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Instructions for Use – *syngo*.CT Myocardial Perfusion VB20A

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Legend

	Indicates a hint Is used to provide information on how to avoid operating errors or information emphasizing important details
»	Indicates the solution of a problem Is used to provide troubleshooting information or answers to frequently asked questions
■	Indicates a list item
✓	Indicates a prerequisite Is used for a condition that has to be fulfilled before starting a particular operation
◆	Indicates a one-step operation
1 2 3	Indicates steps within operating sequences
Italic	Is used for references and for table or figure titles
→	Is used to identify a link to related information as well as previous or next steps
Bold	Is used to identify window titles, menu items, function names, buttons, and keys, for example, the Save button
Blue	Is used to emphasize **particularly** important sections of the text
Courier	Is used for on-screen output of the system including code-related elements or commands
`Courier`	Is used to identify inputs you need to provide
Menu > Menu Item	Is used for the navigation to a certain submenu entry
<variable>	Is used to identify variables or parameters, for example, within a string
⚠ CAUTION	CAUTION Used with the safety alert symbol, indicates a hazardous situation which, if not avoided, could result in minor or moderate injury or material damage. CAUTION consists of the following elements: ■ Information about the nature of a hazardous situation ■ Consequences of not avoiding a hazardous situation ■ Methods of avoiding a hazardous situation

WARNING

Indicates a hazardous situation which, if not avoided, could result in death or serious injury.

WARNING consists of the following elements:

- Information about the nature of a hazardous situation
- Consequences of not avoiding a hazardous situation
- Methods of avoiding a hazardous situation

WARNING

Legend

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1 *syngo*.CT Myocardial Perfusion

Indications for use

The Siemens *syngo*.CT Myocardial Perfusion software package has been designed to evaluate perfusion of the myocardium.

The software can calculate blood flow, blood volume, and other hemodynamic parameters from sets of images reconstructed from dynamic CT data acquired after the injection of contrast media.

It supports evaluation of regions of interest and the visual inspection of time attenuation curves.

Intended use

syngo.CT Myocardial Perfusion allows assessment of parameters related to myocardial tissue perfusion by means of a rapid sequence of CT scans (typically prospective triggered cardiac sequence or shuttle mode scans).

Contraindications

There are no known specific situations that contraindicate the use of this device.

Legal notes

The functions described in this document are not commercially available in all countries. Some functions may be protected by a software license that is currently restricted for regulatory reasons. Some functions may be available with an optional software license. Please contact your local Siemens representative for further details.

1.1 Safety advice

CAUTION

Not observing the Instructions for Use of the software and its applications!

Wrong basis for diagnosis.

- Always use this Instructions for Use in conjunction with all Instructions for Use provided.
- Follow the safety instructions.

CAUTION

Operation of the system, applications, or functionalities by non-trained user!

Wrong basis for diagnosis or treatment.

- The system must only be used after appropriate training by persons with the certified necessary specialist knowledge according to country-specific regulations, for example, physicians, radiologists, or technologists. Consult your Siemens representative for appropriate training.

CAUTION

The pixel lens has a constant size and is independent of the zoom factor of the image!

Wrong diagnosis due to misleading image information.

- Please note that the pixel lens is only a pointer indicating the position (not the size) of the measured area.

CAUTION

Loading image data sets of different patients!

Mix-up of patients and incorrect diagnosis possible.

- When loading reference and model series, make sure that you select the data of the correct patient.

CAUTION

User is not instructed in how to operate the applications!

Wrong basis for diagnosis.

- The operator must be qualified to use the applications.

CAUTION

Wrong motion correction of input data sets!

Wrong basis for diagnosis.

- Ensure that the motion correction results are adequate. The user should navigate through all volumes of the time series. If motion correction is not correct, reset to original data.

CAUTION

Removal of relevant body parts due to automatic segmentation!

Wrong basis for diagnosis.

- Make sure that the segmentation results are adequate. If segmentation is not proper, correct manually or reset to original data.

CAUTION

Definition of wrong reference vessel!

Wrong basis for diagnosis.

- Make sure that the suggested reference vessel is correct before accepting it.

CAUTION

Automatically saved results may be sent to another DICOM node!

Wrong diagnosis due to wrong information.

- Check all results of the currently active workflow. If applicable, remove intermediate or incorrect results.

  Send only correct results to other DICOM nodes, such as image viewers or PACS.

CAUTION

Displayed information about changed patient data is not observed!

Wrong diagnosis due to wrong information.

- Always read and observe the displayed information about changed patient data.

  Follow the instructions provided with the displayed information, if applicable.

  Check all results and delete results that include outdated patient data.

CAUTION

Patient data is changed using the correct and rearrange function while a time-critical workflow for this patient is in progress!

Delayed diagnosis due to restart of workflow.

- Do not perform correct and rearrange actions while time-critical cases are in progress. Always check the **Workflows** section in the **Job View** for time-critical workflows.

1.2 Functionality of *syngo*.via

syngo.via is a software solution intended to be used for viewing, manipulation, communication, and storage of medical images. It can be used as a stand-alone device or together with a variety of cleared and unmodified *syngo* based software options. The functionality of the *syngo*.via software that is used in combination with a *syngo*.CT medical device is described in the *syngo*.via Basic Operator Manual. The *syngo*.via Basic Operator Manual and the *syngo*.via Administrator Manual are the Instructions for Use of *syngo*.via.

CAUTION

Not observing the Instructions for Use of the software and its applications!

Wrong basis for diagnosis.

- Always use this Instructions for Use in conjunction with all Instructions for Use provided.
- Follow the safety instructions.

1.3 Layouts

For each step, a specific layout is applied. You cannot select another layout.

The arrangement of segments in the provided layouts depends on your current monitor configuration. There are dedicated layouts for single-monitor and dual-monitor configurations, and also for different aspect ratios (4:3, 16:10, and portrait orientation).

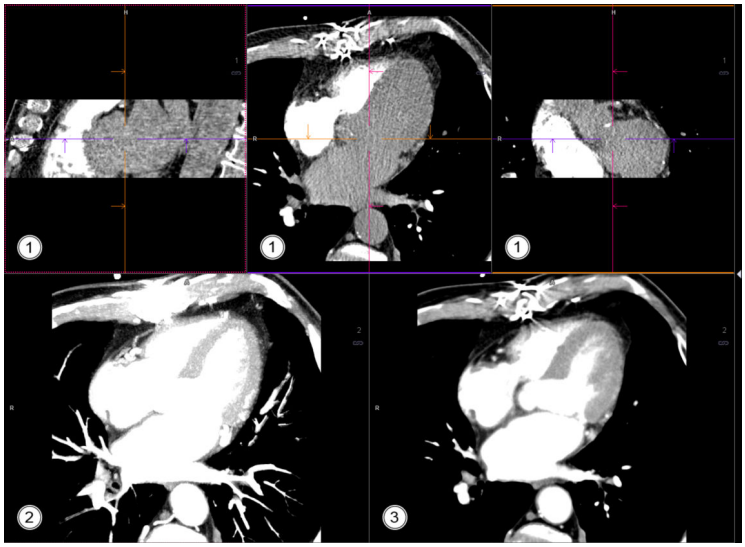
Double-click a segment to expand it. Note that this does not apply to segments of the Result Gallery. To inspect the result volumes in detail, drag them from the Result Gallery to the larger segments.

1.3.1 Basic layout

This layout is applied in the following steps:

- **Motion Correction**
- **Segmentation**
- **Vessel Definition**

The following example shows the basic layout for a single-monitor configuration:



(1) Synchronized segments

These segments display the axial, coronal, and sagittal orientation of one volume, by default.

