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syngo MR E11

Operator Manual – Body

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Legend

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

WARNING

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

WARNING consists of the following elements:

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

WARNING

Legend

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1 Introduction

In order to operate the MR system accurately and safely, the operating personnel must have the necessary expertise as well as knowledge of the complete operator manual. The operator manual must be read carefully prior to using the MR system.

1.1 Layout of the operator manual

Your complete operator manual is split up into several volumes to improve readability. Each of these individual operator manuals covers a specific topic:

- Hardware components (system, coils, etc.)
- Software (measurement, evaluation, etc.)

Another element of the complete operator manual is the information provided for the system owner of the MR system.

The extent of the respective operator manual depends on the system configuration used and may vary.

All components of the complete operator manual may include safety information that needs to be adhered to.

The operator manuals for hardware and software address the authorized user. Basic knowledge in operating PCs and software is a prerequisite.

1.2 The current operator manual

This manual may include descriptions covering standard as well as optional hardware and software. Contact your Siemens Sales Organization with respect to the hardware and software available for your system. The description of an option does not infer a legal requirement to provide it.

The graphics, figures, and medical images used in this operator manual are examples only. The actual display and design of these may be slightly different on your system.

Male and female patients are referred to as “the patient” for the sake of simplicity.

1.3 Intended use

Your MAGNETOM MR system is indicated for use as a magnetic resonance diagnostic device (MRDD) that produces transverse, sagittal, coronal and oblique cross sectional images, spectroscopic images and/or spectra, and that displays the internal structure and/or function of the head, body, or extremities. Other physical parameters derived from the images and/or spectra may also be produced. Depending on the region of interest, contrast agents[1] may be used. These images and/or spectra and the physical parameters derived from the images and/or spectra when interpreted by a trained physician yield information that may assist in diagnosis.

[1] The drugs mentioned herein shall be used consistent with the approved labeling and/or indications for use of the drug. The treating physician bears the sole responsibility for the diagnosis and treatment of patients, including drugs and doses prescribed in connection with such use.

Your MAGNETOM MR system may also be used for imaging during interventional procedures when performed with MR compatible devices such as in-room displays and MR Safe biopsy needles.

The MAGNETOM MR system is not a device with measuring function as defined in the Medical Device Directive (MDD). Quantitative measured values obtained are for informational purposes and cannot be used as the only basis for diagnosis.

For the USA only: Federal law restricts this device to sale, distribution and use by or on the order of a physician.

Your MR system is a medical device for human use only!

1.4 Authorized operating personnel

The MAGNETOM MR system must be operated according to the intended use and only by qualified persons with the necessary knowledge in accordance with country-specific regulations, e.g. physicians, trained radiological technicians or technologists, subsequent to the necessary user training.

This user training must include basics in MR technology as well as safe handling of MR systems. The user must be familiar with potential hazard and safety guidelines the same way the user is familiar with emergency and rescue scenarios. In addition, the user has to have read and understood the contents of the operator manual.

Please contact Siemens Service for more information on available training options and suggested duration and frequency of such training.

1.4.1 Definitions of different persons

Term used	Explanation
User/Operator/ Operating personnel	Person who operates the system or software, takes care of the patient or reads images Typically physicians, trained radiological technicians, or technologists
System owner	Person who is responsible for the MR environment. This includes legal requirements, emergency plans, employee information and qualifications, as well as maintenance/repair.

Term used	Explanation
MR worker	Person who works within the controlled access area or MR environment User/Operator as well as further personnel (for example, cleaning staff, facility manager, service personnel)
Siemens Service/service personnel	Group of specially trained persons who are authorized by Siemens to perform certain maintenance activities References to “Siemens Service” include service personnel authorized by Siemens.

2 Preparation

2.1 Preparing and positioning the patient

2.1.1 Reducing motion artifacts

1 Instruct the patient to hold completely still during the entire examination.

2 Instruct the patient to take shallow and gentle breaths during free-breathing measurements.

Respiratory cushion

When performing measurements with respiratory triggering:

- Attach the respiratory cushion to the patient using the respiratory belt.

Breathhold commands

When performing breathhold measurements:

- Ensure that the patient wears the headset so that the breathhold commands can be understood despite the gradient knocking.

2.1.2 Preparing the contrast agent injection

Prior to moving the patient table into the magnet, you route the tube for the infusion.

1 Insert an intravenous port into the forearm vein of the patient.

2 Connect the port to the extension tube.

The tube should be long enough so that it can be accessed from the outside when the patient is in the magnet bore.

3 Connect the tube to the contrast agent injector.

2.1.3 Preparing dark lumen colonography

Preparation includes full cleansing of the bowels the day before the examination followed by one night of fasting.

1 Inform the patient about the entire examination.

2 Explain the filling of the intestines with water.

3 Practice holding one's breath with the patient.

4 Position the patient on one side on the patient table.

5 Position the inflow for filling the intestines with water.

6 Move the patient into the prone or supine position.

7 Prepare the contrast agent injection.

2.1.4 Preparing ECG-triggered examinations

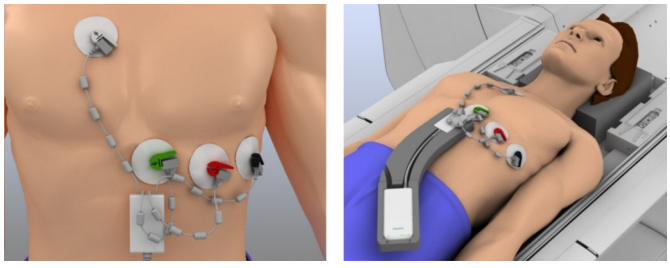
Positioning the electrodes and PERU

Electrodes: Positioning of the electrodes varies according to the position of the heart. An example is provided in the figure below.

Use only disposable ECG electrodes as released by Siemens.
(→ Page 20 *Procurement addresses*)

PERU: The ECG sensor in the PERU ensures transfer of the ECG signal. Typically, the PERU is aligned in the direction of the foot end of the **patient table** even though the patient may be positioned feet first in the direction of the magnet bore.

- Position the PERU in the appropriate support or add absorbent material between the ECG cables, PERU and skin. The distance between PERU and patient should be at least 2 cm.



Positioning the ECG electrodes (left) and the PERU (right).

The transmitter unit of the PERU includes three LEDs for signaling the battery status and one LED as fault indicator (e.g. insufficient skin contact of the ECG electrodes).

Battery status and electrode fault are also indicated on the Dot display above the magnet bore and the **Physiological Display** dialog window.

If the red LED **Electrode fault** on the PERU flashes, the ECG electrodes are not attached correctly. Check to ensure that the electrodes are not falling off.

Attaching ECG electrodes

The electrodes must be positioned and attached with care to ensure a sufficient and consistent ECG signal.

1 Discuss the breathholds and respective commands with the patient.

2 Ensure satisfactory contact between the electrodes and the patient's skin.

3 Thoroughly clean the patient's skin with a dry cloth or **NUPREP ECG & EEG Abrasive Skin Prepping Gel** . (→ Page 20 *Procurement addresses*)

4 If the patient is hirsute, shave the location where you want to attach the electrodes.

5 Dry the skin carefully.

6 Check the signal at the Dot display above the magnet bore.

7 If the signal received is not satisfactory and consistent, vary the location of the electrodes. Use new electrodes every single time.

8 If one of the leads does not provide a sufficient signal, change to a single ECG lead in the **Physiological Display** dialog window.

Procurement addresses

Disposable ECG electrodes may be ordered from:

Siemens Commercial goods (Catalog Med & More), CONMED 2700 Cleartrace

- Item no. 07437598 (600 pieces)

or from:

CONMED CORPORATION, 310 Broad Street, Utica, New York 13501, USA

Cleaning gel: NUPREP ECG & EEG Abrasive Skin Prepping Gel

Weaver and Company, 565 Nucla Way, Unit B, Aurora, Colorado 80011, USA

2 Preparation

3 Measurement

3.1 General information

Radiological requirements on the one hand, and anatomical or physiological requirements on the other, present certain challenges in the area of body imaging.

The organs of the abdomen are affected by a number of motions that make it difficult to obtain images free of artifacts.

- Respiratory motion
- Peristalsis
- Pulsation of different arteries, especially the aorta

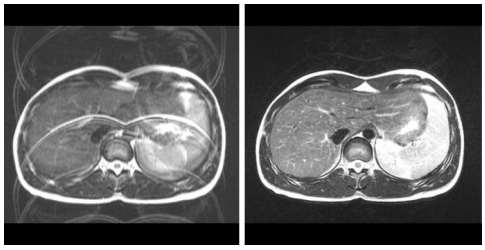


Image with (left) and without respiratory artifacts (right).

3.1.1 Sequences

Fast or ultra-fast sequences are used for body imaging.

- Single-shot sequences (e.g. TurboFLASH, HASTE)
- Multi-shot sequences for 2D and 3D measurements (e.g. TSE, GRE)
- VIBE for 3D measurements

3.1.2 Measurement techniques

Techniques for reducing respiratory artifacts include measurements during one or several respiratory breathholds as well as measurements with triggering during normal breathing.

- Single/multi-breathhold techniques (without 2D PACE) (→ Page 40 *Performing multi-breathhold examinations*)
- Measurement with navigator triggering during normal breathing (→ Page 43 *Performing examinations with navigator triggering*)
- Measurement with respiratory triggering during normal breathing (→ Page 58 *Performing examinations with respiratory triggering*)

3.1.3 iPAT: Application hints

To avoid aliasing artifacts, iPAT protocols can be used.

Ensure that the FoV is sufficiently large in the iPAT mode "mSENSE" or use phase oversampling.

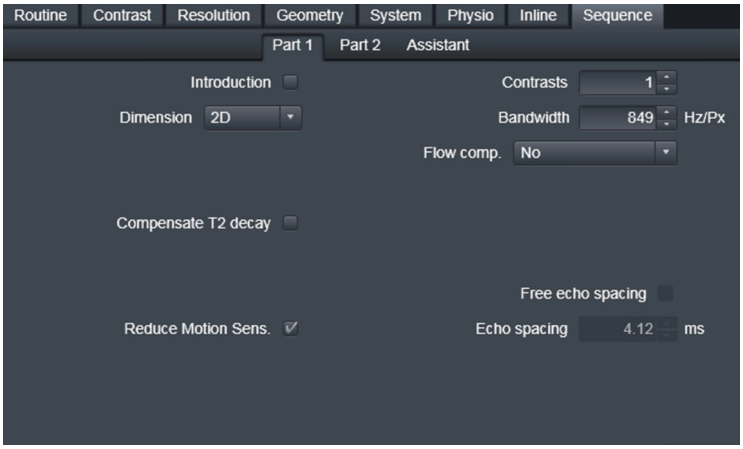
Use a sagittal localizer to ensure that all transverse slices have a sufficiently large FoV.

Use spacer pads to prevent aliasing artifacts.

Multi-contrast FLASH sequences can be used only in the iPAT mode "GRAPPA".

3.1.4 Reduced motion sensitivity

For small patient movements, motion artifacts are reduced significantly by enabling the **Reduce Motion Sens.** checkbox on the **Sequence Part 1** parameter card of the TSE sequence.



Applications:

- T2-weighted measurements of head, spine, pelvis, and hip
- T2-weighted abdominal applications based on TSE with PACE free breathing

The technique is less effective for application setups with higher Turbo factors. For this reason, breathhold measurements of the lungs or abdomen are **not** recommended.

For the TSE sequence, the BLADE technique may also be used to reduce motion sensitivity. Detailed information about BLADE is available in the **Application Brochure Pulse Sequences**.

Single excitation

For abdominal measurements, a motion-insensitive single-excitation TSE DIXON sequence is provided. Measurements can be performed using breathhold and respiratory-triggering techniques.

WARNING

When using the DIXON method, water and fat swaps might occur!

Incorrect diagnosis

- Diagnosis should be confirmed by a second contrast and/or a different orientation.

In order to reduce motion artifacts, enable **Fast Dixon** in the **Contrast Common** parameter card.

Radial trajectory

Imaging methods using radial trajectories are more robust to motion, compared to cartesian sampling. A motion-insensitive VIBE sequence with trajectory acquisition is available with StarVIBE. The sequence supports free-breathing measurements.

In order to reduce motion artifacts, select **Radial** from the **Trajectory** dropdown menu in the **Resolution Common** parameter card.

3.1.5 Fat suppression

	STIR	SPAIR		Fat saturation		Water excita-tion	Dixon
		Standard	Mode weak/ strong	Standard	Mode weak/ strong		
TSE/SE	Yes	Yes	Yes	Yes	Yes	Yes	Yes
HASTE	Yes	Yes	Yes	Yes	Yes	No	No
SPACE	Yes	Yes	Yes	Yes	Yes	No	No

	STIR	SPAIR		Fat saturation		Water excitation	Dixon
FLASH-2D	No	No	No	Yes[1)]	Yes[2)]	No	No
VIBE	No	Yes[3)]	No	Yes[4)]	No	Yes	Yes
REVEAL	Yes	Yes	No	Yes	No	Yes	No
TFL	No	No	No	No	No	Yes	No
TrueFISP	No	No	No	Yes	No	Yes	No

Recommended fat/water selective techniques[1)2)3)4)]

Technique	Advantages	Disadvantages	Applications
STIR	■ Insensitive to B_0 inhomogeneities	■ Timing changes TR, TA ■ Contrast affected	■ Detection of metastasis in the abdominal region
SPAIR	■ Insensitive to B_1 inhomogeneities ■ High performance (quick mode) ■ Contrast not affected	■ Timing changes TR, TA	■ Abdominal breathhold applications with TSE, SPACE, HASTE, and VIBE ■ Fast T1-weighted breathhold applications based on VIBE (with proper setting of the parameter “Lines per shot”)
FatSat	■ High performance (quick mode) ■ Contrast not affected	■ Sensitive to B_0 and B_1 inhomogeneities ■ Timing changes TR, TA	■ T2-weighted abdominal applications with fat saturation based on TSE, SPACE, and HASTE ■ Fast T1-weighted breathhold applications with Quick FatSat based on FLASH-2D, and VIBE

1) both FatSat and Quick FatSat are available
2) available only with Quick FatSat
3) “Lines per shot” can be selected
4) with Quick FatSat, “Lines per shot” can be selected

Technique	Advantages	Disadvantages	Applications
Water excitation	■ Insensitive to B_1 inhomogeneities ■ Contrast not affected	■ Timing changes TE, TR	■ Frequently used on low field systems where spectral fat suppression is inapplicable ■ Transverse TurboFLASH applications with breathhold or PACE free breathing ■ REVEAL applications in breathhold technique
Dixon	■ Insensitive to B_0 and B_1 inhomogeneities ■ Multiple contrasts generated ■ Contrast not affected	■ Timing changes TR	■ Robust fat/water imaging in abdominal applications ■ Fat measurements

Comparison of different fat suppression techniques

Optimizing fat suppression

SPAIR fat suppression is available for TSE, SPACE, HASTE, VIBE, and EPI diffusion sequences.

The main advantages are:

- decreased sensitivity to B0 inhomogeneities
- increased saturation homogeneity
- increased saturation strength

For abdominal imaging with 3T, SPAIR fat saturation can be optimized for specific regions:

- abdomen and pelvis
- thorax

The optimized fat suppression regions **Abdomen & Pelvis** or **Thorax** can be selected in the **Fat Suppression Optimization** dialog window.

To open the dialog window, click the button on the right side of the **Fat suppr.** dropdown menu.

Prerequisite: **SPAIR** is selected.

For further information, please refer to Operator Manual - Parameters and Image Text.

3.1.6 REVEAL: diffusion-weighted measurements

Diffusion-weighted imaging shows an increased potential for differential diagnosis in evaluating body lesions. Accurate lesion detection is necessary for subsequent therapy planning or follow-up of lesions.

Technique

Principle of DWI: DW MRI is based on the principle that random motion of molecules during the interval of excitation and signal measurement reduces the amplitude of the resulting signal. The application of appropriate pulse sequences (using, for example, bipolar gradient pulses in one or several directions) allows you to measure signal cancellation due to diffusion in the given direction. While normal tissue exhibits gross signal loss, areas with restricted molecular motion such as densely packed tumor cells show less signal loss and become **bright** in diffusion-weighted images.

Auto calibration scan: In general, segmented reference scan techniques produce artifacts if acquired during different breathholds. With iPAT including auto calibration scan (ACS), motion artifacts can be reduced for iPAT values higher than 2. Raw data filtering for the ACS is not required.

Separate GRE reference scan: For iPAT acceleration factors higher than 2, the separate GRE reference scan is less sensitive to subject motion than the separate EPI reference scan.

ADC map: The value of the diffusion of water in tissue is called the apparent diffusion coefficient (ADC). Based on the diffusion-weighted images, an ADC map can be calculated, which shows the ADC value of each voxel in every slice. Restricted water movement in tumors with high cellularity leads to lower ADC values.

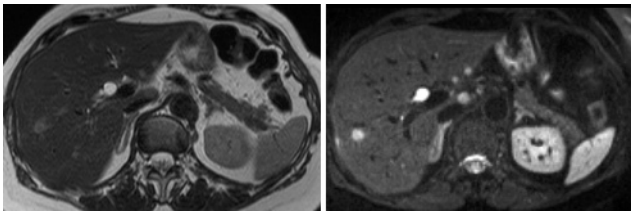
Body diffusion: For body diffusion, trace-weighted single-shot EPI sequences are used (ep2d_diff, see **Application Brochure Pulse Sequences**), which apply diffusion gradients of specific strength and direction.

The strength of the diffusion gradients is determined by the b-value [s/mm^2]. Typically, an iPAT factor of 2 (GRAPPA) is used to shorten the echo train and reduce sensitivity to susceptibility. For a good fat suppression, which is essential for single-shot EPI applications, a fat saturation pulse is applied or STIR in difficult regions with artifacts caused by unsaturated fat (e.g., for breast diffusion with REVEAL).

Finally, images are generated which clearly show the diffusion status within the anatomy.

Low b-value imaging

Application using a low b-value (b ≤50 s/mm^2) to obtain high lesion conspicuity with dark vessels. No differentiation between benign and malignant lesions is possible. Image acquisition can be performed within one breathhold or with a freely breathing patient to increase SNR. This technique is beneficial for, e.g. liver examinations as a fast acquisition add-on to the standard program.

