

SIEMENS

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syngo MR E11

Supplement – Parameters and Image Text

Answers for life.

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1 Parameter Cards

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1.1 Routine

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
Slice group	1	+	-			FoV read	380 mm
Slices	30					FoV phase	84.4 %
Dist. factor	20 %					Slice thickness	3.0 mm
Position	Isocenter		...			TR	700.0 ms
Orientation	Coronal		...			TE	11 ms
Phase enc. dir.	F >> H		...			Averages	1
AutoAlign	Hip > Cor L+R		...			Concatenations	2
Phase oversampling	80 %					Filter	Distortion Corr. (2D), E
						Coil elements	BC

Slab group

Shows the number of slab group currently displayed. All slice parameters currently seen on the **Routine** or **Geometry** card refer to this slab group.

Slabs

Determines the number of slabs in this group.

Dist. factor

Determines the gap between slices and/or slabs of a group in percentages.

At a 100% value the gap corresponds exactly to one slice and/or slab thickness. Negative values lead to overlapping.



Negative distance values cannot be entered for 3D measurements.

Position

Defines the position of the object center.

- **Table position**

Table position of the protocol, referenced to the whole body patient coordinate system.

- **Phase offcenter**

Shift in phase-encoding direction

- **Read offcenter**

Shift in readout direction

- **Slice shift**

Shift in slice-selection direction



The selection list is dimmed if the position matches the isocenter.



Opens the **Position** dialog window for the slice selected.
(→ Page 188 *Position dialog window*)

Orientation

Indicates the position of the object in space based on the whole body patient coordinate system.



Opens the **Orientation** dialog window for the slice selected.
(→ Page 187 *Orientation dialog window*)

Phase enc. dir.

Changes the phase-encoding direction. This will swap the phase-encoding and readout directions. Using this method allows you to prevent aliasing artifacts in the phase-encoding direction or change the direction of flow and motion artifacts.



In the **Phase enc. dir.** selection list you are only offered configurations suitable to the current orientation.



Opens the **Inplane Rotation** dialog window for the slice selected. (→ Page 190 *Inplane Rotation dialog*)

AutoAlign

Used in two different variants:

AutoAlign Head

AutoAlign scout protocols: In AutoAlign scout protocols the **AutoAlign** parameter is used to specify the anatomical region where the AutoAlign matrices will be computed.



Predefined AutoAlign scouts are found in the localizer libraries of the Siemens protocol tree (e.g. \\SIEMENS\\head\\library\\localizers).

AutoAlign Spine > Cervical

AutoAlign clinical protocols: AutoAlign clinical protocols are protocols which use only one of the AutoAlign matrices. Almost all protocols can be used as an AutoAlign clinical protocol.

The AutoAlign parameter specifies which of the AutoAlign matrices will be used to align this clinical protocol. The displayed value is a composite of the AutoAlign region and an AutoAlign reference.



The content of the **AutoAlign** parameter is ignored if the referenced AutoAlign matrix is not yet computed.



Opens the **AutoAlign** dialog window. (→ Page 190 *AutoAlign dialog*)

Phase oversampling

Increases the phase-encoded area symmetrically at both sides of the field of view (FoV). The expanded FoV area is not shown. It is used to avoid overfolding artifacts.

Phase oversampling is shown as a percentage of the FoV in the phase-encoding direction.



Phase oversampling increases the measurement time. The signal-to-noise ratio is improved.

Oversampling is always automatically performed in the readout direction so it does not lead to an increase in measurement time.

Slice oversampling

Enlarges the phase-encoding area symmetrically on both sides of the slab in the slice selection direction. This extended FoV area is not shown. It is used to avoid overfolding artifacts.

Slice oversampling is indicated as a percentage of the slab thickness.



The measurement time is prolonged through slice oversampling. The signal-to-noise ratio is improved.

Slices per slab

Determines the number of slices per slab:

Changes of the **Slices per slab** affect the following:

- Thickness of slab
- The absolute slice oversampling as percentage of the slab.

FoV read

Determines the size of the anatomical region to be displayed (extension of the measurement in the readout and phase-encoding direction) and its resolution (pixel size).



When the **Tim CT mode** is active, this parameter determines the anatomical region required during RF excitation.

FoV phase

Displays the FoV in the phase-encoding direction (**FoV phase**) as a percentage of the FoV in the readout direction (**FoV read**).

Slice thickness

Determines the extension of the measurement area in the slice selection direction together with the number of slices.

2D measurements

The slice thickness corresponds to the thickness of a slice within a slice group.

