# 11 MR QFlow Analysis

This postprocessing package calculates quantitative information as flow velocity or flow rate, visualized as 2D color flow maps overlaid on anatomical references. These flow maps can be used to view stroke volumes or analyze CSF flow.

A QFlow scan is a scan where multiple acquisitions take place within one cardiac cycle, resulting in multiple phases.

Results from QFlow analysis include stroke volume, forward and backward flow volumes, flux, stroke distance, mean velocity, maximum velocity, minimum velocity, peak velocity, and vessel area.

### Benefits

If the device is used as specified in the Indications for Use, under the circumstances and conditions as specified in the Indications for Use, the ISP MR QFlow application assists users to view and interpret anatomy and flow related MR (phase-contrast) datasets. The application assists to exclude or confirm the presence of ambiguity in flow-through vessels, valves or spinal cord/aqueduct.

The expected patient benefits are: With the use of the application, the investigating radiologist or cardiologist can specify the flow related conditions and can use MR QFlow results solely or in conjunction with other cardiac related qualitative and quantitative application results to define a report for the referring physician. Based on the results of the requested flow conditions, the referring physician can define and/or advise a diagnosis and treatment path to the patient or propose actions to control risk factors with healthy lifestyle changes and/or medicines or further investigations.

### Valid Imaging Series

Suitable scans are QFlow scans that are triggered PCA scans containing at least PCA/Phase images and FFE/Modulus, and optionally PCA/Modulus images.

Reliable results are achieved when the scan has been acquired perpendicular to the vessels of interest, although scans in the same plane as the vessels can also be loaded for viewing.

### Phase Wrapping

Phase wrapping may occur if the VENC value (the (maximum) velocity encoding value) used during acquisition is too low compared to the actual maximum blood flow velocity in the vessel or structure. Phase wrapping causes incorrect value of the velocity in QFlow analysis.

Directly after acquisition, you should inspect the MRI data for phase wraps. If phase wraps are present, you should repeat the acquisition using a higher VENC value.

## Indications for Use

The MR Qflow application supports the visualization and quantification of fluid (blood and CSF) flow dynamics by assisting in reviewing of MR phase-contrast data.

# User Interface

## Screen layout

The QFlow Analysis package has a default layout of two image viewports, a graph viewer, a table viewer, and toolbar and panels.

### Viewports

The slice that is selected for viewing is displayed in both viewports in the upper part of the main display area. The first viewport displays the source image displaying the first slice in the imaging volume (FFE/M image). The second viewport displays a PCA/P image. The image type of each viewport can be changed independently using the viewport control in the lower-left corner of the viewport. You can also add a color overlay indicating flow to the second viewport using the right-mouse menu.

## Task Guidance

Similar to all packages on the IntelliSpace portal, the QFlow Analysis package provides a task guidance panel in the left part of the screen. The task guidance panel provides the following steps:

- Create Segmentation
- Verify Contours
- Review Results

The Workflow section later in these Instructions for Use is based on this Task Guidance. For details, see section “Workflow” on page 250.

**NOTICE**

Follow the steps of the Task Guidance to make optimal use of the QFlow Analysis function.

## Toolbar

### Speed (frames per second)

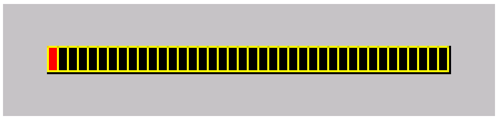
To change the playback speed of the slices in movie mode, click the up or down arrow in the **Speed** box.

### Movie Mode

Use the Movie Mode tool to play or pause review of the slices:

- ◀ **Play backward**
- ❚❚ **Pause**
- ▶ **Play forward**

### Image Navigator



The phases of the displayed series are represented by a row of blocks in the Image Navigator. Each block represents a phase that can be displayed in the main display area, and the currently displayed phase is highlighted. You can display a phase by clicking a block.

Phase or slice positions that contain an ROI are colored gray.

If a phase or slice position contains a red cross in the Image Navigator, this indicates that the contours are crossing. This should be fixed before moving to the Results screen.

### Settings

To change the application settings, click **Show settings dialog**. You can configure the following settings:

- Select different units to be used for analysis.
- Display forward flow analysis as always positive in the analysis graph and numerical results.

## More Functions within the QFlow Analysis package

In IntelliSpace Portal MR packages, the most important functions can be performed via the Task Guidance and the toolbar. However there are more functions which you can access via the right mouse menus.

For more information, see section “Right mouse menus” on page 12.

### Additional right mouse functions with QFlow Analysis

In addition to the standard right mouse functions, QFlow Analysis provides the following package-specific functions in the right mouse menu:

| Function | Description |
|---|---|
| Show Overlay | Displays an overlay in the image to provide additional information about the velocity in the anatomy. |
| Propagate | Propagates the contour to other slices. Choose from the following options:<br>• **Propagate next**<br>• **Propagate all**<br>• **Propagate previous** |
| Probe | Adds a probe at the selected point to measure velocity per pixel. |
| Drop Seed / Draw Bezier / Draw Ellipse | Activates / Deactivates the currently selected contour method. |
| Show settings dialog | Opens the **Settings** dialog box, allowing you to change the units used to display analysis results. |
| Export results and segmentation | Opens the **Export results and segmentation** dialog box providing options to save the analysis results in CSV format to a repository or directory. |

# Workflow

## Launch the QFlow Analysis package

▷ In the 'Directory' tab of the activity bar:

1. Select a suitable QFlow scan (triggered PCA scan).

   If you do not select a scan, the system finds appropriate QFlow series (based on DICOM information) when you start the QFlow Analysis package.