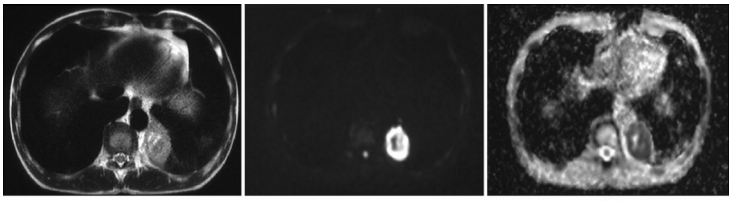


Dark vessel liver imaging with single-shot EPI diffusion sequence with fat saturation, b-value = 50 s/mm^2, in one breathhold (left) compared to T2-weighted breathhold Turbo spin echo with fat saturation (right). Improved visibility of lesions as compared to the standard T2-weighted liver imaging with Turbo spin echo sequence normally showing bright vessels.

High b-value imaging

Diffusion-weighted imaging with three b-values in the range from 50–1000 s/mm^2.

With a b-value above 800 s/mm^2, a very good suppression of normal tissue is obtained and essentially tissue with a high cellularity is displayed. Image acquisition can be performed within one breathhold or in free breathing to increase SNR.



(1) (2) (3)

(1) T2-weighted image

(2) High b-value diffusion-weighted image: The malignant lesion shows up bright (b-value = 1,000 s/mm^2)

(3) ADC map. Due to restricted diffusion, the tumor has a low ADC

3.1.7 Measuring dynamic signal changes

2D and 3D protocols are available for measuring dynamic changes in signal in different organs and tissues.

Temporal resolution/planning

Fast temporal changes in signal intensity require the highest possible temporal resolution for the measurement. To realize very short temporal intervals between measurements, the number of slices possible as well as their spatial resolution is limited. This is why slice planning plays an important role in acquiring the organs that are of interest.

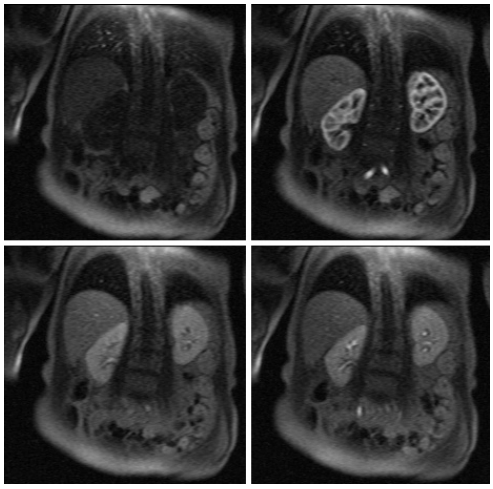
The multi-slice TrueFISP localizer in the protocol tree is suitable for displaying the kidneys and the renal artery.

When selecting and adjusting a protocol, it is important to take into account the temporal resolution for the changes in signal to be monitored.

2D measurements

During 2D measurements, a low measurement time is selected for individual slices so that a respiratory shift in the organ seems to be frozen during image acquisition time and is of negligible importance.

The measurement protocols consist of a sequence of slices that are acquired in the single-shot technique, one after the other. The orientation of the individual slices may be different. The temporal resolution is determined by the number of slices. The organ is motion-corrected during image post-processing.



Example: Measurement of dynamic signal changes with SR-FLASH.

3D measurements

Using the same parameters, 3D measurements show a better SNR than 2D techniques. However, by necessity their measurement time is longer.

This is why motions and their effects play a role during the measurement. It is important to either avoid or, if present, correct respiratory motion.

The breathhold technique is a simple and effective method for reducing spatial shifts in organs and for performing measurements of high temporal and/or spatial resolution.

Where temporal changes are considered slow in relationship to the measurement time, the signal course can be documented by using repeated measurements at suitable intervals.

Base line

The base line plays an important role when evaluating the time course of the signal. The base line is determined by the constant signal value of a tissue prior to observing temporal signal changes.

Several sequence techniques require a number of excitation cycles until a steady state is reached.

Measurements should be performed that allow for easy definition of the base line without adversely affecting the monitoring of fast signal changes. For this reason, separate measurements are performed including only a few repeats prior to dynamic changes.

Saturation

Non-selective saturation: When using saturation pulses, the protocol name includes **_sr_**. Non-selective saturation is characterized by generating a uniform magnetic state with vanishing longitudinal magnetization for all tissues. Once in this state, the sequence-specific signal is generated as a function of the tissue-specific relaxation times.

Saturation with an IR pulse: Magnetization prepared by an inversion pulse with suitable inversion time is often used for displaying differences in signal. What needs to be considered in this case is the occurrence of signal fluctuations with long relaxation times. With signal changes with short T1 relaxation, ambiguous signal contributions may occur. For this reason, examinations with time-dynamic imaging are run **without** using a protocol with inversion pulse.

Slice-selective saturation: During slice-selective preparation, the signal is also affected by the blood flowing into the slice. These types of effects should be avoided for signal analyses that are largely based on changes in relaxation time.

Selection of saturation pulse: For a comparison of the signal time curves of different tissues, it is necessary to assess a complete and homogeneous saturation over the complete selected imaging volume. In order to achieve this, an optimized saturation pulse should be used which can be accessed via the **Contrast Common** parameter card.

Aliasing artifacts

Examinations with time-dynamic imaging of the kidneys are usually performed in the coronal orientation. The phase-encoding direction runs in this case from left to right. With small fields of view (FoV), aliasing artifacts may occur caused by the arms aligned along the sides of the patient. These artifacts are acceptable only if they do not adversely affect the signal for the kidneys.

Otherwise, the FoV has to be enlarged or phase-oversampling has to be used.

Evaluation software

Mean Curve may be used for displaying signal-time curves. This program is suitable for drawing tissue regions and performing base line corrections.

3.1.8 Time-dynamic imaging with 2D PACE

Usually, the early phase of the measurement should be performed with high temporal resolution. During this time interval, breathhold acquisition is performed. The images that follow can be measured, however, at a larger time interval using navigator triggering.

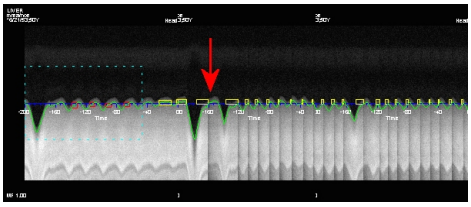
Both phases of this type of measurement follow one another automatically. The number of breathhold measurements as well as the number of slices per respiratory cycle are shown on the **Physio PACE** parameter card.

Learning phase: The learning phase is at the beginning of the time-dynamic image acquisition with combined breathhold measurements and triggering. The parameters determined during this phase are used for subsequent measurements with triggering.

Imaging phase: After the learning phase, a respiratory command is issued and the requested number of images is acquired without interruption. Following this procedure, the automatic navigator-triggered measurement begins up to the end of the repetitions set.

It is important that the position of the diaphragm during the breathhold closely corresponds to the learned breathing position for triggering.

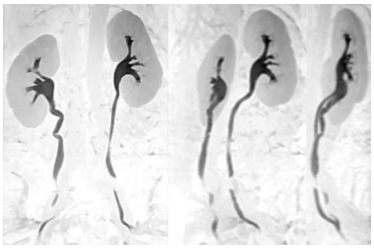
Advantages: By combining the two methods of fast data acquisition and triggering, signal evaluation across a longer acquisition time has been improved. Whenever possible, organs and vessels are acquired during the same respiratory position and partial volume effects vertical to the slice plane due to motion are reduced. Currently, these methods are implemented in the **tfl** sequence.



Course over time for a time-dynamic image acquisition using navigator signals: After the learning phase, a deep respiratory intake period is visible. A temporal high-resolution measurement (red arrow) is acquired when the trigger conditions are subsequently met. The navigator signals are not displayed at the end of the breathhold measurements. However, all following acquisitions are measured with respiratory triggering.

Urographic display

Using dynamic procedures, it is possible to display renal calyces, the renal pelvis, and the urinary tract collection system with a 3D sequence.



Different projection angles of a MIP reconstruction during a dynamic measurement (inverted display).

You can either compute a maximum intensity projection (MIP) or a multiplanar reconstruction (MPR).

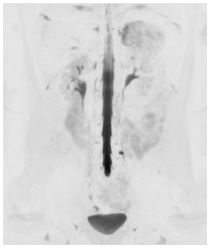
Due to their peristaltic movement and anatomical position, it is frequently impossible to fully display ureters. However, it is also possible to repeat the measurement several times to acquire peristaltic waves.

Additionally, it is helpful to provide patients with as much fluids as possible during urographic examinations.

During a dynamic measurement, the kidneys act to filter out any substances in the blood. This will result in an increased concentration of the substance in the kidneys. A corresponding extreme shortening of relaxation times is then likely.

MR urography at low concentration levels (inverted display). Selective display of the renal calyces as well as the urinary tract collection system.

It is also possible to perform urography with strongly T2-weighted sequences. Strong hydrogenation of the patient is especially advantageous including compression of the lower abdomen, if required.



MIP reconstruction of a T2-weighted 3D TSE image (inverted display). The spinal canal is clearly displayed.

3.1.9 Multi-arterial phase imaging with TWIST-VIBE

For liver multi-arterial phase imaging, the VIBE sequence is extended by the TWIST technique in combination with CAIPIRINHA and DIXON with fat/water separation. This allows multi-arterial phase imaging in a single breathhold with high temporal and spatial resolution.

The advantages are:

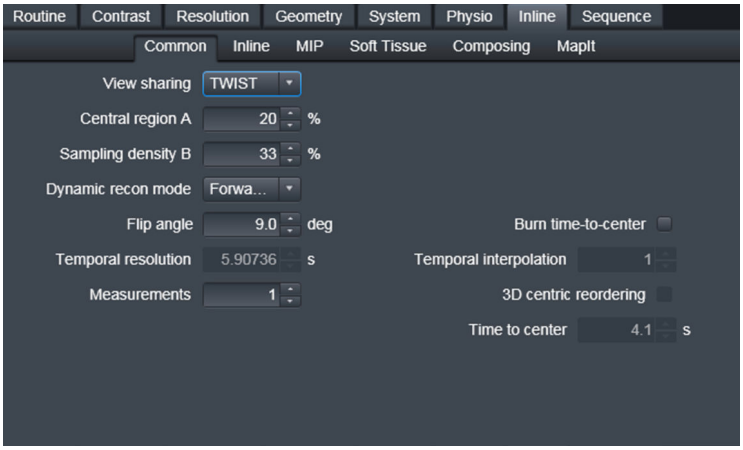
- high temporal resolution for multiple measurements with TWIST view sharing
- high iPAT factors with CAIPIRINHA

The multi-arterial phase sequence is available in the abdomen dot library under "multi arterial phase". To run liver dynamics with multi-arterial phases, replace the entire ABLE block within the Abdomen Dot Engine with the steps from the abdomen dot library in the **Dot Cockpit**.

In the **Common Inline** parameter card, following parameters can be defined for TWIST-VIBE:

- the size of the **Central region A**
- the **Sampling density B** used during each pass through the outer region
- the **Dynamic recon mode** defines the sharing direction of the raw data (forward sharing, backward sharing, symmetric sharing)

For a detailed description of the TWIST technique, please refer to: Operator Manual- Vascular.



3.2 Performing multi-breathhold examinations

3.2.1 Single/multi-breathhold techniques

If the patient can hold their breath sufficiently long, the entire measurement can be completed in a single breathhold. In this way respiratory artifacts are largely avoided. However, this requires excellent cooperation on the patient's part, since the patient has to hold this breath for about 20 s.

Usually, several breathhold intervals are required to fully cover the anatomy of interest. The number of breathhold intervals depends on the number of concatenations.

Concatenations: Concatenations subdivide the overall measurement into partial measurements. The number of concatenations corresponds to the number of partial measurements.

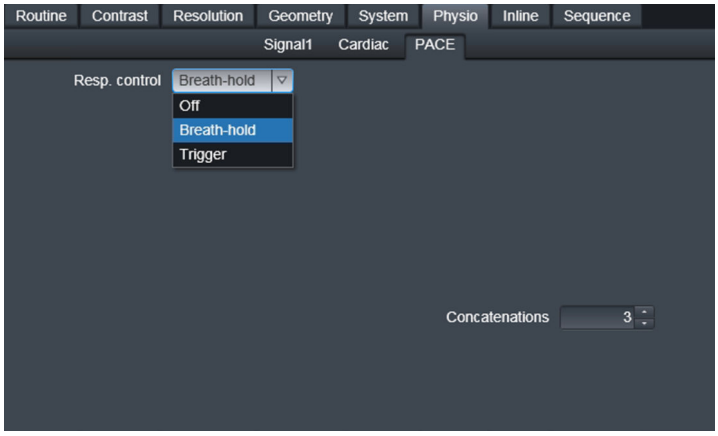
3.2.2 Planning the examination

Using multi-breathhold protocols, you are able to plan all slices in a single examination protocol and manually measure the slices of each breathhold interval.

✓ Localizer has been measured

✓ Multi-breathhold protocol has been opened

1 Open the **Physio PACE** parameter card.



2 Select the **Breath-hold** option under the respiratory control parameter.

In order to use automatic voice commands, you have to adapt the protocol parameters in the **Step Properties – Voice Commands** dialog.

For a detailed description of the parameters, please refer to: Operator Manual - Dot Cockpit.

In this case, the voice commands are only given at the beginning and the end of the protocol.

If you want to use automatic voice commands at each measurement, make sure that the **Breath-hold** option is selected in the **Physio PACE** parameter card.

The duration of the breathhold is available as a tool tip of the measurement time.

3 Select as many concatenations as necessary to ensure that the patient is comfortable with the duration of the breathholds.

4 Plan the slices as usual.

Measurement time

The **predicted measurement time** is computed from the measurement time of the breathhold interval (= duration of breathhold) and the number of breathhold intervals per measurement. The **actual measurement time** depends also on the length of the pauses between respiratory intervals and is not known beforehand.

- If necessary, adjust additional parameters relevant to the measurement time (e.g., TR, Turbo factor, phase resolution).

Minimizing shifts within the measurement

1 Acquire all partial measurements during the end inspiration or end expiration phase.

2 In the **Geometry Common** parameter card: Select the interleaved in breathhold excitation sequence.

3.2.3 Performing the measurement

1 Start the measurement.

The **Wait for user to start** option (flagman) in the **Protocol step properties** dialog window is not required and should **not** be selected for multi-breathhold protocols.

2 Open the Inline Display.

3 Start the first breathhold command as soon as **Press Scan in Inline Display when patient holds breath** appears at the bottom left in the measurement time display.

4 Start the measurement after the patient is holding his breath with **Scan** in the Inline Display.

The slices of the first breathhold interval are measured.

During the measurement, the time remaining for the breathhold interval is counted down in the measurement time display.

The number n in the measurement time display **Scanning breath hold... (1 of n)** stands for the number of breathhold intervals measured and **not** the number of individual measurements.

5 Repeat the last step for each breathhold interval.

The number of manual starts required for the complete measurement equals the number of concatenations set.

3.3 Performing examinations with navigator triggering

3.3.1 Navigator triggering

During navigator triggering, a navigator is used for monitoring respiratory motion. Data acquisition is performed during normal breathing.

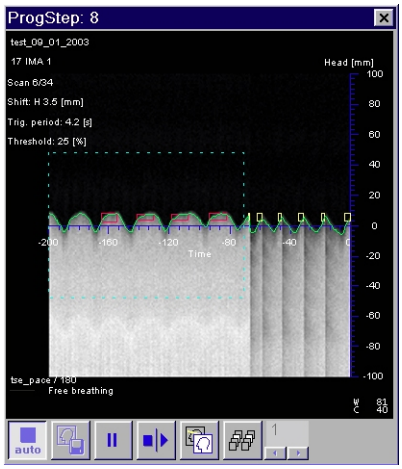
Trigger: The trigger is the reference point in the physiological signal that releases data acquisition. It synchronizes respiratory motion and data acquisition.

Learning/imaging phase

The navigator-triggered measurement can be divided into two phases: the learning phase and the imaging phase.

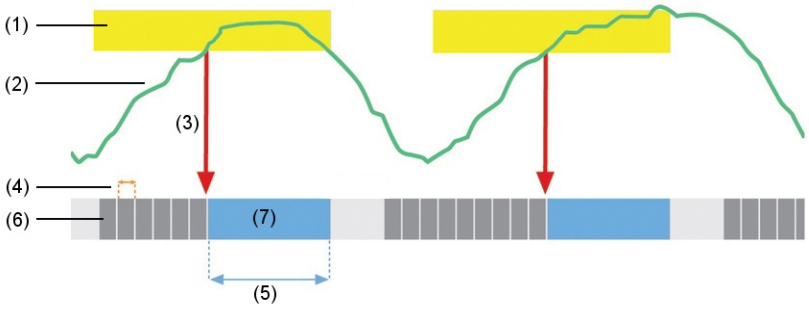
Learning phase: During the learning phase, the "respiratory pattern" of the patient is learned to establish the center position of the acceptance window during the imaging phase. During the first five respiratory cycles, the navigator acquires the respiratory cycle without interrupting the measurement. During this period, respiratory motion is continuously shown in the Inline Display. Beginning with the second respiratory cycle, a red rectangle shows the period proposed for data acquisition. The position of the red rectangles is based on the parameters set and on the evaluation of preceding respiratory cycles.

Width/height of the red rectangle: The width of the red rectangle corresponds to the acquisition duration. Height and vertical position of the red rectangles are set so that they fully cover the motion of the diaphragm during the proposed period. The parameters are set correctly when the data are acquired toward the end of expiration.



Navigator-triggered respiratory curve. The turquoise rectangle (position of the navigator) marks the learning phase.

Imaging phase: At the beginning of the imaging phase, the navigator is repeated at constant time intervals (**Scout TR**) in order to acquire the positions of the diaphragm. As soon as the detected diaphragm position falls within the acceptance window, the navigator is no longer repeated, and the first block of the actual imaging sequence is started. The measurement time for one block corresponds to the acquisition duration.



Imaging phase of navigator-triggered sequence. After completing one block of the imaging sequence, the navigator is repeated until the next suitable respiratory phase is located. No triggers are generated during inspiration (acceptance window is interrupted).

