QMass® 7.6

User Manual

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Regulatory Information

Intended Use

QMass has been developed for the objective and reproducible analysis of LV and RV function based on cardiac MR and reformatted CT data sets. The software enables the display of images for use by trained medical personnel.

The intended purposes are:

- Supporting clinical diagnoses on the status of the global and regional function and anatomy of the cardiac chambers.
- Supporting the subsequent clinical decision making processes.

WARNINGS

QMass 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 QMass should not be used for purposes other than those indicated in the section Intended Use.

Users must make sure to read this manual to become familiar with the software and be able to obtain reliable analysis results.

European Regulations

CE 0120	QMass 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.

North American Regulations

QMass 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, with the exception of the first-pass perfusion analysis, late-enhancement analysis and T1 mapping modules, as the use of contrast agents for cardiac MR procedures is not FDA-approved. The first-pass perfusion analysis, late-enhancement and T1 mapping analysis modules are available in the United States for scientific research purposes only.

QMass complies with the requirements of the Canadian Medical Devices Regulations and has been licensed 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 left mouse button. If you are left-handed, you may have set the right mouse button as your primary mouse button.
Double-click	Press and release the left mouse button rapidly twice. If you are left-handed, you may have set the right mouse button as your primary mouse button.
Right-click	Press and release the right 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.

Keyboard

SHIFT+click	Press and hold down the SHIFT 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. You can find an overview of keyboard shortcuts in Chapter 20.

Typographical Conventions

On the **Display** tab, under **Display Settings**, 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.
Contours can be saved in a `.CON` file.	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 QMass®

QMass is the Medis software solution for the quantitative analysis of cardiac MRI and 'CT reformatted' studies. QMass features:

- ventricular function analysis (MRI and 'CT reformatted studies')
- scar tissue analysis (referred to as Delayed Signal Intensity or DSI analysis)
- edema tissue analysis
- area at risk analysis (referred to as AAR or Area at Risk analysis)
- 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 and T2* analysis
- left ventricular diameter analysis (referred to as LV Diameter analysis)

The software provides guided workflows for ventricular function analysis, LV diameter analysis, scar tissue analysis, T1, T2 and T2* analysis, T2 weighted based edema analysis and area at risk analysis so that you can perform these quantitative analyses quickly and accurately.

QMass provides 2D and 3D representations of the analysis results. Reports can be complemented with your visual scoring of a study and with your own observations.

QMass also provides support for functional analysis of CT reformatted data.

All in all, QMass helps you get more out of cardiac MR and CT reformatted studies, while providing support for an efficient workflow that is geared toward your needs.

2 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 in 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 **Help > About** in the menu bar.

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3 Starting QMass and Opening Studies

This chapter explains how to:

- start QMass
- open studies from a location on your system or network
- load contour files

3.1 Starting QMass

QMass must be installed and licensing must be enabled before you can start working with it.

For instructions on installing QMass and on enabling the license mechanism, refer to the QMass Installation Manual.

To start QMass

- Double-click the QMass icon on your desktop.

Or,

- Select **Start > (All) Programs > Medis QMass > QMass 7.6**.

3.2 Opening Series from System or Network

In QMass, you now select the series that you want to view and analyze.

To open a series from your system or network

1. Click  , press CTRL+O or select **File > Open Study…** from the menu bar.

   In the dialog window, browse the directory structure and select the directory in which the series you want to analyze are located.

2. In the top right pane of the dialog window, select the series and then click **OK**, or double-click the series.

   You can also select a number of series. To select consecutive series, press and hold down the SHIFT key, select the first series, and then select the last series. To select non-

consecutive series, press and hold down the CTRL key, and then select the various series. Click **OK** to open the selected series.

If the series are located in different subdirectories, select the top directory in the browser, select the **Recursive** option in the top right corner, and then click **Rescan**. This displays all series from all subdirectories in the top right pane.

If you want to load a number of series in a specific order, create a loading list. In the upper pane, select the series you want to load first, and click **Add to Loading List**. This adds the series to the lower pane. Repeat this for every series you want to load, then click **OK**.

3. Click **OK**.

When you are opening stress level series, make sure to select the **Comparison mode** check box when the Comparison Selection dialog window opens, and then click **Load**.

Make sure to leave the **Comparison mode** check box **unselected** when you are opening series that do **not** make up a stress level study.

In functional short axis, QMass requires parallel-scanned short-axis data.

3.3 Loading Contour Files

Contours are the basis for calculations in QMass. They are created automatically or manually when you perform an analysis. Contours are saved in contour files.

The contour file is loaded automatically with the associated series if the contour file was saved in the default contour directory with the file name proposed by QMass. Otherwise, you must load the contour file manually.

You can enable or disable automatic loading of contour files by editing the configuration settings. For instructions, refer to the QMass Reference Manual.

To change the default contour directory, select **Tools > Options…**, and then select a new directory on the **General** tab, under **Folders**, behind **Contour Folder**.

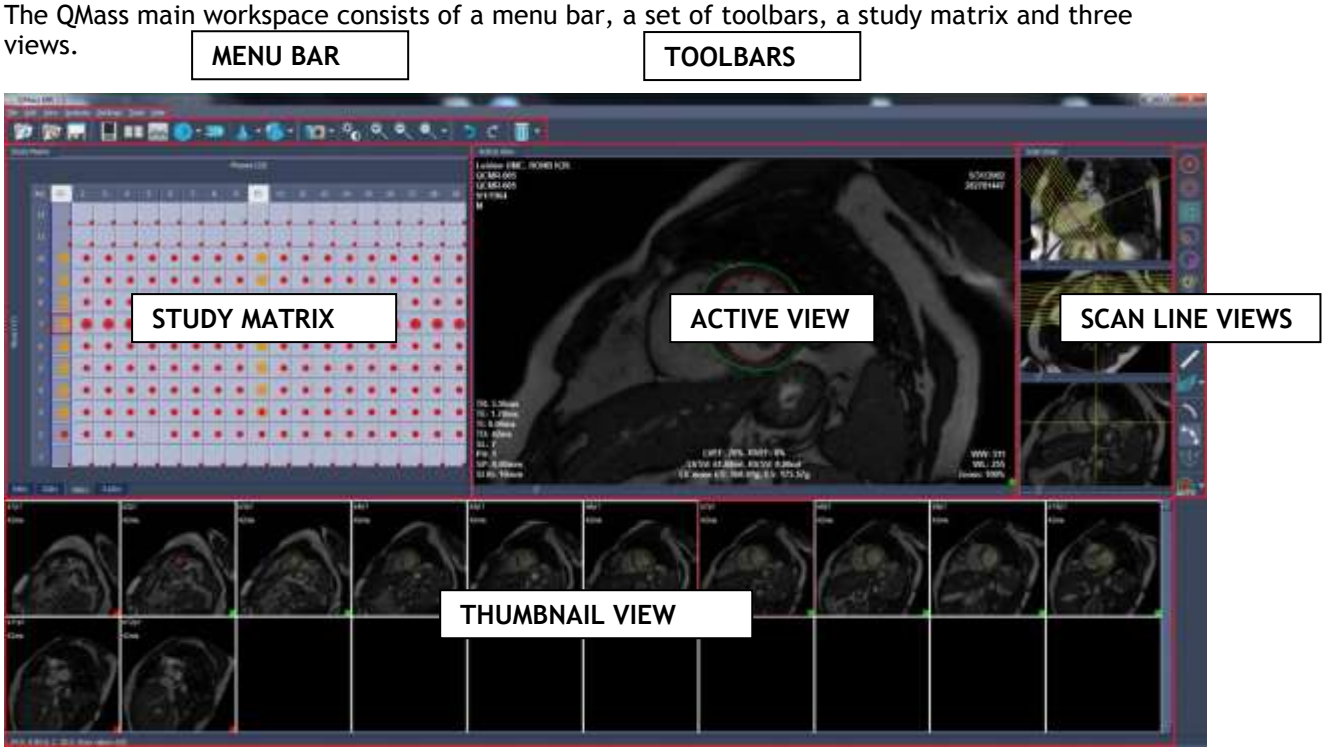
Integrated versions of the application, can select “Findings” by clicking the button. 

To load a contour file

1. If the series is not opened yet, follow the instructions in section 3.2.
2. Click  or select **File > Load…**
3. In the Open Files dialog window, select the directory in which the contour file is saved.
4. Double-click the contour file, or select the contour file and click **Open**.

4 The QMass Workspace

The QMass main workspace consists of a menu bar, a set of toolbars, a study matrix and three views.



4.1 The Toolbars

Tool Icons	Use To
File Toolbar	
	open a series.
	load a set of contours.
	save a set of contours.

	show findings dialog.
View Toolbar	
	open the reporting window.
	show the selected slice or phase as a movie.
	show analysis results in a graph.
	show analysis results in a bull's-eye diagram. Click the arrow next to this icon to select the type of representation.
	show a 3D representation of the contours.
	take a snapshot of the Active View, which you can save, e-mail, or add to a report. Click the arrow next to this icon to select the type of action.
	open a wizard to start a guided workflow for performing an analysis. Click the arrow next to this icon to select the type of analysis.
	perform a T1 analysis.
	perform a T2* analysis.
	perform a Edema analysis.

	perform a DSI analysis.
	perform a AAR analysis.
	open an LV diameter wizard.
	open a visual scoring diagram. Click the arrow next to this icon to select the type of visual scoring.
Panning and Zooming Toolbar	
	switch between editing mode and window/level mode. You can see which mode is active by checking the type of cursor.
	zoom in.
	zoom out.
	apply the zoom percentage that you specified in the zoom drop-down list. You can access the zoom drop-down list by clicking the arrow next to this icon.
Undo/Redo Toolbar	
	undo your editing actions.
	redo your editing actions.
	delete the selected contour or point. Click the arrow next to this icon to select an item to delete.

QFlow Toolbar	
	launch Medis QFlow®. This icon is only available if Medis QFlow has been installed on your system.
Medis Global Toolbar	
	launch Medis Website.
	launch Medis help manuals.
Contour Toolbar The icons shown as active in the contour toolbar vary, depending on the image orientation and on the type of study selected.	
Contour Toolbar – Short-Axis Icons	
	indicate that you are detecting, drawing, or editing an LV endocardial contour.
	indicate that you are detecting, drawing, or editing an LV epicardial contour.
 	indicate that you are drawing or editing a papillary contour.
	indicate that you are detecting, drawing, or editing an RV endocardial contour.
	indicate that you are drawing or editing an RV epicardial contour.

	specify an LV center point in an image. This automatically creates an LV endocardial contour.
	specify a reference point at the inferior or anterior end of the interventricular septum as the starting point for myocardial segment analysis.
Contour Toolbar – Long-Axis Icons	
	indicate that you are detecting, drawing or editing an LV endocardial contour.
	indicate that you are detecting, drawing, or editing an LV epicardial contour.
 	indicate that you are drawing or editing a papillary contour.
	set base and apex reference points to detect the LV endocardial contour.
	interpolate long-axis reference points between the ED and ES phases.
	automatically exclude slices and images in the short-axis study based on the reference points that you placed in the long-axis study.
Contour Toolbar – Icons for TSI analysis, DSI analysis, Edema analysis, T1 or T2/T2*analysis	
	indicate that you are detecting, drawing, or editing an LV endocardial contour.
	indicate that you are detecting, drawing, or editing an LV epicardial contour.

   	indicate that you are detecting, drawing, or editing the contour of a region of interest.
	specify a reference point at the inferior or anterior end of the interventricular septum as the starting point for myocardial segment analysis.
	transfer the contours from the short-axis cine series to the DSI or Edema series. This icon is only available when a short-axis cine series and a DSI or Edema series are being analyzed.
	register contours in a TSI analysis. This icon is only available when a TSI series is being analyzed.

Contour Toolbar – Additional Icons	
	perform a distance measurement.
	draw a custom volume.
	perform an area measurement.
	draw or edit a contour by tracing.
	draw or edit a contour by placing points.
	apply rubberband editing to a contour.
	perform automatic contour detection. Click the arrow next to this icon to select the type of contour detection and the range of images.

Mask Toolbar	
	Indicates that you are drawing or editing the core tissue mask.
	Indicates that you are drawing or editing the micro-vascular tissue mask.
	Indicates that you are drawing or editing the gray zone mask.