2. Click 'QFlow Analysis'.

   The QFlow Analysis package opens.

## Create Segmentation

In this step of the QFlow Analysis process, you create a contour that defines a vessel or valve in the scan.

1. Use the Image Navigator to select a phase that clearly displays the vessel or valve that you want to analyze, and where the area of interest contains the highest velocity.

⇨ The selected phase is displayed in the main display area.

⇨ If desired, you can change the type of image displayed using the "image type" viewport control. You can set the image type independently in each image viewport. The following image types are available:

- FFE/M (anatomical)
- PCA/M (model)
- PCA/P (phase, showing velocity with colored areas of high and low intensity, this type of image is typically used as an overlay)

⇨ When using a PCA overlay, you can use the **Change window level** tool to reduce noise in the image (drag up or down). Dragging right or left with the **Change window level** tool changes the upper limit of the velocity scale on the right side of the viewport.

2. Select a contour tool in the task guidance panel.

   The following contour tools are available (click the arrow next to the contour tool to show all options):

   - **Drop Seed**
   - **Draw Bezier**
   - **Draw Ellipse**

3. When using the bezier or ellipse method, select the **Fit contour to vessel** check box next to the contour tool to allow the contour to automatically find the edges of the vessel or valve.

**NOTICE**

If anatomical structures cover only a few pixels (e.g. small vessels), contours should be verified carefully in order to avoid inaccurate results.

**NOTICE**

The drop seed method is suitable for large vessels. For smaller vessels, better results can be obtained using the bezier or ellipse method. When using the bezier or ellipse method to define a contour on a small vessel, we recommend that you clear the **Fit contour to vessel** check box.

4. To create a contour with the **Drop Seed** contour tool, click on the vessel or valve.

⇨ The position of the vessel or valve is calculated automatically from the seed and a contour is displayed.

5. To create a contour with the **Draw Bezier** tool, do the following:

   - Click on the edge of the vessel or valve.
   - Continue clicking around the edge of the vessel or valve.

- Double-click to complete the contour.

6. To create a contour with the **Draw Ellipse** tool, do the following:
    - Click on the edge of the vessel or valve.
    - Click at the opposite edge of the vessel or valve, or drag to set the size of the ellipse.
    - If desired, you can adjust the width of the completed contour by dragging.
7. After creating a contour, select a label from the **Choose vessel name** dialog box (displayed automatically).

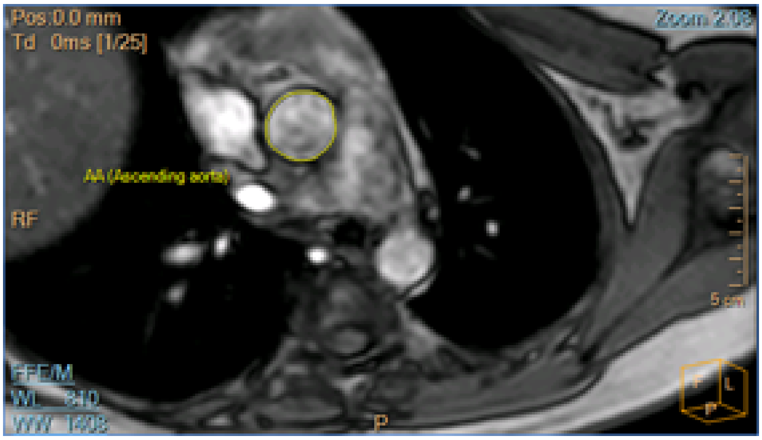


**Fig. 108:** Labeled contour

## Verify Contours

In this step of the QFlow Analysis process, you verify that the contour accurately defines the vessel or valve in every phase of the slice.

1. Click **Play forward** to start movie mode.

    Movie mode provides a good overview of all slices.
2. Click **Pause** to stop movie mode.
3. Drag horizontally to verify the accuracy of the contour in all phases.
4. In the Image Navigator, click the first phase in the series.

**NOTICE**

We recommend that you work with phases from left to right when correcting the contour.

5. Use the **Zoom** interactor to display the contour in detail in the displayed slice.
6. Verify the accuracy of the contour and make corrections if needed:
    - Select any of the interactor tools.
    - Pause the pointer over the edge of the ROI to display the ROI nodes.

- Drag an existing node to a new position, or click and drag on the edge of the contour to create and reposition a new node.
- To delete one or more nodes, drag a node to another node; this action combines the nodes and deletes any nodes in between them.

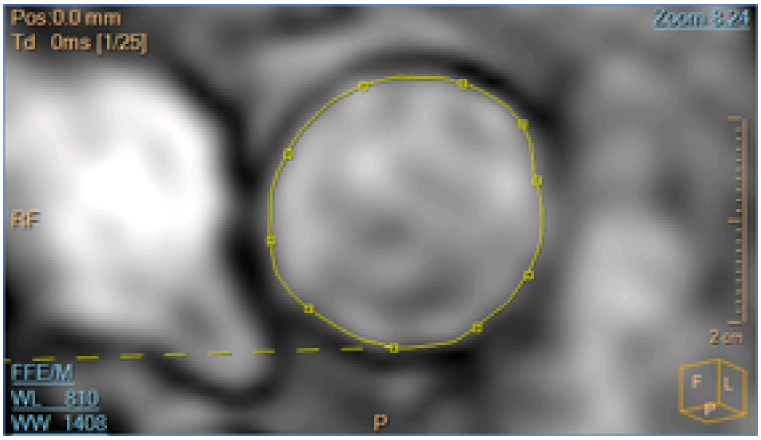


**Fig. 109:** ROI nodes

7. To move a contour, move the pointer over the edge of the contour, press CTRL and drag the contour to a new position.
8. If you are working on a large vessel, select **With fit** in the task guidance panel.

