# Medis
## MEDICAL IMAGING

# QMass 8.1
## User Manual

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# 1. Starting QMass

QMass is started from Medis Suite.

⮕ For a detailed description on starting applications and loading data in the applications, refer to the Medis Suite Quick Start/User Manual.

Using Drag 'n Drop (D'nD) one can load data into QMass. Depending on the modifier keys pressed during the D'nD QMass will have a different load behavior:

| D'nD | Data will be added to the current session and the first series will be made active. |
|---|---|
| D'nD + Shift | Data will be added. Current active series will remain active. |
| D'nD + Ctrl | Current data will be closed. New data will be loaded. First series will be made active. |

**To load existing local contours**

- Click Menu ⦂ and select **File > Load Contours …**

Select the QMass analysis file you are interested in.

**To select a series**

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

  Move the mouse over a tab to view a tooltip that shows the series name.
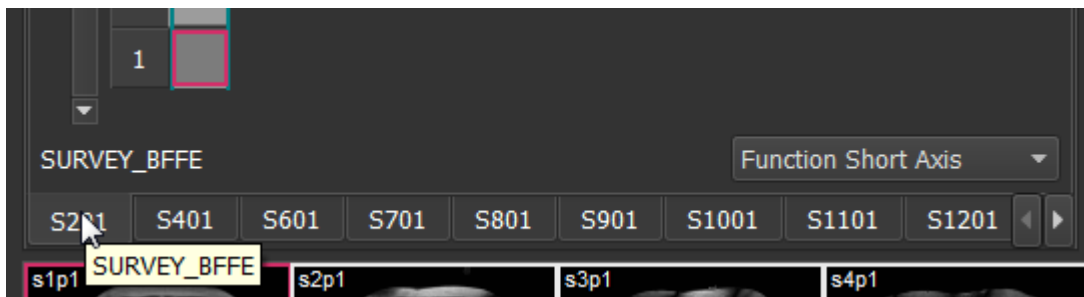


**To browse through the images of a series**

- Use the arrow keys on your keyboard to scroll the images in the Thumbnail View and in the Active View.

**To select an image**

- Click an image in the Thumbnail View to select it.

  This displays the image in the Active View.

  In the Thumbnail View, the selected image is marked with a red frame.

**To view a series in the Movie window**

- Click  in the toolbar or press F5.

**To scroll through the images of the series in the Movie window**

- Use the arrow keys on your keyboard.

**To switch between series in the Movie window**

- Press the PgUp or PgDn key on your keyboard.

**To zoom in or out**

- Use the slider under the Viewport or set the edit mode to Zoom mode  and use the LMB.

**To pan**

- Press the middle mouse button or mouse wheel, hold it down and drag.

  This pans the image.

  To return to editing mode, release the middle mouse button or mouse wheel.

**To adjust window width and level**

- Press 2 on the keyboard to optimize window width and level.

Or,

- Click RMB and drag in the Active View. Move the mouse to the left or right to adjust window width, move it up or down to adjust window level.

**To load series for a Comparison analysis**

- Click Menu  and select **File > Open Series Selection …**

Select the series you are interested in. Turn on the Comparison check box and load the data.

**To change the auto-combine settings**

- Click Menu ⠿ and select **File > Open Series Selection …**

Turn on or Off the auto combine checkbox. By selecting multiple series one can create a new combined series.

**To create a snapshot from a graph or viewport**

- Click  in the toolbar of the dialog.

# 2.    QMass Workspace

The QMass main workspace consists of a set of toolbars, a study matrix and three views. Which icons are active in the toolbars, depends on the type of study that is being analyzed and on its orientation.

The scan line views present the slice position of the selected series. In the first two views, you can switch to another series by right-clicking and selecting the new series. You can also pan, and you can zoom in or zoom out by using the sliders.
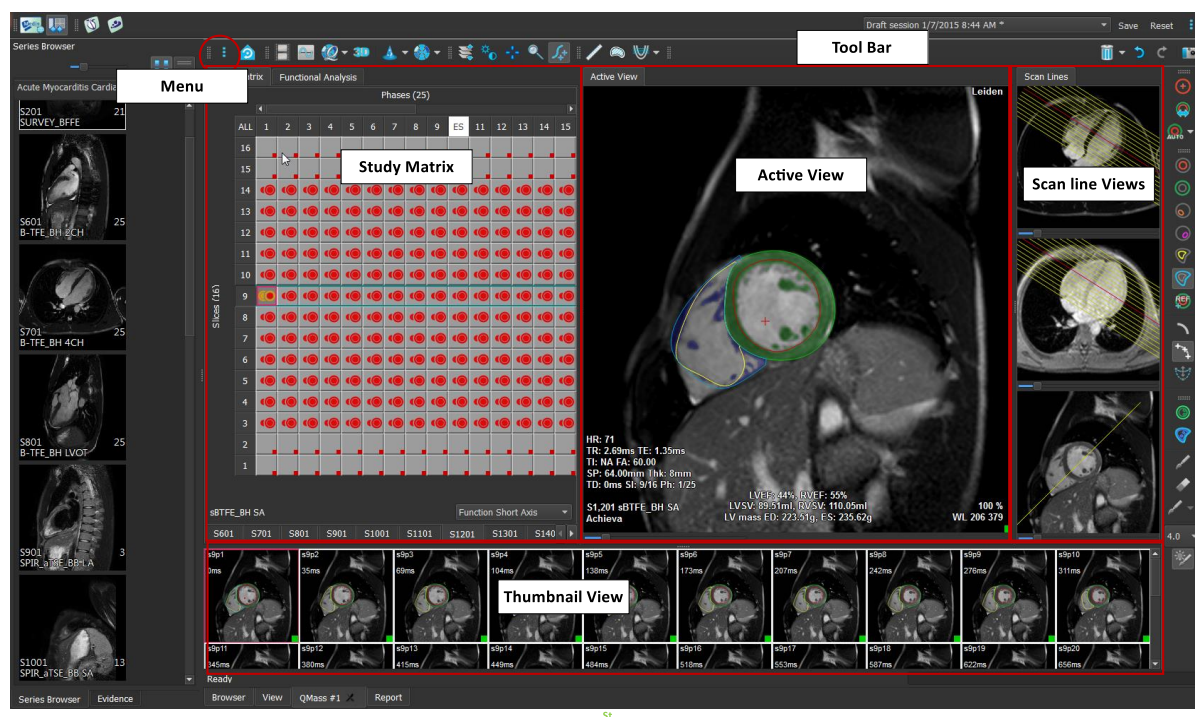


In this quick tour, you will get to know QMass's key features and basic workflow. You will open a study, review it, perform an LV function analysis, view analysis results.