(2) Temporal maximum intensity projection (tMIP) segment

This segment displays a calculated volume created from all loaded time points of the series. Each voxel in this volume displays the maximum HU value of all time point voxels at the same image position.

(3) Temporal average (tAVG) segment

This segment displays a calculated volume created from all loaded time points of the series. Each voxel in this volume displays the average HU value of all time point voxels at the same image position.

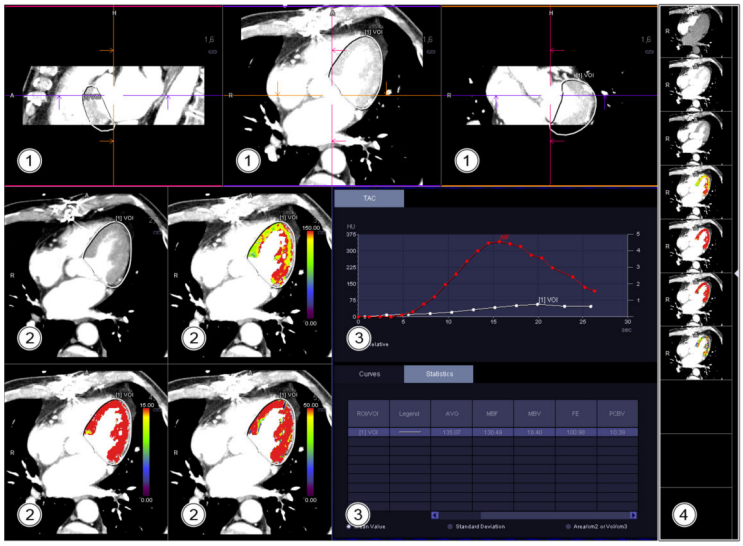
When the TAC tool has been activated, the table and curve segment covers the tAVG segment in a single-monitor environment.

1.3.2 Results layout

This layout is applied in the following steps:

- **Results Preview**
- **Results**

The following example shows the default layout for a single-monitor configuration.



(1) Synchronized segments

These segments display the axial, coronal, and sagittal orientation of one result volume, by default.

(2) Result segments

These segments display up to six available result volumes. A color scale is available for each result volume. The color scale shows the window width of the result volume as the upper value of the scale.

(3) Time Attenuation Curve (TAC) tool

The TAC tool covers two result segments if activated.

(4) Result Gallery

These 10 segments display the available result volumes.

1.4 Selecting a template

To start evaluation, you need to select a template from the list of default templates in the **Case Navigator**. If only one template is available, it is automatically selected.

✓ A data set is loaded that meets requirements.

◆ In the **Case Navigator**, select a template for evaluation.

The **Motion Correction** step is opened.

1.5 Navigating through time points and inside volumes

You can inspect each time point series in the upper three MPR segments, which are orthogonally synchronized. Each time point series represents one particular point in time of a CT examination. You can navigate from one time point series to another or you can scroll through the images of a single time point series.

Time Navigation

Use one of the following methods to navigate through time point series, for example to review the contrast enhancement in particular regions:

- Press and hold the **Alt** key and scroll with the mouse wheel.
- Right-click and drag the mouse pointer to the right or to the left.
- Press the left and right arrow keys.
- Use the Time Slider.

Volume Navigation

Use one of the following methods to navigate inside a time point series:

- Scroll with the mouse wheel.
- Right-click and drag the mouse pointer up and down.
- Use the reference lines.

1.6 Time Slider

The Time Slider allows you to to scroll though the time point series of the data set by using the left arrow and the right arrow.

The small white triangle represents the motion correction base:

The bright bar represents the segmentation baseline:

The position marker indicates the currently displayed time point series, which is displayed in the orthogonal MPRs and indicates the time in seconds within the acquisition.

2 The CT Myocardial Perfusion workflow

The CT Myocardial Perfusion workflow allows you to evaluate the perfusion of the myocardium.

The basic CT Myocardial Perfusion workflow contains the following steps:

- Select a template.
- Prepare the images and/or check the preparation of images in each step.

  To automatically apply cardiac planes when preparing images, select Cardiac Planes from the lower right corner menu. Cardiac planes will be automatically applied in the **Results Preview** step. This allows you to view the heart for diagnosis without the need to rotate or zoom manually.
- Check the quality of the CT examination.
  - Navigate through the time points of the data set, for example, by using the Time Slider.
  - Use the **Motion Correction** step to improve images that show movements. See (→ Page 25 *Correcting motion artefacts*). If there are motion artefacts left, you may exclude the affected images (time points) from evaluation. See (→ Page 27 *Excluding a time point from evaluation*), and (→ Page 27 *Excluding a range of time points from evaluation*).
  - If the images are very noisy because of low kV or low dose, you can reduce the image noise in the **Segmentation** step. See (→ Page 32 *Reducing image noise*).

- Use the **Segmentation** step to check and define the volume and structures for evaluation.
  - You can define a volume of interest (VOI) to evaluate a specific organ or volume only. See (→ Page 29 *Defining a myocardial VOI*).
  - You can exclude structures by adjusting the values of the HU-based segmentation. See (→ Page 31 *Using the HU-based segmentation*).
- Click the **Vessel Definition** step when the segmentation results are satisfactory.
  - Check the reference artery (cranial and caudal; red circle), the vessels and heart cavities (purple overlay).
    - Define an artery manually if the identification did not work properly. See (→ Page 34 *Defining arteries manually*).
    - Correct the representation if the purple overlay also covers structures other than vessels and heart cavities. See (→ Page 35 *Windowing vessels*).
    - If necessary, change the artery definition by adapting the values of the **Max. Enhancement**. See (→ Page 35 *Changing the maximum enhancement value*).
    - Check the arterial input function (AIF) curve in the Time Attenuation Curve (TAC) tool.
- Click the **Results Preview** step once the vessels are properly defined.
  - Check the displayed result volumes.
  - Select the result volumes to be saved for further evaluation and accept the results to proceed to the **Results** step. See (→ Page 37 *Checking the Results Preview*).
- Perform measurements and define ROIs and VOIs to create findings in the **Results** step.
- Evaluate result data that is already calculated by clicking the **Perfusion Evaluation** workflow step. The measurements performed in the **Results** step and in the **Perfusion Evaluation** workflow step are synchronized and listed in the **Findings Navigator** with sequential numbering. See (→ Page 52 *Evaluating perfusion results*).

When you repeat a previously performed step, you must also repeat all subsequent steps. You can reset the workflow to its initial state at any time by clicking the **Reset** icon in the **Case Navigator**.

2 The CT Myocardial Perfusion workflow

3 Motion correction step

In the **Motion Correction** step, you can perform a correction of motion artefacts.

Motion correction is based on a time point series that does not contain motion artefacts. This time point should be representative for all other time points series and defines the motion correction base.

On the Time Slider, the motion correction base is referenced by a small white triangle.

The default motion correction base can be configured for the workflow. You can adapt this motion correction base for the currently active workflow during case preparation, for example, if this time point shows motion artefacts itself..

In the **Motion Correction** step, you can also exclude time points from evaluation if the images cannot be aligned correctly. You can either exclude a single time point or you can exclude all time points from the currently displayed to the last available time point.

3.1 Correcting motion artefacts

Perfusion scans of the myocardium are performed in the heart perfusion scanning mode. In this mode, an ECG trigger scan is performed that covers alternatively the caudal part and the cranial part of the heart. This mode might cause a shift between the caudal part and the cranial part.

In the **Motion Correction** step, possible shifts between the caudal part and the cranial part are corrected, followed by a non-rigid registration of the volume.