   For smaller vessels, if there is not much movement between the different phases, we recommend that you leave this check box clear.
9. Click **Propagate next** in the task guidance panel to apply the correction to the following phases.
10. In the Image Navigator, click the next slice in the series and repeat the "verify, correct, and propagate" process.
11. Continue sequentially through all the slices until all phases are verified and corrected.
12. To add a probe, right-click at the desired probe location and then click **Probe** in the right mouse menu.

⇨ You can add a probe to either image. The velocity per pixel is displayed next to the probe.

## Using Background Correction

If you are analyzing a series acquired with a non-Philips scanner, you can manually apply background correction to correct for bias or eddy current in the images.

**NOTICE**

Series acquired with a Philips scanner are automatically corrected for bias or eddy current.

To use background correction, do the following:

1. In the task guidance panel, click **Contour** to select the contour tool.
2. If the study is a multi-slice study, select the slice of interest.

**NOTICE**

The correction should be done in the slice of interest because the background correction ROI can only be used in one slice.

3. Draw the background correction ROI on stationary tissue as close to the vessel ROI as possible, but where no velocity from vessels is expected.

⇨ The contour is copied to all phases.

⇨ A row is added to the numerical results table indicating the background correction value (**BC**).

4. In the task guidance panel, select whether to calculate **Correction per phase** or **Correction mean over phases**.

## Review Results

**NOTICE**

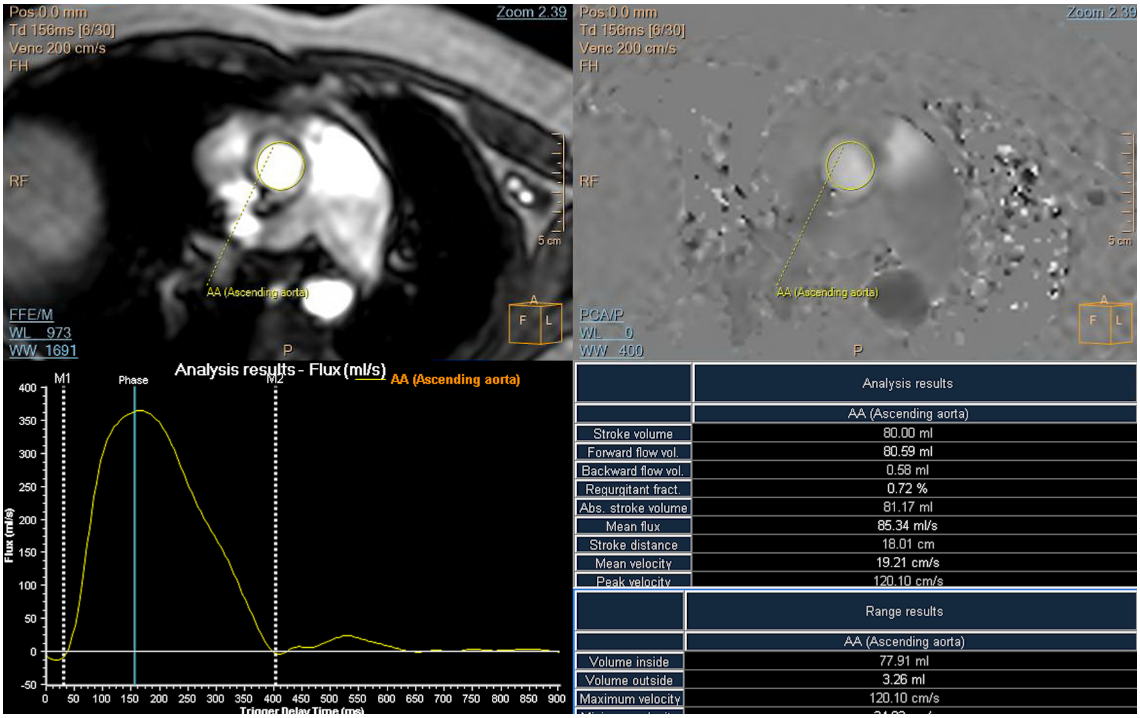
The results of analysis depend on the quality of the acquisition. Ensure that the scan settings are set correctly for the patient at the time of acquisition to assure best results.

**NOTICE**

When the field-of-view (FOV) is not positioned in the isocenter of the magnet, incorrect Q-Flow calculations may occur.

The results of the analysis are displayed automatically in the lower part of the main display area after at least one contour has been defined.

