syngo MBF

Operator Manual
VB30

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syngo MBF

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VB30

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 Is used for on-screen output of the system including code-related elements or commands
Orange	Is used to emphasize particularly important sections of the text
`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	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

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1 *syngo* MBF

Siemens *syngo* MBF is a software product intended for visualization, assessment and quantification of PET images.

The application performs quantitative measurements of tracer uptake over time to aid in the interpretation of myocardial perfusion PET images.

The product is intended for use by trained professionals. The clinician retains the ultimate responsibility for making the pertinent assessment based on their standard practices and visual comparison of the information.

syngo MBF, a part of *syngo*.via MI workflows, can be deployed on the *syngo*.via and MI View&GO platform.

1.1 Intended use

An individual software program, or group of programs, routines, or algorithms that add specific image processing and/or analysis capabilities to a positron emission tomography (PET) imaging system configuration. A basic set of application programs and routines is included with such computer-controlled imaging systems and they can be upgraded to correct programming errors or to add new system capabilities. Some packages must be combined with specific hardware or firmware accessories or configurations in order to function as intended. Application program packages are typically identified by a proprietary name and “version” or “upgrade” number.

1.2 Indications for use

- *syngo*.via MI Workflows Indications for Use

  syngo.via Molecular Imaging (MI) workflows comprise medical diagnostic applications for viewing, manipulation, quantification, analysis and comparison of medical images from single or multiple imaging modalities with one or more time-points. These workflows support functional data, such as positron emission tomography (PET) or nuclear medicine (NM), as well as anatomical datasets, such as computed tomography (CT) or magnetic resonance (MR). *syngo*.via MI workflows can perform harmonization of SUV (PET) across different PET systems or different PET reconstruction methods.

  syngo.via MI workflows are intended to be utilized by appropriately trained health care professionals to aid in the management of diseases associated with oncology, cardiology, neurology, and organ function. The images and results produced by the *syngo*.via MI workflows can also be used by the physician to aid in radiotherapy treatment planning.

- MI View&GO Indications for Use

  MI View&GO is a medical diagnostic application for viewing, manipulation, quantification, analysis and comparison of medical images with one or more time-points. MI View&GO supports functional data, such as positron emission tomography (PET) or nuclear medicine (NM), as well as anatomical datasets, such as computed tomography (CT) or magnetic resonance (MR). MI View&GO is intended to be utilized by appropriately trained health care professionals to aid in the management of diseases associated with oncology, cardiology, neurology, and organ function. The images and results produced by MI View&GO can also be used by the physician to aid in radiotherapy treatment planning.

1.3 Contraindications

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

1.4 Authorized users

The system must only be used by persons with the necessary specialist knowledge, for example, physicians, trained radiologists, or trained technologists, after an appropriate application training. Use of this application by untrained or unqualified users may lead to incorrect diagnosis or treatment.

CAUTION

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

1.5 Clinical benefits

The *syngo* MBF application achieves its intended performance under normal conditions of use. The *syngo* MBF application has a positive impact on the health of an individual by its use as an aid in detecting, localizing, diagnosing, staging and restaging of lesions, tumors, disease and organ function for the evaluation of diseases and disorders. The *syngo* MBF application has a positive influence on the health of an individual when used as an aid in managing cardiology and other diseases.

1.6 Patient population

This device is not limited in the patient population it can be used for.

Limiting factors are determined by scanner system and modality that this post-processing software is used with.

The decision whether to use this device for specific populations is at the discretion of the physician.

The clinician retains the ultimate responsibility for making the pertinent diagnosis based on their standard practices and visual comparison of the separate unregistered images. This device is a complement to these standard procedures.

1.7 Availability of products and features

Due to international regulatory restrictions, some products and features described in this document are not commercially available in all countries. Features may be blocked or enabled by optional software licenses. Future availability of these features cannot be guaranteed. Some features may not be explicitly marked as optional. Please contact your local Siemens Healthineers representative for further details.

1.8 Serious Incident Reporting

Any serious incident that has occurred in relation to the device should be reported to the manufacturer and the competent authority of the EU Member State in which the user and/or patient is established.

1.9 System and software representations

The photographs, graphics, figures, and medical images used in this documentation are examples only. Their actual display and design may be slightly different on your system.

1.10 Legal notice

Siemens reserves the right to modify the design and specifications contained herein without prior notice. Please contact your local Siemens Sales Representative for the most current information.

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The parameters mentioned herein were specified to the best of our knowledge. We assume no responsibility whatsoever for the correctness of this information. Variations may prove necessary for individual patients. The treating physician bears the sole responsibility for all of the parameters selected.

Third-party software should not be added to your system except by Siemens-authorized personnel. The customer takes full responsibility for any damage or loss of data resulting from the use of unauthorized third-party software. Siemens Healthcare GmbH makes no warranty with respect to third-party software.

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Other trademarks are used for identification purposes only and are the property of their respective owners.

In some instances, the color scheme and the resolution of illustrations or original medical images shown in this document has been modified for illustrative purposes. It is not the purpose of illustrations in this guide to provide definitive examples of statistics or image alignment, unless otherwise indicated.

This software must be installed with the *syngo*.via or MI View&GO platform in order to function properly.

The original language of this document is English.

2 About *syngo* MBF

Always use this operator manual in conjunction with all operator manuals provided.

Familiarize yourself with the analysis methods described.

Follow the safety instructions.

Not observing the operator manuals of the software and its applications could result in using the wrong basis for diagnosis.

The *syngo* MBF application provides tools for looking at information obtained from dynamic cardiac PET scans.

This application supports scans acquired with either ^{82}Rb, or $^{13}NH_3$ tracers. If you are using the application to look at two scans, the same tracer must have been used in both scans.

Before using this application please read the section (➔ Page 18 *Before you Start*), for essential information on patient positioning, data acquisition and data quality.

2.1 Before you Start

2.1.1 Data Acquisition and Data Quality

To compute myocardial blood flow or "MBF", the blood input function or BIF is estimated from the reconstructed images and plays an important role in determining the accuracy of the quantification results. Best results are likely to be obtained when the tracer is injected in a **bolus mode** which is captured with the appropriate number of dynamic frames. It is recommended that the **acquisition is synchronized with the injection** such that scan is started before the injection bolus reaches the left ventricular cavity to make sure the blood input function is entirely covered. A good quality blood input function can be obtained when the **sampling rate of the dynamic framing** is sufficient to represent the changing distribution of the radiotracer as it reaches the ventricles of the heart. If the early frames are too short, the images may contain significant statistical noise due to low counts; conversely, if the frames are too long, the BIF may be under sampled. Particular care must therefore be taken in determining framing for the early part of the acquisition in order to achieve the best accuracy.

The dose injected to the patient should be such that the scanner operates within the linear range of its detection response. Should the count rate exceed this range, the early bolus phase of the scan may be underestimated, leading to overestimation of flow values.

In order to be quantitative, necessary corrections must be applied during image reconstruction including scatter correction, decay correction and attenuation correction. The data should also be calibrated. It is important to ensure that the CT attenuation image is correctly aligned with the PET data in the region of the left ventricle. The *syngo* MBF application assumes that these corrections have been applied. When corrections and calibrations have been applied, the data can be represented in units of Bq/ml. If the dataset uses units other than Bq/ml, the *syngo* MBF application will display a warning and the quantification results will be generated without any units displayed. It is the user's responsibility to interpret the results.

2.1.2 Patient Positioning

The *syngo* MBF application assumes the patient is scanned in head first supine position. Other patient positions could result in the presentation of the results in a wrong region of the polar plots and vessel beds.

2.1.3 Data Orientation

The automatic heart reorientation may need further adjustment for either stress or rest data. If both stress and rest datasets are loaded it is important to assess the alignment between the two datasets and adjustment may be necessary. Results should not be accepted without user review. In some instances the automatic heart localization may fail, and the heart region may need to be identified manually. This is more likely to happen in very noisy data, when the location of the heart is very close to either end of the field of view, or when unusually high extracardiac activities, right ventricular or major infarctions are present in the image.

Be aware that when the base and apex locations of the long axis are manually adjusted, this information is used to *assist* in the automatic segmentation. The position of base will be fixed at the manually selected location. The exact position of apex is determined by the automatic processing. Both locations will be displayed to the user.

2.1.4 Calculation of Myocardial Flow Reserve when Rest Flow is Very Low

When stress and rest datasets are loaded, 'reserve' is calculated as the ratio of stress flow to rest flow. When the resting values are very low or close to zero, this can result in unusually high reserve values. These values have no clinical meaning and can bias the statistical results.

2.1.5 Automatic Segmentation and Motion Correction

It is important to review data for possible intra-scan patient motion. Segmentation of the left ventricle is computed for each frame of the image and displayed as an overlay. By stepping through the frames of the series, it is possible to assess the amount of motion that may occur. A typically acceptable range of motion is observed when the points of peak intensities of the left ventricle stay within the contour.

In rare circumstances, automatic segmentation can fail to compute a reasonable result. This can be identified by checking the myocardium segmentation contour overlay. This is normally localized and attributed to regional noise in the data or high uptakes in the neighborhood of the failure. Quantitative values computed from the wrongly segmented region should not be used for interpretation.

The *syngo* MBF application has an automatic motion correction function to compensate for heart movement during the scan. Motion correction is applied to late time frames when the tracer has diminished from the blood pool and is being taken up in the myocardium and earlier blood pool uptake frames are not motion corrected. Motion correction is based on adjustment of the myocardium segmentation contours for each late frame and is subject to the same possible failures as the automatic segmentation described above.

2.1.6 Residual Correction

To use the 'residual correction' function for $^{13}NH_3$ studies, the first frame of the image needs to be acquired before the injection of the $^{13}NH_3$ tracer.

2.1.7 Rate-Pressure Product Normalization

The *syngo* MBF application provides a function to normalize the rest flow quantification results and thereby the reserve. This is done by means of the product of the heart rate and the blood pressure.

This normalization allows the user to compare rest values with stress values more accurately without any pseudo-stress effects caused by high heart rate or blood pressure. Furthermore, normalizing in this way allows for comparison of values between patients with physiological differences.

2.2 Using *syngo* MBF

2.2.1 Cautions and Warnings

Image Quality Assumptions:

CAUTION

syngo MBF assumes that datasets are quantitative attenuation corrected (AC) (and decay corrected) PET volumes that have been calibrated and accurately reflect a measure of radioactivity in units proportional to number of disintegrations per second. This will not be checked explicitly by the *syngo* MBF application, however, the user may assess the quality of the input data using features of the *syngo* MBF application.

Using datasets that do not meet this criteria may result in inaccurate calculation, potentially leading to incorrect diagnosis

- Acquisition protocols must ensure that datasets meet these assumptions.

syngo MBF is designed for use as a visualization tool only. Siemens takes no liability for any misuse or clinical outcome resulting from the use of the software as an aid to diagnosis. The functionality of the software package is available to the user in the belief that the software is only an aid or adjunct to processes or decisions that can be made without the use of the software.

The software tool may, by virtue of its usage, contain confidential patient information. The security and configuration of the computing hardware used to execute the software is the responsibility of the end-user. This includes secure imaging local area networks (LANs), appropriate fire-wall provision, network directory permissions etc.

CAUTION

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

2.2.2 Diagnostic and Therapeutic Restrictions

Image compression:

syngo MBF is not intended for use on data that has been compressed using lossy compression techniques. Data that has been compressed in this way may be inaccurate and should not be used for interpretation of medical data.

Use of the software:

The software is designed as a visual aid and as such it is not recommended for use in applications where the image geometry as displayed by the software application cannot be confirmed by other means. The software should not be used as a direct control mechanism for delivery of treatment, and should not be used as the sole basis for evaluating the success/response to treatment, as a direct control mechanism for biopsy guidance mechanisms (either hardware or software based) or as the sole basis for surgical planning, the preparation, execution or post-operative assessment of surgical practices.

2.3 Statement of Accuracy

The accuracy of measurements derived from *syngo* MBF are difficult to assess due to the nature of the physiological measurement that is being made. There are methods defined in the literature which compare the flow computed from dynamic PET imaging with reference methods, themselves having recognized accuracy [1-7].