	Indicates that you are drawing or editing the edema tissue mask.
	Indicate that you are drawing or editing the right ventricular muscle mass.
	Indicate that you are drawing or editing the left ventricular muscle mass.
	Add pixels to a mask.
	Remove pixels from a mask.
	Brush tool: Pain or erase using a square brush
	Brush tool: Pain or erase using a square brush
	Smart brush: When on, pixels from other masks are not modified when editing the current mask.
Functional Graph icons	
	Indicates the left ventricular blood volume
	Indicates the left ventricular myocardial volume
	Indicates the right ventricular blood volume
	Indicates the right ventricular myocardial volume

4.2 The Study Matrix

The Study Matrix shows a representation of the images in the currently loaded study. Right-click in the Study Matrix to access a context menu with options.

As you analyze a study, symbols are added to the matrix. This gives you an overview of the status of the images and the elements added to them. The following symbols are used in the Study Matrix.

Symbol	Meaning
	marks the image currently shown in the Active View.
	indicates that the image is excluded from automatic contour detection.
	indicates that the image contains a custom volume.

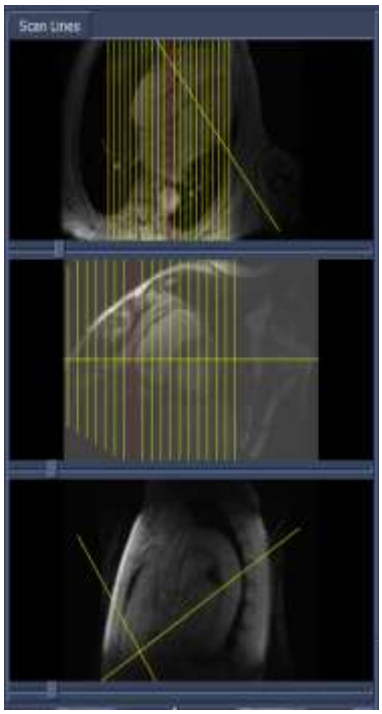
LV Endocardial Contours	
	represents an image with an automatically detected LV endocardial contour.
	represents an image with an LV endocardial contour that you have drawn or edited.
	represents an image with an LV endocardial contour that you have accepted.
LV Epicardial Contours	
	represents an image with an automatically detected LV epicardial contour.
	represents an image with an LV epicardial contour that you have drawn or edited.
	represents an image with an LV epicardial contour that you have accepted.
RV Endocardial Contours	
	represents an image with an automatically detected RV endocardial contour.
	represents an image with an RV endocardial contour that you have drawn or edited.
	represents an image with an RV endocardial contour that you have accepted.
RV Epicardial Contours	
	represents an image with an RV epicardial contour that you have drawn or edited.
	represents an image with an RV epicardial contour that you have accepted.

4.3 The Scanline Views

The scanline views present different perspectives of multiple series. It shows the current slice or phase in red. Normally parallel slices reflect the same series. All other non-parallel slices indicate a different series.

In the first two views, you can switch to another series. You can pan and zoom by using the given sliders.

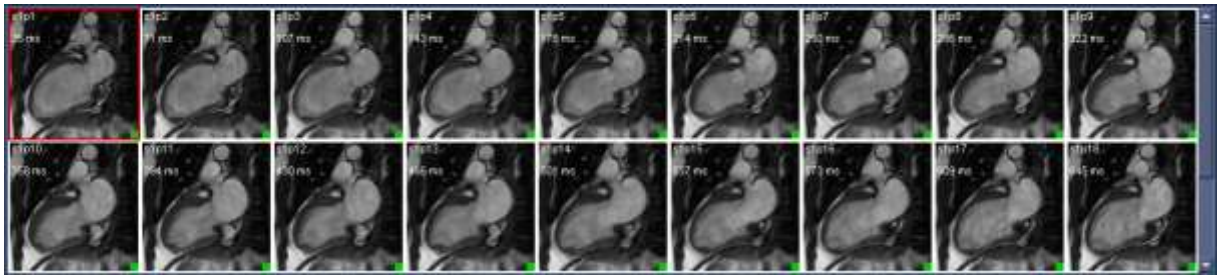
Scanlines are only displayed if it is possible to calculate them.



To change the series shown in a scanline view

1. Right-click in a scanline view.
2. In the **Series Selection** window, select the series you want to view.
3. Click **OK**.

4.4 The Thumbnail View



The Thumbnail View shows the slice or phase that you have selected in the Study Matrix. You can use the Thumbnail View to select and display an image in the Active View. You can also access a context menu with image and contour editing options.

A red frame marks the image currently shown in the Active View. Colored squares in the bottom right corners of the thumbnails indicate if the images are included for or excluded from automatic contour detection.

- ***green*** squares indicate that the images are marked as ***included*** for contour detection
- ***red*** squares indicate that the images are marked as ***excluded*** from contour detection

To access the context menu

- Right-click in the Thumbnail View.

  You can now select one of the commands for image and contour editing.

5 Reviewing

This chapter explains how to:

- review series
- zoom
- pan
- adjust window width and level
- adjust contrast and brightness
- hide or show patient and study data
- hide or show contours and other overlay elements
- view study properties
- perform distance measurements

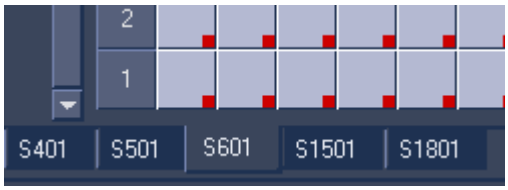
5.1 Reviewing Series

You can review series in the QMass main window or in the Movie Tool.

To select a series in the Study Matrix

- If you have opened more than one series, you can switch between the series by clicking the corresponding tabs under the Study Matrix.

  To view a tooltip that shows the series name, move the mouse over the tab.



To browse a series

- Use the arrow keys on your keyboard to scroll the images in the Thumbnail View and 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 the series in the Movie window

- Use the arrow keys on your keyboard.

To switch between series in the Movie window

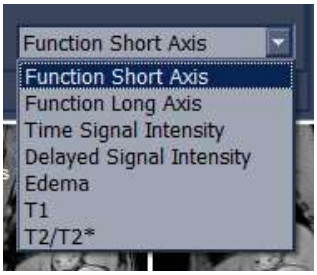
- Press the PgUp or PgDn key on your keyboard.

To change the slice orientation or the series label

If needed, you can change the slice orientation of a series from short-axis to long-axis or vice versa. You can also change the series label (time signal intensity, delayed signal intensity, T1, T2/T2*, Edema), if necessary.

- In the bottom-right corner of the Study Matrix, select the correct series label from the menu.

The following illustration shows an example.



Or,

- Select the correct orientation from the **Analysis** menu.

5.2 Zooming

To zoom in

- In the toolbar, click  .

Or,

- Press +.

Or,

- Drag the slider under the Active View or the Scanline View to the right.

Or,

- Press and hold down both the left mouse button and the mouse wheel, then drag the mouse up.

To zoom out

- In the toolbar, click  .

Or,

- Press -.

Or,

- Drag the slider under the Active View or the Scanline View to the left.

Or,

- Press and hold down both the left mouse button and the mouse wheel, then drag the mouse down.

To specify a default zoom factor

1. Select **View > Zoom** or click the arrow next to  , and select a zoom percentage from the drop-down menu.

2. To store this zoom percentage for the next time you work with this series, press CTRL+S or select **File > Save > Current Series**.

   This saves the new zoom percentage with the contours.

To apply the default zoom factor

- Click  .

  This applies the zoom factor specified in the zoom list.

5.3 Panning

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.

5.4 Adjusting Window Width and Level

You can have QMass determine the optimal window width and level settings. You can do this for the currently selected series, or for the current image, slice, phase, for all series loaded, for all images with the same geometry or orientation, or for all series with the same orientation.

You can also adjust window width and level settings manually.

To optimize window width and level automatically

- In the Active View, right-click and select **Optimize W/L**.

Or,

- Press 2 on the keyboard.

To adjust window width and level manually

- In the Active View, right-click and drag the mouse.

  Moving the mouse to the left or right adjusts window width. Moving the mouse up or down adjusts window level.

Or,

1. Click  in the toolbar.

   QMass is now in window width and level mode.

2. In the Active View, drag the mouse anywhere in the image using the left mouse button.

Moving the mouse to the left or right adjusts window width. Moving the mouse up or down adjusts window level.

Or,

1. Select **Settings > Main…**
2. On the **Image** tab, drag the **Window and Level** sliders.

   You can also enter a value in the text fields or select a value by clicking the selection arrows.

To return to the original window width and level settings

- In the Active View, right-click and select **Reset W/L**.

Or,

- Press 1 on the keyboard.

Or,

1. Select **Settings > Main…**
2. On the **Image** tab, behind the **Window and Level** sliders, click **Reset**.

5.5 Adjusting Contrast and Brightness

You can manually adjust the contrast and brightness for the current series.

To adjust contrast and brightness

1. Select **Settings > Main…**
2. On the **Image** tab, drag the **Contrast** and **Brightness** sliders.

   You can also enter a percentage in the **Contrast** and **Brightness** text fields or select a percentage by clicking the selection arrows.

To return to the original contrast and brightness settings

1. Select **Settings > Main…**
2. On the **Image** tab, behind the **Contrast** and **Brightness** sliders, click **Reset**.

5.6 Hiding and Showing Patient and Study Data

The Active View and Thumbnail View display a number of patient and study data by default. You can hide these data or redisplay them.

To hide or show patient and study data

- In the Active View, click and hold down the middle mouse button or mouse wheel.

  Release the middle mouse button to show the data again.

To hide or show patient and study data during the current session

1. Select **Settings > Main…**.
2. On the **Display** tab, under **Image Annotation Settings**, select the **Hide all annotations** check box to hide study and image details, including analysis results. Clear the check box to show them.

   You can also choose to hide or show specific types of information. Use the check boxes under **Hide all annotations** to hide or show them.

5.7 Hiding and Showing Contours and Other Overlay Elements

You can hide the contours, center points, reference points, and chords that are shown in the Active View and Thumbnail View. You can choose to hide them all or to hide specific elements.

To hide or show elements

- In the Active View, click and hold down the middle mouse button or mouse wheel.

  Release the middle mouse button to show the elements again.

To hide or show elements during the current session

1. Select **Settings > Main…**.
2. To hide all contours, center points, and reference points, select the **Display** tab, and under **Display Settings**, select the **Hide all drawings** check box.

   Clear this check box to display these elements again.

   To hide specific types of overlay elements, under **Display Settings**, clear the check boxes of the contours or other elements you want to hide.

5.8 Viewing Study Properties

In QMass, you can access details about the patient as well as study acquisition parameters that were included in the study's DICOM header.

To view study properties

1. Select **View > Study Parameters…** or press F6.

   This opens a window that lists the study properties.

2. Click **OK** to close the window.

5.9 Performing Distance Measurements

QMass enables you to perform measurements, for example of the left or right atrium, or of the aortic root.

To perform a distance measurement

1. Click  in the Contour toolbar.
2. In the Active View, click to place the starting point in the image.

   This inserts a yellow cross.

3. Click to place the end point.

   This opens the Set Distance Measurement dialog window.

4. Select a label for the distance.

   For instructions on changing the default labels, refer to the QMass reference manual.

5. Click **OK**.

   The distance in millimeters is now shown in the image. It is also included in reports.

To delete distance measurements

- Select **Edit > Delete Distance Labels**, and then select a distance label or select **All Labels**.

Or,

- Right-click in the Active View, select **Delete > Distance Labels** and then select a distance label or select **All Labels**.

5.10 Performing Area Measurements

QMass enables you to perform area measurements, for example measure the area of the left or right atrium, or of the aortic root.

To perform a area measurement

6. Click  in the Contour toolbar.
7. Create a contour using the trace  or point  method.
8. Select a label for the distance, either a default or user defined.

   For instructions on changing the default labels, refer to the QMass reference manual.
9.

   The area measurements are in centimeters square and they are included in the reports.

To delete area measurements

- Select **Edit > Delete Area Measurement Labels**, and then select an area measurement label or select **All Labels**.

Or,

- Right-click in the Active View, select **Delete > Area Measurements Labels** and then select an area measurement label or select **All Labels**.

6 Visual Scoring

This chapter explains how to visually score wall motion series, first-pass perfusion series (referred to in QMass as time-signal intensity series) and late-enhanced series (referred to in QMass as delayed signal intensity series). This chapter also explains the segmentation model used.

6.1 About Visual Scoring in QMass

You can access the visual scoring windows by clicking the arrow next to  . You enter your assessment in the plot, which you can then print, save, e-mail, or add to the report.