# 3.     Performing LV Function Analysis

Now that we have reviewed the series, we are going to perform an LV function analysis using the Ventricular Analysis wizard. There are a number of wizards in QMass, which provide a guided workflow to help you perform an analysis quickly and easily. The Ventricular Analysis wizard consists of four steps:

- selecting the long-axis series and the short-axis series, and placing valve and apex markers in the ED phase of the long-axis series

- placing markers in the ES phase of the long-axis series, and selecting the type of contours to be detected

- reviewing the detected contours

- reviewing the results

💡 The Ventricular Analysis wizard is only available when the study contains both long-axis and short-axis cine images. If you have no long-axis images, you can still perform an analysis using the standard automatic detection feature. Refer to the QMass User Manual for instructions.

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

**To perform an LV function analysis using the Ventricular Analysis wizard**

1.  In the Study Matrix, select the tabs of the various series and check for each series if the correct study type is set.

    If needed, you can correct the labeling of a series by right-clicking its tab and selecting the correct label from the menu.

2.  Select **Analysis > Ventricular Analysis Wizard**.

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

    If you have loaded a long-axis radial scan, you can select the long-axis slice you want to use in the **LAX Slice** field.

    From the **SAX series** drop-down list, select the short-axis cine series you want to analyze.

    Under **ED Phase**, check if the phase presented as the LV ED phase is correct.

    In the Active View, pick up the long-axis markers and drag them to the correct positions. Place the A marker over the apex, and place the B markers over the mitral valves.

    

    Click **Next**.

4.  Under **ES Phase**, check the phase. In the Active View, place the A and B markers as described in the previous step.

    Under **Contour Selection**, select the type of contours that you want to be detected in the short-axis images.

     If you want to calculate the peak ejection rate and the peak filling rate, leave **All** selected in the **LV Endo** box.

    Click **Next**.

5.  When the automatic contour detection has finished, review the detected contours. Review both the ED phase and the ES phase by selecting the corresponding **View** icon.

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

     For an overview of all detected contours, you can switch to the Study Matrix tab.

    To edit a contour, click  ,  or  and then start editing.

     For detailed instructions on editing, refer to the QMass User Manual.

    To switch between viewing the ED and the ES phase in the Thumbnail View, click the corresponding **View** button in the wizard.

    To change the ED or ES phase and automatically redetect contours, select the new phase number under **Redetect Contours** in step 3 of the wizard, and click **Apply**.

    To exclude or include individual images, click the green or red square in the bottom right corner in the Thumbnail View. This automatically removes or detects contours.

    Click **Next**.

6.  To obtain regional analysis results, make sure that  is selected, and then click in the Active View to mark the posterior or anterior septum in the current slice. Repeat this for the other slices you are analyzing.

     If you place the reference point at the <u>anterior</u> septum, make sure to first change the bull's-eye settings, so that the cardiac segments are labeled correctly. Select Menu  > **Settings > Bull's-Eye…** On the **Display** tab, under **Reference Point Location**, select **Anterior** and click **OK**.

7.  Click  to view analysis results. Click  to view regional analysis results.

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

8.  Click **Done** to close the wizard.

# 4.     Performing QStrain Analysis

Now that we have functional analysis results we can start a QStrain analysis.

- Click  to start the QStrain analysis.

All data and all contours are given as input to the QStrain analysis.

Contours are not strictly necessary to start a QStrain analysis.

# 5.     Performing extended LV Function Analysis

The MassK (blood muscle segmentation) checkbox in the Functional Analysis offers an alternative method to determine blood and muscle volumes for functional analysis, in addition to papillary muscle volume.

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

**To perform a functional analysis using MassK mode**

1.  Select the tab **Functional Analysis** and select the checkbox **MassK.**

2.  Draw the Epicardial contours in all slices and phases.

3.  Draw the Endocardial contours if one needs to distinguish between Papillary volume and Myocardial volume.

4.  Drag the LV or RV thresholds slider to modify the blood muscle classification.

5.  Click the toolbar button, **"Edit LV Papillary"** tissue to manually add or remove muscle tissue.

6.  View the results in the Volume graph in the **Functional Analysis Tab**

    Or,

    The Results Pane or the Report pane of Medis Suite.

The MassK mode is dependent on the EPI cardial contours. Always review all EPI-cardial contours to be available and correct.