✓ The **Motion Correction** step is active.

◆ In the **Case Navigator**, click the **Myocardial Motion Correction** icon.

After the motion correction has been performed, the system displays the aligned images for all time points within the series. The Temporal Maximum Intensity Projection (tMIP), the Temporal Average (tAVG), and the Baseline volume are recalculated. This may take several minutes.

3.2 Setting the motion correction base

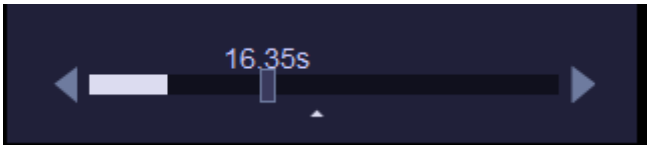
The motion correction base is the reference volume to which the other volumes are aligned. If the motion correction base shows a strong misalignment to the other volumes, you can define another timepoint within the series.

✓ The **Motion Correction** step is active.

1 On the **Time Slider**, navigate to the time point that should be defined as the motion correction base.

2 In the **Case Navigator**, click the **Motion Correction Base** icon.

On the Time Slider, the triangle jumps to the position of the current time point, which is now the motion correction base.



3.3 Excluding a time point from evaluation

You can exclude a single time point from evaluation, if the images show strong movements. At least four time points of the series have to be kept for evaluation. You can repeat this process several times.

✓ The **Motion Correction** step is active.

1 On the Time Slider, navigate to the time point that you want to exclude.

2 In the **Case Navigator**, click the **Time Point Exclusion** icon.

3.4 Excluding a range of time points from evaluation

You can exclude all time points from the currently displayed to the last available time point, if the last time points in the series are not required for evaluation. At least four time points of the series have to be kept for evaluation. You can repeat this process several times.

✓ The **Motion Correction** step is active.

1 On the Time Slider, navigate to the time point from which on you want to exclude data.

2 In the **Case Navigator**, click the **Time Range Exclusion** icon.

The selected time range is excluded.

3 Motion correction step

4 Segmentation step

CT Myocardial Perfusion defines the baseline that is used for HU-based segmentation. To calculate the segmentation baseline, CT Myocardial Perfusion uses the first time point series of the study. This volume is referred to as the Baseline volume.

In the Time Slider, brightly colored bars represent the segmentation baseline.

For calculation of results, you can define a volume of interest (VOI) to restrict the evaluation to the myocardial volume. Additionally, you can exclude structures from evaluation.

See (→ Page 29 *Defining a myocardial VOI*) and (→ Page 31 *Using the HU-based segmentation*).

CT Myocardial Perfusion provides a specific noise reduction algorithm that preserves time-density information and smoothes the display of images. See (→ Page 32 *Reducing image noise*).

4.1 Defining a myocardial VOI

If the existing segmentation is not as expected, you can delete, edit, or define a Volume of Interest (VOI) to evaluate the perfusion of the myocardium.

✓ The **Segmentation** step is active.

1 In the **Case Navigator**, click the **Segment Myocard** icon.

An editing mini toolbar is displayed and the **Draw Contour** icon is activated. The mouse pointer changes its shape.

2 To delete all existing contours, press the **Delete All** button.

– or –

You can edit a single contour.

3 If there is no myocardial VOI, or if you have deleted the VOI, define a VOI.

4 Click and drag the mouse pointer to define a contour. Double-click to finish the contour.

5 Scroll through the slices and create more contours to cover the required volume. Interpolation between the slices is calculated (dashed magenta lines).

If necessary, you can delete a single contour or all contour lines.

6 In the temporal MIP, scroll to a slice with a magenta contour and click the **Delete Single Contour** icon.

– or –

Click the **Delete All Contours** icon.

7 After you have created all required contours, click the **Complete Contour Drawing** icon to finish editing.

The mini toolbar changes to correction mode. The myocardial VOI contour is displayed in all segments.

If necessary, you can correct a single contour or delete all contours and return to the editing mode.

8 Scroll through the slices and check the contours. To correct a contour, click and drag the mouse pointer to draw a freehand line. To add an area to the existing contour, start at the contour line and draw outside the contour. To cut off an area from the existing contour, start at the contour line and draw inside the contour. Double-click to finish the contour editing.

The new contour is displayed as a dotted path in magenta.

After editing the contour, *syngo*.via may not be able to decide which part of the contour has to be discarded. In this case, the manual cutting mode is activated automatically.

The mouse pointer changes its shape to scissors with a question mark.

The part of the contour that has to be discarded is displayed as a dotted line.

9 Click the part that you want to cut off.

10 Click the **Delete VOI and Draw Manual Contour** icon to discard all contours and start editing from the beginning.

– or –

Click the **Complete Contour Drawing** icon to finish the myocardial VOI.

The myocardial VOI is displayed in all segments and can be used to calculate results.

4.2 Using the HU-based segmentation

You can change the values of the HU thresholds if the displayed segmentation results are not as expected. All voxels with HU values within the range you specify are kept for display, calculation, and measurements, while all other voxels are excluded from the Baseline volume. You can specify the values within the complete range from -1024 to 3071 HU.

✓ The **Segmentation** step is active.

1 In the **Case Navigator**, click the **HU Segmentation** icon.

2 If necessary, enter new values in the min or max HU fields and press the **Return** key. The values can only be modified when the segmentation mode is active.

If you deactivate the mode, all structures that were excluded by the HU segmentation are visible again. The segmentation results are used to calculate the result volumes whether or not this mode is activated.

If you want to use your values as default values, you can adjust the values in the **CT Myocardial Perfusion Configuration** dialog box. See (→ Page 56 *Setting the segmentation thresholds*).

4.3 Defining the baseline for HU-based segmentation

CT Myocardial Perfusion defines the segmentation baseline that is used for HU-based segmentation. By default, the first time point series of the study is used. The segmentation baseline should not show contrast medium. You can define a new segmentation baseline if the default one is not appropriate. CT Myocardial Perfusion calculates the Baseline volume from the time points that are defined as the segmentation baseline.

✓ The **Motion Correction** step is active and the **Segmentation** step has not been activated yet.

1 On the Time Slider, navigate to the last time point without contrast medium.

2 In the **Case Navigator**, click the **Segmentation Baseline** icon.

The Baseline volume is recalculated and updated in the Result Gallery. The brightly colored bars of the Time Slider are updated.

When you remove a time point from the segmentation baseline, a new Baseline volume is automatically calculated and updated.

4.4 Reducing image noise

You can reduce image noise that results from low kV or low dose to preserve time-density information and smooth the display of images.

✓ The **Segmentation** step is active.

◆ In the **Case Navigator**, click the **4D Noise Reduction** icon.

The Temporal Maximum Intensity Projection (tMIP), the Temporal Average (tAVG), the time points, and the baseline volume are automatically recalculated.

5 Vessel definition step

After you have performed and checked the segmentation, you must identify vessels as a basis for calculation in the **Vessel Definition** step. Vessels are indicated by purple overlays and the defined reference artery is indicated by a red circle.

- You can define the reference artery manually. See (➔ Page 34 *Defining arteries manually*).
- You correct the value of the **Max. Enhancement** in the artery. See (➔ Page 35 *Changing the maximum enhancement value*).
- In the TAC tool, the arterial input function (AIF) curve is displayed.

5.1 Checking the vessel identification

CT Myocardial Perfusion identifies vasculature. The vessels are indicated by purple overlays and the reference artery is indicated by a red circle.

CAUTION

Definition of wrong reference vessel!

Wrong basis for diagnosis.

- Make sure that the suggested reference vessel is correct before accepting it.