The lower-left viewport displays a graph of the analysis results and the lower-right viewport displays numerical results in a results summary table. The vertical blue line in the graph display (**Phase**) indicates the position of the displayed slice.



| | Analysis results |
|---|---|
| | AA (Ascending aorta) |
| Stroke volume | 80.00 ml |
| Forward flow vol. | 80.59 ml |
| Backward flow vol. | 0.58 ml |
| Regurgitant fract. | 0.72 % |
| Abs. stroke volume | 81.17 ml |
| Mean flux | 85.34 ml/s |
| Stroke distance | 18.01 cm |
| Mean velocity | 19.21 cm/s |
| Peak velocity | 120.10 cm/s |

| | Range results |
|---|---|
| | AA (Ascending aorta) |
| Volume inside | 77.91 ml |
| Volume outside | 3.26 ml |
| Maximum velocity | 120.10 cm/s |

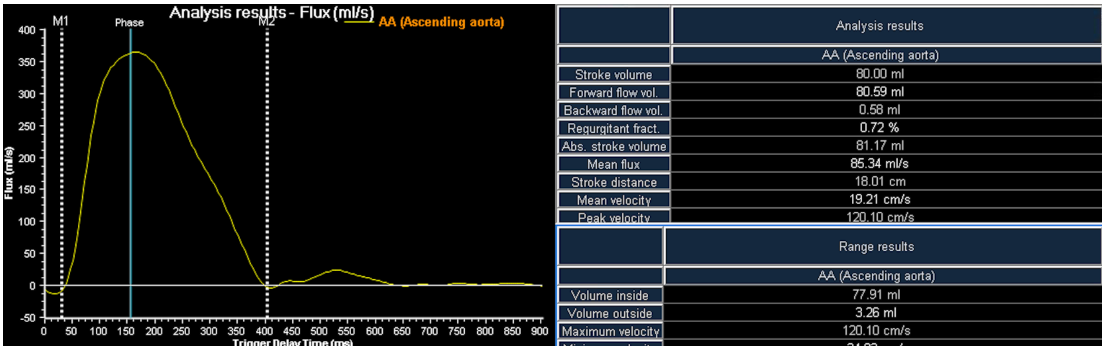
**Fig. 110:** Analysis results

## Defining a Range in the Analysis Results

You can focus the analysis results on part of the flow curve by defining a range in the analysis results graph.

To define a range, do the following:

1. In the analysis results graph, drag the line **M1** to start position of the range.
2. Drag the line **M2** to end position of the range.



| | Analysis results |
|---|---|
| | AA (Ascending aorta) |
| Stroke volume | 80.00 ml |
| Forward flow vol. | 80.59 ml |
| Backward flow vol. | 0.58 ml |
| Regurgitant fract. | 0.72 % |
| Abs. stroke volume | 81.17 ml |
| Mean flux | 85.34 ml/s |
| Stroke distance | 18.01 cm |
| Mean velocity | 19.21 cm/s |
| Peak velocity | 120.10 cm/s |

| | Range results |
|---|---|
| | AA (Ascending aorta) |
| Volume inside | 77.91 ml |
| Volume outside | 3.26 ml |
| Maximum velocity | 120.10 cm/s |

**Fig. 111:** Defining a range in the analysis results graph

⇨ An additional numerical results table is displayed below the main summary table. The additional table is titled **Range results** and it displays analysis results for the defined range only.

**NOTICE**

Setting a range defines all applicable results for this temporal range. If multiple ROIs are drawn, the displayed results include this range for all available curves.

## Understanding the Results

### General Parameters

| | |
|---|---|
| **Heart Rate** | As derived from acquisition. |
| **Velocity Encoding** | As derived from acquisition. |
| **Velocity Direction** | As derived from acquisition. |

Right-click the results summary table and click **Analysis results**. These results are only generated for multiphase scans.

### Stroke volume

- The net amount of blood that passes the contour (1 RR-interval).

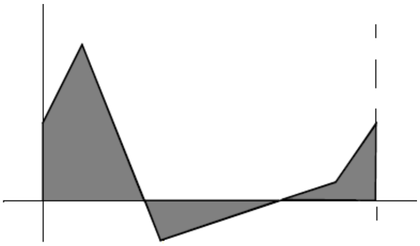


**Fig. 112:** Stroke volume (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

### Forward flow volume [ml]

- The amount of the blood that passes the contour in the positive flow direction (1 RR-interval).

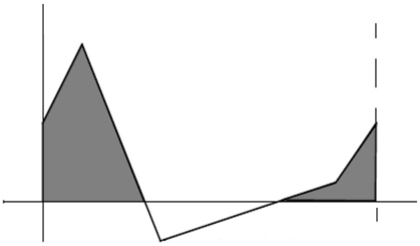


**Fig. 113:** Forward flow volume (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

### Backward flow volume [ml]

- The amount of blood that passes the contour in the negative flow direction (1 RR-interval).

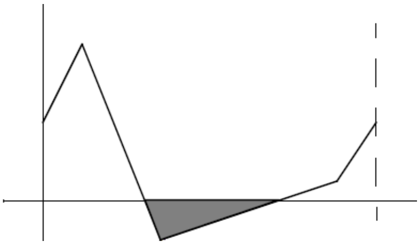


**Fig. 114:** Backward flow volume (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

### Regurgitant fraction

- Fraction of backward to forward flow.

### Absolute stroke volume

- Absolute value of forward flow PLUS absolute value of backward flow (1 RR-interval).

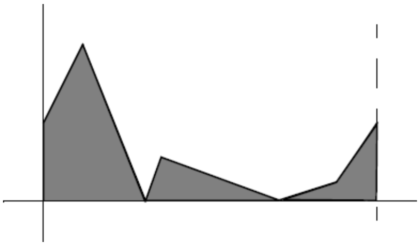


**Fig. 115:** Absolute stroke volume (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

### Mean flux [ml/s]

- Stroke volume x heartbeat / 60 (1 RR-interval).

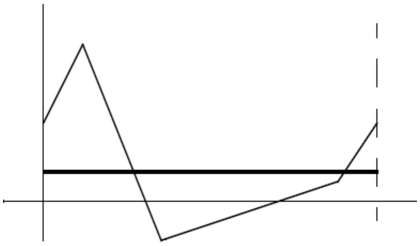


**Fig. 116:** Mean flux, indicated by the horizontal line in the graph (x-axis = trigger delay time (ms), y-axis = flux (ml/s))

### Stroke distance

- Net distance the blood proceeds in the vessel in 1 RR-interval.