In case all derived results (Ejection Fraction, Stroke volume, Cardiac output) are zero, check whether all EPI contours are available.
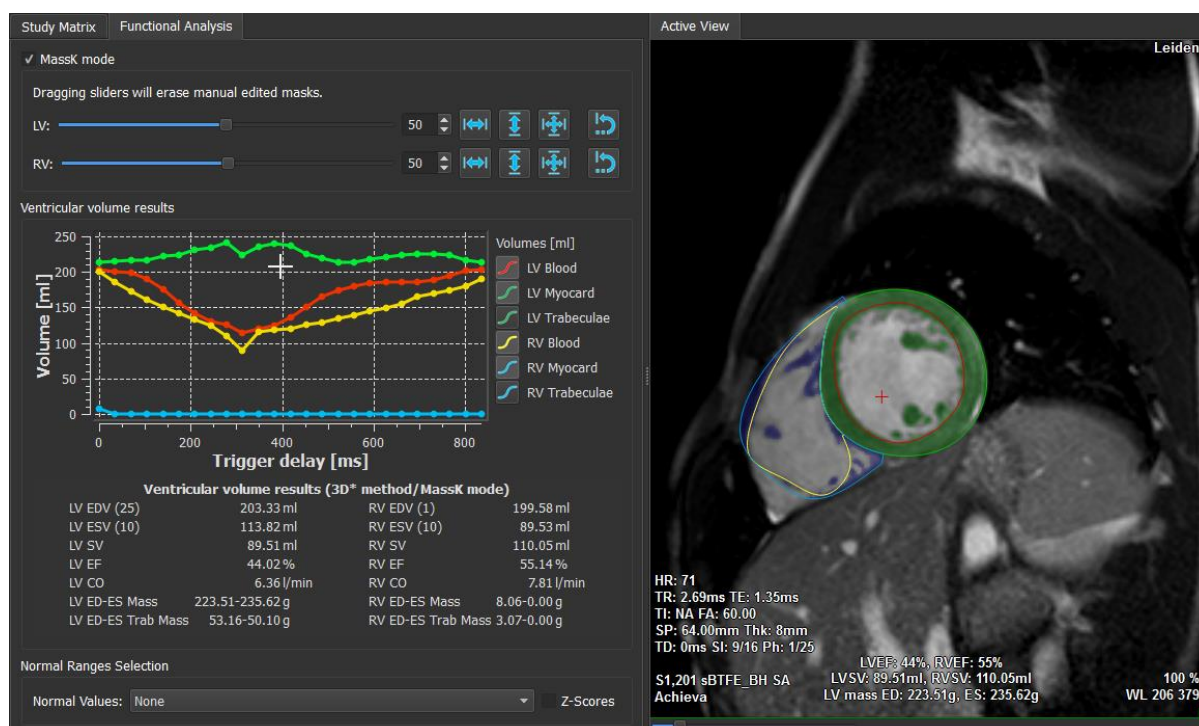
You can add a normal range and Z-score to the Results or Report. QMass automatically selects a set of normal ranges based on the patient gender, age and the magnetic field strength of the scanner or you may choose a different set of normal values in the Functional Analysis Pane:
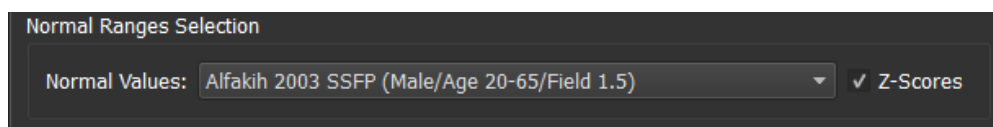


To add Z-scores to text report, click the check box .

The default normal values are based on the following articles: [1,2,3,4,5].

# 6.     T2w Analysis

The T2-weighted (T2w) analysis helps you determine the amount of volume of high T2w signal intensity in the myocardium which has been applied extensively in imaging edema in various myocardial diseases.

This chapter explains how to perform an analysis using the T2w analysis.

**Performing a T2w Analysis**

QMass features a T2w analysis. It is a simple one page analysis tool. One should:

- Create LV endocardial and epicardial contours

- Detect and verify the areas of high and low signal intensity within the myocardium.

- Verify the T2w threshold and segmentation

**To perform an T2w analysis**

1. Load a T2w dataset into QMass.

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

2. Select the series you want to analyze.

3. Start the **T2w Analysis Wizard** by pressing next to  and select  **T2w Analysis Wizard**.

4. In the wizard, click  and draw LV endocardial contours in each slice of the series in the Active View. Similarly, click  to draw LV epicardial contours in each slice of the series.

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

5. Click Detect  and check if the ROI1 contour is detected in low signal intensity part of the myocardium and if ROI2 is detected in high signal intensity part of the myocardium. If necessary, you can edit the contours or re-detect them using the Detect button.

6. Check the T2w threshold by reviewing the segmentation of high intensities in all slices. You can override the calculated threshold by dragging the slider under **Intensity Threshold**.

   💡 You can copy a manually set threshold value to other slices using **Copy to all slice numbers**  , **Copy to lower slice numbers**  or **Copy to higher slice numbers**  .

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

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

   💡 You can hide the masks by deselecting **Menu**  > **Settings > Main Settings > Display > masks**.

   💡 View the results in the T2w Pane, or the Results Pane or the Report pane of Medis Suite.

**To perform a T2 ratio measurement**

1. Use the ROI icon  to determine an area within the myocardial region by drawing the corresponding contour.

2. Use the ROI icon  to determine the skeletal muscle by drawing the corresponding contour.
3. From the two ROIs the mean, minimum, and maximum signal intensities are calculated and used to calculate the T2 ratio between the two defined regions.

💡 The T2 ratio value can be seen on the report pane.

**Transferring contours from short axis cine series**

If contours are already available in the short axis cine series, you can load the series and transfer the contours from this series to the T2w series by clicking . Contour transfer works best if you manually create contours in the phase of the short axis cine series in which the T2w series was scanned.

# 7.  DSI Analysis

A Delayed Signal Intensity (DSI) analysis can help you to determine the infarct size as well as the extent of infarct transmurality which appears to delineate viable and nonviable myocardium and the recovery of function after revascularization.

For further reading, see the following article: *Gibbons, Raymond J., et al. "The quantification of infarct size." Journal of the American College of Cardiology 44.8 (2004): 1533-1542.*

The wizard consists of four steps:

- creating LV endocardial and epicardial contours

- verifying the areas of healthy and hyper-intense myocardium

- verifying the DSI threshold and segmentation

- placing a reference point, setting the transmurality threshold.

**To perform a DSI analysis**

1. Load a DSI dataset into QMass.

    See also, "**Automatic contour detection in DSI series.**"

2. Select the DSI series you want to analyze.

3. Start the **DSI Analysis Wizard** by pressing next to       and select       **DSI Analysis Wizard**.

4. In the wizard, click       and draw LV endocardial contours in each slice of the series in the Active View. Similarly, click       to draw LV epicardial contours in each slice of the series.