Measurement using microsphere using a classic model have been performed on 11 subjects [7]. Mean MBF was compared between the microsphere results and *syngo* MBF ^{82}Rb, and statistically tested for deviation from the line of Identity using Passing-Bablok regression with 95% confidence interval.

Mean MBF (±standard deviation) was found to be 2.1±1.2 [min 0.52...max 3.0] for the microspheres, 1.7±1.1 [0.35...3.7] for *syngo* MBF. Within a 95% confidence interval, no deviation from the line of identity was found for the reference MBF versus the two quantification approaches (*syngo* MBF and microsphere).

1. K. Yoshida, N. Mullani, and K. L. Gould, Coronary Flow and Flow Reserve by PET Simplified for Clinical Applications Using Rubidium-82 or Nitrogen-13-Ammonia, J Nucl Med 37: 1701-1712.

2. P. Herrero, J. Markham, M.E. Shelton, and S.R. Bergmann, Implementation and evaluation of a two-compartment model for quantification of myocardial perfusion with rubidium-82 and positron emission tomography, Circ. Res. 1992, 70: 496-507.

3. M. Lortie, R.S. Beanlands, K. Yoshinaga, R. Klein, J.N.Dasilva, R.A. DeKemp, Quantification of myocardial blood flow with 82Rb dynamic PET imaging. Eur J Nucl Med Mol Imaging 2007; 34: 1765-1774.

4. Georges El Fakhri, Arash Kardan, Arkadiusz Sitek, Sharmila Dorbala, Nathalie Abi-Hatem, Youmna Lahoud, Alan Fischman, Martha Coughlan, Tsunehiro Yasuda, and Marcelo F. Di Carli, Reproducibility and Accuracy of Quantitative Myocardial Blood Flow Assessment with 82Rb PET: Comparison with 13N-Ammonia PET, J Nucl Med 2009, vol 50: 1062-1071.

5. Riikka Lautamäki, Richard T. George, Kakuya Kitagawa, Takahiro Higuchi, Jennifer Merrill, Corina Voicu, Anthony DiPaula, Stephan G. Nekolla, João A. C. Lima and Albert C. Lardo, et al. Rubidium-82 PET-CT for quantitative assessment of myocardial blood flow: validation in a canine model of coronary artery stenosis, EJNMMI,Volume 36, Number 4, 576-586, 2009.

6. Muzik et.al. Validation of Nitrogen-13-Ammonia Tracer Kinetic Model for Quantification of Myocardial Blood Flow Using PET JNM 34:83-91 (1993).

7. Stephan G. Nekolla, Hossam Sherif, Sibylle Reder, Xiao-Bo Pan, Eliane Weidl, Anne Preissel, Christine Baumgartner, Jérôme Declerck, Markus Schwaiger, Validation of myocardial blood flow measurements with 82Rb and a 3D PET tomograph, J Nucl Med. 2011; 52 (Supplement).

2.4 Illustrations used in this Help System

It is not the purpose of illustrations used in this guide to provide definitive examples of statistics, regions of interest, or other analysis, unless otherwise indicated. In some instances the resolution of illustrations or original images has been modified for illustrative purposes. Note that original images always lose a certain amount of detail when reproduced.

2.5 Glossary and Abbreviations

Dynamic Series or Dynamic Dataset - A single dataset, acquired in a single scan, containing multiple images which represent the change in tracer uptake in a subject over a relatively short period of time.

HLA - Horizontal Long Axis. One of three cardiac orthogonal views

LAD - Left anterior descending artery

LCX - Left circumflex artery

LUT - In image processing, lookup tables or LUTs give an output value for each of a range of index values. One common LUT, called the colormap or palette, is used to determine the colors and intensity values with which a particular image will be displayed.

MPI - Myocardial Perfusion Imaging

^{13}**NH$_3$** - Ammonia. Commonly used myocardial perfusion tracer for PET

Outlier - Segments of a polar plot determined from the kinetic modeling process, where the value of the segment is considered as statistically not valid in the kinetic model fitting of the dynamic study.

PET - Positron Emission Tomography

^{82}**Rb** - Rubidium. Commonly used myocardial perfusion tracer for PET

RCA - Right coronary artery

ROI - Region of Interest

SA - Short Axis. One of three cardiac orthogonal views

Spillover factor - Parameter for spill-in/spill-out effects. A high spillover factor can be an indicator that the myocardial blood flow and the reserve values are not accurate.

TAC - Time Activity Curve

VLA - Vertical Long Axis. One of three cardiac orthogonal views

3 Getting Started

Please read the section Before you Start, see (➔ Page 18 *Before you Start*) to help you get the best results when using the application.

3.1 Using the Application

The *syngo* MBF application has two main stages:

- data set-up
- analysis

3.1.1 Data Set-up

Before data analysis, you may need to complete some data set-up:

- Identify the tracer used.
- Set data as Stress or Rest.
- The position of the Long Axis of the heart may require adjustment.

This data set-up is usually done automatically by *syngo* MBF. However, in some instances you may need to assign Stress and Rest or set the tracer, if these values are not clear from the data.

For more information see the sections on:

- Selecting the Tracer (➔ Page 40 *Selecting the Tracer*)
- Set Datasets as Stress or Rest (➔ Page 39 *Assign Data as Stress or Rest*)

The long axis of the heart is also defined automatically, but this can be changed if you are not happy with the automatic placement.

See the section on (➔ Page 41 *Realigning the Long Axis of the Heart*).

3.1.2 Analysis

The second stage of the application provides quantitative information on the data.

Polar Plots

Polar plots are used to display:

- tracer uptake;
- quantitative results;
- myocardial blood flow;
- reserve, or the ratio of stress flow to rest flow, if two datasets have been loaded.

You can select segments of the polar plots and display activity for a segment in the graph.

Statistics Table

The table shows mean and standard deviation for each region of the heart according to the three vessel model. If you have two datasets loaded, it also gives myocardial flow reserve: that is, the ratio of stress flow to rest flow.

Graph

The graph displays:

- the blood input time activity curves;
- tissue activity curves for a selected segment of the polar plots, see (➔ Page 65 *Selecting a Segment for Analysis*);
- the global time activity curve which represents the amount of tracer for the entire myocardium.

3.2 Shortcuts

Show or Hide, see (➔ Page 35 *Show or Hide: Reference Lines*):	
Ctrl + L	Show or Hide Reference Lines
Ctrl + P	Show or Hide Patient Information

Ctrl + I	Show or Hide Series Information
Ctrl + T	Show or Hide Segmentation Overlay and Blood Input ROI
Ctrl + 3	Show or Hide 3 Segment Overlay
Ctrl + 17	Show or Hide 17 Segment Overlay
Ctrl + 0	Hide Segment Overlay
Data Set-up, see (➔ Page 39 *Setting up Data before Analysis*):	
Ctrl + C	Motion Assessment Mode
Ctrl + M	Adjust Long Axis Location
Esc	Exit Long Axis Location Mode
Ctrl + U	Reset Long Axis Location
Ctrl + H	Reset Crosshair Location
File:	
Ctrl + S	Save Screen
Edit:	
Ctrl + W	Set Automatic Window Level
View:	
Ctrl + R	Show Results
Ctrl + D	Show Database
Ctrl + N	Show or Hide RPP Normalized Results
Help:	
F1	Open the online Help

4 Preparation for Reading: Imaging and Navigation Tools

syngo MBF provides a number of imaging and navigation tools to improve the visualization of data in the Analysis stage.

The window level controls allow you to change the window (contrast) or level (brightness) of cardiac orthogonal views. To change the window level you can use:

- the sliders;
- click and drag using the middle mouse button;
- keyboard shortcuts;
- the window level adjustment automatically performed by the system.

You can also change the LUT or colormap of the polar plots and the cardiac views, and show or hide overlays and on-screen information.

You can navigate through the data using:

- the reference lines, see (➔ Page 34 *Reference Lines*);
- the mouse Wheel, see (➔ Page 30 *Mouse Wheel*).

4.1 Interpolation

Interpolation refers to the different ways of displaying an image, depending upon how much "smoothing" is applied.

Both the polar plots and the cardiac orthogonal views are displayed using a linear interpolation method. Linear method is the standard method for interpolating values between adjacent pixels, to give a smoother image for a more pleasing visual effect on the screen.

The interpolation method used to display the cardiac views and the polar plots cannot be changed.

4.2 Mouse Wheel

Click on an orthogonal view and move through the dataset by moving the mouse wheel.

4.3 Dynamic Frames

You can review the dynamic frames by left-clicking and dragging on the frame number at the bottom right of the image window.

The first number below the Frame index is the start time of the current frame, and the second number is the duration of the current frame in seconds.

4.4 LUT

You can change the LUT or colormap of the polar plots and the cardiac views.

1 To change the polar plot colormap, right-click on a polar plot color bar. To change the cardiac view colormap, right-click on a cardiac view color bar.

   This opens a context menu of colormap options. You can also select either **Select Orthogonal View LUT** or **Select Polar Plot View LUT** from the **Edit** menu.

2 Select a new colormap.

4.5 Information Overlays

You can show or hide the dataset information and the patient information separately.

You can review the dynamic frames by left-clicking and dragging on the frame number at the bottom right of the image window.

Information on the dataset is shown on each cardiac view - this includes:

- a label indicating whether the dataset is Stress or Rest data;
- information on the data such as tracer;
- frame number. The first number below the Frame index is the start time of the current frame, and the second number is the duration of the current frame in seconds;
- a value in Bq/ml at the point of the crosshair;
- orientation hints.

Patient information is shown at the top of the screen, including:

- name;
- ID;
- age;
- sex;
- date of birth;
- BMI;
- name of hospital or clinic.

4.6 Orientation Hints

Orientation hints are displayed on the orthogonal cardiac views, and provide information on the orientation of the data.

Ant - Anterior

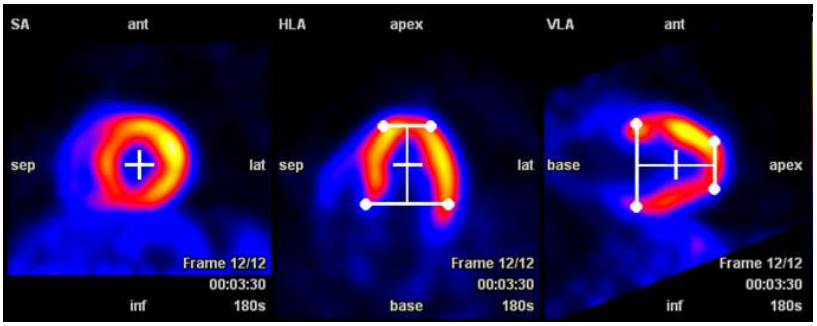
Sep - Septum

Lat - Lateral

Inf - Inferior

Apex

Base



Example showing the orientation of the heart

4.7 Manually Changing Window Level

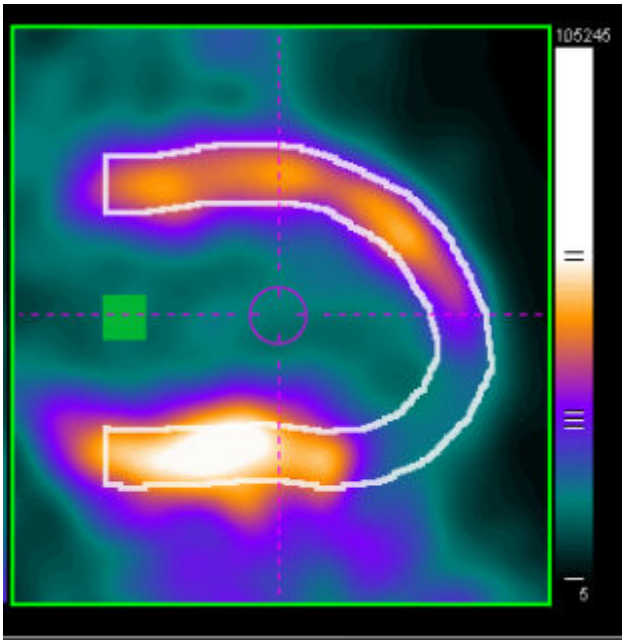
You can change the window level of the cardiac orthogonal views either by the sliders of the color bar or by using the mouse.