✓ The **Vessel Definition** step is active.

1 Inspect the displayed images and check if the vessels are correctly identified.

If the results are not as expected, you can adjust the vessel identification. See (➔ Page 35 *Windowing vessels*) .

2 Check the **Max. Enhancement** value.

If the results are not as expected, you can adjust the **Max. Enhancement** value. See (→ Page 35 *Changing the maximum enhancement value*).

3 Check the ROI that represents the reference vessels and verify the correct position.

If the results are not as expected, define a reference artery manually. See (→ Page 34 *Defining arteries manually*).

4 In the TAC tool, check if the red arterial input function (AIF) curve is smooth.

5.2 Defining arteries manually

You can define the cranial artery and the caudal artery manually if the results of the identification are not as expected.

✓ The **Vessel Definition** step is active.

1 In the **Case Navigator**, click the **Cranial Artery Definition** icon.

– or –

In the **Case Navigator**, click the **Caudal Artery Definition** icon.

In the tMIP segment, you are guided to the slice where the ROI could be placed. The mouse pointer changes its shape. In the tMIP segment, all colored overlays are hidden.

2 In the tMIP segment, scroll to a slice with a main artery.

3 In the tMIP segment, click and drag the mouse to draw a ROI that almost covers the artery.

The scans of the cranial part and the caudal part are combined. In the MPR images, the purple overlays for vessels are updated. The two curves from the ROIs are combined to the AIF (arterial input function). The AIF contains all the points from the cranial scan and from the caudal scan. Use both, the cranial ROI and the caudal ROI to get a smooth AIF.

4 Click the **Cranial Artery Definition** icon again to finish editing.

– or –

Click the **Caudal Artery Definition** icon again to finish editing.

5 Check the results to verify the vessel definition. See (➔ Page 33 *Checking the vessel identification*).

5.3 Changing the maximum enhancement value

After the reference vessel has been defined, the application automatically calculates the value of the **Max. Enhancement**. You can change the value for maximum enhancement of the reference vessel if the value is underestimated or the reference vessel was not properly identified.

✓ The **Vessel Definition** step is active.

◆ In the **Case Navigator**, enter a value in the **Max. Enhancement** field and press the **Return** key.

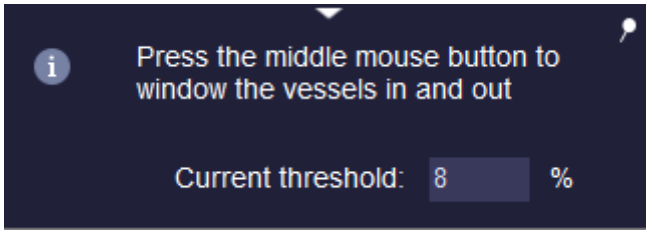
The corresponding information in the TAC tool is updated.

5.4 Windowing vessels

In the **Vessel Definition** step, you can window vessels in and out.

✓ The reference vessel is properly defined.

1 In the **Case Navigator**, click the **Window** icon.



2 Use the middle mouse button to window vessels in and out. You can directly control the effects on the vessels by changing the thresholds of the image. This allows you to control what is vessel, and what is not, inside the segment.

3 Use the middle mouse button to window vessels in and out until only the vessels are colored and no flying pixels are left. When the vessels are correctly indicated, click the **Window** icon again.

6 Results preview step

This step provides you with a preview of the calculation results. A snapshot is automatically created that contains the parameters that were used for the calculation and provides the information needed to reproduce the results.

You can check the result volumes before saving them for further evaluation. Additionally, you can define which of the result volumes should be saved with the data set for further evaluation.
(→ Page 37 *Checking the Results Preview*)

To inspect result volumes in detail, you can drag them from the Result Gallery into the image area. See (→ Page 37 *Expanding volumes from the Result Gallery*).

6.1 Expanding volumes from the Result Gallery

✓ The **Results** layout is displayed.

You can drag the result volumes from the Result Gallery into the larger segments, but not vice versa.

You can also display the same volume in several segments at the same time.

◆ From the Result Gallery, drag a volume to a segment.

Dragging a volume into one of the upper three segments automatically replaces the volume in all three segments.

6.2 Checking the Results Preview

✓ Case preparation has been performed and the **Results Preview** step is active.

1 Check the result volumes to ensure they are adequate for further evaluation.

If the results are not as expected, return to a previous step or reset the workflow.

2 In the Result Gallery, click the **Result Storage** icon of the result volume you want to exclude from evaluation and archiving.

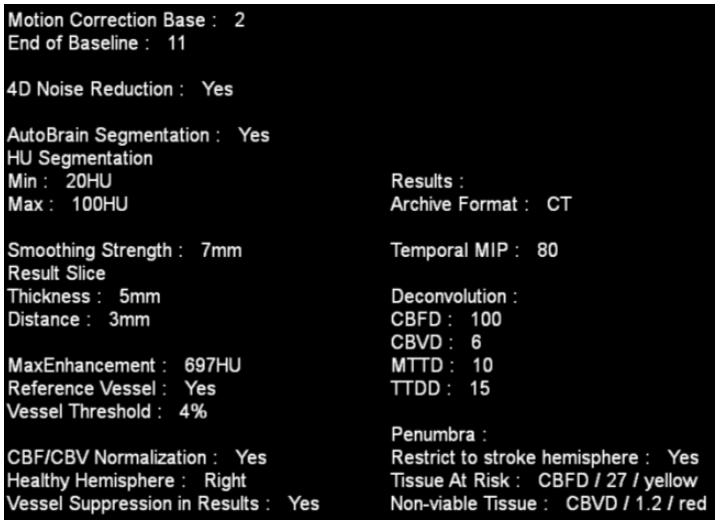
The check mark is removed.

Original images can be saved if motion correction results are available. This may take several minutes.

The tMIP is selected by default and cannot be deselected.

3 In the **Case Navigator**, click the **Confirm Results** icon.

Upon clicking the **Confirm Results** icon, a snapshot is automatically created that contains the parameters that were used for the calculation.



The selected result volumes are saved with the data set. The result volumes can be further evaluated in the **Results** step and can be opened with another workflow or in the **Perfusion Evaluation** workflow step.

When switching to reduced image text mode while visualizing perfusion results, the type of result is not written into the image comment because fused images are displayed. In full text mode, the type of result is written into the image comment.

6 Results preview step

7 Reading

CT Myocardial Perfusion provides various result volumes depending on the configured calculation method. For further evaluation, you can perform ROI and VOI quantifications. See (→ Page 41 *Results step*).

7.1 Results step

The **Results** step displays the calculation results in a multi-parameter layout, showing a maximum of six result volumes in an axial view and one result volume in axial, sagittal, and coronal default orientation. Free rotation is supported in all segments. The six result volumes are synchronized for navigation, rotation, and zooming and panning. In the Result Gallery, up to nine result volumes and the dynamic input data are listed. These results can be dragged into one of the larger segments.

For further evaluation, you can perform ROI and VOI quantifications. See (→ Page 41 *Time attenuation curves*) and (→ Page 44 *Defining a volume of interest*).

7.2 Time attenuation curves

Local vessel or tissue enhancement can be visualized by using ROI-specific or VOI-specific time attenuation curves (TAC).

7.2.1 Displaying the time attenuation curves

After drawing, for example a TAC ROI Ellipse, the respective time attenuation curve (TAC) and the related parameters are displayed automatically in the TAC tool.

You can hide or show the TAC tool manually.

- In the **Case Navigator**, click the **Time Attenuation Curves and Parameters** icon.

The TAC tool is hidden or displayed. The **TACs** and **Curves** tabs are displayed by default.