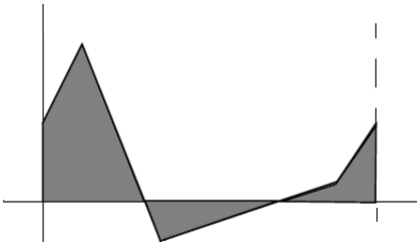


**Fig. 117:** Stroke distance (x-axis = trigger delay time (ms), y-axis = mean velocity (cm/s))

### Mean velocity

- Stroke distance x heartbeat / 60 (1 RR-interval).

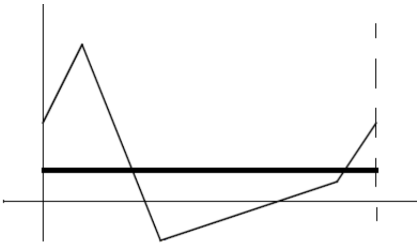


**Fig. 118:** Mean velocity, indicated by the horizontal line in the graph (x-axis = trigger delay time (ms), y-axis = mean velocity (cm/s))

### Peak velocity

- Peak blood flow velocity

### Current Phase Results for each ROI (vessel contour)

Right-click the results summary table and click **Current phase results**. The results are available per slice, per phase and per vessel.

- Positive flow is flow into the plane (maximum positive: displayed white), e.g. in Feet-to-Head direction and in Right-to-Left direction.
- Negative flow is flow out of the plane (maximum negative: displayed black), e.g. in Head-to-Feet direction and in Left-to-Right direction.

| | |
|---|---|
| **Trigger delay [ms]** | • Time between R-peak and acquisition of the specific slice. |
| **Flux [ml/s]** | • Blood volume that passes the contour per second. This is the same as ’mean velocity * area'. Note that this value is only calculated if the flow direction is perpendicular to the image. |
| **Area [cm2]** | • Area of the pixels that are partially or fully included in the contour. To visualize this area, right-click in an image viewport and select 'Filled graphics'. |
| **Nr. of pixels** | • Pixels that are partially or fully included in the contour. |
| **Mean velocity [cm/s]** | • Mean blood flow velocity. |
| **Maximum velocity [cm/s]** | • Highest measured positive flow in the contour. |
| **Minimum velocity [cm/s]** | • Highest measured negative flow in the contour. |
| **Peak velocity [cm/s]** | • Either maximum velocity or minimum velocity, whichever has the highest absolute value. |
| **Velocity Standard Deviation [cm/s]** | • Standard deviation of the mean velocity. |

**NOTICE**

To show Cardiac Output, change the unit for Flux to L/min in the settings dialog (see below). In the mean analysis results the Cardiac Output can be read from the parameter Mean Flux.

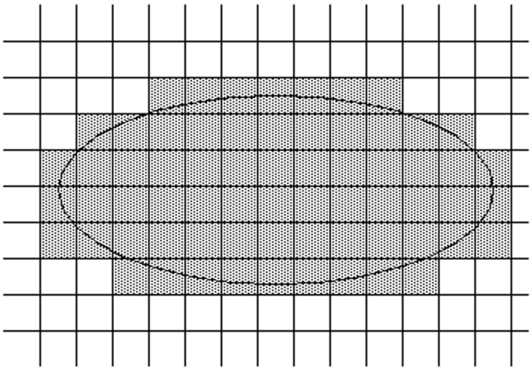


**Fig. 119:** The pixels that are taken into account for quantitative flow calculations.

Note that the units for each result type can be chosen by the user. Available units are:

| Result | Available units | Default unit |
|---|---|---|
| **Area** | mm$^2$, cm$^2$ | cm$^2$ |
| **Distance** | cm, mm, m | cm |
| **Dynamic Time** | ms, s | depends on length of series |
| **Flux** | mm$^3$/s, ml/s, ml/min, L/min | ml/s |
| **Trigger Delay Time** | ms, s | ms |
| **Velocity** | mm/s, cm/s, m/s | cm/s |
| **Volume** | mm$^3$, ml, cc, cm$^3$ | ml |

## Saving the Results

1. To change the result type used to display the results, right-click the graph display and select a parameter.
2. To include or exclude vessels and valves in the results, right-click the graph display and select or clear vessels and valves as desired.

   Only vessels or valves for which a contour has been defined are available to be included in the results.
3. To save the contours, use the **Save Results** tool in the common tools panel.
4. To create a derived series from the current series, including the segmentation, use the **Generate Series** tool in the common tools panel.

⇨ The **Save batch** dialog box is displayed allowing you to select a file name, file format, and destination. You can save the series in DICOM format, or in non-DICOM format. If you select a non-DICOM format, you should additionally select a filesystem destination to export the series to.

5. To save numerical results, use the **Save All Tables** tool in the common tools panel.

⇨ The **Save all tables** dialog box is displayed allowing you to select a file name, file format, and destination. You can save the tables in DICOM format, or as HTML, text, or comma-separated values.

6. To save the contents of a numerical results table, right-click the table and click **Copy**. You can then paste the data to a desktop application, such as a text editor, a spreadsheet, or presentation software.

7. To save the complete layout in the main display area, use the **Save Bookmark** tool in the common tools panel.

**NOTICE**

Before saving a bookmark, you should save any key images that you have created.