When you change the slice thickness for 2D measurements, you also change the distance between the slices.

3D measurements

The slice thickness is the thickness of a slice within a slab (partitions).

When you change the slice thickness with 3D measurements, you change the thickness of the slab as well.



Increasing the slice thickness improves the signal-to-noise ratio, but degrades the spatial resolution in the slice-selection direction.

TR (repetition time)

Determines the repetition time TR that elapses between two successive excitations. (At times an alternative designation *Repetition time* is used).

Changing the repetition time affects image contrast and measurement time.

If you would like to enter several repetition times, additional keys are superimposed for scrolling between the individual times.

TE (echo time)

Determines the echo time (TE) that elapses between the RF excitation pulse and the pulse for the echo to be measured.



This parameter is not active for all sequences.



You may enter several echo times for multi-echo sequences. You scroll through the echo times below the field names by using the arrow keys. When you change a given echo time, the following echo times will be adjusted accordingly.

Averages

Determines the number of repeat measurements to improve the signal-to-noise ratios. The results of repeat measurements are averaged by the system.



The greater the number of measurements, the longer the measurement time.

Concatenations

Defines into how many repetition times TR the measurement of the planned slices should be divided. The system then determines the number of single sequential measurements across which the slices will be distributed.

Using this method, you can acquire many slices with a short repetition time (T1 weighted imaging) and prevent slice crosstalk.



When you selected a measurement in **multiple breathhold mode** and chose **Breath-hold** under **Respiratory control**, the number of breathhold intervals is determined via the **Concatenation** parameter.

- In the **Interleaved** multi-slice mode, the number of breathhold intervals results from the product of the parameter values **Measurements** and **Concatenations**.
- In the **Single Shot** multi-slice mode, the number of breathhold intervals is the product of the parameter values **Measurements**, **Concatenations** and **Averages**.



With triggered multislice measurements ("interleaved" excitation sequence), it is sometimes not possible to acquire all slices in one measurement. The slices missing from one measurement will then be acquired in the next measurement.



This field is active only when the **Interleaved** or **Single Shot** option was selected in the **Multi-slice mode** on the **Geometry - Common** parameter card.

Filter

Displays the selected filter.



You set the filters on the **Resolution - Filter** parameter card.

Coil elements

Displays the coils for this protocol.



You set the coils on the **System - Coils** parameter card.

Slice group

Shows the number of the slice group currently displayed. All slice parameters that are currently seen on the **Routine** or **Geometry** task card refer to this slice group.

Slices

Determines the number of slices in this group.

1.2 Contrast

1.2.1 Contrast - Common

The screenshot shows the 'Contrast - Common' parameter card. It features a dark background with white text and input fields. The parameters are organized into two columns. The left column includes TR (2000 ms), TE (30 ms), Averages (80), and Flip angle (90 deg). The right column includes Water suppr. (Water sat.), Water suppr. BW (50 Hz), Spectral suppr. (None), and Measurements (1). Each parameter has a small up/down arrow icon next to its value.

Parameter	Value	Unit
TR	2000	ms
TE	30	ms
Averages	80	
Flip angle	90	deg
Water suppr.	Water sat.	
Water suppr. BW	50	Hz
Spectral suppr.	None	
Measurements	1	

T1, T2, and proton density contrast

With spin-echo sequences, you obtain T1, T2 or proton density contrast weighting by setting the parameters TR (repetition time) and TE (echo time). The following applies:

- Short TR and short TE produces T1 contrast.
- Long TR and long TE produces T2 contrast.
- Long TR and short TE produces proton density contrast.

Spin preparation

You are planning an RF pulse (so-called spin preparation) before the actual measurement when you want changes in contrast or want to suppress certain signals (e.g., inversion recovery sequence).

Magnitude, phase, and real images

Signal suppression

The MR signal comprises the sum of signals from water and fat protons. This may result in chemical shift artifacts. Motion artifacts may be enhanced, and contrast may be degraded.

Signal suppression may be used to decrease these effects.

The **Contrast** parameter card provides a list of the image types for reconstruction:



Reconstruction of image types is not possible in every protocol and every sequence.

- **Magnitude images**

Show the intensity of the MR signal.

- **Phase images**

Show the phase positions of the spins

- **Real images**

Show the amplitude plus algebraic sign of the longitudinal magnetization after an inversion pulse.

Suppression of fat and water signals

Using the Dixon method, you can split the MR signal into a fat and a water signal and display the two signals separately.

TR (repetition time)

Determines the repetition time TR that elapses between two successive excitations. (At times an alternative designation *Repetition time* is used).