    See also, "**Automatic contour detection in DSI series**".

5. Click **Detect**       and check if the ROI1 contour is detected in healthy myocardium and if ROI2 is detected in hyper-intense myocardium. If necessary, you can edit the contours or re-detect them using the **Detect** button.  The DSI hyper-enhanced threshold is also calculated when the **Detect** button is pressed.

    The calculated threshold value is copied automatically to all other slices if the option **Auto copy** is selected. If you use the **Apply** button without **Auto copy** selected, then the ROI contours and threshold value are determined for the current slice only. You can repeat this for each slice separately.

6. Check the DSI threshold by reviewing the infarct size segmentation in all slices. You can override the calculated threshold by dragging the slider under **Intensity Threshold**.

Click  and  to draw areas with hypo-enhancements.

To start erasing pixels, click  .

💡 You can copy a manually set threshold value to other slices using **Copy to all slice numbers**  , **Copy to lower slice numbers**  or **Copy to higher slice numbers**  .

💡 You can calculate another threshold value based on the healthy contour area by specifying a calculation method.

💡 You can increase the tip size of the brush or the eraser by increasing the **Draw size**.

💡 Select **Smart brush** or click  in the toolbar if you want to edit the current mask without overwriting or erasing other masks.

💡 You can hide the masks by deselecting **Display masks**.

7. Set a reference point. You can place a reference point by clicking  and setting a reference point in the Active view at the inferior or anterior end of the interventricular septum.

🛑 Make sure a reference point is placed in every slice you are analyzing.

🛑 If you place the reference point at the <u>anterior</u> septum, make sure to change the bull's-eye settings, so that the cardiac segments are labeled correctly. Select Menu ⋮ > **Settings > Bull's-Eye…** On the **Display** tab, under **Reference Point Location**, select **Anterior**.

💡 If you want to change the default transmurality threshold of 50 %, you can modify the threshold under **Transmurality Threshold**.

💡 You can click  to open a bull's-eye window. You can also select the diagram of your choice from the **Show** drop-down list. Right-click in the window to access options for saving the diagram and for adding it to Results.

💡 View the results in the DSI Pane, or the Results Pane or the Report pane of Medis Suite.

**Automatic contour detection in DSI series**

The contours can be detected automatically in DSI series by clicking .

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

# 8.    Combined T2w-DSI Analysis

The Combined T2w-DSI analysis helps you determine the index and difference between T2w analysis results and DSI result.

This chapter explains how to perform a T2w-DSI analysis.

**Performing a T2w-DSI Analysis**

QMass features a T2w-DSI analysis. It is a simple analysis tool. One should:

- Load and create LV endocardial and epicardial contours in both T2w and DSI series.

- Do a T2w and DSI analysis on the respective datasets.

**To perform a T2w-DSI analysis**

1. Load a DSI and T2w dataset into QMass.

2. Start the **T2w-DSI Analysis Wizard** by pressing next to  and select  **Combined T2w-DSI**.

3. Complete a DSI analysis on the DSI dataset.

4. Complete a T2w analysis on the T2w dataset.

 View the results in the DSI/T2w and Combined T2w-DSI Pane, or the Results Pane or the Report pane of Medis Suite.

 In the Combined T2w-DSI analysis, the high T2w volume is always assumed to be larger or equal to the volume of the infarct volume. If the infarct is greater in volume than the high T2w volume then the volume and calculations will be rounded to zero as opposed to showing the negative values.

# 9.    TSI Analysis

In QMass, you can perform a first-pass perfusion analysis, which is called a Time Signal Intensity (TSI) analysis. To do this, you must take the following steps:

- draw endocardial and epicardial contours

- place reference points

- register the contours

**To draw endocardial and epicardial contours**

1. Load a TSI dataset into QMass.

2. Select the TSI series you want to analyze and click **OK**.

3. If the Time Signal Intensity toolbar with the  icon does not appear, select the Study Matrix tab, and check if the series is labeled correctly. You can do this by right-clicking the series tab.

4. In the Thumbnail View, select an image that shows sufficient contrast in both the left and the right ventricle.

5. By default, the drawing mode is set to tracing. To draw in point mode, click .

6. In the Active View, draw the endocardial contour, then click  and draw the epicardial contour.

    Make sure to exclude the LV and RV blood pool by drawing correct endocardial contours, to avoid that its high intensity signal affects the results.

7. If you want to analyze signal intensity over time in a region of interest, click . In the Active View, draw a contour around the region of interest (ROI).

   If you want to compare one or more ROIs with each other, click one of the other ROI icons , , or  and draw the corresponding contour or contours in the Active View.

**To place reference points**

1. Click .

2. In the Active View, place a reference point at the inferior or anterior junction of the right ventricle and the left ventricle.

    If you place the reference point at the <u>anterior</u> septum, make sure to first change the bull's-eye settings, so that the cardiac segments are labeled correctly. Select Menu  > **Settings > Bull's-Eye…** On the **Display** tab, under **Reference Point Location**, select **Anterior** and click **OK**.

**To register contours**

1. If you have drawn one or more ROIs, select the corresponding menu item or items from the Registration submenu. Click the arrow next to  and then select **Register ROI1 Contours** and the other menu items that apply.

2. Click  .

   This copies the selected contours to the other images in the slice and performs breathing motion correction.

    Contour registration is performed based on the contour registration settings. To access and modify these settings, select **Menu** , **Settings > Registration Settings**

3. Check the contours in the Thumbnail View or in the Movie Tool to see if the automatic positioning of the contours needs correcting.

   To move a set of contours to another position, press SHIFT+CTRL and drag them to their new position.

    Do **not** edit the contours using the drawing tools. If you want to add new ROIs after performing registration, make sure to create the ROI contours in the same image in which you created the initial contours.

