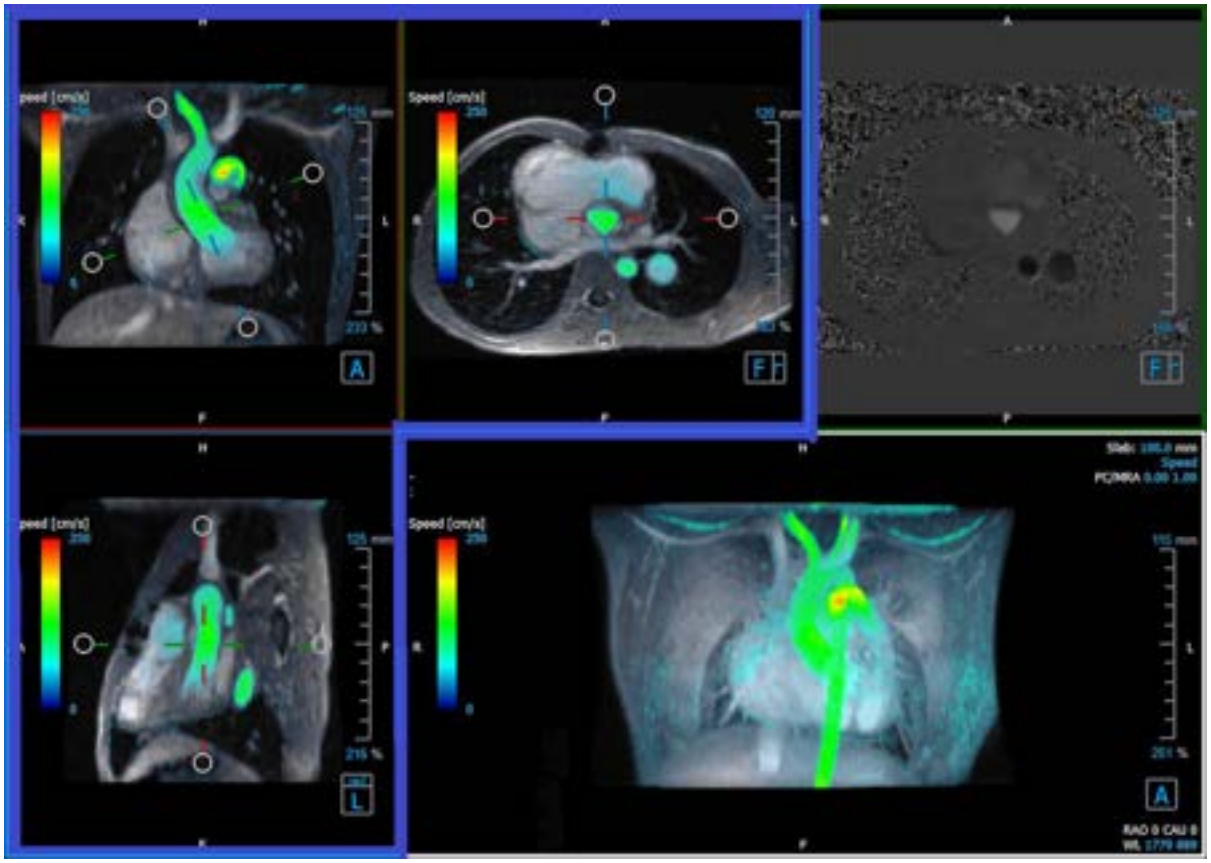


Figure 6-5 Double Oblique Viewport Layout

3D View

The 3D view viewport is highlighted in blue in Figure 6-6 3D View, viewport.

The 3D view is a viewport that shows the series rendered in 3D.

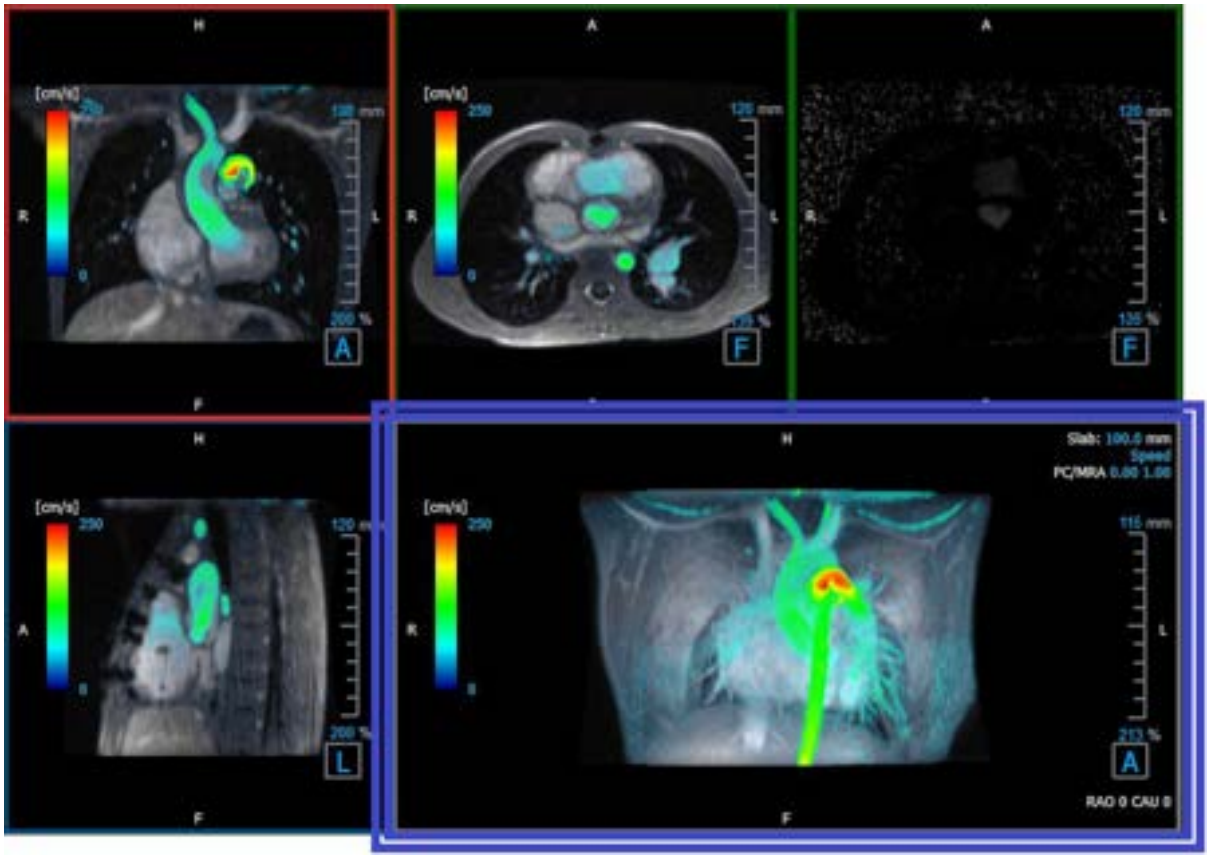


Figure 6-6 3D View, viewport

Change the slab thickness and or the window width/level to optimize the view on the heart.

Flow 2D Representation

The top middle and top right viewports show the series at the reconstruction plane defined by the user for Flow Analysis procedure. The top middle viewport shows the reconstructed modulus image and the top right viewport shows the perpendicular velocities of that plane.

These two planes, marked in red in Figure 6 The Modulus and Phase series, shows the data that is used for the Flow Analysis.

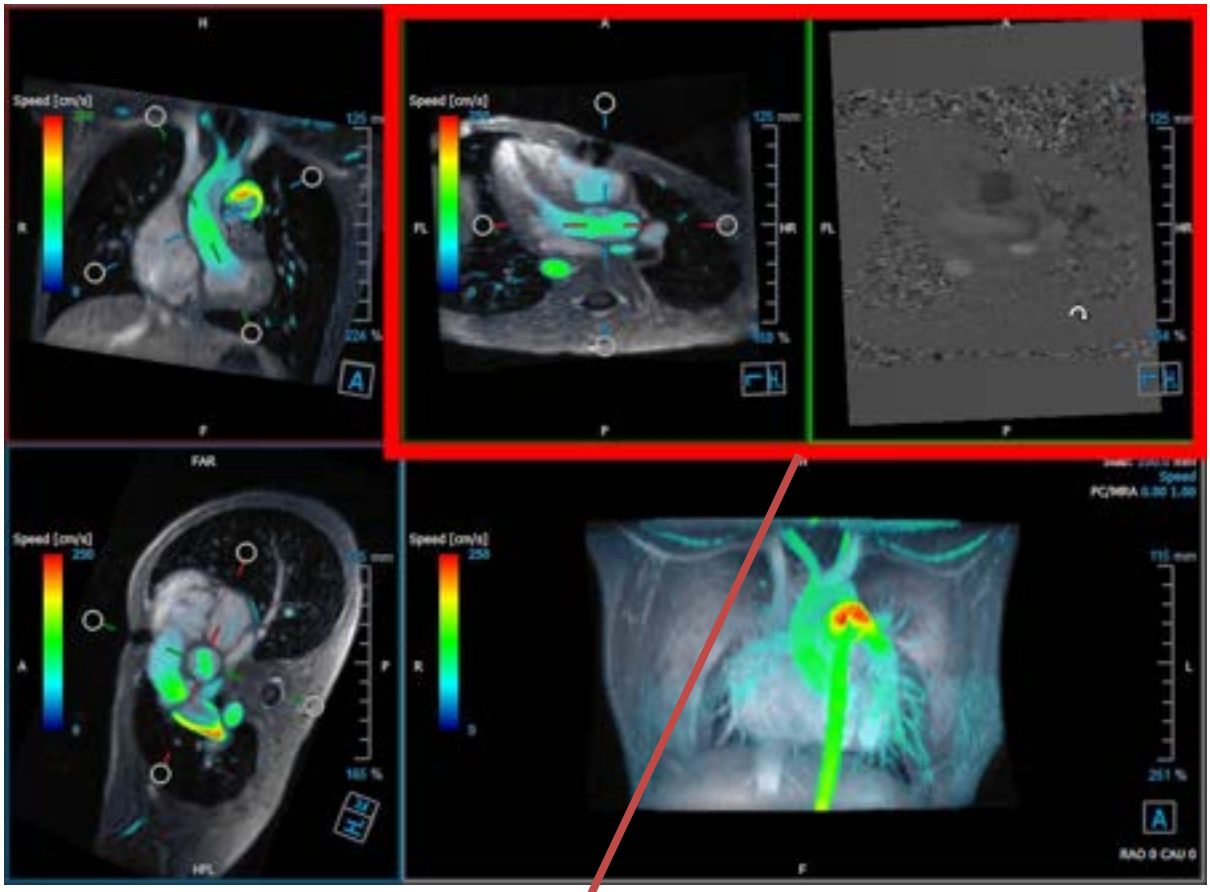


Figure 6-7 The Modulus and Phase images

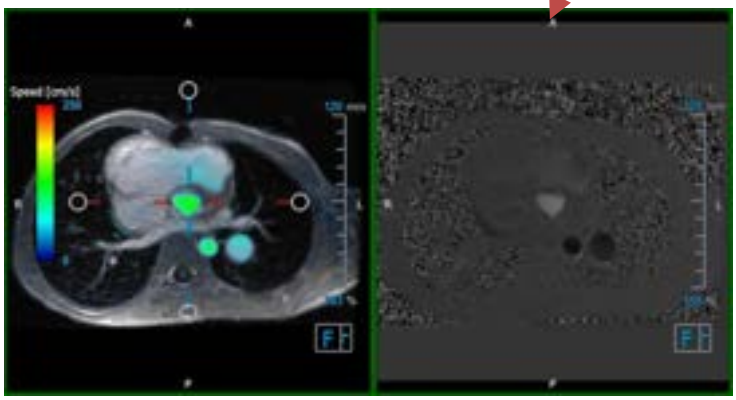


Figure 6-8 Flow Analysis Plane of Modulus and Phase images

2D View Layout

All viewports show 2D orientation images. Optionally, Speed, Vectors and Streamlines can be displayed.

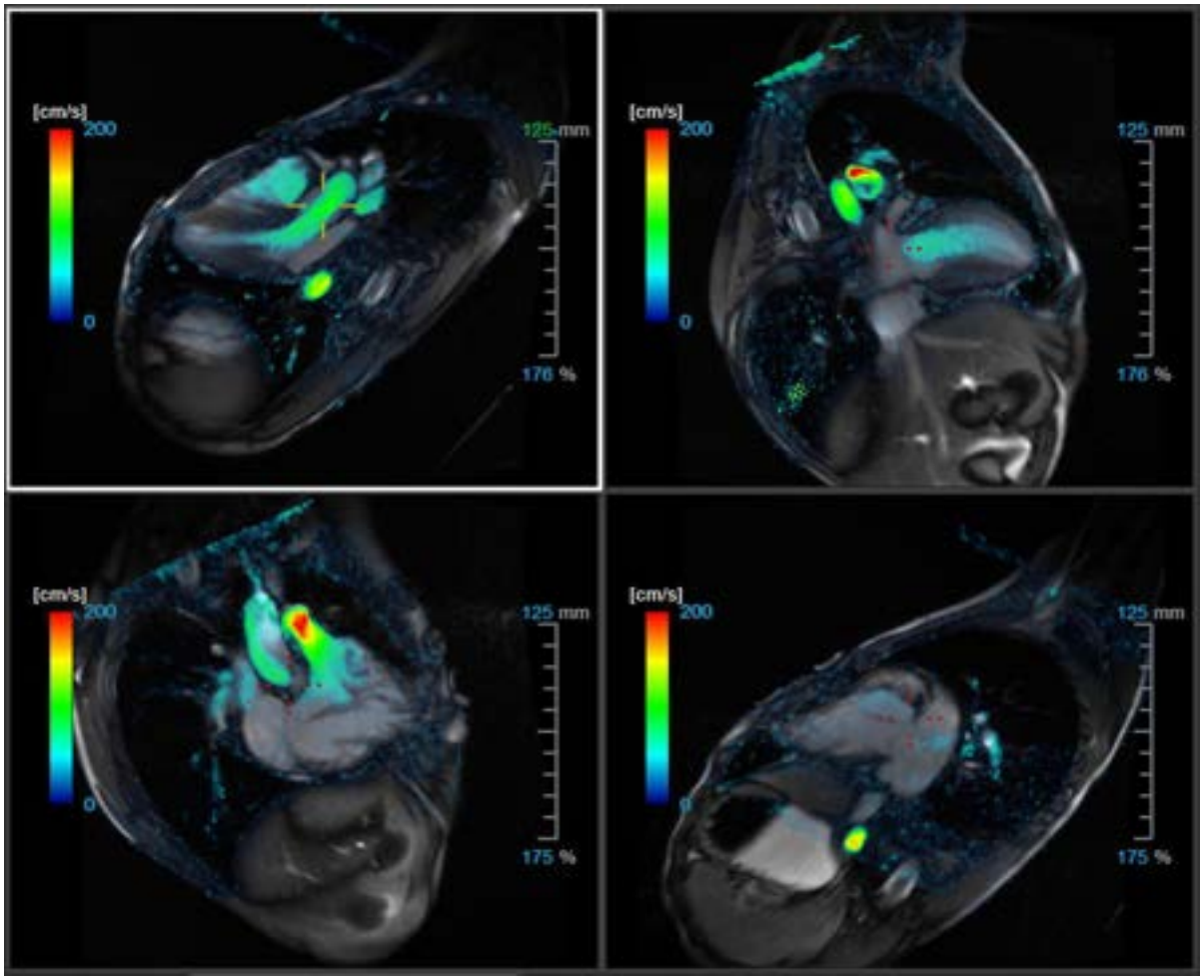
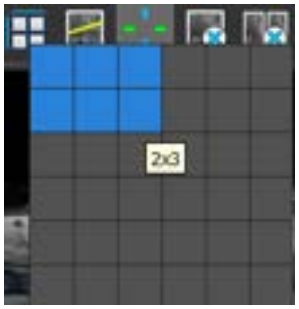


Figure 6-9 2D View Layout with 4 high-resolution series. A speed overlay is shown on these images.

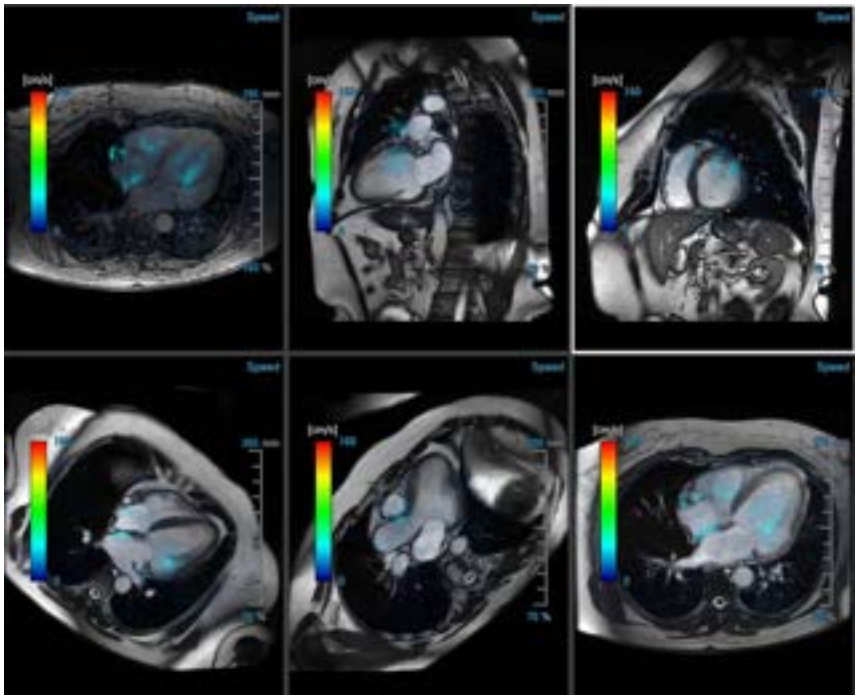
Adjusting the layout

To adjust the viewport layout

- Click  in the general toolbar. A table of rows and columns will appear.
- Drag the mouse to determine the number of viewport rows and columns.



- The viewport layout will be applied



To clear a series from a viewport

- Select the viewport
- Click  in the general toolbar

To clear all series from all viewports

- Click  in the general toolbar

Loading new series into 2D View layout

Series can be loaded in the viewport from the **Series Browser**.

To load series in the viewport

1. Click an item in the image view or text view of the Series Browser to select it.
2. Click and drag the selected series from the **Series Browser** to the viewport.
   This will load the series into the viewport. When multiple slices are contained in the series, the middle slice is displayed by default. When multiple time points are contained in the series, the first time point is displayed by default.

To review all series in the active study

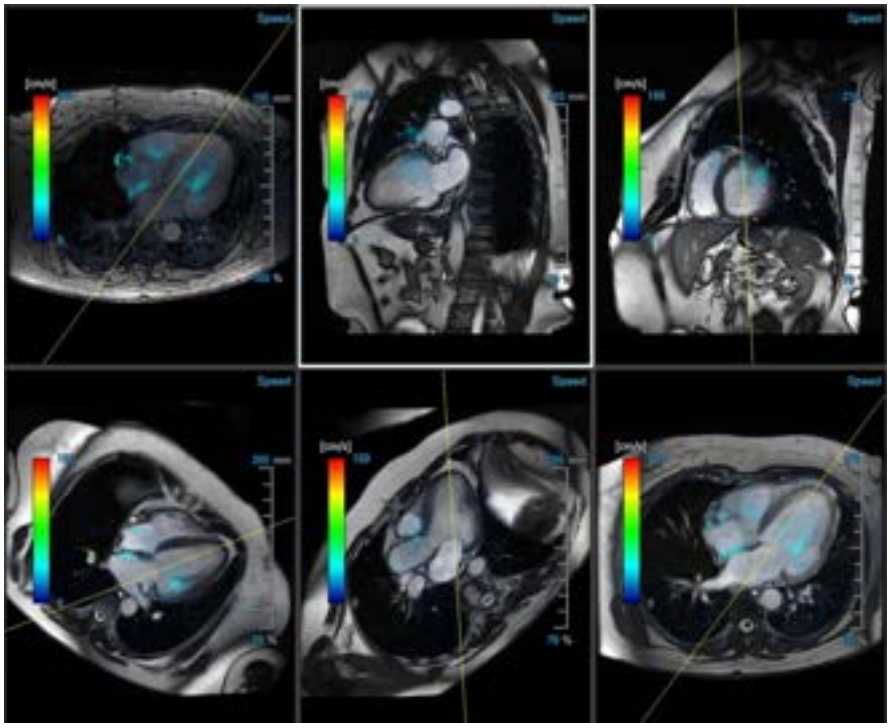
1. Press **Page Down** on your keyboard to load the next series into the viewport.
2. Press **Page Up** on your keyboard to load the previous series into the viewport.

Cross Referencing

The scanline  and cross hair  tools enable the user to visually relate the active image and image position with that of the different series loaded in other viewports. Cross referencing is visible when multiple related series are loaded.

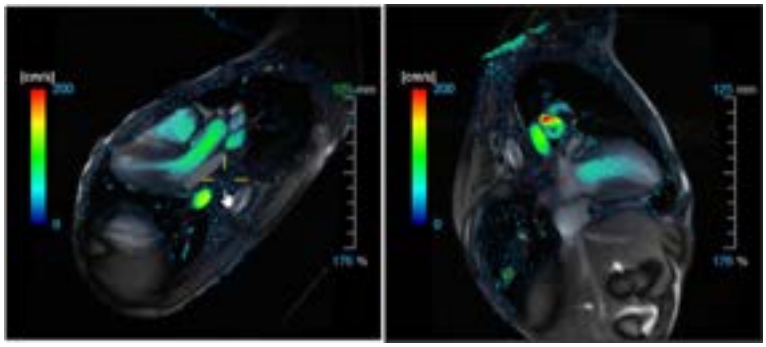
To enable/disable the scanlines

- Click  in the general toolbar to enable or disable the scanlines



To enable/disable the crosshairs

- Click  in the general toolbar to enable or disable cross hair.



A cross hair reference of the same color implies there is an exact or nearby position cross reference. A different color cross hair indicates the position is out of range of the cross hair in the active image.

6.2.4 Noise Removal

QFlow 4D Noise Removal is a utility for visualization only. It is available when viewing images in the **Flow Analysis 3D View Layout** and **2D View Layout**. It filters out the air and the surrounding static tissue, essentially highlighting motion velocity of the blood-pool. When Noise Removal is enabled, it will be automatically applied to the three double-oblique views, the 3D and **2D View layout** viewports. The velocity viewport on the top right of the **Flow Analysis 3D Layout**, is unaffected.

There are two parameters governing the behavior of the Noise Removal, the standard deviation threshold and the modulus threshold.

- The standard deviation threshold can take values from 0-1%. It defines the static tissue to be removed based on the velocity of the tissue.
- The modulus threshold can take values from 0-100% and the area to be removed based on the intensity of the modulus image. The area removed is based on the intensity of modulus image and corresponds mainly to the surrounding air and the lungs.

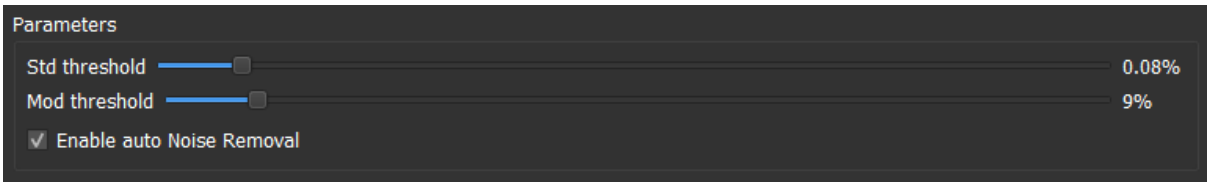
QFlow 4D Noise Removal has no effect on quantification or numerical results, and it is not applied to any data.

Please ensure that QFlow 4D Noise Removal only removes noise from the images.

Noise Removal Options

To modify Noise Removal settings:

1. Select  **> Options**, **Noise Removal**.



Higher values, in both cases, will cause more of the speed overlay to be removed from the image.

If Enable auto Noise Removal is selected, Noise Removal will be applied after loading the data.

Enable/Disable Noise Removal

To enable/disable noise removal:

1. Select  in the toolbar to enable Noise Removal.

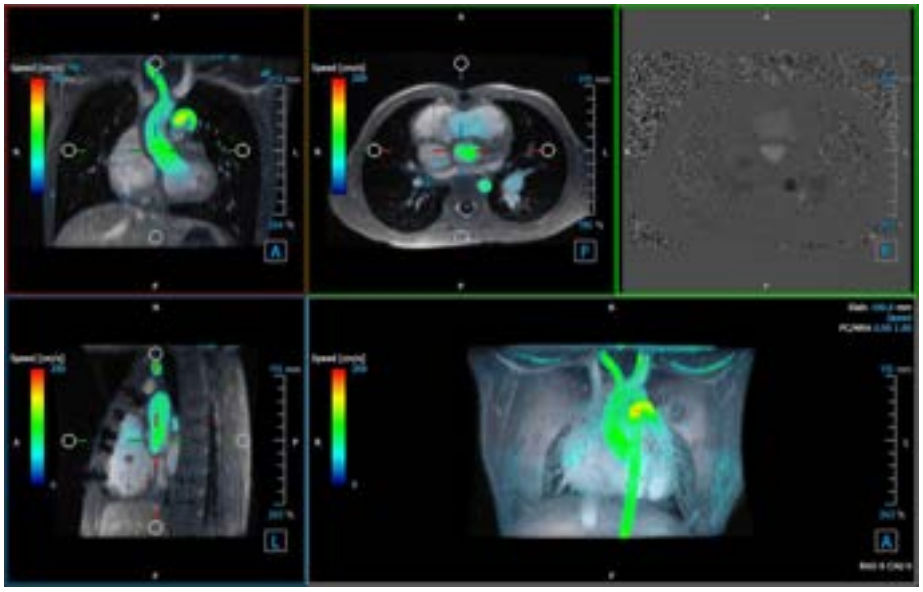


Figure 6-10 Noise Removal Enabled

2. Select  in the toolbar to disable Noise Removal.

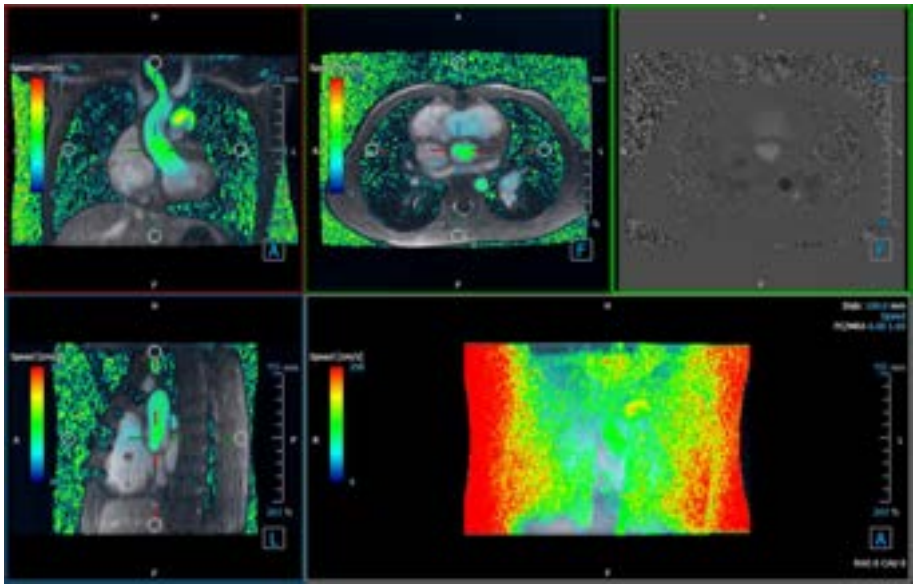


Figure 6-11 Noise Removal Disabled

6.2.5 Viewport Overlay Visualization

QFlow 4D provides multiple overlay types, each defining different visual aspects of the data.

- PCMRA

- Speed
- Streamlines
- Vectors

Toggle Overlay Representation

Overlays showing speed, streamlines or vectors may be enabled or disabled. In the Flow Analysis 3D layout, they are visible in the three double oblique viewports and the 3D MIP viewport. In the 2D View Layout, the overlays are visible in all viewports with a loaded series.

To modify the overlay representation in the Flow Analysis Layout:

1. Select the top right-hand corner text in the 3D MIP viewport. It will toggle from
   - **No Overlay**
   - **Speed**
   - **Streamlines**
   - **Vectors**

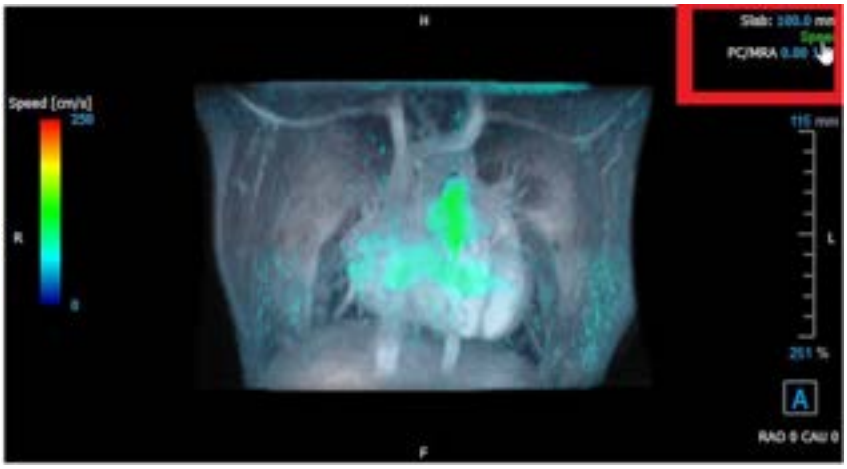


Figure 6-12 Select Overlay Type Annotation in the Flow Analysis 3D Layout

Or,

1. Right-click the top right-hand corner text in the 3D MIP viewport. This opens a context menu.
2. Select **No overlay**, **Speed, Streamlines or Vectors**.

To modify the overlay representation in the 2D View Layout:

1. Right-click the top right-hand corner text in any viewport. This opens a context menu.
2. Select **No overlay, Speed, Streamlines or Vectors**.

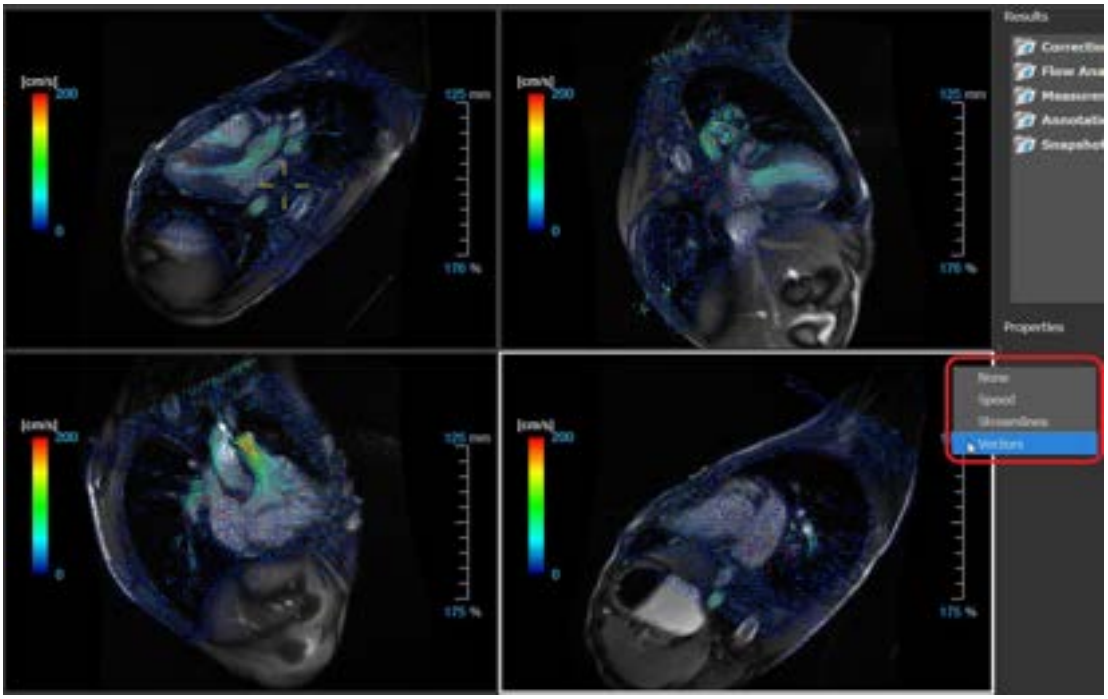


Figure 6-13 Select Overlay Type Context Menu in the 2D View Layout

To modify the Vector overlay size and quantity in the Flow Analysis Layout:

1. Select the top right-hand corner text in the 3D MIP viewport.
2. Toggle or select Vectors
3. Hoover over either the Size or Number values.
4. Right-click the value to modify it.

Or,

5. Scroll the mouse wheel up and down to modify the value.

Or,

6. Reset to the value to its default setting, by clicking the middle mouse button.

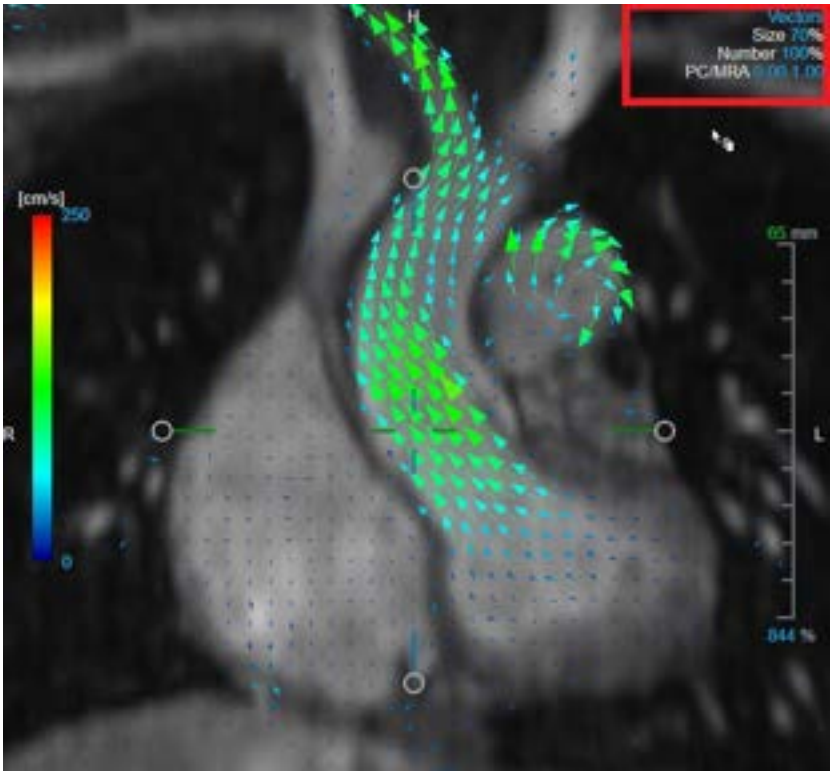


Figure 6-14 Select Vector Overlay & Modify the Size and Quantity in the Flow Analysis 3D Layout

Streamlines Plane of Origin overlay

When Streamlines are shown in the 3D MIP viewport the plane of origin of the streamlines is also visible. The plane of origin represents the axial view, that is the top middle double oblique viewport (DOV) marked in green. The plane also represents the reconstructed modulus image position and orientation.