(1) Acceptance window

(2) Position of diaphragm

(3) Trigger

(4) Scout TR

(5) Acquisition duration

(6) Navigators

(7) Imaging sequence (block)

Respiratory curve: In the imaging phase, the respiratory curve is no longer displayed during data acquisition. As soon as expiration begins, the acceptance window is shown as a yellow rectangle. The height of the acceptance window corresponds to the value of the **Accept Window ±** parameter on the **Physio PACE** parameter card. The center of the acceptance window is either determined by the system during the learning phase or is set manually. As soon as the detected diaphragm position (green curve) falls into the acceptance window, the first block of the imaging sequence is started.

3.3.2 Planning the examination

Selecting the coil elements

1 To avoid unnecessary noise or artifacts select only relevant coil elements in the imaging field of view.

2 Select also a coil element near the navigator.

Measuring the localizers

To enable optimal navigator positioning, the localizers are measured in free-breathing technique.

- Start the measurement of the localizer.

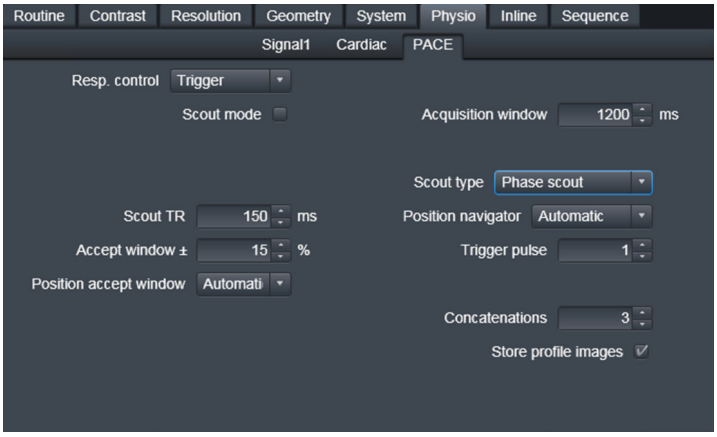
Several transverse and coronal slices through the dome of the liver are measured.

Adding the navigator

✓ Coronal and transverse localizer slices have been measured

✓ Free-breathing protocol has been opened

1 Open the **Physio PACE** parameter card.



2 Select the **Trigger** option under the respiratory control parameter.

The system automatically adds a navigator to the measurement protocol.

The acquisition duration is available as a tool tip of the measurement time. To display the tool tip, float the cursor over the measurement time. In line 2 you will find the number of required respiratory cycles (5 respiratory cycles for the learning phase plus X respiratory cycles for the imaging phase).

3 Plan the slices.

4 Set the imaging parameters (e.g. number of slices per concatenation, Turbo factor) so that the duration of acquisition either equals or is reduced by 1/3 of the expected average respiratory period.

(For a description of reducing the acquisition duration, please refer to: (→ Page 55 *Reducing the acquisition duration (optional)*).)

For healthy adults, the respiratory period (interval maximum inspiration to maximum inspiration) is approx. 4–6 s. However, this period may be shorter for children[1] or the ill.

[1] MR scanning has not been established as safe for imaging fetuses and infants less than two years of age. The responsible physician must evaluate the benefits of the MR examination compared to those of other imaging procedures.

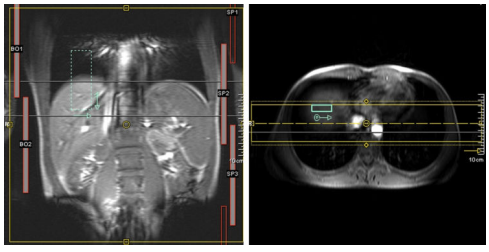
3.3.3 Setting the navigator

✓ Navigator is switched on

1 Open the **Geometry Navigator** parameter card.

2 Set the parameters of the navigator, for example, position, and orientation.

The navigator is displayed as a turquoise rectangle in the GSP.



Coronal and transverse localizer with navigator.

A phase navigator is only visible in the GSP if the **Manual** option is selected. (→ Page 51 *Manually positioning the phase navigator*)

3.3.4 Positioning the navigator

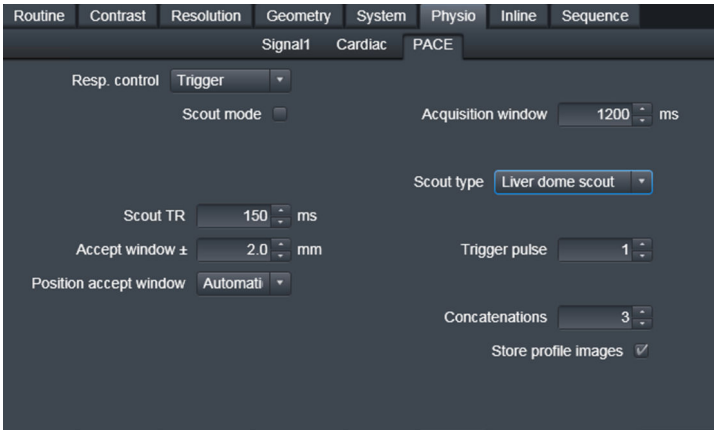
Depending on the type of examination, you can select between two types of navigator.

- Liver dome navigator (➔ Page 48 *Positioning the liver dome navigator*)
- Phase navigator (➔ Page 51 *Manually positioning the phase navigator*)

Positioning the liver dome navigator

✓ Navigator is switched on

1 Open the **Physio PACE** parameter card.



2 From the **Scout type** list: Select the **Liver dome scout**.

In the GSP: The navigator is displayed as a turquoise rectangle with dashed lines.

3 Select the navigator.

Positioning the navigator on coronal localizers

1 In the coronal localizers: Select the best image of the dome of the liver.

2 Shift the navigator to this coronal plane by selecting **Protocol > Shift to image plane** from the main menu.

In the GSP: The navigator is displayed as a turquoise rectangle with **continuous** lines.

3 Position the navigator centered on the dome of the liver, where half of the turquoise rectangle is in the liver and the other half is in the lung.

Please consider whether the localizer was acquired during inspiration or expiration.

- Inspiration: Position the navigator higher (more cranial)
- Expiration: Position the navigator lower (more caudal)

Positioning the navigator on transverse localizers

1 In the transverse localizers: Select the best image of the dome of the liver.

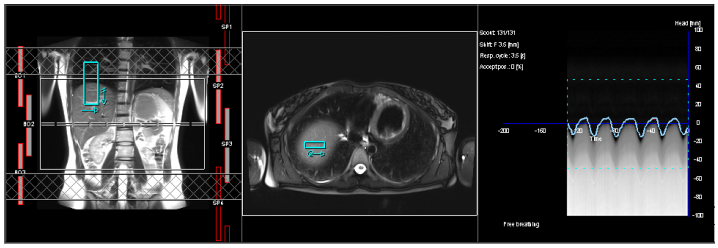
2 Position the navigator in the center of the dome of the liver.

3 Double check that the navigator is still centered on the coronal image.

Checking the navigator position

1 Start the measurement.

2 In the Inline Display: Check whether the navigator is positioned correctly.

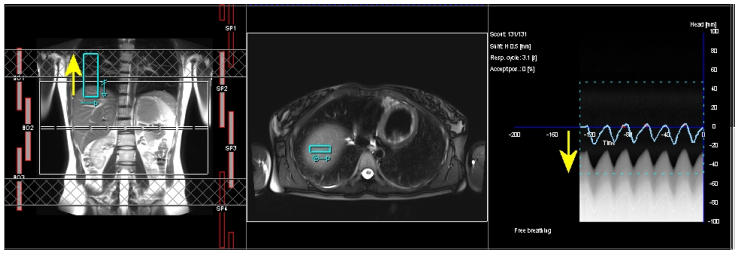


Accurate positioning of the navigator: Display of clearly separated borders between the lung and liver is seen. The green line will show the patients breathing motion.

The green line and the transition between liver/lung do **not** have to be congruent.

Examples: Wrong navigator positions

Navigator is positioned too high

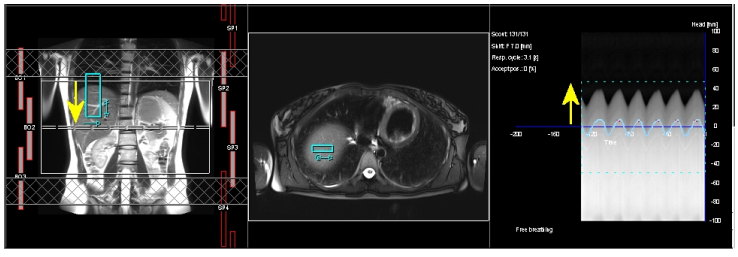


The navigator is positioned too far towards the lung parenchyma. Apart from that the detected breathing signal is ok.

In general: The border between the bright signal of the liver and the dark signal from lung parenchyma has to be within the turquoise rectangle with dashed lines. In the example, this requirement is barely met.

- Correct the position of the navigator. (➔ Page 53 *Correcting the position of the liver dome navigator (optional)*)

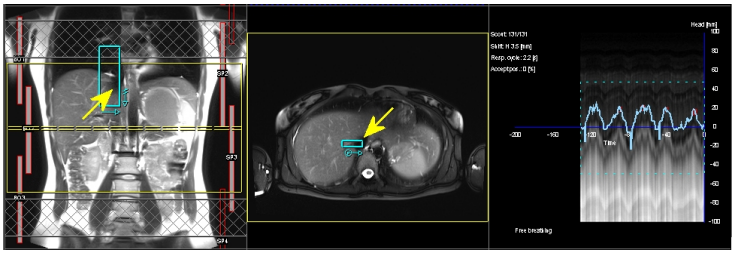
Navigator is positioned too low



The navigator is positioned too far into the liver parenchyma. Apart from that the detected breathing signal is ok.

- Correct the position of the navigator. (➔ Page 53 *Correcting the position of the liver dome navigator (optional)*)

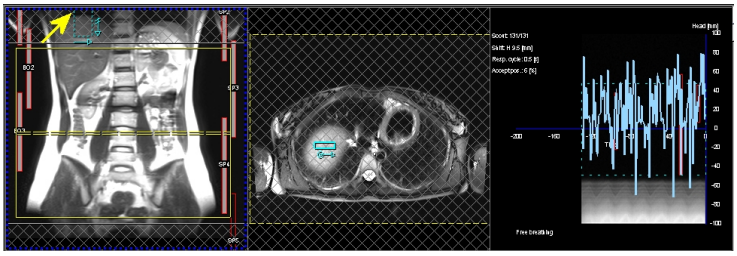
Navigator is cutting a vessel



The navigator is cutting a vessel (vena cava). The detected breathing curve is irregular and not feasible.

- Correct the position of the navigator. (→ Page 53 *Correcting the position of the liver dome navigator (optional)*)

Navigator is not within the homogeneous magnetic field



The navigator is positioned at the border of magnet homogeneity. The detected signal is jagged and not feasible.

- Reposition the patient so that the dome of the liver is within the area of homogeneity.

With large patients it may be difficult to position the imaging volume as well as the navigator in the homogeneity volume of the scanner. In these cases, consider using the phase navigator.

Manually positioning the phase navigator

Normally, the phase navigator is positioned automatically and is not visible in the GSP.

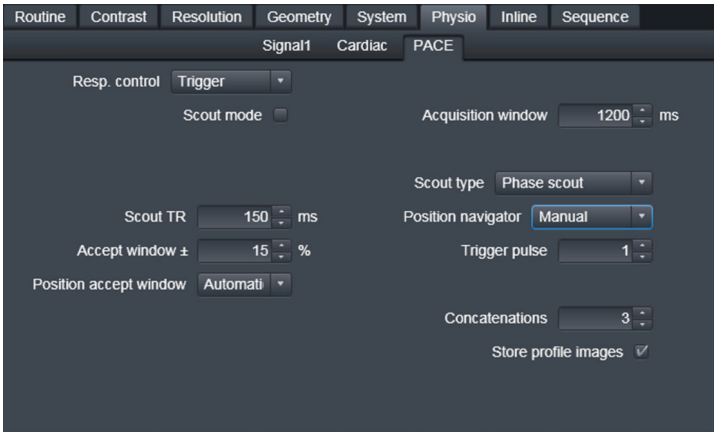
The automatic positioning mode is not available for spectroscopy single voxel spin-echo measurements (svs_se). In this case, you have to position the phase navigator manually.

✓ Phase navigator is switched on

To check and, if necessary, correct the position of the navigator, proceed as follows.

1 Open the protocol.

2 Open the **Physio PACE** parameter card.



3 From the **Position navigator** list: Select the **Manual** option.

In the GSP: The navigator is displayed as a turquoise rectangle with dashed lines.

Optimal positioning

1 Position the phase navigator within the homogeneous liver parenchyma.

2 Exclude bigger vessels, if possible.

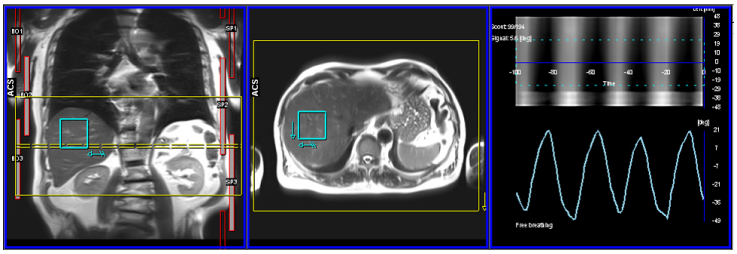
Please consider whether the localizer was acquired during inspiration or expiration.

- Inspiration: Position the navigator higher (more cranial)
- Expiration: Position the navigator lower (more caudal)

Verifying the positioning

1 Start the measurement.

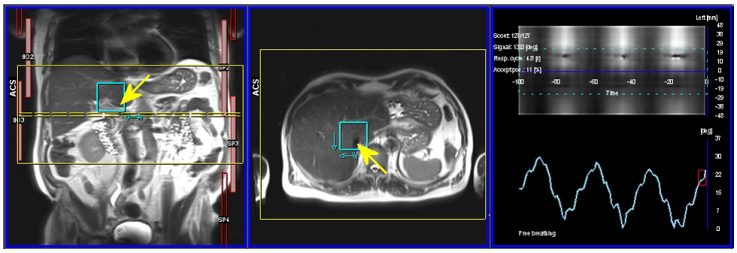
2 In the Inline Display: Check whether the navigator is positioned correctly.



Due to the movement of the liver during the breathing cycle, phase changes will occur, which are detected and represented in the breathing curve as displayed in the right image.

Example: Wrong navigator position

Navigator is cutting a vessel



The navigator is cutting a vessel (vena portae). The detected breathing curve is still ok, but may be not feasible, when too much pulsation is involved.

- Correct the position of the navigator.

3.3.5 Correcting the position of the liver dome navigator (optional)

✓ Liver dome navigator has not been positioned correctly

You may correct the position of the liver dome navigator when, e.g., the localizer was generated while the patient was deeply inhaling or exhaling.

Example: The liver dome navigator is located completely in the liver (is located too far down). The transition between the dark signal of the lung and the bright signal of the liver takes place above the turquoise rectangle.

1 Terminate the measurement.

2 Track the navigator asymmetrically to the edge of the diaphragm.

3 Shift the navigator upward (toward the head).

The navigator in the localizer no longer appears symmetrically to the edge of the diaphragm.

3.3.6 Measuring the respiratory period (optional)

You are able to check whether or not the navigator records the respiratory signal as required.

- On the **Physio PACE** parameter card: Select the **Scout mode** checkbox and start the measurement.

  After a complete respiratory interval (at least two end expirations), the average respiratory period is shown in the Inline Display (respiratory cycle).

The **Scout mode** **cannot** be selected during the actual measurement.

3.3.7 Performing the measurement

The breathing behaviour of the patient is strongly affecting the image quality.

1 Instruct the patient to breathe normally during the entire measurement (do not stop breathing).

2 Start the measurement.

3 Check the acquisition window during the learning phase. For this purpose, monitor the width of the red rectangles on the Inline Display.

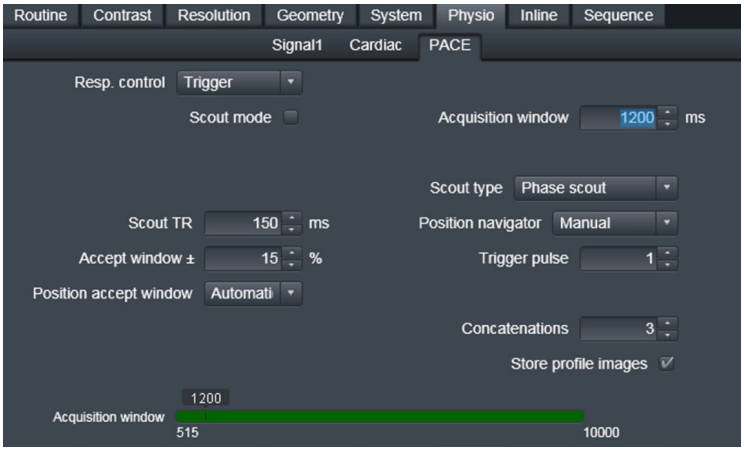
3.3.8 Reducing the acquisition duration (optional)

The acquisition duration is the acquisition time per breathing cycle. (For a detailed description, please refer to: (→ Page 43 *Learning/ imaging phase*) .) If the width of the red rectangles is larger than 1/2 of the breathing period (horizontal distance from maximum inspiration to maximum inspiration), the measurement must be terminated and the acquisition duration reduced. In this manner, artifacts can be avoided.

The acquisition duration is available as a tool tip of the measurement time.

Modifying the acquisition window

On the **Physio PACE** parameter card you can limit the acquisition duration with the help of the **Acquisition window** parameter. Two modes are to be distinguished: **Manual** and **Automatic**.



Using the Manual mode

In the **Manual** mode, you can enter a fixed value for the acquisition window.

3D measurements only support the **Manual** mode.

1 From the **Select acquisition window** list: Select the **Manual** mode.

2 Enter the new value for the **Acquisition window**, for example, 1300 ms.

This value is limiting the maximum acquisition duration.

If you choose the acquisition window significantly shorter than one third of the individual breathing period, this can lead to unnecessarily long acquisition times.

To ensure a robust triggering, acquisition duration should be no more than one third of the individual breathing period of the patient.

The individual breathing period of the patient is displayed in the left corner of the Inline Display during a current measurement or as a tool tip of the **Acquisition window** parameter (if prior to that a PACE measurement had been performed).