6.2 Visual Scoring

You score all types of series in the same way: first you visually assess the study in the Movie Tool, in the Thumbnail View, or in the Active View, then you fill in the plot.

To visually score studies

1. In the toolbar, click the arrow next to  and select **Wall Motion…, Time Signal Intensity…,** or **Delayed Signal Intensity….**

    You can also press F10 for wall motion scoring, CTRL+F10 for first-pass perfusion (time-signal intensity) scoring, or CTRL+SHIFT+F10 for late-enhanced (delayed signal intensity) scoring.

2. When scoring, make sure to first select the appropriate check box on the right.

3. In the plot, click the segments that you want to mark.

4. You can now print, save, or e-mail the plot, or add it to a report.

   Click **Print** to print the plot.

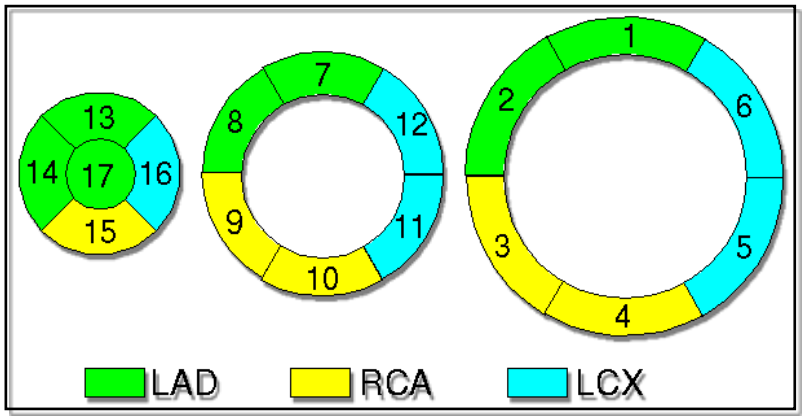
   Right-click in the plot window to access a menu with options for saving to file system, e-mailing and adding the plot to a report.

    For detailed instructions on adding the plot to a report, refer to section 10.2.

6.3 About the Segmentation Model

Visual scoring in QMass is based on the American Heart Association's model for segmentation of the left ventricle. The following illustration shows how this model divides the myocardium into segments.

AHA Model for Segmentation of the Left Ventricle



Coronary Artery Territories

LAD Left Anterior Descending Artery
RCA Right Coronary Artery
LCX Left CircumfleX Artery

Left Ventricular Segments

1. basal anterior
2. basal anteroseptal
3. basal inferoseptal
4. basal inferior
5. basal inferolateral
6. basal anterolateral
7. mid anterior
8. mid anteroseptal
9. mid inferoseptal
10. mid inferior
11. mid inferolateral
12. mid anterolateral
13. apical anterior
14. apical septal
15. apical inferior
16. apical lateral
17. apex

Source: Standardized Myocardial Segmentation and Nomenclature for Tomographic Imaging of the Heart. *Circulation* 2002; 105: 539-542.

7 Detecting and Drawing Contours

This chapter explains how to:

- detect contours in short-axis and in long-axis images
- exclude images from the automatic contour detection
- draw contours
- save contours

7.1 About Detecting and Drawing Contours

There are two ways of creating LV endocardial, LV epicardial, and RV endocardial contours in both short-axis and long-axis images: automatically detecting them and manually drawing them. RV epicardial contours must always be drawn manually.

With LV endocardial, LV epicardial, and RV endocardial contours, you can use automatic contour detection. These types of contours must only be drawn manually when automatic contour detection fails or when part of the automatic contour detection must be re-traced.

7.1.1 Detecting Contours

You can automatically detect short-axis and long-axis contours in a single image or in a slice. Short-axis contours can also be automatically detected in a phase, in the orientation currently shown in the Study Matrix or in the entire series at once.

Typically, you create one or two contours, preferably in ED and ES, to guide the automatic contour detection in an entire slice, phase or series.

To detect a single LV endocardial contour in a short-axis image

1. In the Thumbnail View, select the image.
2. Click  .
3. In the Active View, click in the center of the LV blood pool.
4. Make sure to review and edit the detected contour.

   You can pick up and drag the center point to create a new contour.

To detect a single LV endocardial contour in a long axis image

1. In the Thumbnail View, select the image.

2. Click  in the toolbar.

   If this icon is not shown, make sure to switch to long axis mode first. Select **Settings > Main…** On the **Quantification** tab, under **Slice orientation**, select **Long axis 2ch** or **Long axis 4ch**.

3. In the Active Image View, click at the level of the mitral valve, and then click on the apex, on the inside of the myocardium.

   This detects the LV endocardial contour.

4. Make sure to review and accept the contour.

To detect multiple LV contours and RV endocardial contours in short axis images

1. Examine the slices and determine which slices or images must be excluded from the analysis to obtain accurate results. The rule of thumb is that you exclude all slices and images that show less than 50% of the myocardium. Slices below the apex and slices displaying the outflow tract must be excluded.

   If a corresponding long axis study is available, QMass can automatically exclude these slices. Open both the short axis and long axis series, and select the tab showing the long axis series. Select the ED image, click  and place the markers, then select the ES image, click  and place the markers. Click  to interpolate. Now click  to exclude slices from the short axis series based on the long axis information.

2. To manually exclude a slice, right-click the number of the slice in the Study Matrix and select **Exclude Image**. To exclude a single image, right-click the image in the Study Matrix and select **Exclude Image**.

   To exclude more than one slice, press CTRL, click the numbers of the slices you want to exclude in the Study Matrix, then right-click the selection and select **Exclude Image**. To exclude a range of slices, click the first slice in the Study Matrix, press SHIFT, click the last slice, and then right-click the selection and select **Exclude Image**.

3. Before starting the automatic contour detection, make sure that a slice is selected in the Study Matrix. This sets the detection orientation to slice.

   You must do this, regardless of the range of images in which you want to detect contours.

4. You can detect or draw one or more contours to guide the automatic contour detection. Refer to the previous section for instructions on detecting contours in a single image. Refer to section 7.1.2 for instructions on drawing contours.

5. Click the arrow next to  . From the submenu, select the type of contours you want to detect and the range of images in which you want them to be detected. Then click  .

Or, select **Contours > Selection…** to specify the type of contours you want to detect and the range of images in which you want them to be detected.

6. In the Study Matrix in the main window, symbols appear in the matrix cells as contour detection progresses. Circles indicate endocardial contours, rings indicate epicardial contours.

7. Make sure to review and accept the detected contours.

   To ensure that analysis results are accurate, all automatically detected contours must be reviewed and edited where necessary.

To exclude images from automatic contour detection

Some of the images and slices in a series must be excluded to ensure accurate results. The rule of thumb is that you exclude all slices and images that show less than 50% of the myocardium. Slices below the apex and slices displaying the outflow tract must always be excluded.

When you use the Ventricular Analysis Wizard, these slices are excluded automatically.

- To exclude a single image, right-click the red square in the image in the Thumbnail View, and then select **Exclude Image** from the submenu.

- To exclude a slice, right-click the number of the slice in the Study Matrix and then select **Exclude Image**.

- To exclude more than one slice, press CTRL, click the numbers of the slices in the Study Matrix, then right-click the selection and select **Exclude Image**.

To detect contours in a slice, phase or series

1. Make sure that there are model contours in ED and ES to guide the automatic contour detection, and that irrelevant images or slices are excluded.

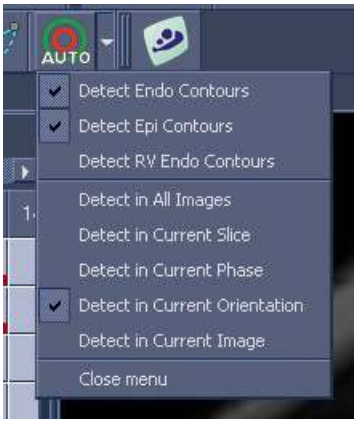
   For detailed steps, refer to the previous instructions.

2. If the type of contours and the image range have already been specified, you can click 

or press CTRL+D to immediately start the automatic contour detection.

   To specify the type of contours and the image range, click the arrow next to 

.



In the submenu, make the appropriate selections, and select **Close Menu**, then click 

.

3. Make sure to review and edit the detected contours.

   To ensure that analysis results are accurate, all automatically detected contours must be reviewed and, where necessary, edited.

7.1.2 Drawing Contours

You can draw contours using the Point Tool or the Trace Tool, depending on your personal preference.

To draw or edit a contour using the Point Tool

1. In the toolbar, click the icon of the contour that you want to draw.
2. Click 
.
3. Click in the Active View to mark the starting point of the contour. This can be any point along the contour that you want to create.
4. Mark the rest of the contour by placing more points. Avoid changing direction while you do this. You can place the points in either clockwise or counterclockwise direction.
5. When you place the last point, double-click.

   This automatically creates the contour along the points that you have placed.

To draw or edit a contour using the Trace Tool

1. In the toolbar, click the icon of the contour that you want to draw.
2. Click 
.

3. Click in the Active View at the starting point of the contour, hold down the mouse button and start tracing.

4. When you reach the end of the contour, release the mouse button.

To edit a contour using the Rubberband Tool

1. In the toolbar, click the icon of the contour that you want to edit.

2. Click  .

3. Move the mouse over the contour, and pick up the middle of the section that you want to reposition.

4. Position the contour over the place in the image where it fits, and release the mouse button.

To draw and edit custom volumes

1. In the toolbar, click left of  to open the menu of available custom volumes:

2. By means of the Point or Trace Tool, draw the custom volume.

7.2 Saving Contours and Image Settings

Contours can be saved in a contour file that is associated with the series. The contour file also stores the image settings you specified and any comments or labels that you added to the report.

You can save a contour file as a QMass `.CON` file or a DICOM file in the default contour directory or in a directory on your system or network.

A contour file does ***not*** store the DICOM metadata or the MRI images. It only stores the contours created in QMass, the settings specified and the comments and labels added to the report.

To save a contour file in the default contour directory

1. Click  or select **File > Save > Current Series** or **All Series**.

   This saves the current contours to the default contour directory.

    You can change the default contour directory by selecting **Tools > Options…**, and then selecting a new directory on the **General** tab, under **Folders**, behind **Contour Folder**.

2. You can save any changes you make by pressing CTRL+S or by clicking  again.

To save a contour file in another directory on your system or network

1. Select **File > Save As…** or press CTRL+SHIFT+S.

   This opens the Save Contours and Settings As dialog window.

2. Select the directory in which you want to save the contours, then select `.CON` or `.DCM` as the file type from the **Save as type** drop-down list.

   The directory initially specified is the default contour directory. If you save the contour file in this directory, it is automatically loaded with the associated series the next time it is opened in QMass. If you save it in another directory, you must load the contour file manually as described in section 3.3.

3. Click **Save**.

   This only saves the contours of the currently active series. If you want to save the contours analyzed in other series, you must repeat these steps for each series.

   You can save changes by pressing CTRL+S or by selecting **File > Save**.

8 Performing Function Analysis

This chapter explains for MR and CT how to:

- perform a function analysis using the Ventricular Analysis wizard
- perform a function analysis using the LV Diameter wizard
- perform a long-axis analysis using the area-length method
- perform a long-axis volume analysis using the bi-plane method
- perform a regional analysis in a short-axis study
- launch QFlow and import flow analysis results into QMass

8.1 About Performing Function Analysis

QMass offers two wizards for function analysis:

- the **Ventricular Analysis wizard**
- the **LV Diameter wizard**

The **Ventricular Analysis wizard** provides a guided workflow for the analysis of a short-axis cine series. This analysis provides the following results for the left and the right ventricle:

- ED and ES volumes
- ejection fraction
- stroke volume
- LV myocardial mass
- LV peak ejection rate and LV peak filling rate
  (if all endocardial contours are present)

The **LV Diameter wizard** provides a guided workflow for an analysis based on images in ED and ES in a single slice of a short-axis cine series. This analysis provides the following results:

- LV diameter in ED and in ES
- anterior septal wall thickness in ED and in ES
- posterior lateral wall thickness in ED and in ES
- fractional shortening

8.2 Performing an LV Function Analysis Using the Ventricular Analysis Wizard

The Ventricular Analysis wizard is only available if you have loaded a study that contains both long-axis and short-axis cine series. This 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

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 icons (short-axis or long-axis) are displayed in the toolbar.

   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**.