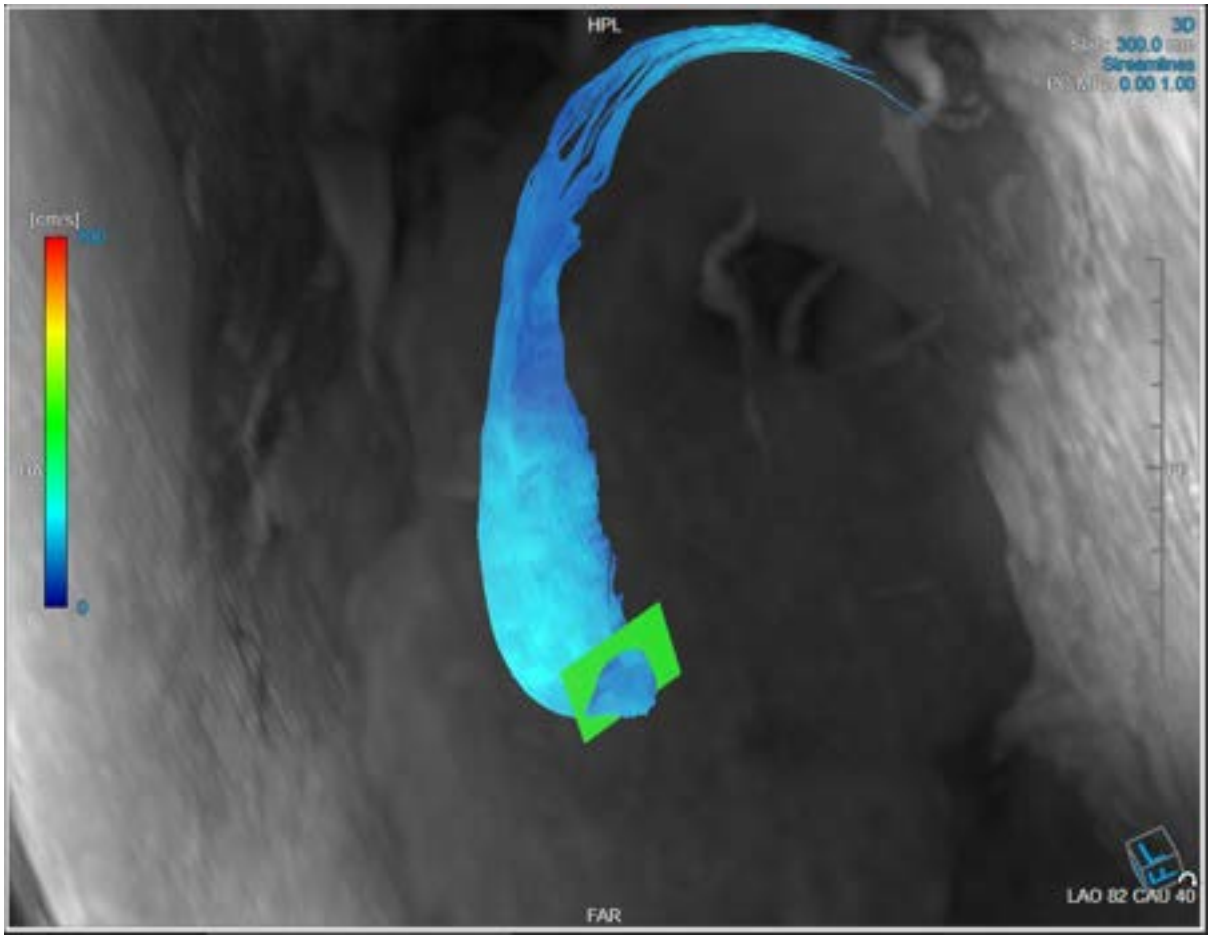


Figure 6-15 The 3D MIP viewport showing Streamlines and the Plane of Origin in the Flow Analysis 3D Layout

To modify the Plane of Origin in the Flow Analysis Layout:

1. Select either the sagittal viewport which has a blue border, or the coronal viewport with a red border.

2. Modify the position of the axes.

To Modify the position of the axes.

1. Move the mouse to a circular grip at the end of one axis. The mouse cursor changes to the Rotate cursor .
2. Click and drag the axes to the desired angle.
   Or,
3. To drag the axes vertically, press the Ctrl key after pressing the mouse key, then drag.

4. To drag the axes horizontally, press the SHIFT key after pressing the mouse key, then drag.

6.2.6 Frame Selection

You can move forward or backward through the frames in the image in several ways.

Moving through frames can be done by using buttons:

- Press  or  on the Viewing toolbar to move to the previous or next frame.

Or,

- Press  or  on the Viewing toolbar to play a cine through the frames in backward or forward direction. Click  to stop the cine.

Or,

- Press  or  on the Viewing toolbar to move to the first or last frame.

Moving through frames can be done by using keys:

- Press the left or right arrow key to move to the previous or next frame.

Or,

- Press CTRL + left arrow, CTRL + right arrow to play a cine through the frames in backward or forward direction. Press Esc to stop the cine.

Or,

- Press HOME or END to move to the first or last frame.

Moving through frames can be done by using interactive graphics:

- Select the interactive graphics for frame selection (‘Frame’) on the viewports to move to the next frame.

Or,

- Right-click the interactive graphics for frame selection (‘Frame’) and enter the desired frame number.

 The cine speed can be modified with the slider  in the Viewing toolbar.

6.2.7 Mouse Controls

Stacking

You can move through the frames using **Stacking** when you see the stack cursor .

To activate the stacking mouse control:

- Press  in the mouse controls toolbar.

Or,

- Select **Stacking** from the viewport context menu.

To stack forward or backward through frames:

- Click and drag the mouse left and right or down and up to scroll through the frames. It will loop to the first or last frame.

Or,

- Independent of the stacking mouse control status, you can scroll the mouse wheel to stack through the frames. It will stop at the first or last frame.

Zooming

You can zoom in and out of the viewport using **Zooming** when you see the magnify cursor .

To activate the zooming mouse control:

- Press  in the mouse controls toolbar.

Or,

- Select **Zooming** from the viewport context menu.

To zoom in and out:

- Click and drag the mouse forward and backward to zoom in and out.

Or,

- Independent of the zooming mouse control status, you can click and drag on the interactive zoom scale graphics, or hold Ctrl and scroll the mouse wheel up and down, to zoom in and out.

The current zoom factor is displayed on the scale graphics in the viewport.
The value above the scale is the physical size of the scale.
The number below the scale indicates the relative zoom:
100% means one display pixel equals one acquisition pixel.

Panning

You can move the image within the viewport left, right, up and down using **Panning** when you see the hand cursor .

To activate the panning mouse control:

- Press in the mouse controls toolbar.

Or,

- Select **Panning** from the viewport context menu.

To pan the image:

- Click and drag the mouse in any direction.

Or,

- Independent of the panning mouse control status, you can middle-click and drag the mouse in any direction to pan the image.

Window Width and Level

You can adjust the window width and level (WWL) when you see the WWL cursor .

To activate the window/level mouse control:

- Press in the mouse controls toolbar.

Or,

- Select **Window/Level** from the viewport context menu.

To adjust the window width and level:

- Click and drag in the viewport
  - Right or left to increase or decrease the width.
  - Down or up to increase or decrease the level.

Or,

- Independent of the window/level mouse control status, right-click and drag
  - Right or left to increase or decrease the width.
  - Down or up to increase or decrease the level.

Or,

- Independent of the window/level mouse control status, click on the window width or level interactive graphics and drag up or down to increase or decrease the window width or level.

Or,

- Independent of the window/level mouse control status, right-click on the window width or level interactive graphics and enter the desires values.

 The current window width and level values are displayed in the lower-right overlay graphics in the viewport.

Initial View State

To reset the zooming, panning and window width and level settings to the initial view state:

- Press  to reset the zooming, panning and window width and level.

6.2.8 Standard Measurements

QFlow 4D supports the following standard measurements:

- Annotations,
- Distance measurements,
- Area measurements,
- Snapshots.

Annotations

You can add annotations to a viewport to mark it for analysis or to draw attention to specific details. Annotations are displayed in the viewport. All annotations of the active study are listed on the **Results** pane.

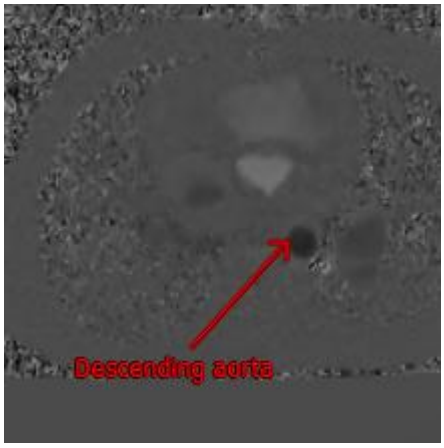


Figure 6-16 Example Annotation

When you select another series or navigate to another time point in the active series, your annotation is no longer displayed in the viewport. This is because the point to which the annotation refers does not lie on the currently visible image. To see your annotation again, right-click on the annotation on the **Results** pane and select **Locate**; or double-click on the annotation on the **Results** pane.

For details on creating, editing and deleting annotations, see the Medis Suite User Manual.

Distance Measurements

A procedure to measure the distance from one point to another. When you have measured a distance, you can modify the annotation and the end points of the measurement. All distance measurements of the active study are listed on the **Results** pane. All distance measurements of the active session are listed on the **Results** pane of Medis Suite.

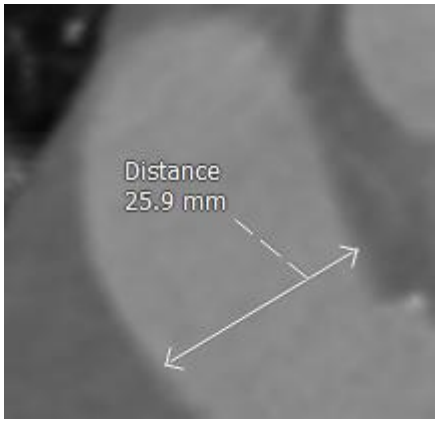


Figure 6-17 Example Distance Measurement

When you select another series or navigate to another time point in the active series, your distance measurement may not be displayed on the viewport. This is because the points between which you measured do not lie on the currently visible image. To see your measurement again, right-click on the measurement on the **Results pane** and select **Locate**; or double-click on the measurement on the **Results pane**.

For details on creating, editing, and deleting distance measurements and copying the results to clipboard, see the Medis Suite User Manual.

Area Measurements

You use the area measurement tool to draw and measure 2D areas. When you have measured an area, you can modify the area contour or annotation. All area measurements of the active study are listed on the **Results pane**. All area measurements of the active session are listed on the **Results** pane of Medis Suite.

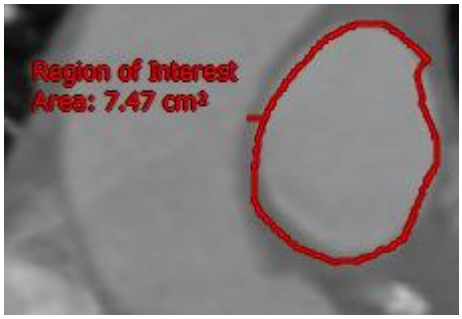


Figure 6-18 Example Area Measurement

When you select another series or navigate to another time point in the active series, your area measurement may not be displayed on the viewport. This is because the image on which you measured the area is not the same as the currently visible image. To see your measurement again, right-click on the measurement on the **Results pane** and select **Locate**; or double-click on the measurement on the **Results pane**.

For details on creating, editing, and deleting area measurements and copying the results to clipboard, see the Medis Suite User Manual.

Snapshots

You can save snapshots as evidence of an analysis or diagnosis. Snapshots are displayed on the **Properties** pane and are listed on the **Results pane**. When a snapshot is created, you can modify the name at any time.

When you select another series or navigate to another time point in the active series, the annotations and measurements shown in the snapshot may not be displayed on the viewport. This is because the points at which the annotations and measurements were created do not lie on the currently visible image. To return to the same series and time point where a snapshot was created, right-click on the snapshot on the **Results pane** and select **Locate**; or double-click on the snapshot on the **Results pane**.

For details on creating, editing and deleting snapshots, see the Medis Suite User Manual.

6.3 Performing a QFlow 4D Analysis

The Flow Analysis procedure reformats a series of time-resolved 3D volumes, into a 2D CINE series, which can then be quantified in QFlow.

To perform a QFlow 4D flow analysis, you may use the following guidelines.

- Load series
- Visually inspect the data
  Apply Noise Removal: Refer to, **Error! Reference source not found.** Noise Removal [5.4].
- Optional: Verify All Flow Velocity Directions
- Optional: Create a Phase Unwrapping
- Optional: Create a Background Correction
- Start a Flow Analysis
- Review Reporting
- Save the Session

6.3.1 Verify Flow Velocity Directions: Overview

A 4D flow MRI dataset consists of time-resolved, three-dimensional series encoded in three velocity directions and a single modulus (or magnitude) series. In QFlow4D, the three velocity orientations are as follows

- LR/RL (Left-Right/Right-Left)
- HF/FH (Head-Feet/Feet-Head) and
- AP/PA (Anterior-Posterior/Posterior- Anterior)

If velocity encoding is positive, the pixels are white and if it is negative, the pixels are black. In a series where the data is encoded in RL direction, the areas showing the flow from right to left would be positive and visually seen as white pixels, while areas showing the flow left to right would be negative and seen as black.

Given that there is no standardization in the velocity encoding directions in the 4D Flow MRI field, the directions in the data should be verified.

The user must check all orientations.

Not all Siemens and Philips scanners have 4D Flow MR acquisition protocol available for their series. As such, the correct velocity directions cannot be warranted and therefore should be verified.

Post processing packages may change the velocity encoding directions.

If QFlow 4D did not correctly determine the velocity encoding, contact Installation & Support for assistance in correctly configuring your system. Refer to the Support section.

Figure 6-19 Modulus Image

H, P, A and F are indicators that assist in determining the flow direction and image orientation.

The orientation cube located at the bottom right corner can be modified to change the viewing orientation. Refer to Figure 6-19 Modulus Image.

Verify All Flow Velocity Directions

To verify all velocity directions:

1. Press  in the toolbar.

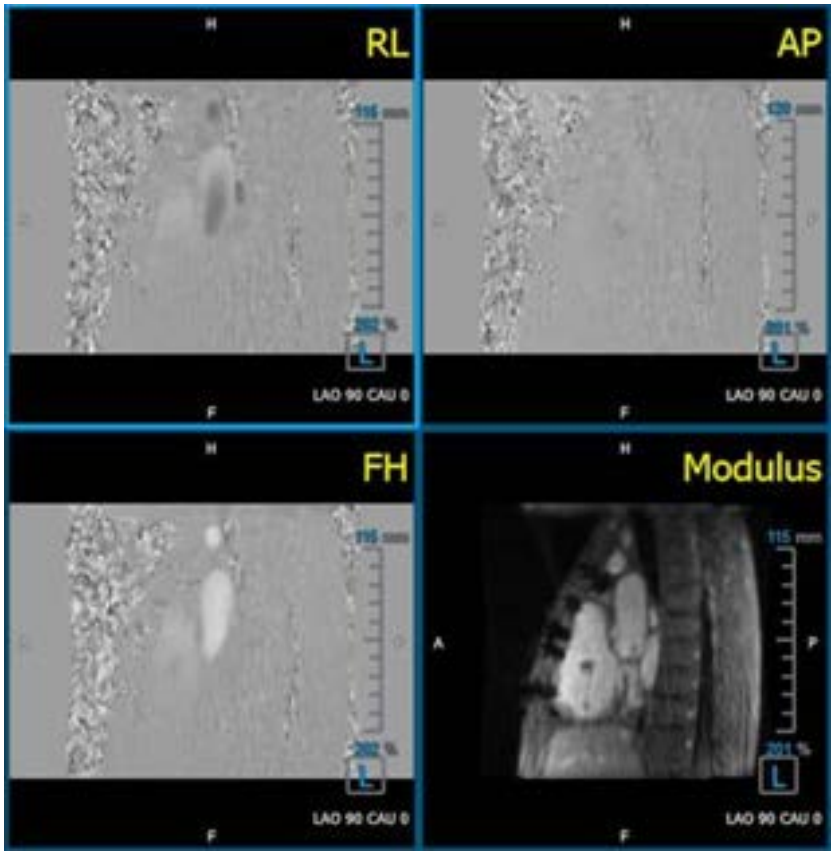


Figure 6-20 Verify Flow Velocity Direction Layout

2. Make the MODULUS viewport orientation LEFT

   “L” in the square at the right bottom corner of the viewport.

3. In the MODULUS viewport, scroll through the images to find a slice including the descending aorta and the heart chambers.

4. Determine the systolic time frame where the images have the highest velocity intensity signal.

5. **Error! Reference source not found.**

6. **Error! Reference source not found.**

7. **Error! Reference source not found.**

Verify HF / FH Velocity Direction

To verify the HF / FH velocity direction:

1. Press  in the toolbar.

2. Make the MODULUS viewport orientation LEFT

“L” in the square at the right bottom corner of the viewport.

3. In the MODULUS viewport scroll through the images to find a slice including the descending aorta and the heart chambers.

4. Determine the systolic time frame where the images show a definitive velocity signal.

5. Please verify at least one of the following situations described below is correct. If not, contact Medis Support.

If the descending aorta is white, in the viewport containing HF / FH view, then the velocity encoding direction should be HF.

If the descending aorta is black, in the viewport containing HF / FH view, then the velocity encoding direction should be FH.

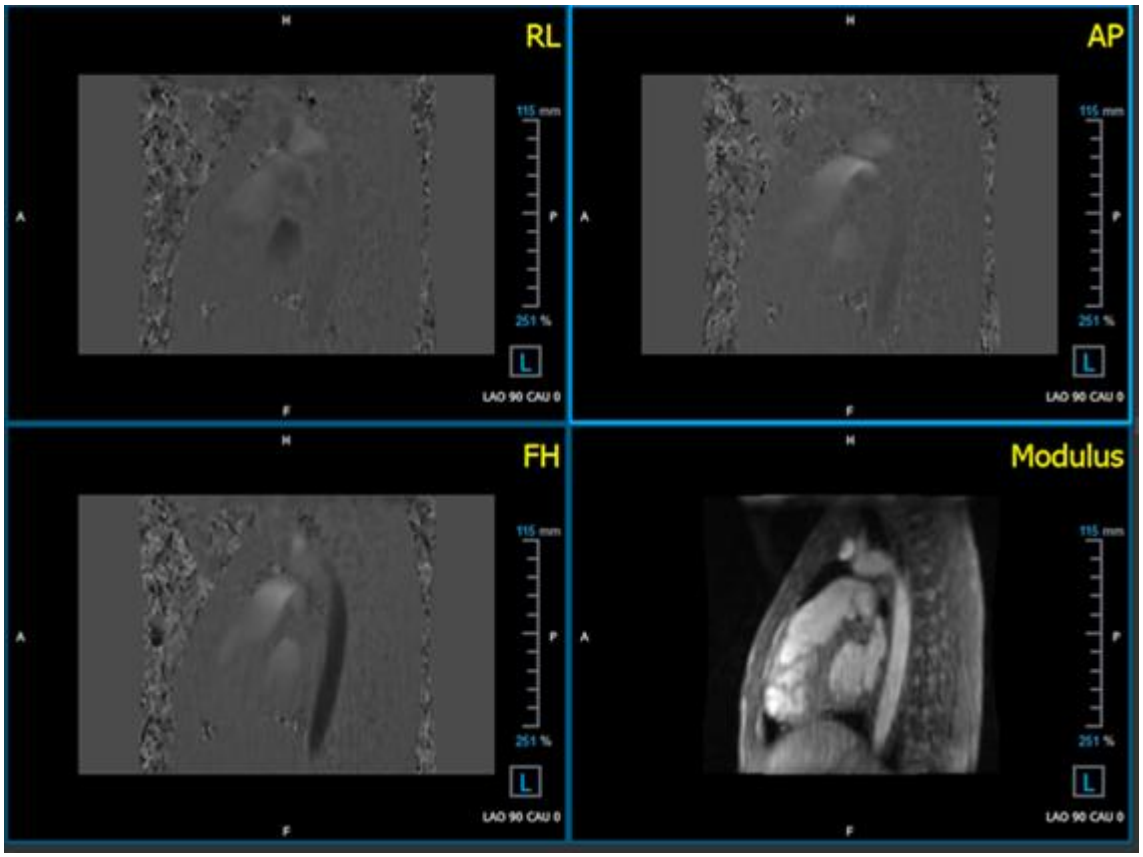


Figure 6-21 Verify Flow Velocity Direction Layout

Verify AP / PA Velocity Direction

To verify the AP / PA velocity direction:

1. Press  in the toolbar.

2. Make the MODULUS viewport orientation LEFT (“L” in the square at the right bottom corner of the viewport.

3. In the MODULUS viewport find the aortic arch.

4. Determine the systolic time frame where the images show a definitive velocity signal.

5. Please verify at least one of the following situations described below is correct. If not, contact Medis Support.

   If the aortic arch is white, in the viewport containing PA / AP view, then velocity encoding direction should be AP.

   If the aortic arch is black, in the viewport containing PA / AP view, then velocity encoding direction should be PA.

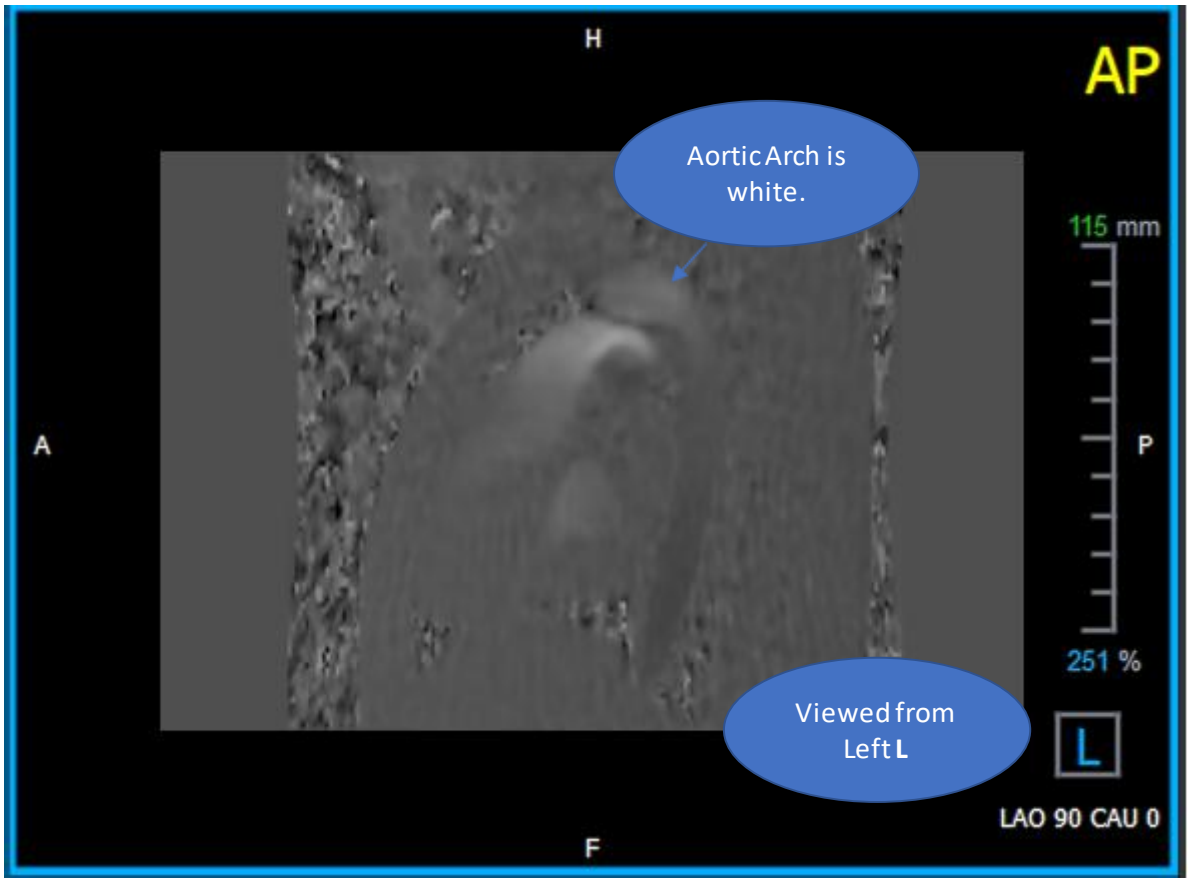


Figure 6-22 AP Positively encoded viewport, with a white aortic arch and a darker descending aorta.

Verify RL / LR Velocity Direction

To verify the AP / PA velocity direction:

1. Press  in the toolbar.

2. Make the MODULUS viewport orientation ANTERIOR

   “A” in the square at the right bottom corner of the viewport.

3. In the MODULUS viewport find the slice including the ascending aorta.

4. Determine the systolic time frame where the images show a definitive velocity signal.

5. Please verify at least one of the following situations described below is correct. If not, contact Medis Support.

   In the viewport containing RL / LR view, the orientation is LR if the proximal ascending aorta is white and the distal ascending aorta is black.
   In the viewport containing RL / LR view, the orientation is RL, if the proximal ascending aorta is black and the distal ascending aorta is white.

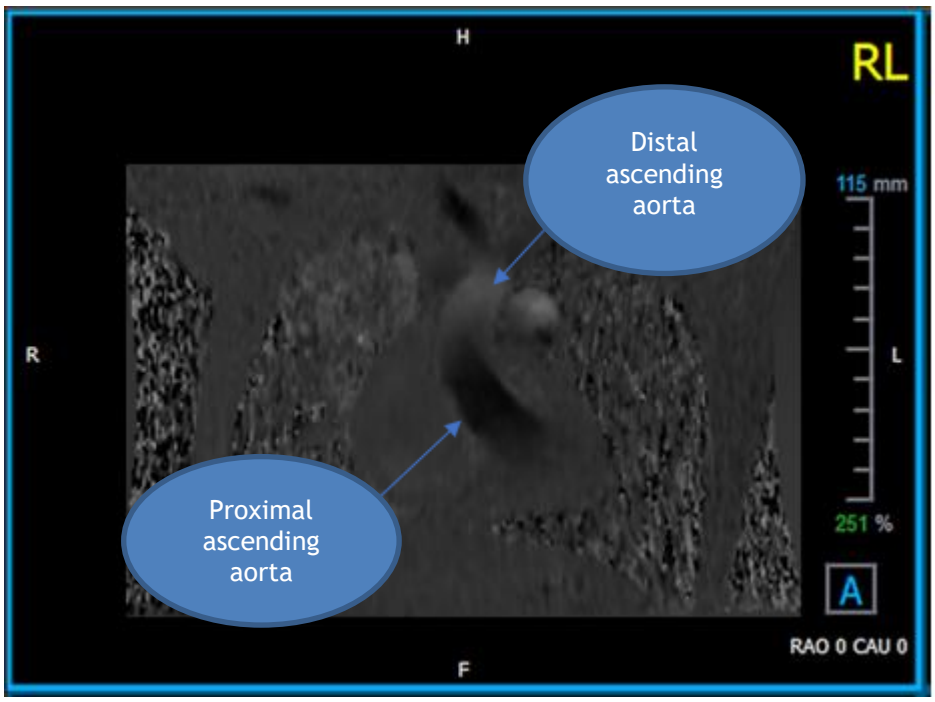


Figure 6-23 RL Positively encoded viewport, with proximal and distal ascending aorta

Close the Velocity Direction Verification View

1. Press  in the toolbar. The layout will return the QFlow 4D analysis layout.

Custom System Options

If the velocity direction are incorrect for a particular dataset, please contact Medis Installation & Support.

6.3.2 Background Correction

The quality of the phase velocity data may be compromised as a result of background phase distortions. These distortions can be corrected by applying a stationary flow fit algorithm to the data. The Background correction utility is a quantitative tool which removes phase offset errors from the data, thereby correcting phase offset errors.

The background correction which is also known as stationary flow fit algorithm, has two configurable settings, the **Standard Deviation Threshold** to define the static tissue mask and the **Fitting order** which defines the level of complexity of the fitting.

Standard Deviation Threshold.

A low standard deviation threshold value might cause inclusion of insuffient static tissue volume to obtain an accurate background correction
A high standard deviation threshold value might cause inclusion of flow area as static tissue which would result in an inaccurate background correction.
25% standard deviation threshold is the default.

Fitting order

The fitting order of the stationary flow fit algorithm defines the complexity of the fitting planes used to correct the phase offset error. There are three fitting orders, 1st 2nd and 3rd, which in theory, respectively produce more sophisticated background corrections, although they require longer computational time.

The Background Correction settings are used for all Reconstructions and they are published as part of each reconstruction output in the **Results** pane, the **Report** tab in Medis Suite.

The background correction affects the reconstruction procedure(s). When a background correction is modified or completed, all existing reconstructions in the current session, will be updated to use the new background corrected data.

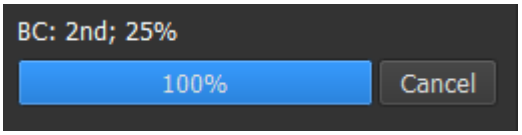
Noise Removal has no effect on background correction.

Enable Background Correction

To enable background correction.

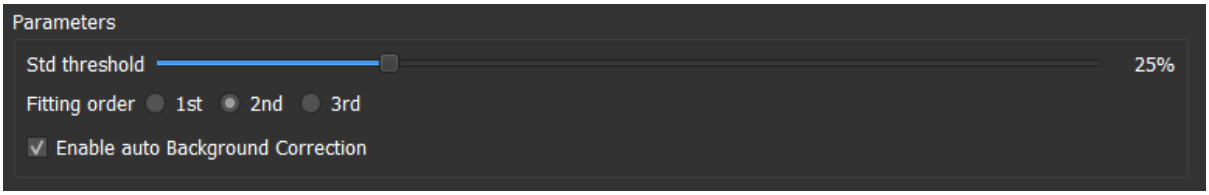
1. Press  in the toolbar.

   The **Properties** pane of the Background Correction displays the following;

   - Background Correction progress
   - The selected threshold
   - The selected fitting order
   - **Cancel** button, to cancel the correction

2. Select  **> Options**, **Background Correction** and check the “Enable auto Background Correction” option.



The Background Correction can be selected in the Corrections list on the Results pane, which will show the corresponding Properties pane.

Any changes to Background Corrections threshold or fitting order are applied to all reconstructions in the current session.

Deleting Background Correction

You can delete any Background Correction that was created.

To delete a Background Correction:

1. Select the Background Correction in the **Corrections** list on the **Results pane**.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the Background Correction.

Removing a Background Correction updates **all** reconstructions in the current session.

Background Correction Options

You can change and apply the Background Correction settings using the options menu.

To modify Background Correction settings:

1. Select  **> Options**, **Background Correction**.

   - The Std Threshold can be modified with the slider  .
   - The Stationary Flow Fit, Fitting Order can be selected.
   - The Enable auto Background Correction, can be selected.

Any changes to Background Corrections threshold or fitting order are applied to **all** reconstructions in the current session.

If Enable auto Background Correction is selected, Background Correction will be applied after loading the data.

6.3.3 Phase Unwrapping

The quality of the phase velocity data may be compromised as a result of an incorrectly chosen Venc. Velocities higher than Venc cannot be encoded in the phase velocity data, and show up

“wrapped”, i.e. with a lower value, a phenomenon known as aliasing. The Phase Unwrapping algorithm detects aliasing in the data and undoes it by applying a corresponding shift to the phase velocity data.

The phase unwrapping algorithm has two parameters, and upper and a lower threshold, the values of which can be changed in the options. The initial computation of the phase unwrapping algorithm yields an amount of aliasing that can be any value. However, it is assumed that the aliasing always is 2 Venc. To constrain the algorithm output accordingly, there is an **Upper Threshold** above which values are rounded to 2 Venc, and a **Lower Threshold** below which values are rounded to -2 Venc.

Upper Threshold

> The upper threshold can take values between 0 and 2 Venc. Higher values of this threshold cause the algorithm to be more conservative in identifying aliasing in the positive velocity direction, while lower values cause the algorithm to identify aliasing more readily. An upper threshold below 0.5 Venc is not advised.

Lower Threshold

> The lower threshold can take values between -2 Venc and 0. Lower values of this threshold cause the algorithm to be more conservative in identifying aliasing in the negative velocity direction, while higher values cause the algorithm to identify aliasing more readily. A lower threshold above -0.5 Venc is not advised.

The Phase Unwrapping is used for all reconstructions, and whether one is present is published as part of each reconstruction output in the **Results** pane, the **Report** tab in Medis Suite.

The Phase Unwrapping affects the reconstruction and Background Correction procedure(s). When a Phase Unwrapping is completed, an existing Background Correction, and afterwards all reconstructions in the current session, will be updated to use the new unwrapped data.

For performance, apply Phase Unwrapping before Background Correction, and prevent the recompute of the Background Correction after the Phase Unwrapping finishes.

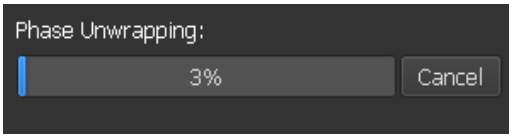
Noise Removal and Background Correction have no effect on Phase Unwrapping.

Enable Phase Unwrapping

To enable Phase Unwrapping.