⇨ If desired, you can enable the **Autosave Bookmark** function in the **Viewing Applications** section of the **Preferences** dialog box in the **Directory** screen. This function automatically saves a bookmark when you exit the analysis application.

8. To export the analysis results in CSV format, right-click one of the upper viewports (displaying the slice) and click **Export results and segmentation**.

⇨ The **Export results and segmentation** dialog box is displayed, allowing you to select a destination for the CSV file. You can save the file to a repository, or export the file to a directory on your workstation.

**NOTICE**

"CSV" stands for "Comma-Separated Values". CSV files can be opened in a spreadsheet application.

9. To save an image as a key image, press the spacebar when the image is displayed.

⇨ You can view saved images by clicking **Key Images** in the task menu of the task guidance panel.

⇨ After performing analysis on a study, you can access the key image viewer in the Directory. Using the key image viewer, you can provide a title and a comment for each image.

## Procedure for Analyzing E/A Ratio for Mitral Valve

To analyze E/A ratio, we recommend that you use the following procedure.

1. Plan a QFlow series for the mitral valve when it is nearly at the end of the diastolic stage (opening stage).

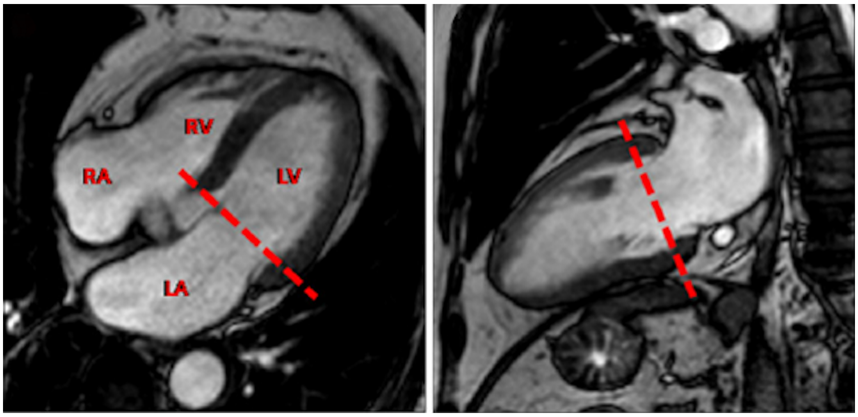


**Fig. 120:** Example of the recommended planned situation for the series (these images are provided by courtesy of Ricardo Duarte and Gabriel Fernandez "Assessment of LV DF by MRI")

⇨ Avoid being too close to the cardiac base as this may cause distortion or include LA inflow tract or aortic outflow tract. This position includes both LV inflow and LV outflow.

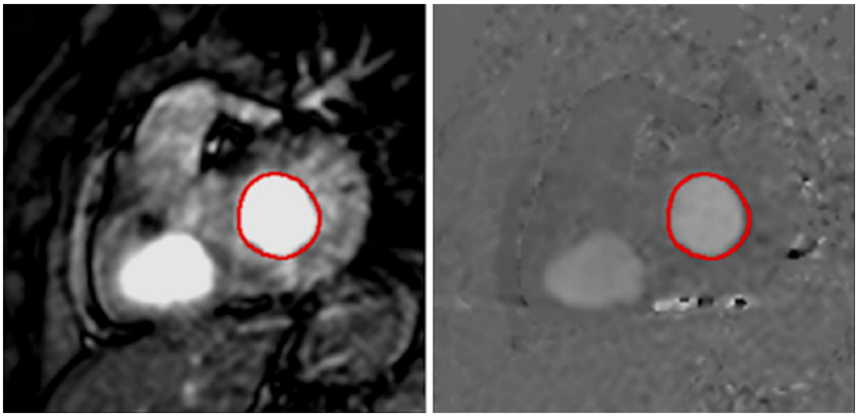


**Fig. 121:** Example of an optimal result (these images are provided by courtesy of Ricardo Duarte and Gabriel Fernandez "Assessment of LV DF by MRI")

2. To create the contour, use the following steps. (These steps minimize the need for editing as the entire LV inflow and outflow is included.)
   - Select the **Bezier** ROI tool.
   - Ensure that **Fit contour to vessel** is not selected.
   - Display the LV ED phase.
   - Create the contour.
   - Select **Mitral Valve** in the vessel name list.

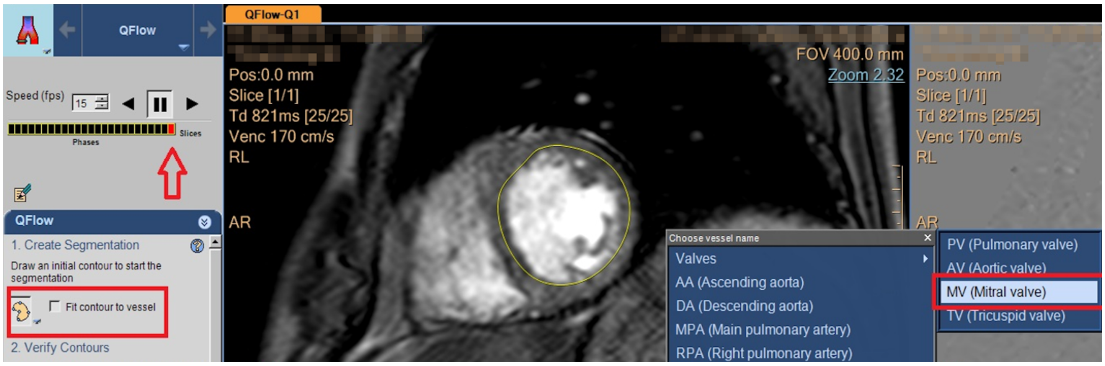


**Fig. 122:** Optimal settings for creating the contour

⇨ After you define the contour, the analysis results are displayed.