**To view TSI analysis results**

1. Click  to display the analysis results in a graph.

2. From the **Show** drop-down list, select the **Myo Intensity – Time** or **ROI Intensity – Time** graph.

Or,

1. Click  to display the analysis results in a bull's-eye diagram.

2. From the **Show** drop-down list, select **SI Analysis**.

   This adds a drop-down list to the dialog window.

3. Select the type of diagram that you want to view.

    For a detailed description of the bull's-eye diagrams, refer to the User Manual.

 Click the Right mouse button to select 'toad snapshot to Results' to add the snapshot of the graph to the Reporting.

 View the results in Results Pane or the Report pane of Medis Suite.

# 10.   T1 Analysis

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

This chapter explains how to:

- Perform a T1 analysis

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

**To perform a T1 analysis**

- Load a T1 dataset into QMass.

- Select the T1 series you want to analyze.

💡 In the Study Matrix, right-click the series tab and check if the series is labeled correctly as a T1 series. If needed, you can change the series label in the submenu.

- Select the T1 Analysis tab.

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

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

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

- Click ◎ and draw the epicardial contour.

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

- Mark one or more regions of interest in the septum. Select the region of interest icon, for example, ①, and draw a region of interest in the myocardium.

💡 You can deselect **Auto copy** under **Contours** to prevent copying the contours of the regions of interest to the other images.

- The T1 Analysis tab now shows two curves per region of interest: the curve of the measured values in the color of the region of interest, and the fitted curve as a dotted line.

- The "Time [ms]" box now shows the T1 recovery time.

💡 You can click on the icons in the "Time [ms]" box to show or hide the various regions of interest.

💡 You can select and display the T1, T1*,, or the Residual overlay by selecting an **Overlay** from the drop-down selection box.

💡 You can select the Acquisition type, Look-Locker (LL) which displays the T1*, T1 or the t0 results or Progressive Saturation (PS), which displays the T1 and the t0 results.

| Result | Description |
|---|---|
| **T1** <br><br> **(Progressive saturation)** | T1 for progressive saturation studies corresponds to the following equation: <br><br> I = A – B • EXP (-t/T1) |
| **T1\* (Look-Locker)** | T1* for Look-Locker studies corresponds to the following equation: <br><br> I = A – B • EXP (-t / T1*) |
| **T1 (Look-Locker)** | T1 value for Look-Locker studies corresponds to the following equation: <br><br> T1 = T1 • (B / A – 1) |
| t0 | t0 is the "Nulling time", i.e. the time at which the signal intensity crosses the zero on the horizontal axis. One can also roughly estimate the t0 value from the graph. |

You can also view the recovery rate per pixel using mouse cursor tracking. Click , and then hover the mouse over the pixel in the image. This displays the currently tracked pixel's recovery rate.

💡 Please refer to the following article for information about T1 mapping in Look-Locker studies: Daniel R. Messroghli et al, Modified Look-Locker Inversion Recovery (MOLLI) for High-Resolution $T_1$ mapping of the Heart, Magnetic Resonance in Medicine 52: 141-146 (2004).

💡 View the results in the T1 Pane, or the Results Pane or the Report pane of Medis Suite.

**To set a color range and color map setting**

1. Select Menu ⁝ > **Settings > T1 Settings**.

   This opens the T1 Settings dialog window.

Under **Color range**, choose your preferred color range of colors. Under **Color Map**, choose your preferred overlay color map.

💡 You can specify a default color map in the Configuration File Editor.

**To export the relaxation times per slice to DICOM**

Click  the "Add parametric map to Results" button.

💡 The maps will automatically appear in the current QMass session and can be selected on the Study Matrix tab for further analysis.

➡ For instructions on series selection, see: Starting QMass.

# 11.   T2/T2* Analysis

With the T2/T2* analysis it is possible to determine T2/T2* relaxation times. Quantification of T2* relaxation time helps characterizing iron loading in heart and liver.

This chapter explains how to:

- perform a T2 or T2* decay time analysis

A T2 or T2* decay time analysis consists of two steps: first you must draw a contour around the region of interest in the myocardium, and then you must exclude the measurements from the curve that are biased by MR noise.

**To perform a T2 or T2* analysis**

1. Load a T2/T2* dataset into QMass.
2. Select the T2/T2* series you want to analyze.
3.
In the Study Matrix, right-click the series tab and check if the series is labeled correctly as a T2/T2* series. If needed, you can change the series label in the submenu.

4. Select the T2/T2* Analysis tab.

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

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

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

7. Click  and draw the epicardial contour.

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

8. Mark one or more regions of interest in the septum. Select the region of interest icon, for example,  , and select  . Click the epicardial contour to mark the beginning of the septal segment, and then double-click the endocardial contour to mark the end.

    This creates the region of interest. The following illustrations show an example.
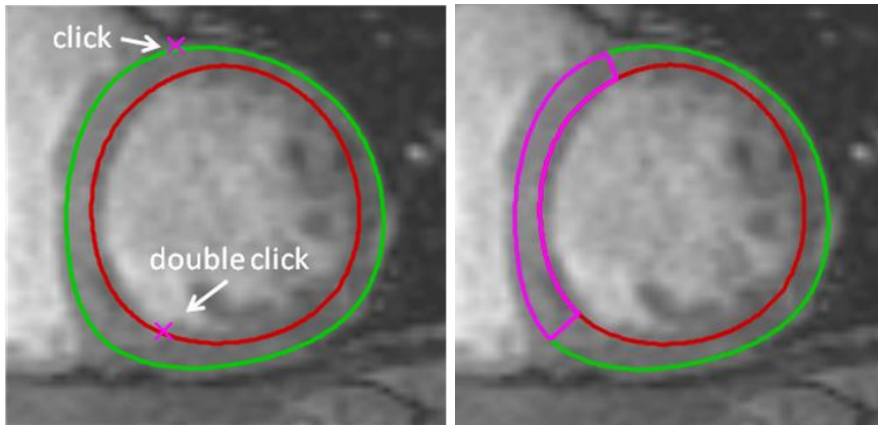
💡 You can deselect **Auto copy** under **Contours** to prevent copying the contours of the regions of interest to the other images.