Using the Automatic mode

In the **Automatic** mode, you can enter the percentage of the individual breathing period.

1 From the **Select acquisition window** list: Select the **Automatic** mode.

2 Enter the new value for the **Acquisition window**, for example, 30%.

The concatenations are adapted automatically so that the acquisition duration is smaller or equal to the specified percentage of the individual breathing period. Therefore, the sequence adapts automatically to the individual breathing of the patient.

Modifying further measurement parameters

TSE sequences

- Increase the number of concatenations.

SPACE sequences

- Reduce the Turbo factor.

3.3.9 Performing a measurement with double triggering (optional)

Proceed as follows for a combined cardiac-triggered examination.

1 On the **Physio PACE** parameter card: Select the **Trigger** option under the respiratory control parameter.

2 Select the desired trigger signal on the **Physio Signal 1** parameter card (e.g. **ECG/Trigger**).

3 Set the other parameters (acquisition window, trigger delay) as usual.

3.3.10 Optional measurement parameters

In general you do not have to change the remaining parameters on the **Physio PACE** parameter card.

Accept window ±	Set the height of the yellow acceptance window in the Inline Display. There is no display during inspiration.
Position accept window	If **Automatic** has been selected, the system sets the center of the acceptance window during the learning phase. In the **Manual** mode, you can set the value in percent (%) under **Accept position**.
Accept position	Shift the center of the acceptance window between the mean end expiration (0%) and the mean end inspiration (100%).
Scout TR	The repetition time of the navigator, when the sequence tracks the patient's respiratory curve.
Store profile images	Store the repiratory curve as an extra series in the patient database.
Trigger pulse	For **n** value, **n – 1** respiratory cycles are omitted between neighboring gates. Normally, the parameter is set to a minimum to minimize the measurement time.

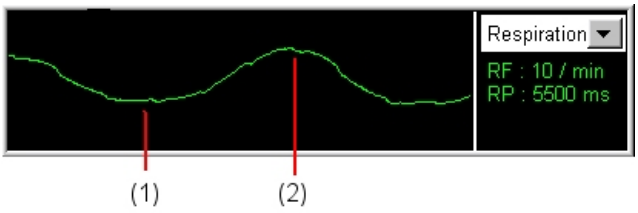
3.4 Performing examinations with respiratory triggering

3.4.1 Respiratory triggering

Respiratory triggering is used to keep artifacts caused by respiratory motion to a minimum. Data acquisition is performed during normal breathing.

Trigger: The trigger is the reference point in the physiological signal that releases data acquisition. It synchronizes respiratory motion and data acquisition.

Respiratory cushion: Respiratory motion is transferred to a respiratory cushion. The cyclic expansion or contraction of the thorax is displayed as a respiratory curve in the **Physio Display**. The respiratory signal rises during inspiration and falls off during expiration. It is used to generate the trigger signal as a function of the respiratory phase selected.



(1) End expiration phase

(2) End inspiration phase

Acquistion window: When using a respiratory cushion, selection of the acquisition window is of great importance. To minimize motion artifacts, you typically set the acquisition window during expiration. As soon as the respiratory signal falls below the threshold set, you start a partial measurement. The maximum duration of the partial measurement is set by the length of the acquisition window. When the respiratory curve falls again below the trigger threshold, you start the next partial measurement, etc. until all data have been fully acquired.

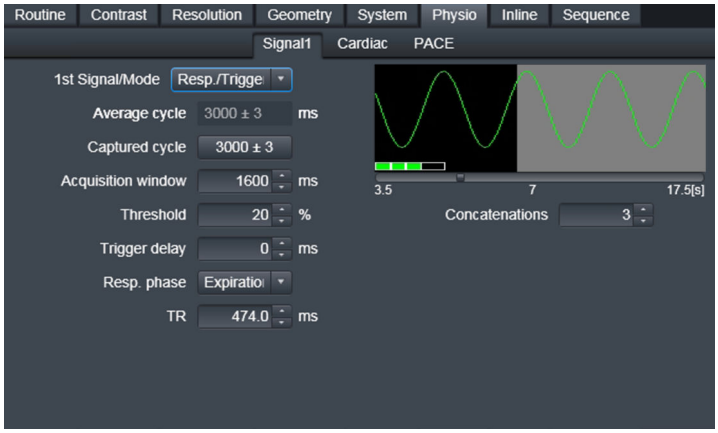
3.4.2 Setting the acquisition window

✓ Respiratory cushion has been attached to the patient

✓ Localizer has been measured

✓ Free-breathing protocol has been opened

The display of the respiratory signal on the **Physio Signal 1** parameter card facilitates correct setting of the acquisition window.



Acquisition window during expiration of the respiratory period.

- Select the acquisition window as large as possible to reduce the measurement time. However, to avoid motion artifacts, limit yourself to the exhaled, relative motionless area of the respiratory period.

The duration of the acquisition window is a compromise between reducing the examination time (large acquisition window) and the best possible insensitivity to motion artifacts (small acquisition window).

The duration of the acquisition window depends on the average respiratory period of the patient. It should include between 1/3 and max. 1/2 of the average respiratory period.

3.4.3 Performing T1-weighted measurements

Since the average respiratory period is typically between 4–6 seconds, measurement pauses of several seconds occur during which the system waits for the next respiratory period. While these measurement pauses facilitate acquisition of T2-weighted images, T1 weighting is difficult to obtain due to the relaxation of the magnetization.

gre sequence

The gradient echo sequence **gre** is suitable for this particular application. To ensure T1 weighting despite respiratory triggering, the measurements between the two acquisition windows are continued, however, without data acquisition. The number of measurements with data acquisition corresponds to the number of segments on the **Physio Signal 1** task card.

To keep the examination time as short as possible, the sequence automatically selects the largest possible number of segments for a given acquisition window.

1 If you would like to use saturation pulses, select the **Quick** saturation mode.

  The measurement time is reduced.

2 If your are using several averages, select the **Long term** averaging mode.

  Motion artifacts are suppressed.

3.5 Performing a dark lumen colonography

With dark lumen colonography, the interior of the intestines is shown as hypointense as compared to the intestinal wall. Intravenous contrast agent is added for increasing contrast.

3.5.1 Performing dark lumen colonography

✓ Patient has been positioned (→ Page 18 *Preparing dark lumen colonography*)

✓ Contrast injector is ready

1 Begin to fill the intestines with water.

2 Inject medication for relaxing the intestines.

Control measurement

- Check the filling and expansion of the large intestines by using a TrueFISP or HASTE sequence.

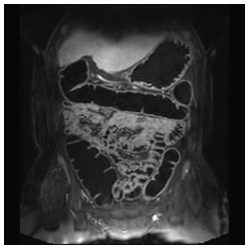
Measuring pre-contrast images

- As soon as the intestines are filled and sufficiently expanded, perform a pre-contrast measurement (3D VIBE sequence) with respiratory triggering.

Measuring post-contrast images

1 Inject contrast agent.

2 Repeat the 3D VIBE sequence 75 seconds after administering contrast agent.



Dark lumen image.

Subsequently, you are able to perform a 3D image evaluation (MPR, MIP, VRT).

3.6 Performing fast T1 mapping

Fast T1 mapping uses a VIBE measurement with variable flip angles. Corresponding protocols are provided in the **Dot Cockpit** (Abdomen/Library/MapIt). To calculate T1, this technique utilizes spoiled gradient echo (GRE) measurements, each identical except for different flip angles. *syngo* MapIt calculates T1 on a pixel-by-pixel basis. To improve the accuracy of T1 mapping for abdominal imaging, *syngo* MapIt is combined with a B1 correction.

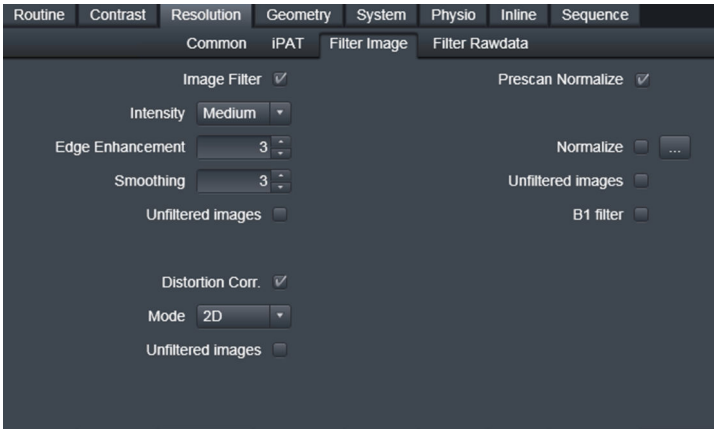
The B1 mapping has to be performed prior to the T1 MapIt measurement. The FoV and slice coverage have to be identical for both measurements. For this reason, a copy reference is set in the corresponding Siemens protocol. Prerequisite: The B1 and T1 mapping protocols have to be moved simultaneously into the queue.

3.6.1 Performing B1 mapping

1 Use the B1 mapping sequence to determine the actual flip angle for each voxel.

In addition, **Prescan Normalize** can be performed to reduce the inhomogeneities due to local coils in the anatomical images.

2 Select **Prescan Normalize** in the **Resolution Filter Image** parameter card.



B1 correction for T1 MapIt cannot be combined with TimTX TrueShape B1 Shimming (only valid for pTx-Systems).

For further information, please refer to Operator Manual - TimTX TrueShape.

3.6.2 Performing T1 mapping

1 For T1 mapping, use the VIBE sequence.

2 Select **T1 map** in the **Inline MapIt** parameter card.

T1 mapping allows more than two measurements with individual flip angle for each measurement separately. This improves the T1 value accuracy in addition to the B1 correction. In addition, T1 can be determined within several breathhold measurements.

3 Enter the number of measurements to be performed.

4 If the **Auto angle calculation** is switched **On**, the flip angles are chosen automatically, based on the T1 values defined in the protocol. If you want to freely enter **Flip angle** values, switch off **Auto angle calculation**.

3.7 Abdomen Dot Engine

The **Abdomen Dot Engine** covers MR examinations of the liver, the biliary and pancreatic system, and the kidneys (morphology). The reduction of organ motion artifacts is essential for examinations of the abdominal region. Techniques for reducing respiratory artifacts include measurements during one or several respiratory breathholds as well as measurements with navigator triggering during normal breathing.

The Dot Engine user interfaces shown in this operator manual are examples only. The actual guidance texts and the design may be slightly different on your system.

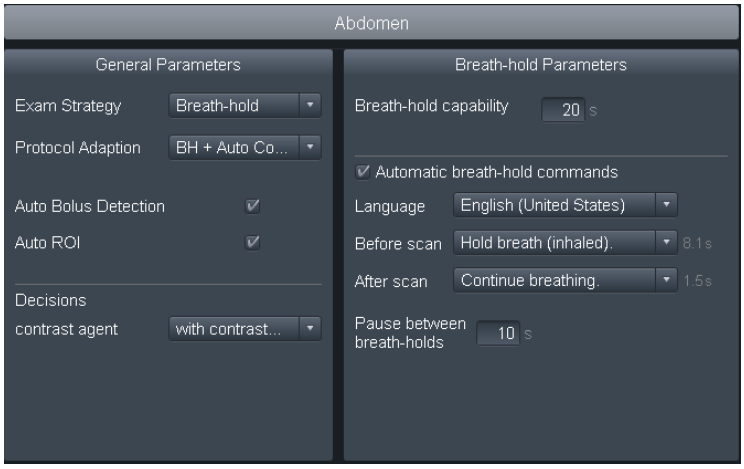
3.7.1 Planning the examination and measuring the localizer

✓ Patient has been registered

✓ **Abdomen Dot Engine** has been selected

Adapting the examination to the patient

After registration, the **Patient View** opens automatically. The default examination parameters are loaded.



In the **Patient View** you select a suitable examination strategy, activate automatic functionalities, and adapt the breathhold parameters to the patient's need. In addition, you can decide whether contrast agent is to be administered or not. The pending protocols of the measurement queue are updated upon your selection.

Selecting the examination strategy

- From the list: Select a suitable **Exam Strategy** for the patient.

Breath-hold	Measurements are performed with single/multi-breathhold techniques. This means that reduced measurement times are achieved resulting in reliable and reproducible image quality. A mostly automated liver dynamic examination is included. During the liver dynamics, a single-shot MRCP measurement is performed.
Resp synchronized	Some measurements are performed in free breathing with navigator triggering (PACE), with higher resolution as its focus. A mostly automated liver dynamic examination is included.
Motion-insensitive	For uncooperative/moving patients, motion-corrected protocols and triggering are used. Liver dynamics are not included. Instead, a pre- and a post-contrast measurement is performed.

In the following example, the strategy **Breath-hold** is selected.

Setting the breathhold parameters

1 Enter the **Breath-hold capability** of the patient.

The sequence parameters of the breathhold protocols will be adapted automatically.

2 If you want to use **Automatic breath-hold Commands** throughout the entire examination, activate the checkbox and set the timing and language for the commands. The language of the breathhold commands is freely selectable and does not depend on the language of the system.

You are also able to set the breathhold commands individually for each protocol (in the **Step properties** dialog window).

Calculating the FoV automatically

- Select **Auto Coverage** in the **Protocol Adaption** drop-down menu.

  In case of breathhold examinations, select **Auto Coverage + BH**.

Activating automatic functionalities

- Activate the automatic functionalities, if necessary.

Auto ROI	Position of the ROI is suggested by the system.
Auto Bolus Detection	Automatic detection of the contrast bolus arrival in the region of interest and proper start of the arterial phase measurement.

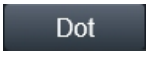
Using contrast agent

- Select **with Contrast agent** from the drop-down menu if contrast agent is to be used.

Contrast agent protocols will be added in the measurement queue.

Accessing the Patient View

You can access the **Patient View** at any time during the examination.



1 To open the view, click the icon.

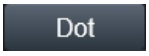
2 To confirm the settings and close the view, click the icon.

Modifying parameters of measured protocols

Changes in the **Patient View** only apply to pending protocols in the measurement queue.

1 To change the status of a protocol from measured to pending, select the measured protocol.

2 Select **Rerun from here** from the context menu (right-click with the mouse)



3 Open the **Patient View**.

or

4 Select **Rerun from here with** from the context menu (right-click with the mouse).

The **Patient View** opens automatically.

5 Enter the requested modifications.

Starting the measurement of the localizer

- Confirm the patient-specific settings.

The sagittal, coronal and transverse localizers are measured and displayed.

Subsequently, T2-weighted coronal images are measured and displayed. Breathhold commands are output before and after the measurement.

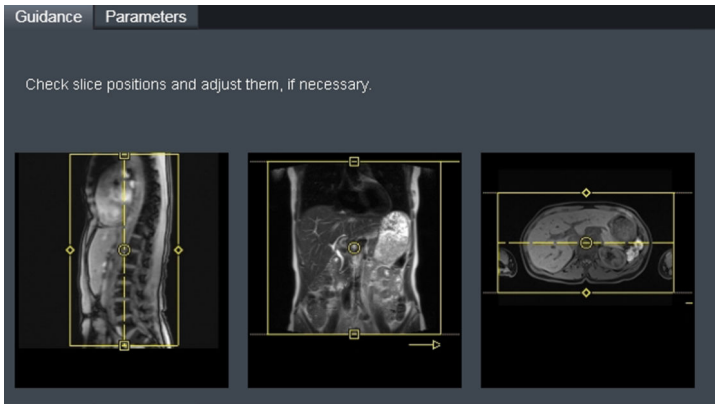
The T2-weighted transverse protocol opens for planning.

3.7.2 Planning transverse measurements

✓ Localizer images and T2-weighted coronal images are displayed

Within this step, you define the FoV and the slice position for all subsequent transverse measurements.

In the GSP segments, the system makes a proposal for the FoV and the slice positioning.



1 Check the FoV and the slice position in the GSP segments and adapt them, if necessary.

2 If necessary, select the **Parameter** view to adapt additional settings for the transverse measurements.

To increase lesion conspicuity, you may insert a diffusion-weighted measurement in free breathing mode after the T2-weighted transverse measurement. For this, select the corresponding clinical decision point **Diffusion** in the measurement queue. Result images show the b values and the ADC maps.

3 Start the measurement.

After measuring the T2-weighted transverse images, the pre-contrast protocol opens.

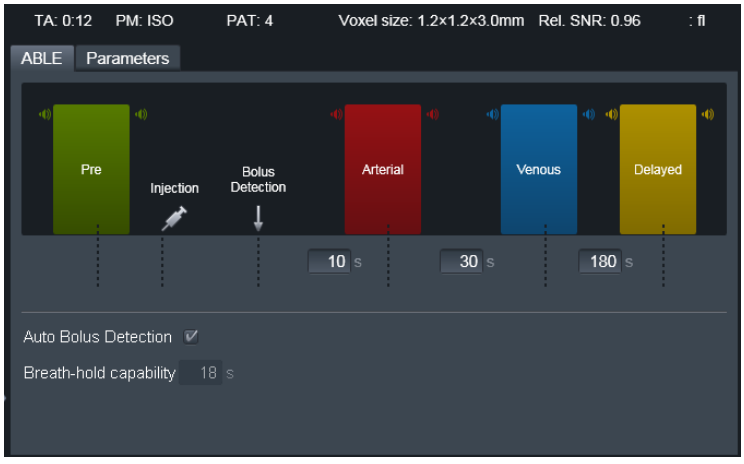
3.7.3 Planning liver dynamics with Care Bolus

✓ T2-weighted transverse images have been measured

✓ Care Bolus workflow has been selected

Setting the dynamic parameters

The liver dynamic measurement consists of four T1-weighted transverse VIBE-DIXON measurements with breathhold technique. Within this step, you define the presets for all subsequent dynamic measurements.



1 Check and adapt the preset delays between the predefined phases, if necessary.

2 Activate or deactivate **Auto Bolus Detection**.

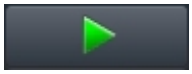
Even while **Auto Bolus Detection** is activated, you can manually start the subsequent arterial phase with **Stop&Continue** in the **Inline Display**.

If **Automatic breath-hold commands** is deactivated, the user is informed by the system when to give the breathhold commands.

Starting the dynamic measurements

1 Start the pre-contrast measurement.

If **Automatic breath-hold commands** is deactivated, the system waits for the first breathhold command. For the following breathhold commands, the system informs the user when to give the breathhold command.