4.7.1 Changing Window Level by Using the Sliders

Next to the cardiac orthogonal views there is a color bar, which represents the full range of intensity values in the image. On this color bar there are **sliders** for changing the window level. You can use these sliders to alter the minimum, maximum, and center.

To change window level:

- To change window, click and drag on the top and bottom sliders.
- To change level, click and drag on the center slider.



Example of a color bar at the right of the cardiac view, showing the sliders

4.7.2 Changing Window Level by Using the Mouse

You can change the window level using a click and drag method with the mouse.

In one of the cardiac orthogonal views, click on the center mouse button and drag:

- To change window, click and drag right to increase the window width; moving left decreases the width.
- To change level, click and drag up to increase the value; moving down decreases the value.

4.8 Setting Window Level Automatically

You can apply the default window level values of each frame of a dynamic series automatically by the system. This saves adjustment time, reduces the performance of repetitive tasks, and prevents the display of over-saturated frames.

If you perform any manual adjustment for either the Stress or the Rest series, the automatic window level setting is switched off.

- Select **Set Automatic Window Level** from the **Edit** menu or click the button from the toolbar.

  The default values for window level are automatically applied to all frames of the series.

4.9 Reference Lines

Reference lines enable you to navigate between and within datasets. You can move reference lines by click and drag with the mouse.

To use the reference lines, first click on one of the cardiac views.

4.9.1 Moving the Reference Lines

Hovering the mouse over the center of the reference lines activates (and animates) the lines.

Left-click and drag to move the reference lines over the image.

4.9.2 Using the Arms of the Reference Lines

Move the cursor over an arm of the reference lines.

Left-click and drag to move the reference line arm.

To reset the reference lines to their original position, click the button.

4.10 Show or Hide: Reference Lines

- Select **Hide Reference Lines** from the **View** menu, or click the **Hide Reference Lines** button. This applies to all reference lines.

4.11 Show or Hide: Information Labels

4.11.1 Data Information and Orientation Hints

You can show or hide the information that is shown on the cardiac orthogonal views. This includes series information and the orientation hints.

Select **Hide Series Information > View** from the menu, or click the **Hide Series Information** button.

4.11.2 Patient Information

To display or hide patient information that is shown at the top of the screen, select **Hide Patient Information > View** from the menu, or click the **Hide Patient Information** button.

4.12 Selecting Polar Plot Overlays

You can select whether the polar plots should display overlays (either outliers or spillover factor) or not.

1 On the toolbar, click the **Polar Plot Overlay Options** button.

2 From the context menu, select the option of your choice:

- **Spillover factor**: Displays the spillover factor values overlayed on the polar plots.
- **Outliers**: Displays the outlier values overlayed on the polar plots.
- **None**: No values are displayed overlayed on the polar plots.

The polar plots are displayed depending on your choice.

4.13 Show or Hide: Segmentation Overlays

1 The segmentation overlay is shown over the cardiac orthogonal views, and shows the extent of the myocardium.

2 Select **Hide Segmentation Overlays** from the **View** menu or click the **Hide Segmentation Overlays** button.

4.14 Show or Hide: Switching Between Segment Overlays

You can switch between the three segment overlay, the 17-segment overlay, or no segment overlay.

◆ From the **View > Overlay Mode** menu, select from 3, 17 segment, or None.

On the toolbar, your most recent selection is displayed as a toolbar button: click on this button for a menu to select between these options.

Three Segment

17 Segment

None

5 Setting up Data before Analysis

The *syngo* MBF application automatically identifies the tracer, sets data as Stress or Rest, and positions the long axis of the heart. However, in some instances you may need to confirm these settings. For example, you may need to confirm that the tracer has been correctly identified, if it is not clear from the data.

For more information see the sections on:

- Set Datasets as Stress or Rest, see (➔ Page 39 *Assign Data as Stress or Rest*);
- Selecting the Tracer, see (➔ Page 40 *Selecting the Tracer*);
- Changing the automatic positioning of the Long Axis of the Heart, see (➔ Page 41 *Realigning the Long Axis of the Heart*).

5.1 Assign Data as Stress or Rest

When you are loading two datasets, the application automatically detects which dataset is Stress, and which is Rest. However, you may be prompted to confirm that the datasets are correctly assigned as Stress or Rest.

If more than two dynamic datasets have been passed to *syngo* MBF, or if the system cannot automatically determine the stress/rest assignment, then a selection window appears. This lists the available datasets, with the acquisition date, acquisition time, and a short description of the data, where this information is available.

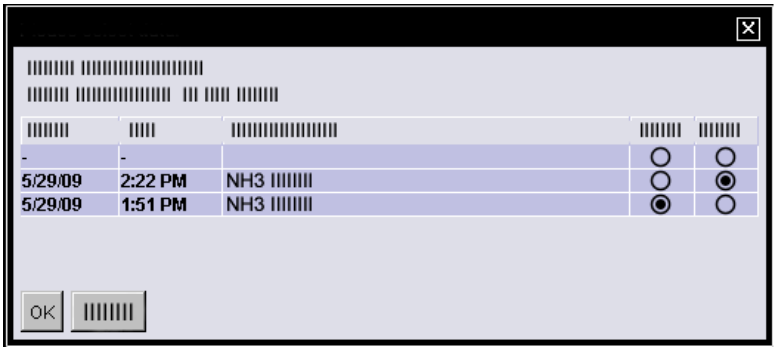
A maximum of two datasets can be processed by *syngo* MBF at any one time.

Data may be automatically assigned as Stress or Rest but it is important to ensure you are happy with the automatic assignment.

1 To the right of each dataset displayed in the table, click the radio button to assign the data as **Stress** or **Rest**.

2 If you wish to load one dataset only as Stress, click the **No Dataset Selected** button in the **Rest** column of the table. Similarly, if you wish to load one dataset only as Rest, click the **No Dataset Selected** button in the **Stress** column of the table.

3 Click **OK**.



5.1.1 One Dataset Only

If you are only looking at one dataset, you may also be prompted to confirm that the dataset is Stress or Rest.

5.1.2 Swap Stress and Rest

You can swap Stress and Rest when in the analysis stage of the application. This automatically swaps the cardiac orthogonal views and recalculates the polar plots. There is no need to re-position the vertical long axis, unless you are unhappy with the current position.

- From the **Edit** menu, select **Swap Stress / Rest Datasets**.

5.2 Selecting the Tracer

The tracer is usually identified automatically (➔ Page 41 *Automatic Tracer Selection*).

However in some instances you may need to confirm the tracer that has been used.

5.2.1 Automatic Tracer Selection

The application automatically detects what tracer has been used - i.e. either ^{82}Rb; or $^{13}NH_3$.

If the tracer is not ^{82}Rb or $^{13}NH_3$, an error message is displayed to indicate that the tracer is not supported by the application.

5.2.2 Manually Setting the Tracer Used

syngo MBF usually automatically identifies the tracer used. However in some instances it may not be possible for the application to automatically determine what tracer was used - for example, if this information is not clear from the data. In this instance, you can select the appropriate tracer.

- Click on a selection button to select the correct tracer and click **OK**.

5.3 Realigning the Long Axis of the Heart

The three orthogonal cardiac views of the heart are displayed with the long axis shown as an overlay: in white, as illustrated in the example shown below.

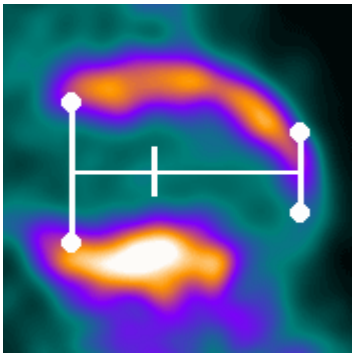
The initial placement of the long axis is automatic. However, you can adjust the base and apex location and pan and rotate the cardiac slices in relation to the long axis to change its position.

See (➔ Page 43 *Changing the Position of Base and Apex Planes*), (➔ Page 42 *Changing the Position and Orientation of the Long Axis*)

Once you are happy with the placement of the long axis, click the **Process** button to start analysis.

Be aware that when the base and apex locations of the long axis are manually adjusted, this information is used to *assist* in the automatic segmentation. The exact position of apex is determined by the automatic processing.

In the following example, the long axis of the heart is shown in white, on the vertical long axis view:



Long axis of the heart

5.3.1 Automatic Positioning of the Long Axis and Base and Apex Planes

The *syngo* MBF application automatically positions the long axis and base and apex planes. If you are happy with the automatic positioning, click the **Process** button. The analysis stage of the application then opens.

If you want to re-run the analysis with a new long axis placement, you can return to this stage, see (➔ Page 44 *Changing the Long Axis from the Analysis Stage*).

5.3.2 Changing the Position and Orientation of the Long Axis

If you are not happy with the automatic positioning of the long axis, it can be changed manually.

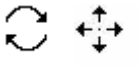
To adjust the position of the long axis, you can use Pan and Rotate tools, to move or rotate the orthogonal cardiac slices to align the center of the heart with the long axis center. Note that the axis itself does not move, but you can move the cardiac slices in relation to the axis.

1 Move the cursor over the cardiac views.

2 The Pan or Rotate cursor appears, depending on where you move the cursor:

- The Pan cursor appears when you are in the center of one of the cardiac views.
- The Rotate cursor appears when you move the cursor away from the center of the cardiac views, i.e. towards the outer edges of the view.

3 Click and drag to rotate or pan.



Rotate cursor, left, and Pan cursor, right

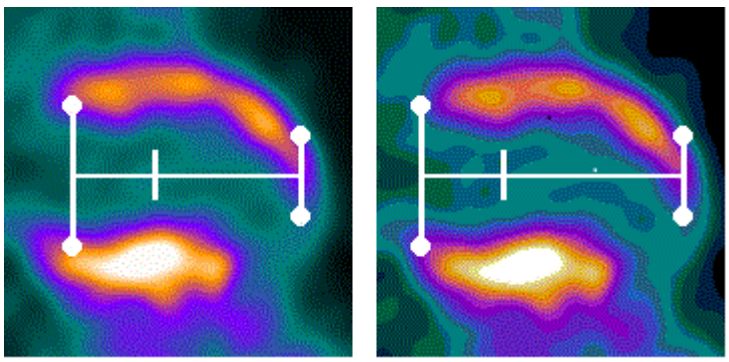
5.3.3 Changing the Position of Base and Apex Planes

If you are not happy with the automatic positioning of the base and apex planes, it can be changed manually.

◆ Move the cursor over the base or apex planes and click and drag to change.

When you click on the base or apex planes they become thicker, and the cursor changes to a selection cursor.

In the following example, the original axis, shown in the first illustration, has been stretched, as shown in the second illustration. Note that these examples are for illustrative purposes only.



Original and stretched axis

5.3.4 Sending the Long Axis and Base and Apex Position to Another Dataset

When you have two datasets loaded, you can copy the position of the long axis from one dataset to the other.

This can be useful where both scans have an unusual orientation or base and apex planes, and similar changes need to be made for both scans.

It may also be useful if the automatic placement has accurately positioned the long axis on one dataset but not the other. The correct positioning information can be sent to the other dataset to provide a reasonable approximation of the correct placement.

The copied position of the long axis may need to be refined manually, to get the best results.

1 To send a long axis position and base and apex location to another dataset, right-click on the long axis views of the correctly-positioned dataset. This opens a context menu.

2 Select an option from the context menu.

Copying the long axis position is only available when both Stress and Rest datasets have been loaded.

5.3.5 Reset

You can revert back to the original automatic long axis placement. From the **Edit** menu, select **Reset Long Axis Location**, or click the **Reset** button.

5.3.6 Changing the Long Axis from the Analysis Stage

If you are in the Analysis stage of the application, you can change the long axis placement. This re-runs the analysis using the new axis placement.

1 From the **Edit** menu, select **Adjust Long Axis Location** or click the corresponding button.

This takes you back to the initial data set-up screen.

2 Change the placement and length of the long axis as required.

3 Re-start the quantitative analysis by clicking the **Process** button.

For more information see the sections on (➔ Page 51 *Analysis*) and (➔ Page 41 *Realigning the Long Axis of the Heart*).

5.4 Advanced Options

In some cases, one or both datasets may need additional adjustment that cannot be achieved with the standard data set-up tools.