9. The T2/T2* Analysis tab now shows two curves: the curve of the measured values in the color of the region of interest, and the fitted curve in a light and semitransparent version of that color.

   To remove the measurement points that are biased by MR noise and calculate the correct T2/T2* value of the region of interest, you must drag the cut-off slider to the point where the curve starts to level off.

   ⓘ If the curve slopes upward instead of downward at the end, make sure to first exclude the corresponding images. You do this by clicking the green squares in the bottom right corner of the images in the Thumbnail View.

   Pick up the white triangle at the bottom of the diagram and drag it up.

   This marks the points under the slider as excluded and makes the fit curve the non-excluded part of the measured curve. Make sure that the fit curve runs through the first measured points.

   The following illustration provides an example.
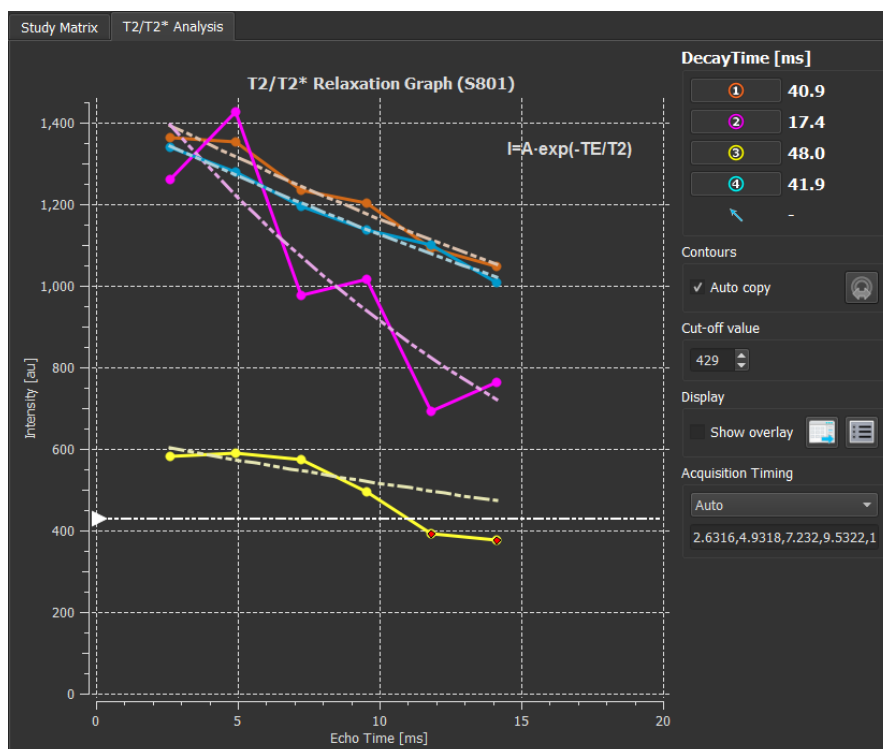
10. Define the Acquisition Timing. Choose "Auto" to use the timing derived directly from the scanner, or use the configurable Acquisition Timings, such as "T2Prep_4", if the values are not available from the scanner.

💡 Using the Configuration File Editor, in the Acquisition Timing section, you can specify the timing values. T2Prep_4 is an example of a timing configuration.

🛑 Using Acquisition Times that have been configured may lead to incorrect results. Make sure to review them and correct if necessary.

11. The Decay Time box now shows the T2 or T2* decay time.

Use the icons in the Decay Time box to show or hide the various regions of interest.

You can display a color overlay of the decay time by selecting **Show overlay** under **Display**.

| Result | Description |
|---|---|
| **T2 or T2*** | The result corresponds to the following equation:<br><br>$I = A \bullet EXP\ (-TE\ /\ T2)$<br><br>where TE is the Echo Time in ms and whereT2  indicates  T2 for T2 analysis or T2* for T2* analysis |

You can also view the decay rate per pixel using mouse cursor tracking. Click , and then hover the mouse over the region of interest. This displays the currently tracked pixel's decay rate in the status bar at the bottom of the QMass window.

💡 View the results in the T2/T2* Pane, or the Results Pane or the Report pane of Medis Suite.

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

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

    This opens the T2/T2* Settings dialog window.

Under **Color Map**, choose your preferred color scheme.

After **Cut-off value**, specify the default to be used during the current session.

💡 You can specify a persistent default cut-off value in the Configuration File Editor.

**To set the Acquisition Timing**

1. Select the Acquisition Timing.

Under **Color Map**, choose your preferred color scheme.

After **Cut-off value**, specify the default to be used during the current session.

💡 Using the Configuration File Editor, in the Acquisition Timing section, you can specify the timing values. T2Prep_4 is an example of a timing configuration.

🛑 Using Acquisition Times that have been configured may lead to incorrect results. Make sure to review them and correct if necessary.

**To export the decay times per slice to DICOM**

Click ⊞ the "Add parametric map to Results" button.

💡 The maps will automatically appear in the current QMass session and can be selected on the Study Matrix tab for further analysis.

➡ For instructions on series selection, see: Starting QMass.

# 12. Finishing a QMass analysis

When you have finished analyzing, press the save session button on the Medis Suite.

 For a detailed description on stopping a Medis Suite session, refer to the Medis Suite Quick Start/User Manual.

# Accuracy of Measurements

In QMass all measurements are derived from calculations performed on the loaded DICOM images.

Both during development and with each new release of the product, measurements and calculations are extensively validated. The accuracy of the measurements and calculations exceeds that of the displayed results, by at least one decimal point.

In practice, the image is the limiting factor of the accuracy of measurements. Limiting factors, such as, image resolution both spatial and time-based, image noise, inhomogeneity in the magnetic field and patient determines the accuracy of any given measurement.