1. Press  in the toolbar.

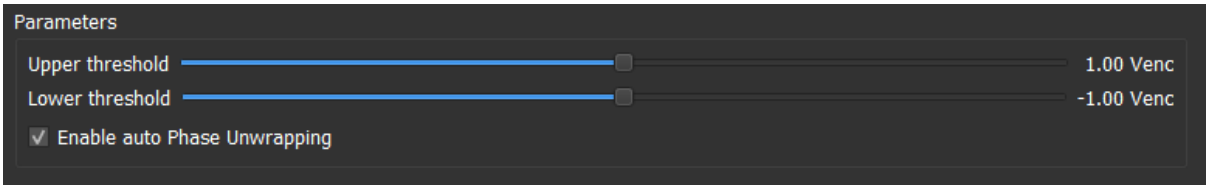
   The **Properties** pane of the Phase Unwrapping displays the following;

   - Phase Unwrapping progress
   - **Cancel** button, to cancel the unwrapping

   or

2. Select  **> Options**, **Phase Unwrapping** and check the “Enable auto Phase Unwrapping” option.



The Phase Unwrapping can be selected in the Corrections list on the Results pane, which will show the corresponding Properties pane.

From the **Results** pane Phase Unwrapping can be located, deleted and renamed. The **Properties** pane shows the Phase Unwrapping progress.

Deleting Phase Unwrapping

You can delete any Phase Unwrapping that was created.

To delete a Phase Unwrapping:

1. Select the Phase Unwrapping in the **Corrections** list on the **Results pane**.
2. Press Delete on your keyboard or right-click and select **Remove**.

   This deletes the Phase Unwrapping.

Removing a Phase Unwrapping updates **all** reconstructions in the current session.

Phase Unwrapping Options

You can change and apply the Phase Unwrapping settings using the options menu.

To modify Phase Unwrapping settings:

1. Select  **> Options**, **Phase Unwrapping**.

   - The Upper Threshold can be modified with the top slider  .
   - The Lower Threshold can be modified with the bottom slider.
   - The Enable auto Phase Wrapping can be selected.

Any changes to the Phase Unwrapping parameters Upper Threshold and Lower Threshold are applied to **all** Background Corrections **and** Reconstructions.

If Enable auto Phase Unwrapping is selected, Phase Unwrapping will be applied after loading the data.

6.3.4 Flow Analysis

The QFlow 4D Flow analysis is referred to as a **Reconstruction**. The Flow Analysis procedure enables reformatting the time-based 3D volume, into a 2D series, which is then quantified in another app, QFlow 2D.

These are the steps to complete a Flow analysis.

1. Locate the plane of interest. Refer to Double Oblique View.
2. Start a Flow analysis
    - Optionally: Rename the reconstruction
3. Complete a Flow analysis
4. Rename the Flow analysis label, from “Reconstruction” to an appropriate label.

All Flow Analyses results are stored in the QFlow 4D results, reports and session.

Multiple Flow analyses may be started.

The flow analysis in QFlow 4D is performed in a separate tab outside QFlow 4D using the existing QFlow application.

Start Flow Analysis

QFlow 4D supports locating, renaming, exporting and removing of the flow analyses. Flow Analysis is labelled by default “Reconstruction”.

To start a flow analysis

- Select  from the toolbar.

Or,

1. Right-click in the viewport area. This opens a context menu.

Select **Flow Analysis**

Flow Analysis App

Flow analysis will be started with the QFlow 4D reformatted dataset.

- Press F1.
- Pushing the  help button.
- Select the Medis Suite main menu button in the upper right corner  > **Help** > **User Documents**. For detailed instructions on using Flow 2D, refer to the QFlow 2D User manual.

Figure 6-24 QFlow2D hosting the Flow analysis

Multiple Flow Analysis's

QFlow 4D supports multiple Flow analyses. Each new Flow analysis creates a new tab.

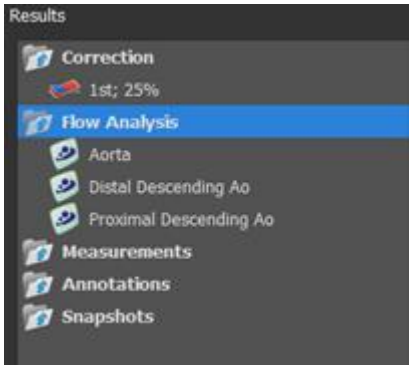


Figure 6-25 Results Pane with multiple flow analysis

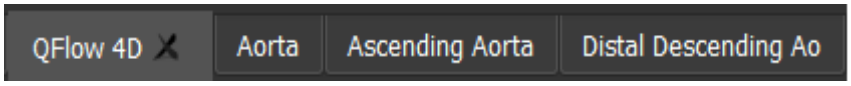


Figure 6-26 List of multiple tabs, each with a flow analysis

6.3.5 Mitral Valve analysis

The Mitral Valve procedure enables the quantification of valvular blood flow. The QFlow4D data is a time-based 3D series, which is automatically reformatted into a 2D series before it is quantified by QFlow 2D.

These are the steps to complete a Mitral Valve analysis.

1. Load a QFlow 4D dataset, in addition to a 2 chamber, and 4 chamber cine series.
2. Start a Mitral Valve analysis.
3. Change the plane of interest, for each phase, if it is required.
4. Complete a QFlow 2D analysis.
5. Rename the analysis label, from “Mitral Valve” to an appropriate label.

The procedure requires both 2 and 4 chamber cine series to determine the Mitral valve location.

All Mitral Valve Analyses results are stored in the QFlow 4D results, reports and session.

Multiple Mitral Valve analyses may be started.

The flow analysis in QFlow 4D is performed in a separate tab outside QFlow 4D using the existing QFlow 2D application.

Start Mitral Valve analysis

QFlow 4D supports locating, renaming, editing, duplicating and removing of the Mitral Valve analyses. The analysis is labelled by default “Mitral Valve”.

To start a Mitral Valve analysis

- Select  from the toolbar.

Or,

1. Right-click in the viewport area. This opens a context menu.
2. Select Mitral Valve.

Change the plane of interest

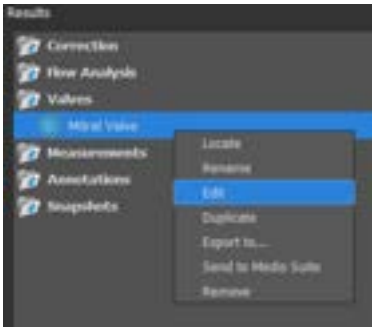
The Mitral Valve procedure allows you to move the plane of interest for each phase by individually positioning the axes. The default plane of interest is based on the automated Mitral Valve location. You can adjust this plane by applying a positive or negative **“offset”**, which effectively moves the plane parallel to the default Mitral Valve plane.

- A positive offset moves the plane toward the cardiac apex.
- A negative offset moves the plane toward the atrium.

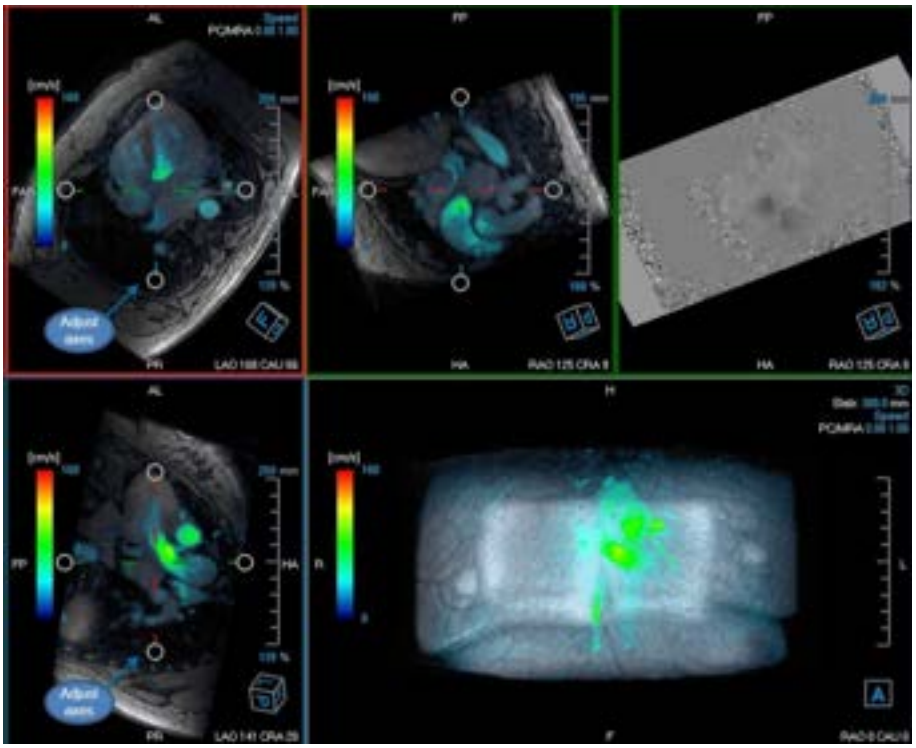
This offset is measured in millimetres and can be copied to all phases.

To adjust the plane of interest

- Select “Edit” in context menu.



- Navigate to the phase that needs correction.
- Adjust the plane of interest, by adjusting the axes in either top left or bottom right viewport.

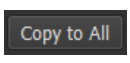


- Navigate to another phase that needs correction

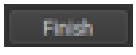
Or,

- Apply an offset to each plane for all phases in the properties pane

Or,

- Click  to copy the current plane location and orientation to all phases.

Or,

- Click  to accept all changes.

The existing Flow analysis results for the Mitral Valve procedure are deleted when finalizing editing.

Flow Analysis App

Flow analysis will be started with the QFlow 4D reformatted dataset. For more information see chapter 7.

6.4 Reporting

QFlow 4D results are made available in the Medis Suite Results pane and in the Medis Suite report.

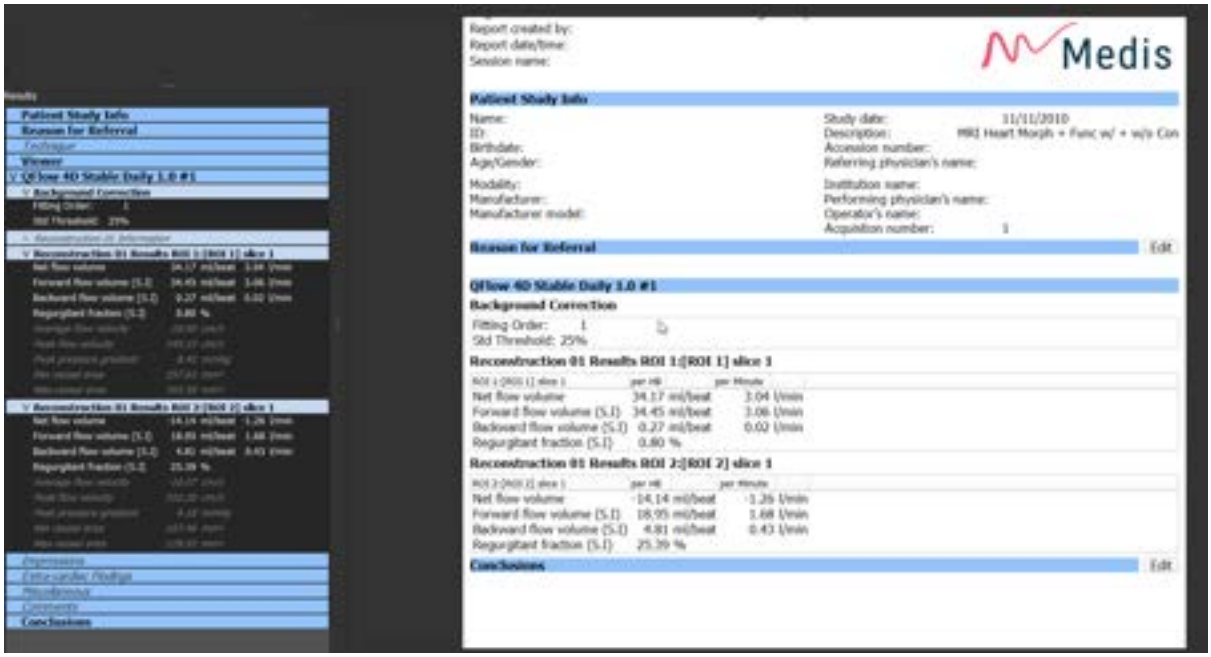


Figure 6-27 Medis Suite Report with QFlow 4D Results

The Reporting functionality of Medis Suite is described in the Medis Suite user manual. The Medis Suite documentation is available from the User documents tab, which can be opened as follows;

- Press F1.
- Pushing the  help button.
- Select the Medis Suite main menu button in the upper right corner  > **Help** > **User Documents**

6.5 Sessions

The QFlow 4D state can be saved in a Medis Suite session. The session can be reloaded to continue or review the analyses.

The session functionality in Medis Suite is described in the Medis Suite user manual. The Medis Suite documentation is available from the User documents tab, which can be opened as follows;

- Press F1.

- Pushing the  help button.

Select the Medis Suite main menu button in the upper right corner  > **Help** > **User Documents**

6.6 Accuracy of Measurements

QFlow 4D measurements are not intended for a specific clinical purpose and therefore there is no clinical validation, with exception to the length and area measurement calculations, which are validated based on the pixel sizes.

In QFlow 4D all measurements are derived from calculations performed on the loaded DICOM images.

The accuracy of the measurements and calculations exceeds that of the displayed results, by at least one decimal point.

In practice, the image is the limiting factor of the accuracy of measurements. Limiting factors, such as, image resolution both spatial and time-based, image noise, inhomogeneity in the magnetic field and patient determines the accuracy of any given measurement.

Result	Unit	Precision	Accuracy source
Distance measurement	mm	0.1	Not intended for specific clinical measurement.
Area measurement - area	mm^2	0.01	Not intended for specific clinical measurement.
Area measurement - circumference	mm	0.1	Not intended for specific clinical measurement.
Area measurement min and max diameter	mm	0.1	Not intended for specific clinical measurement.

6.7 Shortcut Keys

When you are working with QFlow 4D, you can use several combinations of keys on your keyboard and mouse actions to quickly perform the following tasks.

Press	To
Layout	
F11	Show or hide the workspace window panes
Image control	

Press	To
Middle-click and hold	Hide all graphics
Middle-click and drag, or Ctrl and drag	Pan
Ctrl+Shift and drag	Zoom
Alt+Shift and drag	Stack
Procedures	
A	Create an area measurement
D	Create a distance measurement
S, or CTRL+SPACE	Create a snapshot
Esc	Stop editing the procedure
Delete	Delete the currently selected procedure
SHIFT+Delete	Delete all procedures
Navigation Controls	
HOME	Display the first time point
END	Display the last time point
Arrow up	Display the previous slice
Arrow down	Display the next slice
Arrow left	Display the previous time point

Press	To
Arrow right	Display the next time point
CTRL+arrow left	Play cine backward
CTRL+arrow right	Play cine forward
Esc	Stop playing cine
Page Up	Display the previous series
Page Down	Display the next series

6.8 Reference

Anterior (or **ventral**) Describes the front or direction toward the front of the body. The toes are anterior to the foot.

Posterior (or dorsal) Describes the back or direction toward the back of the body. The popliteus is posterior to the patella.

Streamlines Describes the blood flow along a anatomical structure, such as a blood vessel. They represent a group of connected lines, where the color of each line indicates the velocity at a given location.

Vectors Describe a microscopic blood particle traversing through the structure of interest. It portrays the direction with an arrowhead and the velocity with color.

7 QFlow

7.1 Starting QFlow

This chapter explains how:

- How QFlow is started and how data is loaded into QFlow

QFlow can be started from Medis Suite. Series that have been loaded in Medis Suite can be selected and dropped onto the QFlow icon using the left mouse button, which will start QFlow. Exactly 1 phase and 1 magnitude image series need to be selected and dragged onto the QFlow app. The selected series are then displayed in QFlow.

The following image shows how a phase and a magnitude image can be dropped simultaneously onto the QFlow icon.

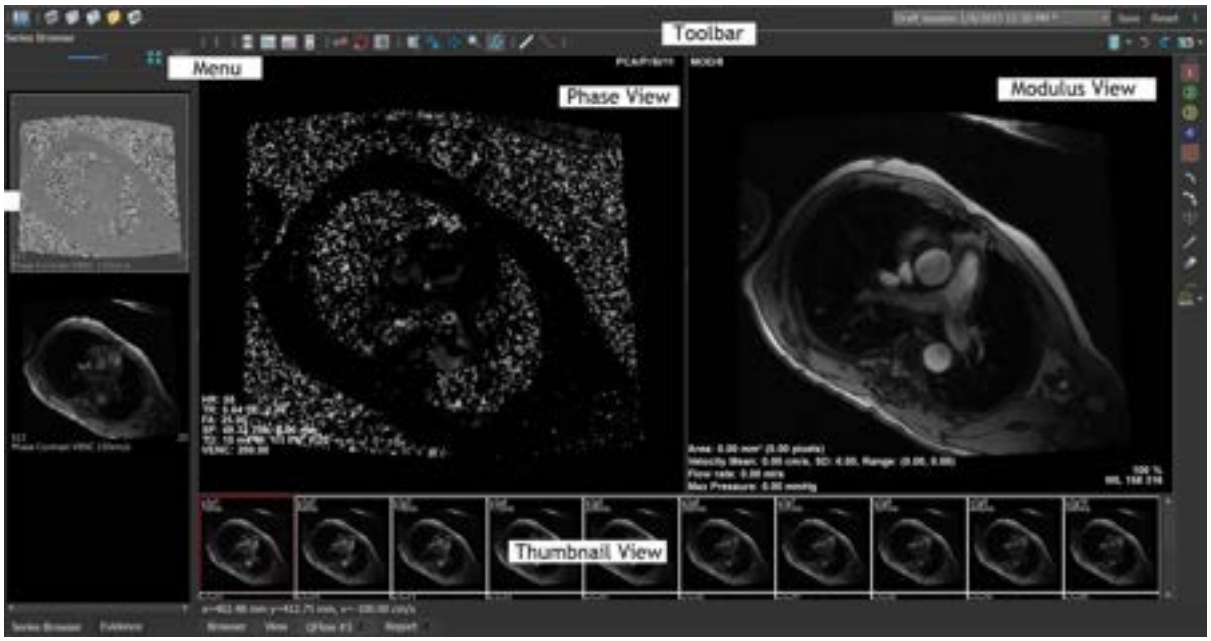
QFlow requires both phase and modulus series. An error occurs if only one of these types is loaded.

7.2 The QFlow Workspace

This chapter explains:

- The contents of the QFlow workspace

The QFlow main workspace consists of a set of toolbars, a phase view, a modulus view and a thumbnail view. The application menu is accessible through a menu icon in the toolbar.



Phase view
The phase view shows a velocity image of the selected series.

Modulus View
The modules view shows a modules image of the selected series.

Thumbnail View
The thumbnail view shows thumbnail images of the selected series. The thumbnail view shows either phase images or modulus images. This can be configured through through the application menu. The thumbnail marked with the red border corresponds to the image displayed in either the phase view or the modulus view.

Toolbar
The toolbar area consists of a Medis Suite toolbar and several QFlow toolbars. The QFlow toolbars can be used to access the application menu, to start a movie, to show a graph, to access the main settings, and to perform some basic image manipulations like panning or zooming. The QFlow toolbars can also be used to undo and redo some actions, to create a snapshot, to detect or draw contours and to edit or delete them.

Menu

The application menu is accessible through the button and can be used for example to reset the layout, to view graphs, to view reports, to view study parameters, to change settings, to detect and edit contours, to undo or redo actions and to cut, copy and paste elements.

7.3 Reviewing Studies

This chapter explains how to:

- Browse the images in the Modulus View and Phase View

- Select an image
- Switch between phase and modulus images in the Thumbnail View
- View the series in the Movie window
- Scroll through the images
- Zoom in or out
- Pan
- Adjust the window width and level
- Select the Edit mode

To browse the images

- Use the arrow keys on your keyboard to browse the images in the Modulus View and Phase View.

To select an image

- Click an image in the Thumbnail View to select it.

  This displays the image in the Phase and Modulus Views.

To switch between phase and modulus images in the Thumbnail View

- Click  to open the application menu and Select **View > Modulus Images** or **View > Phase Images**.

To view the series in the Movie window

- Click  in the toolbar or press F5.

To scroll through the images

- In the toolbar, click  . Pressing the left mouse button and moving the mouse from left to right allows you to scroll through the phases. Pressing the left mouse button and moving the mouse up and down allows you to scroll through the slices.

Or,

- Press the left and right mouse button simultaneously and move the mouse from left to right to scroll through the phases. Pressing the left and right mouse button and moving the mouse up and down allows you to scroll through the slices.

To zoom in or out

- In the toolbar, click  . You can zoom in by pressing the left mouse button and moving the mouse down. You can zoom out by pressing the left mouse and moving the mouse up.

Or,

- Press + to zoom in or – to zoom out.

Or,

- Press the left and middle mouse buttons and move the mouse down to zoom in or move the mouse up to zoom out.

To pan

- In the toolbar, click  . You can pan by pressing the left mouse button and dragging the mouse.

Or,

- Press the middle mouse button and drag the mouse.

 Panning only works when the images are zoomed in.

To adjust the window width and level

- In the toolbar, click  . In the Phase View or Modulus View, hold down the left mouse button and drag.

  Or,

- Press the right mouse button and drag the mouse.

To select the Edit mode

- In the toolbar, click  . In the edit mode you are able to draw contours, distance measurements, profile lines etc.

7.4 Performing Vascular Flow Analyses

This chapter explains how to:

- Perform a vascular flow analysis
- Apply background correction
- View analysis results
- Perform a Qp/Qs analysis

Now that we have reviewed the series, we are going to perform a vascular flow analysis using the automatic contour detection.

If you want to perform a transvalvular flow analysis, you have to create contours manually. For detailed instructions, refer to the QFlow User Manual.

Automatic contour detection is performed based on the settings specified in the Contour Detection Settings window. You can access these settings by selecting **Settings > Contour Detection Settings**… from the application menu.

When you are using the analysis to obtain results on the average flow velocity, make sure that contours are present in every phase.

Automatically and manually created contours can lead to incorrect results. Make sure to review them and correct if necessary.

To perform a vascular flow analysis

1. Select the image that shows most contrast between the vessel and the background.
2. Click  in the toolbar.
3. Click  .
4. In the Phase or Modulus View, click to select the center point of the vessel you want to analyze.
5. Verify that the contour is correct.

   The maximum velocity pixel within the contour in this phase is marked by an orange square, the minimum velocity pixel is marked by a blue square.

   To create a new contour, you can place the center point again.

   To draw or edit the contour, click  or  and trace the contour in the Modulus or Phase View, or click  and drag the contour. To reshape the contour, right-click in the view, select **Contour Shape**, and select one of the reshaping options from the submenu.

6. If you want to analyze a second, third, or fourth vessel in the same series, click  ,  ,or  in the toolbar, and repeat steps 3 through 5 for each vessel.

7. Click  or press CTRL+D to automatically detect contours in the other images of the series.

    You can detect contours for all vessels you marked in one go. Click the arrow next to this icon  , and from the submenu, select **Detect Contours of All ROIs**. This detects contours for all vessels (regions of interest) you marked in the entire series.

8. Check if all contours have been detected correctly. Make sure to edit incorrect contours. Click  or press CTRL+D again to automatically redetect the contours.

To view analysis results

1. Click  , press F7, or select **View > Graph** from the application menu.

   This displays the Volume diagram.

    Click a point in the curve to display the corresponding image in the Phase View and Modulus View.

2. Select the diagram of your choice from the **Show** drop-down list.

To add or hide curves in flow diagrams

In the diagram window, click  ,  ,  , or  to show or hide the corresponding curves in the diagram.

To apply background correction using the ROI4 area method

If needed, you can apply background correction. The ROI4 area method is one of four methods for background correction that are available.

 Refer to the QFlow User Manual for instructions on performing background correction using one of the other methods.

1. Click  to open the application menu and Select **Settings > Main**…or click 

2. On the **Background subtraction** tab, from the **Subtract background flow** drop-down list, select **ROI 4 area** and close the settings dialog.

3. In the toolbar, select  , and then select  or  .

4. In the Phase or Modulus View, trace a contour in an area where you expect no flow. Make sure that you do so as close to the vessel as possible.

5. Press CTRL+C and then CTRL+SHIFT+V.

   This copies the contour to the other images.

6. Check the area in all images to verify that it does **not** cover areas where flow is to be expected. Edit the contours if necessary.

    You can move a contour as follows. Select its ROI icon in the toolbar, then press CTRL and use the left mouse button to move the contour.

7. Any results that you now view are corrected for background flow.

To calculate the pulmonary-to-systemic flow ratio

1. Open a new instance of QFlow with series that show Pulmonary blood flow.

2. Click  in the toolbar to perform a regular vascular flow analysis and follow the steps above.

3. Click  in the toolbar to mark the analysis as a Pulmonary blood flow analysis.

4. Open a new instance of QFlow with series that show Systemic blood flow.

5. Click  in the toolbar to perform a regular vascular flow analysis and follow the steps above.

6. Click  in the toolbar to mark the analysis as a Systemic blood flow analysis.

   The Qp/Qs results are automatically displayed in the report in Medis Suite.

7.5 Creating reports

This chapter explains:

- How to view a Medis Suite report.
- How to manually add a snapshot to the Medis Suite report.
- How to create a text or XML report.

Reports contain a summary of patient and study information and a number of analysis results. You can create plain text reports, XML reports or a Medis Suite report.

To view a Medis Suite report

Flow results and distance measurements are automatically added to a Medis Suite report. You can access a Medis Suite report by selecting the **Report** tab in Medis Suite.

Refer to the Medis Suite User Manual for instructions on how to customize a Medis Suite report.

To manually add a snapshot to the Medis Suite report

QFlow allows you to create a snapshot from an image or a graph and to add the snapshot to a Medis Suite report.

1. Press the right mouse button on an image or a graph and select the right mouse button menu.
2. Select **Add… To Results.**
3. The snapshot is added to the Medis Suite report.

To create a text or XML report

1. Click to open the application menu and select **View > Report** or press F9.
2. To create a text or XML report, click Plain text or XML.

   If you are creating a text report, you can select the results you are interested in by selecting the corresponding check boxes under Contents.

7.6 Accuracy of Measurements

In QFlow all measurements are derived from calculations performed on the loaded DICOM images.

Both during development and with each new release of the product, measurements and calculations are extensively validated. The accuracy of the measurements and calculations exceeds that of the displayed results, by at least one decimal point.

In practice, the image is the limiting factor of the accuracy of measurements. Limiting factors, such as, image resolution both spatial and time-based, image noise, inhomogeneity in the magnetic field and patient determine the accuracy of any given measurement.

The effective accuracy of measurements has been evaluated with multiple validation studies. The following table gives the expected accuracy for the different types of measurement.

Functional measurement	Accuracy
Automatic segmentation algorithm for the calculation of flow rates	Inter-observer variability areas [1]: Manual: 6.28 %. Automatic: 2.15 %.
Application of background correction, by means of stationary flow fit or phantom correction	Lankhaar method [2] has been implemented.
Calculation of flow curves for flow, velocity, peak values and regurgitation	Inter-observer variability volumes [1]: Manual: 0.85 %. Automatic: 1.2 %.
CSF flow analysis calculations	Error in absolute CSF flow [3]: In images from RPC: 1.15 %. In images from CPC: 8.91 %.

References used in table above:

1. van der Geest, Rob J, Niezen, Andre R, van der Wall, Ernst E, de Roos, Albert, Reiber, Johan HC, “Automated Measurement of Volume Flow in the Ascending Aorta Using MR Velocity Maps: Evaluation of Inter- and Intra-observer Variability in Healthy Volunteers”, J Comput Assist Tomogr, vol. 22(6) (1998): 904-911.
2. Lankhaar JW et al, “Correction of Phase Offset Errors in Main Pulmonary Artery Flow Quantification”, Journal of Magnetic Resonance Imaging 22 (2005):73-79.
3. Wentland, Andrew L., Oliver Wieben, Frank R. Korosec, and Victor M. Haughton. "Accuracy and reproducibility of phase-contrast MR imaging measurements for CSF flow." American Journal of Neuroradiology 31, no. 7 (2010): 1331-1336.

7.7 Troubleshooting

Multiple slices in one series

If there are multiple flow locations combined in one series and you are not able to separate them, the arrows up and down keys will then allow you to switch slices.

7.8 Function Keys

When you are working with QFlow, you can use the function keys on your keyboard to quickly perform the following tasks.

Press	To
F5	play the current study as a movie.
F6	display the study properties.
F7	show the graph window.
F8	view the flow profile.
F9	open the report window.

7.9 Shortcut Keys

Shortcut keys are combinations of keys that you can press on your keyboard to give a command.

Shortcut	Use to
Images	
CTRL+drag	move the active contour relative to the image in the Phase or Modulus View.
middle mouse button or mouse wheel and drag	pan the image.
left and right mouse button simultaneously and drag	scroll through the images. A horizontal movement lets you scroll through the phases. A vertical movement lets you scroll through the slices.
left and middle mouse button and drag	zoom the images. An upward movement zooms out, and a downward movement zooms in.
right mouse button and drag	adjust the window width and window level of the images. A horizontal movement adjusts the window width, and a vertical movement adjusts the window level.
+ or =	zoom in on the images.
-	zoom out.
→	scroll forward through the Thumbnail View.
←	scroll backward through the Thumbnail View.
1	reset window width and level.
2	optimize window width and level.
Elements	
CTRL+Z	undo the last action.
CTRL+Y	redo the action that was undone.

CTRL+X	cut the currently active element and place it onto the clipboard.
CTRL+C	copy all elements from the active image to the clipboard.
CTRL+V	paste the element to the selected image.
CTRL+F	paste the element or elements to all images from the selected image onward.
CTRL+B	paste the element or elements to all images from the selected image backward.
CTRL+SHIFT+V	paste the element to all images.
DEL	delete the currently active element from the active image.
SHIFT+DEL	delete all elements in the active image.
CTRL+SHIFT+DEL	delete all elements in the entire slice.
CTRL+D	automatically detect contours based on the active contour.
CTRL + →	move the profile line to the right.
CTRL + ←	move the profile line to the left.
SHIFT + S	smoothen the active contour.
SHIFT + C	make the active contour more convex.
SHIFT + D	make the active contour decurved.
Tool icons	
CTRL+1	make the tool icon of the first contour active in the toolbar.
CTRL+2	make the tool icon of the second contour active in the toolbar.

CTRL+3	make the tool icon of the third contour active in the toolbar.
CTRL+4	make the tool icon of the fourth contour active in the toolbar.
F	make the profile line icon active in the toolbar.
Spacebar	switches between ROIs.

8 QMass

8.1 Starting QMass

QMass is started from Medis Suite.

For a detailed description on starting applications and loading data in the applications, refer to the Medis Suite Quick Start/User Manual.

Using Drag 'n Drop (D'nD) one can load data into QMass. Depending on the modifier keys pressed during the D'nD QMass will have a different load behavior:

D'nD	Data will be added to the current session and the first series will be made active.
D'nD + Shift	Data will be added. Current active series will remain active.
D'nD + Ctrl	Current data will be closed. New data will be loaded. First series will be made active.

To load existing local contours

- Click Menu and select **File > Load Contours …**

Select the QMass analysis file you are interested in.

To select a series

- If you have opened more than one series, you can switch between the series by clicking their tabs under the Study Matrix.

  Move the mouse over a tab to view a tooltip that shows the series name.

To browse through the images of a series

- Use the arrow keys on your keyboard to scroll the images in the Thumbnail View and in the Active View.

To select an image

- Click an image in the Thumbnail View to select it.

  This displays the image in the Active View.

  In the Thumbnail View, the selected image is marked with a red frame.

To view a series in the Movie window

- Click  in the toolbar or press F5.

To scroll through the images of the series in the Movie window

- Use the arrow keys on your keyboard.

To switch between series in the Movie window

- Press the PgUp or PgDn key on your keyboard.

To zoom in or out

- Use the slider under the Viewport or set the edit mode to Zoom mode  and use the LMB.

To pan

- Press the middle mouse button or mouse wheel, hold it down and drag.

  This pans the image.

  To return to editing mode, release the middle mouse button or mouse wheel.

To adjust window width and level

- Press 2 on the keyboard to optimize window width and level.

Or,

- Click RMB and drag in the Active View. Move the mouse to the left or right to adjust window width, move it up or down to adjust window level.

To load series for a Comparison analysis

- Click Menu  and select **File > Open Series Selection …**

Select the series you are interested in. Turn on the Comparison check box and load the data.

To change the auto-combine settings

- Click Menu  and select **File > Open Series Selection …**

Turn on or Off the auto combine checkbox. By selecting multiple series one can create a new combined series.

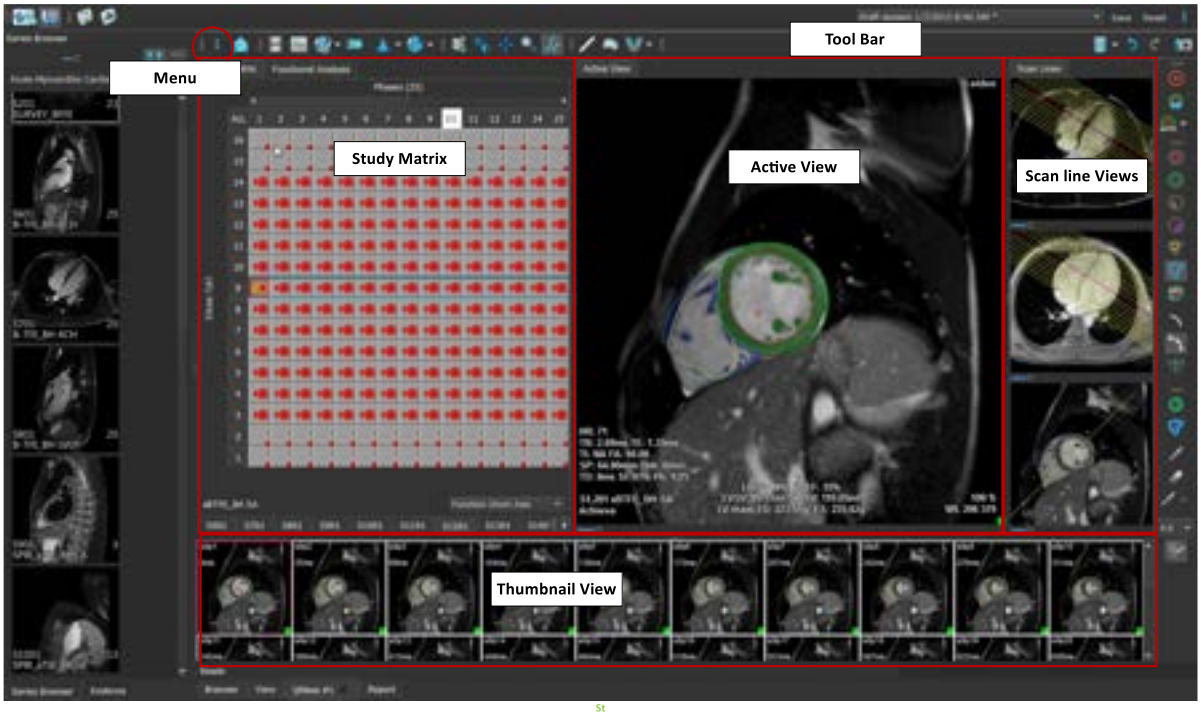
To create a snapshot from a graph or viewport

Click  in the toolbar of the dialog.