The **Advanced Options** panel on the data set-up screen provides you with options for advanced motion correction, residual activity correction, and rate-pressure product normalization.

(➔ Page 45 *High Motion Correction*)

(➔ Page 47 *Residual Activity Correction*)

(➔ Page 48 *Rate-Pressure Product Normalization*)

You can return to **Advanced Options** if initial results in the Analysis screen suggests that additional corrections are needed. See the section (➔ Page 49 *Returning to Advanced Options*)

5.4.1 High Motion Correction

By default, *syngo* MBF will attempt to correct motion between dynamic frames. This default correction may not be sufficient for high motion between frames, or when the motion includes significant rotation of the patient's chest. When you feel the default correction is insufficient for a particular case you can select a **High Motion Correction** from **Advanced Options** to apply to one or both datasets.

For information on how High Motion Correction works see the section on (➔ Page 47 *Effects of High Motion Correction*).

Firstly assess the motion in the datasets. This can be done by assessing the data as it appears in the orthogonal views on the initial set-up screen.

In some instances it can be helpful to proceed to the **Analysis** stage and assess if the default motion correction is sufficient for the data.

1 Click the **Process** button to process data with the default motion correction.

  This opens the Analysis screen. The resulting segmentation of the myocardium has been processed using the default motion correction.

2 Assess the results shown by scrolling through the frames of the dynamic data and reviewing the position of the myocardial segmentation outline to determine if high motion correction or additional adjustment of the position of the long axis may be useful, see (➔ Page 74 *Motion Assessment*).

3 If you decide that high motion correction would be useful, you can return to the data set-up screen.

4 From the **Edit** menu, select **Adjust Long Axis Location**.

Using High Motion Correction

If your assessment suggests advanced motion correction would be useful, you can use the High Motion Correction tool.

When you click **Process**, processing the data with this additional motion correction may take longer than the default motion correction processing.

1 From the **Advanced Options** panel, select **High Motion Correction** for one or both datasets.

2 Click the **Process** button to process data with high motion correction.

  If your assessment of resulting segmentation suggests that High Motion Correction may not be appropriate for the data, you can return to the set-up screen and deselect **High Motion Correction** then re-process the data.

Effects of High Motion Correction

The default motion correction used in *syngo* MBF will regenerate the myocardial segmentation on each dynamic frame, using the same long axis position on each. As the base and apex positions will not vary between frames, this can be effective at coping with lateral patient motion but may not cope fully with larger motion. *syngo* MBF will perform this process from the final frame backwards to a point where the images become too dissimilar to provide reliable results.

High Motion Correction takes the single segmentation generated on the summed image of the last few dynamic frames and moves it as required from one frame to the next to track the observed motion. This will include translation and rotation in each axis. The amount of correction is based on image registration methods used to align each dynamic frame to its neighbor to minimize differences between them. *syngo* MBF will perform this process from the final frame backwards to a point where the images become too dissimilar to provide reliable registration results.

As the segmentation from the summed image is being moved to suit each frame, the result will be a consistently-shaped segmentation on all frames. This makes the **High Motion Correction** more robust against extra-cardiac activity being included in the segmentation.

5.4.2 Residual Activity Correction

This option applies only to Ammonia scans.

The half-life of Ammonia $^{13}NH_3$ is long enough that Stress and Rest scans for a single patient carried out on the same day may show traces of the first injection in the second scan. This may bias the flow calculation as the residual activity cannot be distinguished from the newly-injected activity.

To compensate for this you can take the activity seen in the first frame of the second scan before the injection as being an effective indicator of the residual activity that should be accounted for. To do this your acquisition protocol must ensure that the scan starts sufficiently before the injection, so that the first frame as reconstructed is entirely before the new injection.

- In the **Advanced Options** panel, select **Residual Activity Correction**.

When the **Residual Activity Correction** option is selected the intensities in the first frame are subtracted from each subsequent frame, after appropriate decay-correction, to compensate for that activity's contribution.

Residual Activity Correction: Assumptions

This method makes the assumption that there is negligible further movement of the tracer from the first injection due to cellular activity by the time of the second scan. The residual activity is also assumed to be Ammonia (rather than resulting from an earlier scan, cardiac or otherwise, with a different tracer) and the decay correction used is based on the half-life of Ammonia.

The subtraction is made on the time-activity curves generated from the segmentation, rather than on the dynamic images themselves.

This option is always available for Ammonia datasets so that the later scan can be reviewed on its own if required. You are also able to correct both **Stress** and **Rest** in this way, if an additional Ammonia scan was taken prior to these.

5.4.3 Rate-Pressure Product Normalization

The rate-pressure product normalization normalizes the rest myocardial blood flow and the reserve polar plots. This is done by setting the values for the rest heart rate and the rest systolic blood pressure manually to get more realistic values without any pseudo-stress effects.

The rate-pressure product normalization is applied, if the following requirements are fulfilled:

- The **Normalize using Rate-Pressure Product** option is selected.
- The calculated value for the rate-pressure product is higher than the value of the rate-pressure product threshold.

1 From the **Advanced Options** panel, select **Normalize using Rate-Pressure Product**.

The **Rest Heart Rate** and **Rest Systolic Blood Pressure** fields become editable.

2 Enter the rest heart rate and the rest systolic blood pressure.

The rate-pressure product is calculated and displayed in the **Rate-Pressure Product** field.

3 To change the rate-pressure product threshold, click the **Edit** button.

The **Rate-Pressure Product Threshold** field becomes editable.

4 Type the value of the rate-pressure product threshold.

The **Edit** button changes to a **Set** button.

5 Click the **Set** button.

The new value for the rate-pressure product threshold is set.

6 Click the **Process** button to process data with the calculated rate-pressure normalization.

This opens the Analysis screen. The polar plots for the rest myocardial blood flow and the reserve are displayed normalized. The table indicates the normalized rest mean values and reserve mean values with an asterisk. The input data for the normalization (rest heart rate, rest systolic blood pressure, rate-pressure product, rate-pressure product threshold) are displayed in a legend under the table (even if no normalization was performed).

7 To toggle between normalized and non-normalized display, select **View Results Normalized by Rate-Pressure Product > View > Edit** from the menu or click the button on the toolbar.

5.4.4 Returning to Advanced Options

You can return to Advanced Options if initial analysis suggests that additional corrections are needed. For example, after you have clicked the **Process** button and moved to the **Analysis** screen, the results may indicate that the default motion correction was not satisfactory to cope with the type or amount of motion between dynamic frames in one or both scans.

So you can return to the set-up screen and change the advanced options before re-processing the data.

1 In **Analysis**, select **Adjust Long Axis Location** from the **Edit** menu.

2 This takes you back to the initial data set-up screen. Change Advanced Options as needed.

3 Re-start the quantitative analysis by clicking the **Process** button.

6 Analysis

The second stage of the *syngo* MBF application is for analysis.

6.1 Overview of the Analysis Screen

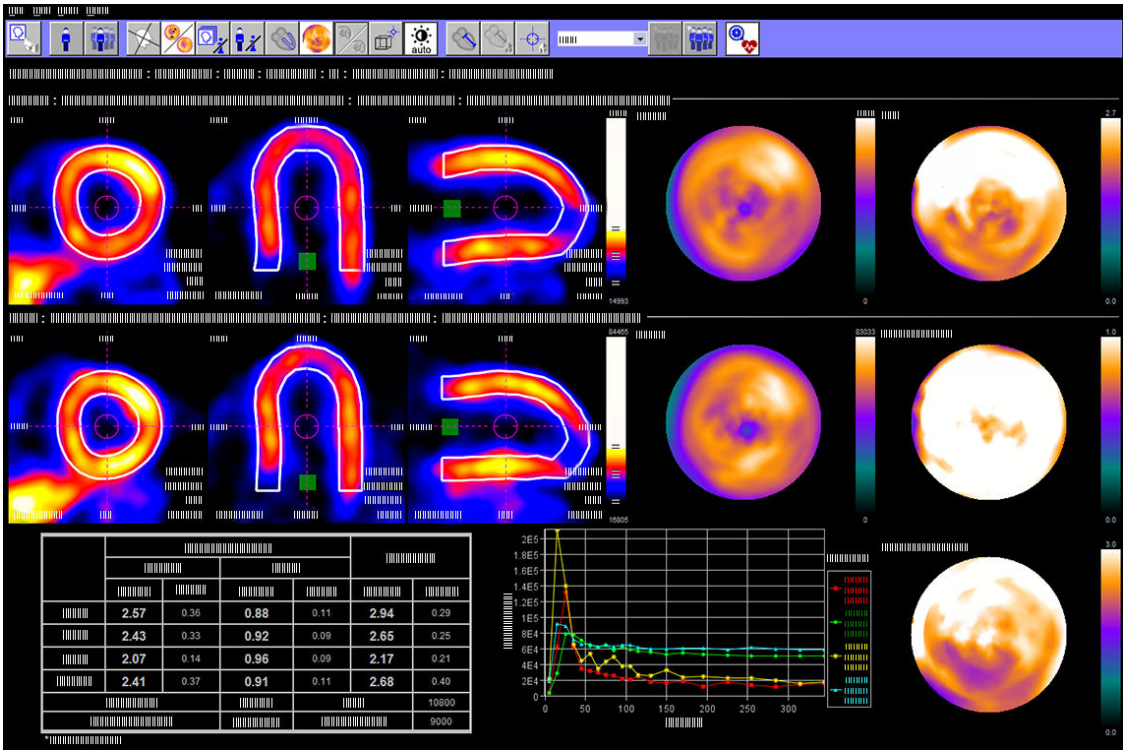
The analysis screen displays:

- Three cardiac orthogonal views of the data at the top left of the screen. In this example, a Stress and a Rest dataset has been loaded, so two datasets are shown. The views displayed are:
  - SA - Short Axis;
  - HLA - Horizontal Long Axis;
  - VLA - Vertical Long Axis;
- A graph showing activity curves for each dataset:
  - Time activity curves for blood input, for Stress and Rest;
  - A tissue uptake curve for a selected segment;
  - A global time activity curve for the entire myocardium (Stress and Rest).
- Polar plots for each dataset of:
  - tracer uptake;
  - myocardial blood flow;
  - reserve - the ratio of Stress flow to Rest flow;
- At the bottom left of the screen, a table displaying quantitative values for each of the main coronary arteries.

Note that if only one dataset had been loaded, the screen would appear slightly different. Only one set of polar plots would be shown.

Note that if a rate-pressure product normalization was performed, the screen would appear slightly different. See section (➔ Page 48 *Rate-Pressure Product Normalization*) for more information.

Patient and other data information is also shown. See the sections on (➔ Page 30 *Information Overlays*) and (➔ Page 31 *Orientation Hints*) for more information.



6.2 Cardiac Orthogonal Views

Data is displayed in cardiac orthogonal views at the top left of the **Analysis** screen.

The Cardiac Views display the **Blood Input ROI** and cardiac orientation information and a color bar which displays the color map used.

The **Segmentation Overlay** can also be displayed.

For more information see the sections on:

(➔ Page 53 *Cardiac Views*)

(➔ Page 53 *Segmentation Overlay and Blood Input ROI*)

6.2.1 Cardiac Views

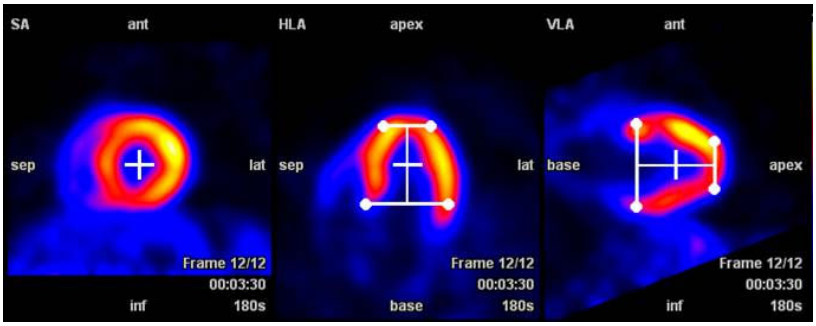
Data is displayed in cardiac orthogonal views at the top left of the **Analysis** screen.