Changing the repetition time affects image contrast and measurement time.

If you would like to enter several repetition times, additional keys are superimposed for scrolling between the individual times.

1 Parameter Cards

TE (echo time)

Determines the echo time (TE) that elapses between the RF excitation pulse and the pulse for the echo to be measured.



This parameter is not active for all sequences.



You may enter several echo times for multi-echo sequences. You scroll through the echo times below the field names by using the arrow keys. When you change a given echo time, the following echo times will be adjusted accordingly.

MTC (magnetization transfer)

Determines whether the signal of tissue with a high portion of macro molecules is weakened by a special RF excitation pulse.



By activating the **MTC** checkbox, you obtain better contrast in images for e.g., vessel examinations.

Magn. Wrap-up / Restore Magnetization

Determines how the remaining magnetization is treated immediately after each data acquisition shot.

Option	Description
None	No wrap-up
Restore	Accelerates restoring the longitudinal magnetization. This increases the signal for T2 weighted acquisitions (even if short repetition times are used).
Suppress	Remaining magnetization is destroyed to suppress artifacts from long T1 fluids



The option **Suppress** is only available for segmented sequences. The option **Restore** corresponds to the Parameter **Restore Magn.** in previous software versions.

Magn. preparation

During inversion recovery (IR), double inversion recovery (DIR), and saturation recovery (SR), this parameter determines whether an RF pulse is transmitted prior to each measurement to affect contrast.

You can send the inversion pulse as slice-selective or non-selective. Consider whether your current sequence is an inversion recovery sequence (IR), double inversion recovery (DIR), or a saturation recovery sequence (SR).

The following options are available:

Option	Description
Slice sel./slab sel. (IR, DIR, or SR)	Selective preparation is performed (slice or slab).
Non-sel. (IR, DIR, or SR)	Non-selective preparation is performed.
T2 prep	A special preparation module is applied to the entire volume to enhance T2 contrast. The preparation pulse suppresses signals from tissue with short T2 times. Go to the Contrast parameter card and determine the duration of the preparation pulse in the T2 Prep. duration field.
T2 prep. adiab	This option works similar to T2 prep. Compared to the T2 prep. option these are the main differences: ■ Preparation module is more B1-insensitive ■ Leads to better image homogeneity ■ Requires more RF power
TI Scout	This scout generates a series of images with different inversion time. Based on this series, you can determine the most suitable inversion time and enter the value in the TI parameter.
Non-sel. T2-IR	A special inversion preparation pulse is transmitted for the entire volume. This pulse effects that only tissue with a long T2-time (fluids) is fully inverted. Tissue with short T2 is only inverted in part. In a subsequent excitation, it is possible to display it with a higher signal (e.g. for protocols with dark fluid contrast).

1 Parameter Cards

Option	Description
None	No inversion pulse is sent.



When you select the **None** option in the **Magn. preparation** list, you are usually not offered the **TI** parameter on the **Contrast - Common** card.

TI (Inversion time)

Determines whether an additional T1 contrast is added with spin preparation. For this purpose, a 180° RF pulse is used (inversion pulse) that inverts the spins.

■ For inversion recover sequences:

In this case, TI is the time between sending the inversion pulse and the excitation pulse of the subsequent measurement (e.g., a spin-echo pulse sequence). Depending on the TI, certain signals are suppressed (e.g., fat) and additional T1 contrast is applied to the signal.

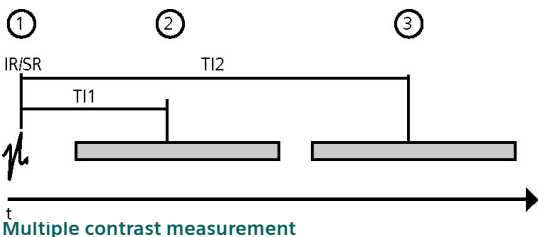
■ For Turbo FLASH sequences:

TI describes the time between sending the inversion pulse and reading out the echo signal, sorted in the center of the raw data matrix (this echo determines the contrast).

IR Contrast / SR Contrast

Enables multiple contrasts with different times for inversion recovery (IR) or saturation recovery (SR).

Determines the number of editable contrast times.



- (1) Inversion pulse or saturation pulse
- (2) First contrast
- (3) Second contrast



IR Contrasts parameter is visible only if **Magn.Preparation** is set to **Slice-sel. IR** or **Non-sel. IR**.
SR Contrasts parameter is visible only if **Magn.Preparation** is set to **Slice-Sel. SR** or **Non-sel. SR**.



Available only for a few sequences.