**NOTICE**

When you label a contour as Mitral Valve, you can assess diastolic function by investigating the ratio between early diastolic filling peak and the atrial kick. This tool also allows you to measure the deceleration time.

3. In the **Select Result Protocol** step in the task guidance panel, select **E/A ratio for Mitral Valve**.
4. Set the position of the rulers correctly in the analysis graph.

⇨ Rulers are added to the analysis graph allowing you to indicate the following positions:

- Early peak (Emax)
- Deceleration time (Emin)
- Atrial peak (Amax)

⇨ A red line is displayed between Emax and Emin. This line provides assistance with positioning Emin; the line reflects the deceleration slope of the flow when Emin is positioned correctly.

⇨ Emin should be set such that the deceleration line has a similar downslope to the graph between Emax and Amax.

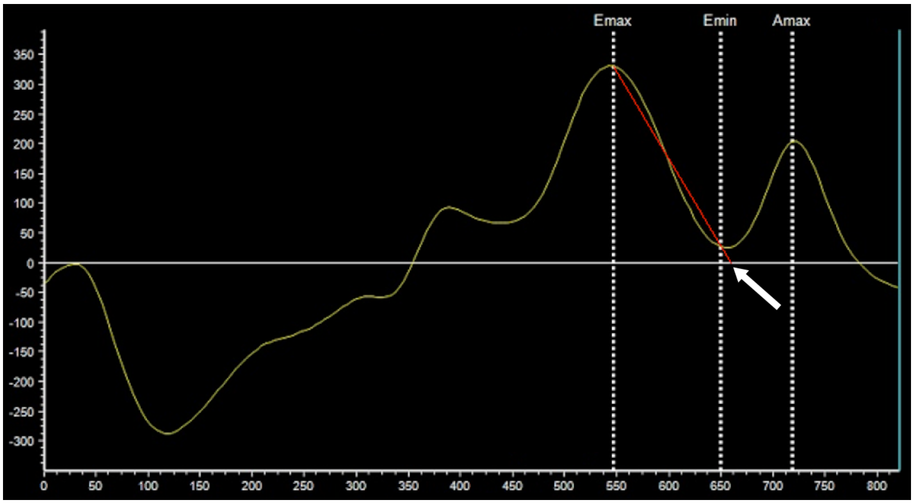


**Fig. 123:** Setting the position of the E/A ratio rulers in the analysis graph

⇨ The deceleration time is calculated as the time between Emax and the point where the slope intersects the baseline (indicated by the arrow in the figure above). The normal range for the deceleration time is 140-220 ms.

⇨ The deceleration rate represents the measured upslope from the deceleration line.

5. Verify the position of the rulers.

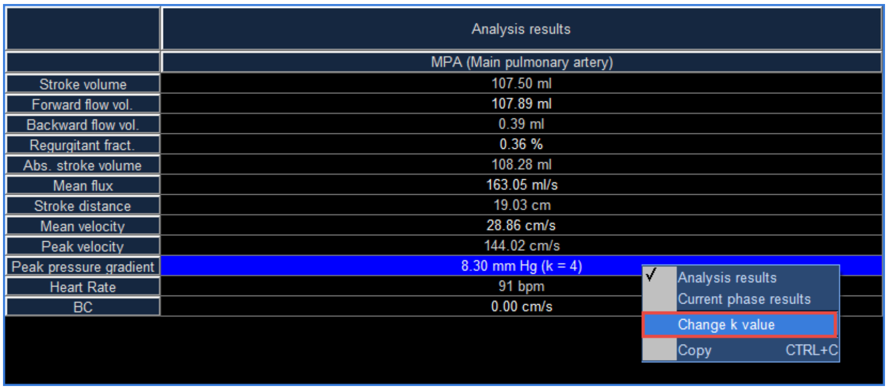
⇨ Numerical values of the ruler positions are displayed in the task guidance panel. You can adjust these values directly in the task guidance panel, if desired.

⇨ A section is added to the numerical results table indicating the **E/A Ratio**, the **Deceleration Time**, and **Deceleration Rate**.

## Peak Pressure Gradient

The pressure gradient over, for example, stenotic cardiac valves or aortic stenosis is considered to be a measure of severity of the disease. It is important to measure the maximum flow velocity (Vmax) distal from the expected stenosis, which can be performed with QFlow MRI.

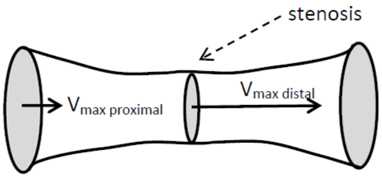
The peak pressure gradient is available in QFlow by using the simplified Bernoulli equation as defined in literature (see references below).



| | Analysis results |
|---|---|
| | MPA (Main pulmonary artery) |
| Stroke volume | 107.50 ml |
| Forward flow vol. | 107.89 ml |
| Backward flow vol. | 0.39 ml |
| Regurgitant fract. | 0.36 % |
| Abs. stroke volume | 108.28 ml |
| Mean flux | 163.05 ml/s |
| Stroke distance | 19.03 cm |
| Mean velocity | 28.86 cm/s |
| Peak velocity | 144.02 cm/s |
| Peak pressure gradient | 8.30 mm Hg (k = 4) |
| Heart Rate | 91 bpm |
| BC | 0.00 cm/s |

In reference [1], it is explained that the decrease in pressure (the pressure gradient) ΔP over a stenosis can be calculated using the modified Bernoulli equation:

$$(P_{\text{distal}} - P_{\text{proximal}}) = K \times (V_{\text{max distal}} - V_{\text{max proximal}})^2,$$



$P_{\text{distal}}$ and $P_{\text{proximal}}$ are the pressures distally and proximally of the stenosis, respectively, $V_{\text{max distal}}$ and $V_{\text{max proximal}}$ the maximum velocities distally and proximally of the stenosis, and K a constant.