- Short Axis - SA
- Horizontal Long Axis - HLA
- Vertical Long Axis - VLA

Patient and data information is shown above the cardiac views. Each view also displays cardiac orientation information.

Next to the cardiac views is a color bar which displays the color map used in the views. You can also use the color bar to change the window level values for the cardiac views.

Each view - i.e. Short Axis, Horizontal Long Axis and Vertical Long Axis view - appears in its own image window. If you click on a view, it becomes the *active* window. This is indicated by a colored border. Actions such as changing slice are affected on that view.



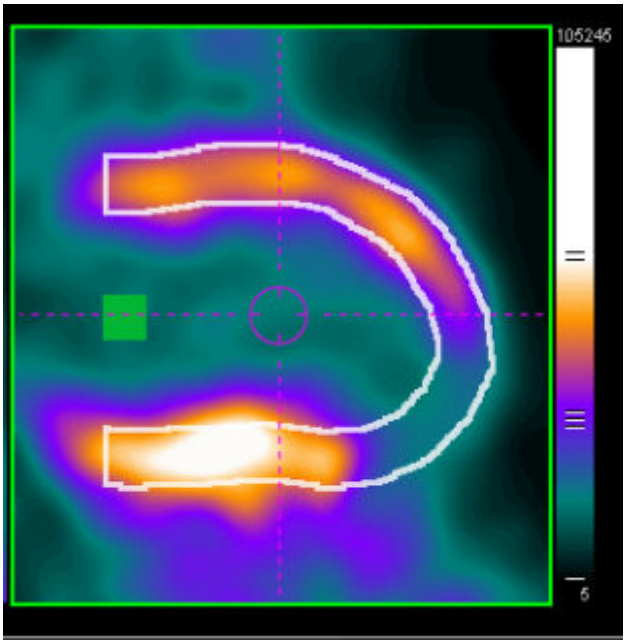
Example showing the orientation of the heart used in the cardiac views

6.2.2 Segmentation Overlay and Blood Input ROI

A white outline indicates the extent of the myocardium. This is the segmentation overlay. This overlay can be hidden.

When the segmentation overlay is shown, the blood input region of interest is also shown, as a green square. This is the area used to derive the blood input for the blood input curve.

The following example shows a vertical long axis view. This is the active view; the colored border is visible. The color bar is shown to the right of the view. The segmentation overlay is also shown, in white. Data information and orientation hints have been hidden.



Example of a vertical long axis view

6.3 Polar Plots

A polar plot or polar map is a 2D representation of activity in the myocardium. It enables you to view the whole surface of myocardial activity in a single polar image.

Polar plots show the whole left ventricle in a 2D-overview image, where the apex position is shown in the image center and the base is located at the periphery.

For information on how the polar plots are created, see the section on (➔ Page 55 *How are Polar Plots Created*).

6.3.1 Selecting a Segment of a Polar Plot

You can select a segment of the myocardium by clicking on a polar plot. Information on this segment is then displayed at the base of the polar plot and in the graph.

See the section on (➔ Page 65 *Selecting a Segment for Analysis*) for more information.

6.3.2 Overlay Options

The kinetic modelling process for the polar plots can produce inaccurate values. You should be able to identify such values in order to decide whether values are reliable or not. Therefore, these values are displayed as an overlay on the polar plots. You can select between two types of overlay information:

- Spillover factor, see (➔ Page 61 *Spillover Factor*) for more information.
- Outliers, see (➔ Page 63 *Outliers*) for more information.

6.3.3 Polar Plot Display and Color Bar

For more information on the polar plot display see the section on (➔ Page 56 *Polar Plot Display*).

Next to each polar plot is a color bar, representing values within that polar plot. See (➔ Page 61 *Polar Plot Color Bar*)

6.3.4 How are Polar Plots Created

The method used in this application to create the polar plots is the cylindrical-spherical model: for more information see the reference listed in this section.

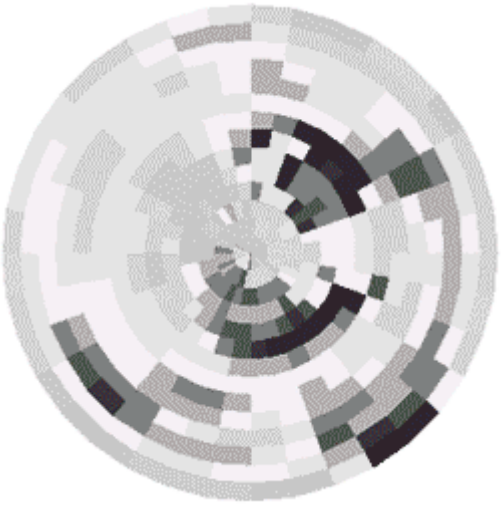
Segmentation of the Polar Plots

The polar plot segmentation is created by division of the myocardium into 15 'slices', from the base to the apex. Each slice is then divided into smaller radial segments at ten degree intervals. The average quantitative value for each of these segments can then be determined. This information is mapped to a 2D representation to create the polar plot.

Therefore, the polar plot is essentially divided into 15 rings: each ring is mapped to a myocardial 'slice'. The most inner ring corresponds to the most apical slice, the outer ring to the basal slice. The left side of the polar plot is Septal, the right side is Lateral. The top of the polar plot is Anterior, and bottom is Inferior.

When you click on a polar plot, the selected segment is highlighted. As there are 540 possible segments, only the boundaries of the selected segment are shown, for clarity.

The following diagram illustrates polar plot segmentation. Note this is for illustrative purposes and is not included in the application itself.



Polar plot segmentation

Reference

Sharat Lin, G, Hines H, Grant G, Taylor K, and Ryals C. Automated Quantification of Myocardial Ischemia and Wall Motion Defects by Use of Cardiac SPECT Polar Mapping and 4-Dimensional Surface Rendering. Journal of Nuclear Medicine Technology. 2006. Vol 34: pages 3-17.

6.3.5 Polar Plot Display

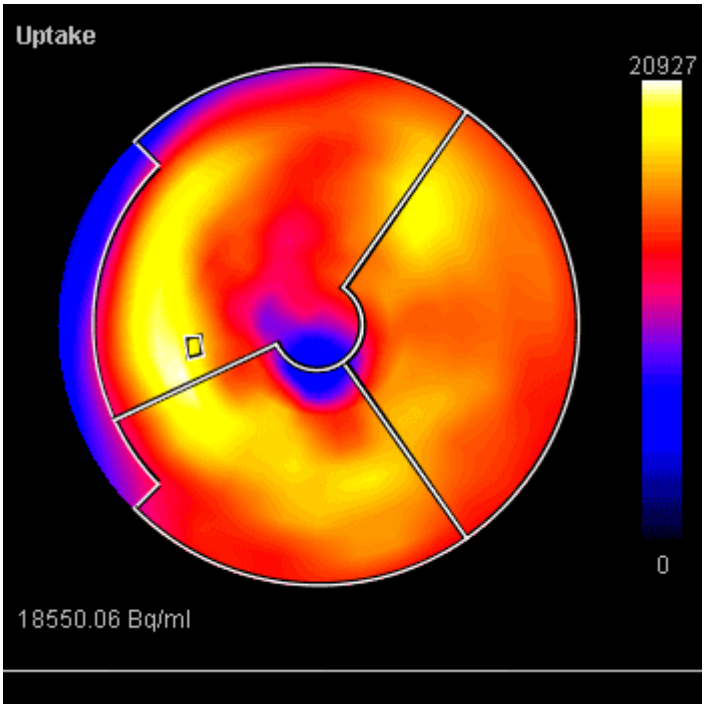
Polar plots display:

- tracer uptake;
- myocardial blood flow;
- a color bar for each polar plot, which represents the range of values in the polar plot;
- the percentage of outliers for myocardial blood flow polar plots;
- the boundaries of the segment that has been selected;
- the value of a selected segment;
- overlays:
  - (→ Page 61 *Spillover Factor*)
  - (→ Page 63 *Outliers*)
  - (→ Page 69 *Three Vessel Model*)
  - (→ Page 70 *Seventeen Segment Model*)

If Stress and Rest datasets have been loaded, Reserve, the ratio of the myocardial blood flow of stress flow to rest flow, is displayed.

Example of an uptake polar plot, showing:

- the three vessel overlay;
- the polar plot color bar, right;
- a selected segment, and the value of this segment at the bottom left.



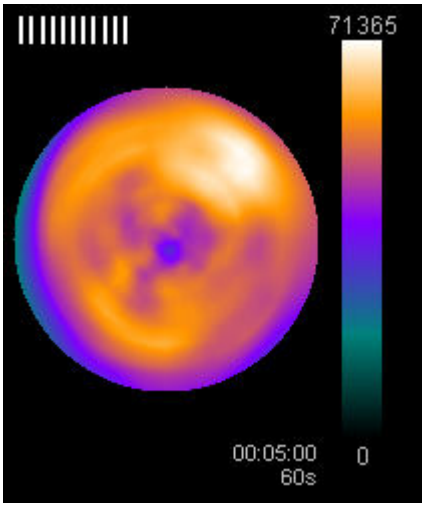
6.3.6 Uptake Polar Plot

The uptake polar plot is derived from the weighted sum of the late frames. The first number on the bottom right is the start of the summed frames, and the second number is the total duration of all the summed frames.

The uptake value for a selected segment is shown at the bottom left of the polar plot.

The color bar on the right indicates the range of values. Note the range of values for uptake polar plots cannot be changed.

The uptake value for a selected segment is given in Bq/ml, unless the data uses units other than Bq/ml. In this instance, no units are displayed: it is the user's responsibility to interpret the results. See (➔ Page 18 *Before you Start*) for more information.



Example of an uptake polar plot

6.3.7 MBF and Reserve Polar Plots

The MBF polar plots display values in milliliters per gram per minute - ml/g/min - for selected segments of the polar plot. The reserve polar plot displays the ratio of stress flow to rest flow for the selected region. As this is a ratio no units are shown. The value for a selected segment is shown at the bottom left of the polar plot.

The segments where the spillover factor (SF) is above the threshold are displayed in green. The SF value is displayed for selected segments in the bottom right of the Stress and Rest polar plot (not for Reserve plots). For spillover factors above the threshold, the MBF values on the bottom are displayed in red.

The percentage of outliers for the whole polar plot is also shown. Individual outliers are shown on the polar plot in black. Outliers can also be hidden.

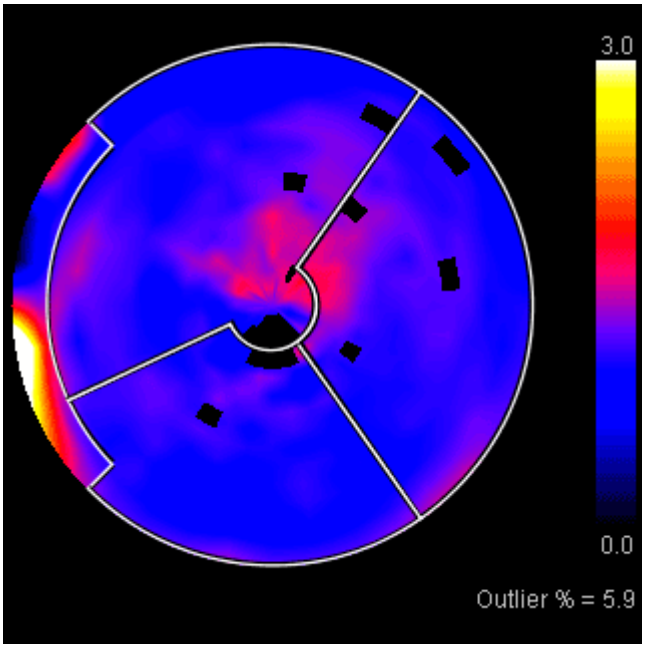
Color Bar and Range

The color bar on the right indicates the range of values. To change the range, select **Configure Polar Plots > Edit** from the menu.

You can change the LUT or colormap by right-clicking on the color bar.

When stress and rest datasets are loaded, 'reserve' is calculated as the ratio of stress flow to rest flow. When the resting values are very low or close to zero, this can result in unusually high reserve values. These values have no clinical meaning and can bias the statistical results.