7.2.2 Drawing a circular or an elliptical TAC ROI

To evaluate tissue regions, you can draw elliptical or circular ROIs.

1 In the **Case Navigator**, click the **Circular** icon.

– or –

From the upper right corner menu, choose **TAC ROI Ellipse**.

The TAC ROI mode starts and the mouse pointer changes its shape.

2 To draw a circle, click and drag the mouse until the circle is of the required size.

– or –

To draw an ellipse, press and hold the **Shift** key while drawing.

The evaluation results are displayed in the segment, preceded by the graphic identification tag. The time attenuation curve of this ROI and its curve and statistical values are displayed in the TAC tool.

7.2.3 Drawing a freehand TAC ROI

To evaluate tissue regions, you can draw freehand Regions of Interest (ROIs).

1 In the **Case Navigator**, click the **Freehand** icon.

– or –

From the upper right corner menu, choose **TAC ROI Freehand**.

The TAC ROI mode starts and the mouse pointer changes its shape.

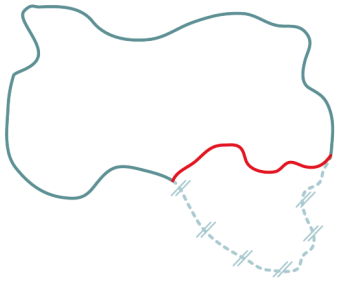
2 To draw a freehand ROI, click and drag the mouse while drawing the required shape.

The evaluation results are displayed, preceded by the graphic identification tag. The time attenuation curve of this ROI and its curve and statistical values are displayed in the TAC tool.

To change the size of a freehand ROI, select it and move the handles to resize the geometric figure.

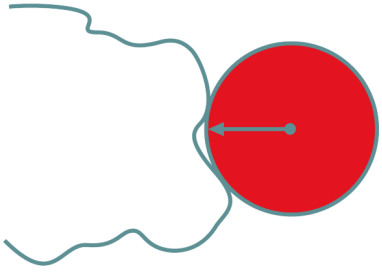
7.2.4 Correcting a freehand ROI using the correction pen

- To edit a part of a freehand ROI, right-click the ROI, choose **Correction Pen** from the context menu and redraw the part of the figure you want to correct. The smaller part of the original line will be removed.



7.2.5 Correcting a freehand ROI using the nudge tool

1. To fit a freehand ROI to a certain section of the image, right-click the ROI and choose **Nudge Tool** from the context menu.



2. Click the required point in the segment. The size of the **Nudge Tool** is determined by the distance between the point you have clicked and the nearest point of the line.
3. Click and drag the mouse to move the borders of the ROI.

7.2.6 Analyzing the ROI statistics

✓ Time attenuation curves are displayed.

1 On the TAC tool, click the **Statistics** tab to display the ROI statistics.

You can choose between the following parameters:

- **Mean Value**
- **Standard Deviation**
- **Area/cm² or Vol/cm³**

2 Change the display of ROI parameters according to your needs.

The values are adapted according to your selection. You can also export the ROI statistics for further analysis. See (→ Page 51 *Exporting statistics*).

7.2.7 Defining a volume of interest

✓ The **Results** step or the **Perfusion Evaluation** workflow step is active.

1 In the **Case Navigator**, click the **VOI** icon.

– or –

From the upper right corner menu, choose **TAC VOI**.

A mini toolbar for editing is displayed. The mouse pointer changes its shape.

2 Click and drag the mouse pointer to define a contour. Double-click to finish the contour.

3 Scroll through the slices and create more contours to cover the required volume. Interpolation between the slices is calculated automatically (dashed magenta lines).

If necessary, you can delete a single contour or all contour lines.

4 Scroll to a slice with a magenta contour and click the **Delete Single Contour** icon.

– or –

Click the **Delete All Contours** icon.

5 After you have created all required contours, click the **Complete Contour Drawing** icon to finish editing.

The mini toolbar changes to correction mode. The VOI contour is displayed in all segments.

If necessary, you can correct a single contour or delete all contours and return to the editing mode.

6 Scroll through the slices and check the contours. To correct a contour, click and drag the mouse pointer to draw a freehand line. To add an area to the existing contour, start at the contour line and draw outside the contour. To cut off an area from the existing contour, start at the contour line and draw inside the contour. Double-click to finish the contour editing.

The new contour is displayed as a dotted path in magenta.

After editing the contour, *syngo*.via may not be able to decide which part of the contour has to be discarded. In this case, a manual cutting mode is activated automatically.

The mouse pointer changes its shape to scissors with a question mark.

The part of the contour that has to be discarded is displayed as a dotted line.

7 Click the part that you want to cut off.

8 Click the **Delete VOI and Draw Manual Contour** icon to discard all contours and start editing from the beginning.

– or –

Click the **Complete Contour Drawing** icon to finish the VOI.

The VOI is listed in the **Findings Navigator** and the VOI specifics are displayed in the TAC tool.

7.2.8 Analyzing the VOI statistics

✓ The TAC tool is displayed.

1 On the TAC tool, click the **Statistics** tab to display the VOI statistics.

You can choose between the following parameters:

- **Mean Value**
- **Standard Deviation**
- **Area/cm² or Vol/cm³**

2 Change the display of VOI parameters according to your needs.

The values are adapted according to your selection. You can also export the VOI statistics and histogram data for further analysis. See (→ Page 51 *Exporting statistics*) and (→ Page 51 *Exporting histogram data*).

7.3 Resetting the workflow

You can reset the workflow to its initial state at any time. All unsaved results will be lost.

- In the **Case Navigator**, click the **Reset** icon.

7 Reading

8 Documenting results

When examining images, you can document your findings by using markers and snapshots. All findings are listed in the **Findings Navigator**.

You can further evaluate your findings in the **Perfusion Evaluation** workflow step. The findings that are added for saved result volumes in the **Perfusion Evaluation** workflow step and in the **Results** step are synchronized.

Additionally, you can evaluate and compare your findings in the **Results** step of the **MM Reading** workflow step after you have saved the result volumes.

8.1 Checking the Results Preview

✓ Case preparation has been performed and the **Results Preview** step is active.

1 Check the result volumes to ensure they are adequate for further evaluation.

If the results are not as expected, return to a previous step or reset the workflow.

2 In the Result Gallery, click the **Result Storage** icon of the result volume you want to exclude from evaluation and archiving.

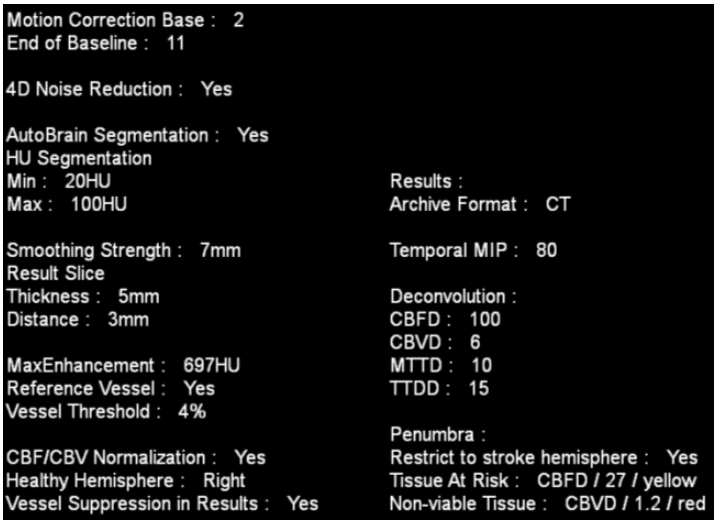
The check mark is removed.