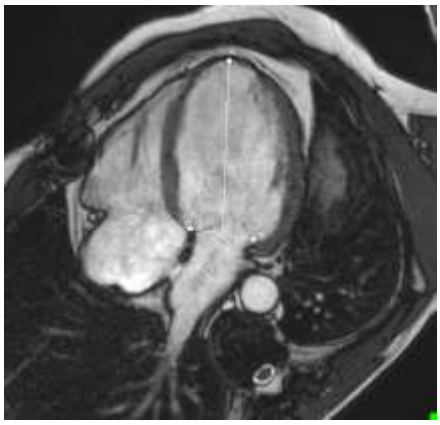
3. Under **Series Selection**, from the **LAX series** drop-down list, select the long-axis series you want to use as a reference to specify the locations of the mitral valve and the apex.

   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. For instructions on viewing these results in a graph, refer to section 9.1.1.

   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, where necessary, edited.

   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 section 7.1.2.

   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 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. The last wizard step shows an overview of the main analysis results. Make sure to review the results.

   To start performing a regional analysis, click  . For detailed instructions on performing regional analysis, refer to section 8.6.

7. Click  ,  or  to view analysis results.

   To save the contours you created, select **File > Save** from the menu bar.

8. Close the wizard by clicking **Done**.

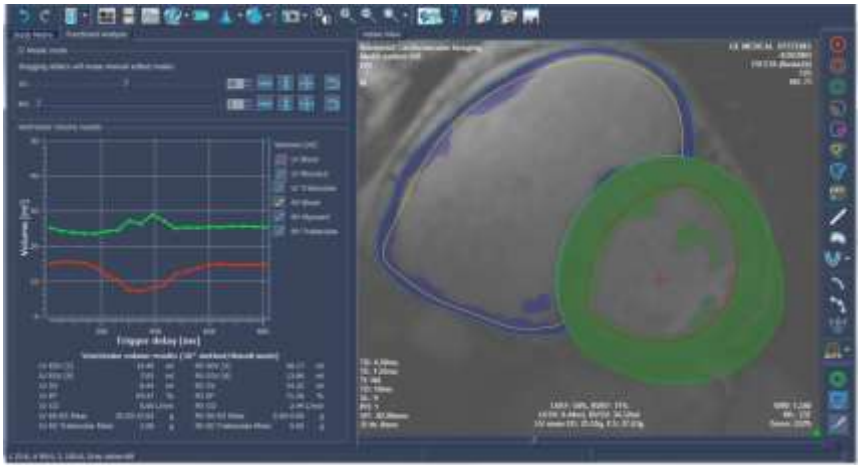
8.3 Performing a Functional Analysis: MassK mode.

The MassK mode checkbox in the functional Analysis tab allows for automatic segmentation of blood and muscle inside the epicardial border.

Using a threshold slider one can determine a threshold that distinguishes blood from muscle in both the Right Ventricular aswell as the Left Ventricular chambers. The threshold can be copied to other slices or phases.

To perform a functional analysis using blood and muscle segmentation

1. Select the tab **Functional Analysis** and select the checkbox **Blood muscle segmentation**.
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. Click  to view analysis results, or view the results in the Volume graph in the **Functional Analysis Tab**



8.4 Performing an LV Diameter Analysis

The LV diameter analysis is available when you have loaded a study that contains short-axis cine images. This wizard consists of two steps:

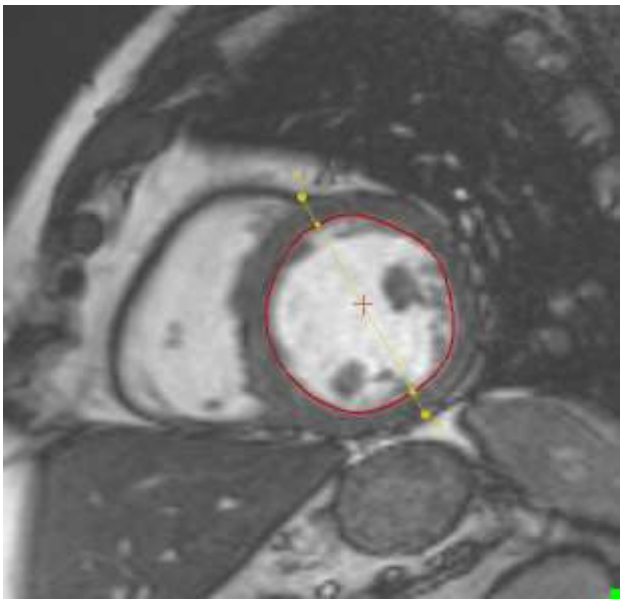
- measuring the LV diameter in the ED phase
- measuring the LV diameter in the ES phase

To perform an LV diameter analysis

7. Select **Analysis > LV Diameter Wizard**.
8. In the wizard, under **ED phase**, use the **Slice** field arrows to select a basal slice that shows the papillary muscle.

   Under **ED phase**, also select the end-diastolic phase in the **LV ED Phase** field.

   In the Active View, click on the outside of the anterior septum to place the anterior marker, and then click on the outside of the posterior wall to place the posterior marker.

   You can pick up and drag the markers to change their position.

   Click **Next**.
9. Under **ES phase**, select the end-systolic phase in the **LV ES Phase** field.

   In the Active View, click on the outside of the anterior septum to place the anterior marker, and then click on the outside of the posterior wall to place the posterior marker.

   Review the analysis results shown in the Results pane. The abbreviations used are:

   LVDd - left-ventricular diameter in diastole
   LVDs - left-ventricular diameter in systole

ASd – anterior septum in diastole
ASs – anterior septum in systole
PWd – posterior wall in diastole
PWs – posterior wall in systole

10. Click  or  to view analysis results.

    To save the contours you created, select **File > Save > Current Series** from the menu bar.

11. Close the wizard by clicking **Done**.

8.5 Performing Long-Axis Function Analysis

There are two methods to obtain volume results in long-axis series:

- the area-length (single-plane) calculation method
- the bi-plane calculation method

The following instruction describes both methods.

To perform an LV volume analysis in a long-axis series

1. Select the long-axis series by clicking its tab under the Study Matrix.
2. In the Thumbnail View, select the ED phase.
3. Click  in the toolbar.

   In the Active View, click to place two markers over the ventricular base, then click to place a marker over the apex.

   This automatically detects the endocardial LV contour in the ED phase. The base is marked with two B markers, the apex is marked with an A.

    Review the contour and, where necessary, edit it.

4. In the Thumbnail View, select the ES phase and repeat the actions described in step 3.
5. If you are performing a bi-plane analysis, repeat the actions described in steps 1 through 4 for the other 2-chamber or 4-chamber series.

    Make sure to use the same phases as ED and ES that you used in the other series.

   If you also want to calculate mass, wall motion, wall thickness and wall thickening, you must draw epicardial contours in ED and ES in both series. Otherwise, continue with step 6.

   Click  and draw the epicardial contour in the ED phase, and then in the ES phase. Do the same in the ED and ES phases in the other series.

For detailed instructions on drawing, refer to section 7.1.2.

6. Select **Settings > Main…**

   On the **Quantification** tab, under **Volume Calculation method**, select **Bi-Plane**, and check that the correct series are selected.

7. Click  .

   The lower left corner of the dialog window displays the volume results.

   From the **Show** drop-down list, select **Wall Thickness**, **Wall Thickening**, or **Wall Motion**.

8. Click  to view more analysis results.

   To save the contours you created, select **File > Save > Current Series** from the menu bar.

8.6 Performing Regional Analysis in Short-Axis Studies

When LV contours are present in the ED and ES phases of a short-axis study, you can obtain regional analysis results simply by placing a reference point. Results include wall motion, wall thickness and wall thickening. When endocardial and epicardial contours are present in all phases, results also include wall thickness over time.

To perform a regional analysis

1. Check that LV endocardial and epicardial contours are present in at least the ED and ES phases of the slices for which you want to obtain regional analysis results.

2. Click  and click in the Active View to mark the inferior septum. By default, this adds the reference point to all images in the current series.

   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 **Settings > Bull's-Eye…** On the **Display** tab, under **Reference Point Location**, select **Anterior** and click **OK**.

3. Check if the reference point is located in the correct position in every slice.

   To reposition a reference point, pick it up and drag it. Make sure that  is selected in the toolbar.

4. Click  ,  or  to view the regional analysis results.

   To save the contours you created, select **File > Save > Current Series** from the menu bar.

8.7 Launching QFlow® and Importing Flow Analysis Results

QFlow is the Medis software solution for the analysis of flow and velocity in phase-contrast MR studies. If you also have a QFlow license and QFlow is installed on the same system as QMass, you can launch QFlow from QMass, perform a flow analysis, and import the flow analysis results into QMass.

You can only launch QFlow if the version installed on your system has the same release number as QMass. To see which version you have, select **Help > About**. The box at the top of the window shows the release number. The last two numbers should be identical for QMass and QFlow.

To launch QFlow and import flow analysis results

1. In QMass, click  .

   This launches QFlow.

2. Open the series and perform a flow analysis in QFlow.

   For detailed instructions on performing flow analysis, refer to the QFlow user manual.

3. In QFlow, click  to close QFlow and return to QMass.

   Click **Yes** to confirm saving the contours if you had not saved them yet.

4. In QMass, click  to open the report window.

5. You can add the QFlow results to a graphic report, a text report, or an XML report.

   On the **Graphic** tab, from the **Report Layout** drop-down list, select **Congenital**, **LV/RV Volume**, or **LV Volume**, and then click **Redraw**.

   On the **Text** tab, under **Contents**, select **QFlow**, and then click **Generate**.

   On the **XML** tab, click **Generate**.

9 Viewing Analysis Results

This chapter explains how to:

- view graphs
- display peak ejection rate (PER) and peak filling rate (PFR) in the LV volume graph
- view bull's-eye diagrams
- view results as 3D representations or movies

9.1 Viewing Graphs

In QMass, you can view graphs that show the results of global and regional function analysis and of myocardial intensity analysis.

To view LV and RV results in a graph

1. Click  , press F7, or select **View > Graph…**

   This opens a window that shows the LV volume curve by default.

2. From the **Show** drop-down list, select the type of diagram that you want to view.

   If you make changes to the contours, you can redraw the graph by clicking **Redraw**.

   Right-click in the graph to access commands for saving it, e-mailing it and for adding it to a report. Chapter 10.7 explains these commands in detail.

9.1.1 Displaying Peak Ejection Rate and Peak Filling Rate

When you have performed a ventricular analysis and have detected all LV endocardial contours, you can display the peak ejection rate and peak filling rate in the LV volume graph.

To display peak ejection rate and peak filling rate

1. Click  , press F7, or select **View > Graph…**

2. Right-click in the graph and select **Graph Settings**. In the Graph Settings window, on the **Display** tab, under **Volume graph show**, select the **Ejection/filling dynamics** check box.

   This displays the PER and PFR in the legend of the graph. The vertical lines in the graph mark the TPER (Time to Peak Ejection Rate) and TPFR (Time to Peak Filling Rate).

9.2 Viewing Bull's-Eye Diagrams

In QMass, you can view bull's-eye diagrams that show the results of regional myocardial function analysis, delayed signal intensity (DSI) analysis and time signal intensity (TSI) analysis.

To view analysis results in a bull's-eye diagram

1. Select **View > Bull's Eye**, then select a representation scheme from the submenu.

   Or, click the arrow next to  , then select a representation scheme from the submenu.

   16 Segment Model presents results per segment (segment definition according to the AHA 16 segment model)
   Segmented per Slice presents average results per segment
   No Segments (Chords) presents the results per chord

   This opens a window that displays the Wall Thickness in ED.

   For more information about the AHA 16 segment model, refer to section 6.3.

2. From the drop-down list, select the type of bull's-eye diagram that you want to view.

   If you make changes to the contours, you can redraw the diagram by clicking **Redraw**.

   Right-click in the diagram to access commands for saving it, e-mailing it, and for adding it to a report. Chapter 10.7 explains these commands in detail.

9.3 Viewing 3D Contours

The 3D Viewer generates 3D images and movies of the contours that you created.

To view contours as 3D images or movies

1. Click  , press F11, or select **View > 3D Viewer…**

   This displays the LV endocardial, LV epicardial, and RV endocardial contours by default.

2. In the 3D Viewer, from the **Named Settings** drop-down list, select the contour type that you want to view.

   Right-click in the 3D image to access commands for saving the image, sending it by e-mail, and adding it to a report. Chapter 10.7 explains these commands in detail.