IR Scheme

Defines whether IR pulses of different slices may be interleaved.

Option	Description
Automatic	The system tries to use the idle time between the IR pulse and the acquisition module of a particular slice to play out IR pulses or acquisition modules of other slices. If T1 is too short interleaving of IR pulses is not possible.
Sequential	Forbids interleaving of IR pulses. This can enable an optimized utilization of the gradient system.

If interleaved IR pulses are possible the **Automatic** mode allows the shortest minimum TR and hence the most efficient scan.

If interleaved IR pulses are not possible the optimized utilization of the gradient system in mode **Sequential** may allow a shorter minimum TR.



Available only for a few sequences.

Flip angle

Determines the extent the RF pulse deflects the longitudinal magnetization from the Z-direction of the magnetic field. The flip angle directly affects image contrast.

With a 90° excitation pulse, for example, the longitudinal magnetization is rotated by 90° out of the Z-direction of the magnet. If a smaller flip angle is used, the magnetization returns to equilibrium more quickly allowing you to reduce the repetition time TR (for gradient echo sequences).

For spin echo sequences, you can enhance the T1 contrast by reducing the flip angle.

Fat suppr.

Suppresses the signal from fat protons in a targeted way.

The following options are available:

Option	Description
Fat sat.	Suppresses the fat signal and has no effect on TE, TR is greatly prolonged. This extends the measurement time as well. For MSK imaging, fat saturation can be optimized region-specific in the Fat suppression Optimization dialog window, which is accessible via the button next to the Fat suppr. parameter field. Possible values are: ■ "Default": standard Fat sat. mode behavior ■ "Joints": optimized Fat sat. mode for MSK imaging
Water excit. normal	Suppresses the fat signal, effects moderate extension of TE and TR.
Water excit. fast	Suppresses the fat signal and causes slight extension of TE and TR. The effect on fat saturation is slightly less than in Water excit. normal mode.

Option	Description
Q-fat sat.	Suppresses the fat signal. This mode is only available when selecting Quick mode in the Saturation mode .
SPAIR	Prior to image saturation, the fat signal is suppressed via a frequency-selective adiabatic inversion pulse. However, this option is only available with certain sequences for 1.5 T and 3 T systems.
None	Does not suppress the fat portion in the MR signal.



To shorten the measurement time in connection with fat sat, select **Quick** Mode in the **Saturation Mode** parameter.

Fat sat. mode

Determines the extent of fat suppression.

Water suppr.

Suppresses the signal of water protons in a targeted manner.

The following options are available:

Option	Description
Water sat.	Suppresses the water signal, has no effect on TE, TR is greatly prolonged. This extends the measurement time as well.
Fat excit.	Suppresses the water signal and has a moderate effect on TE and TR. This leads to a slightly longer measurement time.
None	Does not suppress the water portion in the MR signal.



When you select **Quick** setting in the **Saturation mode** parameter in connection with fat saturation, you are able to shorten the measurement time.

Blood Suppression

Determines whether the blood signal is suppressed by weak diffusion weighting. This is done by gradient moments (first order).

The following options are available:

Option	Description
On	Optimized gradient moments for the current protocol
< Body region >	Typical gradient moments for imaging the corresponding body region
Free	The parameters can be changed freely in the Blood Suppression dialog window
None / Off	No blood suppression



Opens the **Blood Suppression parameters** dialog window.
(→ Page 191 *Blood Suppression parameters dialog*)

SWI

Activates reconstruction of susceptibility-weighted images.

T2 prep. Duration

Defines the duration of the T2 preparation pulse train to increase T2 contrast.



This parameter is active only when the **T2 Preparation** option has been selected in the **Magn. Preparation** selection list.

Dixon

Determines whether the fat and water signal are displayed separately. For this purpose, the Dixon method separates the MR signal into a fat and water signal.

The following options are available via the button next to the parameter field:

Option	Description
Original echoes	The original image for each echo time is reconstructed.
Water	The Dixon method is performed, and an image is reconstructed that contains the water signal only.
Fat	The Dixon method is performed, and an image is reconstructed that contains the fat signal only.
In Phase	Dixon is used, and the original in-phase image is reconstructed.
Opposed Phase	Dixon is used, and the original opposed-phase image is reconstructed

Dixon evaluation

Specifies the parameters for Dixon evaluation. The following options are available via the button next to the parameter field:

- Fat fraction
- Water fraction
- T2*
- R2*
- Report

Fast Dixon

Enables single excitation to reduce motion artifacts.

Lines per shot

Defines the number of slices to be measured with one shot. For example, the number of lines that are acquired after a fat sat pulse.