The following image shows an example of a reserve polar plot. In this example outliers are shown, but no segment has been selected.



Example of a reserve polar plot

For more information on showing or hiding MBF and reserve values on polar plots, see (➔ Page 36 *Show or Hide: Switching Between Segment Overlays*) and (➔ Page 36 *Selecting Polar Plot Overlays*).

In case that a rate-pressure product normalization was applied, the polar plots for the rest myocardial blood flow and the reserve are displayed normalized as indicated by the title **Normalized MBF**, **Normalized Reserve**.

For information about normalizing the rest MBF and reserve values for the rest database, see (➔ Page 48 *Rate-Pressure Product Normalization*).

6.3.8 Polar Plot Color Bar

Each polar plot also has an associated **color bar** on the right, which shows the range of values in the polar plot in relation to the colors of the colormap.

MBF and Reserve Polar Plots

For MBF and reserve polar plots, the color bar represents the range of values shown in the polar plot, and the colors with which these values are represented.

Maximum and minimum values are shown at the top and bottom of the color bar. The default ranges of these values are:

- Stress - minimum 0.0, maximum 2.7
- Rest - minimum 0.0, maximum 1.0
- Reserve - minimum 0.0, maximum 3.0

You can change the maximum and minimum values.

◆ Select **Configure Polar Plots** from the **Edit** menu.

Uptake Polar Plots

For uptake polar plots, the color bar represents the full range of the data. The option to change the minimum and maximum is not available for uptake polar plots.

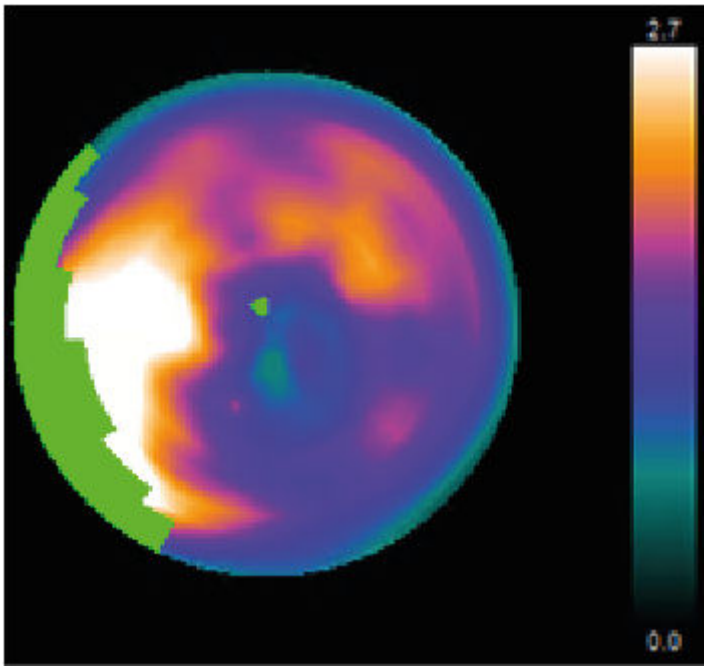
6.3.9 Spillover Factor

Calculation for the myocardial blood flow can be distorted by spill-in/spill-out effects:

- Spill-in:- When radiation from the background tissue spreads into target tissue.
- Spill-out: When radiation from the target tissue spreads into background.

A high spillover factor, for example in case of high motion or infarcted myocardium tissues, indicates that the MBF value is not computed accurately.

You can show or hide the spillover factor display in the polar plots, see (➔ Page 36 *Selecting Polar Plot Overlays*). The spillover factor is also displayed in the Statistics table, see (➔ Page 67 *Displaying MBF and Reserve Statistics: Table*).



Example polar plot showing spillover factor

6.3.10 Setting the Spillover Factor Threshold

You can set a threshold value for the spillover factor. Spillover factor values above this threshold will be displayed in the MBF polar plots.

1 Select **Configure Polar Plots** from the **Edit** menu.

  The **Configure Polar Plots range configuration** dialog opens.

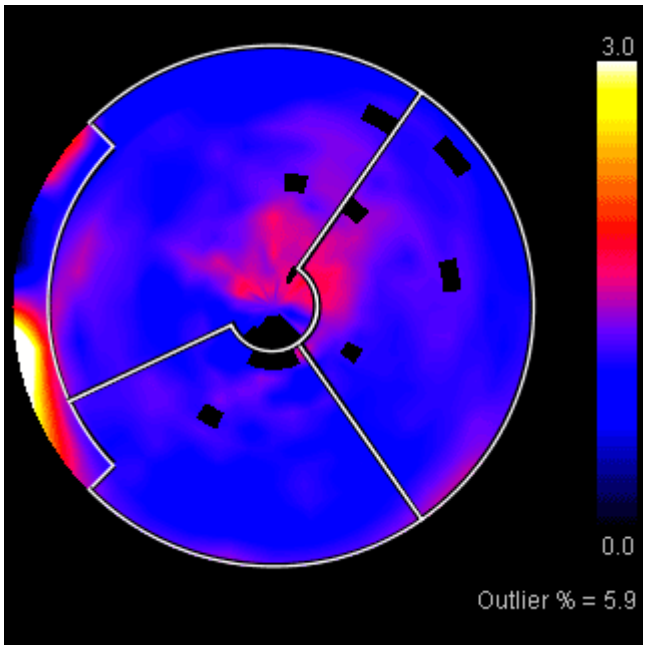
2 In the **Spillover Threshold Factor** field, set the desired value for the threshold, and click **OK**.

6.3.11 Change LUT or Colormap

You can change the colormap for a polar plot. Note that this does not change the values as represented by the color bar.

1 Right-click on a color bar for a menu of colormaps, or select **Change LUT** from the **Edit** menu.

2 Select a colormap from the list.



Example polar plot illustrating the color bar

6.3.12 Outliers

Calculation of the myocardial blood flow and reserve polar plots for each dynamic PET series will sometimes produce a number of 'outlier' segments, determined from the kinetic modeling process. An outlier means its value is considered as not valid in the kinetic model fitting of the dynamic study.

Outliers are shown as black in the polar plot. The percentage of outliers is shown at the bottom of the respective polar plot.

You can show or hide the outliers associated with each polar plot, see (➔ Page 36 *Selecting Polar Plot Overlays*).

Hiding Outliers

An interpolated value for an outlier can be calculated. The correlation of uptake values to non-outlier regions is established: this is then applied to the uptake value for any outlier segments.

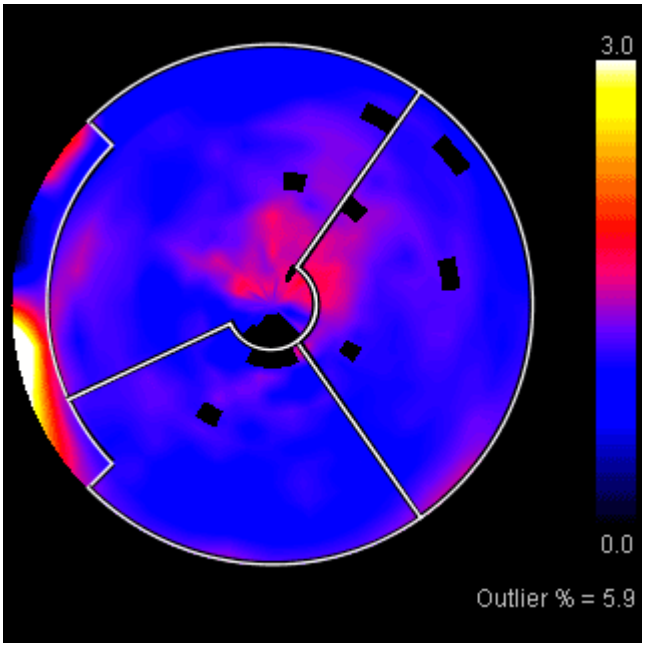
If outliers are hidden, any outliers are replaced with the interpolated value. Visually, this means that the black outliers are replaced with a colored interpolated value.

Outliers and Statistics

The interpolated value of the outliers are **not** counted in the statistical calculation of the mean and standard deviation displayed in the table.

The value for a selected outlier segment, shown at the bottom left of the polar plot, is the original non-valid value and is shown in red.

In rare situations when all or most of the segments in a vessel bed region are outliers, then the mean and standard deviation will not be computed.



Example polar plot showing outliers

6.4 Selecting a Segment for Analysis

You can select a small segment of the myocardium to display information for that segment in the Analysis screen. To select a segment click on a polar plot or click one of the cardiac orthogonal views.

See the sections on (➔ Page 65 *Selecting a Segment using the Polar Plots*) and (➔ Page 66 *Selecting a Segment using the Cardiac Views*).

6.4.1 Selecting a Segment using the Polar Plots

To select a segment click on a polar plot.

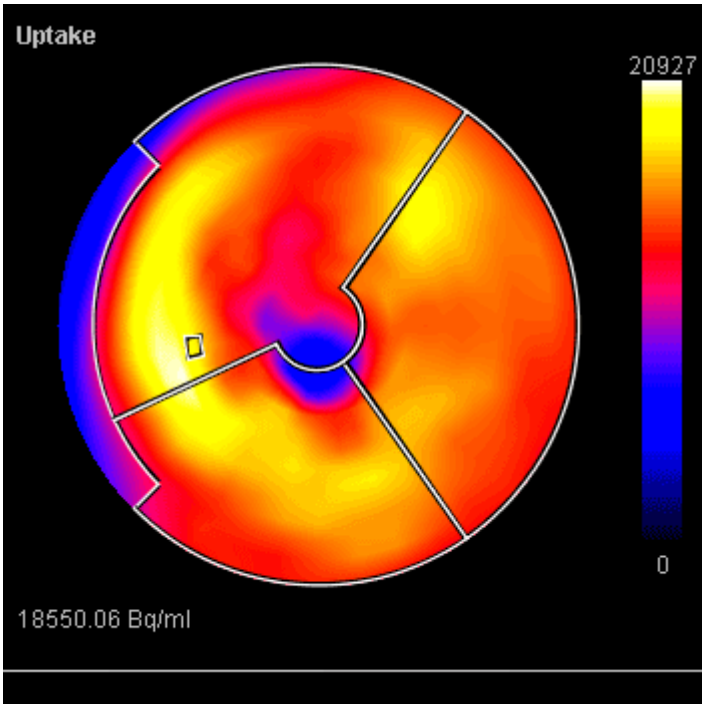
The selected segment is highlighted by an overlay of the segment boundaries. The corresponding segments in other polar plots are also highlighted.

The crosshairs in the cardiac orthogonal views move to the center of the corresponding region. See (➔ Page 52 *Cardiac Orthogonal Views*)

Values for the segment are shown:

- in the tissue uptake curve in the graph;
- in the value at the bottom left of each polar plot.

In the following example polar plot, the selected segment is indicated by a white outline.



Selected segment indicated by a white outline

6.4.2 Selecting a Segment using the Cardiac Views

To select a segment click on a location in a cardiac view.

The crosshairs in each view move to the same point, and the corresponding segment in all polar plots is highlighted.

When you select a segment:

- the tissue uptake curve for that segment is shown on the graph;
- values for the segment are shown at the bottom left of each respective polar plot.

If you click outside of the myocardium, there is no corresponding area in the polar plots. Therefore no segment is shown in the polar plots.

6.5 Displaying MBF and Reserve Statistics: Table

Statistics for each dataset are shown in a table at the bottom left of the screen. If both a Stress and a Rest dataset have been loaded, values are shown for both datasets respectively. Reserve, or the ratio of stress flow to rest flow, is also shown. The table displays, in milliliters per gram per minute, the following values:

- the mean value for:
  - LAD - left anterior descending artery;
  - LCX - left circumflex artery;
  - RCA - right coronary artery;
- standard deviation for the same three arterial regions;
- mean and standard deviation for the average of all of these regions.
- In case that the spillover factor is enabled, the table will display the average spillover factor values instead of the standard deviation. For more information, see (➔ Page 61 *Spillover Factor*).
- In case of an applied rate-pressure product normalization: The table indicates the normalized rest mean values and reserve mean values with an asterisk. The input data for the normalization (rest heart rate, rest systolic blood pressure, rate-pressure product, rate-pressure product threshold) are displayed in a legend under the table (even if no normalization was performed). For more information, see section (➔ Page 48 *Rate-Pressure Product Normalization*).