8.2 QMass Workspace

The QMass main workspace consists of a set of toolbars, a study matrix and three views. Which icons are active in the toolbars, depends on the type of study that is being analyzed and on its orientation.

The scan line views present the slice position of the selected series. In the first two views, you can switch to another series by right-clicking and selecting the new series. You can also pan, and you can zoom in or zoom out by using the sliders.



In this quick tour, you will get to know QMass's key features and basic workflow. You will open a study, review it, perform an LV function analysis, view analysis results.

8.3 Performing LV Function Analysis

Now that we have reviewed the series, we are going to perform an LV function analysis using the Ventricular Analysis wizard. There are a number of wizards in QMass, which provide a guided workflow to help you perform an analysis quickly and easily. The Ventricular Analysis wizard consists of four steps:

- selecting the long-axis series and the short-axis series, and placing valve and apex markers in the ED phase of the long-axis series
- placing markers in the ES phase of the long-axis series, and selecting the type of contours to be detected
- reviewing the detected contours
- reviewing the results

The Ventricular Analysis wizard is only available when the study contains both long-axis and short-axis cine images. If you have no long-axis images, you can still perform an analysis using the standard automatic detection feature. Refer to the QMass User Manual for instructions.

Automatically and manually created contours can lead to incorrect results. Make sure to review them and correct if necessary.

To perform an LV function analysis using the Ventricular Analysis wizard

1. In the Study Matrix, select the tabs of the various series and check for each series if the correct study type is set.

   If needed, you can correct the labeling of a series by right-clicking its tab and selecting the correct label from the menu.

2. Select **Analysis > Ventricular Analysis Wizard**.

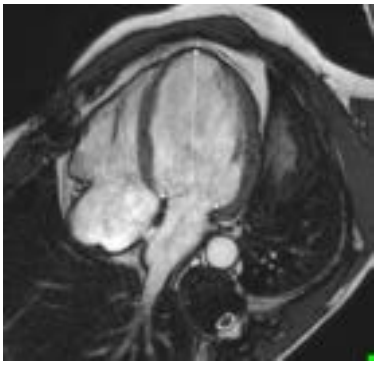
3. Under **Series Selection**, from the **LAX series** drop-down list, select the long-axis series you want to use as a reference to specify the locations of the mitral valve and the apex.

   If you have loaded a long-axis radial scan, you can select the long-axis slice you want to use in the **LAX Slice** field.

   From the **SAX series** drop-down list, select the short-axis cine series you want to analyze.

   Under **ED Phase**, check if the phase presented as the LV ED phase is correct.

   In the Active View, pick up the long-axis markers and drag them to the correct positions. Place the A marker over the apex, and place the B markers over the mitral valves.

   Click **Next**.

4. Under **ES Phase**, check the phase. In the Active View, place the A and B markers as described in the previous step.

Under **Contour Selection**, select the type of contours that you want to be detected in the short-axis images.

If you want to calculate the peak ejection rate and the peak filling rate, leave **All** selected in the **LV Endo** box.

Click **Next**.

5. When the automatic contour detection has finished, review the detected contours. Review both the ED phase and the ES phase by selecting the corresponding **View** icon.

   To ensure that analysis results are accurate, all automatically detected contours must be reviewed and edited where necessary.

   For an overview of all detected contours, you can switch to the Study Matrix tab.

   To edit a contour, click  ,  or  and then start editing.

   For detailed instructions on editing, refer to the QMass User Manual.

   To switch between viewing the ED and the ES phase in the Thumbnail View, click the corresponding **View** button in the wizard.

   To change the ED or ES phase and automatically redetect contours, select the new phase number under **Redetect Contours** in step 3 of the wizard, and click **Apply**.

   To exclude or include individual images, click the green or red square in the bottom right corner in the Thumbnail View. This automatically removes or detects contours.

   Click **Next**.

6. To obtain regional analysis results, make sure that  is selected, and then click in the Active View to mark the posterior or anterior septum in the current slice. Repeat this for the other slices you are analyzing.

   If you place the reference point at the anterior septum, make sure to first change the bull's-eye settings, so that the cardiac segments are labeled correctly. Select Menu  > **Settings > Bull's-Eye**… On the **Display** tab, under **Reference Point Location**, select **Anterior** and click **OK**.

7. Click  to view analysis results. Click  to view regional analysis results.

   To save the contours you created, select Menu  > **File > Save** from the menu bar.

8. Click **Done** to close the wizard.

8.4 Performing QStrain Analysis

Now that we have functional analysis results we can start a QStrain analysis.

- Click  to start the QStrain analysis.

All data and all contours are given as input to the QStrain analysis.

Contours are not strictly necessary to start a QStrain analysis.

8.5 Performing extended LV Function Analysis

The MassK (blood muscle segmentation) checkbox in the Functional Analysis offers an alternative method to determine blood and muscle volumes for functional analysis, in addition to papillary muscle volume.

Using a threshold slider one can determine a threshold that distinguishes blood from muscle in both the Right Ventricular as well as the Left Ventricular chambers. The threshold can be copied to other slices or phases.

To perform a functional analysis using MassK mode

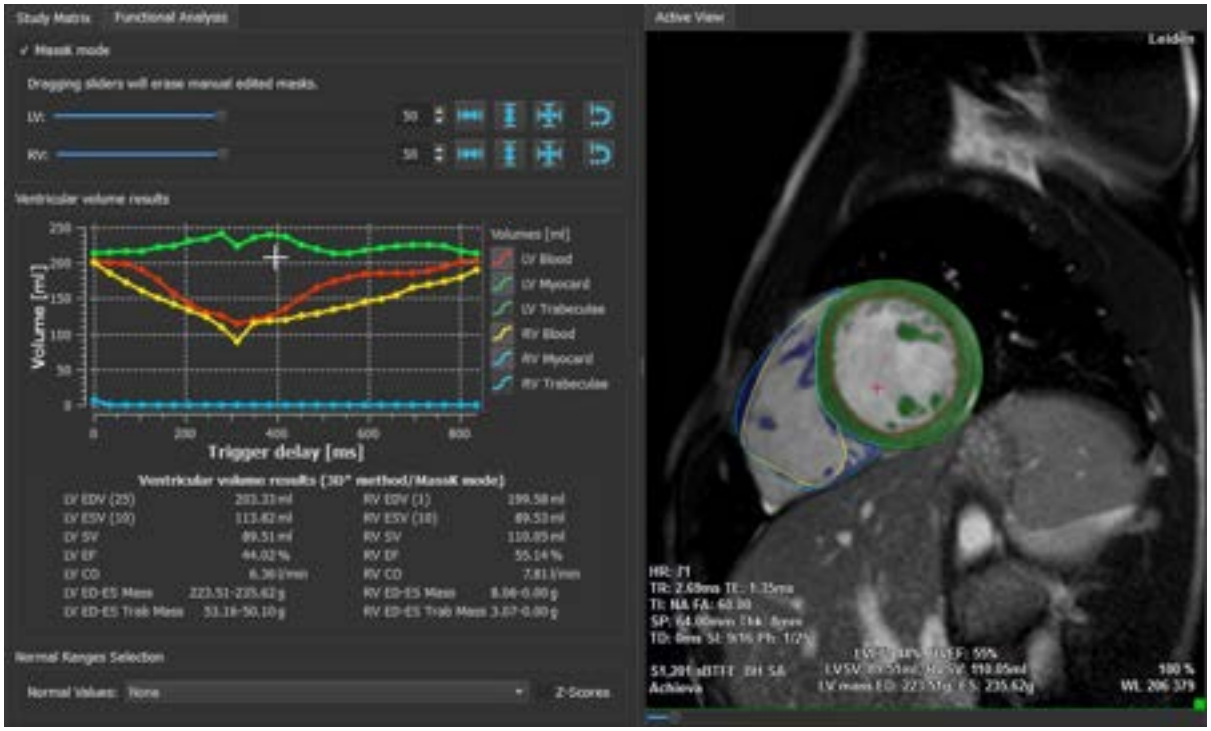
1. Select the tab **Functional Analysis** and select the checkbox **MassK**.
2. Draw the Epicardial contours in all slices and phases.
3. Draw the Endocardial contours if one needs to distinguish between Papillary volume and Myocardial volume.
4. Drag the LV or RV thresholds slider to modify the blood muscle classification.
5. Click the toolbar button, **"Edit LV Papillary"** tissue to manually add or remove muscle tissue.
6. View the results in the Volume graph in the **Functional Analysis Tab**

   Or,

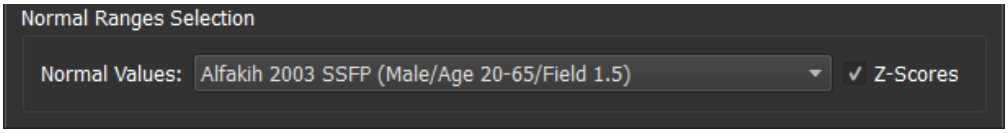
   The Results Pane or the Report pane of Medis Suite.

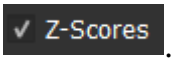
The MassK mode is dependent on the EPI cardial contours. Always review all EPI-cardial contours to be available and correct.

In case all derived results (Ejection Fraction, Stroke volume, Cardiac output) are zero, check whether all EPI contours are available.



You can add a normal range and Z-score to the Results or Report. QMass automatically selects a set of normal ranges based on the patient gender, age and the magnetic field strength of the scanner or you may choose a different set of normal values in the Functional Analysis Pane:



To add Z-scores to text report, click the check box 

.

The default normal values are based on the following articles: [1,2,3,4,5,6].

8.6 T2w Analysis

The T2-weighted (T2w) analysis helps you determine the amount of volume of high T2w signal intensity in the myocardium which has been applied extensively in imaging edema in various myocardial diseases.

This chapter explains how to perform an analysis using the T2w analysis.

Performing a T2w Analysis

QMass features a T2w analysis. It is a simple one page analysis tool. One should:

- Create LV endocardial and epicardial contours
- Detect and verify the areas of high and low signal intensity within the myocardium.

- Verify the T2w threshold and segmentation

To perform an T2w analysis

1. Load a T2w dataset into QMass.
   See also, **"Transferring contours from short axis cine series."**
2. Select the series you want to analyze.
3. Start the **T2w Analysis Wizard** by pressing next to  and select  **T2w Analysis Wizard**.
4. In the wizard, click  and draw LV endocardial contours in each slice of the series in the Active View. Similarly, click  to draw LV epicardial contours in each slice of the series.

   See also, **"Transferring contours from short axis cine series".**
5. Click Detect  and check if the ROI1 contour is detected in low signal intensity part of the myocardium and if ROI2 is detected in high signal intensity part of the myocardium. If necessary, you can edit the contours or re-detect them using the Detect button.
6. Check the T2w threshold by reviewing the segmentation of high intensities in all slices. You can override the calculated threshold by dragging the slider under **Intensity Threshold**.

   You can copy a manually set threshold value to other slices using **Copy to all slice numbers**  , **Copy to lower slice numbers**  or **Copy to higher slice numbers**  .

   You can calculate another threshold value based on the low intensity contour area by specifying the **Standard Deviation** calculation method and to supply a standard deviation.

   Click  to draw areas with high intensity tissue. To start erasing pixels, click  .

   You can hide the masks by deselecting **Menu**  > **Settings > Main Settings > Display > masks**.

   View the results in the T2w Pane, or the Results Pane or the Report pane of Medis Suite.

To perform a T2 ratio measurement

1. Use the ROI icon  to determine an area within the myocardial region by drawing the corresponding contour.
2. Use the ROI icon  to determine the skeletal muscle by drawing the corresponding contour.
3. From the two ROIs the mean, minimum, and maximum signal intensities are calculated and used to calculate the T2 ratio between the two defined regions.

The T2 ratio value can be seen on the report pane.

Transferring contours from short axis cine series

If contours are already available in the short axis cine series, you can load the series and transfer the contours from this series to the T2w series by clicking  . Contour transfer works best if you manually create contours in the phase of the short axis cine series in which the T2w series was scanned.

8.7 DSI Analysis

A Delayed Signal Intensity (DSI) analysis can help you to determine the infarct size as well as the extent of infarct transmurality which appears to delineate viable and nonviable myocardium and the recovery of function after revascularization.

For further reading, see the following article: *Gibbons, Raymond J., et al. "The quantification of infarct size." Journal of the American College of Cardiology 44.8 (2004): 1533-1542.*

The wizard consists of four steps:

- creating LV endocardial and epicardial contours
- verifying the areas of healthy and hyper-intense myocardium
- verifying the DSI threshold and segmentation
- placing a reference point, setting the transmurality threshold.

To perform a DSI analysis

1. Load a DSI dataset into QMass.

   See also, **“Automatic contour detection in DSI series.”**

2. Select the DSI series you want to analyze.

3. Start the **DSI Analysis Wizard** by pressing next to  and select  **DSI Analysis Wizard**.

4. In the wizard, click  and draw LV endocardial contours in each slice of the series in the Active View. Similarly, click  to draw LV epicardial contours in each slice of the series.

    See also, **"Automatic contour detection in DSI series".**

5. Click **Detect**  and check if the ROI1 contour is detected in healthy myocardium and if ROI2 is detected in hyper-intense myocardium. If necessary, you can edit the contours or re-detect them using the **Detect** button. The DSI hyper-enhanced threshold is also calculated when the **Detect** button is pressed.

    The calculated threshold value is copied automatically to all other slices if the option **Auto copy** is selected. If you use the **Apply** button without **Auto copy** selected, then the ROI contours and threshold value are determined for the current slice only. You can repeat this for each slice separately.

6. Check the DSI threshold by reviewing the infarct size segmentation in all slices. You can override the calculated threshold by dragging the slider under **Intensity Threshold**.

   Click  and  to draw areas with hypo-enhancements.

To start erasing pixels, click  .

 You can copy a manually set threshold value to other slices using **Copy to all slice numbers**  , **Copy to lower slice numbers**  or **Copy to higher slice numbers**  .

 You can calculate another threshold value based on the healthy contour area by specifying a calculation method.

 You can increase the tip size of the brush or the eraser by increasing the **Draw size**.

 Select **Smart brush** or click  in the toolbar if you want to edit the current mask without overwriting or erasing other masks.

 You can hide the masks by deselecting **Display masks**.

7. Set a reference point. You can place a reference point by clicking  and setting a reference point in the Active view at the inferior or anterior end of the interventricular septum.

Make sure a reference point is placed in every slice you are analyzing.

If you place the reference point at the anterior septum, make sure to change the bull's-eye settings, so that the cardiac segments are labeled correctly. Select Menu > **Settings > Bull's-Eye…** On the **Display** tab, under **Reference Point Location**, select **Anterior**.

If you want to change the default transmurality threshold of 50 %, you can modify the threshold under **Transmurality Threshold**.

You can click to open a bull's-eye window. You can also select the diagram of your choice from the **Show** drop-down list. Right-click in the window to access options for saving the diagram and for adding it to Results.

View the results in the DSI Pane, or the Results Pane or the Report pane of Medis Suite.

Automatic contour detection in DSI series

The contours can be detected automatically in DSI series by clicking .

Automatically and manually created contours can lead to incorrect results. Make sure to review them and correct if necessary.

8.8 Combined T2w-DSI Analysis

The Combined T2w-DSI analysis helps you determine the index and difference between T2w analysis results and DSI result.

This chapter explains how to perform a T2w-DSI analysis.

Performing a T2w-DSI Analysis

QMass features a T2w-DSI analysis. It is a simple analysis tool. One should:

- Load and create LV endocardial and epicardial contours in both T2w and DSI series.
- Do a T2w and DSI analysis on the respective datasets.

To perform a T2w-DSI analysis

1. Load a DSI and T2w dataset into QMass.
2. Start the **T2w-DSI Analysis Wizard** by pressing next to and select **Combined T2w-DSI**.
3. Complete a DSI analysis on the DSI dataset.
4. Complete a T2w analysis on the T2w dataset.

View the results in the DSI/T2w and Combined T2w-DSI Pane, or the Results Pane or the Report pane of Medis Suite.

In the Combined T2w-DSI analysis, the high T2w volume is always assumed to be larger or equal to the volume of the infarct volume. If the infarct is greater in volume than the high T2w volume then the volume and calculations will be rounded to zero as opposed to showing the negative values.

8.9 TSI Analysis

In QMass, you can perform a first-pass perfusion analysis, which is called a Time Signal Intensity (TSI) analysis. To do this, you must take the following steps:

- draw endocardial and epicardial contours
- place reference points
- register the contours

To draw endocardial and epicardial contours

1. Load a TSI dataset into QMass.
2. Select the TSI series you want to analyze and click **OK**.
3. If the Time Signal Intensity toolbar with the  icon does not appear, select the Study Matrix tab, and check if the series is labeled correctly. You can do this by right-clicking the series tab.
4. In the Thumbnail View, select an image that shows sufficient contrast in both the left and the right ventricle.
5. By default, the drawing mode is set to tracing. To draw in point mode, click  .
6. In the Active View, draw the endocardial contour, then click  and draw the epicardial contour.

   Make sure to exclude the LV and RV blood pool by drawing correct endocardial contours, to avoid that its high intensity signal affects the results.
7. If you want to analyze signal intensity over time in a region of interest, click  . In the Active View, draw a contour around the region of interest (ROI).

   If you want to compare one or more ROIs with each other, click one of the other ROI icons  ,  , or  and draw the corresponding contour or contours in the Active View.

To place reference points

1. Click  .

2. In the Active View, place a reference point at the inferior or anterior junction of the right ventricle and the left ventricle.

   If you place the reference point at the anterior septum, make sure to first change the bull's-eye settings, so that the cardiac segments are labeled correctly. Select Menu > **Settings > Bull's-Eye**... On the **Display** tab, under **Reference Point Location**, select **Anterior** and click **OK**.

To register contours

1. If you have drawn one or more ROIs, select the corresponding menu item or items from the Registration submenu. Click the arrow next to and then select **Register ROI1 Contours** and the other menu items that apply.

2. Click .

   This copies the selected contours to the other images in the slice and performs breathing motion correction.

   Contour registration is performed based on the contour registration settings. To access and modify these settings, select **Menu** , **Settings > Registration Settings**

3. Check the contours in the Thumbnail View or in the Movie Tool to see if the automatic positioning of the contours needs correcting.

   To move a set of contours to another position, press SHIFT+CTRL and drag them to their new position.

   Do **not** edit the contours using the drawing tools. If you want to add new ROIs after performing registration, make sure to create the ROI contours in the same image in which you created the initial contours.

To view TSI analysis results

1. Click to display the analysis results in a graph.

2. From the **Show** drop-down list, select the **Myo Intensity - Time** or **ROI Intensity - Time** graph.

Or,

1. Click to display the analysis results in a bull's-eye diagram.

2. From the **Show** drop-down list, select **SI Analysis**.

   This adds a drop-down list to the dialog window.

3. Select the type of diagram that you want to view.

   For a detailed description of the bull's-eye diagrams, refer to the User Manual.

Click the Right mouse button to select ‘toad snapshot to Results’ to add the snapshot of the graph to the Reporting.

View the results in Results Pane or the Report pane of Medis Suite.

8.10T1 Analysis

If you have the T1 analysis module, you can use QMass to analyze the T1 relaxation time of a region of interest.

This chapter explains how to:

- Perform a T1 analysis

A T1 analysis determines the rate of magnetization recovery of a region of interest.

To perform a T1 analysis

- Load a T1 dataset into QMass.
- Select the T1 series you want to analyze.

  In the Study Matrix, right-click the series tab and check if the series is labeled correctly as a T1 series. If needed, you can change the series label in the submenu.
- Select the T1 Analysis tab.
- In the Thumbnail View, select an image that shows sufficient contrast.
- Select your preferred drawing tool and draw the endocardial contour.

  Make sure to exclude the LV blood pool, to avoid its high intensity signal affecting the results.
- Click and draw the epicardial contour.

  Make sure to exclude the RV blood pool, to avoid its high intensity signal affecting the results.
- Mark one or more regions of interest in the septum. Select the region of interest icon, for example, , and draw a region of interest in the myocardium.

You can deselect **Auto copy** under **Contours** to prevent copying the contours of the regions of interest to the other images.

- The T1 Analysis tab now shows two curves per region of interest: the curve of the measured values in the color of the region of interest, and the fitted curve as a dotted line.

- The "Time [ms]" box now shows the T1 recovery time.

You can click on the icons in the "Time [ms]" box to show or hide the various regions of interest.

You can select and display the T1, T1*,, or the Residual overlay by selecting an **Overlay** from the drop-down selection box.

You can select the Acquisition type, Look-Locker (LL) which displays the T1*, T1 or the t0 results or Progressive Saturation (PS), which displays the T1 and the t0 results.

Result	Description
T1 **(Progressive saturation)**	T1 for progressive saturation studies corresponds to the following equation: I = A – B • EXP (-t/T1)
T1* (Look-Locker)	T1* for Look-Locker studies corresponds to the following equation: I = A – B • EXP (-t / T1*)
T1 (Look-Locker)	T1 value for Look-Locker studies corresponds to the following equation: T1 = T1 • (B / A – 1)
t0	t0 is the "Nulling time", i.e. the time at which the signal intensity crosses the zero on the horizontal axis. One can also roughly estimate the t0 value from the graph.

You can also view the recovery rate per pixel using mouse cursor tracking. Click  , and then hover the mouse over the pixel in the image. This displays the currently tracked pixel's recovery rate.

Please refer to the following article for information about T1 mapping in Look-Locker studies: Daniel R. Messroghli et al, Modified Look-Locker Inversion Recovery (MOLLI) for

High-Resolution T_1 mapping of the Heart, Magnetic Resonance in Medicine 52: 141-146 (2004).

View the results in the T1 Pane, or the Results Pane or the Report pane of Medis Suite.

To set a color range and color map setting

1. Select Menu > **Settings > T1 Settings**.

   This opens the T1 Settings dialog window.

Under **Color range**, choose your preferred color range of colors. Under **Color Map**, choose your preferred overlay color map.

You can specify a default color map in the Configuration File Editor.

To export the relaxation times per slice to DICOM

Click the “Add parametric map to Results” button.

The maps will automatically appear in the current QMass session and can be selected on the Study Matrix tab for further analysis.

For instructions on series selection, see: Starting QMass.

8.11T2/T2* Analysis

With the T2/T2* analysis it is possible to determine T2/T2* relaxation times. Quantification of T2* relaxation time helps characterizing iron loading in heart and liver.

This chapter explains how to:

- perform a T2 or T2* decay time analysis

A T2 or T2* decay time analysis consists of two steps: first you must draw a contour around the region of interest in the myocardium, and then you must exclude the measurements from the curve that are biased by MR noise.

To perform a T2 or T2* analysis

1. Load a T2/T2* dataset into QMass.
2. Select the T2/T2* series you want to analyze.
3.

In the Study Matrix, right-click the series tab and check if the series is labeled correctly as a T2/T2* series. If needed, you can change the series label in the submenu.

4. Select the T2/T2* Analysis tab.

5. In the Thumbnail View, select an image that shows sufficient contrast.

6. Select your preferred drawing tool and draw the endocardial contour.

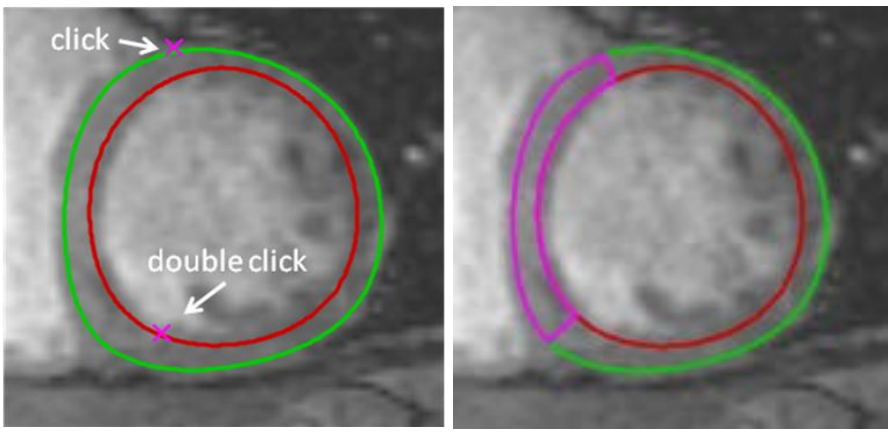
   Make sure to exclude the LV blood pool, to avoid its high intensity signal affecting the results.

7. Click and draw the epicardial contour.

   Make sure to exclude the RV blood pool, to avoid its high intensity signal affecting the results.

8. Mark one or more regions of interest in the septum. Select the region of interest icon, for example, , and select . Click the epicardial contour to mark the beginning of the septal segment, and then double-click the endocardial contour to mark the end.

   This creates the region of interest. The following illustrations show an example.



   You can deselect **Auto copy** under **Contours** to prevent copying the contours of the regions of interest to the other images.

9. The T2/T2* Analysis tab now shows two curves: the curve of the measured values in the color of the region of interest, and the fitted curve in a light and semitransparent version of that color.

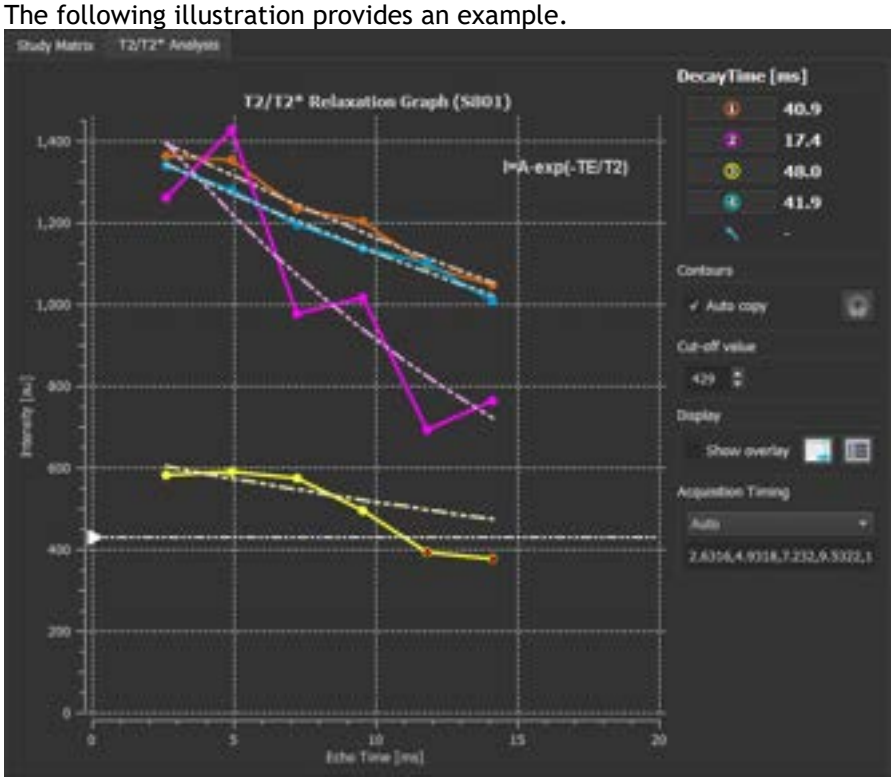
   To remove the measurement points that are biased by MR noise and calculate the correct T2/T2* value of the region of interest, you must drag the cut-off slider to the point where the curve starts to level off.

   If the curve slopes upward instead of downward at the end, make sure to first exclude the corresponding images. You do this by clicking the green squares in the bottom right corner of the images in the Thumbnail View.

   Pick up the white triangle at the bottom of the diagram and drag it up.

This marks the points under the slider as excluded and makes the fit curve the non-excluded part of the measured curve. Make sure that the fit curve runs through the first measured points.

The following illustration provides an example.



10. Define the Acquisition Timing. Choose “Auto” to use the timing derived directly from the scanner, or use the configurable Acquisition Timings, such as “T2Prep_4”, if the values are not available from the scanner.

    Using the Configuration File Editor, in the Acquisition Timing section, you can specify the timing values. T2Prep_4 is an example of a timing configuration.

    Using Acquisition Times that have been configured may lead to incorrect results. Make sure to review them and correct if necessary.

11. The Decay Time box now shows the T2 or T2* decay time.

    Use the icons in the Decay Time box to show or hide the various regions of interest.

    You can display a color overlay of the decay time by selecting **Show overlay** under **Display**.

Result	Description
T2 or T2*	The result corresponds to the following equation: I = A • EXP (-TE / T2) where TE is the Echo Time in ms and whereT2 indicates T2 for T2 analysis or T2* for T2* analysis

You can also view the decay rate per pixel using mouse cursor tracking. Click  , and then hover the mouse over the region of interest. This displays the currently tracked pixel's decay rate in the status bar at the bottom of the QMass window.

View the results in the T2/T2* Pane, or the Results Pane or the Report pane of Medis Suite.

To set a default for the cut-off value and for the overlay colors

1. Select Menu > **Settings > T2/T2* Settings**.

   This opens the T2/T2* Settings dialog window.

Under **Color Map**, choose your preferred color scheme.

After **Cut-off value**, specify the default to be used during the current session.

You can specify a persistent default cut-off value in the Configuration File Editor.

To set the Acquisition Timing

1. Select the Acquisition Timing.

Under **Color Map**, choose your preferred color scheme.

After **Cut-off value**, specify the default to be used during the current session.

Using the Configuration File Editor, in the Acquisition Timing section, you can specify the timing values. T2Prep_4 is an example of a timing configuration.

Using Acquisition Times that have been configured may lead to incorrect results. Make sure to review them and correct if necessary.

To export the decay times per slice to DICOM

Click  the "Add parametric map to Results" button.

The maps will automatically appear in the current QMass session and can be selected on the Study Matrix tab for further analysis.

For instructions on series selection, see: Starting QMass.

8.12 Finishing a QMass analysis

When you have finished analyzing, press the save session button on the Medis Suite.

 For a detailed description on stopping a Medis Suite session, refer to the Medis Suite Quick Start/User Manual.

8.13 Accuracy of Measurements

In QMass all measurements are derived from calculations performed on the loaded DICOM images.

Both during development and with each new release of the product, measurements and calculations are extensively validated. The accuracy of the measurements and calculations exceeds that of the displayed results, by at least one decimal point.

In practice, the image is the limiting factor of the accuracy of measurements. Limiting factors, such as, image resolution both spatial and time-based, image noise, inhomogeneity in the magnetic field and patient determines the accuracy of any given measurement.

The effective accuracy of measurements has been evaluated with multiple validation studies. The following table gives the expected accuracy for the different types of measurement.