Original images can be saved if motion correction results are available. This may take several minutes.

The tMIP is selected by default and cannot be deselected.

3 In the **Case Navigator**, click the **Confirm Results** icon.

Upon clicking the **Confirm Results** icon, a snapshot is automatically created that contains the parameters that were used for the calculation.



The selected result volumes are saved with the data set. The result volumes can be further evaluated in the **Results** step and can be opened with another workflow or in the **Perfusion Evaluation** workflow step.

When switching to reduced image text mode while visualizing perfusion results, the type of result is not written into the image comment because fused images are displayed. In full text mode, the type of result is written into the image comment.

8.2 Editing the findings details

In the **Findings details** window, you can edit the details of measurements and markers. The different types of findings are listed on the following tabs:

- **Markers**
- **Other**: General measurements

8.3 Exporting statistics

✓ At least one TAC ROI or VOI is drawn and the TAC tool is displayed.

1 In the TAC tool, right-click and choose **Export Statistics and Curves** from the context menu.

The **Save As** dialog box opens.

2 Navigate to the target folder and click **OK**.

The TAC and corresponding statistics are exported to a file which is saved in the selected folder.

8.4 Exporting histogram data

✓ At least one TAC ROI or VOI is drawn and the TAC tool is displayed.

1 In the TAC tool, right-click and choose **Export Histogram Data** from the context menu.

The **Browse For Folder** dialog box opens.

2 Navigate to the target folder and click **OK**.

The histogram data is exported to a file which is saved in the selected folder.

8.5 Perfusion Evaluation

In the **Perfusion Evaluation** workflow step, you can further evaluate your findings even at a later point in time. The findings that are added for saved result volumes in the **Perfusion Evaluation** workflow step and in the **Results** step are synchronized.

See (→ Page 52 *Evaluating perfusion results*).

8.5.1 Evaluating perfusion results

In the **Perfusion Evaluation** workflow step, you can review your findings and further evaluate previous perfusion results.

The **Perfusion Evaluation** workflow step can be used with results in either the CT Grayscale or the Enhanced CT format but not with the Color RGB format.

✓ The **Perfusion Evaluation** workflow step is active.

✓ Perfusion results are available in the Series Navigator or in the Result Gallery.

1 From the Series Navigator, drag a single result volume into the image area.

- or -

From the Series Navigator, drag a result series into the image area.

- or -

From the Result Gallery, drag a result into the image area.

The result volume or result series is displayed in the image area. Time attenuation statistics are displayed.

2 Use the perfusion evaluation tools to evaluate a result.

Define ROIs. (→ Page 42 *Drawing a circular or an elliptical TAC ROI*) and (→ Page 42 *Drawing a freehand TAC ROI*)

- or-

Define VOIs.

- or-

Set markers.

9 CT Myocardial Perfusion configuration

No special user rights are necessary to change settings in the **CT Myocardial Perfusion Configuration** dialog box. Note that your settings apply only for the currently active workflow. Applying changed settings while you read data may require a reset and the recalculation of results in the currently active workflow. This reset can affect the calculation and visualization, even of resumed data sets.

As a Clinical Administrator, you can change the settings permanently for all users.

In the **CT Myocardial Perfusion Configuration** dialog box, you can configure the following settings:

- You can create or delete user-specific templates for evaluation.

  (→ Page 54 *Creating a template*) and (→ Page 54 *Deleting a template*)

- **Common** tab

  You can select a time point as the motion correction base. (→ Page 55 *Setting the default motion correction base*)

- **Calculation** tab

  You can adjust the calculation parameters.

  – (→ Page 56 *Setting the segmentation thresholds*)

  – (→ Page 56 *Defining the smoothing strength for image calculation*)

- **Visualization** tab
  - You can adjust the initial display of images for workflow-specific series and results.

    (→ Page 57 *Setting the display properties for specific volumes*)
  - You can define the initial display of the time attenuation curves and tables.

    (→ Page 58 *Setting the display properties for curves and tables*)
- **Results** tab

  You can define the display and archiving properties of results.
  - (→ Page 58 *Selecting result volumes for archiving and further evaluation*)
  - (→ Page 59 *Setting window values for result volumes*)
  - (→ Page 60 *Defining the archive format of result volumes*)
  - (→ Page 61 *Defining the myocardial parameter maps*)

9.1 Creating a template

Only a clinical administrator can create new templates.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1. From the **Template** list, select the required template as a basis for the new template.
2. On the tabs of the **CT Myocardial Perfusion Configuration** dialog box, change the settings accordingly.
3. Click the **Create New** button.
4. In the **New Template** dialog box, enter a name and click **OK** to save the template.

   The new template is now available in the **Case Navigator**.

9.2 Deleting a template

Only a clinical administrator can delete templates.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 From the **Template** list, select the template that you want to delete.

2 Click the **Delete** button.

The template is deleted and is no longer available in the **Case Navigator**.

9.3 Setting the default motion correction base

You can select the time point position within the series that is used as the motion correction base by default. The motion correction base is used to align images that show strong movements.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

For the motion correction base you can select one of the following options:

- **First**: to use the first time point of the series
- **Second**: to use the second time point of the series
- **Middle**: to use the middle of all time points in the series
- **Custom**: to specify a time point of your choice

1 On the **Common** tab, select the **First**, **Second**, or **Middle** option.

– or –

Select the **Custom** option and enter a number to specify a time point of your choice. The number reflects the position of the time point within the loaded series.

2 Click **OK**.

The **Reset** dialog box opens.

3 Click **Yes** to reset the workflow including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9.4 Setting the segmentation thresholds

You can specify the default range of values to be used by the HU-based segmentation algorithm. The values you define in the configuration are displayed in the **Min. HU** and **Max. HU** fields of the **Segmentation** step. All voxels with HU values within the range you specify are kept for display, calculation, and measurements, while all other voxels are excluded. You can specify the values within the complete range from -1024 to 3071 HU.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 On the **Calculation** tab, enter a value in the **Min. HU** and in the **Max. HU** field to specify the **HU Thresholds**.

2 Click **OK**.

The **Reset** dialog box opens.

3 Click **Yes** to reset the workflow including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9.5 Defining the smoothing strength for image calculation

The smoothing filter is another possibility to soften images besides the 4D noise reduction. It is applied during the result volume calculation in the **Results** step.

You can specify the default diameter of the smoothing filter to provide a soft-focus effect for noisy input images. The bigger you choose the filter, the softer the images will be displayed. Note that fine structures in the images will be displayed blurred when a big filter was chosen.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 On the **Calculation** tab, enter a value for the **Smoothing Strength** in mm.

2 Click **OK**.

The **Reset** dialog box opens.

3 Click **Yes** to reset the workflow including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9.6 Setting the display properties for specific volumes

You can define the display type and, if applicable for the display type, also the slice thickness and the windowing values.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 On the **Visualization** tab, select a **Display Type** from the list of the **Volume** you want to change.

- For the **MPR Thick** and **MIP Thin** display types, you can adjust all fields.
- For the **MPR** display type, you can adjust the **Window Values** fields.
- For the **MPR** display type selected in the **Original Data** fields, the **Window Values** and the **Slice Thickness** from the DICOM image header are used.

2 Enter a value for the **Slice Thickness** in mm.

3 Enter a value for the **Width** (contrast) and the **Center** (brightness) to specify the window in HU.

4 Click **OK**.

The **Reset** dialog box opens.

5 Click **Yes** to reset the workflow including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9.7 Setting the display properties for curves and tables

You can specify the default display of curves and tables in the TAC tool.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 On the **Visualization** tab, select the **Absolute** option for **Time Attenuation Curves** to display the curves with absolute scaling.

