



# QMass<sup>®</sup> MR 7.6

## Release Notes

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These release notes provide an overview of new and improved features, and point you to more detailed information.

## What's New

### QMass MR 7.6.32.4

- **Version number alignment with QFlow.**  
No changes.

### QMass MR 7.6

- **Enhanced contour accuracy QMass.**  
Over the last decade, the image quality of MRI scanners has been steadily improving, allowing smaller and smaller structures to be imaged and researched reliably. To keep up with these developments, calculations in QMass MR are now performed with sub-pixel accuracy. This has significantly enhanced the way QMass MR handles contours ensuring reliability now and in the future. As a consequence, results with the new version can differ from previous versions, but Medis assures that the differences caused by this have been found small and clinically insignificant.

In case you are carrying out a research study, we always recommend using one fixed product version, as the use of different versions might influence the outcome of the study. The changes described in the previous paragraph are an example of differences that can occur between product versions.

- **Ventricular analysis: new analysis tab.**  
A new analysis tab has been introduced to enhance the ventricular analysis workflow.
- **MassK mode: Automatic segmentation of papillary muscles and trabeculae by pixel intensity based thresholding.**  
The MassK algorithm has been added to allow for segmentation of blood and muscle based on pixel intensities. This enables the automatic segmentation of papillary muscles and trabecular

Improving the reproducibility of MR-derived left ventricular volume and function measurements with a semi-automatic threshold-based segmentation algorithm. Jaspers K, et al., Int J Cardiovasc Imaging. 2013 Mar.

- **CT.**  
It is now possible to perform a functional analysis on CT series. A separate license is needed for this.
- **Enhanced DSI workflow.**  
The DSI analysis has been redesigned and the workflow is now enhanced in various ways:
  - **Enhanced GUI:** the multiple step wizard is now organized nicely in a one-step analysis pane.
  - **2 Thresholding methods** have been added: 50% max and automatic SCAR.
  - **SCAR:** an advanced automatic algorithm for detection scar has been added based on a method described in:

*Automated segmentation of myocardial scar in late enhancement MRI using combined intensity and spatial information. Tao Q, et al. Magn Reson Med. 2010*

- Manual editing is now even easier: The brush size can be changed easily with ctrl + scroll wheel and the shape can be chosen.
- Workflow with thresholds per slice has been enhanced.
- Automatic detection of normal ROI's has been changed. The ROI is now larger encompassing more remote/normal myocardium. If needed, the ROI size and shape can still be manually adjusted.
- **Edema analysis.**  
A new analysis has been added to allow for quantification of edematous tissue on T2 weighted series. The workflow is very similar to the workflow in the DSI analysis.
- **AAR analysis and quantification of Myocardial salvage.**  
A new analysis wizard is available to allow for quantification of myocardial salvage.
- **T1 corrected (including support for SR sequence).**  
T1 corrected with support for SR sequences is now supported.
- **T1-T2/T2\* export of parametric maps.**  
It is now possible to export parametric maps and subsequently perform further analysis.
- **Area Measurements.**  
The area measurement is now accessible from the main GUI.
- **Visual scoring.**  
Results from visual scoring are now available in table format in the text report.

## QMass MR 7.6.32.2

- **AAR: Myocardial Salvage**  
The myocardial salvage value was displayed incorrectly in the AAR analysis. This has been corrected.
- **Functional Analysis: pane updates**  
The Functional Analysis pane was not automatically updated when changing ED & ES manually. This has been solved.
- **Functional Analysis:, graph color**  
The color for the myocardial mass curve in the Functional Analysis pane was grey and has been changed to green.
- **T1 mapping: name changes**  
T1c and T1 have been renamed to T1 and T1\*, respectively. These new names follow the definitions used in the landmark paper by Messroghli et al. *Magnetic Resonance in Medicine* 52:141-146 (2004). For further information, refer to Deichmann & Haase, *Journal of Magnetic Resonance*, 96:608-612 (1992)

## QMass MR 7.6

- **Incorrect XML tags.**  
In the XML report of T1 several tags have been corrected or added. “DecacyTimes” has been corrected to “DecayTimes”. The following tags are added “T1DecayTimes”, “T1DecayTimesCorrected” (only in IR mode), “T1DecayTimesZeroCrossings”, “T1DecayTimesResiduals”, “T1DecayTimesScalings”, “T1DecayTimesOffsets”.  
  