This parameter is available only, when the **Q-fat sat.** or **SPAIR** mode has been selected under the **Fat suppr.** parameter.

Save original images

This parameter determines whether the original in-phase and opposed-phase images are saved.



This parameter has to be activated when the **Dixon** parameter is enabled.

Freeze suppressed tissue

When selecting this parameter, the system computes the T1-value of the tissue that is currently suppressed by the TR/TI combination selected and saves it. Effective immediately, a change in the repetition time (TR) automatically adjusts the inversion time (TI), so that the tissue with the saved T1-value is suppressed by the new TR/TI combination as well.

Minimize Inflow

Liquor-suppressed head measurements may be affected by liquor from the neighboring slices. Since this inflow of liquor was not inverted at the inversion time, it results in undesirable signal contributions. This signal contribution is minimized as much as possible when selecting this parameter.



When activating this parameter, the max.possible number of slices per TR may be reduced.

1.2.2 Contrast - Dynamic

The screenshot shows the 'Contrast - Dynamic' parameter card in the syngo MR E11 software. The interface has a dark theme with a top navigation bar containing tabs: Routine, Contrast, Resolution, Geometry, System, Angio, and Sequence. Below this, there are sub-tabs: Common and Dynamic. The Dynamic tab is currently selected. The main area contains several controls: 'Measurements' is set to 40; 'Pause after meas. 1' is set to 0.0 s with left and right arrow buttons; 'Reconstruction' is set to Magnitude; and 'Multiple series' is set to Each measurement. Each control has a small up/down arrow icon.

Averages

Determines the number of repeat measurements to improve the signal-to-noise ratios. The results of repeat measurements are averaged by the system.



Please note that the greater the number of measurements, the longer the measurement time.

Averaging mode

Determines the method for averaging measurements when several measurements are performed.

■ Short term

effects a better signal-to-noise ratio while maintaining optimal resolution

■ Long term

effects a better signal-to-noise ratio while maintaining optimal resolution

Reconstruction

Determines the image type(s) that have to be reconstructed.

Image type	Description
Magnitude images	MR images are usually so-called magnitude images. The MR signal intensity is displayed directly in these images.
Phase images	The grayscales in phase images correspond to the spin phases (between -180° and $+180^\circ$). These depend on the velocity with which spins move in the body (e.g., blood flow velocity). Spins with the same phase position (i.e., velocity) have the same grayscale value in this type of image.
Real images	The grayscale distribution in real images shows the real alignment of the longitudinal magnetization after an inversion pulse.



Real images can be selected only when an inversion pulse has been chosen.

Infinite measurement

For real-time sequences, this parameter sets the number of measurements to the max. value.



When the **Infinite measurement** checkbox is activated, the **Measurement** parameter is hidden.

Measurements

Determines how often a measurement is to be performed.

Delay in TR

Determines the time between two subsequent measurements. The parameter is relevant for all ep2d sequences.



The delay time set applies to all measurements.

Multiple series

Determines whether the images for each measurement cycle are stored in their own series.

The following options are available:

Option	Description
Each measurement	A separate series is generated for each series.
Each slice (not for BOLD sequences)	A separate series is generated for each slice.
Each slice and measurement (not for BOLD sequences)	A separate series is generated for each measurement and each slice.
Off	All images of a measurement are stored together in one series.

Pause after Meas.

During dynamic measurements, this parameter determines a delay time (in seconds) between the individual measurements. You separately determine the pause for each measurement:

- ◆ Click the lower arrow keys to get to the pause the duration of which you want to change.
- ◆ Enter the desired value in the input field.



Up to 64 individual pauses are possible. In most cases, you are setting the same pause time for all measurements or set the pause time to zero. Beginning with 65 pauses, you can only enter a general pause time.

Proton Dens. Map

Defines whether proton density maps are reconstructed for dynamic cardiac imaging.

Proton density maps are images without magnetization preparation.

Useful for correction and calibration purposes.

1.2.3 Contrast - ASL

Routine
Contrast
Resolution
Geometry
System
Physio
Perf
Sequence

Common
Dynamic
ASL

Perfusion mode PICORE Q2T
Bolus Duration 700 ms
Inversion Time 1800.0 ms
Inversion Array Size 1
Flow limit 100.0 cm/s

Perfusion mode

Determines the ASL perfusion preparation.
The following settings are presently available:

Option	Description
PICORE Q2TIPS	The PICORE label scheme is used in combination with periodic saturation pulses (Q2TIPS). FOCL pulses are used together with inversion.