The effective accuracy of measurements has been evaluated with multiple validation studies. The following table gives the expected accuracy for the different types of measurement.

| QMass Results | Common value | Unit | Expected accuracy | Precision | Accuracy justification and source is applicable |
|---|---|---|---|---|---|
| **Left and right ventricular volume results** | | | | | |
| Body Surface Area | 2 | m² | 5% | 0.01 | Accuracy entirely dependent on the manual user input |
| ED phase number | 2 | | | 1 | Is accurate, as long as the contours are drawn correctly |
| ES phase number | 9 | | | 1 | Is accurate, as long as the contours are drawn correctly |
| ED phase time | 39.75 | ms | 25 ms | 0.01 | Depends on the acquisition sample frequency, given for a typical 20 frames/ heartbeat, 60 bpm |
| ES phase time | 272.25 | ms | 25 ms | 0.01 | |
| ED volume | 129.43 | ml | 5%-10% | 0.01 | [1] - Depends strongly on the acquisition number of slices. Value given for typical 10 slices |
| ED volume index | 64.71 | ml/m² | 5%-10% | 0.01 | - derived |
| ED volume/HT (HT=height) | 71.9 | ml/m | 5%-10% | 0.01 | - derived |
| ES volume | 63.63 | ml | 5%-10% | 0.01 | [1] - Depends strongly on the acquisition number of slices. Value given for typical 10 slices |
| ES volume index | 31.81 | ml/m² | 5%-10% | 0.01 | - derived |
| Stroke volume | 65.8 | ml | 8%-15% | 0.01 | Derived from ED an ES volume accuracy |
| Stroke volume index | 32.9 | ml/m² | 8%-15% | 0.01 | - derived |
| Cardiac output | 4.76 | l/min | 8%-15% | 0.01 | Derived from Cardiac output |

| | | | | | |
|---|---|---|---|---|---|
| Cardiac output index | 2.38 | l/(m²*min) | 8%-15% | 0.01 | - derived |
| Ejection fraction | 50.84 | % | 8%-15% | 0.01 | Derived from Cardiac output and ED volume |
| LV mass ED | 109.45 | g | 25% | 0.01 | Derived from volume, however, cardia muscle density is not a constant [12] |
| LV mass ED index | 54.72 | g/m² | 25% | 0.01 | - derived |
| LV mass ED/HT | 60.81 | g/m | 25% | 0.01 | - derived |
| LV mass ES | 117.88 | g | 25% | 0.01 | See LV mass ED |
| LV mass ES index | 58.94 | g/m² | 25% | 0.01 | - derived |
| **Ejection / filling dynamics** | | | | | |
| Parameter | Value | | | | |
| PER | 535.46 | ml/s | 10% | 0.01 | Derived from volume, limited by acquisition frequency. |
| PER/EDV | 4.14 | EDV/s | 10% | 0.01 | - derived |
| TPER | 66.63 | ms | 25ms | 0.01 | Depends on the acquisition sample frequency, given for a typical 20 frames/ heartbeat, 60 bpm |
| TPER phase number | 4 | | | 1 | Is accurate, as long as the contours are drawn correctly |
| PFR | 325.11 | ml/s | 10% | 0.01 | Derived from volume, limited by acquisition frequency. |
| PFR/EDV | 2.51 | EDV/s | 10% | 0.01 | - derived |
| TPFR | 232.63 | ms | 25ms | 0.01 | Depends on the acquisition sample frequency, given for a typical 20 frames/ heartbeat, 60 bpm |
| TPFR phase number | 16 | | | 1 | Is accurate, as long as the contours are drawn correctly |
| **Time intensity** | | | | | |
| Amplitude | 780.7 | AU | | 0.1 | Since this is an arbitrary unit, there is no specific accuracy. |
| Max upslope | 364.8 | AU/s | | 0.1 | Since this is an arbitrary unit, there is no specific accuracy. |
| Time max upslope | 14.6 | s | 2 | 0.1 | Determined by time interval between acquisitions. Based on a typical one acquisitions / 2 seconds |

| Mean intensity | 1348.8 | AU | | 0.1 | Since this is an arbitrary unit, there is no specific accuracy. |
|---|---|---|---|---|---|
| Time to 50% max | 15.7 | s | 2 | 0.1 | Determined by time interval between acquisitions. Based on a typical one acquisitions / 2 seconds |
| T0 intensity | 1,020.1 | AU | | 0.1 | Since this is an arbitrary unit, there is no specific accuracy. |
| Baseline intensity | 930.6 | AU | | 0.1 | Since this is an arbitrary unit, there is no specific accuracy. |
| Relative upslope | 58.7 | % | 2 | 0.1 | [2] |
| **Wall thickness / motion** | | | | | |
| Chords wall thickness | 20.00 | mm | 5% | 0.01 | [10] - error based on 2 standard deviations |
| Chords wall motion | 10.00 | mm | 11% | 0.01 | [10] - error based on 2 standard deviations |
| Chords wall thickening | 100.00 | % | 16% | 0.01 | [10] - error based on 2 standard deviations |
| Mean wall thickness | 20.00 | mm | 0.1% | 0.01 | [10] - error based on 2 standard deviations |
| Mean wall motion | 10.00 | mm | 0.1% | 0.01 | [10] - error based on 2 standard deviations |
| Mean wall thickening | 100.00 | % | 0.1% | 0.01 | [10] - error based on 2 standard deviations |
| **Long axis volumes / wall motion** | | | | | |
| ED Volume | 110.00 | ml | 8% | 0.01 | Typical for long axis volume approximation |
| ES volume | 50.00 | ml | 8% | 0.01 | Typical for long axis volume approximation |
| ED Mass | 120.00 | g | 25% | 0.01 | Derived from volume, however, cardia muscle density is not a constant. [12] |
| ES Mass | 55.00 | g | 25% | 0.01 | Derived from volume, however, cardia muscle density is not a constant. [12] |
| Ejection Fraction | 55.00 | % | 15% | 0.01 | Based on volume accuracy |
| Stroke Volume | 60.00 | ml | 12% | 0.01 | Based on volume accuracy |
| Wall thickening | 100.00 | % | 0.1% | 0.01 | Based on short axis accuracy calculations |
| Wall thickness | 20.00 | mm | 0.1% | 0.01 | Based on short axis accuracy calculations |