3. If you want to view the 3D contours as a movie, select the type of movie from the **Movie Type** drop-down list, then click **Movie** at the bottom of the window.

10 Creating Reports

This chapter explains how to:

- create graphic reports
- add graphic elements to a graphic report
- create text reports
- create XML reports
- add comments to reports
- create reports with normalized data

10.1 About Reports

Reports contain a summary of patient and study information and a number of analysis results.

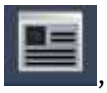
You can generate three types of reports:

- **graphic reports**, which you can save in HTML or PDF format, or as a DICOM SC.
- **text reports**, which you can save in TXT format. TXT reports can be viewed in any text editor and imported into spreadsheet or database applications.
- **XML reports**, which contain data structured in XML format. This type of report can be shared between XML-enabled applications.

10.2 Creating Graphic Reports

Graphic reports contain text and graphics. You can add predefined texts and your own comments to a graphic report. You can also add images, such as the active image, graphs, visual scoring, standard or 3D movie frames, movies, and diagrams.

To create a graphic report

1. Click  , press F9 or select **View > Report…**

   This creates a report in the layout last selected.

2. From the **Report Layout** drop-down list, you can select another type of report.

   This immediately creates the new report.

   You can create your own report templates. For more information, contact the Medis helpdesk.

To add a graphic element to a report

1. Right-click in the image or in the movie window and select the menu option for adding the image or movie to a report.

   For example, in the Active View, right-click and select **Snapshot > Add Image to Report**.

2. In the **Image Name** text field you can type a new name for the image, movie frame, or movie. In the main field of the dialog window you can enter additional comments. Click **OK**.

   This adds the image, movie frame, or movie to the report.

3. On the **Graphic** tab, all images you added are shown at the bottom of the main window.

   The left pane of the **Graphic** tab shows thumbnail images representing movies you added. Drag the thumbnail to the main window to include the movie in your report.

   Including a movie may take some time.

   Movies are displayed as thumbnails in the Report window. When you save the report in HTML format, the thumbnail is replaced by the original movie.

4. Click **Save** to save the report.

To remove a graphic element from a report

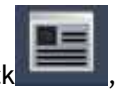
- Click the **Remove** hyperlink under the graphic element.

  This moves the graphic element to the pane on the left. To include it in the report again, drag it to the main part of the report.

10.3 Creating Text Reports

Text reports contain text only. In the report window, you can select the type of information and the level of detail that you want to see in the report.

To create a text report

1. Click  , press F9 or select **View > Report…**
2. Select the **Text** tab.
3. Under **Contents**, select the type of information that you want to include in the report.

   The option **16 Segment Model** adds analysis results for each of the segments of the AHA 16 segment model
4. From the **Detail** drop-down list, select the level of detail.

   Select **Normal** to create a report that shows overall results.

   Select **Advanced** to create a report with more detailed results.

   Select **Full** to create a report that shows the highest level of detail.
5. If you want to export the data to a spreadsheet or database application, make sure to select the correct marker for the end of each column from the **Column Separator** drop-down list.
6. Click **Generate**.

10.4 Creating XML Reports

XML reports contain data structured in XML format. This type of report can be imported into applications that support XML.

To create an XML report

1. Click  , press F9 or select **View > Report…**
2. On the **XML** tab, click **Generate**.

10.5 Adding Comments to Reports

You can add predefined labels and your own comments to a report. Comments can be linked to a predefined label or added separately.

There are two types of predefined labels:

- remarks concerning a patient's ***history***, condition, and current symptoms, for example, `high blood pressure`, `diabetes I`, or `nausea`
- remarks that give your ***impression*** of the patient's condition and of the anatomical location of problematic areas

Changes that you make to a comment or predefined label in a report, apply to all reports and report formats of the currently selected study.

To add predefined labels

1. Click **Add Text** at the bottom of the report window, and select the type of remark you want to add: **History** or **Impression**.
2. Select a term from the **History** drop-down list or from the **Impression** and **Anatomical location** drop-down lists.

   This shows the term or terms in the Preview pane.

   You can type additional comments in the **Comments** field.
3. Click **Add**.
4. You can add more labels and comments by repeating steps 2 and 3.

   When you have finished adding labels and comments, click **Done**.

To add comments to a report

1. Click **Add Text** at the bottom of the report window, and select **Comment**.
2. Type your comments in the main field of the dialog window and click **Add**.

   You can add multiple comments.

   When you have finished adding comments, click **Done**.

To edit or delete labels and comments in graphic reports

- On the **Graphic** tab, click the **edit** or **delete** hyperlink behind the label or comment that you want to edit or delete.

  This opens the dialog window for editing or prompts you to confirm deletion.

  When you are editing, make your changes and click **Add**. Click **Done** when you have finished editing.

To modify or delete labels and comments in text or XML reports

- At the bottom of the report window, click **Remove Texts**.

  This deletes all comments and labels you added.

10.6 Creating Reports with BSA Normalized Data

If the study's DICOM header includes values for the patient's weight and height, your report already contains values that relate the analysis results to the patient's body surface area (BSA). If the

DICOM header does not include the patient's weight or height, you can add normalized data as follows.

Make sure to check that values already filled in for the patient's weight and height are correct. The accuracy of the results depends on these data.

There are five different BSA calculation methods that you can use: Dubois & Dubois, Mosteller, Gehan & George, Haycock, and Boyd. The default is Dubois & Dubois. To change the default BSA calculation method, modify the **Body Surface Area Calculation Method** setting under **Quantification** in the Configuration File Editor.

For instructions on modifying settings, refer to the Configuration File Editor documentation.

To add normalized data

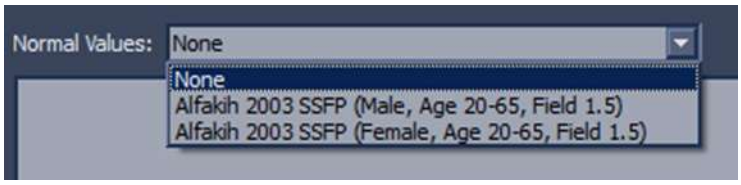
1. Click  , press F9 or select **View > Report…**
2. At the bottom of the report window, click **Set Weight and Height**.
3. In the Study Parameters window, double-click **Patient weight** and type the correct value. Do the same for the **Patient height** entry, then click **OK**.

   The report on the **Graphic** tab now lists normalized results.
4. On the **Text** tab or on the **XML** tab, click **Generate**.

   This creates a text or XML report with normalized results.

10.7 Creating reports with normal values

You can add a normal range and Z-score to the 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:



Press **Generate** in the Text report to generate results with the chosen normal values.

Press **Redraw** in the Graphic report to generate results with the chosen normal values.

To add Z-scores to text report, click the check box 

.

To view Z-scores in the Graphic report, select the "Congenital" template.

The default normal values are based on the following article: *Alfakih K, Plein S, Thiele H, Jones T, Ridgway JP, Sivananthan MU. Normal human left and right ventricular dimensions for MRI as assessed by turbo gradient echo and*

steady-state free precession imaging sequences. Journal of magnetic resonance imaging : JMRI [Internet]. 2003 Mar [cited 2013 Mar 21];17(3):323-9. Available from: http://www.ncbi.nlm.nih.gov/pubmed/12594722.

10.8 Adding custom normal values

You can edit the default sets of normal values or create additional sets. The default normal range file is extensively documented to assist in customizing the normal ranges.

1. After installation, start QMass at least once.

Open, review and edit the *QMassNormalRangeValuesDefault.nrf* in the *All Users* folder on your operating system. You can copy this file to other workstations to let QMass use the same normal values.

2. You can edit the QMassNormalRangeValuesDefault.nrf file with any suitable text editor.

In summary, setting up a new normal range set involves the following details:

1. Each set of normal ranges consists of the following header information:
    - SET NAME: A test template name
    - SET BSAMETHOD: Gehan and Boyd
    - AVAILABLE: NO
    - QUALIFIER: Gender = Male
    - QUALIFIER: Agerange = 20 65
    - QUALIFIER: fieldstrength = 1.5
2. Each set of normal ranges then has a list of values. E.g.
    - # Mean SD
    - LV ED Volume: 134.9 19.3 # ml
    - LV ED Volume / BSA: 77.7 10.8 # ml/m2
    - LV ED Volume / Height: 82.6 10.9 # ml/m
    - LV ES Volume: 48.9 10.7 # ml
3. # at the beginning of a line indicates commentary.
4. Undefined items may be listed as "—" or can be omitted altogether.

Where multiple normal ranges are defined, QMass will automatically select the first matching set.

Disclaimer

Medis medical imaging systems bv accepts no liability for the values entered by the user in *QMassNormalRangeValuesDefault.xml*, or for the consequences of any actions taken on the basis of the newly entered values. Values entered in *QMassNormalRangeValuesDefault*.xml are solely those of the user and do not necessarily represent those of Medis medical imaging systems bv.

11 Printing, Saving and E-Mailing

This chapter explains how to:

- print reports, snapshots of the Active View, graphs, bull's-eye diagrams, and visual scoring plots
- save reports, snapshots of the Active View, movie frames, movies, graphs, bull's-eye diagrams, visual scoring plots, and 3D images to a location on your system or network
- save reports, snapshots of the Active View, movie frames, graphs, bull's-eye diagrams, visual scoring plots, and 3D images as DICOM secondary captures
- e-mail reports, snapshots of the Active View, movie frames, movies, graphs, bull's-eye diagrams, visual scoring plots, and 3D images

11.1 Printing

You can print graphs, diagrams, visual scoring plots or images with a short overview of basic patient and study details.

You can also print reports that may include a number of graphs and images. Refer to Chapter 10 for information on how to create and customize reports.

To print a graph or image or to print a report

1. If you want to print a graph, click **Print Preview** in the graph window. You cannot modify the contents of this preview.

   If you want to print an image, right-click in the Active View, and select **Print Preview…** or **Print…**

   If you want to print a report, click **Print** in the Report window.

2. In the Print window, specify your printing preferences and click **Print**.

3. Click **Close**.

11.2 Saving

You can save images, movie frames, movies, graphs, snapshots and reports in various file formats or as DICOM secondary captures to a location on your system or network.

 For instructions on saving the contour files that store contours, image settings and report comments, refer to section 7.2.

 You can change the default directories in which studies, reports, and contour files are stored. Select **Tools > Options…** On the **General** tab, under **Folders**, specify or select the new directories.

To save a report or graphical object to a location on your system or network

1. If you want to save the current image, right-click in the Active View, and select **Snapshot > Save Image…**

   If you want to save a report, click **Save** at the bottom of the Report window.

   If you want to save another graphical object, right-click it in its window and select the save option.

2. In the dialog window that opens, you can change the location where the report or graphical object is saved by clicking **Browse…**, selecting another directory, and clicking **OK**.

3. If you want to change a report's or graphical object's file name, click in the **Filename** text field and type the new name.

4. Select the file format of your choice from the drop-down list.

5. Click **OK**.

   This saves the report or graphical object to the specified location.

11.3 E-Mailing

QMass has a custom e-mail tool that allows you to e-mail images, movie frames, movies, graphs, bull's-eye diagrams, visual scoring plots, 3D images, and reports directly from QMass.

To e-mail a report or graphical object

1. If you want to e-mail the current image, right-click in the Active View, and select **Snapshot > Send Image by E-mail…**

   If you want to e-mail a report, click **Send** at the bottom of the Report window. If you want to e-mail any other graphical object, right-click it in its window and select the send option.

2. In the dialog window that opens, type the e-mail address of the person to whom you want to send the item in the **To** text field.

   You can change the standard subject of the e-mail in the **Subject** text field and write an accompanying message in the **Comments** text field.

3. Click **Send**.

4. The bar at the bottom of the dialog window indicates progress.

   A dialog appears if the mail has been sent successfully.

 If you want to send the e-mail to another recipient, type the new recipient's e-mail address in the **To** field and click **Send** again.
To close the e-mail window, click **Close.**

1.

11.4 Closing QMass

When you have finished analyzing, you close QMass as follows.

To close QMass, select **File > Quit** or press CTRL+Q.