Saving the Table

The export of the Table includes the patient metadata (such as name, age and gender) and the metadata for each scan. Flow and Reserve values are exported for the Three-Vessel model as shown in the table, and also for the Seventeen-segment model. When comparing the current patient to a database of values, the comparison results table will also be exported to the file, with values for Three-Vessel model and Seventeen-segment model. The export will also include the values for the spillover factor.

The calculation of values in the table does not include the interpolated values for outliers within that region. The mean and standard deviation values of a region may not be representative if the region has significant number of outliers, in particular in regions with defects. See the section on (➔ Page 63 *Outliers*) for more information.

- Right-click on the table and select **Save to Clipboard**. This saves the table values in a comma separated values format.

  – or –

  From the **File** menu, select **Export**. This will allow you to save the table values to a comma separated file on disk.

Note that the comma separated file uses US English defaults for list delimiters and number separators. This can cause issues if the comma separated file is opened in another application such as Microsoft Excel where a different set of number separators may be in use. If you are using other applications to open exported comma separated files, check if the results are consistent with what is displayed in the original table in *syngo* MBF. You may need to update settings in other applications such as Microsoft Excel in order to correctly display results.

If a rate-pressure product normalization was performed, the exported file also includes the normalized rest and normalized reserve values along with their corresponding standard deviations. The input parameters of the rate-pressure product will also be included (even if no normalization was performed).

6.5.1 Three Vessel Model

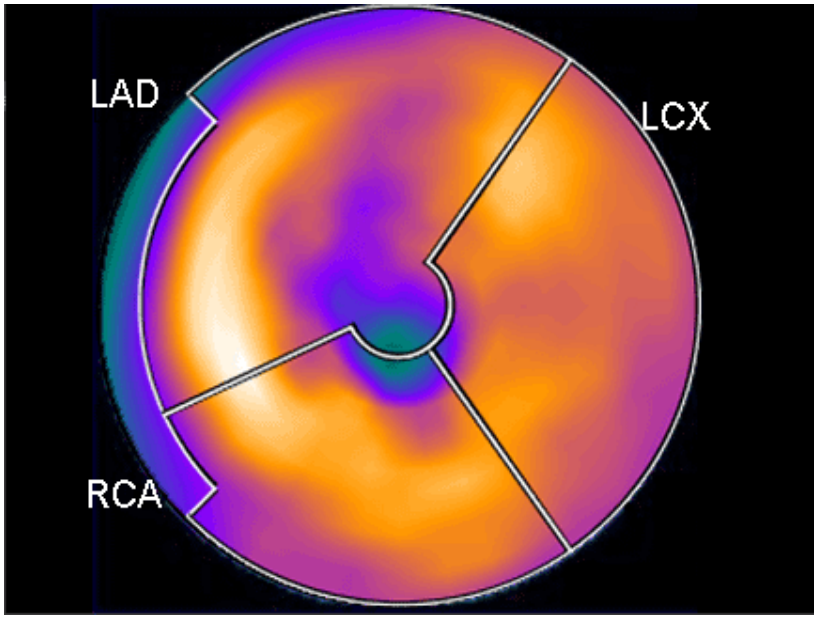
The three vessel model divides the heart into the three sections:

- LAD - left anterior descending artery;
- LCX - left circumflex artery;
- RCA - right coronary artery.

You can display these regions as an overlay on the polar plots.

The excluded region on the polar plot, on the left between LAD and RCA, corresponds to the septal base region. The shape of the left ventricle is such that the septal side is shorter than the lateral side: consequently the excluded region corresponds to an area where there is no myocardial muscle. So when computing the vessel bed statistics, excluding this region improves the accuracy of results.

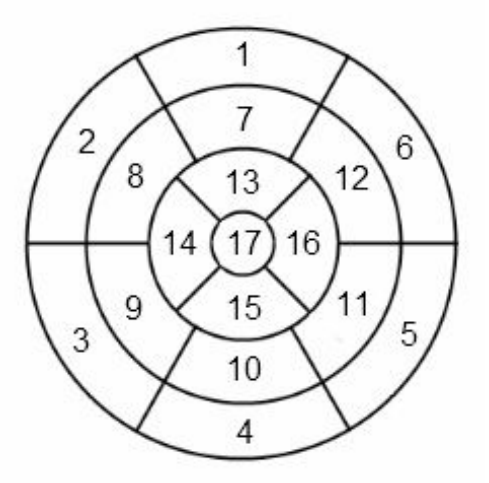
The following example of a polar plot shows the three vessel model overlay. Note that this example is for the purpose of illustrating the three vessel model and not intended to represent actual analysis results.



Polar plot showing the three vessel model overlay

6.5.2 Seventeen Segment Model

The 17 segment model divides the heart into segments conforming to the standardized AHA myocardial segmentation and nomenclature as described in the reference listed in this section. These regions completely cover the polar plot, including the septal base region that is excluded from the three vessel model. You can display these regions as an overlay on the polar plots.



Given an appropriate initial orientation of the long axis when setting up the data before analysis, these numbered segments correspond to the following regions of the myocardium:

1 - basal anterior

2 - basal anteroseptal

3 - basal inferoseptal

4 - basal inferior

5 - basal inferolateral

6 - basal anterolateral

7 - mid anterior

8 - mid anteroseptal

9 - mid inferoseptal

10 - mid inferior

11 - mid inferolateral

12 - mid anterolateral

13 - apical anterior

14 - apical septal

15 - apical inferior

16 - apical lateral

17 - apex

When saving the table the mean and standard deviation for each of the seventeen segments will be saved in addition to the three vessel values shown on-screen in the table.

Reference

Manuel D Cerqueira, MD, Neil J. Weissman, MD, Vasken Dilsizian, MD, Alice K. Jacobs, MD, Sanjiv Kaul, MD, Warren K. Laskey, MD, Dudley J. Pennel, MD, John A. Rumberger, MD, Thomas Ryan, MD, Mario S. Verani, MDH, and American Heart Association Writing Group on Myocardial Segmentation and Registration for Cardiac Imaging, "Standardized myocardial segmentation and nomenclature for tomographic imaging of the heart: A statement for healthcare professionals from the Cardiac Imaging Committee of the Council on Clinical Cardiology of the American Heart Association", J Nucl Cardiol 2002;9:240-5

6.6 Displaying Graph and Kinetic Model Fitting Statistics

The graph displays:

- the blood input time activity curve, which represents the blood input level. This is displayed automatically;
- if a segment of the myocardium has been selected, the tissue uptake time activity curve for that segment is also shown. This represents the amount of tracer in the myocardial tissue for that segment;

- if a segment of the myocardium has been selected that is not the myocardium tissue, the global time activity curve which represents the amount of tracer for the entire myocardium is displayed.
- chi-squared results for each dataset.

If two datasets have been loaded, curves for both datasets are displayed.

You can change the appearance of the graph, including:

- the scale used - log or linear;
- the range of the graph;
- the zoom level - you can enlarge a section of the graph.

See the section on (➔ Page 72 *Changing the Graph*).

To save the graph, select **Export Graph > File** from the menu.

6.6.1 Changing the Graph

You can change:

- the x and y values to be linear or log;
- the zoom level of the graph;
- the range of the graph.

Log or Linear Scale

Right-click on the graph for a menu.

- Select x log scale or x linear scale.

or

- Select y log scale or y linear scale.

The graph is updated automatically.

Zoom and Reset Zoom

You can zoom and enlarge a section of the graph.

1 Left-click and drag on the graph to select a section where you would like to zoom in.

2 Release the mouse button. The graph updates automatically.

To reset the zoom to the original level, right-click for the menu and select **Reset Zoom**.

Properties

Right-click on the graph and select **Properties**.

- You can change the range of values of the graph: minimum and maximum for x and y.
- You can display or hide the Grid.

6.6.2 Kinetic Modeling

The application automatically determines which kinetic model to use, based on the tracer.

- For ^{82}Rb the one tissue compartment model is used - see reference 1.
- For $^{13}NH_3$, the two tissue compartment model is used - see reference 2.

References

For Rubidium:

1. Lortie, M, Beanlands, R, Keiichiro Yoshinaga, K, Klein, R, DaSilva, J and deKemp, R. Quantification of myocardial blood flow with ^{82}Rb dynamic PET imaging. European Journal of Nuclear Medicine and Molecular Imaging. 2007, Vol 34: p 1765-1774

For Ammonia:

2. Hutchins, G.D. et l. Noninvasive Quantification of Regional Blood Flow in the Human Heart using N-13 Ammonia and Dynamic Positron Emission Tomographic Imaging. Journal of the American College of Cardiology. 1990, Vol 15, 5: p 1032-42.

6.7 Motion Assessment

The cardiac orthogonal views shown in the Analysis screen provide a visual indication of the motion correction applied. The positioning of the myocardial segmentation against the dynamic frames indicates the application's current positioning of the myocardium in each frame. Moving through the dynamic frames allows you to assess how the application has tracked the myocardium across the frames, as a quality control step.

- If you have used High Motion Correction, the myocardial segmentation is based on the uptake in the sum of later frames in the acquisition, see (➔ Page 45 *High Motion Correction*). This segmentation is repositioned on each dynamic frame to track the patient movement from each frame to the next, by moving the long axis position with the identified movement. The segmentation remains constant with respect to the long axis position.
- For cases where default motion correction is applied, the long axis remains fixed, and the segmentation is regenerated on each dynamic frame to adapt to minor changes in myocardial positioning.

Two navigation modes are available, which allow you to optionally assess the motion correction. These can be toggled through the Motion Assessment tool on the toolbar in the Analysis screen.

- By default, as you move between different dynamic frames, the selected position in the polar plots remains constant. The crosshair position in the cardiac orthogonal views will track the myocardial segmentation, keeping consistent with polar plots at each stage. In this mode, your identified position in the body remains constant as you navigate dynamic frames with the default applied motion correction. This default mode ensures that you do not have to adjust position when examining a potential defect region across dynamic frames, but can make assessment of motion more difficult. As the positioning in each frame applies the motion correction, the changes in physical position within the field of view may be more difficult to assess in this mode; their effects are hidden by tracking the applied motion correction.
- Motion Assessment mode (enabled through the Motion Assessment tool on the toolbar retains the same physical position within the acquisition field of view as you change dynamic frame. This can allow easier assessment of level of motion, and of the application's correction for the motion, by making the motion evident. As you change dynamic frame, the crosshairs remain constantly positioned, and movement of the myocardial segmentation becomes apparent.

In this mode the crosshairs and the polar plots can become separated, as the myocardium moves away from the crosshairs. The same physical position within the scanner field of view may relate to one segment of the polar plot in a given dynamic frame, but to a different segment in another frame (or be outside the myocardium altogether). Selecting a segment on the polar plot will always reposition the crosshairs to the equivalent position on the current frame.

When loading Stress and Rest datasets together, the crosshair correlation between the two datasets will always be based on the position relative to the segmentation. This may mean that the position in 3D space changes in one dataset when you navigate across dynamic frames in the other dataset, with Motion Assessment mode active.

6.8 Database Comparison

syngo MBF provides absolute flow quantification to assist diagnosis of myocardial perfusion defects. The values indicate the rate of flow in the current patient's scans, but a range of other factors are important when making a diagnosis: for example, the age, gender and medical history of the patient may often be considered.

syngo MBF provides **Database Comparison** tools for this purpose. For each segment in the myocardium you can compare the current patient's MBF and Reserve values with the mean value for the population of a selected database. Statistics are then calculated for each region to assist you in determining how closely this patient matches the database values. For each segment in the myocardium, the difference between the current patient and the database mean is expressed in terms of the **number of standard deviations** that the patient is away from the database mean value.

If a rate-pressure product normalization has been done for the patient, the normalized values of the current patient are compared with the mean value for the population of a selected database.

Database comparison can be used to compare your patient's values with those of healthy patients, from a demographic range you feel is appropriate. Similarly, you can select databases that do not match the current patient's demographic data but include patient groups with medical histories you consider relevant.

syngo MBF provides numerical values to quantify comparison, and flexible database selection to enable comparison with different types of database population.