| Wall thickness segment | 20.00 | mm | 0.5% | 0.01 | Based on short axis accuracy calculations and segment size |
|---|---|---|---|---|---|
| **Delayed Signal Intensity** | | | | | |
| Infarct size volume | 39.81 | ml | 5% | 0.01 | [5], combined with generic accuracy [1] |
| Infarct size mass | 41.80 | g | 10% | 0.01 | [5], combined with generic accuracy [1], and [12] |
| Infarct size percentage | 34.02 | % | 5% | 0.01 | [5] |
| High transmural extent volume | 32.90 | ml | 5% | 0.01 | [5], combined with generic accuracy [1] |
| High transmural extent mass | 34.54 | g | 10% | 0.01 | [5], combined with generic accuracy [1], and [12] |
| **T2*** | | | | | |
| Relaxation time | 43.6 | ms | 5% | 0.1 | [9] |
| Relaxation rate | 22.9 | Hz | 5% | 0.1 | Is the inverse of the relaxation time |
| Cardiac Iron Load T2 (1.5T) | 0.44 | mg/g | 0.01% | 0.01 | [13] |
| Liver Iron Load T2 (1.5T) | 0.78 | mg/g | 0.01% | 0.01 | [13] |
| Cardiac Iron Load T2 (3.0T) | 0.38 | mg/g | 0.01% | 0.01 | [13] |
| Liver Iron Load T2 (3.0T) | 0.63 | mg/g | 0.01% | 0.01 | [13] |
| **T1/T1*** | | | | | |
| T1* Decay Time | 1620 | ms | 5% | 1 | [11] |
| T1 Decay Time | 1560 | ms | 5% | 1 | [11] |

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**Adding Results To Excel**

To add results into excel you can you the CSV format. To get the results in excel do the following:

- Go to the text report
- Select the desired text and or tables
- RMB > Select **Copy CSV**.
- In Excel > **Paste Special** > Select **CSV**.


**Cine Grid with holes**

Sometimes the Cine image matrix may appear irregular in the number of images per slice or phase, or there are holes where images are missing. This is caused by duplicated slices in the series.

- Go to the file browser
- Check that filter duplicates is selected and press rescan
- Load the data again
- Now the image matrix should be nice and regular.


**No Short Axis results**

Sometimes when you have a Short Axis and a Long Axis series with the same series description the sorting and splitting of these series is wrong. One of the consequences is that no Short Axis results are shown. To avoid this, make sure the LA series and SA series have different series descriptions.


**No results in the Combined T2w-DSI Report**

**Combined T2w-DSI** results are only available when the **Combined T2w-DSI** wizard is open. Once the **Combined T2w-DSI** wizard is open all **Combined T2w-DSI** results are available in the Results and the Report.

# 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. |

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# Shortcut Keys

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

The following shortcut keys are applicable to all views.

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| Shortcut | Use to |
|---|---|
| **Studies and Contour Files** | |
| CTRL+O | open a study browser. |
| CTRL+F5 | refresh the directory tree of the browser. |
| **Images** | |
| + | zoom in. |
| - | zoom out. |
| **Elements** | |
| CTRL+D | detect contours automatically. |
| CTRL+Z | undo the actions you performed. |
| CTRL+Y | redo the actions you undid. |
| CTRL+C | copy all elements from the active image to the clipboard. |
| CTRL+V | paste the active element to the selected image. |
| CTRL+SHIFT+V | paste all elements to the selected image. |
| DEL | delete the currently selected element. |
| CTRL+T | transfers the contours from the short-axis cine series to the DSI series. |
| CTRL+R | registers the created contours to the other images in the series. |
| F5 | Open the movie dialog |
| F6 | Open the Study parameter dialog |

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| F7 | Open the Graph dialog |
|---|---|
| F8 | Open the bull's eye dialog – 16 segment model |
| Ctrl + F8 | Open the bull's eye dialog – segmented per slice |
| Ctrl + Shift + F8 | Open the bull's eye dialog – no segments. |
| X | Toggle inclusion or exclusion of selected images for automatic contour detection. |

The following shortcut keys are applicable to the active view.

| Shortcut | Use to |
|---|---|
| drag using the middle mouse button | pan the image. |
| press W, then drag | adjust the window width and level of the images. By default, a horizontal movement adjusts the window width, and a vertical movement adjusts the window level.<br><br>Press the W key on the keyboard or make sure that  is selected to make the window width and level mode active. |
| 1 | reset window width and level to the original values. |
| 2 | optimize window width and level. |
| click+hold down the middle mouse button or mouse wheel | hides the contours and all patient and study properties shown in the Active View. Release the middle mouse button to show the contours again. |
| CTRL+drag | move the active contour relative to the image in the Active View and Thumbnail View. |
| CTRL+SHIFT+drag | move all elements relative to the image in the Active View and Thumbnail View. |
| CTRL+SHIFT+ALT +drag | move all elements in the entire slice stack relative to the images in the Active View and Thumbnail View. |
| SHIFT + S | reshapes a contour by removing small irregularities. |
| SHIFT + D | reshapes a contour by removing curves. |
| SHIFT + C | reshapes a contour by removing all curves that point inward. |
| SHIFT + E | reshapes a contour by redetecting the edge, using the existing contour as a model. |
| S | add the image in the Active View to the report. |

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| | |
|---|---|
| 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 |

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| [ or ] | Increases and decreases the brush size, when using DSI, T2w or Functional MassK mode analysis. |

The following shortcut keys are applicable to the movie window.

| Shortcut | Use to |
| --- | --- |
| PgUp | Scroll to the next series in the Movie window. |
| PgDn | Scroll to the previous series in the Movie window. |
| P | play the movie |
| S | stop the movie |
| up | show the next slice |
| down | show the previous slice |
| right | show the next phase |
| left | show the previous phase |
| F2 | toggle between slice and phase looping |

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