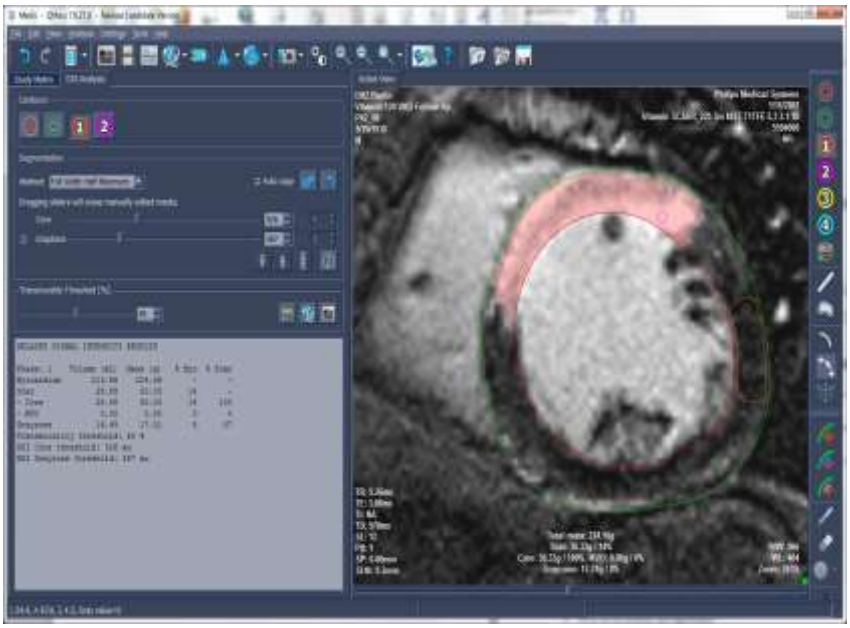
 When data has changed during the user session but has not yet been saved, a warning will be issued upon exit, offering the user a chance to save any unsaved data.

12 Performing Delayed Signal Intensity Analysis

A Delayed Signal Intensity (DSI) analysis helps you determine the amount of scar tissue in the myocardium.

In QMass, you can perform a scar tissue analysis using the Delayed Signal Intensity (DSI) wizard if your organization has obtained the DSI module.

This chapter explains how to perform an analysis using the Delayed Signal Intensity (DSI) wizard.



12.1 Performing a DSI Analysis

QMass features a DSI analysis. It is a simple one page analysis tool. One should:

- Create LV endocardial and epicardial contours
- Detect and verify the areas of healthy and hyper-intense myocardium
- Verify the DSI threshold and segmentation
- Place a reference point, set the transmurality threshold and view the results.

To perform a DSI analysis

1. Load a DSI dataset into QMass.

   See also, **"Transferring contours from short axis cine 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, **"Transferring contours from short axis cine series".**

5. Click **Apply**  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 **Apply** button. The DSI core threshold is also calculated when the **Apply** 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 core threshold by reviewing the scar tissue segmentation in all slices. You can override the calculated threshold by dragging the slider under **Intensity Threshold**.

   Click  and  to draw areas with micro-vascular obstructions. To start erasing pixels, click  .

   You can copy a manually set threshold value to other slices using **Copy to All**  , **Copy Down**  or **Copy Up**  .

   You can calculate another threshold value based on the healthy contour area by specifying the **Standard Deviation** calculation method and to supply a standard deviation.

   You can specify areas at risk by selecting **Dual Threshold** in the DSI analysis box. Two threshold sliders will appear. You can define a gray-zone threshold by moving the bottom slider or start drawing a gray-zone mask by clicking  .

   You can increase the tip size of the brush or the eraser by increasing the **Draw size**. You can increase or decrease the brush size using the shortcut key, **Ctrl->Scroll wheel**.

You can alter the brush type, either  or  .

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** in the Settings.

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 **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 reports.

   You can click  to create a DSI report.

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 DSI series by clicking  . Contour transfer works best if you manually create contours in the phase of the short axis cine series in which the DSI series was scanned.

Clearing ROI contours bitmasks and thresholds

Ther button  can be used to clear all the thresholds, bitmasks, and the ROI's used to determine the threshold.

13 Performing an EDEMA Analysis

An Edema analysis helps you determine the amount of Edema tissue in the myocardium. This chapter explains how to perform an analysis using the Edema wizard.

Performing an Edema Analysis

QMass features an Edema analysis. It is a simple one page analysis tool. One should:

1. Create LV endocardial and epicardial contours
2. Detect and verify the areas of healthy and edema myocardium
3. Verify the Edema threshold and segmentation

To perform an Edema analysis

1. Load an Edema study into QMass.

   See also, **"Transferring contours from short axis cine series."**

2. Select the Edema series you want to analyze.
3. Start the **Edema Analysis Wizard** by pressing next to  and select **Edema 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 healthy myocardium and if ROI2 is detected in Edema myocardium. If necessary, you can edit the contours or re-detect them using the **Detect** button.
6. Check the Edema core threshold by reviewing the edema tissue segmentation 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**  ,

Copy Down  or **Copy Up**  .

You can calculate another threshold value based on the healthy contour area by specifying the **Standard Deviation** calculation method and to supply a standard deviation.

Click  to draw areas with Edema tissue. To start erasing pixels, click  .

You can increase the tip size of the brush or the eraser by increasing the **Draw size**. You can increase or decrease the brush size using the shortcut key, **Ctrl->Scroll wheel**.

You can alter the brush type, either  or  .

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** in the Settings.

You can click  to create an Edema report.

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 Edema series by clicking 

. Contour transfer works best if you manually create contours in the phase of the short axis cine series in which the Edema series was scanned.
scanned.

Clearing ROI contours bitmasks and thresholds

The button  can be used to clear all the thresholds, bitmasks, and the ROI's used to determine the threshold.

14 Performing an AAR Analysis

Area At Risk (AAR) analysis helps you determine the amount of edema tissue in the myocardium that is defined as salvageable tissue.

This chapter explains how to perform an AAR analysis.

14.1 Performing an AAR Analysis

QMass features an AAR analysis. It is a simple analysis tool. One should:

- Load and create LV endocardial and epicardial contours in both Edema and DSI series.
- Do an Edema and DSI analysis on the respective datasets.

To perform a AAR analysis

1. Load a DSI and Edema dataset into QMass.
2. Start the AAR **Analysis Wizard** by pressing next to  and select AAR.
3. Complete a DSI analysis on the DSI dataset.
4. Complete an Edema analysis on the Edema dataset.
5. Review the AAR Results in the AAR tab of the AAR analysis.

 In the AAR analysis, the edema volume is always assumed to be larger or equal to the volume of the scar (DSI core) tissue. If the scar tissue is greater in volume than the edema volume then the volume and calculations will be rounded to zero as opposed to showing the negative values.

15 Performing Time Signal Intensity Analysis

In QMass, you can perform a Time Signal Intensity (TSI) analysis to analyze a first-pass perfusion study.

This chapter explains how to:

- perform a TSI analysis
- correct for body array inhomogeneity
- specify the transmural range
- calculate signal intensity in a region of interest
- view TSI analysis results in graphs and bull's-eye diagrams
- compare myocardial upslope with the upslope in a region of interest

15.1 Performing a Myocardial TSI Analysis

To perform a time signal intensity (TSI) analysis, you must take the following steps:

- draw endocardial and epicardial contours
- place reference points
- register the contours

You can also analyze signal intensity over time in specific regions of interest (ROIs). You can specify up to four different ROIs after creating the endocardial and epicardial contours.

To draw endocardial and epicardial contours

1. Select **File > Open Study…** and select the series you want to analyze.

   For detailed instructions on opening series, refer to section 3.2.

2. If the Time Signal Intensity toolbar with the 

icon does not appear, select the correct series label for the series.

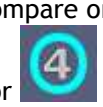
   You can do this by right-clicking the series tab. This shows the label submenu. You can also change the series label using this menu.

3. In the Thumbnail View, select an image that shows sufficient contrast in both the left and the right ventricle.
4. By default, the drawing mode is set to tracing. To draw in point mode, click  .
5. 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, to avoid its high intensity signal affecting the results.
6. If you want to analyze signal intensity over time in a region of interest, click  in the toolbar. In the Active View, draw a contour around the ROI.

   You can mark a sub-endocardial infarct using part of the existing endocardial contour. Start drawing at the endocardial contour, continuing along the epicardial contour. When you reach the endocardial contour again, release the mouse button if you are in Trace Mode, or double-click to place the last point on the contour if you are in Point Mode.

   You can quickly mark a segment by doing the following. Click the epicardial contour to mark the beginning of the septal segment, and then double-click the endocardial contour to mark the end.

   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

If you prefer to place the reference point at the anterior junction, make sure to change the bull's-eye settings, so that the cardiac segments are labeled correctly in bull's-eye representations. Select **Settings > Bull's-Eye…** On the **Display** tab, under **Reference Point Location**, select **Anterior**.

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.

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 **Settings > Registration…**

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.

   Refer to section 15.3 for detailed instructions on viewing results and creating reports.

15.2 Specifying Calibration Methods and Transmural Range

The TSI module has settings for:

- correcting for body array inhomogeneity (calibration method settings)
- specifying the transmural range (transmural range settings)

To calibrate

1. Select **Settings > Main…**
2. On the **SI Analysis** tab, from the **Calibration** drop-down list, select a calibration method.

   Divide by baseline intensity divides signal intensity by the mean intensity in the range you specified.

   Divide by ROI4 divides signal intensity by the intensity measured in a region that you specified.

   Subtract ROI4 subtracts signal intensity from the intensity measured in a region that you specified.

3. If you select **Divide by baseline intensity**, you must make sure to indicate a baseline. You can specify which phases must be considered the baseline by typing the phase number in the **T0 Phase** box.

   You can also mark the baseline in the TSI curves or in the Study Matrix.

   To mark the baseline in a TSI curve, click  . From the **Show** drop-down list, select **Myo Intensity –Time** or **ROI Intensity – Time**. Under the curve, drag the slider to define the

range of phases to be considered the baseline. The slider is the white triangle.

To mark the baseline in the Study Matrix, review the thumbnails in the Thumbnail View, then select the appropriate phase in the Study Matrix, right-click, and select **Set T0 Phase**.

The phase you selected as T0 is shown in the Study Matrix.

4. If you select **Divide by ROI4** or **Subtract ROI4**, specify the region of which the baseline signal intensity must be used to calibrate.

   Click  and use your preferred drawing tool to mark a region with the same signal intensity as the myocardium, such as muscle tissue. Copy this area to all images by pressing CTRL+C, and then selecting **Edit > Paste Active Element… > Paste to Phases of Current Slice**.

5. Click **OK**.

To specify the transmural range

By default, the transmural range is the entire distance between endocardium and epicardium (0% - 100%). You can set a specific range.

1. Select **Settings > Main…**
2. On the **SI Analysis** tab, the Transmural Range slider indicates the range used to calculate signal intensity.

   By default, the transmural range is 0% - 100%.

3. Specify the transmural range.
4. Click **OK**.

15.3 Viewing TSI Analysis Results

You can view various types of TSI analysis results in graphs and in bull's-eye diagrams.

To view TSI analysis results in graphs

1. Click  to display the analysis results in a graph.
2. From the **Show** drop-down list, select the type of graph that you want to view. You can select **Myo Intensity - Time**, **Myo Intensity Profile**, **ROI Intensity – Time**, or **ROI Histogram**.

Or, To view TSI analysis results in bull's-eye diagrams

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.

   The table below explains the bull's-eye diagrams. The terms used in the table are explained in the following illustration.