2 Apply the breathhold command and click this icon.

If **Automatic breath-hold commands** is activated, all breathhold commands are given by the system.

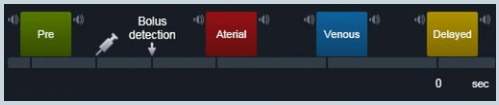
Check the pre-contrast images in the GSP. If the quality is insufficient, proceed as follows:

3 Select the pre-contrast step and then select **Repeat & Open** from the context menu.

Adapt the protocol parameters and start the measurement.

The pre-contrast images are measured. The Care Bolus protocol opens.

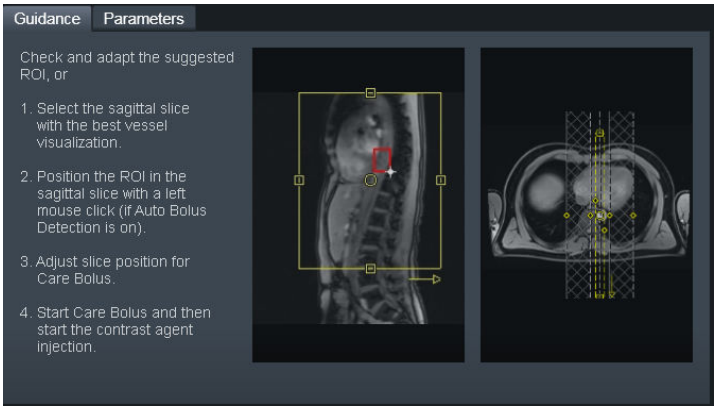
Monitoring the dynamic measurements: In the monitoring window on the left-hand side of the screen, you can follow the progression of the dynamic measurements.



Positioning the slice and ROI for the Care Bolus

✓ Pre-contrast images have been measured

You use the Care Bolus protocol to monitor the contrast agent inflow in real time on the **Inline Display**.



1 Check and adapt the suggested ROI positioning.

or

2 Select an adequate sagittal slice for best vessel visualization.

3 Position the ROI in the sagittal slice by clicking in the GSP (**Auto Bolus Detection On**, only).

4 Adjust the slice position for the Care Bolus.

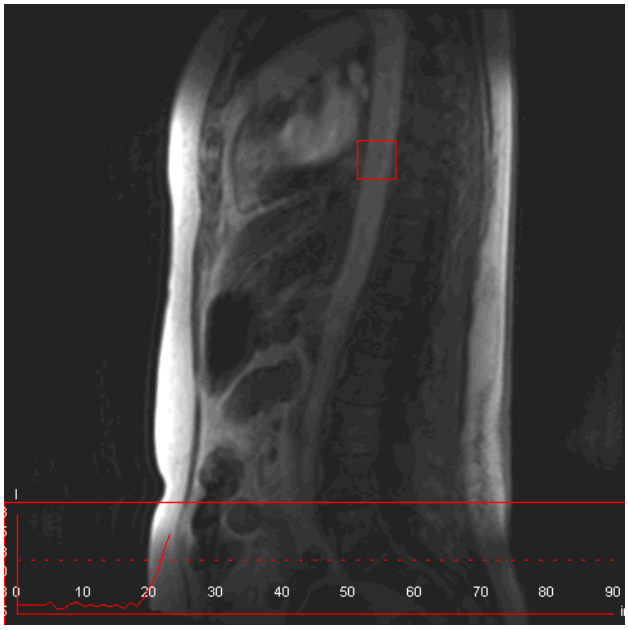
Starting dynamic contrast agent measurements

✓ Care bolus slice has been positioned

✓ ROI for bolus detection has been positioned

1 Start the Care Bolus measurement.

The main vessel for bolus monitoring is displayed in the **Inline Display** at an image rate of approximately 1 image/sec.



2 Begin with the contrast agent injection as soon as images appear in the **Inline Display**.

The bolus arrival is monitored in the ROI with **Auto Bolus Detection On** and visualized via a corresponding signal curve.

A **Stop&Continue** icon is available in the icon bar for manual start or override of the automatic start of arterial phase measurement.

3 With **Auto Bolus Detection On**, you may check if contrast agent arrival is detected in time.

4 Override with the **Stop&Continue** icon if the automatic bolus detection fails.

– or –

With **Auto Bolus Detection** **Off**, manually start the arterial phase measurement with the **Stop&Continue** icon upon visual detection of bolus arrival in the **Inline Display**.

The consecutive measurement of arterial, venous, and delayed phase is performed automatically. The delay time settings are taken into account. Breathhold commands are output before and after each measurement, if **Automatic breath-hold commands** is activated. Otherwise you will be informed when to give voice commands.

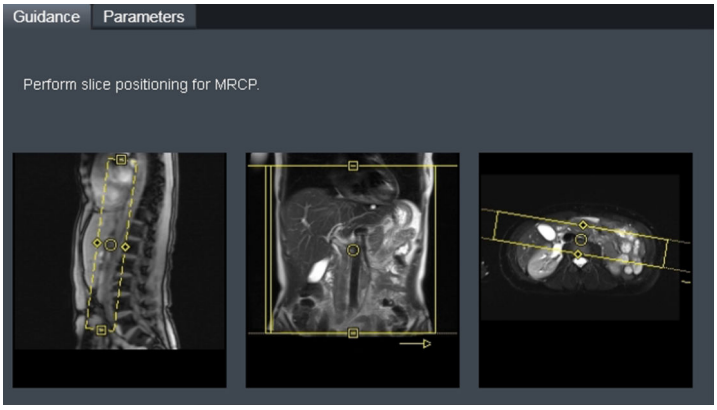
The following image data are generated:

- Series of original data of all phases
- Subtraction series

Performing MRCP and post-contrast measurements

✓ Measurement of the arterial phase is running

You can perform a single-shot T2-weighted coronal measurement for MRCP between the venous and the delayed phase. You position the slices for MRCP between the arterial and delayed phase and start the measurement such that it is finished before the start of the delayed phase.



1 Position the slices for MRCP.

2 Confirm the settings.

The MRCP measurement is started automatically after completion of the venous phase.

As soon as the measurement of the delayed phase is completed, a T1-weighted coronal VIBE-DIXON measurement with breathhold complements the preceding transverse measurements, allowing a detailed analysis of the anatomy in two planes.

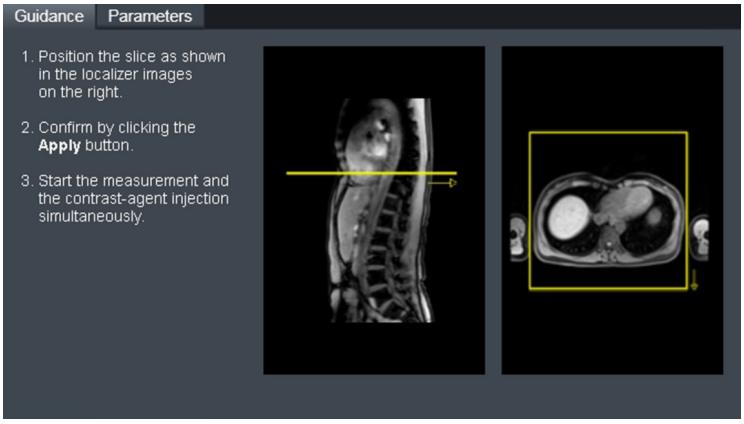
3.7.4 Planning liver dynamics with Test Bolus

Test bolus: Prior to the actual post-contrast measurements, you inject a small amount of contrast agent at the same injection rate as for subsequent measurements. A rapid 2D measurement, typically 40–80 images with a temporal resolution of one image per second, is used to view the passage of the test bolus in the vicinity of the target vessel.

Planning and measuring the test bolus

✓ Test Bolus workflow has been selected

✓ Pre-contrast images have been measured



1 On the localizer: Position the test bolus slice axially on the aorta on the level of the diaphragm.

2 Complete the slice positioning.

The **Exam paused** dialog window opens.

3 Start the test bolus measurement with **Continue** and **simultaneously** inject the contrast agent.

4 Use the same injection scheme as that used subsequently with the actual post-contrast measurements.

The test bolus images are displayed.

Determining the transit time

To determine the transit time, you draw a region of interest (ROI) in an artery (aorta) of the test bolus images. The signal-time curve for the arterial phase is subsequently computed.

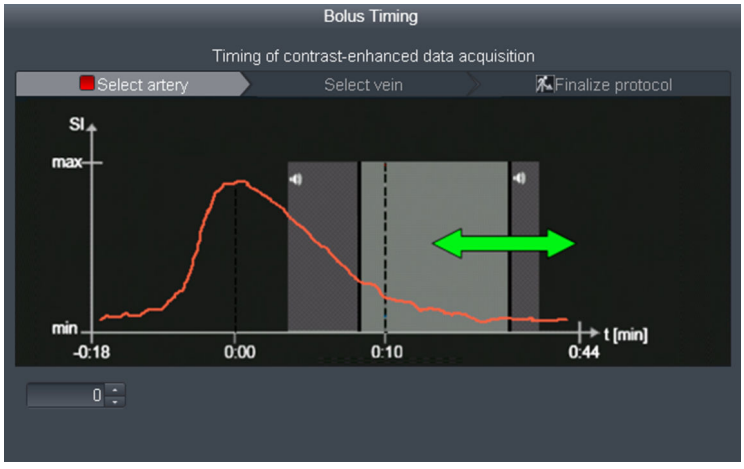
✓ Test bolus images have been measured

1 Scroll through the test bolus series and select a suitable test bolus image.

2 Draw a ROI by clicking an artery.

The signal-time curve for the arterial phase is computed and displayed. The system makes a proposal for the data acquisition window, so that the center of the k-space of the arterial phase is acquired at the contrast agent arrival in the target organ (liver).

For a description of configuring the bolus timing, please refer to:
(→ Page 75 *Configuring the bolus timing*)



The quality of the curve depends on the physiology of the individual patient. If the curve is not satisfactory, simply draw new ROI.

Setting the timing parameters and performing post-contrast measurements

1 If necessary, adapt the position of the data acquisition window in relation to the curve by moving it with the mouse.

2 Check for optimal vessel contrast (the center of the k-space is acquired at maximum vessel contrast).

3 Check the duration of the automatic breathhold command (if selected in the **Patient View**).

4 Complete the planning.

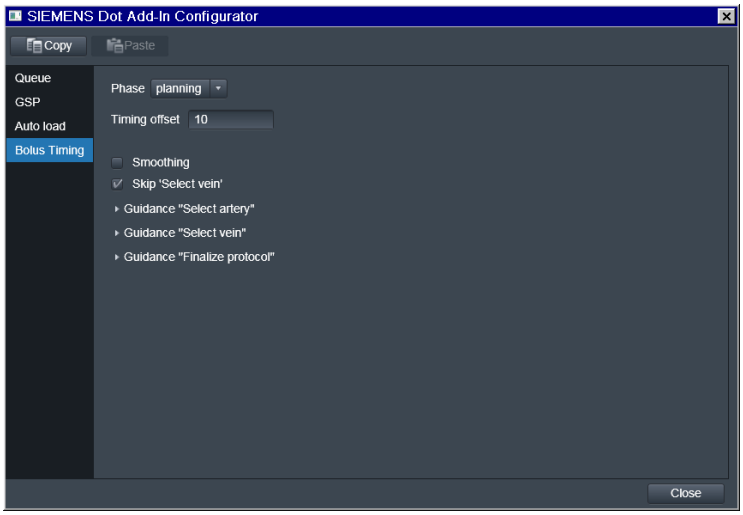
If selected, breathhold commands are output before and after the measurement. The post-contrast images are displayed.

Configuring the bolus timing

Using the **Bolus Timing Dot Add-In** you can configure the position of the data acquisition window relative to the peak of the signal time curve.

Setting the acquisition window

On update of the arterial signal-time curve, the system adapts the position of the data acquisition window relative to the signal-time curve.



- Set the **Timing offset** to **0 s**, to position the data acquisition window so that the center of the k-space is acquired at the peak of the arterial phase.

If you set the **Timing offset**, for example, to **10 s**, then the data acquisition window is shifted accordingly.

3.8 Liver evaluation (LiverLab)

CAUTION

Evaluated parameter values are only estimated!

Wrong diagnosis

- As the given protocol settings are preconfigured but not standardized always consider that the evaluated parameter values are only estimated. Therefore you are responsible for the interpretation of such estimated results.

Through advanced signal modeling and parameter fitting algorithms, both HISTO and multi-echo VIBE Dixon estimate fat signal fraction and transverse relaxation largely independent of each other, and hence largely independent of measurement parameters in appropriate ranges.

Nevertheless, the parameter estimation may be confounded by additional signal effects and/or inappropriate measurement parameters, refer to (→ Page 82 *Settings for multi-echo VIBE Dixon evaluation*) and (→ Page 83 *Checking the evaluation results*) below. The operator is responsible for the interpretation of results.

The **Abdomen Dot Engine Liver Eval CB** provides a workflow for examining the hepatic fat and iron overload as important biomarkers for various disease processes. For this purpose, two evaluation methods (HISTO and multi-echo VIBE Dixon) are available.

The workflow corresponds mainly with the **Abdomen Dot Engine CB**. After confirming the **Patient View** and measuring the localizer, the pre-measurement is performed. The pre-measurement consists of:

- automatic liver segmentation
- pre-evaluation which provides a first overview of possible overload in the whole liver

After the subsequent liver dynamics measurements, the evaluation is performed. The evaluation includes:

- spectroscopy (HISTO) and image-based (multi-echo VIBE Dixon) methods for reproducible evaluation
- inline ROI analysis of image-based parameter maps
- inline evaluation reports

The **HISTO** evaluation is an easy to use spectroscopy technique based on single voxel spectroscopy. The advantages are:

- complete data acquired in one breathhold
- accurate fat signal fraction evaluation due to integrated T2 correction
- significant correlation between the R2 of water and the amount of iron

The advantages of the image-based **multi-echo VIBE Dixon** evaluation are:

- spatially resolved whole liver coverage
- simultaneous estimation of fat signal fraction, and R2* as a measure of iron. Phantom measurements show a reproducibility better than +/- 1.6 % for fat signal fraction and +/- 6 s^{-1} for R2* (based on provided Siemens protocols).
- correction for transverse relaxation effects

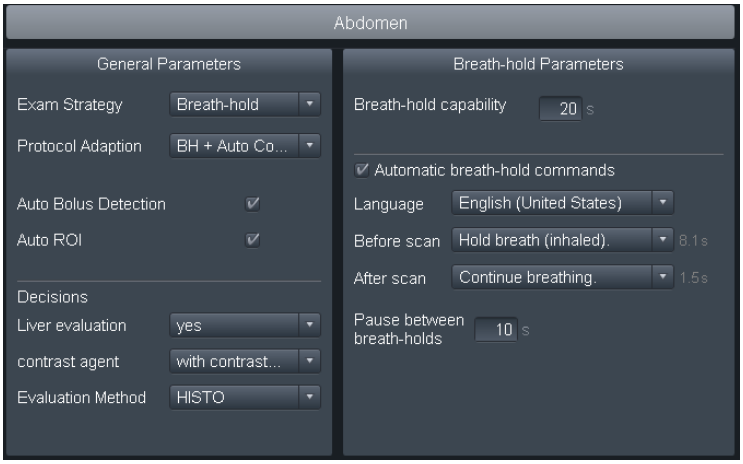
3.8.1 Planning the examination

✓ Patient is registered

✓ **Abdomen Dot Engine Liver Eval CB** is selected

Adapting the examination to the patient

After registration, the **Patient View** opens automatically. The default examination parameters are loaded.



In the **Patient View** you select a suitable examination strategy, activate automatic functionalities, and adapt the breathhold parameters to the patient's need. The pending protocols of the measurement queue are updated upon your selection. In addition to the **Abdomen Dot Engine** following decisions for liver evaluation can be selected.

1 Select **Yes** in the **Liver evaluation** dropdown menu.

2 Select the **Evaluation Method**: **HISTO**, **multi-echo VIBE Dixon** or **Both**.

3.8.2 Settings for pre-evaluation

✓ T1-weighted Dixon protocol for evaluation is selected

✓ **Contrast Common** parameter card is opened

For performing pre-evaluation the following settings are required at the pre-contrast step:

- dual echo Dixon enabled (**TE 1** and **TE 2** for Opposed phase/In phase)
- only **Report** enabled under **Dixon evaluation**

The pre-evaluation determines:

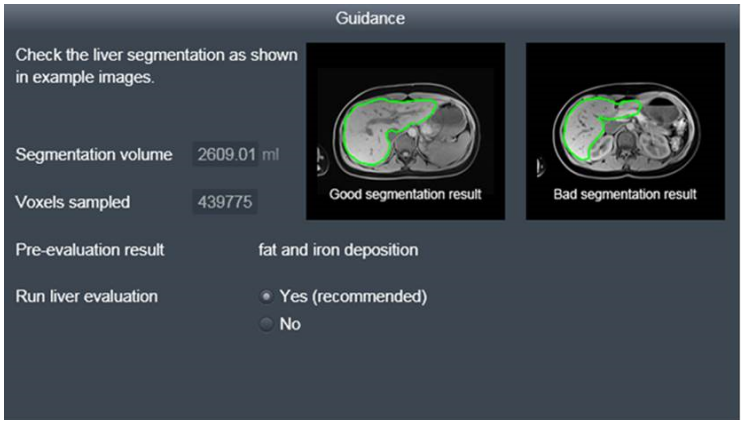
- segmented liver volume
- ROI or HISTO-voxel position
- recommendation for more detailed tissue characterization (fat deposition, iron deposition, fat and iron deposition, normal, unclear) based on dual-ratio Dixon discrimination of fat/water and in-phase/opposed-phase signal ratios

3.8.3 Checking the pre-evaluation report

After the liver dynamics measurement (ABLE) and the T1-weighted coronal VIBE-DIXON measurement, the queue is halted at the decision point **Evaluation**. Images of the segmented liver are displayed in the right segment of the GSP. In the **Guidance View**, the results of the pre-evaluation are displayed and the selection for **Run liver evaluation** is pre-configured.

✓ **Liver evaluation** has been selected in the **Patient View**

✓ pre-evaluation has already been performed



1 Check the liver segmentation in the GSP as shown in the guidance images.

2 Based on the pre-evaluation result, decide whether to run liver evaluation.

By clicking **Yes**, the **Evaluation method** selected in the **Patient View** will be subsequently performed.