Under the assumption that $V_{\text{max proximal}}$ is small compared with $V_{\text{max distal}}$ this can be further simplified to:

$(P_{\text{distal}} - P_{\text{proximal}}) = 4 \times V_{\text{max distal}}^2$ or $\Delta P=4V_{\text{max}}^2$

In reference [2], a method is proposed to measure $V_{\text{max}}$, namely: “the peak velocity was calculated as the average of the top 10% velocities from contiguous pixels within the vessels. The final peak velocity was calculated as the maximum of the peak velocities at systole”.

### Using a User-Defined Pressure Gradient

Using a series of anatomically accurate models of aortic coarctation, the laboratory portion of a study (reference [3]) found that the loss coefficient (K), commonly taken to be 4.0 in the simplified Bernoulli equation P =KV2, was a function of stenosis severity. The values of the loss coefficient ranged from 2.8 for a 50% stenosis to 4.9 for a 90% stenosis.

For this reason the user is able to change the loss coefficient (K) in the results table.

**NOTICE**

This function and option should only be used by certified MR Cardiac users.

### References

[1] M.B. Srichai et al., "Cardiovascular applications of phase-contrast MRI”, AJR 2009; 192:662–675.

[2] C.D. Lew et al., “Peak velocity and flow quantification validation for sensitivity-encoded phase-contrast MR imaging”, Ac. Rad 2007;14(3):258-269.

[3] JonN. Oshinski, et al., “Improved Measurement of pressure Gradients in Aortic Coarctation by Magnetic Resonance Imaging’; J am Coll Cardiol.1996;28(7):1818-1826

# References

Kozerke, S., Botnar, R., Oyre, S., Scheidegger, M. B., Pedersen, E. M., Boesiger, P. "Automatic Vessel Segmentation Using Active Contours in Cine Phase Contrast Flow Measurements". *Journal of Magnetic Resonance Imaging*, No. 10: 41-51, 1999.

Lotz, J., Meier, C., Leppert, A., Galanski, M. "Cardiovascular Flow Measurement with Phase-Contrast MR Imaging: Basic Facts and Implementation". *RadioGraphics*, No. 22: 651-671, 2002.

Pandey, T., Jambhekar, K. "Evaluation of Diastolic Dysfunction Using Cardiac Magnetic Resonance Imaging". *European Cardiology*, Vol. 6, No. 1: 21-25, 2010.

**Diastolic Function: Planning and Interpretation of Analysis**

Duarte, R., Fernandez, G. "Assessment of left ventricular diastolic function by MR: why, how and when". *Insights Imaging*, Vol. 1: 183-192, 2010.

Danzmann, L. C., Bodanese, L. C., Köhler, I., Torres, M. R. "Left atrioventricular remodeling in the assessment of the left ventricle diastolic function in patients with heart failure: a review of the currently studied echocardiographic variables". *Cardiovascular Ultrasound*, Vol. 6, No. 56, 2008.

Daneshvar, D., Wei, J., Tolstrup, K., Thomson, L. E. J., Shufelt, C., Merz, N. B. "Diastolic dysfunction: Improved understanding using emerging imaging techniques". *American Heart Journal*, Vol. 160, No. 3: 394-404, 2010.

Rathi, V. K., Doyle, M., Yamrozik, J., et al. "Routine evaluation of left ventricular diastolic function by cardiovascular magnetic resonance: A practical approach". *Journal of Cardiovascular Magnetic Resonance*, Vol. 10, No. 36, 2008.

Rubinshtein, J., Glockner, F., Feng, DL., et al. "Comparison of Magnetic Resonance Imaging Versus Doppler Echocardiography for the Evaluation of Left Ventricular Diastolic Function in Patients With Cardiac Amyloidosis". *The American Journal of Cardiology*, 2008.

Zile, M. R., Brutsaert, D. L. "New Concepts in Diastolic Dysfunction and Diastolic Heart Failure: Part I (Diagnosis, Prognosis, and Measurements of Diastolic Function)". *Circulation*, No. 105: 1387-1393, 2002.

**Background Correction**

Lan, T., Erdogmus, D., Hayflick, S. J., Szumowski, J. U. "Phase Unwrapping and Background Correction in MRI". IEEE Workshop on Machine Learning for Signal Processing, 239-243, 2008.

Rigsby, C. K., Hilpipre, N., McNeal, G. R., et al. "Analysis of an automated background correction method for cardiovascular MR phase contrast imaging in children and young adults". *Pediatr Radiol*, No. 44: 265-273, 2014.

Delfino, J. G., Bhasin, M., Cole, R., et al. "Comparison of Myocardial Velocities Obtained With Magnetic Resonance Phase Velocity Mapping and Tissue Doppler Imaging in Normal Subjects and Patients With Left Ventricular Dyssynchrony". *Journal of Magnetic Resonance Imaging*, No. 24: 304-311, 2006.