Quality check

Activates inline image quality check.
The level of motion within an image series is analyzed. Images with excessive motion are excluded from the calculation of parameter maps.

Inversion time

Specifies the array of inversion times to be measured in the sequence.

Flow limit

Used in ASL to limit flow in order to attenuate the signal from large arteries.



The flow limit is switched off when set to maximum.

Averaging mode

Sets the mode for distributing averages over the specified TI array.

1.3 Resolution

1.3.1 Resolution - Common

Routine	Contrast	Resolution	Geometry	System	Physio	Perf	Sequence
Common iPAT Filter Image Filter Rawdata							
FoV read 256 mm							
FoV phase 100.0 %							
Slice thickness 8.0 mm							
Base resolution 64							
Phase resolution 100 %							
Phase partial Fourier 6/8							
Interpolation ☐							

FoV read

Determines the size of the anatomical region to be displayed (extension of the measurement in the readout and phase-encoding direction) and its resolution (pixel size).



Changing the FoV in the readout direction also changes the FoV in the phase-encoding direction. This changes the pixel size.



When the **Tim CT mode** is active, this parameter determines the anatomical region required during RF excitation.

FoV phase

The FoV in the phase-encoding direction (**FoV phase**) is shown as a percentage of the FoV in the readout direction (**FoV read**).



You can only set the extent in the phase-encoding direction to be less than or equal to the extent in the readout direction. If you change the FoV in the phase-encoding direction, the number of phase-encoding steps is always adapted to keep the resolution ratio constant.



If you increase the number of phase-encoding steps, the measurement time will be adjusted accordingly.

Slice thickness

Determines the extension of the measurement area in the slice selection direction together with the number of slices.

2D measurements

In the case of 2D measurements, the slice thickness corresponds to the thickness of a slice within a slice group.

When you change the slice thickness for 2D measurements, you also change the distance between the slices.

3D measurements

For 3D measurements, the slice thickness is the thickness of a slice within a slab (partitions).

When you change the slice thickness with 3D measurements, you change the thickness of the slab as well.



Increasing the slice thickness improves the signal-to-noise ratio, but degrades the spatial resolution in the slice-selection direction.

Base resolution

Determines the number of pixels in the readout direction. This determines the spatial resolution in the readout direction.

The base resolution is also the reference value for specifying the percentage of resolution in the phase-encoding direction.

The basic resolution also determines the size of the image matrix that can be doubled by selecting interpolation.

Phase resolution

Determines the resolution of the slices in the phase-encoding direction and is provided in percentages referenced to the basic resolution.

If phase resolution is 100%, the resolution in the readout and phase-encoding directions will have the same value and the pixels are square. At e.g., 75%, the pixels are rectangular, and resolution decreases.

Slice resolution

In 3D measurements, phase-encoding is performed in addition to the slice selection and phase-encoding directions.

This parameter determines the resolution in the slice-selection direction. The resolution ratio is expressed as a percentage of the readout steps.

With slice resolution at 100%, the phase-encoding table in the slice-selection direction has as many steps as the number of slices (partitions) to be reconstructed.

For < 100% slice resolution, fewer phase-encoded steps are measured in the slice-selection direction. This reduces the measurement time. Additional slices are subsequently calculated using interpolation. The slice thickness displayed in the image text does not change. An "i" is simply appended to its numeric value to identify it (e.g., **SL 2.0i**).

Phase partial Fourier

If partial Fourier matrices are used for 2D measurements, only part (at least half) of the phase-encoding steps are acquired.

This parameter determines that the k-space is asymmetrically sampled in the slice selection direction. As a result, the measurement is reduced at an unchanged spatial resolution. However, the signal-to-noise ratio is reduced.

1 Parameter Cards

The following options are available:

Option	Description
4/8 (half Fourier), 5/8 , 6/8 , 7/8	Number of acquired phase-encoding steps
Allowed	The sequence automatically computes and uses the most optimal setting of the phase partial Fourier.
Off	The entire image matrix is used.



Different modes are available depending on the sequence.

Slice partial Fourier

During 3D measurements, you are able to change the image matrix and measurement time not only via the phase-encoding and readout direction, but also via the slice-selection direction.

This parameter determines that the k-space is asymmetrically sampled in the slice selection direction. As a result, the measurement is reduced at an unchanged spatial resolution. However, the signal-to-noise ratio is reduced.

The following options are available:

Option	Description
4/8 (half Fourier), 5/8 , 6/8 , 7/8	Number of acquired phase-encoding steps
Allowed	The sequence automatically computes and uses the most optimal setting of the phase partial Fourier.
Off	The entire image matrix is used.