3.8.4 Performing the evaluation

The evaluation measurement depends on the selected **Evaluation method** in the **Patient View**. In the following, the **multi-echo VIBE Dixon** evaluation will be described.

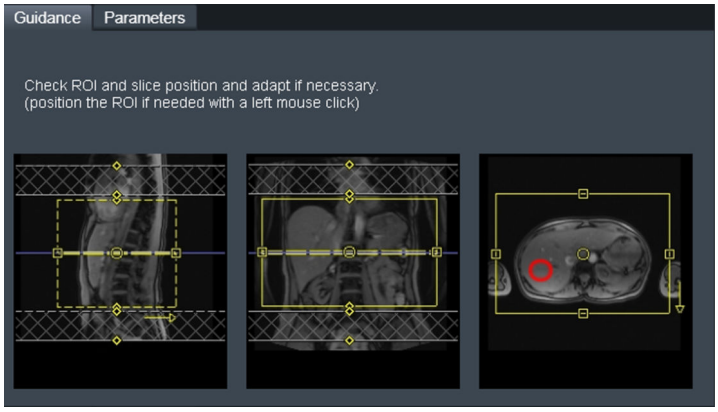
✓ **Evaluation Method** is selected in the **Patient View**

✓ **Run liver evaluation** is selected in the **Guidance View**

Liver evaluation can also be activated by selecting **Yes** at the **Evaluation** decision point in the queue.

Adapting the ROI and the slice position

A ROI is provided for inline analysis of the parameter maps. The position of the ROI is preset by the pre-evaluation, and can be adapted in the GSP subsequently.



1 Check the ROI and the slice position in the GSP.

2 If necessary, adapt the position and the size of the ROI with the mouse.

For **HISTO** evaluation, check and adapt the voxel position, if necessary.

Position the ROI/voxel on liver parenchyma, avoid positioning on large vessels and border areas of the liver.

3.8.5 Settings for multi-echo VIBE Dixon evaluation

✓ **Contrast Common** parameter card is opened

The following settings are required at the multi-echo VIBE Dixon evaluation step:

- multi-echo VIBE Dixon enabled (6 echoes)
- for **Dixon evaluation** the options **Fat fraction**, **Water fraction**, **T2***, **R2*** and **Report** may be selected

For the evaluation of fat and iron deposition **Fat fraction**, **R2*** and **Report** are recommended.

To avoid T1 bias, the flip angle of multi-echo VIBE Dixon protocols must be low, for example, 4° at TR 10 ms for 1.5 T. Higher flip angles may lead to over-estimated fat signal fractions.

Echo times for multi-echo VIBE Dixon must span the "opposed-phase" and "in-phase" conditions for water and fat, for example, 2.4 ms ... 4.8 ms for 1.5 T, and must reflect typical T2* times, for example, 5 ms ... 25 ms in the liver. The first two echo times should be near the opposed-phase and in-phase conditions. The use of Siemens protocols is recommended, which use 6 echoes between, for example, 2 ms and 10 ms at 1.5 T.

Echo times for HISTO must reflect typical T2 times, for example, 30 ms ... 100 ms for liver water signal. The use of Siemens protocols is recommended, which use 5 echoes between, for example, 12 ms and 72 ms at 1.5 T.

For high liver iron, transverse relaxation times shorten considerably, and measurement parameters may have to be adapted, in particular by selecting shorter echo times.

3.8.6 Checking the evaluation results

The evaluation results depend on the **Evaluation method** selected in the **Patient View**.

The quality of the parameter estimation can be assessed by the following criteria: Parameter maps and HISTO spectra should not display excessive noise. The parameter fit quality metrics should not deviate substantially from the optimum values: 0% fit error for multi-echo VIBE Dixon, typically below 5%, and R^2 (rsqr) 1.0 for HISTO, typically above 0.95. Results of lesser quality may be inaccurate.

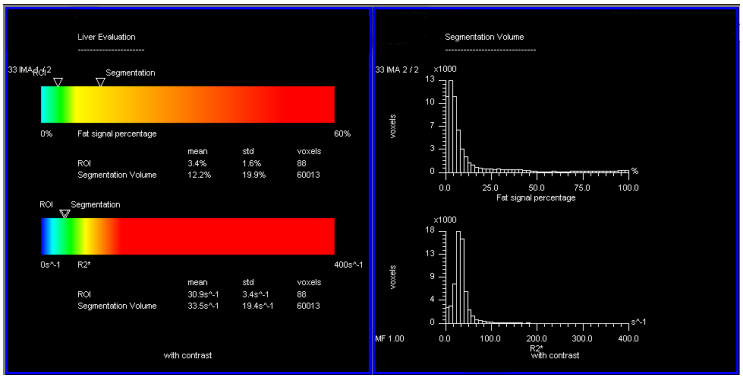
Confounding signal effects, for example, strong B0 inhomogeneity or susceptibility effects near air/tissue interfaces or implants, as well as high tissue iron levels, may cause the parameter estimation to become instable, leading to inaccurate results and water/fat swaps (→ Page 85 *Potential complete swap of fat and water*).

✓ **Viewing** task card is opened

Multi-echo VIBE Dixon evaluation

Parameter maps are calculated for the selected quantities, for example R2* maps in units of s^{-1} and fat signal fraction maps in %. Maps of signal fit error in % are calculated for quality control. The segmented liver and the position of the ROI are displayed within the series: Fat signal fraction, R2*.

A color bar report and a histogram are showing the results of the fat and iron evaluation by displaying fat signal fraction values and R2* values, as well as fit error values.



Example: Color bar report (left side) and histogram (right side) for multi-echo VIBE Dixon

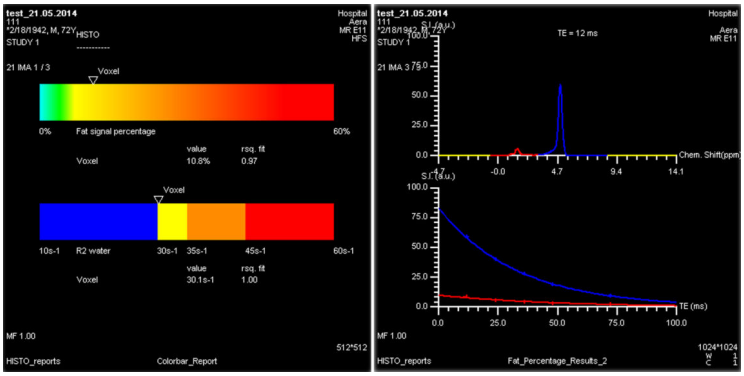
In the color bar report, the following values of fat signal fraction and R2*, as well as fit error, for the liver segmentation volume and the ROI are displayed:

- mean value (see also corresponding triangles above the color bars)
- standard deviation (std)
- number of voxels

In the histogram the following values are displayed:

- distribution of parameter values for the voxels of the segmentation volume

HISTO evaluation



Example: Color bar report (left side) and spectra (right side) for HISTO

The HISTO results include:

- The report sheet containing average fat signal fraction within voxel and R2 of water as text and color bar.
- The spectra for shortest echo time (TE=12 ms) and fitted curves for fat and water signal for quality control.
- A table containing fat signal percentage and R2 of water, the quality of fit and the individual echo values for water and lipid signals.

3.8.7 Potential complete swap of fat and water

WARNING

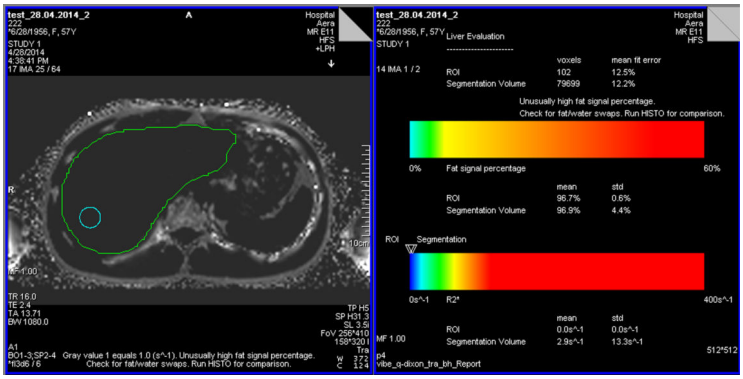
When using the DIXON method, water and fat swaps might occur!

Incorrect diagnosis

- Diagnosis should be confirmed by a second contrast and/or a different orientation.

If a complete swap of fat and water occurs, unusually high fat signal percentage values as well as a respective message are displayed in the corresponding maps.

In addition, the triangles in the color bar report are not displayed, if the value is outside the display range.



Example: Complete fat/water swap

1 Check for fat/water swaps.

2 Run **HISTO** evaluation for comparison.

3.8.8 Repeating the evaluation

You can repeat the evaluation with modified parameter settings or a different voxel/ROI position.

1 In case of **multi-echo VIBE Dixon** evaluation, select **Rerun from here** from the context menu.

2 In case of **HISTO**, drag the HISTO protocol from the **Program Card** into the queue again or select **Append** from the context menu.

3.9 Multinuclear MR Spectroscopy

3.9.1 General information

Multinuclear Spectroscopy enables measurements and evaluations for nuclei 3He, 7Li, 13C, 17O (3 T), 19F, 23Na, 31P, and 129Xe. In addition 31P protocols are available for special applications regarding muscles (1.5 T and 3 T), head (3 T), heart and liver (1.5 T).

The Multinuclear Spectroscopy option is not available for MAGNETOM Aera.

In the following, we discuss the characteristics of 31P MRS examinations for the muscles, heart, and liver. A full description of the general spectroscopy workflow is located under head examinations. (Refer to Operator Manual – Neuro.)

31P MRS of the muscle, heart or liver (31P head protocols for 3 Tesla only)

31P MRS acquires the most important energy carriers of the cell such as ATP, creatine phosphate and inorganic phosphate. Based on the relative concentrations of these phosphorous metabolites, information can be collected regarding the energy state of the cell.

The most important examination regions for 31P MRS include the muscles, the heart, and the liver. Various pathologies of these regions result in typical abnormalities as compared to healthy patients.

These abnormalities affect:

- the absolute concentrations of specific phosphorous metabolites
- the pH value
- the speed of recovery from stress

A physiologically triggered measurement via ECG signal is required for 31P MRS of the heart.

1H saturation

The 31P signal may be enhanced via saturation of the 1H spins (**Nuclear Overhauser Effect, NOE**). For this reason, in 31P measurements 1H saturation pulses are transmitted during the examination prior to the excitation pulses.

1H decoupling

When transmitting 1H decoupling pulses during 31P data acquisition, spin-spin coupling between the 31P and the 1H nuclei can be reduced. This results in simplified spectra and increased signal intensities for certain 31P signals.

3.9.2 Performing 31P MRS

Positioning the patient and coil

Siemens provides a Heart/Liver coil for 1.5 T systems. For 3 T systems, coils from other manufacturers are used.

In the following, the use of the Heart/Liver coil is described. Coils of other manufacturers are operated in a similar way.

The Heart/Liver coil has dual resonance, i.e., it is resonant for both 1H and 31P frequencies (63.6 MHz or 25.7 MHz; at 1.5 T) and can be toggled between the two resonance frequencies. (Coils from other manufacturers usually have dual resonance as well.)

The Heart/Liver coil is used for both acquiring 31P spectra as well as anatomical reference images. In addition, the coil is used for frequency adjustment and for shimming based on the 1H signal.

During X-nucleus measurements you must remove all 1H coils ("standard" coils, for example, for the spine) from the patient table. Only use the specific X-nucleus coils.

1 Position the patient.

2 In case of 31P MRS of the heart: Position the electrodes.
(→ Page 19 *Positioning the electrodes and PERU*)

3 Connect the Heart/Liver coil.

4 During registration, select a 31P MRS examination (under **Study**).

Planning the VOI

31P MRS protocols use either the FID or the CSI FID sequence. The signal is not localized by the FID sequence. It comes from the entire sensitive region of the coil. With CSI FID protocols, data acquisition is performed immediately after localization via slice selection and phase encoding.

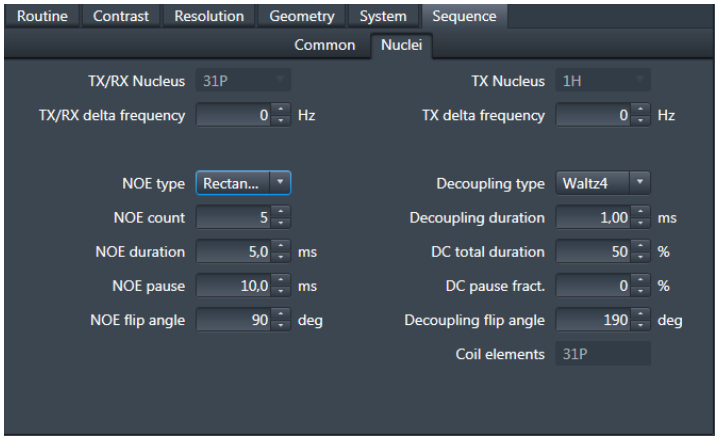
✓ 31P CSI FID protocol has been opened

◆ Due to the absence of a volume selection, select a sufficiently large FoV. Otherwise, aliasing artifacts might occur.

This applies to each spatial direction, because in the CSI FID sequence each spatial direction is resolved via phase encoding.

Setting the measurement parameters

1 Open the **Sequence Nuclei** parameter card.



2 Set the requested parameters. For a detailed description of the parameters, please refer to: Basic Manual - Spectroscopy.

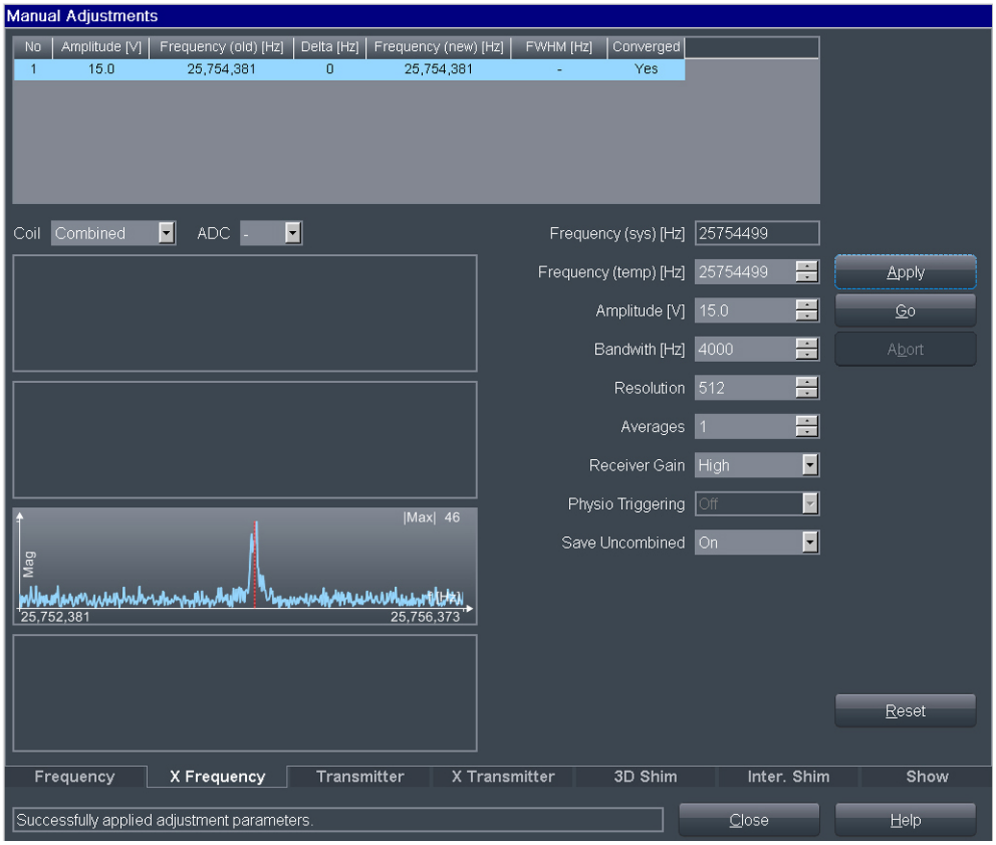
Adjusting the multinuclear frequency

You set the exact resonance frequency for the nucleus determined by the protocol.

1 Select **Options** > **Adjustments** from the main menu.

The **Manual Adjustments** dialog window is opened.

2 Select the **X Frequency** subtask card.



3 Set the adjustment parameters.

4 Ensure that the bandwidth is large enough to receive the signal.

To allow for sufficient signal detection, increase the number of averages for weak signals.

5 Start the frequency adjustment with **Go**.

6 Set the correct frequency by clicking on the acquired signal peak.

7 Transfer the frequency value to the system with **Apply**.

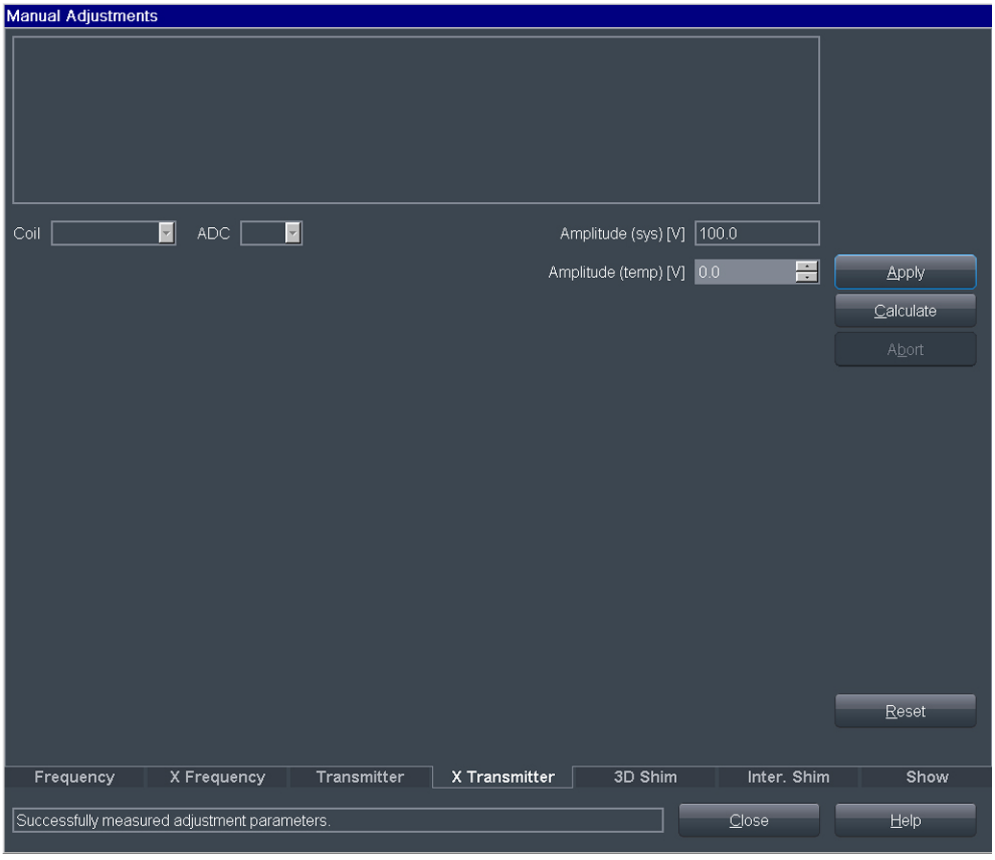
Adjusting the multinuclear transmitter

Since the signal strength is minimal, transmit adjustment measurements are not possible during multinuclear measurements. However, you can define a reference amplitude and apply it as the new system reference amplitude.