QMass Results	Common value	Unit	Expected accuracy	Precision	Accuracy justification and source is applicable
Left and right ventricular volume results					
Body Surface Area	2	m^2	5%	0.01	Accuracy entirely dependent on the manual user input
ED phase number	2			1	Is accurate, as long as the contours are drawn correctly
ES phase number	9			1	Is accurate, as long as the contours are drawn correctly
ED phase time	39.75	ms	25 ms	0.01	Depends on the acquisition sample frequency, given for a typical 20 frames/ heartbeat, 60 bpm
ES phase time	272.25	ms	25 ms	0.01	
ED volume	129.43	ml	5%-10%	0.01	[1] - Depends strongly on the acquisition number of slices. Value given for typical 10 slices
ED volume index	64.71	ml/m^2	5%-10%	0.01	- derived
ED volume/HT (HT=height)	71.9	ml/m	5%-10%	0.01	- derived
ES volume	63.63	ml	5%-10%	0.01	[1] - Depends strongly on the acquisition number of

					slices. Value given for typical 10 slices
ES volume index	31.81	ml/m²	5%-10%	0.01	- derived
Stroke volume	65.8	ml	8%-15%	0.01	Derived from ED an ES volume accuracy
Stroke volume index	32.9	ml/m²	8%-15%	0.01	- derived
Cardiac output	4.76	l/min	8%-15%	0.01	Derived from Cardiac output
Cardiac output index	2.38	l/(m²*min)	8%-15%	0.01	- derived
Ejection fraction	50.84	%	8%-15%	0.01	Derived from Cardiac output and ED volume
LV mass ED	109.45	g	25%	0.01	Derived from volume, however, cardia muscle density is not a constant [12]
LV mass ED index	54.72	g/m²	25%	0.01	- derived
LV mass ED/HT	60.81	g/m	25%	0.01	- derived
LV mass ES	117.88	g	25%	0.01	See LV mass ED
LV mass ES index	58.94	g/m²	25%	0.01	- derived
Ejection / filling dynamics					
Parameter	Value				
PER	535.46	ml/s	10%	0.01	Derived from volume, limited by acquisition frequency.
PER/EDV	4.14	EDV/s	10%	0.01	- derived
TPER	66.63	ms	25ms	0.01	Depends on the acquisition sample frequency, given for a typical 20 frames/ heartbeat, 60 bpm
TPER phase number	4			1	Is accurate, as long as the contours are drawn correctly
PFR	325.11	ml/s	10%	0.01	Derived from volume, limited by acquisition frequency.
PFR/EDV	2.51	EDV/s	10%	0.01	- derived
TPFR	232.63	ms	25ms	0.01	Depends on the acquisition sample frequency, given for a typical 20 frames/ heartbeat, 60 bpm
TPFR phase number	16			1	Is accurate, as long as the contours are drawn correctly
Time intensity					

Amplitude	780.7	AU		0.1	Since this is an arbitrary unit, there is no specific accuracy.
Max upslope	364.8	AU/s		0.1	Since this is an arbitrary unit, there is no specific accuracy.
Time max upslope	14.6	s	2	0.1	Determined by time interval between acquisitions. Based on a typical one acquisitions / 2 seconds
Mean intensity	1348.8	AU		0.1	Since this is an arbitrary unit, there is no specific accuracy.
Time to 50% max	15.7	s	2	0.1	Determined by time interval between acquisitions. Based on a typical one acquisitions / 2 seconds
T0 intensity	1,020.1	AU		0.1	Since this is an arbitrary unit, there is no specific accuracy.
Baseline intensity	930.6	AU		0.1	Since this is an arbitrary unit, there is no specific accuracy.
Relative upslope	58.7	%	2	0.1	[2]
Wall thickness / motion					
Chords wall thickness	20.00	mm	5%	0.01	[10] - error based on 2 standard deviations
Chords wall motion	10.00	mm	11%	0.01	[10] - error based on 2 standard deviations
Chords wall thickening	100.00	%	16%	0.01	[10] - error based on 2 standard deviations
Mean wall thickness	20.00	mm	0.1%	0.01	[10] - error based on 2 standard deviations
Mean wall motion	10.00	mm	0.1%	0.01	[10] - error based on 2 standard deviations
Mean wall thickening	100.00	%	0.1%	0.01	[10] - error based on 2 standard deviations
Long axis volumes / wall motion					
ED Volume	110.00	ml	8%	0.01	Typical for long axis volume approximation
ES volume	50.00	ml	8%	0.01	Typical for long axis volume approximation
ED Mass	120.00	g	25%	0.01	Derived from volume, however, cardia muscle density is not a constant. [12]

ES Mass	55.00	g	25%	0.01	Derived from volume, however, cardia muscle density is not a constant. [12]
Ejection Fraction	55.00	%	15%	0.01	Based on volume accuracy
Stroke Volume	60.00	ml	12%	0.01	Based on volume accuracy
Wall thickening	100.00	%	0.1%	0.01	Based on short axis accuracy calculations
Wall thickness	20.00	mm	0.1%	0.01	Based on short axis accuracy calculations
Wall thickness segment	20.00	mm	0.5%	0.01	Based on short axis accuracy calculations and segment size
Delayed Signal Intensity					
Infarct size volume	39.81	ml	5%	0.01	[5], combined with generic accuracy [1]
Infarct size mass	41.80	g	10%	0.01	[5], combined with generic accuracy [1], and [12]
Infarct size percentage	34.02	%	5%	0.01	[5]
High transmural extent volume	32.90	ml	5%	0.01	[5], combined with generic accuracy [1]
High transmural extent mass	34.54	g	10%	0.01	[5], combined with generic accuracy [1], and [12]
T2*					
Relaxation time	43.6	ms	5%	0.1	[9]
Relaxation rate	22.9	Hz	5%	0.1	Is the inverse of the relaxation time
Cardiac Iron Load T2 (1.5T)	0.44	mg/g	0.01%	0.01	[13]
Liver Iron Load T2 (1.5T)	0.78	mg/g	0.01%	0.01	[13]
Cardiac Iron Load T2 (3.0T)	0.38	mg/g	0.01%	0.01	[13]
Liver Iron Load T2 (3.0T)	0.63	mg/g	0.01%	0.01	[13]
T1/T1*					
T1* Decay Time	1620	ms	5%	1	[11]
T1 Decay Time	1560	ms	5%	1	[11]

References used in table above:

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10. Validation Report Wall Thickness / motion / thickening, Eelco van Akker, Dec 13, 2001
11. T1 Measurements update, Eelco Giele, Mar 5, 2015
12. Cardiac left ventricular myocardial tissue density, evaluated by computed tomography and autopsy, Alexandra G. Gheorghe et al., BMC Med Imaging. 2019; 19: 29
13. Scientific Validation Report: T2* to Iron Loading conversion, E. Giele, January 29, 2025

8.14 Trouble Shooting

Adding Results To Excel

To add results into excel you can you the CSV format. To get the results in excel do the following:

- Go to the text report
- Select the desired text and or tables
- RMB > Select **Copy CSV**.
- In Excel > **Paste Special** > Select **CSV**.

Cine Grid with holes

Sometimes the Cine image matrix may appear irregular in the number of images per slice or phase, or there are holes where images are missing. This is caused by duplicated slices in the series.

- Go to the file browser
- Check that filter duplicates is selected and press rescan
- Load the data again
- Now the image matrix should be nice and regular.

No Short Axis results

Sometimes when you have a Short Axis and a Long Axis series with the same series description the sorting and splitting of these series is wrong. One of the consequences is that no Short Axis results are shown. To avoid this, make sure the LA series and SA series have different series descriptions.

No results in the Combined T2w-DSI Report

Combined T2w-DSI results are only available when the **Combined T2w-DSI** wizard is open. Once the **Combined T2w-DSI** wizard is open all **Combined T2w-DSI** results are available in the Results and the Report.

8.15 Function Keys

When you are working with QMass, you can use the function keys on your keyboard to quickly perform the following tasks.

Press	To
F1	open the online help.
F5	start the Movie Tool and display the currently selected slice or phase as a movie.
F6	display the study properties.
F7	show the graph window.
F8	open a window in which you can create bull's-eye plots that show various types of analysis results. The segment scheme applied in these bull's-eyes is the AHA 16 segment model.
CTRL+F8	open a window in which you can create bull's-eye plots that show various types of analysis results. The segment scheme applied in these bull's-eyes is Segmented per Slice.
CTRL+SHIFT+F8	open a window in which you can create bull's-eye plots that show various types of analysis results. The segment scheme applied in these bull's-eyes is Segmented per Chord.
F9	open the report window.
F10	Open the Wall Motion visual scoring window.
CTRL+F10	Open the Time Signal Intensity visual scoring window.
CTRL+SHIFT+F10	Open the Delayed Signal Intensity visual scoring window.

8.16 Shortcut Keys

Shortcut keys are combinations of keys that you can press on your keyboard to give a command.

The following shortcut keys are applicable to all views.

Shortcut	Use to
Studies and Contour Files	
CTRL+O	open a study browser.
CTRL+F5	refresh the directory tree of the browser.
Images	
+	zoom in.
-	zoom out.
Elements	
CTRL+D	detect contours automatically.
CTRL+Z	undo the actions you performed.
CTRL+Y	redo the actions you undid.
CTRL+C	copy all elements from the active image to the clipboard.
CTRL+V	paste the active element to the selected image.
CTRL+SHIFT+V	paste all elements to the selected image.
DEL	delete the currently selected element.
CTRL+T	transfers the contours from the short-axis cine series to the DSI series.
CTRL+R	registers the created contours to the other images in the series.
F5	Open the movie dialog
F6	Open the Study parameter dialog

F7	Open the Graph dialog
F8	Open the bull’s eye dialog – 16 segment model
Ctrl + F8	Open the bull’s eye dialog – segmented per slice
Ctrl + Shift + F8	Open the bull’s eye dialog – no segments.
X	Toggle inclusion or exclusion of selected images for automatic contour detection.

The following shortcut keys are applicable to the active view.

Shortcut	Use to
drag using the middle mouse button	pan the image.
press W, then drag	adjust the window width and level of the images. By default, a horizontal movement adjusts the window width, and a vertical movement adjusts the window level. Press the W key on the keyboard or make sure that  is selected to make the window width and level mode active.
1	reset window width and level to the original values.
2	optimize window width and level.
click+hold down the middle mouse button or mouse wheel	hides the contours and all patient and study properties shown in the Active View. Release the middle mouse button to show the contours again.
CTRL+drag	move the active contour relative to the image in the Active View and Thumbnail View.
CTRL+SHIFT+drag	move all elements relative to the image in the Active View and Thumbnail View.
CTRL+SHIFT+ALT +drag	move all elements in the entire slice stack relative to the images in the Active View and Thumbnail View.
SHIFT + S	reshapes a contour by removing small irregularities.
SHIFT + D	reshapes a contour by removing curves.
SHIFT + C	reshapes a contour by removing all curves that point inward.
SHIFT + E	reshapes a contour by redetecting the edge, using the existing contour as a model.
S	add the image in the Active View to the report.

CTRL+A	Accept LV endo and LV epi contours.
space	toggle active element
CTRL+space	toggle active edit mode
PgUp	Switch to next series
PgDn	Switch to previous series
CTRL+PgUp	Switch to next level
CTRL+PgDn	Switch to previous level
up	Switch to NEXT phase slice
down	Switch to previous slice
left	Switch to previous phase
right	Switch to next phase
CTRL+left	translate current contour to the left
CTRL+right	translate current contour to the right
CTRL+up	translate current contour upwards
CTRL+down	translate current contour downwards
CTRL+SHIFT+left	translate all contours to the left
CTRL+SHIFT+right	translate all contours to the right
CTRL+SHIFT+up	translate all contours upwards
CTRL+SHIFT+down	translate all contours downwards

[or]	Increases and decreases the brush size, when using DSI, T2w or Functional MassK mode analysis.

The following shortcut keys are applicable to the movie window.

Shortcut	Use to
PgUp	Scroll to the next series in the Movie window.
PgDn	Scroll to the previous series in the Movie window.
P	play the movie
S	stop the movie
up	show the next slice
down	show the previous slice
right	show the next phase
left	show the previous phase
F2	toggle between slice and phase looping

8.17References

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9 QStrain

9.1 Overview

The QStrain generic workflows and the workspace are described in this section.

9.1.1 Workflows

A QStrain analysis can be started either from QMass, or as a standalone application.

The following table describes the steps in the workflow of a QStrain analysis started directly from QMass, or QStrain as a standalone application.

For further details refer to the section, Workflow performing a QStrain analysis

Table 1: QMass + QStrain workflow / QStrain standalone workflow

QMass + QStrain	QStrain standalone
Load Series	
Automatic Contour Detection Review Contours	
Start QStrain Analysis: Automatic load series data & contours	Start QStrain Analysis
QStrain Select Series Select Analysis Type Complete strain analysis	**QStrain** Select Series Select Analysis Type **Manually** draw contours Review Contours Verify ED & ES phase Complete strain analysis

The preferred workflow is to start QStrain from QMass, utilizing the automatically detected contours.

9.1.2 The QStrain Workspace

QStrain is launched from the Medis Suite app toolbar, or the app context menu, or from the app pane by selecting the QStrain app icon  . Detailed information on how to start an application and how to load series into the application, is described in the Medis Suite user manual. QStrain can also be started from QMass.

This chapter covers the following topics:

- Workflows
- Overview
- Toolbars
- Windows layouts
- Mouse controls
- Frame selection

Overview

QStrain application consists of six primary windows each representing a step in the analysis workflow. A vertical toolbar to the right-hand side of the application, shows the buttons required to complete each step in the analysis process.

The following list describes the basic steps to complete a generic QStrain analysis.

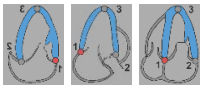
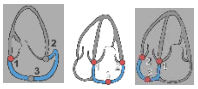
- Series Loading & Analysis selection
- Contour Editing
- ED-ES contour review
- ED-ES phase review (Sequence/M-Mode selection).
- Global Strain Analysis
- Time to Peak detailed regional analysis

Toolbars

A vertical toolbar on the right-hand side of the application allows one to navigate through the different steps of an analysis. In each step of the analysis process, different icons are shown in the toolbar.

The list below describes the purpose of each icon.

Icon	Function
Series & Analysis Selection Toolbar	
	Forward button

Icon	Function
	Back button
	Remove series
Contour Editing Toolbar	
	Phase indicator ES
	Phase indicator ED
	Guide contours LV SAX
	Guide contour LV LAX (2CH, 3CH, 4CH)
	Guide contours Left Atrium | Right Atrium
	Guide Contours RV
Analysis Toolbar	
	About Box.
	Go back to Series & Analysis selection Window
	Send Movie, Snapshot to Medis Suite
	Window Width, Window Level
	Decrease, Increase or go back to initial arrow size
	Go to ES or ED phase
	Mirror the image

Icon	Function
	Switch parametric over B-mode
	Change the visualization method for the contour tracing
	Apply the reference point
	Switch from 2D to 3Dview
	Go to sequence / M-mode selection
	Enable/Disable M / M-mode overlay in the volume graphs.
	Make a new tracing contours from scratch. Modifying the contour for the ED or ES phase.
	Segmental and detailed strain results!
Time to Peak toolbar	
	View results based on Endo contours
	View results based on Endo and Epi contours
	View results based on Epi contours

You cannot move toolbars to another part of the main application window.

You cannot hide toolbars.

The following list describes the icons that are not in the vertical toolbar.

Icon	Function
Viewport Tools	
	Play or stop cine movie
	Go to next or previous phase
	View viewport in Full screen
	View viewport in Normal screen

Windows Layout

QStrain application analysis consists of a sequence of steps to complete an analysis. The following list describes each window or dialog in correspondence with the sequential steps of a QStrain analysis.

- Series & Analysis Selection Window
- Contour Creation Window
- LV SAX Reference Point Placement Dialog
- Sequence / M-Mode Selection Window
- Analysis Window
- Time to Peak Segmental Analysis Window

Series & Analysis Selection Window

The initial series & analysis selection window workspace consists of four sections. The series list overview, CINE viewport, Analysis selection pane and a wizard step vertical toolbar.

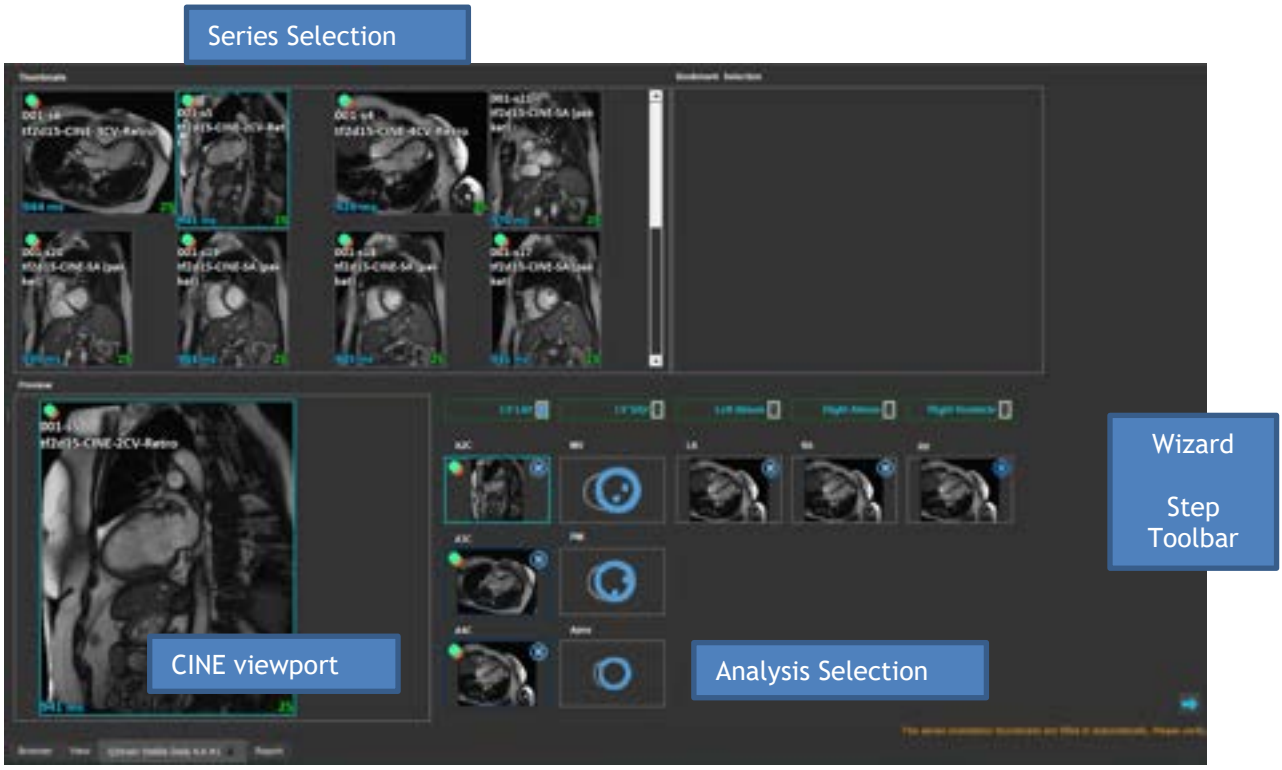


Figure 9-1: Series & Analysis Selection Step

Contour Creation Window

After selecting a series, contours need to be drawn in the selected series before progressing to the analysis. This window consists of two sections, the Viewport and the Toolbars.

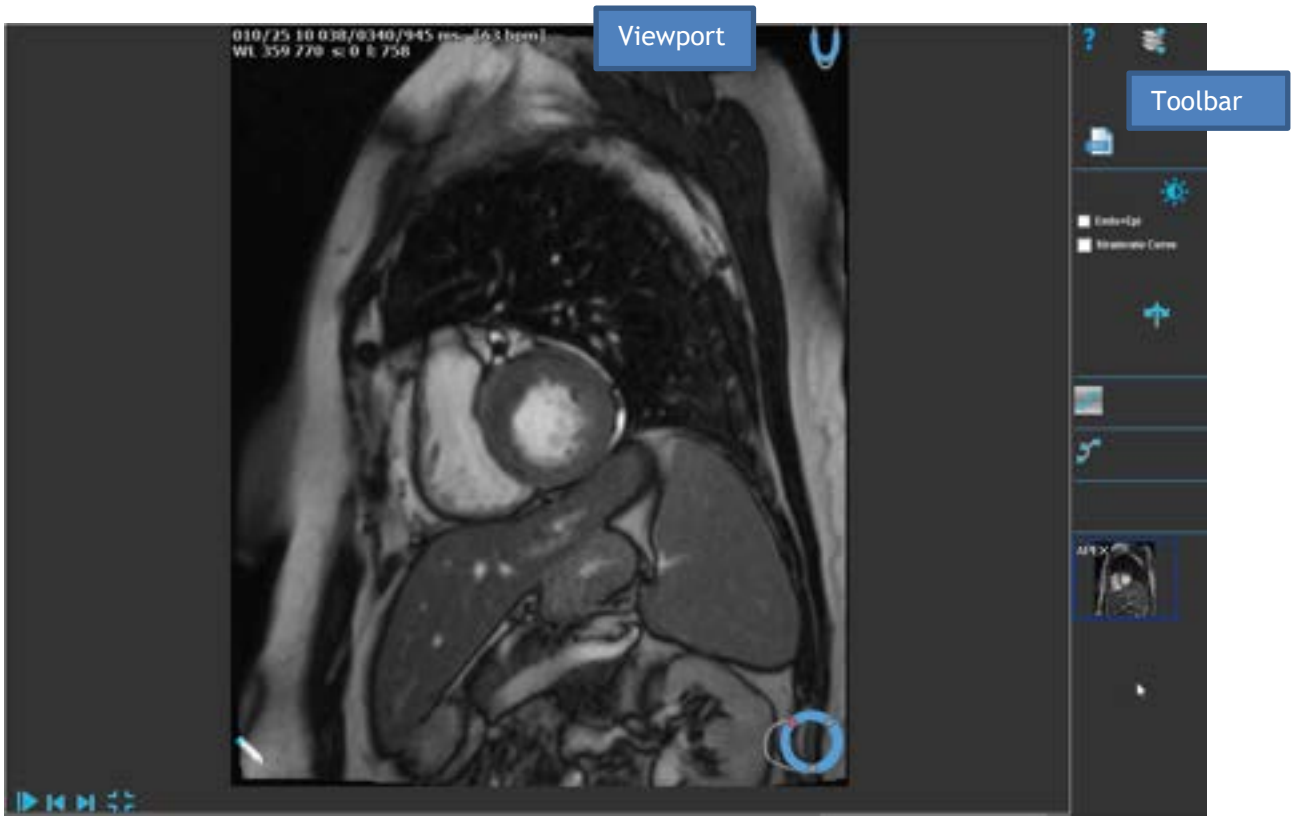


Figure 9-2: Contour Editing Step

ES Contour Review & Modification Window

Once the contours have been created or imported, the ED and ES phases are set.

The ES contours modification window facilitates editing the ES contour edit points. For further details refer to the section, ED ES Management.

The window consists of:

- Viewport
- Cine movie control
- Myocardium expansion and reduction tool.
- Toolbar

There are minor differences between the ED and the ES review and modifications windows.

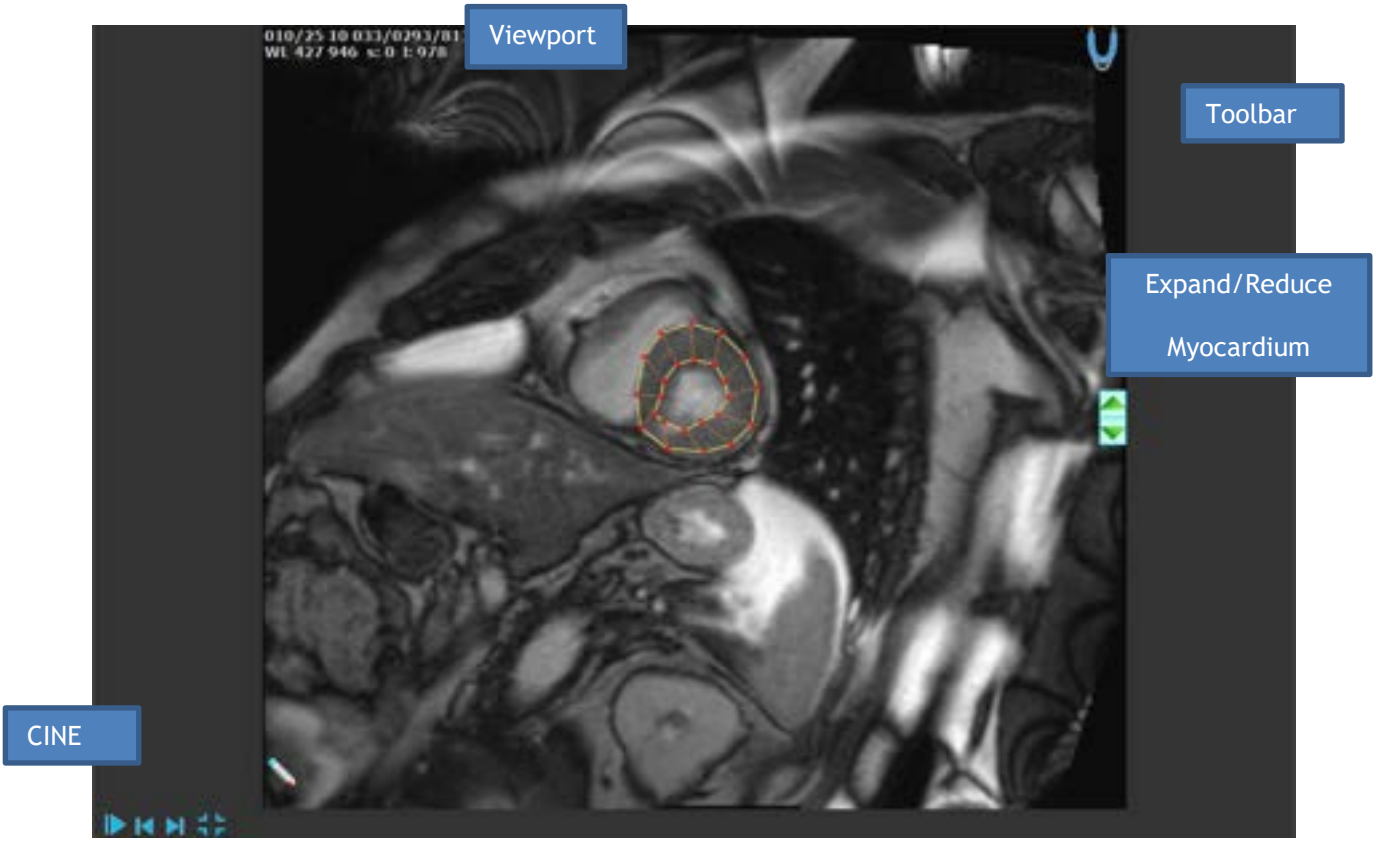


Figure 9-3: ES Review & Modification Window

ED Contour Review & Modification Window

Once the contours have been created or imported, the ED and ES phases are set.

The ED contours modification window facilitates editing the ED contour edit points. The ED & ES review and modification window displays the ED and ES phase position in a volume graph. For further details refer to the section, ED ES Management. The window consists of:

- Viewport
- Volume graphs indication the ED and ES phase position
- Cine control: To scroll through the images.
- Toolbar

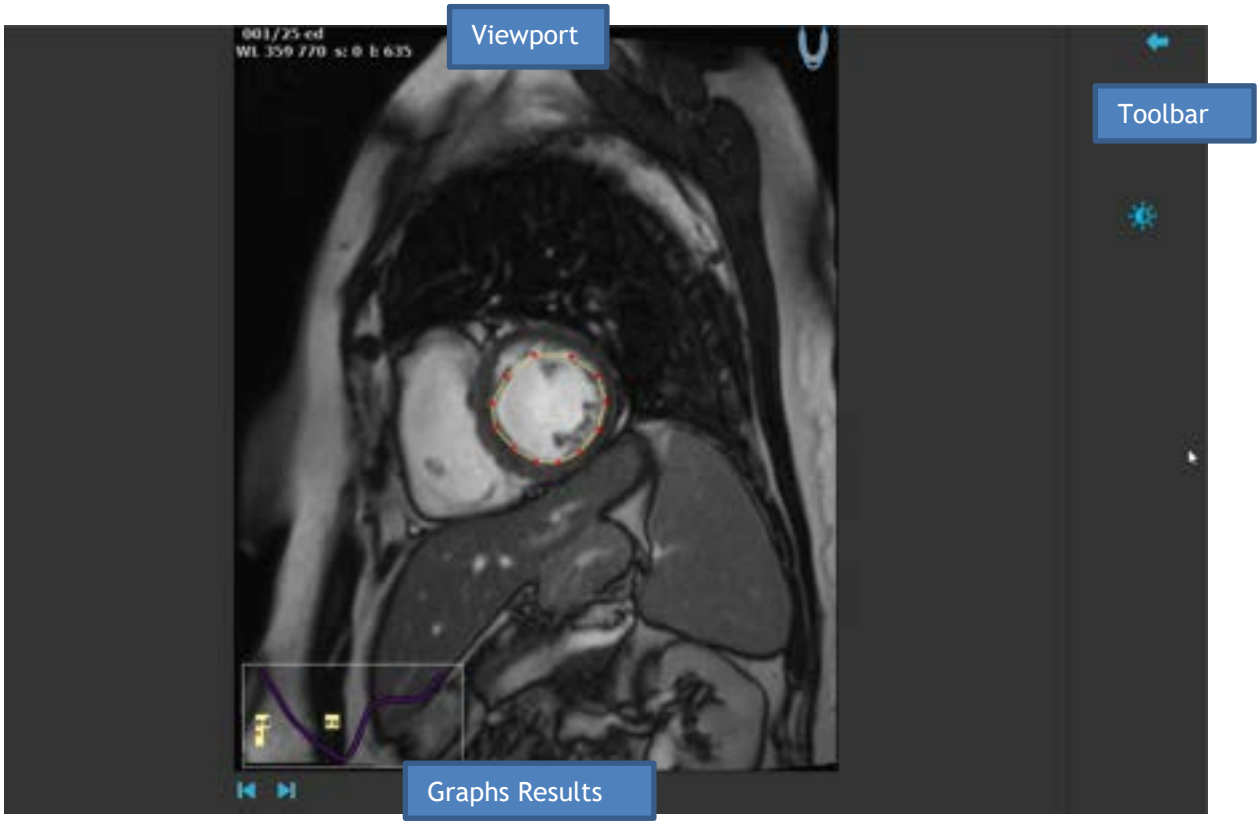


Figure 9-4: ED Review Window

Analysis Window

The analysis window is shown after the data has been selected and the contours have been created or imported.

The analysis window consists of a vertical toolbar and a central viewport which comprises of four sections: The Viewport, graphic result, numeric results, and the 17 segment model results.

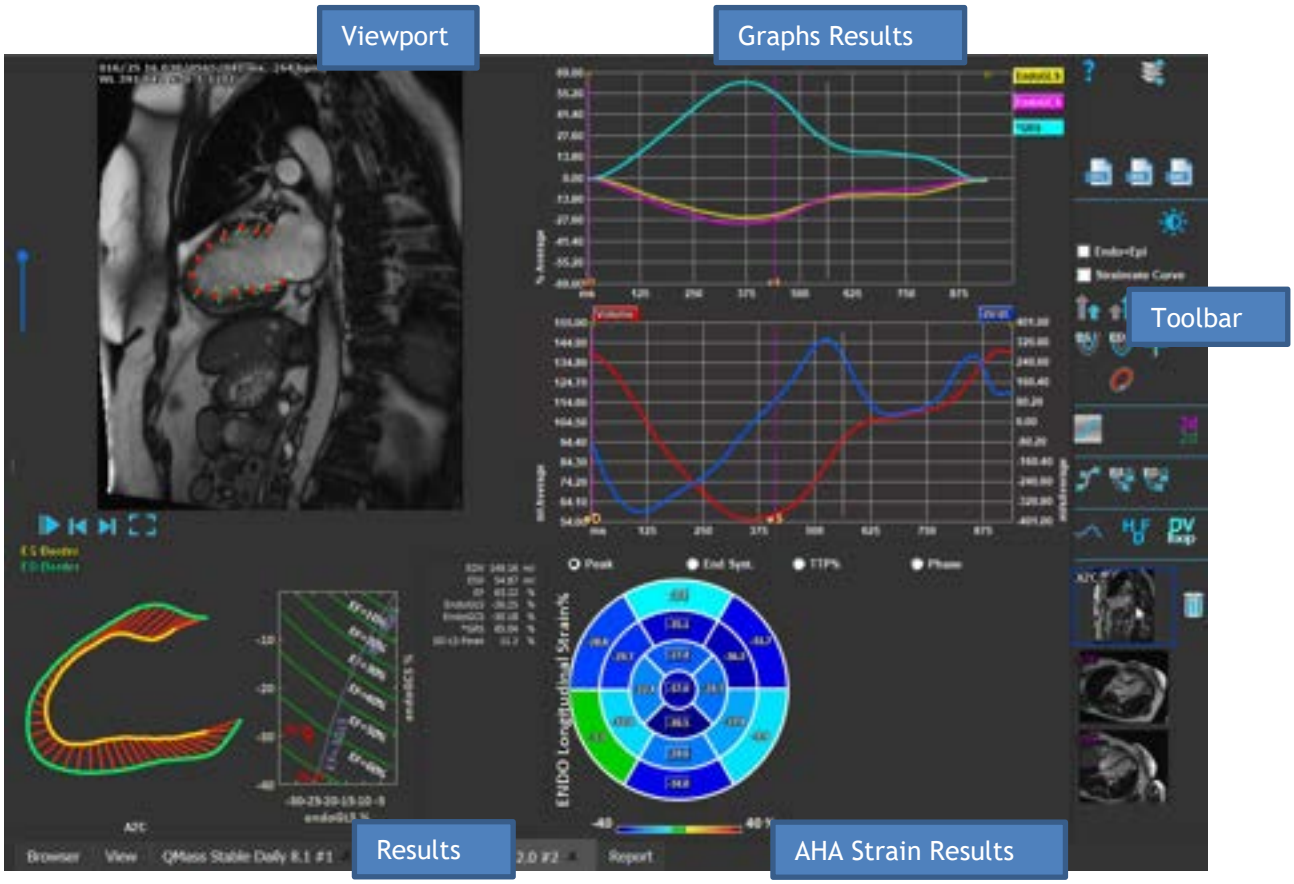


Figure 9-5: Analysis window overview

From the Analysis window you can access the following windows:

- ES/ED modification window
- Reference point
- Sequence/M-Mode
- Time to Peak

LV SAX Reference Point Placement Dialog Box

The LV SAX analysis requires a reference point placement on all slices. The following window facilitates setting the reference point in the correct position.

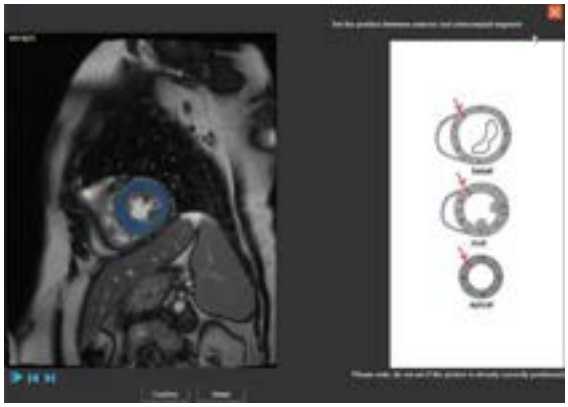


Figure 9-6: LV SAX Reference Point Placement Window

To start the LV SAX Reference Point dialog box:

- In the vertical toolbar, press  to start the LV SAX Reference Point dialog box.

Sequence / M-Mode Selection Window

The sequence / M-Mode selection window is used to verify and modify the ED and ES phase.