Readout Segments

Defines the number of segments in readout direction for multi-shot, readout-segmented sequences.

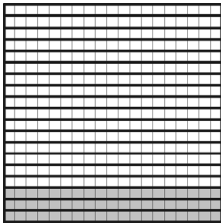


Available only for a few sequences.

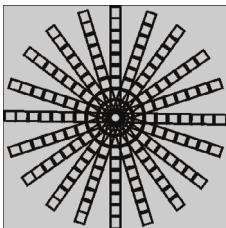
Trajectory

Defines the geometric shape to be sampled in the k-space.

The following shapes are possible:

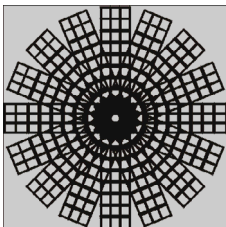


Cartesian: The k-space is sampled as a matrix of rows and columns. The k-space is built up line by line, for example, from the bottom left to the top right.



Radial: The k-space is read out in individual lines. The lines form the shape of a star.

This mode is available for the CV sequence. For the VIBE sequence, it is available with StarVIBE.



BLADE: Data are acquired in so-called blades. Every blade comprises parallel phase-encoding lines. The individual blades are rotated in order to cover a circle in the raw data space.

The number of lines per blade is determined in the **Turbo Factor** parameter on the **Sequence - Part 2** parameter card.

1 Parameter Cards

View sharing

Defines whether k-space data already acquired in a measurement should be reused, for example to obtain higher temporal resolution.

The following options are available:

Option	Description
Off	No data sharing across measurements.
Shared phases	In a CINE acquisition, k-space data are shared across subsequent (cardiac) phases.
TWIST	In a dynamic acquisition, data from the outer k-space region are shared across multiple measurements.

Interpolation

Magnifies the image matrix to twice its size without increasing the measurement time.

After interpolation, the transitions in the image will be softer because the pixels are now smaller. You need four times the memory to store the image in the database.



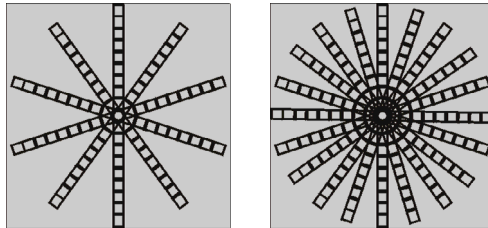
In an interpolated image, the interpolated matrix, *not* the scan matrix, is shown bottom right in the image text. Interpolation is indicated by the **I** after the matrix.



Interpolation doubles the size of the image matrix in the readout and phase-encoding directions. *No* interpolation is performed in the slice-selection direction. If you increase the base resolution, interpolation is deactivated automatically. Otherwise, the reconstruction time will increase considerably. You can activate interpolation at any time.

Radial views

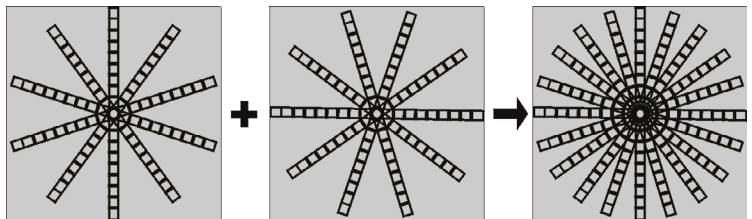
For radial sequences, this parameter determines the number of lines for radial k-space sampling.



Example: k-space sampling with 5 and 10 radial lines

Radial Interleaves

Determines the number of TR intervals required to radially sample all lines of the k-space.



Example: For Radial Interleaves = 2 all requested lines of the k-space are sampled in two TR intervals.

BLADE coverage

Calculates the number of blades of varying rotation angles for k-space sampling.

The value is indicated as a percentage.

■ 100%

The number of blades is selected so that a circle in the k-space is completely covered.

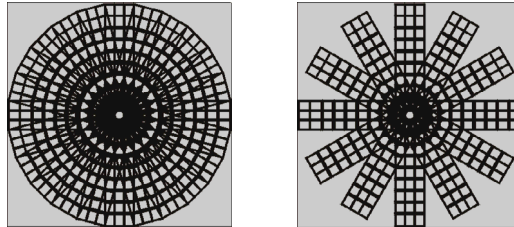
■ Higher than 100%

More blades are measured than necessary for complete coverage. The measurement time increases and the signal-to-noise ratio improves.

■ Less than 100%

Less blades are measured than necessary for complete coverage.