1 Select **Options** > **Adjustments** from the main menu.

The **Manual Adjustments** dialog window is opened.

2 Select the **X Transmitter** subtask card.



3 Define the new reference amplitude.

4 Transfer the amplitude to the system with **Apply**.

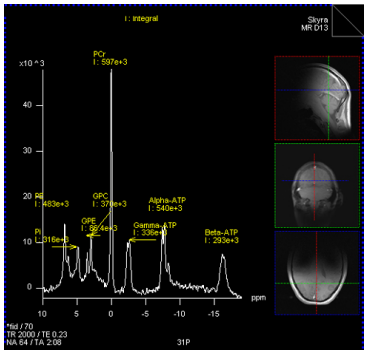
You can now begin with the spectroscopy measurement.

Evaluating spectra

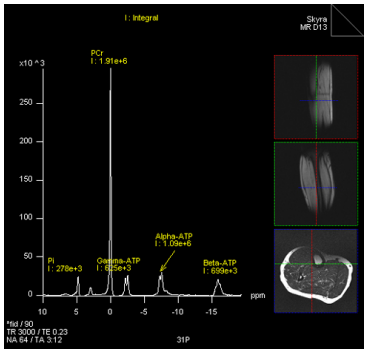
For a detailed description of evaluating MRS raw data, please refer to: Operator Manual- Neuro.

Examples of spectra

We are showing you applications of 31P MRS for the head and muscle.



Example: Spectrum of the head



Example: Spectrum of the muscle

4 Post-processing

4.1 Three-dimensional evaluation with *syngo* 3D

syngo 3D allows you to combine two-dimensional images to obtain a three-dimensional display of the region of interest. In this three-dimensional display, you can reconstruct new images, cut out individual regions and use a range of evaluation functions for special diagnostic problems.

Multiplanar reconstruction (MPR) is used to place slices in other orientations through the region of interest.

The maximum intensity projection (MIP) uses the most intensive gray-scale values of the images for reconstruction. For example, in contrast medium examinations, blood vessels are those structures that have the most intensive values.

The Volume Rendering Technique (VRT) is used for differentiating organs and tissue structures as well as for the colored 3D display of bones, tissues and organs.

MPR, MIP, and VRT reconstruction is applied, for example, to evaluate the images of dark lumen colonography examinations.

The following example describes some typical procedures for working with volume data sets, starting with multiplanar reconstruction (MPR).

4.1.1 Preparing the data

Loading the image data

✓ All images originate from one study of a patient

✓ All images have the same x/y coordinates and FoV

1 Select the data series or at least three images to be analyzed in the **Patient Browser**.

2 Click the **3D MPR** icon to start image processing as MPR.

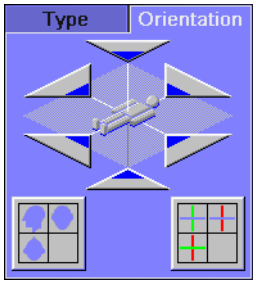
The 3D Series List is displayed.

If this dialog window appears, you have selected more than one series for processing or the series you transferred is not suitable for 3D display.

- Select the desired series in the 3D Series List or load a suitable series.

Optimizing the image display

Adjusting the image views



1 Adjust the image orientation in the segments by using the reference lines and the **Orientation** subtask card.

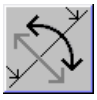
2 Activate **Rotate Images** to tilt and rotate the volume.

An orientation cube is displayed on all images. It indicates the anatomical orientation of the reconstructed image.

3 To display the relevant image area, zoom and pan the image.

4 Window the images to optimize their contrast and brightness.

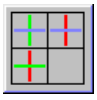
Aligning to the main axis of the organ



1 Activate **Free Mode** to allow rotation of the cut lines.

2 Set a view perpendicular to the main axis of the organ in one segment by rotating the corresponding reference lines.

3 Deactivate **Free Mode** to freeze the orientation.



4 Click the **Ortho Sync** icon to set the orthogonal view in the other segments.

4.1.2 Evaluating the volume data

Reconstructing MIP images

- Select a segment and set the **MIP** display mode with the icon.

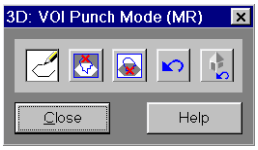
When a volume data set containing wideband noise is rendered using **MIP**, the resultant MIP image can show chessboard or stripe-like artifacts when viewed along one of the volume axes. To reduce these artifacts, select **Type** > **MIP Ultra Quality** from the drop-down menu.

Removing unwanted tissue

With a volume of interest (VOI), you extract a volume of diagnostic interest to you, thus limiting the volume to be reconstructed to a partial volume

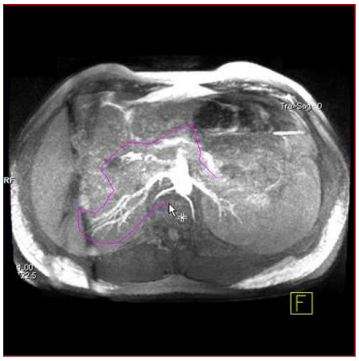
1 Set the **MIP** display mode in a segment suitable for VOI definition (e.g. the axial image).

2 Activate **VOI Punch Mode** with the icon in the **Settings** subtask card.



The **VOI Punch Mode** dialog window opens.

VOI drawing is activated automatically.



3 Draw a contour around the relevant image region. Double-click to finish the VOI definition.

4 Remove the part outside the VOI with the **Keep Inside** icon.

Now the effective VOI is displayed every time you switch to MIP or SSD display and activate the **Visibility Mask**.

Generating parallel ranges

With this option you generate slice images that are parallel to one another and perpendicular to the active segment.

1 Select the **MPR** mode and set up a view you require in one of the segments for positioning the cut lines.

2 Open the **Parallel Ranges** dialog window with the icon.

3 Enter the number and the thickness of images to be generated.

4 Define the position and orientation of the range with the reference lines drawn.

5 Start the calculation with **Start**.

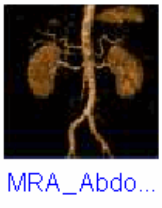
The series of parallel images is displayed in the lower right segment.

Reconstructing VRT images

Adjusting the VRT display

1 Select a segment and set VRT display mode with the icon.

2 To optimize the VRT display, open the **VRT Gallery** (right-click the **VRT** icon).



3 Select a suitable VRT parameter set.

The VRT volume image is displayed including the respective tissue class parameters of the selected parameter set.

You can change individual VRT parameters on the **VRT Definition** subtask card.

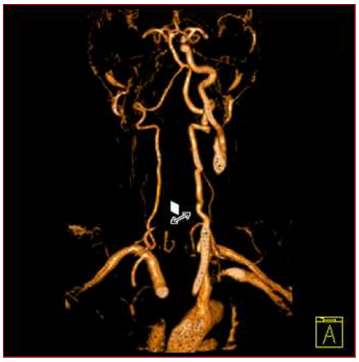
4 Set the **VRT** display mode in the other segments.

5 Window the images to include or exclude anatomy.

Using the clip plane tool

1 Activate **Free View** in the **Settings** subtask card, if necessary.

The clip plane part of the volume is displayed in the lower right segment.



2 Move the mouse cursor with the left mouse button pressed to push/pull the clip plane through the entire volume.

3 To change the tool that is being used, open the smart select context menu of the segment.

Reconstructing VRT thin images

1 Set **VRT thin** mode with the icon.

Volume rendering of thin slices out of the 3D data set is performed. The default slice thickness is 5 mm.

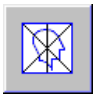
2 To modify the image thickness, right-click the **VRT thin** icon and change the thickness in the dialog window.

Generating radial ranges

With this option you generate radial tomographic images, thus simulating step-by-step rotation around a reference axis.

1 Select the appropriate image for positioning the radial cut lines.

For example, for a left to right rotation, select the axial image.



2 Open the **Radial Ranges** dialog window with the icon.

3 Enter the number of images and the angle between the images to be generated.

4 Define the position and orientation of the range with the reference lines drawn.

5 Start the calculation with **Start**.

The series of radial images is displayed in the lower right segment.

4.2 Fusing images

The **Fusion** function allows you to combine the results of different acquisition techniques or acquisitions performed at different times by overlaying them.

The following example describes how to align and visualize two different image data sets from a patient. Evaluation can be performed by displaying the images side-by-side or overlaid.

4.2.1 Preparing the data

Loading the data to 3D Fusion

✓ Reference and model series cover approximately the same examination range of the patient

Loading the reference series

1 Select the first data series to be analyzed in the **Patient Browser**.

2 Click the **3D MPR** icon to start image processing as MPR.

3 Window the images to optimize their contrast and brightness.

Loading the model series

1 Select the second data series to be analyzed in the **Patient Browser**.

2 Load the data to **3D Fusion** with the icon.

»

The 3D Series List is displayed.

If this dialog window appears, you have selected more than one series for processing or the series you transferred is not suitable for 3D display.

- Select the desired series in the 3D Series List or load a suitable series.

Aligning the image series

1 Open the **Fusion Registration** dialog window with the icon in the **Image** subtask card.

2 Activate **Automatic Registration**, if necessary.

3 For an accurate alignment of the loaded series, select the **Precise registration** option.

4 Start the registration with **Register**.

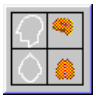
5 Save the registration matrix.

The next time you load two series, the last used matrix is automatically applied.

6 Merge the reference and the model series into a single data set with **OK**.

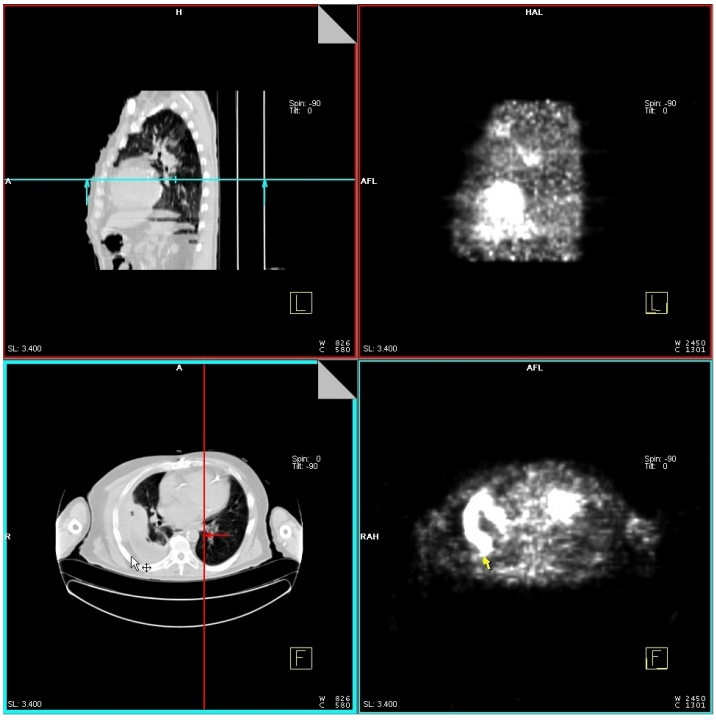
4.2.2 Evaluating the data

Displaying the images side by side

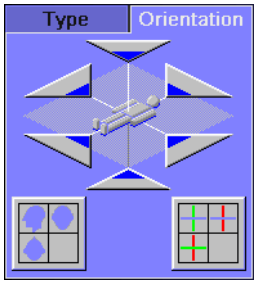


1 Activate the **Side by Side** mode with the icon in the **Image** subtask card.

The left image area is used to display the reference images and the right area for the model images.



2 Use the coupled mouse pointers to compare the data sets synchronously.

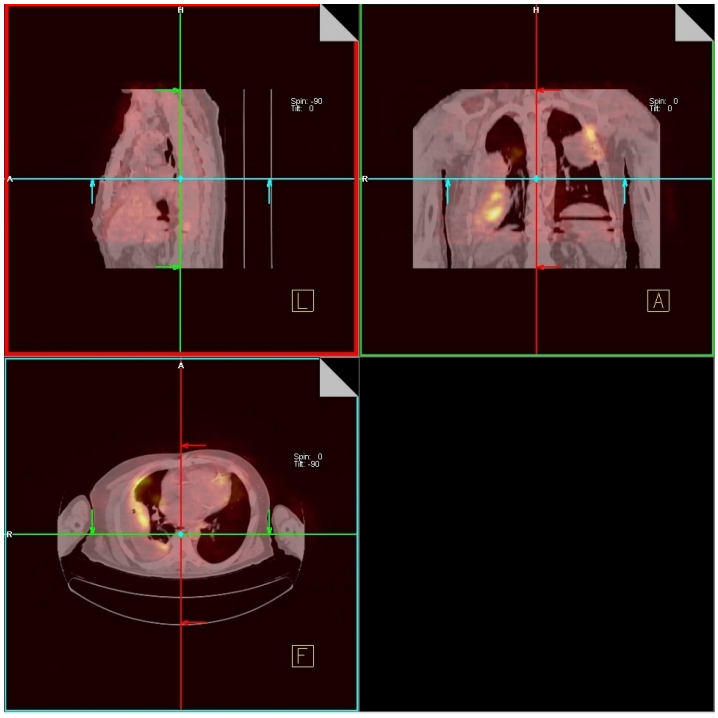


3 Adjust the image orientation by using the reference lines and the **Orientation** subtask card.

Displaying the images overlaid

1 Deactivate the **Side by Side** mode to return to the **Fusion** mode.

The two image data sets are displayed in different colors. The overlaid image data set is displayed in three orthogonal views.



2 To optimize the image display, open the **Fusion Definition MPR** dialog window with **Fusion** > **Fusion Definition**.

4.3 Statistical evaluation with Mean Curve

Statistical evaluation with **Mean Curve** provides information about signal changes as a function of time and place. The resulting curve plots the mean grayscale value against a selectable second variable (X-axis).

The following example describes how to examine the change of the average grayscale value in a region of interest (ROI) depending on slice position, trigger time, or image number.

4.3.1 Preparing the data

Loading the image data

✓ MR measurement series or post-processing series (dynamic analysis, MIP/MPR) are available. All series have the same orientation and spatial resolution.

Loading images for evaluation

1 Select the image data in the **Patient Browser**.

2 Transfer the data with **Applications** > **Mean Curve** to the **Mean Curve** task card.

All images are stacked in the 1st segment (evaluation segment). Sorting is applied **within** each series and **across** multiple series according to initial sort criteria. Image display and evaluation modes are set automatically:

	One series loaded: evaluation mode **within series**. The middle image (acc. to **within** sort criterion) of the stack is displayed.
	Multiple series loaded: evaluation mode **across series**. The middle image (acc. to **within** sort criterion) of the middle series (acc. to **across** sort criterion) is displayed.

Loading images to support evaluation (optional)

1 To facilitate contour determination of the evaluation region, drag & drop suitable images into the 3rd segment.

The image with the same value of the **within** sort criterion as the image in the 1st segment is displayed.

You may load, for example, the subtraction series or the MIP series. The images must have the same orientation and spatial resolution as the images in the 1st segment.

2 To facilitate localization of the evaluation region, drag & drop suitable images into the 4th segment.

You may load, for example, reference images of the exam or images showing the relevant region in a different orientation.

3 To move images into a different segment, reload them via drag & drop.

Optimizing the image display

1 Zoom/pan the images or invert the grayscale values with the corresponding entries in the **Image** menu.

2 Window the images to optimize their contrast and brightness.

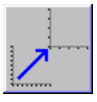
Determining the sorting for evaluation

By selecting the sort criteria, you establish the scrolling sequence in the first and third segments and define the X-axis parameter of the evaluation.

Possible applications of time-related sorting criteria:

- **Trigger Time**: physiologically triggered measurements, e.g. cardiac series
- **Echo Time**: multi-echo sequences, e.g. multi-echo spin-echo sequences
- **Normal Time**: dynamic and/or motion studies

The current sort criterion is displayed in the control area.



1 Open the **Scaling** dialog window with the icon on the **Tools** subtask card.

2 To select the sort criteria in the **within series** mode, use the **X-axis** tab card.

– or –

To select the sort criteria in the **across series** mode, use the **Sort** tab card.

In the **across series** mode, the multiple series are sorted via the sort criterion of the X-axis (**across**). The images within each series are sorted according to the **within** sort criterion.

4.3.2 Defining the evaluation region

You define the regions for statistical evaluation by drawing ROIs in a suitable starting image in the 1st or 3rd segment. The ROIs are then propagated to the other images.

Searching an image for ROI positioning

- Display the evaluation region by scrolling in the 1st or 3rd segment.