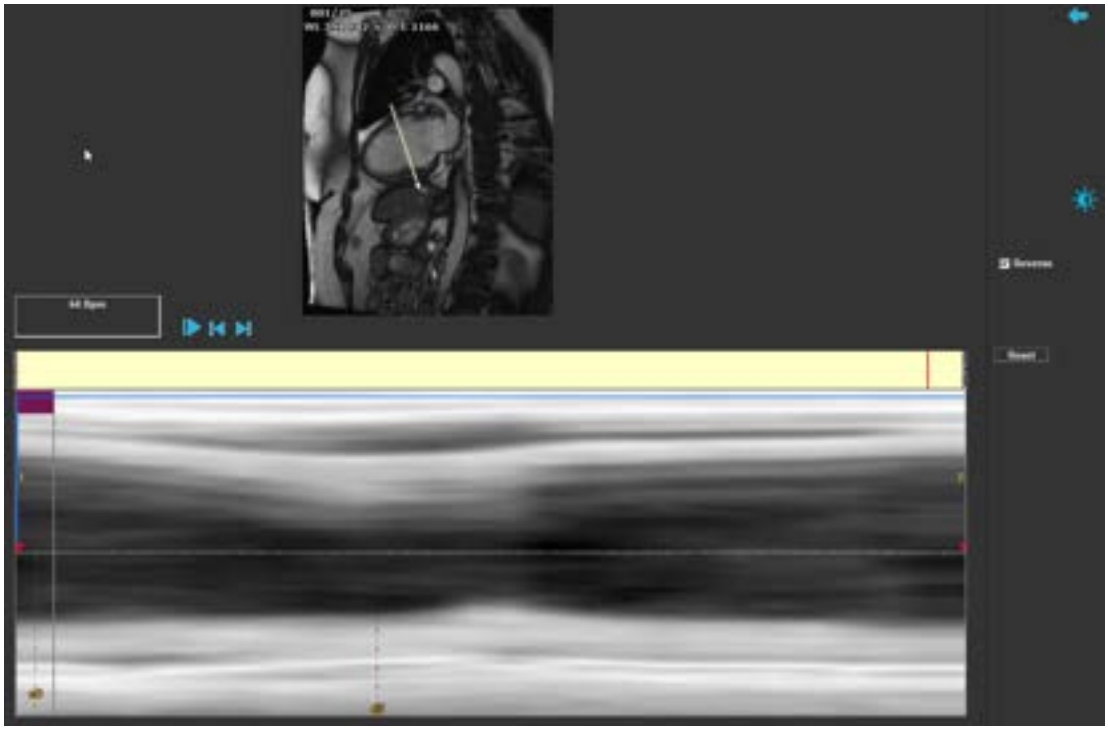


Figure 9-7: Sequence M-Mode Window

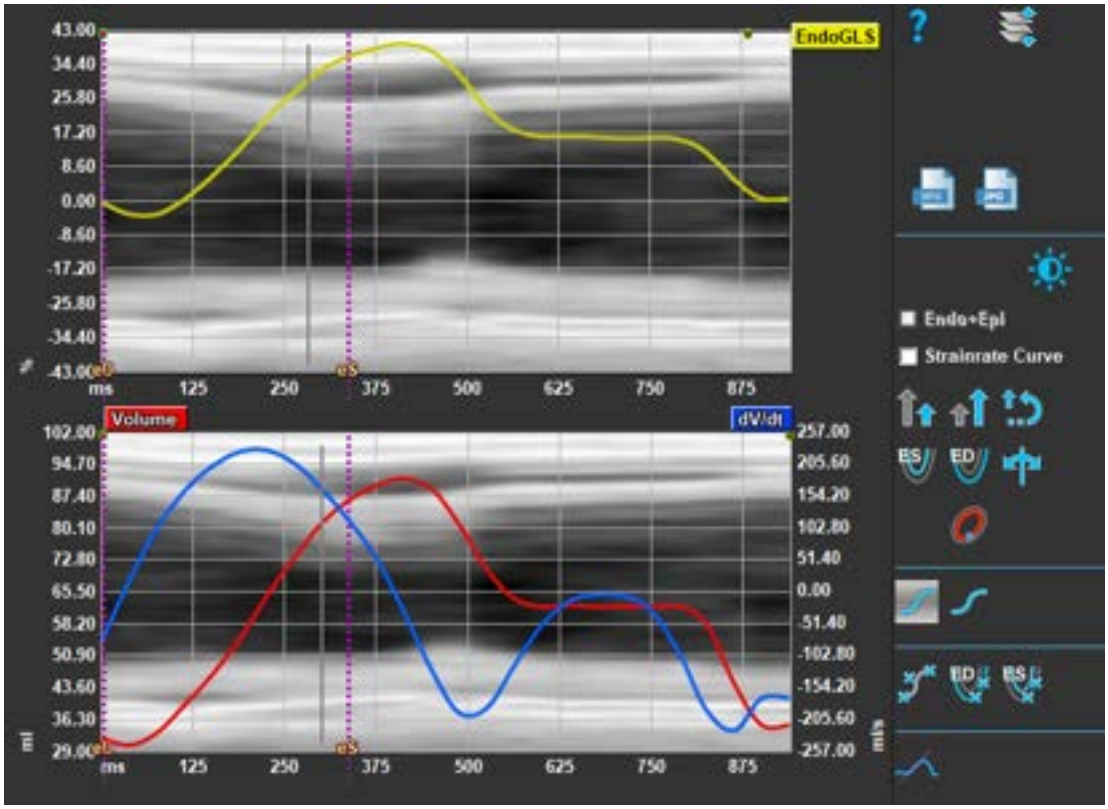


Figure 9-8: Sequence M-Mode in Global Strain Graphs

Time to Peak Segmental Analysis Window

The Time to Peak Segmental Analysis Window shows either LAX or SAX orientational analysis results. The window consists of a vertical toolbar and central viewport with the following sections:

- Image viewing
- Graphic results
- Numerical results
- 17 Segment Model results

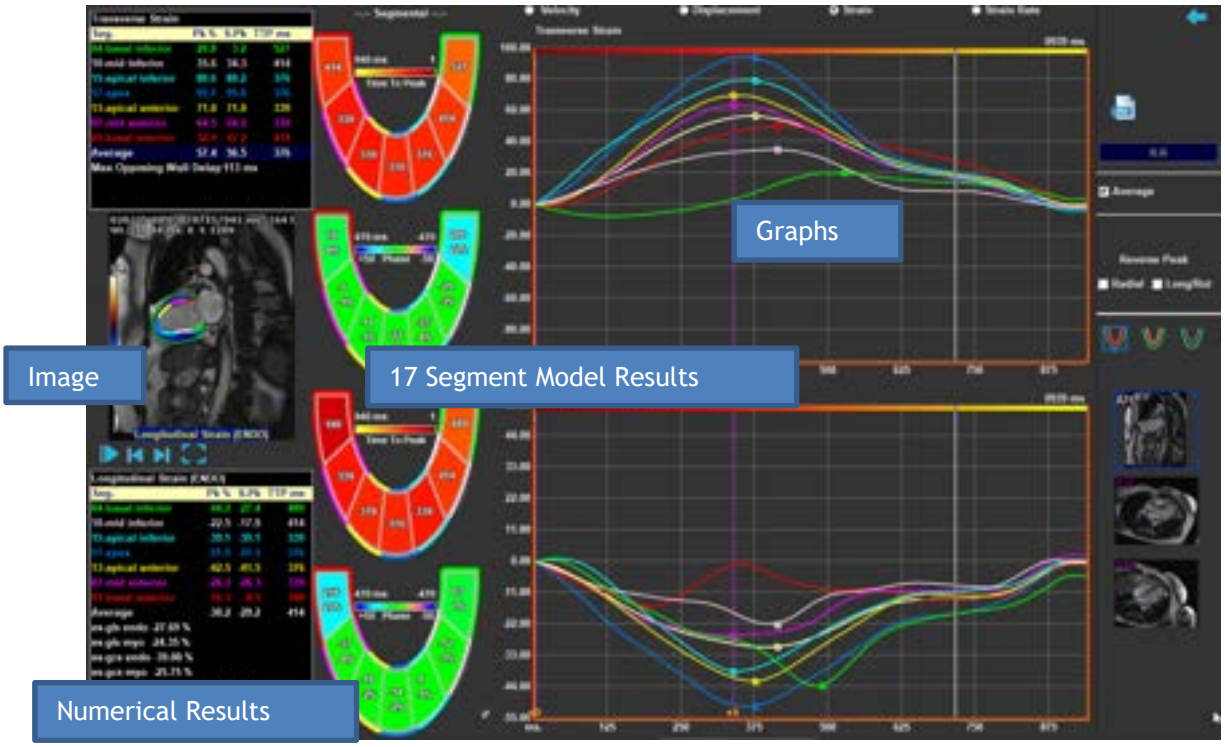


Figure 9-9: Time To Peak Analysis Window (LAX)

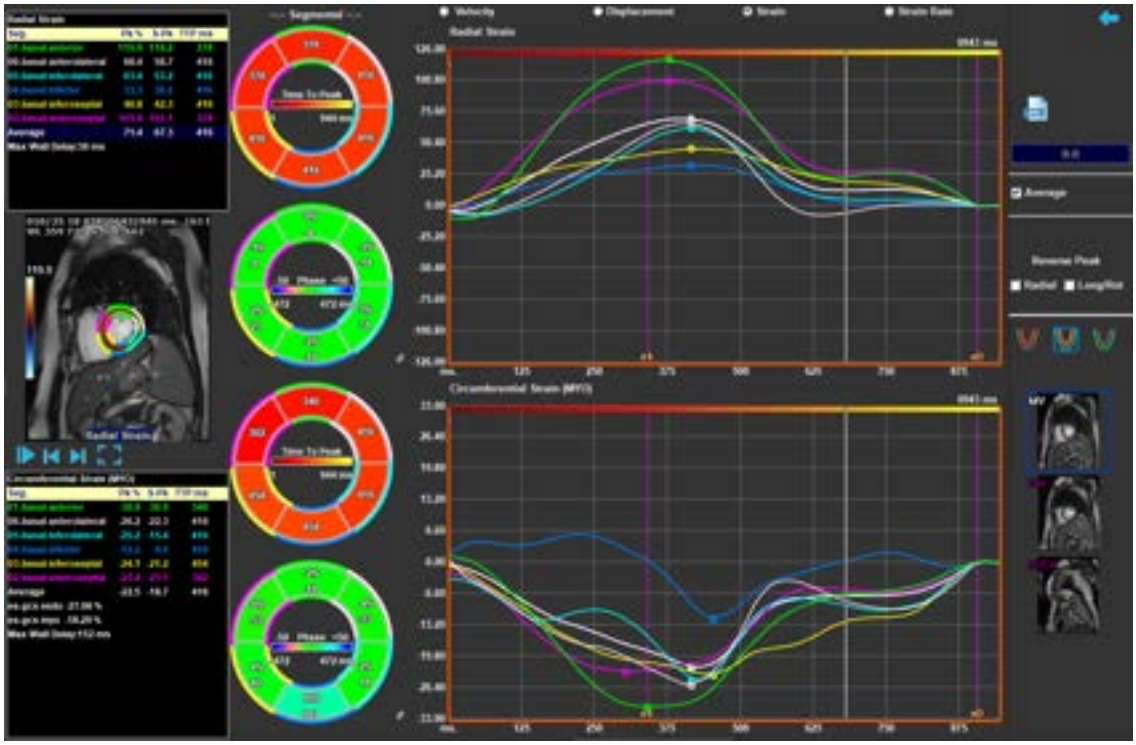


Figure 9-10: Time To Peak Analysis (SAX)

The regional results are distinguishable by color. The 17 segmental model is also interactive, highlighting the numerical region results as well as enabling or disabling the graphs.

9.1.3 Mouse Controls

Zooming

You can zoom in and out of the viewport using **Zooming**.

To activate the zooming mouse control:

- Hover over the image

To zoom in and out:

- Point to the location you want to zoom in on and use your scroll wheel to zoom in and out.

Pan

You can pan an image in the viewport.

To activate the panning mouse control:

- Hover over the image
- Press the left mouse button.

To pan an image:

- Activate the panning mouse control.
- Drag the mouse to pan the image.

Contrast & Brightness & Gamma

You can adjust the contrast, brightness, and gamma. 

To modify the image Contrast

- Press  in the vertical toolbar.
- Click and drag the ruler below the  symbol.

To modify the image Brightness

- Press  in the vertical toolbar.
- Click and drag the ruler below the  symbol.

To modify the image Gamma

- Press  in the vertical toolbar.
- Click and drag the ruler below the  symbol.

To reset the default contrast, brightness, and gamma setting

- Press  in the vertical toolbar.
- Click the symbol  .

9.1.4 Frame Selection

You can move forward or backward through the frames in the image in several ways.

To move through the frames using buttons:

- Press  or  below the viewport to move to the previous or next frame.

Or,

- Press  below the viewport to play a cine through the frames in forward direction. Click again on  to stop the cine.

To move through the frames using keys:

- Press the left or right arrow key to move to the previous or next frame.

To modify the speed of the cine:

- Click and drag the ruler  to the left of the viewport.

Full Screen Selection

The image viewport can be full screen.

To switch to a full screen view.

- Press  below the viewport.

To disable the full screen view.

Press  below the viewport.

9.2 Workflow: Performing a QStrain Analysis

QStrain application supports the following strain related analyses.

- LV long axis (LV LAX)
- LV short axis (LV SAX)
- Left Atrial (Left Atrium)
- Right Atrial (Right Atrium)
- RV images (Right Ventricle)

To navigate through the analysis steps.

- Click  in the vertical toolbar to continue to the next stage of an analysis.
- Click  in the vertical toolbar to go to the previous stage of an analysis.
- Click  in the vertical toolbar to go to the Loading a Series & Analysis stage.
- In the ED/ES Review viewport, click  to accept and click  to reject contour changes.
- In the Sequence / M-Mode Selection Window click  to return to the analysis.
- In the Time to Peak Segmental Analysis Window the button  means return to the analysis window.

9.2.1 QStrain Analysis General Steps

QStrain analyses share the same steps.

- Loading Series
- Analysis Selection

Loading contours

QStrain accepts contours from AutoQ generation and from QMass (when QStrain is started from QMass). In the data selection dialog, you can see if contours are available for a series by the Red/Green dot in the top left of a series.

QMass can provide contours for Left Ventricle Endo and Epi contours for both SAX and LAX series.

AutoQ can provide contours for Left Ventricle Endo and Epi contours for both SAX and LAX series, Right Ventricle Endo and Epi contours for LAX series and can provide Left and Right atrium Endo contours.

When contours are loaded a warning message is presented in the status bar.

Figure 9-11: Message when contours are loaded

Contours are only used when applicable for the selected analysis.

Contours are used as input for the tracking. Therefor the contours after tracking can be slightly different because of the tracking.

- Creating Contours
- Completing Global Strain Analysis.
  - Optional: LV SAX Analysis: Add a reference point, for each slice.
  - ED ES Phase Review: Sequence M-Mode
  - Complete detailed Regional analysis, in the Time to Peak Analysis.

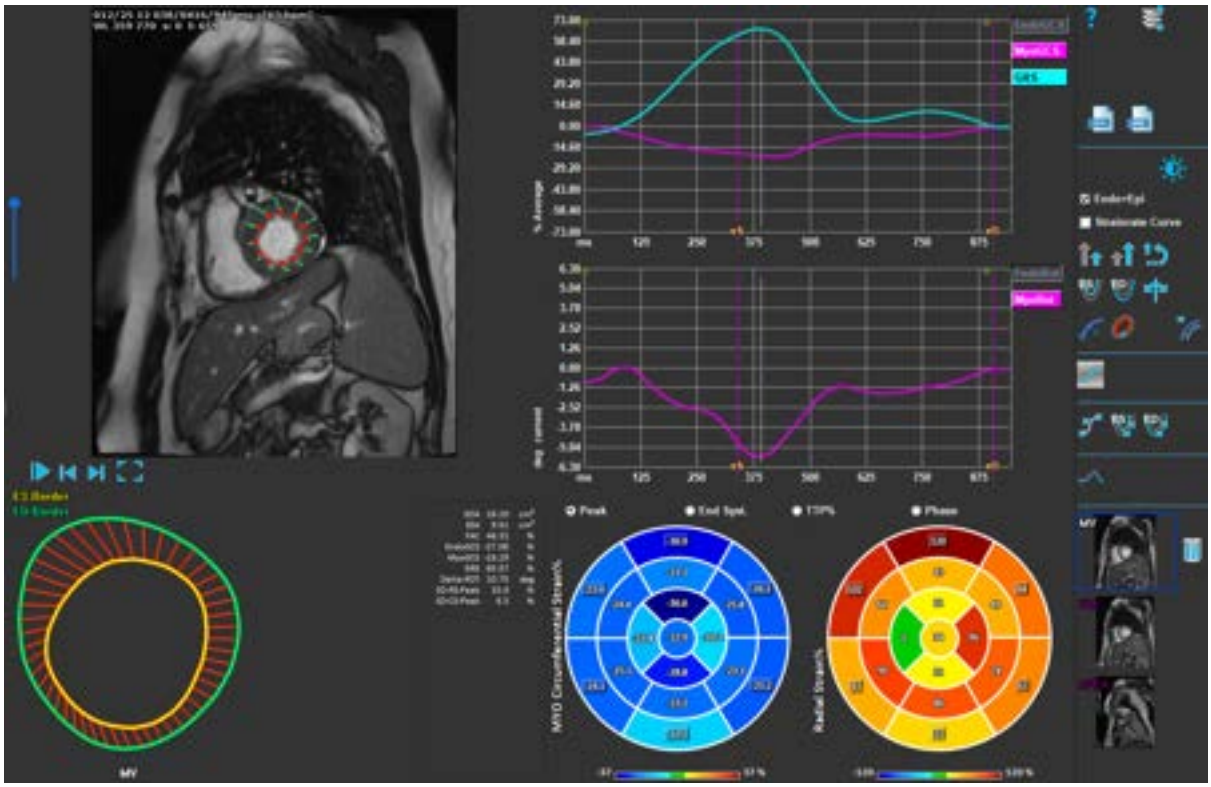


Figure 9-12: LV SAX Analysis

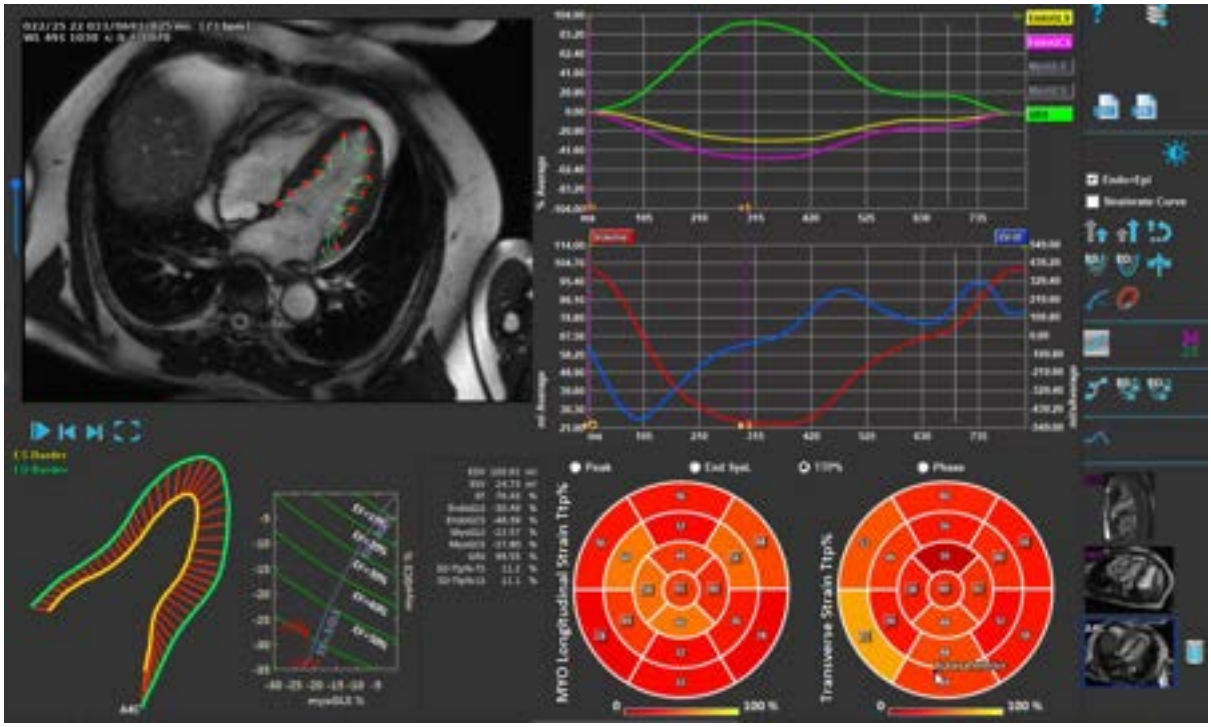


Figure 9-13: LV LAX Analysis

9.2.2 Loading Series

The first step of a strain analysis is loading the series. A series, or multiple series can be loaded into QStrain from the **Series Browser** of Medis Suite. Refer to the Medis Suite user manual for detailed instructions.

QStrain supports MR and CT series.

To load series from the Series Browser of Medis Suite

1. Select the set of strain series in the image or text view of the Medis Suite **Series Browser**.
2. Click and drag the selected items onto the QStrain application icon.

Or,

1. Select all series in the image or text view of the Medis Suite **Series Browser**.
2. Right-click above the selected series to open a context menu.
   Choose QStrain.

This will load the series into the series analysis selection viewport.

To load series from QMass

- Select the icon  in the **General** toolbar in QMass.

All the series data loaded in QMass and their related contours that have been created in QMass, will be loaded into QStrain.

QStrain only loads MR and CT DICOM series.

9.2.3 Analysis Selection

QStrain application supports the following strain related analyses.

- LV long axis (LV LAX)
- LV short axis (LV SAX)
- Left Atrial (Left Atrium)
- Right Atrial (Right Atrium)
- RV (Right Ventricle)

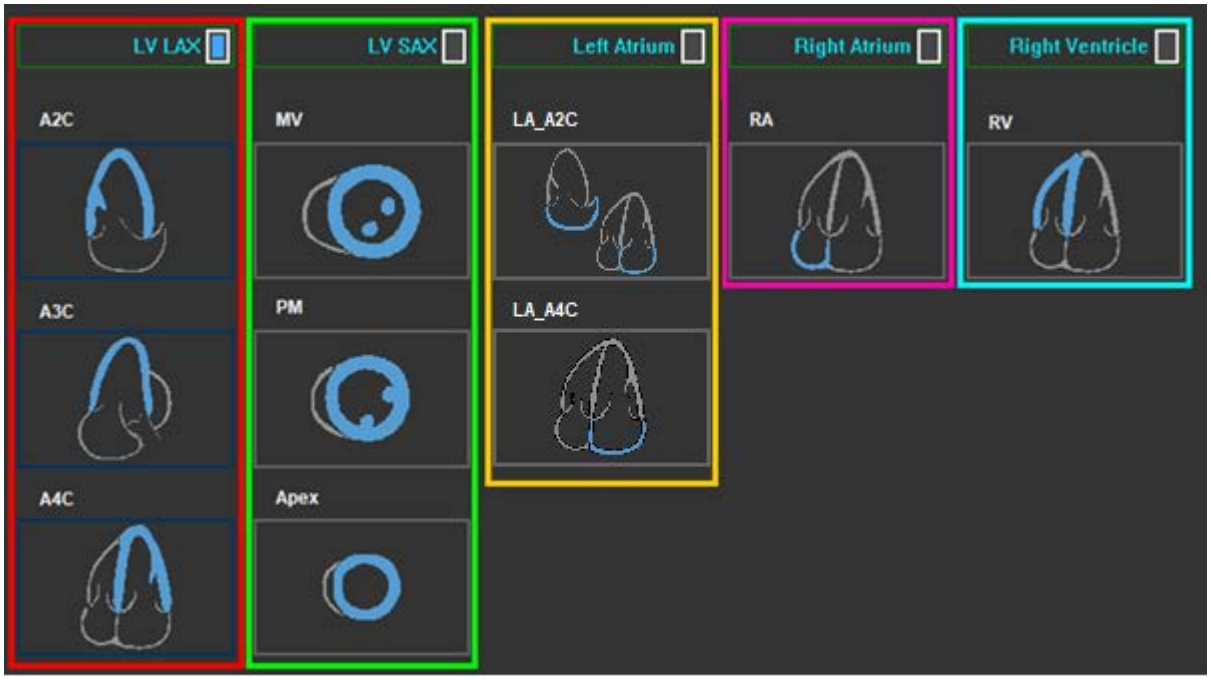


Figure 9-14: Series & Analysis Selection

Automatic series coupling

The loaded series are automatically coupled at start to long axis chamber orientation views if they contain sufficient positional data and if they fit. If multiple series are suitable for a specific image localization, the most recent is coupled. Automatic localization of series can be overridden by manual selection.

If series are automatically coupled a warning is given. The user should always check if the coupled series is the correct series.

Figure 9-15: Message when series are automatically coupled to views

In case multiple series for a series type are available the latest acquisitioned series will be used.

Manual selection and coupling

Series selection.

- Select a series from the left viewport.

Couple a series with an image orientation.

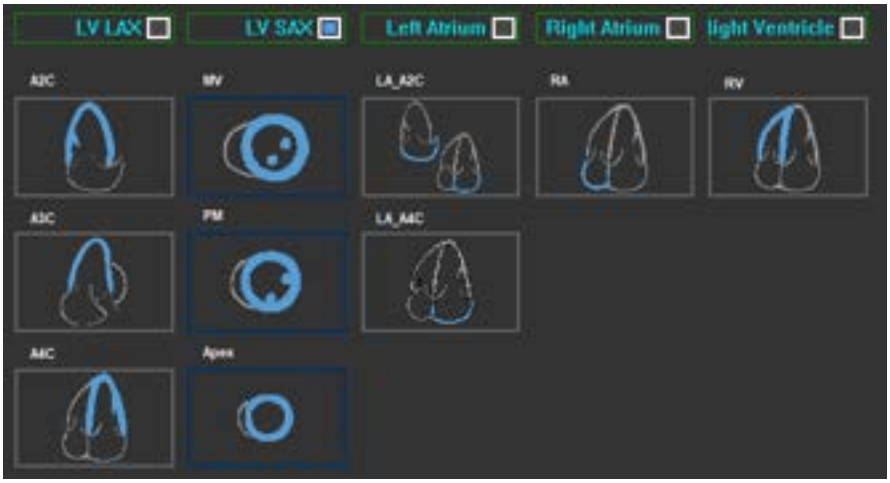


Figure 9-16: Couple a series with an orientation

Choose the analysis type.

- Check the checkbox of the analysis to perform.

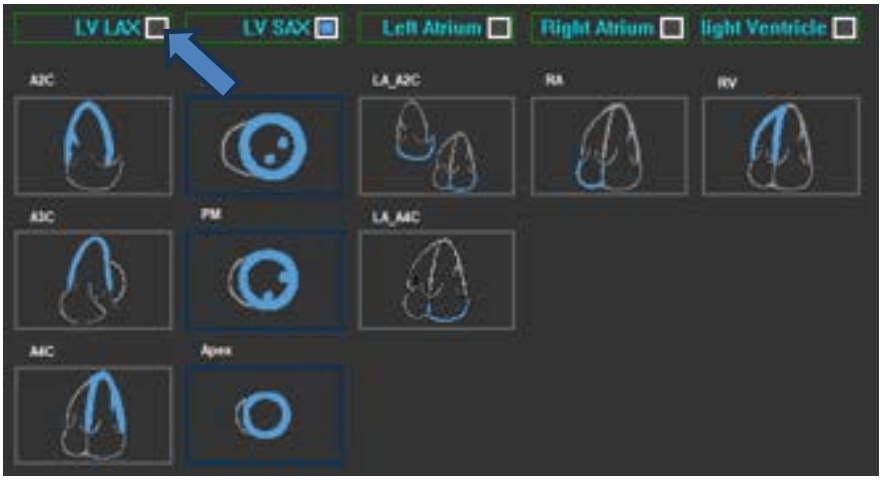


Figure 9-17: Select QStrain Analysis Type

Only one analysis type can be selected.

A green or red circle in the upper left corner of the viewport indicates epi or endo contours are imported with the selected series.

The selected series are coupled with a given QStrain analysis. LV LAX and LV SAX analyses facilitate up to three series, each representing one slice. Left|Right Atrium and RV analyses are limited to one series.

To couple a series with a LV SAX Analysis.

- Select a series in from the series list.

- Click and drag viewport image onto the corresponding level, Mitral Valve  , Papillary Muscle  or Apex  icons.

To couple a series with a LV LAX Analysis.

- Select a series in from the series list.
- Click and drag viewport image onto the corresponding A2C  , A3C  or A4C  chamber view icons.

To couple a series with a Left Atrium Analysis.

- Select a series in from the series list.
- Click and drag viewport image onto the corresponding LA_A2c  or LA_ A4C  chamber view icons.

To couple a series with a Right Atrium Analysis.

- Select a series in from the series list.
- Click and drag viewport image onto the Atrium  icon.

To couple a series with a RV Analysis.

- Select a series in from the series list.
- Click and drag viewport image onto the RV  icon.

To remove a series from an Analysis

- Click on the  icon next to the series you want to remove

To select the series in the viewport already selected in an Analysis orientation.

- Click on the Analysis orientation view icon to select the corresponding series in the viewport

Automatic series mirroring

Series selected for an analysis are checked if mirroring is needed and will be mirrored when the analysis is started.

When one or more series are mirrored a warning message is presented in the status bar.

Figure 9-18: Message when series are automatically mirrored

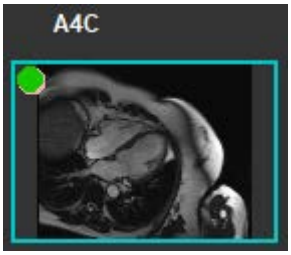
9.2.4 Contours Management

Contours are a prerequisite of a strain analysis. The following section explains the contour management related aspects of QStrain.

When contours are loaded from QMass or AutoQ, the Contour Editing workflow of the analysis is automatically surpassed.

Loading contours

QStrain accepts contours from AutoQ generation and from QMass (when QStrain is started from QMass). In the data selection dialog, you can see if contours are available for a series by the Red/Green dot in the top left of a series.



QMass can provide contours for Left Ventricle Endo and Epi contours for both SAX and LAX series.

AutoQ can provide contours for Left Ventricle Endo and Epi contours for both SAX and LAX series, Right Ventricle Endo and Epi contours for LAX series and can provide Left and Right atrium Endo contours.

When contours are loaded a warning message is presented in the status bar.

Figure 9-19: Message when contours are loaded

Contours are only used when applicable for the selected analysis.

Contours are used as input for the tracking. Therefor the contours after tracking can be slightly different because of the tracking.

Creating Contours

The first step of the QStrain analysis is to define the Endocardium and optionally the Epicardium contours. QStrain contours may be added via the 'Contour Creation Window' viewport or imported with the selected series.

Enable the Contour Creation window.

- After completing the series selection and analysis in the 'Series & Analysis Selection Window', click in the vertical toolbar.

Or,

- In the analysis viewport, click or , or in the vertical toolbar.

Or,

- In the analysis viewport, select the checkbox Endo+Epi in the vertical toolbar.

To create a contour.

When the contour editing window is open, edit the contours as follows:

1. Click to set the first edit point on the image, in the recommended position displayed by the contour point indicator.
2. Click to set the second edit point on the image, in the recommended position displayed by the contour point indicator.
3. Right-click to set the last edit point on the image, in the recommended position displayed by the contour point indicator. A contour will be generated.

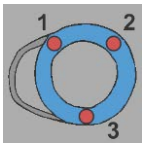
Select the check box Endo + Epi to generate both Endo and Epi contours.

Clear the check box Endo + Epi to generate the Endo contour only.

Creating Contours by Indicators

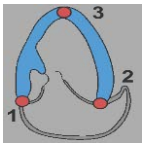
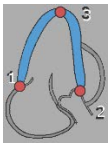
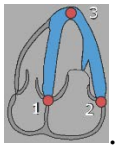
In the bottom right corner of the Contour Editing viewport, a contour position indicator recommends the ideal position placement of the progressive contour points.

LV SAX

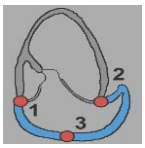
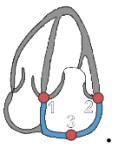
LV SAX placement indicators as follows 

.

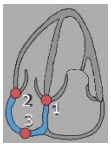
LV LAX

LV LAX placement indicators are as follows  or  or  .

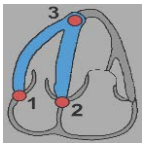
Left Atrium

Left Atrium placement indicators are as follows  or  .

Right Atrium

Right Atrium placement indicators are as follows . 

RV

RV placement indicators are as follows  .

Editing Contours

Modify contours

To modify an existing contour

Moving Edit-points:

- Hover the mouse cursor over the Edit-point. The cursor changes to double-sided arrow cursor.
- Click and drag the mouse to move the edit-point. If the contour is already created (Three edit points present), new contour will be displayed based on the new position of edit-points.
- Release the mouse to end editing and the contour shown while dragging becomes final.

Rubber-banding edit contours:

- Hover the mouse cursor over the contour. The cursor changes to rubber-banding cursor.
- Click the left mouse button and drag the mouse to edit the contour. A section of contour will be edited with mouse motion.
- Release the mouse to end editing and the contour shown while dragging becomes final.

Moving contours (Ctrl + LMB Click and drag):

- Press the Ctrl key and click left mouse button on viewport area and drag the mouse to move the contour. If both Epi and Endo contours are present the contour near to the mouse click point will be selected for move.
- The contour will move the same distance and direction as the mouse moves.
- Release the mouse button to end the move.
- Press Ctrl + Shift + LMB Click and drag to move both Epi and Endo contours simultaneously.

Smoothening contours (Shift + S):

- Press the Shift + S keys to smoothen the selected contour, i.e either ES or ED contour.
- The last contour manually edited, using rubber-band or move edits, will be the selected contour.

Remove all contour points.

- Click on the edit point  in the vertical toolbar.

Undo/Redo edits.

- Press Ctrl + Z to undo the edits done on contour, i.e. moving, rubber-banding, smoothening contour OR moving edit-points.
- Press Ctrl + Y to redo the undo action, provided no new editing is performed after undo.
- Undo/Redo can only be done as long as editing is not finished, or additionally in ED edit page, if frame is not changed.

Finish Contour Editing

After contours have been defined, the analysis can be continued.

To continue from the Contour Editing window to the Analysis window.

- Select the  in the vertical toolbar.

Or,

Right-click in the Viewport

9.2.5 Analysis Accessories

The vertical toolbar in the analysis window, contains utilities that assist in the strain analysis workflow.

Creating a Reference Point for LV SAX Analysis

Reference points enhance the accuracy of the results.

To set a reference point in a LV SAX analysis.

- Choose the LV SAX a slice from the vertical toolbar.

- Select the  in the vertical toolbar.
- Click on the Anterior Septum as indicated in LV SAX Reference Point Placement Dialog.
- Click Confirm.

 LV SAX strain analysis requires a reference point placement on the anterior septum of each slice.

ED ES Management

ED ES Contour Review & Modification

The 'ES Contour Review & Modification Window' facilitates one to update the ED and ES contours.

To enable the ES Contour Review & Modification Window.

- In the analysis window click  in the vertical toolbar.

To enable the ED Contour Review & Modification Window

In the analysis window click  in the vertical toolbar.

ED ES Phase Review: Sequence M-Mode

The Sequence M-Mode is a utility that assists in managing the position of the ED and ES phase. A Sequence M-Mode line is used to create an M-Mode image. Typically, the M-Mode line is drawn from the outer ventricular walls across the diameter of the ventricle. The ED and ES phase positions can then be adjusted on the M-Mode image.

Sequence M-Mode editing consists of three steps.

- Define a line across a ventricle.

- Evaluate the M-Mode image.
- Review/Modify the ED and ES position.