– or –

Select the **Relative** option to display relative curves (all curves start near 0 HU).

2 For the **Result Table**, select the **Curve** option to display the ROI data represented by curves in the foreground.

– or –

Select the **Statistics** option to display the ROI data represented by a table in the foreground.

3 Click **OK**.

The **Reset** dialog box opens.

4 Click **Yes** to reset the workflow including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9.8 Selecting result volumes for archiving and further evaluation

You can send your result volumes to the RIS or PACS when you complete the workflow. Additionally, you can directly perform further evaluation for saved result volumes in the **Perfusion Evaluation** workflow step.

Available result volumes are calculated depending on perfusion maps. On the **Results** tab of the **CT Myocardial Perfusion Configuration** dialog box, these maps are listed according to the calculation mode. You can configure which result volumes should be saved by default. In addition, you can select and deselect result volumes for sending in the Result Gallery. See (→ Page 37 *Checking the Results Preview*).

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 On the **Results** tab, select the check boxes of the required result volumes in the **Archive** section.

2 Click **OK**.

The **Reset** dialog box opens.

3 Click **Yes** to reset the workflow including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9.9 Setting window values for result volumes

In the image area, result volumes are displayed with a colored overlay, together with a color scale. You can define the default value of this scale by setting a value for the window width. You can enter values in a range from 2 to 4096 HU for the selected perfusion maps and volumes.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 From the **Template** list, select either a tumor or a liver template to activate the corresponding calculation modes.

2 On the **Results** tab, enter a window width value in the **Window Value** fields to be used for the required standard and result volumes.

3 Click **OK**.

The **Reset Application** dialog box opens.

4 Click **Yes** to reset the workflow including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9.10 Defining the archive format of result volumes

You can send your calculated result volumes to the RIS or PACS when you complete the workflow. You can select and deselect the result volumes manually or configure which result volumes should be sent by default. See (→ Page 37 *Checking the Results Preview*) and (→ Page 58 *Selecting result volumes for archiving and further evaluation*). Result volumes stored with the data set can be used for further evaluation in the **Perfusion Evaluation** workflow step.

Specify in which format the result volumes should be sent:

- **CT Grayscale**

  Result volume in axial orientation without colored overlays

- **Enhanced CT**

  Multiframe result volume, all frames in axial orientation, including the color palette and real world value mapping (DICOM). Note that this format cannot be displayed by all PACS.

- Additionally, you can combine the selected option with the **Color RGB** format.

  Secondary captures in axial orientation of the result volume. This format cannot be loaded into the **Perfusion Evaluation** workflow step.

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 On the **Results** tab, select the **CT Grayscale** option or the **Enhanced CT** option in the **Archive Format** section.

2 Select the **Color RGB** check box, if required.

3 Click **OK**.

The **Reset** dialog box opens.

4 Click **Yes** to reset the workflow including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9.11 Defining the myocardial parameter maps

You can define the following myocardial parameter map:

- **Myocardial Blood Flow** [mL/100mL/min]
- **Myocardial Blood Volume** [mL/100mL]
- **Flow Extraction Product** [mL/100mL/min]
- **Perfused Capilary Blood Volume** [mL/100mL]
- **Myocardial Blood Flow Corrected** [mL/100mL/min]

  This is an experimental parameter. In this first version, the result is the same as the **Myocardial Blood Flow** parameter.
- **Extravascular Extracellular Volume** [mL/100mL]
- **Time to Peak** [s]
- **Time to Start** [s]
- **Tissue Transit Time** [s]

✓ The **CT Myocardial Perfusion Configuration** dialog box is open.

1 On the **Results** tab, select the applicable check boxes in the **Myocardial Model** section.

2 Adjust the **Window Values** fields, if required.

3 Select the **Archive** check box, if required.

4 Click **OK**.

  The **Reset** dialog box opens.

5 Click **Yes** to reset the workflow, including all results and findings. The workflow is reset to its initial state and all findings are removed from the **Findings Navigator**. Recalculation of the results can be started.

9 CT Myocardial Perfusion configuration

10 Additional information

This section provides background information on *syngo*.CT Myocardial Perfusion.

10.1 Left Ventricle Segmentation

With the left ventricle segmentation it is possible to outline the left ventricle and to outer parts from the evaluation. The outlining of the left ventricle is a semi-automated procedure. The user is able to control, change or delete the contour.

10.2 Perfusion parameter images of *syngo*.CT Myocardial Perfusion

Using a dedicated parametric deconvolution technique, which is derived from the Tofts model and defined by an analytical Impulse Residue Function (IRF, see fig. 1), the voxel time attenuation curves are fit to a simplified two-compartment model of intra- and extravascular space. This technique allows utilization of the high temporal sampling and the high signal of the AIF for the tissue time attenuation curves (TAC) [1].

The following parameter images can be calculated:

- **MBF**:

  Myocardial blood flow [mL/100mL/min] is calculated from the maximum slope of the fit model curve normalized to the peak arterial enhancement.

- **MBV**:

  Myocardial blood volume [mL/100mL] is calculated from the peak of the fit model curve normalized to the peak arterial enhancement.

- **PCBV**:

  Perfused Capillary Blood Volume [mL/100mL] is one of the IRF parameters and proportional to the amount of tracer passing through the capillaries without extraction.

- **FE**:

  Flow Extraction Product [mL/100mL/min] (or KTrans) is one of the IRF parameters and describes the flow of blood from the vessels to the tissue.

- **TTS**:

  Time to Start [s] is one of the IRF parameters and indicates the time to contrast arrival.

- **TTP**:

  Time to Peak [s] indicates the time until the peak of the model fit curve is reached.

- **TTT**:

  Tissue Transit Time [s] is one of the IRF parameters and indicates the mean transit time of contrast agent through the tissue.

- **EEV**:

  Extravascular Extracellular Volume [mL/100mL] is the product of FE and TTT and indicates the blood volume that was exchanged into the extravascular space while the contrast agent passed through the myocardial vessels.

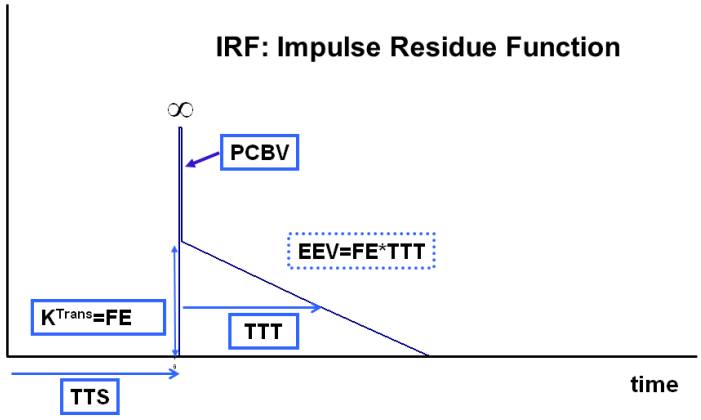


Figure 1

10.3 Application hints on clinical relevance, uncertainties and repeatability

The most important parameter is MBF (myocardial blood flow). This parameter has been validated and tested against SPECT, FFR and microspheres in a number of animal and clinical studies primarily for its capability to depict regions of ischemia under vasodilatory stress downstream of a hemodynamically relevant stenosis and to quantitatively differentiate them from normal regions [1-10]. MBF is the primary output of a perfusion calculation.

Secondary parameters that are calculated in the default setting are MBV, PCBV and FE. These parameters might have potential to provide ancillary information to MBF [1,3,10]; mismatch of MBF and MBV for instance has been linked to infarction [3]. But at this point in time their true clinical relevance has not been established yet.