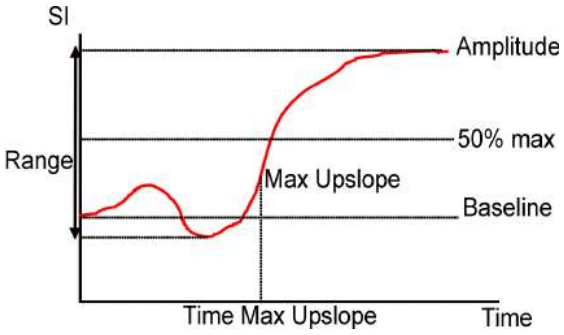


Diagram	Shows	Unit of Measurement
Amplitude	The maximum increase in signal intensity relative to the signal intensity value at time point T0. Only data points between T0 and Tend are taken into account.	Arbitrary units (au)
MaxUpslope	Maximum rate of signal intensity increase per unit time. The upslope is computed by fitting a line on a number of consecutive data points on the intensity-time curve. The number of points used depends on the **Nr of Myo fitting points** setting. To change this setting, select **Settings > Main…** On the **SI Analysis** tab, modify the **Nr of Myo fitting points**.	Arbitrary units (au) / s
TimeMaxUpslope	The time delay between T0 and the moment of maximum upslope.	s
MeanIntensity	Average signal intensity in the phase range between T0 and Tend. You can change the range of phases in the **SI Analysis** settings. Select **Settings > Main…** On the **SI Analysis** tab, type or select other start and end phases in the **T0 Phase** and **T end Phase** settings.	Arbitrary units (au)

Time 50% Max	The time delay between T0 and the moment the intensity-time curve reaches 50% of the maximum intensity.	s
T0 Intensity	Signal intensity at T0. You can change which phase is regarded as T0 in the **SI Analysis** settings. Select **Settings > Main…** On the **SI Analysis** tab, type or select another start phase in the **T0 Phase**.	Arbitrary units (au)
Baseline Intensity	Average signal intensity in the range of baseline phases. You can change which phase is regarded as the last phase of the baseline range. Select **Settings > Main…** On the **SI Analysis** tab, type or select another phase in the **T0 Phase**.	Arbitrary units (au)
Relative Upslope	Upslope of a myocardial segment divided by the upslope of the time-intensity curve of the blood pool signal. The blood pool signal is calculated based on a 5x5 pixel area in the center of the left ventricle.	%/s
Scar Tissue	Percentage of tissue that is above the intensity threshold based on ROIs in hyper-enhanced and/or normal myocardium.	% and mass (g)
Non-Viable Tissue	Scar tissue that has a higher transmurality than the specified transmurality threshold plus the connected normal tissue along a chord.	% and mass (g)

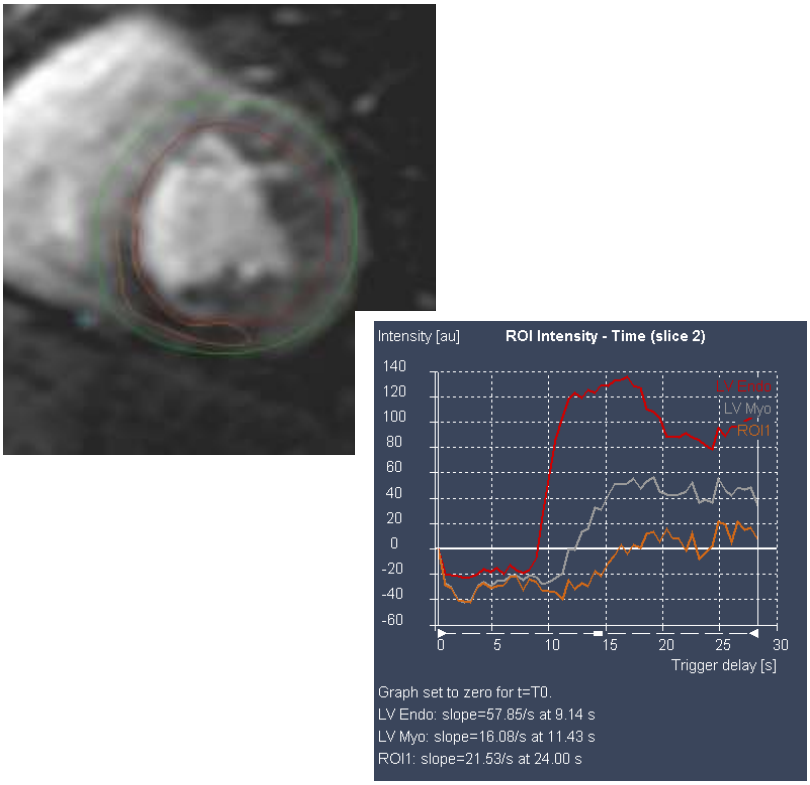
To compare myocardial upslope with the upslope in regions of interest

You can calculate the average TSI value of the entire myocardium and display it as a curve. In this way, you can compare a ROI with the rest of the myocardium.

1. Analyze a ROI as described in the first section of this chapter.
2. Click  .

   In the box to the right of the **ROI Intensity - Time** graph, select the option that displays the ROI curve, and then select the **Myo** option.

   The graph that displays the average TSI values is shown in gray. The illustration on the following page shows an example.


Intensity [au]
ROI Intensity - Time (slice 2)
140
120
100
80
60
40
20
0
-20
-40
-60
LV Endo
LV Myo
ROI1
0
5
10
15
20
25
30
Trigger delay [s]
Graph set to zero for t=T0.
LV Endo: slope=57.85/s at 9.14 s
LV Myo: slope=16.08/s at 11.43 s
ROI1: slope=21.53/s at 24.00 s

16 Performing Stress Level Function Analysis

You can use QMass to view the various stress levels in a stress study simultaneously in the Movie Tool and to analyze function stress level studies for both MR and CT.

This chapter explains how to:

- open a study
- switch between stress levels
- view stress level movies simultaneously
- perform a global stress level analysis
- perform a regional stress level analysis
- view comparison analysis results in graphs and bull's-eye diagrams

16.1 Opening the Stress Level Series

When you open a stress level study, you select Comparison mode and specify the number of levels.

To open the series

1. Select **File > Open Study…** from the menu bar or press CTRL+O.
2. In the upper pane of the Open Study dialog window, select all series that you want to compare and analyze.

    For detailed instructions on opening series, refer to section 3.2.
3. Click **OK**.
4. In the Comparison Selection dialog window, make sure the **Comparison mode** check box is selected, change the number of levels if necessary, and click **Load**.

   This opens the stress level series.

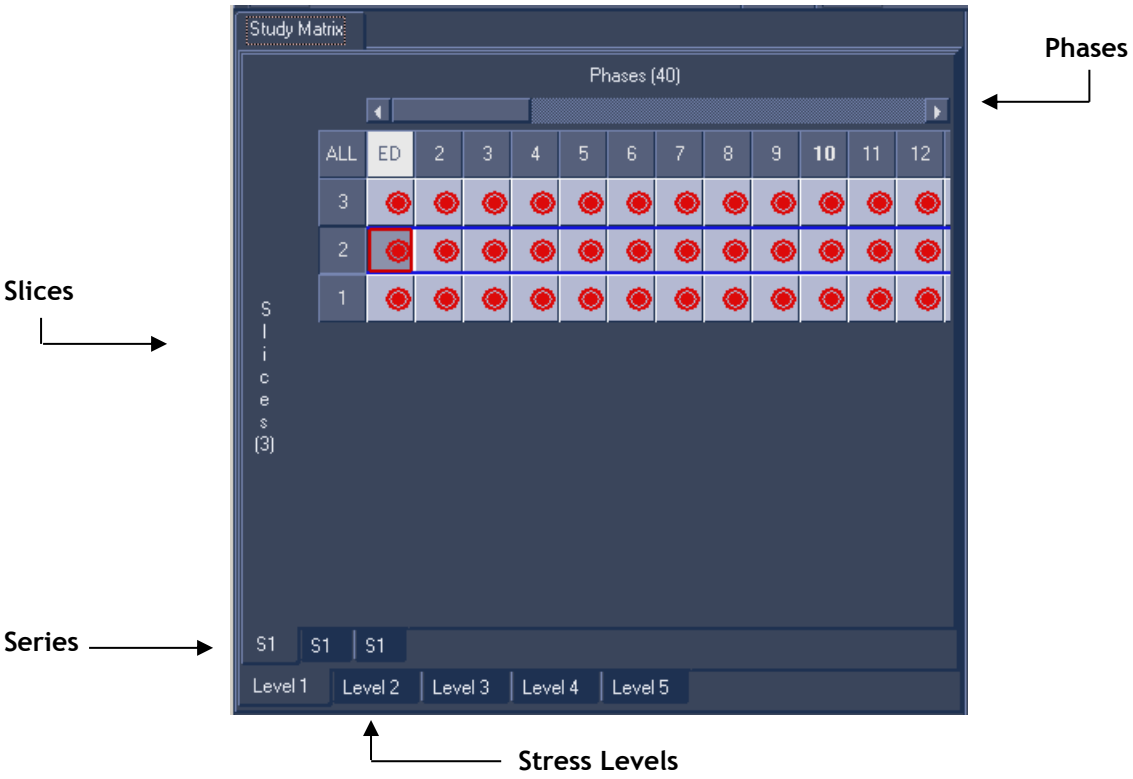
16.2 Reviewing Stress Level Images and Movies

The **Study Matrix** represents the slices, phases, and levels in the stress level study. You can use the tabs at the bottom of the Study Matrix to switch between stress levels.

To switch between stress levels

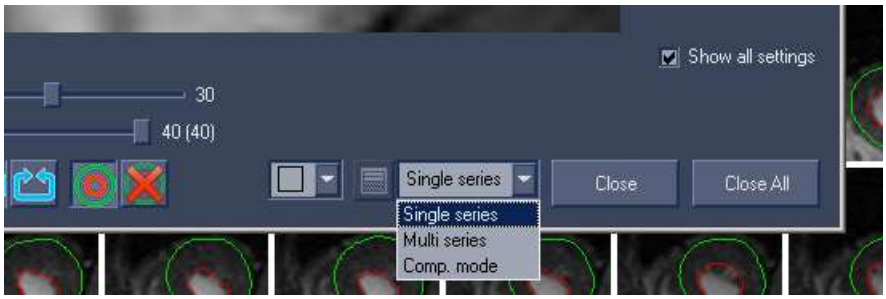
- Click **Level 2**, **Level 3**, and so on to view the next stress level.

  The following illustration shows the Study Matrix with five studies at different stress levels.



To display stress levels simultaneously in the Movie Tool

1. Click  .
2. In the Movie Tool, select the **Show all settings** check box if necessary to display all options.
3. From the drop-down list at the bottom, select the option **Comp. mode** (Comparison mode).



   This displays the various stress levels simultaneously in the Movie Tool.

4. You can click a level or slice button to hide the corresponding level or slice. This enables you to compare specific levels or slices more easily.
5. Click **Close** to close the Movie Tool and return to the main window.

16.3 Performing a Global Stress Level Analysis

When you perform a global stress level analysis, you create endocardial and epicardial contours in all images. This section provides instructions for short-axis images.

If you want to perform a global stress level analysis in long-axis images, create endocardial and epicardial contours in the ED and ES phases using the bi-plane or area length method. For instructions, refer to section 8.4.

To perform a global stress level analysis

1. Click the arrow next to 

and make sure that the following are selected: **Detect Endo Contours**, **Detect Epi Contours**, and **Detect in All Images**. Select **Close Menu**, then click 

.

2. Review the endocardial and epicardial contours.

   To ensure that analysis results are accurate, all automatically detected contours must be reviewed and, where necessary, edited.

3. Detect endocardial and epicardial contours in all other stress levels. You can do this quickly by selecting the stress level, and then clicking 

. Review and edit the detected contours.

4. You can now view analysis results. For instructions, refer to section 16.5.

16.4 Performing a Regional Stress Level Analysis

To obtain regional analysis results for the various stress levels, you must place reference points.

To place reference points

1. If you want to 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 **Settings > Bull's-Eye…** On the **Display** tab, under **Reference Point Location**, select **Anterior**.

2. Click 

in the toolbar.

3. In the Active View, place a reference point at the inferior or anterior end of the interventricular septum.

   To correct for torsion during the cardiac cycle, place a reference point in every slice you are analyzing.

4. Place reference points in the other stress level series in the same way.

5. You can now view analysis results. For instructions, refer to section 16.5.

16.5 Viewing Stress Level Results

You can compare the results for the various stress levels in graphs and in bull's-eye diagrams. Stress level details are added to the standard graphs and bull's-eye diagrams, and you can also view specific stress level graphs and diagrams.

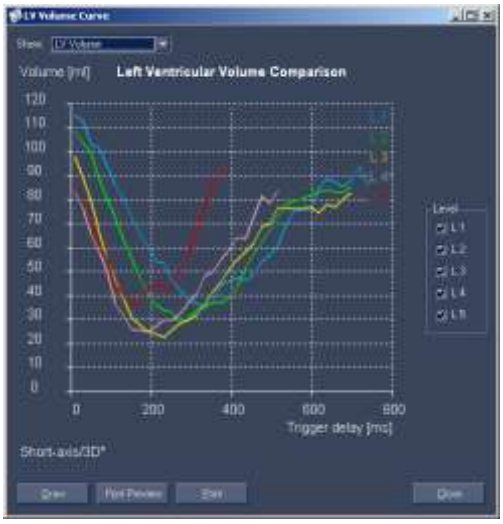
16.5.1 Viewing Graphs

You can view ED volume, ES volume, stroke volume, cardiac output, ejection fraction, and heart rate graphs that show color-coded results for the various stress levels. If you have placed reference points, you can also view wall thickness, wall thickening, wall motion, and wall thickness over time graphs.