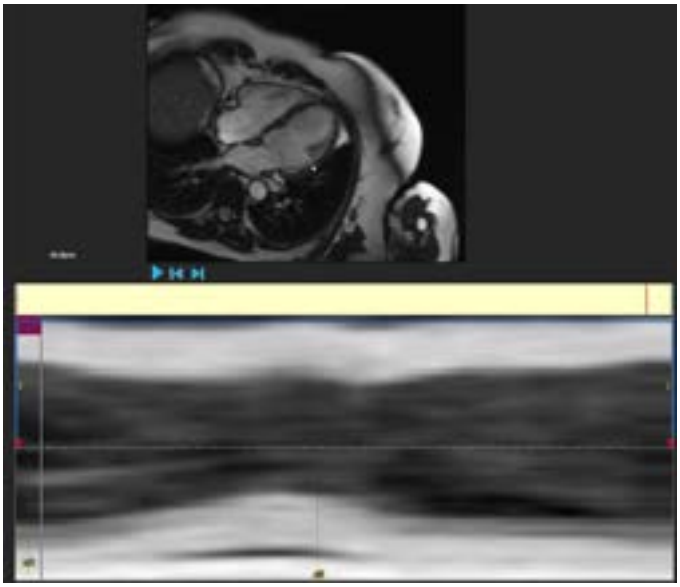


Figure 9-20: Sequence M-Mode ED ES Phase Review

The ED and ES phases can be verified and modified if necessary, using the M-Mode image. The resulting M-Mode overlay image will automatically be displayed in the volume graph of in the analysis window. The overlay can be toggled off and on.

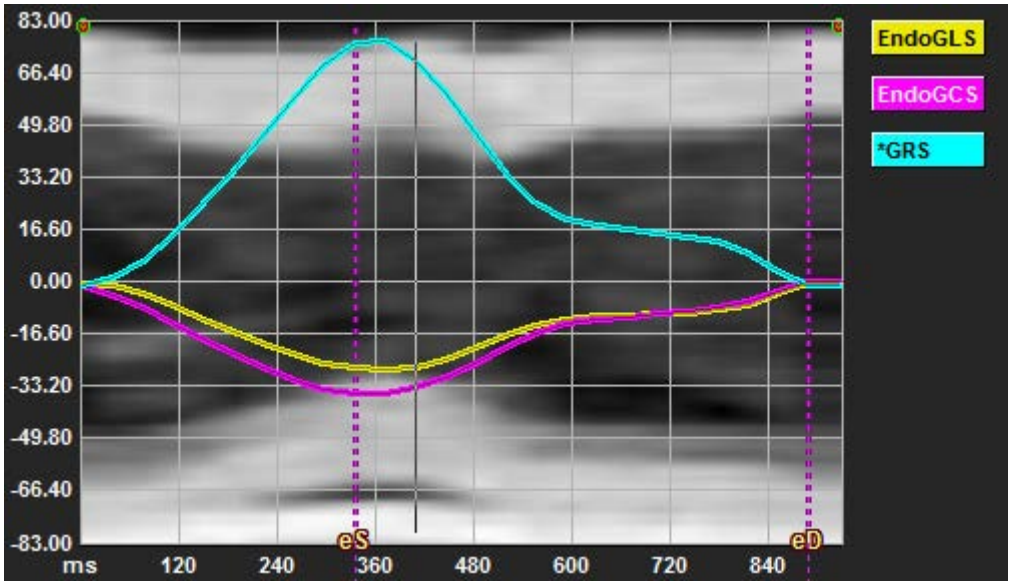


Figure 9-21: M-Mode Overlay in Analysis Window Volume Graph

To draw the M-Mode line.

- In the analysis viewport, click  in the vertical toolbar.
- In the image, click to begin the M-Mode line.
- Right-click to end the M-Mode line.

To update the ED or ES phase.

- Click and drag the ED or ES vertical gridlines in the M-Mode image.
- Click  in the vertical toolbar to return to the analysis window.

To enable / disable M-Mode overlay in volume graphs.

In the analysis window.

- Click to  enable or disable the M-Mode in the strain graph.

Time to Peak Analysis

The Time to Peak analysis provides detailed 17 segment AHA model regional strain results. The regional results are distinguishable by color. The segment model and the corresponding graphs are interactive and facilitate enabling and disabling of the regional results.

The following color scheme is used to distinguish the different segment model regions and their corresponding results.

Basal		**Mid**		**Apical**	
Basal	Anterior	Mid	Anterior	Apical	Anterior
Basal	Anterorlateral	Mid	Anterorlateral	Apical	Inferior
Basal	Inferiorlateral	Mid	Inferiorlateral	Apical	Septal
Basal	Inferior	Mid	Inferior		Lateral
Basal	Inferorseptal	Mid	Inferorseptal		
Basal	Anterorseptal	Mid	Anterorseptal		

To start a Time to Peak analysis.

- Click  in the vertical toolbar to return to the analysis window.

To select a region.

In the Time to Peak Segmental Analysis Window:

- Hover over the Segment model.

Or,

Hover over the graphs.

To enable / disable a region.

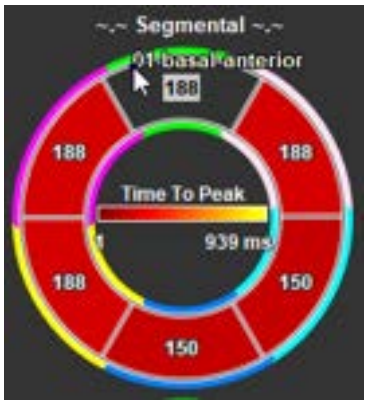


Figure 9-22: Enable/Disable SAX TTP Region

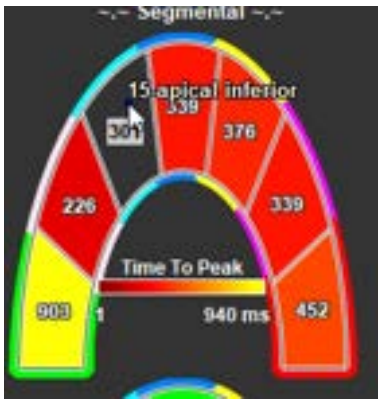


Figure 9-23: Enable / Disable LAX TTP Region

In the Time to Peak Segmental Analysis Window.

- Click the segment to enable or disable.

To enable / disable all regions.

In the Time to Peak Segmental Analysis Window.

Click the center of the segment model to enable or disable all segments.

To switch regional analysis type.

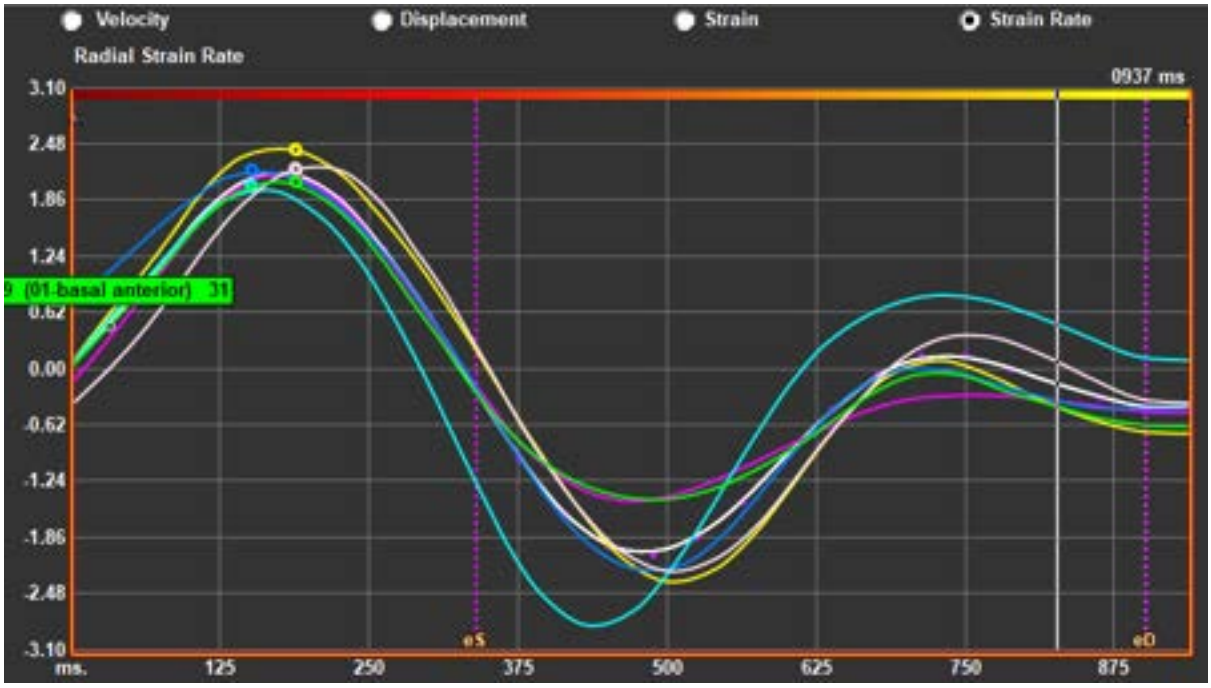


Figure 9-24: Select Strain Results Type

In the Time to Peak Segmental Analysis Window

Select either ‘Velocity’, ‘Displacement’, ‘Strain’ or ‘Strain Rate’.

To switch between Endocardium, Epicardium or Myocardium regional results.

In the Time to Peak Segmental Analysis Window

- Click  in the vertical toolbar for the Endocardial regional results.
- Click  in the vertical toolbar for the Epicardial regional results.
- Click  in the vertical toolbar for the Myocardial regional results.

3D Movie

QStrain has a 2D/3D view to assist in the visualization of strain whilst performing a strain analysis.

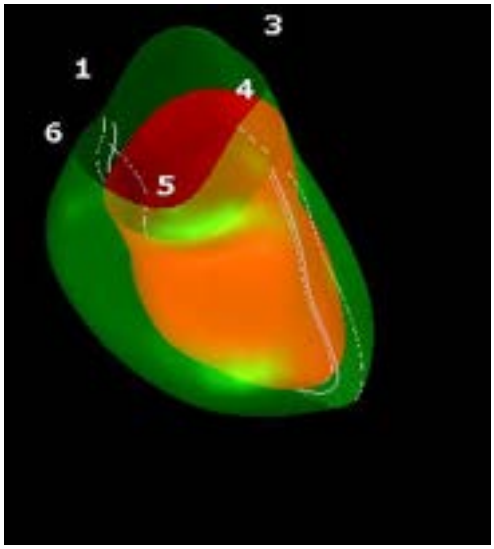


Figure 9-25: 3D View of Strain

To enable 3D view

- Load and complete an analysis of at least 2 LAX series.
- In the analysis viewport, click 

in the vertical toolbar.

Inward Displacement

Inward Displacement is a value defined for each point of the endocardial border, which represents the component of the displacement vector that is directed toward the “center of contraction”. Such center is defined as a point on the LV axis whose position ranges from one half and two-third of the base-apex distance, for the basal to the apical regions, respectively. Inward Displacement computation is carried out only for LAX data.

Inward Displacement is measured starting from the end-diastolic frame, assumed as the rest position. It, therefore, normally increases during systole to reach a positive peak value at end-systole and decrease during diastole to eventually return to zero at end-diastole.

Normalized Inward Displacement (ID %)

Inward Displacement is measured in mm. Moreover, it is normalized with the initial (end-diastolic), local distance to the LV center and expressed in %, where 0% means no contraction and 100% corresponds to a theoretical limit of a regional end-systolic size that shrinks to zero.

Inward Index (II %)

Inward Index (II) is an index that shows the relation between the inward displacement (ID) and a standard reference value (IIsv). Inward Index is computed as ID/IDsv*100 and is expressed in percentage.

Inward Displacement display in Analysis Page

The Inward Displacement measurements are done for each segment individually and are shown in 17-segment AHA model in Analysis window.

The standard deviation calculated on the segmental inward displacement (SD-ID) and inward index (SD-II) are shown as Results section.

In addition, Inward Displacement peak %, Time to peak % and Phase % can be viewed by making selection in vertical toolbar.

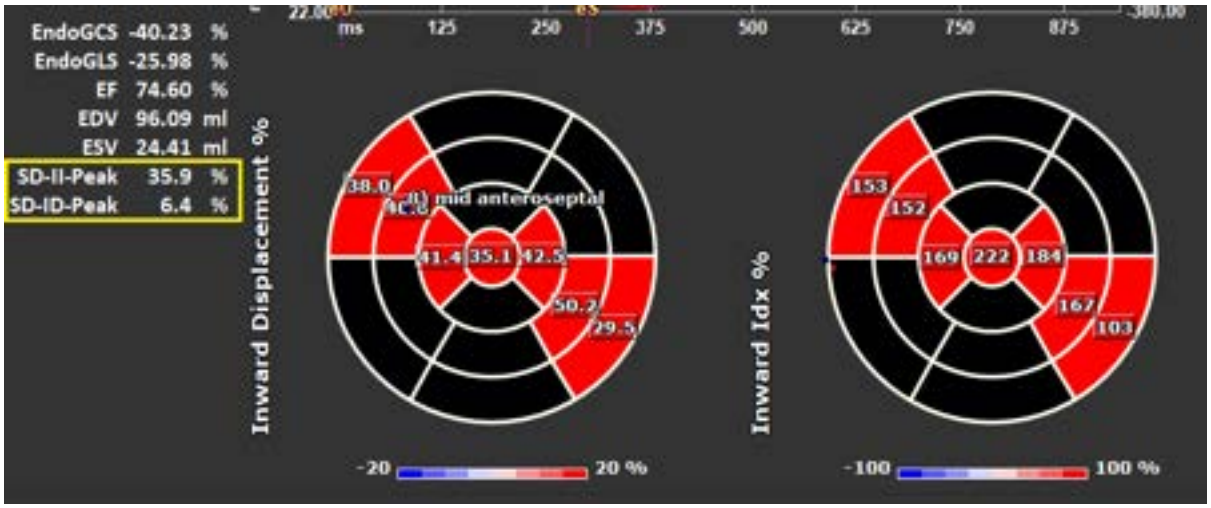


Figure 9-26: Inward Displacement results

To view the Inward Displacement 17 segment AHA model and results

- In the analysis viewport, select the “Inward Displacement” ☑ Inward Displacement checkbox in the vertical toolbar.

On selecting InwD checkbox, the strain results in 17 segment AHA model are replaced by InwD results. To view the strain results again, select “Strain” ☑ Strain checkbox.

Image position

The spatial positioning of an image can be automatically or manually flipped.

To start automatic image position correction

- After completing the series selection and analysis in the ‘Series & Analysis Selection Window’, click  in the vertical toolbar.

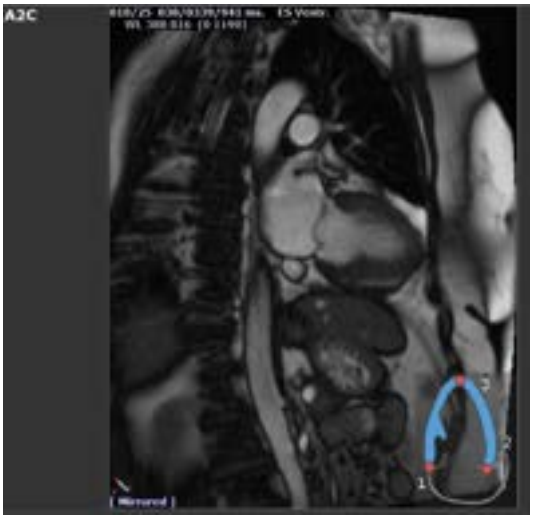


Figure 9-27: Before Image Position Flip

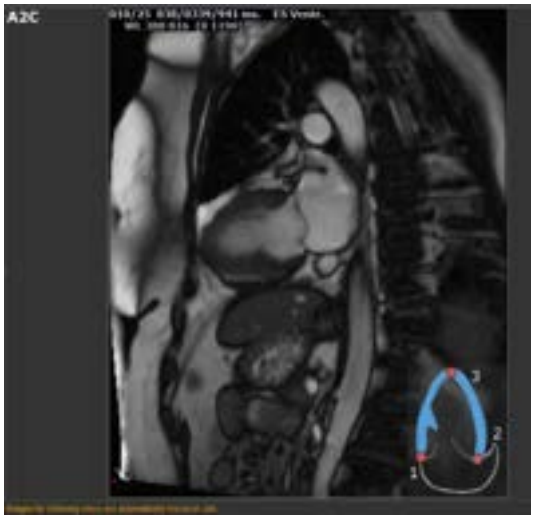


Figure 9-28: After Image Position Flip

To manually flip a series

- In the analysis viewport, click  .

Or,

- In the ‘ES Contour Review & Modification Window’, click  .

Or,

- In the Sequence / M-Mode Selection Window, click  .

The user must ensure that spatial position is accurate. Flipping can modify the results. Make sure to review the spatial position is accurate and correct it if necessary.

A warning message will indicate that the image has been flipped manually or automatically. Make sure to review results and correct if necessary.

9.3 QStrain Results

The QStrain results are visible in Medis Suite, in the Medis Suite Findings and the Medis Suite Report. SnapShots and movies may also be added to the results. QStrain analysis provides the following sets of strain results.

- Global
- Standard Regional
- Detailed Regional (Time to Peak Analysis)

The primary strain results are as follows.

- Global Radial Strain (GRS)
- Global Circumference Strain (GCS)
- Global longitudinal Strain (GLS)

Refer to

Results Overview for further details on the Results

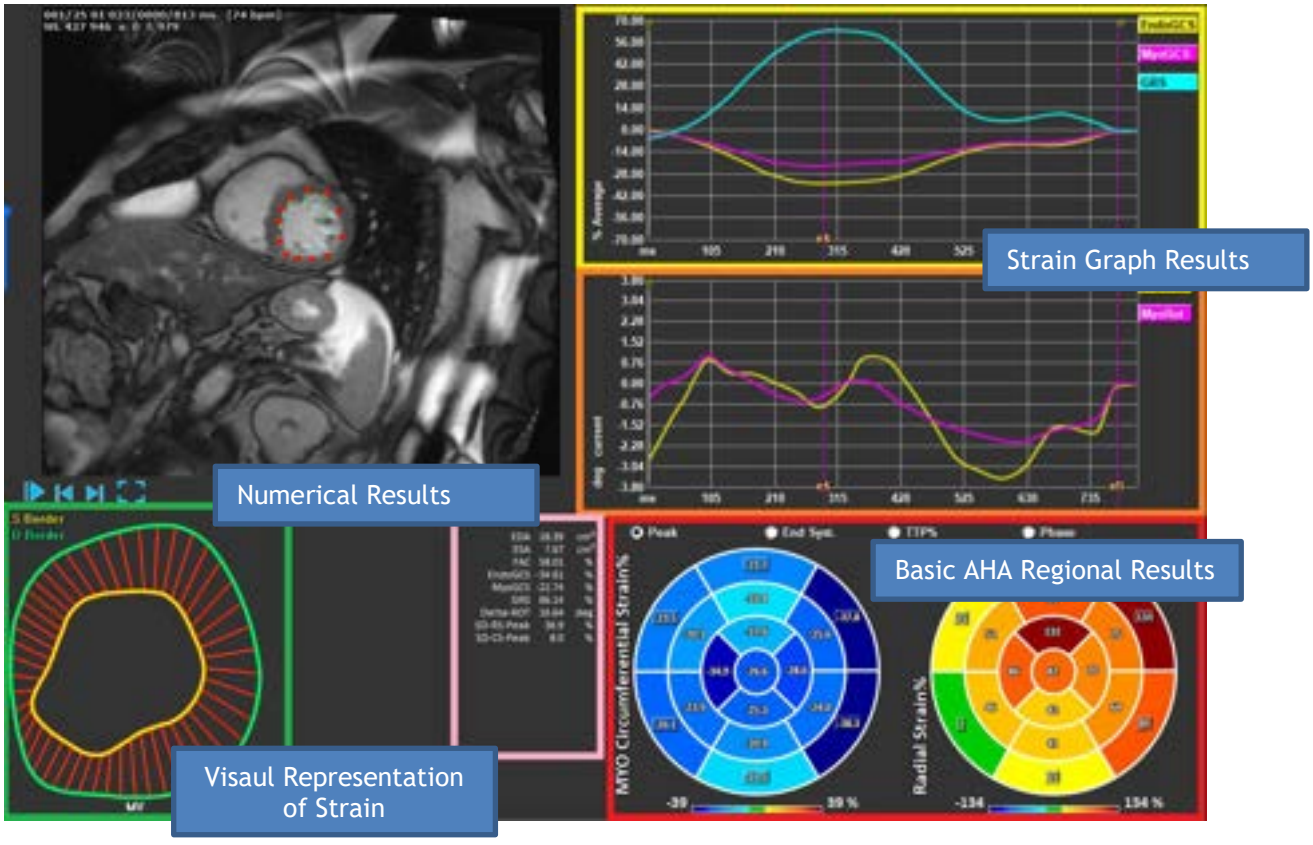


Figure 9-29: Results Sections Overview

9.3.1 Global Strain Results Graphs

The global results are accessible from the analysis window. There are two graphical results graphs. The upper graph shows Global Strain curves, while the lowers shows Rotational Strain curves in LV SAX analysis and Area Curves in the LV LAX, Left Atrium, Right Atrium and RV analysis.

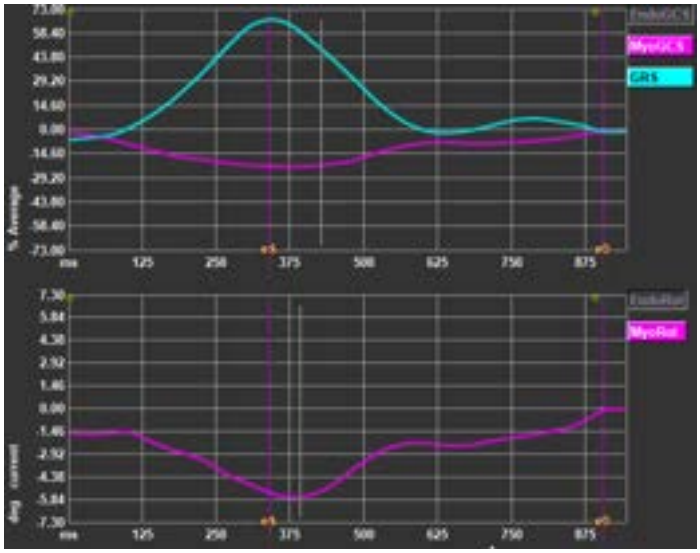


Figure 9-30: Analysis Strain Graphs

To enable Strain Rate curve

In the analysis viewport, select the checkbox Strainrate Curve in the vertical toolbar.

To set ES and ED phases after processing

When the processing of the global results is produced, ES and ED phases are set according to the average volume or area curves. However, the ES and ED phases can be moved manually acting on these graphs: the time position of these phases can be shifted by pressing the mouse on the ES and ED vertical cursors and releasing them at the desired position.

Myocardial Strain results are available when both Endo and Epi contours are available.

The rotation strain is slice dependent and therefore reflects the strain of the selected slice.

9.3.2 Global Strain Numerical Results

The numerical global results are accessible from the analysis window.

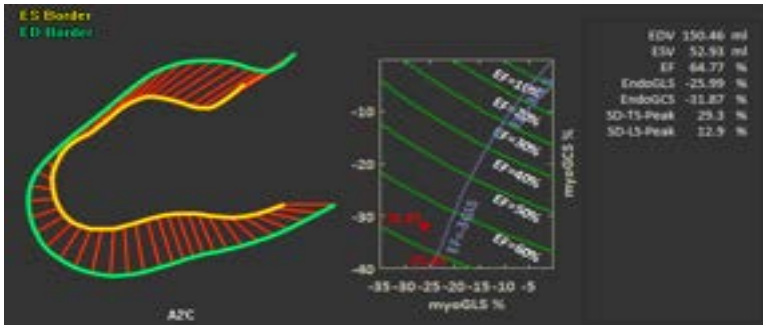


Figure 9-31: LAX Numerical Results

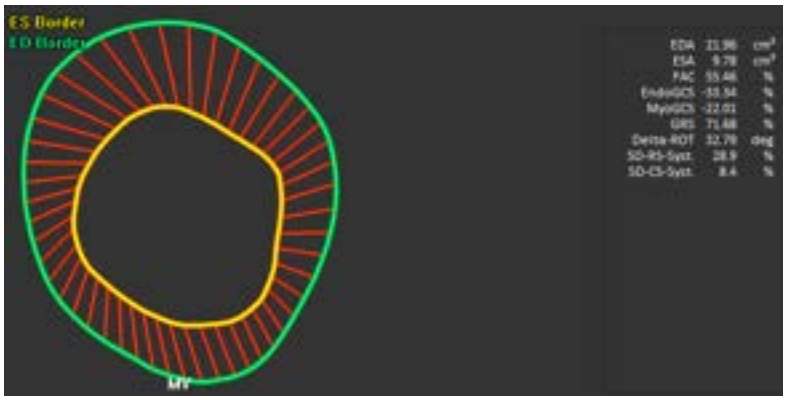


Figure 9-32: SAX Numerical Results

9.3.3 Standard Regional Strain Results

The standard regional results are accessible from the analysis window.

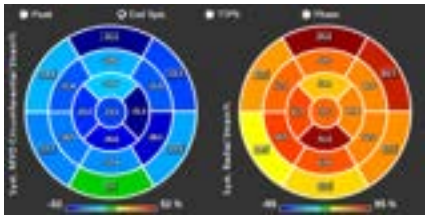


Figure 9-33: Standard Regional Results

9.3.4 Detailed Regional Results (Time To Peak)

Detailed regional results are accessible from the Time to Peak Segmental Analysis Window.

Figure 9-34: Detailed Regional Results. TTP

9.4 Results Overview

The following lists define the results that are available from each QStrain analysis.

9.4.1 LV long axis (LV LAX) results

QStrain provides the following list of results:

- EDV
- ESV
- EF
- Endo GLS
- Endo GCS
- Myo GLS (Only if EPI contour is segmented)
- Myo GCS (Only if EPI contour is segmented)
- GRS (Only if EPI contour is segmented)
- SD-LS-Peak (Only when Peak AHA view is selected)
- SD-TS-Peak (Only when Peak AHA view is selected, and EPI contour is segmented)
- SD-LS-Syst. (Only when End Syst. AHA view is selected)
- SD-TS-Syst. (Only when End Sys. AHA view is selected, and EPI contour is segmented)
- SD-Ttp%-LS (Only when TTP% AHA view is selected)

- SD-Ttp%-TS (Only when TTP% AHA view is selected, and EPI contour is segmented)
- SD-Ph%-LS (Only when Phase AHA view is selected)
- SD-Ph%-TS (Only when Phase AHA view is selected, and EPI contour is segmented)
- SD-II-Peak - % (only when Peak AHA view and Inward Displacement is selected)
- SD-ID-Peak - % (only when Peak AHA view and Inward Displacement is selected)
- SD-II-Syst. - % (only when End Syst. AHA view and Inward Displacement is selected)
- SD-ID-Syst. - % (only when End Sys. AHA view and Inward Displacement is selected)
- SD-Ttp%-ID - % (only when TTP% AHA view and Inward Displacement is selected)
- SD-Ph%-ID – % (only when Phase AHA view and Inward Displacement is selected)

9.4.2 LV Short axis (LV SAX) results

QStrain provides the following list of results:

- EDA
- ESA
- FAC
- Endo Rot
- Endo GCS
- Myo Rot (Only if EPI contour is segmented)
- Myo GCS (Only if EPI contour is segmented)
- GRS (Only if EPI contour is segmented)
- Delta Rot (Only when all slices in LV-SAX are present)
- SD-CS-Peak (Only when Peak AHA view is selected)
- SD-RS-Peak (Only when Peak AHA view is selected, and EPI contour is segmented)
- SD-CS-Syst. (Only when End Syst. AHA view is selected)
- SD-RS-Syst. (Only when End Syst. AHA view is selected, and EPI contour is segmented)
- SD-Ttp%-CS (Only when TTP% AHA view is selected)
- SD-Ttp%-RS (Only when TTP% AHA view is selected, and EPI contour is segmented)
- SD-Ph%-CS (Only when Phase AHA view is selected)
- SD-Ph%-RS (Only when Phase AHA view is selected, and EPI contour is segmented)

9.4.3 Left Atrium or Right Atrium results

QStrain provides the following list of results:

- EDV - ml
- ESV - ml
- EF - %
- EDA – cm^2 (only when one view is selected)
- ESA – cm^2 (only when one view is selected)
- LAS_CT - %
- LAS_CD - %
- LAS_R - %
- FAC - % (only when one view is selected)

9.4.4 Right Atrium results

Medis Suite MRCT provides the following list of results:

- EDV
- ESV
- EF
- Endo GLS
- Endo GCS
- FAC

9.4.5 RV long axis (Right Ventricle)

QStrain provides the following list of results:

- EDA
- ESA
- FAC
- Endo GLS
- Myo GLS (Only when EPI contour is segmented)
- GRS (Only when EPI contour is segmented)

9.5 Reporting

QStrain results are made available in the Medis Suite Results pane and in the Medis Suite report.

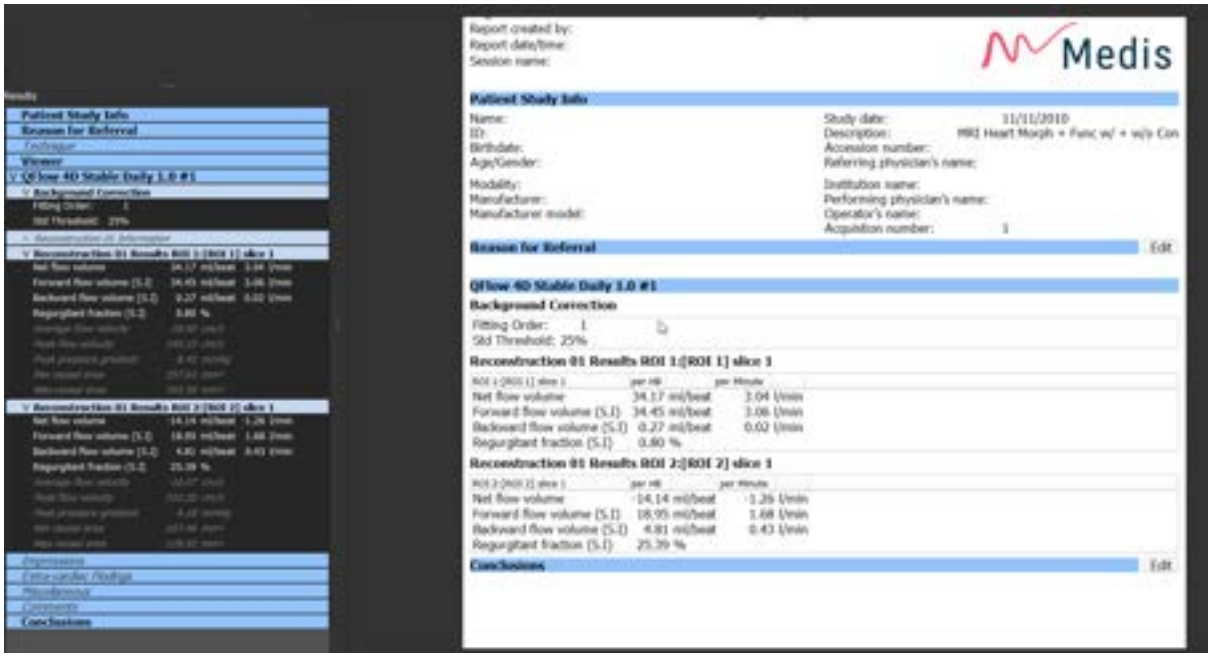


Figure 9-35: Medis Suite Report with QStrain Results

The Reporting functionality of Medis Suite is described in the Medis Suite user manual. The Medis Suite documentation is available from the User documents tab, which can be opened as follows;

- Press F1.
- Pushing the ? help button.

- Select the Medis Suite main menu button in the upper right corner  > **Help** > **User Documents**

9.6 Sessions

The QStrain state can be saved in a Medis Suite session. The session can be reloaded to continue or review the analyses.

The session functionality in Medis Suite is described in the Medis Suite user manual. The Medis Suite documentation is available from the User documents tab, which can be opened as follows;

- Press F1.
- Pushing the  help button.

Select the Medis Suite main menu button in the upper right corner  > **Help** > **User Documents**

9.7 Shortcut Keys

When you are working with QStrain, you can use several combinations of keys on your keyboard and mouse actions to quickly perform the following tasks.