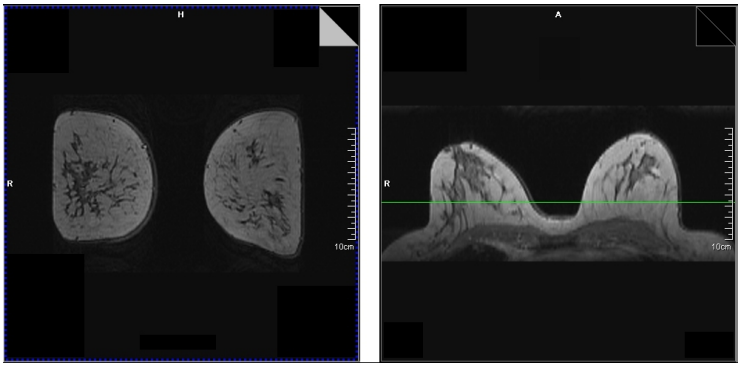
  Upon scrolling in one segment, the other segment displays the image with the same value of the **within** sort criterion.

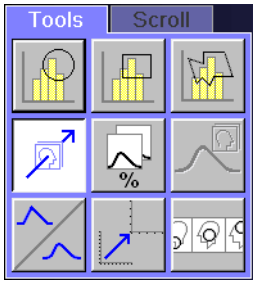
The **across** sort criterion is considered when scrolling from series to series in the 1st segment. The image with the same value of the **within** sort criterion is displayed. If no such image is found, the corresponding series will be skipped.

– or –

Navigate to a suitable image by moving the cut line in the reference image (4th segment).

The 1st and the 3rd segments display the images with positions that best match the position of the cut line.





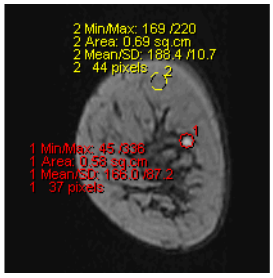
Drawing ROIs

All tools for ROI definition are available on the **Tools** subtask card.

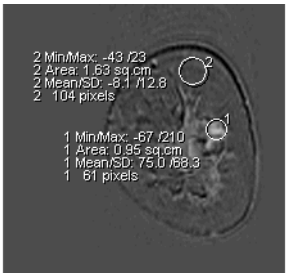
- Draw up to four ROIs in the starting image in the 1st or 3rd segment.

  The ROIs of the first segment are displayed automatically in the third segment and vice versa.

(1)



(2)



(1) ROIs in 1st segment

(2) ROIs in 3rd segment

If the slice positions in the segments differ, the ROIs in the 3rd segment are displayed in white with a solid line.

Adapting and propagating ROIs

ROIs are propagated to the images displayed during scrolling or to images that are not displayed when starting the evaluation. As the default setting, any change of an ROI in one image is reproduced in the other images involved (**Static ROI** mode).

1 To enable individual ROI modification, activate the **Dynamic ROI** mode with the icon.

2 Scroll through the images in the 1st or 3rd segment and check if the ROIs match the anatomy to be evaluated.

3 Correct the size and position of the ROIs, if necessary.

If the **Static ROI** mode is activated, the (modified) ROIs are propagated to all other images. Already existing ROIs are overwritten.

If the **Dynamic ROI** mode is activated, the (modified) ROIs are propagated to the images in the scrolling direction. Already existing ROIs remain unchanged.

You can remove a ROI with the **Del** key. The ROI is deleted in all images regardless of the active ROI mode.

4.3.3 Performing the evaluation

The following modes can be selected for evaluation:

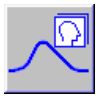
- **Absolute** evaluation (default setting): The signal intensity in the ROIs is assigned to the Y-axis.
- **Relative** evaluation: The difference between the signal intensity and a reference value as well as the ratio of the difference to the reference value are assigned to the Y-axis.

Relative evaluation is used, for example, to evaluate the change of signal intensity in contrast-phase images with respect to the pre-contrast images.

Switching to relative evaluation

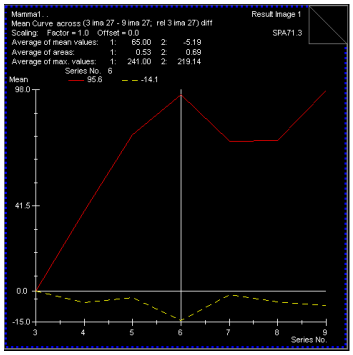
1 Select the **Relative** evaluation mode with the icon on the **Tools** subtask card.
2 Select the reference image (**within** mode) or the reference series (**across** mode) in the dialog window displayed.
3 To exclude the reference image or series from evaluation, uncheck the corresponding checkbox.

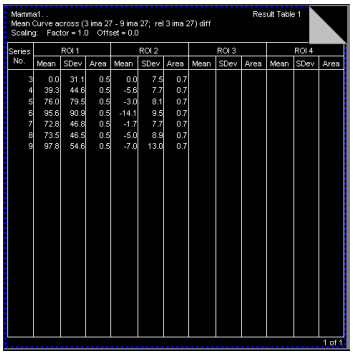
Starting evaluation



1 Click the icon on the **Tools** subtask card.

The resulting diagram shows a curve for each ROI in the color and line style of the corresponding ROIs. A table is generated for each diagram.





2 To display the intensity of the signal for a defined X-value, move the vertical measurement line.

If the vertical line is not visible, it is superimposed directly onto the Y-axis.

3 To smooth the curve, click the icon on the **Tools** subtask card.

4 Edit the commentary line with a double-click, if necessary.

The results will be rejected if you add or delete images, manipulate ROIs, or change the sort criterion. Subsequent recalculation can be performed automatically if **Tools** > **Auto Recalculation** is selected. If you have loaded a large number of series, however, you should deselect this option to save time.

Optimizing the result display by scaling

Scaling the axes

Manual scaling helps you to adjust the graduation of the axes more accurately to the region of interest.

1 Open the **Scaling** dialog window with the icon on the **Tools** subtask card.

2 Set the boundaries of the X and Y-axes in the respective tab cards.

If the **Relative** mode is activated for evaluation, the tab cards **Y-axis (diff)** and **Y-axis (norm)** are displayed for scaling the Y-axes.

3 Subdivide the Y-axis linearly or logarithmically with the **Scale** parameter of the **Y-axis** tab card.

Automatic Scaling is disabled. The manual scaling that has been set applies to all subsequent evaluations.

Scaling the grayscale values

Scaling the measured grayscale values is useful if the grayscale values are proportional to a physiologically relevant value and the proportionality factor is known (e.g., flow velocity of the blood).

- Set the scaling parameters for grayscale values in the **Y-axis** tab card of the **Scaling** dialog window.

Example: Factor = 2, Offset = 20

All Y-values will be multiplied by 2 and shifted 20 units toward the positive Y-axis.

Automatic Scaling is disabled. The manual scaling that has been set applies to all subsequent evaluations.

4.3.4 Documenting the results

Setting the background image for diagrams

1 If necessary, adjust the contrast and brightness in the 1st segment for an optimally visible curve.

2 To use the current image in the 1st segment as the background, select the **View** > **Image with Graphics** option.

You can reset a black background using the **View** > **Graphics only** option.

Reporting the results

✓ Evaluation results are displayed in the 2nd segment

The report includes all evaluation results. It is stored in DICOM format in its own series (the report name is derived from the name of the current series). The **Report Editor** in the **Patient Browser** must be used for further processing.

1 To create a report, click the icon.

2 To add report data for additional evaluations, click the icon.

Use this function, for example, when you have drawn and evaluated new ROIs.

4.4 Evaluation of dynamic 3D datasets with Tissue 4D

syngo **Tissue 4D** is an application card for visualizing and post-processing dynamic contrast-enhanced 3D datasets.

The software allows the application of non-linear fitting with pharmacokinetic models and the creation of parameter maps as color-coded images. The exchange of contrast agents between blood and tissue is described by the following parameters:

- Ktrans (transfer constant)
- Ve (extra-vascular extra-cellular volume fraction)
- Kep (reflux constant)

Pharmacokinetic modeling is performed pixel-by-pixel using a 2-compartment model. Calculation is based on the Tofts model.

The following example describes how to apply pharmacokinetic modeling to dynamic prostate MR examination data for the calculation of parameter images.

4.4.1 Preparing the data

Loading the data to Tissue 4D

✓ Dynamic series have been acquired with fixed flip angle

✓ Pre-contrast series with variable flip angle (i.e. 2°, 15°) are available for T1 map calculation

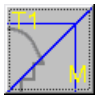
✓ Corresponding morphological images are available (recommended)

Loading the study

1 Select the study to be evaluated in the **Patient Browser**.

2 Click the icon to transfer the data to the **Tissue 4D** task card.

Pre-contrast data is displayed in the 1st segment. Dynamic data is displayed in the 2nd segment.



MPR images at the positions of the dynamic images are calculated from loaded morphological data. This icon allows toggling between the pre-contrast data (T1 maps) and the morphological view in the 1st segment.

Optimizing the image display

1 Use the **Auto Cine** function to get an overview of the loaded dynamic image data.

2 Activate this function if you want to exclude a certain point in time from subsequent evaluations.

3 Zoom and pan the images to display suspicious enhancing regions.

4 Window the images to optimize their contrast and brightness.

Performing motion correction

1 Select the 2nd segment and activate subtraction mode with the icon.

The first volume (reference volume) is substracted. The results are displayed as magnitude images in the same segment.

2 Activate 4D scrolling with the icon.

3 Check for motion artifacts in the subtraction images by scrolling in time (move cursor left/right) and in slice direction (move cursor up/down).

4 If necessary, start motion correction with the icon on the **1. Motion Correction** subtask card.

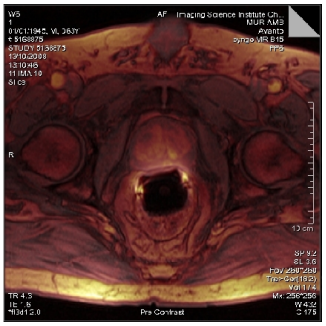
The currently displayed volume of the dynamic data is selected as reference for registration. Motion is corrected in all other volumes.

Registering pre-contrast and morphological data

The reference for registration of the data is a volume of the dynamic series at the currently displayed point in time.

Registering pre-contrast data

1 Open the **2. Registration** subtask card and select the **-PreContrast** mode, if necessary.



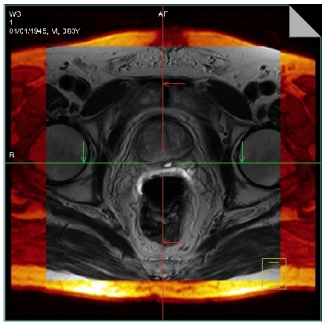
In the 1st segment, the pre-contrast images are overlaid with dynamic images taking the slice positions into account. The reference volume is shown as colored images.

2 Use the blending slider to visually evaluate the registration quality of the pre-contrast data with the selected dynamic volume.

3 If necessary, adjust the registration with the icon.

Registering morphological data

1 Select the **Morphological** mode in the **2. Registration** subtask card.



Fused MPR (three orthogonal MPRs) renderings of the morphological and the dynamic data are displayed in segments 1, 2, and 3. The reference volume is shown as colored images.

2 Use the blending slider to visually evaluate the registration quality of the morphological data with the selected dynamic volume.

3 If necessary, adjust the registration with the icon.

4.4.2 Evaluating the data

Calculating enhancement curves

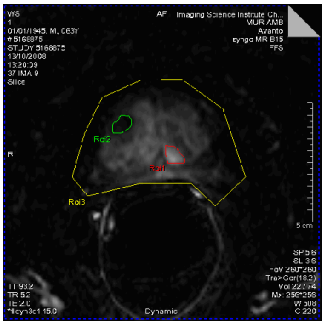
Curve calculation is performed for up to 4 regions defined by ROIs in the dynamic images.

Defining ROIs

1 Open the **3. Curve Calculation** subtask card.

2 Select **ROI1** in the **ROI Selection** list to set the color and the label of the first ROI.

3 Draw the ROI around the lesion in a subtraction image in the 2nd segment.

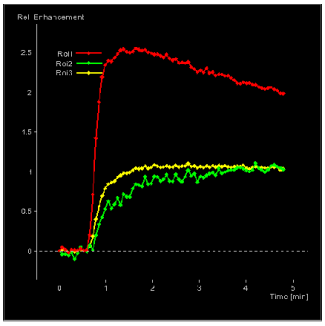


4 To define additional ROIs, select the corresponding ROI labels in the **ROI Selection** list and draw them in the subtraction image.

If you want to delete a selected ROI, press the **Delete** key on the keyboard.

Starting calculation

- Click the icon to plot the signal enhancement curves.



The calculation results for all defined ROIs are displayed in the 4th segment. The curves are shown as relative enhancement curves, the first volume serves as reference.

Preparing pharmacokinetic modeling

Calculating T1 maps

The T1 map masks define the areas to be adjusted for the pharmacokinetic fit. T1 fitting is restricted to pixels with values above a certain noise level value.

1 Open the **4. Pre Evaluation** subtask card.

The T1 map calculation runs automatically. Once the T1 map has been calculated, the pre-contrast data is replaced.

2 Change the threshold value for masking out noise in the **Noise Level** selection list, if neccessary (default: 20).

3 Select the MR acquisition technique in the **MR Protocol** selection list (default: T1 + Dynamic).

If T1 map is not available, dynamic 3D is chosen and an estimated value for T1 can be set.

Setting contrast agent parameters

The contrast agent parameters are used for the application of pharmacokinetic models.

1 Select the contrast agent applied in the **Contrast Ag.** selection list.

Molarity, **Relaxivity** and **Volume** are automatically selected by the system as a function of the contrast agent entered.

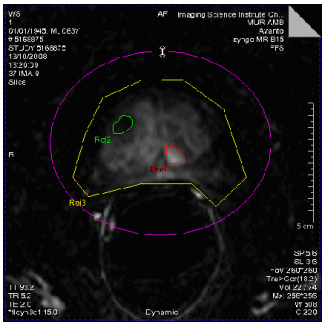
An application specialist can configure a list of preset contrast agents and assign contrast agent parameters.

2 Adapt the contrast agent parameters in the respective input fields, if necessary.

Defining the fitting volume

By defining a VOI, you restrict the application of pharmacokinetic modeling to a subvolume of the dynamic volume data.

1 Activate VOI drawing mode with the icon.



2 Draw an ellipse around the organ or around a subvolume in the 2nd segment enclosing the lesion.

The ellipse is extended to form an ellipsoid in the 3D structure.

3 Scroll through the slices to ensure that the VOI covers the part of the volume relevant for modeling.

4 Modify the VOI, if necessary.

Applying pharmacokinetic modeling

Pharmacokinetic modeling can be applied for the mean curves or voxelwise for the selected ROI/VOI.

Fitting mean ROI curves

1 Open the **5. Evaluation** subtask card and select an ROI in the **Selector** list (e.g. **ROI1**).

2 Select the pharmacokinetic model to be applied in the **Model** selection list.

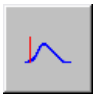
Currently, the two-compartment Tofts model is provided.

3 Select the Model AIF function which provides the applicable information about the concentration of the contrast enhancing media in the blood plasma.

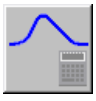
Fast: high temporal resolution, high kinetics.

Intermediate: moderate temporal resolution, moderate kinetics.

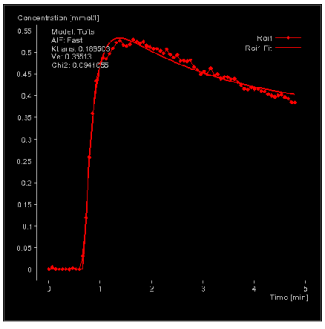
Slow: slow temporal resolution, slow kinetics.



4 Check the value in the **Contrast Arrival Time** field. Adjust the onset time of enhancement with the icon, if necessary.



5 Start pharmacokinetic modeling for mean ROI curves with the icon.



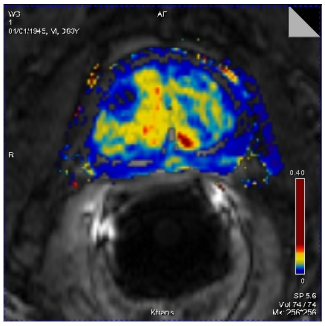
The fitting curve for the selected ROI label is displayed in the 4th segment.

Calculated parameter values for the exchange of contrast agent between blood and tissue are displayed top left in the diagram.

Fitting voxel by voxel

1 In the **Selector** list, select the VOI or the ROI whose parameters should be fitted.

2 Start pharmacokinetic modeling for all voxels of the VOI or ROI with the icon.



Parameter maps describing the contrast media kinetics are calculated for the selected VOI or ROI label. They are displayed as color-coded overlays of the morphological images in the 3rd segment.

Analyzing the results statistically

The parametric data of pharmacokinetic modeling are used to calculate frequency distributions (histograms) and mean values for the ROIs defined in the parameter images.

Defining ROIs

1 Open the **6. Results** subtask card.

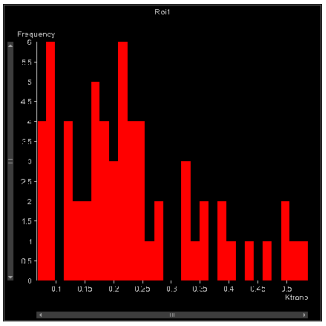
2 In the **ROI Selection** list, select an already existing ROI (e.g. **ROI1**).

3 Click the icon to copy the ROI from the 2nd segment to the parameter image of the 3rd segment.

4 To define new ROIs, use the ROI drawing mode.

Displaying a histogram

- Click the icon to calculate the frequency distribution of parameter values inside the ROI.



The histogram is displayed in the 4th segment.

Displaying mean values

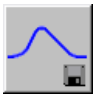
- Click the icon to calculate statistical data of parameter values inside the ROI.

The median, mean and standard deviation for the selected ROI are displayed bottom left in the 3rd segment.

4.4.3 Saving parametric data as ASCII files

1 Click the icon to save all parameter values from the 4th segment for the selected ROI.

The values of the Ktrans, Kep, Ve, Chi^2, FitCode, and iAUC parameters are written to a text file.



2 Click the icon to save the currently displayed curves for the selected ROI to a text file.

You can open and post-process ASCII files, e.g. with Microsoft Excel.

4 Post-processing

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CE 0123

Manufacturer's note:

This device bears a CE mark in accordance with the provisions of Council Directive 93/42/EEC of June 14, 1993 concerning medical devices and the Council Directive 2011/65/EU of June 08, 2011 on the restriction of the use of certain hazardous substances in electrical and electronic equipment.

The CE marking applies only to medical devices which have been put on the market according to the above-mentioned EC Directives. Unauthorized changes to this product are not covered by the CE mark and the related Declaration of Conformity.

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