The other four parameters are either descriptive, TTS for instance can be expected to be increased in patients with certain bypasses, or are used in model fit process as free parameters. They can be switched on as optional parameters for completeness and potential quality control. If they have additional clinical value is unclear.

The repeatability of the calculation of the primary parameter MBF on the same data set is high. In a two center study on 80 patients the variability was determined using intraclass correlation coefficients (ICC's). Intra- and inter-observer ICC's were 0.86 (95% CI: 0.78–0.91) and 0.82 (95% CI: 0.73–0.88), respectively [9].

It has to be emphasized that the uncertainties of all parameters strongly depend on the quality of the original acquisition data. Achieving an optimal breathold during the examination and a good bolus quality are of utmost importance. The software includes means to compensate for residual motion (motion correction), but this correction cannot completely compensate large motion amplitudes.

It is recommended to always check the consistency of the data before and after motion correction by scrolling through the acquisition series in time. A final quality check is possible after the result calculation by placing ROIs over relevant regions of the myocardium and by inspecting their TACs. The continuous solid lines depict the output of the parameter model fitted to the measured data points. Measured time points that are closer to, or optimally on, the model curve indicate higher confidence and lower uncertainty.

Figure 2 shows an example.

The upper TACs (corresponding MBF image middle left) show a high quality case. The AIF (red curve, scale on the right) has a peak enhancement of > 600 HU, the normal TAC is almost perfectly fit by the model, the ischemic TAC is well fit, residual artifacts in the baseline portion are well compensated. This corresponds to the homogeneous image quality with well-defined borders of the myocardial wall.

The lower TACs (corresponding MBF image middle right) show a moderate quality case with considerable motion. The AIF (red curve, scale on the right) has a peak enhancement of only 400 HU and is less well defined: already the normal TAC shows considerable scatter around the model curve. This corresponds to the patchy image appearance and the artifactual hyperintesities in the inferior and lateral endocardium. Nevertheless the ischemic territory is well depicted and the case is diagnostic, but the variability of numbers determined from ROIs will be higher.

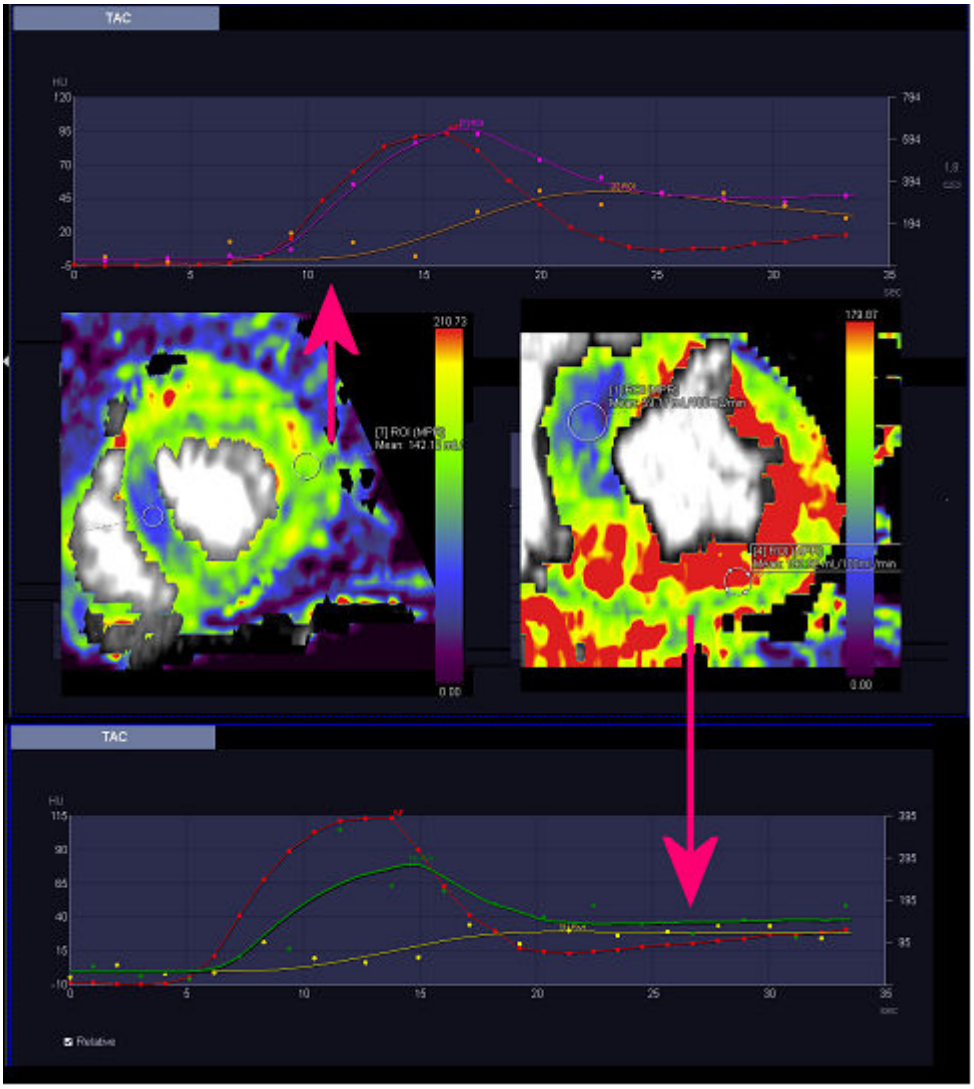

TAC
HU
120
95
70
45
20
-5
0
5
10
15
20
25
30
35
SEC
794
694
394
194
210.73
0.00
179.87
0.00
TAC
HU
115
90
65
40
15
-10
395
295
195
95
Relative

Figure 2

10.4 References

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10.5 Input data suitable for processing with *syngo*.CT Myocardial Perfusion

syngo.CT Myocardial Perfusion is primarily designed to process data acquired with the dedicated scan mode Heart Perfusion Scanning. This mode is optionally available on the SOMATOM Force and the SOMATOM Definition Flash (with or without Stellar Detector).

Heart Perfusion Scanning is a dedicated Dual Source cardiac scan mode that repeatedly acquires data at adjacent alternating table positions employing prospective end-systolic triggering.

10.6 Typical Dose values

Radiation exposure depends on patient size and heart rate. The table below shows typical dose values for a normal size patient scanned with the recommended examination time of 32 s at a heart rate of 90 bpm (i.e. acquisition of 12 time points).

	Cov-erage (cm)	KV	mAs/rot	CTDI-vol (mGy)	DLP (mGycm)	eff. dose (mSv)*
SOMATOM Force	10.5	70	400	35	370	5.2
SOMATOM Definition Flash (with Stellar Detector)	7.3	80	370	54	390	5.5
SOMATOM Definition Flash	7.3	100	300	92	670	9.4

* calculated using a k factor of 0.014

Currently two Siemens scanners, namely SOMATOM Definition Flash (with or without Stellar Detector) and SOMATOM Force, can provide data for *syngo*.CT Myocardial Perfusion. In the future scanners that are fast enough might be able to support scanning with a normal perfusion scan without shuttle because they are wide enough to scan the entire heart.

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Manufacturer's note:

This product is provided with a CE mark in accordance with the regulations stated in Council Directive 93/42/EEC of June 14th 1993, concerning Medical Devices.

The CE marking applies only to Medical Devices which have been put on the market according to the above-mentioned EC Directive.

Unauthorized changes to this product are not covered by the CE mark and the related Declaration of Conformity.

Caution: Federal law restricts this device to sale by or on the order of a physician (21 CFR 801.109(b)(1)).

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