Press	**To**
Layout	
F11	Show or hide the workspace windowpanes
Image control	
Scroll wheel	Zoom
Procedures	
Navigation Controls	
Arrow left	Display the previous time point
Arrow right	Display the next time point

9.8 Parameters / Measurements

9.8.1 Strain Parameters

GLS	Global Longitudinal Strain
GRS	Global Radial Strain
GCS	Global Circumferential Strain
MyoRot	Myocardial Rotation
Delta-ROT	Delta Rotation, difference between basal and apical rotation
Pk%	Peak strain value as a percentage
S-Pk	Strain value at ES as a percentage
TTP ms	Time to peak in milliseconds
LAS_R	Left Atrium Reservoir strain
LAS_CD	Left Atrium Conduit strain
LAS_CT	Left Atrium Contractile strain

9.8.2 Velocity Parameters

Pk	Peak velocity
S-Pk	Velocity at ES
TTP ms	Time to the peak velocity in milliseconds

9.8.3 Displacement Parameters

Pk	Maximum displacement
S-Pk	Displacement at ES
TTP ms	Time to the maximum displacement in milliseconds

9.8.4 Strain Rate Parameters

Pk 1/s	Strain rate peak in 1/s

S-Pk	Strain rate at ES in 1/s
TTP ms	Time to the strain rate peak in milliseconds

9.8.5 General Parameters

ED	End diastolic phase
ES	End systolic phase
EDA	ED Area
ESA	ES Area
FAC	Fraction Area Change
EDV	ED Volume
ESV	ES Volume
EF	Ejection Fraction
TTP	Time to Peak
Max Wall Delay	Difference between lowest and highest TTP

9.9 Accuracy of Measurements

Analysis on long axis data

		Unit	Expected accuracy	Precision QStrain	Precision Medis Suite report	Accuracy source
EDV	ED Volume	ml	2 %	0.01	0.1	AMID Accuracy document
ESV	ES Volume	ml	3 %	0.01	0.1	AMID Accuracy document
EF	Ejection Fraction	%	2	0.01	0.1	From EDV/ESV volume accuracy
EndoGLS	Global Longitudinal Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
EndoGCS	Global Circumferential Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
MyoGLS	Global Longitudinal Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
MyoGCS	Global Circumferential Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
GRS	Global Radial Strain	%	± 4.5	0.01	0.1	AMID Accuracy document
SD-TS-Peak	SD Transversal Strain Peak	%	± 1.5	0.1	0.1	Based on Strain accuracy
SD-LS-Peak	SD Longitudinal Strain Peak	%	± 1.5	0.1	0.1	Based on Strain accuracy
SD-TS-Syst	SD Transversal Strain End Systoly	%	± 1.5	0.1	0.1	Based on Strain accuracy
SD-LS-Syst	SD Longitudinal Strain End Systoly	%	± 1.5	0.1	0.1	Based on Strain accuracy

Analysis on short axis data

		Unit	Expected accuracy	Precision QStrain	Precision Medis Suite report	Accuracy source
EDA	ED Area	cm^2	1.5 %	0.01	0.1	AMID Accuracy document
ESA	ES Area	cm^2	4 %	0.01	0.1	AMID Accuracy document
FAC	Fraction Area Change	%	1	0.01	0.1	From EDA/ESA area accuracy
MyoGCS	Global Circumferential Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
EndoGCS	Global Circumferential Strain	%	± 1.5	0.01	0.1	AMID Accuracy document
GRS	Global Rotational Strain	%	± 4.5	0.01	0.1	AMID Accuracy document
Delta-rot	Delta Rotation	°	1°	0.01	0.1	AMID Accuracy document

SD-RS-Peak	SD Rotational Strain Peak	%	± 4.5	0.1	0.1	Based on Strain accuracy
SD-CS-Peak	SD Circumferential Strain Peak	%	± 1.5	0.1	0.1	Based on Strain accuracy
SD-RS-Syst	SD Rotational Strain End Systoly	%	± 4.5	0.1	0.1	Based on Strain accuracy
SD-CS-Syst	SD Circumferential Strain End Systoly	%	± 1.5	0.1	0.1	Based on Strain accuracy

If the expected accuracy is a percentage, it is relative to the value. If no percentage is mentioned, it is an absolute error. In case the unit is %, interpret the error as percent-point.

9.10 Main Cardiac Mechanics Variables Derived from Tracking Technology

For further reading, see the following articles:

Tissue Tracking Technology for Assessing Cardiac Mechanics
Piet Claus, PHD, Alaa Mabrouk Salem Omar, MD, PHD, Gianni Pedrizzetti, PHD, Partho P. Sengupta, MD, DM, Eike Nagel, MD, PHD

Table 2 Main Cardiac Mechanics Variables Derived From Tracking Technology

Main Cardiac Mechanics Variables Derived From Tracking Technology

	Definition	Parameters
Displacement, cm	Distance between instantaneous and initial (often end-diastolic) position of a myocardial segment	Longitudinal displacement Radial displacement Circumferential displacement
Velocity, cm/s	Velocity of displacement (displacement/time) accuracy is highly frame-rate dependent	Longitudinal velocity Radial velocity Circumferential velocity
Strain, %	Change in length of an object within a certain direction relative to its initial (often enddiastolic) length	Global/segmental longitudinal strain (GLS/LS) Global/segmental radial strain (GRS/RS) Global/segmental circumferential strain (GCS/CS)
Strain rate, 1/s	The speed of deformation accuracy is highly frame-rate dependent	Peak systolic global longitudinal strain rate (GLSR-S) Early diastolic global longitudinal strain rate (GLSR-E) Late diastolic global longitudinal strain rate (GLSR-A) Peak systolic global radial strain rate (GRSR-S) Early diastolic global radial strain rate (GRSR-E) Late diastolic global radial strain rate (GRSR-A) Peak systolic global circumferential strain rate (GCSR-S) Early diastolic global circumferential strain rate (GCSR-E) Late diastolic global circumferential strain rate (GCSR-A)
Rotation	Results from shortening and lengthening of helically oriented myocardial fibers causing counterclockwise rotation of the apex and clockwise rotation of the base as viewed from the apex	Peak systolic apical rotation (apical-R) Peak systolic basal rotation (basal-R) LV twist (LVT) LV torsion (LV-tor) Percentage of LV untwist at mitral valve opening (%LV-UT-MVO) LV untwist rate (LV-UTR) Time to peak untwist (TTP-UT)
LV ¼ left ventricular		

9.11 Inward Displacement standard values

For further reading, see the following articles:

Reference values for inward displacement in the normal left ventricle: a novel method of regional left ventricular function assessment. Hegeman RR, McManus S, Tóth A, Ladeiras-Lopes R, Kitslaar P, Bui V, Dukker K, Harb SC, Swaans MJ, Ben-Yehuda O, Klein P, Puri R. *J Cardiovasc Dev Dis.* 2023;10(12):474. doi: 10.3390/jcdd10120474.

Table 3 Segmental inward displacement standard values

Segment	Region	Mean (%)
Segment 1	Basal anterior	35.6
Segment 2	Basal anteroseptal	28.0
Segment 3	Basal inferoseptal	28.0
Segment 4	Basal inferior	36.4
Segment 5	Basal inferolateral	33.1
Segment 6	Basal anterolateral	35.9
Segment 7	Mid-anterior	38.1
Segment 8	Mid-anteroseptal	34.7
Segment 9	Mid-inferoseptal	32.8
Segment 10	Mid-inferior	48.4
Segment 11	Mid-inferolateral	36.5
Segment 12	Mid-anterolateral	38.3
Segment 13	Apical anterior	29.9
Segment 14	Apical septal	28.8
Segment 15	Apical inferior	30.5
Segment 16	Apical lateral	32.6
Segment 17	Apex	21.0

10 T1/ECV Mapping

The ECV module has not been cleared for clinical use in Europe and Japan.

10.1 Quick Start

The T1/ECV module provides a fully automated workflow for image processing of short-axis T1 data acquired with inversion recovery-based sequences. This includes co-registration, motion correction, contour delineation, reference point placement and results calculation. All intermediate steps can be reviewed and manually adjusted when necessary.

Input requirements

- **T1 analysis:** Pre-contrast T1 data (raw series and/or pre-generated maps) only
- **ECV analysis:** Pre-contrast T1 data and post-contrast T1 data (raw series and/or pre-generated maps)

Workflow steps

1. **Start the application**
   Launch the T1/ECV module via one of the following methods:
   a. Start an automated workflow from the Medis Suite Browser by selecting “Launch Analysis” or “ECV Analysis”.
   b. Select the T1 or ECV icon in the Medis Suite toolbar and drag the required series into the application.
   c. Select the required series in the Medis Suite Series Browser, right-click the selection, and select the T1 or ECV option.
2. **Verify co-registration and motion correction**
   For ECV analysis, verify the co-registration of the pre-contrast and post-contrast datasets and adjust the alignment where necessary. For ECV and T1 analysis, verify the motion correction within a T1 series and correct where necessary.
3. **Verify the contours and reference point**
   Review the automatically generated epicardial, endocardial, and blood pool contours (only displayed in ECV analysis), as well as the reference point, in each slice. Correct when needed.
4. **Verify or enter the hematocrit value**
   A hematocrit value is required to calculate ECV. Confirm the synthetic hematocrit value or enter an obtained hematocrit value.
5. **Add ROIs (optional)**
   Add Regions of Interest (ROIs) when region-specific analysis is required.
6. **Review the results**
   Assess the generated T1 and ECV results, including:
   a. Global myocardial values
   b. ROI-based values
   c. Bullseye plots
   d. Relaxation curves
7. **Reporting**
   Global and ROI-based T1 and ECV results are automatically added to the Medis Suite Report. Snapshots can be manually included.

Detailed information for each step is provided in the following sections.

10.2Application Overview

10.2.1 Workspace Overview

ECV Workspace

The main ECV workspace contains multiple viewports for displaying and comparing pre-contrast, post-contrast, and ECV image series and maps, allowing side-by-side visualization and interaction. Image navigation and contour editing is allowed on each viewport. A separate visualization area displays derived results, such as bullseye plots or relaxation curves. The results panel on the right side of the workspace displays global myocardial T1 and ECV values, and a table of defined ROIs. In the field above the results panel, the hematocrit value required for ECV calculation, can be reviewed and modified. Several toolbars are available for accessing key functions. General image control is available in the viewport directly. The bottom right has options to take snapshots and go the the configuration page. Contour and image controls can be found between the pre- and post-contrast viewport. Figure 10-1 provides an overview of the workspace.

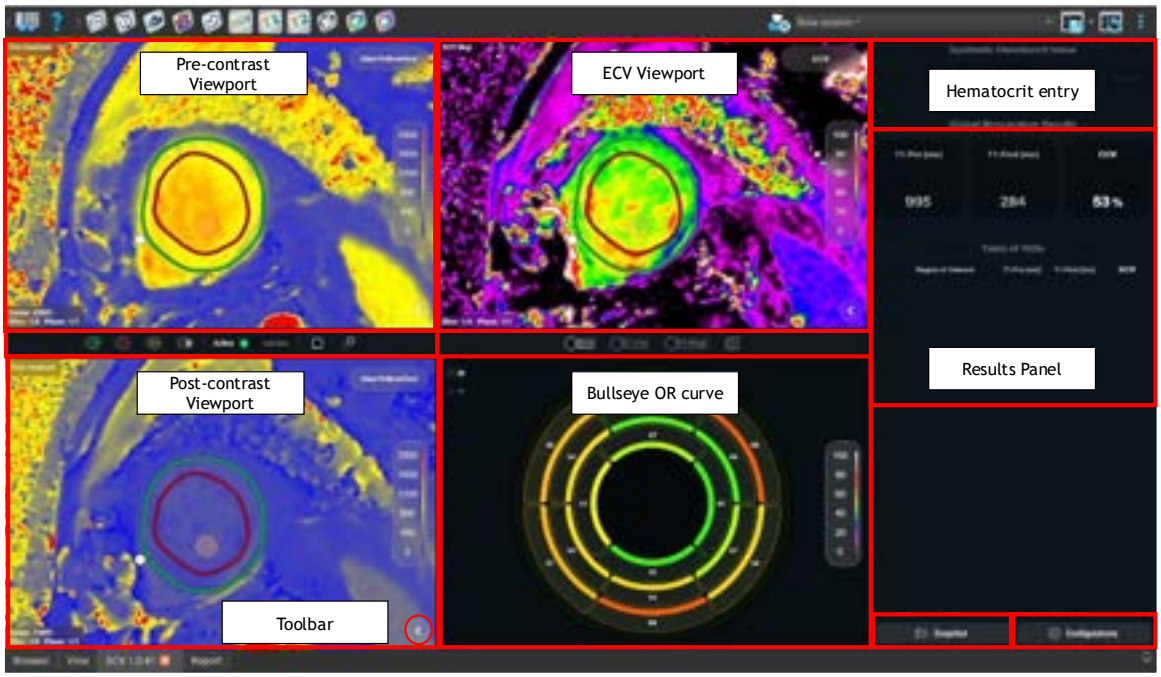


Figure 10-1 ECV Workspace

T1 workspace

The main T1 workspace contains one viewport for displaying pre-contrast T1 images and maps. Image navigation and contour editing is allowed on the viewport. A separate visualization area displays derived results, such as bullseye plots and relaxation curves. The results panel on the right side of the workspace displays the global myocardial T1 value, and a table of defined ROIs. Several toolbars are available for accessing key functions. General image control is available in the viewport directly. The bottom right has options to take snapshots and go the the configuration page. Contour and image controls can be found between the pre- and post-contrast viewport. Figure 10-2 provides an overview of the workspace.

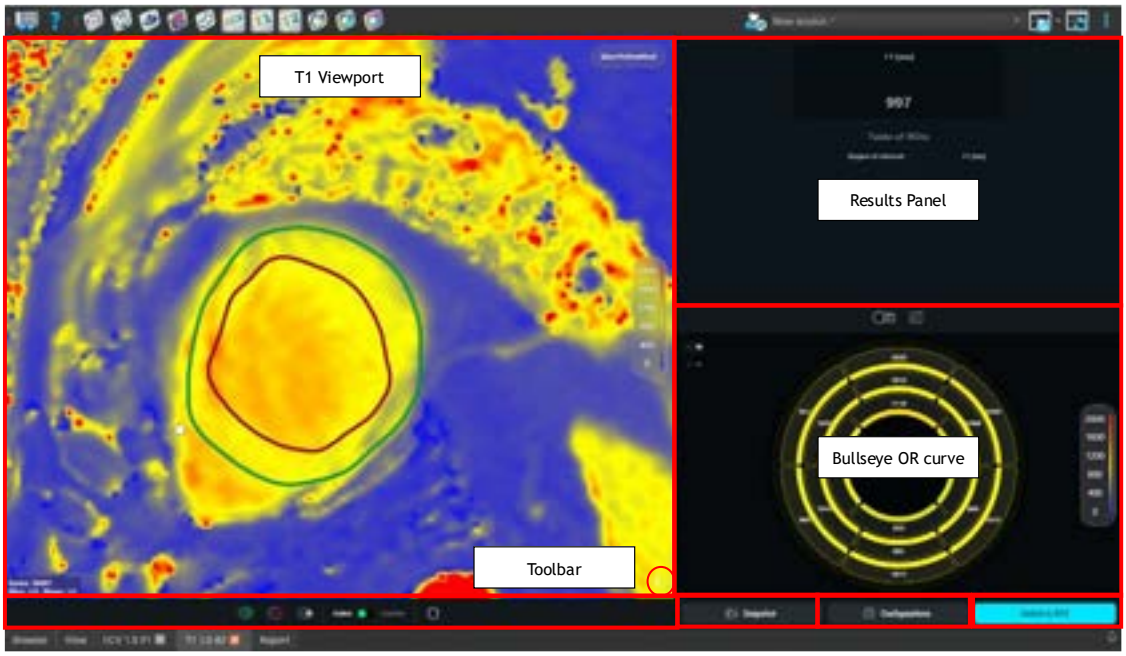


Figure 10-2 T1 Workspace

10.2.2 Toolbars

The table below summarizes the available icons and their functions. The icons are grouped into three categories: contour and image controls, bullseye and curve controls, and general image controls.

Icon	Function
Contour and Image controls	
	Add epicardial contour
	Add endocardial contour
	Add blood pool contour*
	Add ROI
	Co-registration of a slice*
	Motion correction of single image
	Active/Inactive toggle

Icon	Function
Bullseye curve controls	
	Show ECV bullseye*
	Show pre-contrast T1 bullseye
	Show post-contrast T1 bullseye*
	Show T1 bullseye
	Show relaxation curves
	Show two-dimensional bullseye
	Show three-dimensional bullseye
General image controls	
	Stack through images
	Pan images
	Zoom
	Adjust window and level
	Hide contours, hold mouse to activate function
	Reset view
	Zoom to contours

*These icons/functions are only available in ECV analysis and not for T1 analysis

10.2.3 Mouse Controls

The T1/ECV module supports the following mouse controls:

- **Stack through slices:** Hold the left mouse button and move the mouse up or down to navigate through the slices in a series.
- **Scroll through source images:** When raw images are displayed, hold the left mouse button and move the mouse left or right or use the mouse when to navigate through the source images.
- **Zoom:** Hold the Ctrl key and use the mouse wheel.
- **Pan:** Hold the middle mouse button and move the mouse.

- **Window and level:** Hold the right mouse button and move the mouse to adjust image contrast and brightness.

10.3T1 and ECV Workflow

The Quick Start section provides a high-level overview of the workflow. The following sections describe each step of the workflow and in more detail.

10.3.1 Starting the Application

The T1/ECV workflow can be started in three different ways. Below, a detailed description of each procedure is provided.

Automated Workflow

T1 and ECV analyses can be started directly from the Medis Suite Browser. Buttons in the center of the Browser provide access to predefined analysis workflow.

To start an analysis click 

to start a T1 workflow (when only pre-contrast T1 data is available) or an ECV workflow (when both pre- and post-contrast T1 data is available).

The software automatically identifies the appropriate pre-contrast T1 dataset and, for ECV Analysis, the appropriate post-contrast T1 dataset. The selected data are then opened in the T1/ECV module.

If an incorrect series is selected, replace it by dragging the required series from the Medis Suite Series Browser into the T1/ECV module.

For ECV analysis, the software uses timing information to distinguish between pre-contrast and post-contrast datasets.

Manual Workflow

T1 and ECV analyses can also be initiated manually after loading a patient in Medis Suite.

Using the T1/ECV Application Icon

- Select the T1 application icon  or the ECV application  (or  when an ECV license is installed) in the Medis Suite toolbar.
- Follow the instructions displayed on the start screen:
    - Drag a single pre-contrast series from the Series Browser into the application to start a T1 analysis.
    - Drag both a pre-contrast and a post-contrast series into the application to start an ECV analysis.

To select multiple series, hold the Ctrl key while selecting them. The software uses timing information to distinguish between pre-contrast and post-contrast datasets.

Using the Series Browser

- Select a single pre-contrast series to start a T1 analysis.

Or:

- Select both a pre-contrast and a post-contrast series to start an ECV analysis.
- To select multiple series, hold the Ctrl key while selecting them.
- Right-click the selected series and choose the T1 application icon or the ECV application icon (or when an ECV license is installed).
- The software uses timing information to distinguish between pre-contrast and post-contrast datasets.

Both original T1 series and pre-generated T1 maps are supported and can be used as input.

10.3.2 Motion Correction and Co-registration

Motion Correction

Motion correction aligns the images acquired at different inversion times within a T1 image series. Correct alignment is important for accurate T1 fitting.

Motion correction can only be applied to source images of the raw image series. When pre-generated T1 maps are used no additional motion correction is required.

When original T1 image series are used, verify the alignment of the source images before proceeding with the analysis.

Automatic Motion Correction

Automatic Motion Correction can be applied as a preprocessing step.

To perform automatic motion correction from Medis Suite:

- Select the pre-contrast and/or post-contrast T1 image series in the Medis Suite Series Browser.
- Right-click the selected series.
- Select one of the following options:
  - “AutoQ > QMass - T1 Motion Correction”: Applies motion correction without calculating a T1 map.
  - “AutoQ > QMass - T1 MOCO Map”: Applies motion correction and calculates a T1 map.

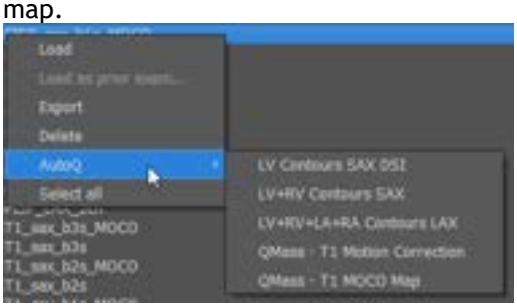


Figure 10-3 AutoQ Motion Correction

- Monitor the processing status via the Status button in Medis Suite.

After processing is complete, new motion-corrected series are generated and can be used for further analysis.

When both pre-contrast and post-contrast T1 image series are selected, the generated datasets are also co-registered.

Manual Motion Correction

The T1/ECV application supports manual motion correction and manual adjustment of images.

To adjust motion correction manually:

- Inspect the source image to determine whether motion correction is required. Raw images can be selected from the drop-down menu in the upper-right corner of the viewport. Use the scroll wheel to navigate through the different images.

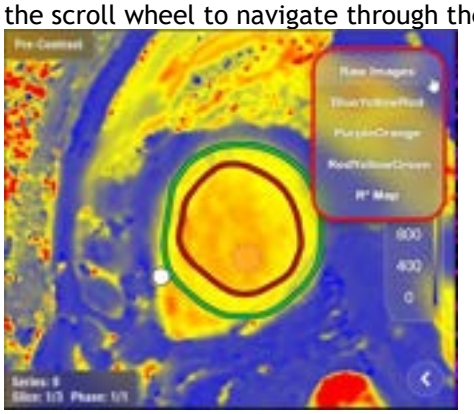


Figure 10-4 Drop down menu to set display

- Select the motion correction tool: 
- In the active viewport, hold the left mouse button and move the image to the required position.
- Repeat these steps for each image that requires adjustment.

Co-registration

Co-registration aligns the pre-contrast and post-contrast datasets used for ECV calculation. Correct alignment is important because ECV values are calculated from corresponding locations in the two datasets.

Co-registration is required for ECV analysis but is not required for T1-only analysis.

It is recommended to verify the alignment before reviewing the ECV results.

Automatic Co-registration

Automatic co-registration can be enabled or disabled in the application settings. Refer to the Application Configurations section for more information.

When automatic co-registration is enabled, the application aligns the pre-contrast and post-contrast datasets when they are loaded.

Manual Co-registration

The ECV application supports manual co-registration and manual adjustment of automatically aligned datasets.

To perform manual co-registration:

- Inspect the pre-contrast and post-contrast datasets to see whether co-registration is required.
- Select the co-registration tool: 
- In the active viewport, hold the left mouse button and move the image to reposition until the datasets are correctly aligned.

When image series are used, manual co-registration adjustments are applied at the slice level. The adjustment does not need to be repeated for every individual image in the slice.

10.3.3 Contour Manipulation

Accurate delineation of the myocardial borders is required for reliable calculation of T1 and ECV values.

The application automatically generates epicardial, endocardial, and blood pool contours (only in ECV analysis). These contours can be reviewed, edited, deleted, or recreated.

A reference point is also placed automatically for bullseye generation. The reference point can be repositioned to ensure correct anatomical orientation.

Editing Contours

The application supports two contour-editing methods. The mode is determined automatically from the mouse interaction:

- **Point-clicking mode:** Click the left mouse button to place individual points along the contour. Double-click to complete the contour.
- **Tracing mode:** Hold the left mouse button and move the mouse along the desired boundary. Release the mouse button to complete the contour.

Deleting a Contour

To delete a contour:

- Move the pointer over the contour.
- Right-click the contour.
- Select **Delete.**

Creating a Contour

To create a contour:

- Confirm that a contour of the same type is not already present. Delete the existing contour when necessary.
- Select the appropriate add-contour button: 
- Draw the contour using the point-clicking or tracing (see section Contour editing)

Adjusting the Reference Point

The reference point is placed automatically at the anterior right ventricular insertion point, where the right ventricle meets the anterior wall of the left ventricle.

In a basal short-axis slice, this position corresponds to the boundary between AHA segment 1, basal anterior, and segment 2, basal anteroseptal.

Correct placement of the reference point is required for accurate reconstruction of the bullseye plot.

To reposition the reference point:

- Select the reference point in the viewport.
- Hold the left mouse button.
- Drag the point to the correct anatomical location.

10.3.4 Regions of Interest

Regions of Interest (ROIs) can be defined to calculate T1 and ECV values for specific regions.

Creating an ROI

To create an ROI:

- Select Add ROI: 
- Draw the ROI in an active viewport using one of the following methods:
    - **Point-clicking method:** Place individual points and double-click to complete the ROI.
    - **Tracing method:** Hold the left mouse button and trace the ROI.
    - **Clipped ROI shortcut**: Click once within the myocardium followed by a double-click at a second location within the myocardium. A clipped ROI that encompasses the area between the first and second point is generated.

After the ROI is created, it is added to the analysis. The corresponding results are displayed in the Table of ROIs on the right side of the workspace.

Managing ROIs

To delete an ROI:

- Right-click the ROI in the viewport and select **Delete.**
  Or:
- Select the delete option for the ROI in the Table of ROIs: 

To rename an ROI:

- Select the ROI name in the Table of ROIs
- Enter the new name.
- Press Enter.

To navigate to an ROI:

- Select the ROI in the Table of ROIs. The corresponding slice is automatically displayed in the viewport.

10.3.5 Switch from T1 Analysis to ECV Analysis

A T1 analysis can be extended to an ECV analysis without repeating already performed workflow steps.

To switch to ECV Analysis:

- While in the T1 application, select the ECV function using the following button: 

.
- The currently loaded T1 dataset is retained as the pre-contrast dataset.
- Drag the corresponding post-contrast dataset into the application.

10.3.6 Hematocrit value

A hematocrit value is required to calculate ECV. The value can be calculated synthetically from the image data or entered manually when a measured hematocrit value is available.

Hematocrit is not required for T1-only analysis.

Synthetic Hematocrit

When using a synthetic hematocrit value:

- Verify that the blood pool contours are correctly delineated.
- Verify that the selected synthetic hematocrit formula is appropriate for the dataset.

The selected formula is shown in the application settings and documented in the Medis Suite Report. Refer to the Application Configuration section for more information.

Entering a Measured Hematocrit Value

To enter a measured hematocrit value:

- Click on the displayed hematocrit value.
- Type the measured value.
- Press Enter or select **Confirm**.

To restore the synthetic hematocrit value, select **Reset**.

Hematocrit values can be entered with a maximum of one decimal place.

10.4 Results

The application provides quantitative and visual results in the following formats:

- Color-coded maps
- Global myocardial values
- ROI-based values
- Bullseye plots
- Relaxation curves

Maps

Depending on the input data, the application generates color-coded maps that are displayed in the viewports.

The colormap and its lower and upper display limits can be configured by the user. Refer to the Application Configuration section for more information.

Each pixel value is represented by a color. The relationship between colors and values is shown in the color bar on the right side of the active viewport.

The visualization of images and maps can be adjusted in the viewport:

- Open the drop-down menu in the upper-right corner of the viewport.
- Select one of the following options:
    - **Raw Images**: Displays the original input images. If pre-generated maps are loaded, this is displayed in grayscale.
    - **Color Map**: Displays the color-coded map. The option name identifies the selected colormap.
    - **R^2 Map**: Displays the coefficient of determination as a measure of T1 fitting quality. This option is available only when original T1 image series are used as input (not for pre-generated maps).

Global Values

Global myocardial values are displayed on the right side of the application.

For ECV analysis, the application displays:

- Pre-contrast T1
- Post-contrast T1
- ECV

For T1-only analysis, only T1 values are displayed.

Global values are calculated from the pixel maps and myocardial contours of all included slices.

Individual slices can be included in or excluded from the global value calculations using the slice toggle: 

When a slice is excluded:

- The slice is not included in the global value calculations.
- Interaction with the slice is disabled.

When the slice is included again:

- The slice is included in the global value calculations.
- Interaction with the slice is restored.

Global myocardial values are automatically added to the Medis Suite Report.

Table of ROIs

ROI-based results are displayed in the Table of ROIs on the right side of the application.

For ECV analysis, the table displays:

- Pre-contrast T1
- Post-contrast T1
- ECV

For T1-only analysis, only pre-contrast T1 values are displayed.

The values are calculated from the pixel maps and the defined ROI contours.

ROI can be deleted, renamed, and used to navigate to the corresponding slice directly from the table. Refer to the Regions of Interest section for more information.

ROI-based results are automatically added to the Medis Suite Report.

Bullseye Plot

The application generates bullseye plots to display segmental myocardial results. The plots use the standardized 16-segment AHA model and presents regional values for each segment of the myocardium.

Use the bullseye controls  to display:

- ECV values
- Pre-contrast T1 values
- Post-contrast T1 values

For T1-only analysis, only the pre-contrast T1 bullseye is available.

The bullseye values are calculated from the pixel maps and contours of all included slices.

When the pointer is moved over a segment:

- The segment is highlighted.
- The corresponding value is displayed.
- The segment name, according to the AHA nomenclature, is displayed.

Figure 10-5 Bullseye segment display

The bullseye is displayed as a two-dimensional plot by default. Select the 2D bullseye control to return to this view: 

.

A three-dimensional representation is also available. This view displays the segments according to their anatomical position in the heart.

The right ventricular insertion point is shown to preserve the correct orientation and support consistent segment identification. Select the 3D bullseye control to display this view: 

.

Individual segments can be included in or excluded from the global myocardial calculation by interacting with the bullseye plot.

To exclude a segment:

- Select the segment in the bullseye plot.
- The excluded segment is displayed in gray and removed from the global calculation.

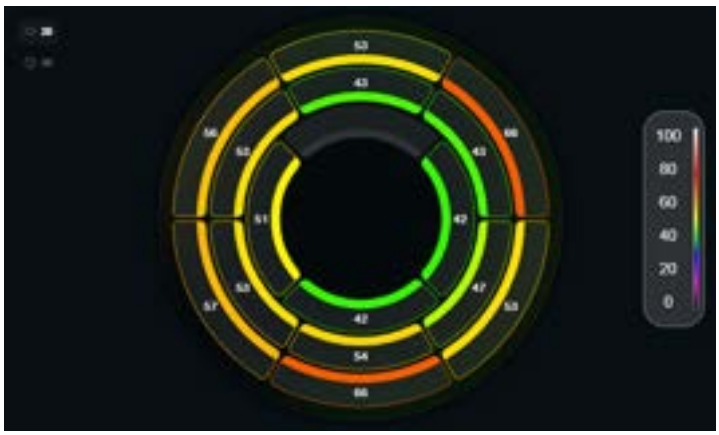


Figure 10-6 Bullseye segment exclusion

Select the segment again to include it

When fewer than three slices are available, the bullseye plot is only partially populated. Segments without corresponding image data are displayed in gray and marked with a "-" (hyphen).

Relaxation Curves

T1 relaxation curves are available when original T1 image series are used as input. Relaxation curves are not available when pre-generated T1 maps are used.

Select the relaxation-curve control to display the curves: 
.

By default, the application displays curves for:

- Myocardium
- Blood pool

Pre-contrast curves are displayed as hollow lines. Post-contrast curves are displayed as solid lines.

Myocardial curves are displayed in blue, and blood pool curves in orange. For T1-only analysis, only pre-contrast curves are available.

When ROIs are defined, corresponding labeled ROI curves can also be displayed.

The following interactions are available:

Showing or Hiding Curves

Use the controls at the bottom of the curve display to show or hide individual curves:

Inspecting Data Points

The measured data points used for curve fitting are displayed as circular markers.

To inspect a data point:

- Move the pointer over the curve to highlight a data point.
- Select the data point.
- The corresponding source image is displayed in the viewport in raw-image mode

This allows the source image associated with each data point to be reviewed directly.

10.5 Application Configuration

Application settings can be accessed using the configuration button: 

After changing the settings:

- Select Save: 

.
- Return to the analysis workspace: 

.

All settings are user-specific and are saved for the current user account

Default Data Type

This setting determines which type of input data is loaded by default when the application starts.

- **Raw Images**: Original T1 image series are loaded by default.
- **Scanned Maps**: Pre-generated T1 maps are loaded by default

Correction Factor

A correction factor can be applied to specific supported Siemens sequences to adjust the calculated values.

The correction factor should be used only for input data to which the configured correction is applicable.

Offset Endocardial and Epicardial Border

Offsets can be applied to the endocardial and epicardial borders to reduce partial-volume effects. These offsets help prevent blood, fat, or other non-myocardial tissue from being included in the myocardial analysis.

The offset is specified as a percentage and reduces the evaluated myocardial region relative to the drawn contours.

Use slider controls to configure the endocardial and epicardial offsets. The selected percentages are displayed in the user interface.

Synthetic Hematocrit Formula

Synthetic hematocrit is estimated from the mean native blood-pool T1 using the selected published regression formula:

Synthetic hematocrit (%) = 100 × (slope / T1blood − intercept)

where **T1blood** is the mean native blood-pool T1 in milliseconds. The calculated value is limited to the range 0% to 100%.

Select one of the following formulas.

Formula	Intended acquisition	Implemented formula
Unspecified	No synthetic hematocrit calculation	A measured hematocrit value must be entered manually.
Treibel 2016, MOLLI	1.5 T Siemens MOLLI	Hct (%) = 100 × (866.0 / T1blood − 0.1232)
Treibel 2016, ShMOLLI	1.5 T Siemens ShMOLLI	Hct (%) = 100 × (727.1 / T1blood − 0.0675)
Fent 2017, 1.5 T MOLLI	1.5 T Philips MOLLI	Hct (%) = 100 × (922.6 / T1blood − 0.1668)
Fent 2017, 3 T MOLLI	3 T Philips MOLLI	Hct (%) = 100 × (869.7 / T1blood − 0.0710)
Ambale-Venkatesh 2019	1.5 T Siemens or GE MOLLI	Hct (%) = 100 × (726.19 / T1blood − 0.0700)
Chen 2022, 3 T, male	3 T Philips MOLLI, male	Hct (%) = 100 × (1763.0 / T1blood − 0.5248)
Chen 2022, 3 T, female	3 T Philips MOLLI, female	Hct (%) = 100 × (1740.0 / T1blood − 0.5233)
Chen 2022, 1.5 T, male	1.5 T Philips MOLLI, male	Hct (%) = 100 × (1319.0 / T1blood − 0.4318)
Chen 2022, 1.5 T, female	1.5 T Philips MOLLI, female	Hct (%) = 100 × (1048.0 / T1blood − 0.2630)

References

- Treibel TA, et al. Automatic measurement of the myocardial interstitium: synthetic extracellular volume quantification without hematocrit sampling. *JACC: Cardiovascular Imaging*. 2016;9(1):54–63.

- Fent GJ, et al. Synthetic myocardial extracellular volume fraction. *JACC: Cardiovascular Imaging*. 2017;10(11):1402–1404.

- Ambale-Venkatesh B, et al. Association of myocardial fibrosis and cardiovascular events: the Multi-Ethnic Study of Atherosclerosis. *European Heart Journal – Cardiovascular Imaging*. 2019;20(2):168–176.

- Chen W, et al. Synthetic extracellular volume in cardiac magnetic resonance without blood sampling: a reliable tool to replace conventional extracellular volume. *Circulation: Cardiovascular Imaging*. 2022;15(4):e013745.

Contour Synchronization

By default, contours are synchronized between the pre-contrast, post-contrast, and ECV viewports. Changes made to a contour are propagated to the corresponding datasets.

Disable contour synchronization when contours must be edited independently.

Automatic Co-Registration

Automatic co-registration is enabled by default.

When enabled, the application automatically aligns pre-contrast and post-contrast datasets when they are loaded.

Disable this setting when alignment must be performed manually.

Colormap Settings

Colormap settings determine which colormaps are available in each viewport and define their display ranges.

To configure the colormaps:

- Select the viewport to configure: 

- Review the active colormap shown at the top of the settings panel. The active colormap is highlighted with a blue border and cannot be disabled.
- Enable or disable additional colormaps using the corresponding controls: 
- Configure the lower and upper limits for each enabled colormap by:
    - Selecting a limit, entering the required value, and pressing Enter.
      or
    - Using the arrow controls  to adjust the value incrementally.

A maximum of seven colormaps can be enabled for each viewport.

Each viewport can be configured independently, including the available colormaps and their display limits.

When the application starts, it uses the colormap most recently selected by the user.