6.8.1 Using Database Comparison

1 The first step is to select a database. For more information see (➔ Page 77 *Selecting a Database*).

2 Select **Comparison** to display comparison polar plots and table. For more information see (➔ Page 78 *Database Comparison View*).

Database Generation

syngo MBF enables you to create your own databases for comparison purposes. This allows you to group patients into databases that may give you the most appropriate comparisons for your typical patient profiles. You may create databases for either Ammonia or Rubidium scans separately, and can restrict by demographic criteria (for example, by age ranges and gender).

For more information see (➔ Page 80 *Editing a Database*).

6.8.2 Selecting a Database

After you click the **Process** button and move to the **Analysis** screen, you can access a list of all databases present on the system.

The database list is automatically filtered by tracer so that only databases matching the tracer of the current scans are shown. If no databases exist on the system for the current tracer, the list will be empty.

This list includes:

- databases that match the demographic criteria of the current patient
- databases that do not match the patient's demographic criteria: these are shown in italics.

Database Comparison is available in the **Analysis** stage.

1 From the **Edit** menu, select **Manage Databases**.

2 Select a database from the list.

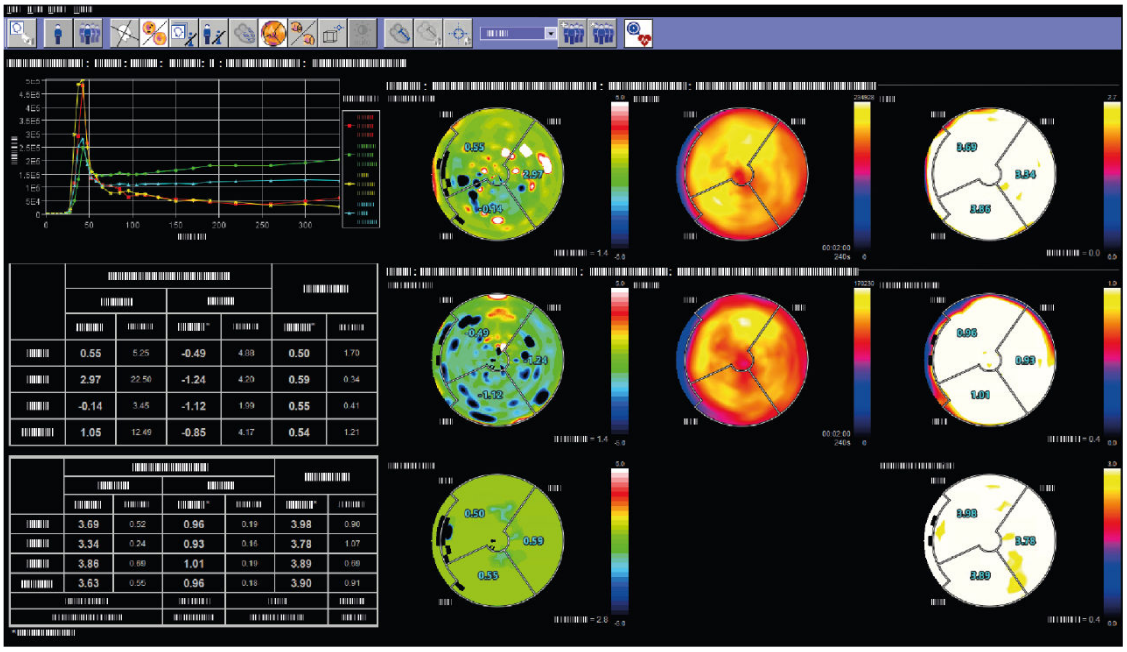
3 To select comparison mode, click **Switch to Database Comparison View** button on the toolbar or select **Database** from the **View** menu. The screen changes to show the database comparison polar plots and table. See (➔ Page 78 *Database Comparison View*)

Exit

To leave database comparison mode, select the **Single Patient** mode.

6.8.3 Database Comparison View

When you have selected a database to compare to your patient, the screen layout changes to show the **comparison polar plots** and the **table of comparison values** for Stress flow values; Rest flow values; and Reserve values. These are expressed in terms of numbers of standard deviations that patient's values are from the database values. If a rate-pressure product normalization has been done for the patient, the normalized myocardial blood flow values and the reserve values of the current patient are compared with the mean value for the population of a selected database. This is indicated by denoting the mean values for the rest and reserve with an asterisk (*) in the comparison table.



	0.55	5.25	-0.49	4.88	0.50	1.70
	2.97	22.50	-1.24	4.20	0.59	0.34
	-0.14	3.45	-1.12	1.59	0.55	0.41
	1.05	12.46	-0.85	4.17	0.54	1.21

	3.69	0.52	0.96	0.19	3.98	0.90
	3.34	0.24	0.93	0.16	3.78	1.07
	3.86	0.69	1.01	0.19	3.89	0.69
	3.63	0.55	0.96	0.18	3.90	0.91

Comparison Polar Plots

The comparison polar plots essentially work in the same way as the uptake, flow and reserve plots. If you select a segment in one polar plot the corresponding segment is highlighted in the other plots.

The color table for the comparison polar plots is fixed. This table is non-linear and is flattened around zero such that values in the range around zero are green: as the values move further from zero the colors move sharply towards the extreme ends of the color table.

Where data is unavailable, the comparison polar plots will show black. If there are insufficient values in the database at any given point, these will be shown black in the same way that outliers are. If one dataset is unavailable (for example, if comparing a Stress and Rest scan pair to a database that only contains Stress datasets) the entire comparison polar plot will show black.

If you have selected Comparison mode without selecting a database to compare against, the Comparison polar plots will also be black.

If a rate-pressure product normalization was performed, the view would appear slightly different. See section (➔ Page 48 *Rate-Pressure Product Normalization*) for more information.

6.8.4 Manage Databases

Database Comparison is available in the **Analysis** stage.

Use **Manage Databases** for viewing, editing or deleting databases, and for creating new databases.

- From the **Edit** menu select **Manage Databases**.

  This opens a dialog listing all databases currently available.

  The databases are shown by name, with entry criteria for the database listed in the columns. These criteria determine what patients are included in the database: criteria may include, for example, gender or a specific age range.

  For more information see the section on (➔ Page 80 *Editing a Database*).

  You can also add patients to a database, and create your own database and add patients to it. See the section (➔ Page 81 *Add Patients to a Database*)

6.8.5 Editing a Database

You can use the **Edit Database** tool to view the contents of a database, check if a rate-pressure product normalization was applied, delete patient results from the database, or add the current patient's results to the database.

Note that changing the contents of a database will mean that the results of database comparison will also change. Patients previously compared to this database may have different comparison results when compared against the edited database.

Where multiple clinicians use the same system it is important to ensure that all users are aware of modifications made to the databases. Each user may need to reassess the appropriateness of the edited database for their specific patient comparisons.

1 From **Manage Databases**, select the database you wish to view.

2 Click **Edit**.

This opens an additional dialog displaying a list of all patient flow results in the database: mean and standard deviation of the results can also be shown. This enables you to browse the individual results that make up the database. This can be helpful when assessing whether the database is appropriate for comparison to a given patient. You can also add new patients to a database, see (➔ Page 81 *Add Patients to a Database*).

Note on Deleting Patients from a Database

Individual patients' results can be deleted from the database by selecting a patient from the list and selecting **Delete**. The database will be recalculated for new mean and standard deviation values.

This action cannot be undone. However the same patient could be reanalyzed in *syngo* MBF and their results from the new analysis added to the database.

6.8.6 Multiple Users Editing a Database

When you are editing a database in *syngo* MBF, the database is locked and cannot be edited by other users. Similarly, if another user is editing a database, this database is locked for editing and the editing tools will not be available to you for this database.

If you are using a database for patient reading and another user opens the database for editing, you can continue to use the database for your read. However, the changes that are made to the database are not available to you until you have exited and then re-started the workflow.

It is recommended that the editing of *syngo* MBF databases is coordinated so as to minimize impact on patient reading.

6.8.7 Add Patients to a Database

You can add patients to an existing database, or create your own database and add patients to it.

Before you add a subject to a database, always anonymize the patient data to prevent unauthorized access to any protected health information (PHI).

Add Current Patients

In the **Analysis** screen, you can add your current patient results to a database.

1 Click the **Add** button on the main toolbar.

This opens **Edit Database**.

2 Click **Add Current**.

Patient results can only be added to a database if the patient meets the database criteria. This prevents inappropriate data being added to a database with a specific population range.

Note that changing the contents of a database will mean that the results of database comparison will also change. Patients previously compared to this database may have different comparison results when compared against the edited database.

Where multiple clinicians use the same system it is important to ensure that all users are aware of modifications made to the databases. Each user may need to reassess the appropriateness of the edited database for their specific patient comparisons.

If a rate-pressure product normalization has been performed for the current patient, the normalized values will be added to the database (regardless whether the normalized or non-normalized results view is displayed on the screen).

Displaying Rate-Pressure Product Normalization details

The **Patient Details** tab displays information regarding whether a rate-pressure product normalization was applied or not. The following table describes the handling:

If	Then
• a rate-pressure product normalization has been set up • and the rate-pressure product normalization has been applied	the information that a rate-pressure product normalization was applied is displayed, including the following parameters: • Resting heart rate • Resting systolic blood pressure • Rate-pressure product • Rate-pressure product threshold

If	Then
• a rate-pressure normalization has been set up • and the rate-pressure product normalization has not been applied	the information that a rate-pressure product normalization was not applied is displayed, including the following parameters: • Resting heart rate Resting systolic blood pressure • Rate-pressure product • Rate-pressure product threshold
a rate-pressure normalization has not been set up	the information that the patient data were not normalized is displayed

6.8.8 Creating a New Database

You may create your own databases using specific population criteria that you feel would be useful for comparisons.

When creating a database you set the database criteria, which cannot be modified once the database is created. This is to reduce the potential for database contents to be changed in a way that other users of the database would not expect. For example, if a database criteria for Gender is initially set to Female, and then is changed to Both, users unaware of the change may assume the database is female only.

◆ From **Manage Databases**, select **New Database**.

This opens a dialog allowing you to configure the new database:

- Name: the short name that will be displayed when selecting a database. Type a name that is sufficiently descriptive to avoid confusion with other existing databases.
- Description: a more detailed description that will be shown in the Manage Databases dialog.
  - Age range: either upper or lower values can be left blank - that is, no upper or lower age limit - or used to restrict the database to a particular age range.
  - Gender: whether the patients in the database are only Male or only Female, or Both. Note that if gender is set to Both this does not mean that a database would need to contain both genders, only that the system will allow patients from either gender in the database.
- Type: Stress only, Rest only, or both Stress and Rest.
  - Note that if both Stress and Rest are allowed in the database, Reserve will also be included.
  - When adding a patient with both Stress and Rest scans to a database that allows either Stress *or* Rest but not both, only the relevant scan's results will be added to the database.
  - It is not possible to add patient results for only Stress or only Rest to a database configured to accept both Stress and Rest.

When you have edited the criteria, click **Save** to create the new database.

Add to New

You can also easily create a new database and add the current patient's results to it by selecting **Add to New** on the toolbar in the Analysis screen. This opens the **New Database** dialog, as described above.

When the new database is created the current patient is added to it automatically. If a rate-pressure product normalization has been performed for the current patient, the normalized values will be added to the database.

6.9 Saving to the Series Panel

You can take a 'snapshot' of the current *syngo* MBF screen.

◆ Select **Save Screen** from the **File** menu or click the **Save Screen** button.

The image is saved as DICOM secondary capture file, and is listed as a series in the **Series** panel. In the **Series** panel a *syngo* MBF secondary capture object is listed as '*syngo* MBF screen image' and labeled with the date and time when the image was taken.

Screen images are also saved as snapshots in the Findings Navigator.

Snapshots taken using any of the cardiac analysis applications such as *syngo* MBF are numbered consecutively in the Findings Navigator, so for example snapshots labeled *Snapshot1* and *Snapshot2* may have been taken using different cardiac applications.

For more information on using the **Series** panel and the Findings Navigator, see the Online Help or Operator Manual.

You can take a screen snapshot at any stage within the application.

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