The XML tags for “BLOOD” and “MYO” have been changed to “LV\_BLOOD” and “LV\_MYO”. “RV\_BLOOD” and “RV\_MYO” have been added.  
  
The XML tag “T2Star” has been renamed to “T2\_T2Star”
- **Mandatory use of the recursive flag with ‘opendirectory’ through activeX.**  
The usage of ‘recursive=true’ is now mandatory when using ‘opendirectory’ through activeX when the recursive behavior is required.

# Known Issues

- **New normal range items not automatically added**

If a previous version of QMass is installed the normal range file from that version will be used. In this case the following (new) items need to be added by hand to all sections if default values are needed for these items:

RV Peak Ejection Rate:	--	--	# ml/s
RV Peak Ejection Rate / ED Volume:	--	--	# fraction (RV EDV/s)
Time to RV Peak Ejection Rate:	--	--	# ms
RV Peak Filling Rate:	--	--	# ml/s
RV Peak Filling Rate / ED Volume:	--	--	# fraction (RV EDV/s)
Time to RV Peak Filling Rate:	--	--	# ms

- **Crash during startup of QMass after selecting a specific default printer**

One of our sites has reported a problem with the startup of QMass when a specific printer was set as default printer. This probably caused by a bug in QT when the correct printer driver and or font is not available. Fixing the printer driver or font issue or selecting a different default printer fixes the problem.

- **T1 mapping sometimes goes wrong on experimental sequences**

It can occur that experimental T1 sequences are not always read correctly by the software, resulting in unusable T1 graphs. If you suspect something is wrong with reading, please contact Medis support for troubleshooting.

- **T1 curve displayed as not flipped**

When using a short imaging period, where the T1 curve doesn't cross the zero line, the T1 curve is displayed as not flipped.

- **Opening the study browser can take a long time**

Slow (or not) responding network shares can result in a slowly populating file browser. This can also be seen when using the explorer and clicking on these mapped drives. Removing or speeding up the response of these drives can resolve this issue.

- **Long-Axis Markers in Ventricular Analysis Wizard Reset**

In step 2 of the Ventricular Analysis Wizard, the apex and base markers get reset to the position of the ED phase when switching between phases.

- **Delete All Does Not Delete Distance Measurements**

The Delete All command discards all contours, reference and center points, and lines, but does not discard the distance measurements.

- **Editing Contours Created in QMass MR Versions 6.x or 7.0**

If you need to edit contours that were created in a previous version of QMass MR, the editing toolbar that is displayed in the QMass MR main workspace may be a toolbar that is associated with another type of study: functional, TSI or DSI studies.

**Workaround:** You can manually change the study type selected to display the correct toolbar. Right-click the study tab in the Study Matrix and select the correct study type from the list.

- **'Disappearing' RV Contours and ROIs**

When you have finished one type of analysis (for example, a functional analysis with LV and RV contours) and then move on to performing the next type of analysis (for instance, a TSI analysis) without saving the contours in a contour file, the RV contours or ROIs seem to disappear.

The contours are still available—they are just not shown because the application focuses on

the information that is relevant for the current analysis type. You can display them as follows. Right-click the study tab in the Study Matrix and select the correct study type from the list.

**Workaround:** Save the contours you created in an analysis before switching to another type of analysis.

- **Asian Character Sets Misrepresented in PDF Reports**

When reports using Asian character sets are saved in PDF format, the characters are misrepresented in the PDF report.

**Workaround:** Save the report in another format, such as HTML.

## More Information

You can find detailed installation instructions and instructions for use in the documentation available on the CD-ROM. The software includes a user manual, which you can access by pressing F1.

For support questions, please contact our Support Team.

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