To view stress level results in a graph

1. Click  .

   The LV volume graph now contains color-coded curves for the various stress levels.



2. Under **Level**, to the right of the graph, you can select or clear check boxes to show or hide stress level curves in the graph.

   Right-click in the graph to access a menu with options.

3. From the **Show** drop-down list you can select other graphs.

16.5.2 Viewing Bull's-Eye Diagrams

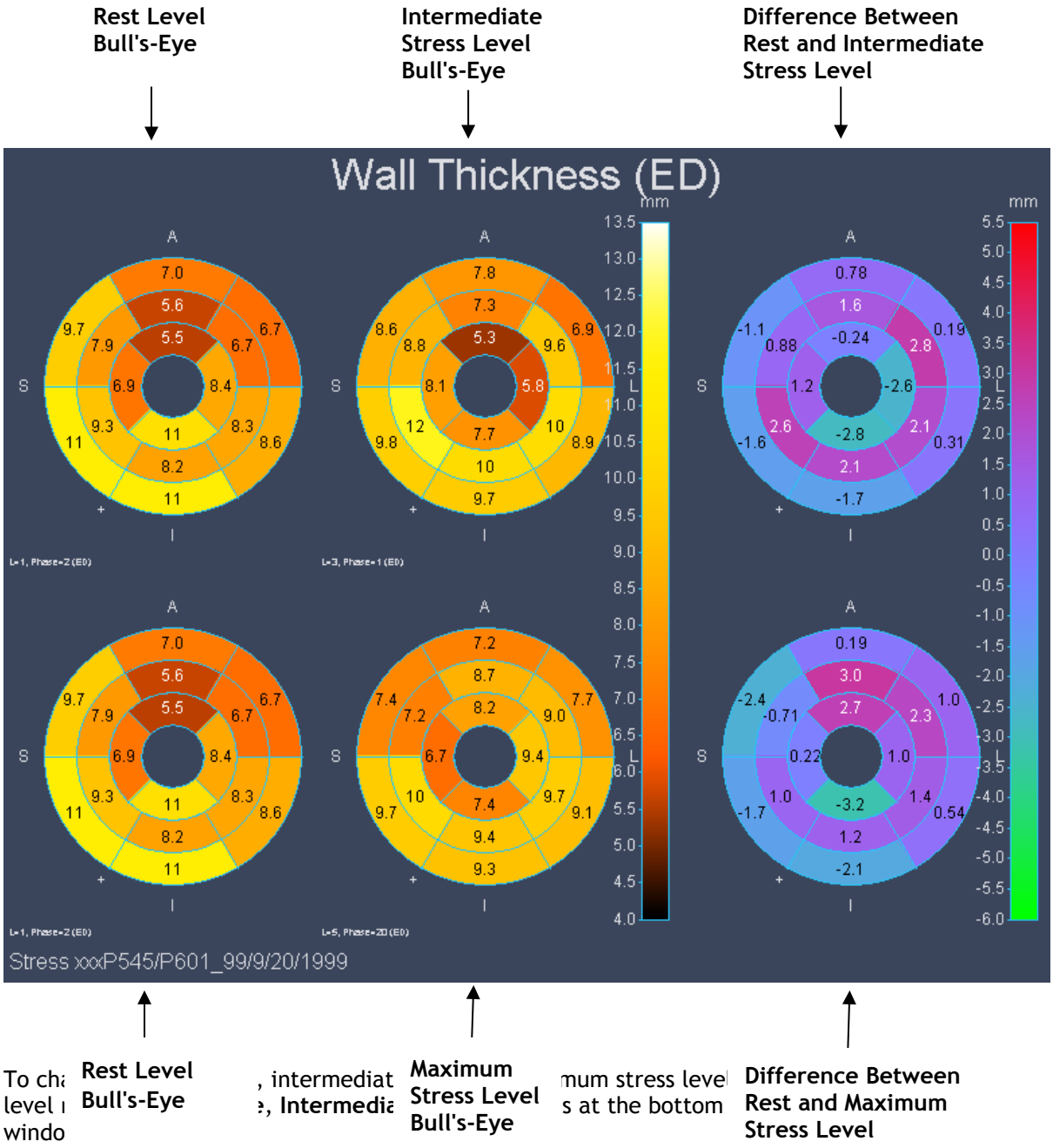
To view stress level results in a bull's-eye diagram

1. Click  .

2. From the **Show** drop-down list, select the diagram of your choice.

   Details are shown for the rest level compared with an intermediate stress level and compared with the maximum stress level. The differences between the levels are also plotted in a diagram. You can specify which levels must be regarded as the rest level, the intermediate level, and the maximum stress level.

   The following illustration shows a wall thickness comparison diagram.



3. To cha… level … windo… …, intermediat… …, Intermedia… …mum stress leve… …s at the bottom…

   Right-click in the diagram window to access a menu with options.

17 Analyzing T1 magnetization recovery

If you have the T1 analysis module, you can use QMass to analyze the T1 magnetization recovery of a region of interest.

This chapter explains how to:

- Perform a T1 analysis
- Create a T1 analysis report

17.1 Performing T1 analysis

A T1 analysis determines the rate of magnetization recovery of a region of interest.

To perform a T1 analysis

1. Select **File > Open Study…** and select the series you want to analyze.

   For detailed instructions on opening series, refer to section 3.2.

2. Set the series label to a T1 series. If needed, you can change the series label in the submenu. 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.

3. Select the T1 Analysis tab.

4. In the Thumbnail View, select an image that shows sufficient contrast.

5. 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.

6. Click  and draw the epicardial contour.

   Make sure to exclude the RV blood pool, to avoid its high intensity signal affecting the results.

7. 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 of contours of the regions of interest to the other images. You can register contours manually by using the left mouse button while pressing Ctrl and Shift simultaneously.

8. 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.

9. 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 studiescorresponds to the following equation: I = A EXP (-t/T1) + B
T1* (Look-Locker)	T1* for Look-Locker studies corresponds to the following equation: I = A EXP (-t/T1*) + B
T1 (Look-Locker)	T1 value for Look-Locker studies corresponds to the following equation: T1 = T1* (-A/B – 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).

To create a T1 report

1. Click  .
2. On the Graphic tab, from the Report Layout drop-down list, select **T1**.

   This creates a T1 report.

To set a color range and color map setting

1. Select **Settings > T1 Settings**.

   This opens the T1 Settings dialog window.
2. 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.

   For instructions on modifying settings, refer to the Configuration File Editor documentation.

To export the relaxation rates per slice to DICOM

1. Click  the “Export …” button.

The exported maps can be saved to disk, to pacs or to an OEM database.

For instructions on modifying export settings, refer to the Configuration File Editor documentation.

18 Performing T2/T2* Decay Time Analysis

If you have the T2/T2* analysis module, you can use QMass to analyze the T2 or T2* decay time of a region of interest in the myocardium.

This chapter explains how to:

- perform a T2 or T2* decay time analysis
- create a T2 or T2* decay time report

18.1 Performing T2 or T2* 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 decayed to zero.

To perform a T2 or T2* analysis

1. Select **File > Open Study…** and select the series you want to analyze.

   For detailed instructions on opening series, refer to section 3.2.

2. Set the series label to a T2/T2* series. If needed, you can change the series label in the submenu.

3. Select the T2/T2* Analysis tab.

4. In the Thumbnail View, select an image that shows sufficient contrast.

5. Select your preferred drawing tool and draw the endocardial contour.

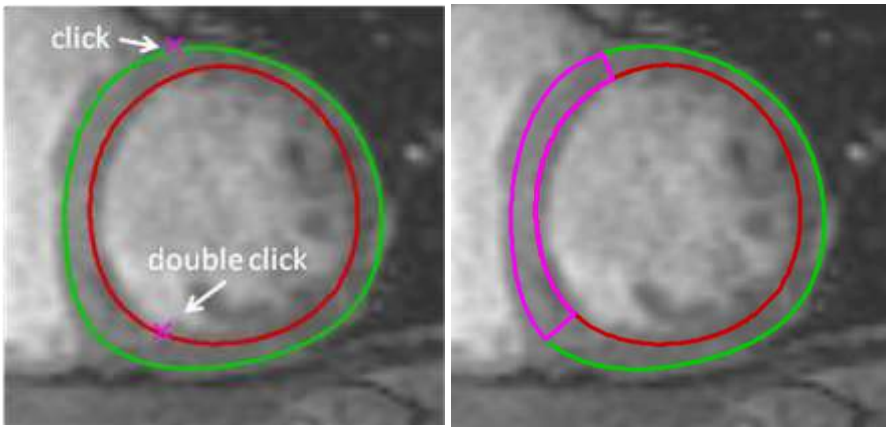
   Make sure to exclude the LV blood pool, to avoid its high intensity signal affecting the results.

6. Click  and draw the epicardial contour.

   Make sure to exclude the RV blood pool, to avoid its high intensity signal affecting the results.

7. 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 of contours of the regions of interest to the other images. You can register contours manually by using the left mouse button while pressing Ctrl and Shift simultaneously.

8. 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 black.

   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 black curve fit the non-excluded part of the measured curve. Make sure that the black curve runs through the first measured points.

   The following illustration provides an example.

9. 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 where T2 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.

To create a T2 or T2* report

1. Click  .
2. On the Graphic tab, from the Report Layout drop-down list, select T2-**T2Star**.

   This creates a T2 or T2* report.

To set a default for the cut-off value and for the overlay colors

1. Select **Settings > T2/T2* Settings**.

   This opens the T2/T2* Settings dialog window.
2. Under **Overlay Colors**, 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.

   For instructions on modifying settings, refer to the Configuration File Editor documentation.

To export the relaxation rates per slice to DICOM

1. Click  the "Export …" button.

 The exported maps can be saved to disk, to pacs or to an OEM database.

 For instructions on modifying export settings, refer to the Configuration File Editor documentation.

Trouble Shooting

Floating license error after a crash of the software

In a floating license setup licenses will be returned to the license server when QMass is closed. In case of a crash, the licenses will not be returned and will remain locked on the license server. Restarting QMass will give a warning that the licenses are not available. To solve this issue, you have to wait 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 install non-expiring license

When you install a temporary 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….

Exporting Results To Excel

To import results into excel you have to create a text report with a delimiter that is easily recognized by excel. The ';' seems to work very well for this. To get the results in excel do the following:

- Go to the text report
- Set the column separator to ;
- Save the file as a .txt
- Open excel
- Open the .txt file
- Select ; as delimiter in the Text import wizard
- Data will now be imported into columns in Excel.

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 AAR Report

AAR results are only available when the AAR wizard is open. Once the AAR wizard is open all AAR results are available in the report.

ES only: communication error between visia and QMass/Qflow

After clicking the QMass/QFlow button in visia an error message appears indicating a communication error has occurred. If this happens, please make sure the Qmass and Qflow installers have run. You need to select all applications from the CMS launcher.

Send email ends up in the junk folder

The send mpeg movie by email, can sometimes end up in the outlook junk folder. A workaround is to save the movie to avi format and send it by email.

19 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.

F11	open the 3D Viewer to view the results of the analysis as 3D images or animations.

20 Shortcut Keys

Shortcut keys are combinations of keys that you can press on your keyboard to give a command.

20.1 All Views

Shortcut	Use to
General	
CTRL+Q	close QMass.
Studies and Contour Files	
CTRL+O	open a study.
CTRL+F5	refresh the directory tree of the browser.
CTRL+L	open a set of contours that were created previously and saved in a contour file.
CTRL+S	save all contours present in the current series.
CTRL+E	save all contours present in all currently opened series.
CTRL+SHIFT+S	save all contours in a contour file.
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.
F1	Help.
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.

20.2 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.
ALT+SHIFT+S	reshapes a contour by removing small irregularities.
ALT+SHIFT+D	reshapes a contour by removing curves.
ALT+SHIFT+C	reshapes a contour by removing all curves that point inward.
ALT+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+P	print the currently selected image and basic patient and study data.
CTRL+SHIFT+P	show a print preview of the currently selected image and basic patient and study data.

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

CTRL+ Scroll mouse wheel	Increases and decreases the brush size, when using DSI, Edema or Functional MassK mode analysis.

20.3 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

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