Measurement time is reduced and image quality degraded.



Example: *BLADE coverage* = 100% (in this case 12 blades) and *BLADE coverage* = 50% (in this case 6 blades)

Central region A

Determines the size of the k-space center that is acquired with full sampling density.

This value is provided as a percentage of the total number of sample points that will be acquired.



This parameter is only active when **TWIST** is selected under the **View sharing** parameter.

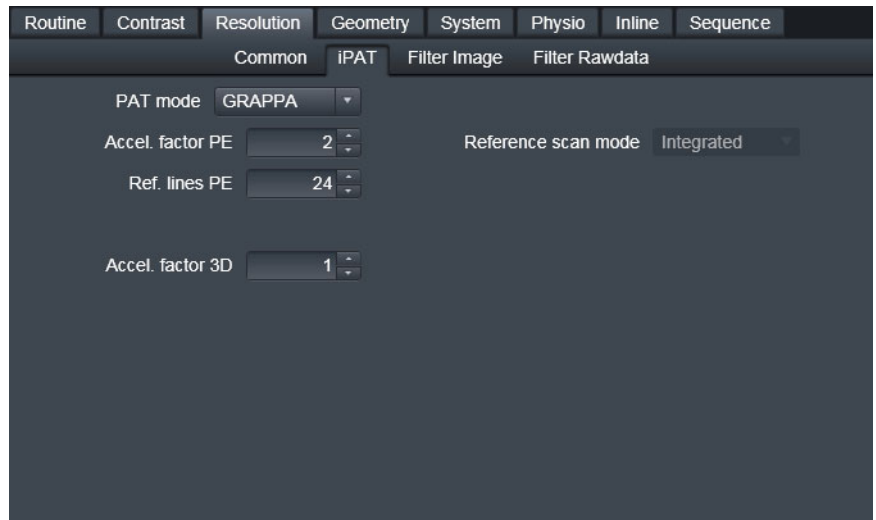
Sampling density B

Determines the sampling density used to sample the individual temporal phases in the outer k-space.



This parameter is only active when **TWIST** is selected under the **View sharing** parameter.

1.3.2 Resolution - iPAT



The screenshot shows the 'Resolution - iPAT' parameter card in the syngo MR E11 interface. The 'Resolution' tab is selected, and the 'iPAT' sub-tab is active. The parameters are as follows:

Parameter	Value
PAT mode	GRAPPA
Accel. factor PE	2
Ref. lines PE	24
Accel. factor 3D	1
Reference scan mode	Integrated

Defines the parameters for PAT reconstruction (PAT = parallel acquisition technology).

PAT reconstruction shortens the measurement time

PAT mode

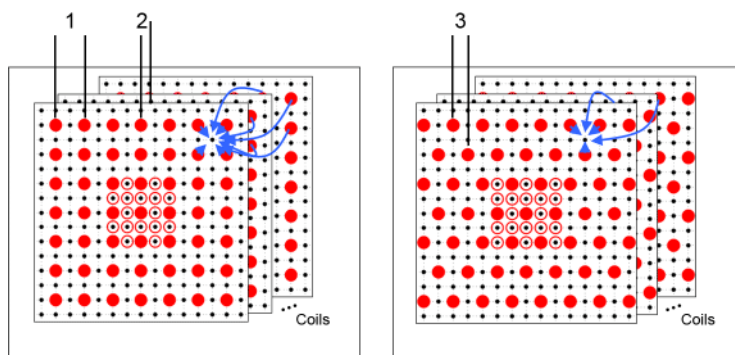
Parallel imaging technique (PAT) accelerates data acquisition by collecting a reduced amount of data.

The following options are available:

Option	Description
None	The PAT reconstruction technology is not being used
GRAPPA	PAT reconstruction mode based on the GRAPPA algorithm
CAIPIRINHA	PAT reconstruction mode based on the CAIPIRINHA algorithm
mSENSE	PAT reconstruction mode based on the mSENSE algorithm



Which options are available depends on the sequence



Reduced data acquisition with GRAPPA and CAIPIRINHA

- (1) Every n th point in phase-encoding direction is acquired (where $n = \text{Accel. factor PE}$)
- (2) Every n th point in slice-encoding direction is acquired (where $n = \text{Accel. factor 3D}$)
- (3) With **CAIPIRINHA**, the acquired pattern can be shifted in slice-encoding direction.
The relative shift of measured neighboring slice-encoding lines is given by the **Reordering Shift 3D**.



A PAT mode can be selected only when at least two coil elements or RF receive channels are available.

Accel. Factor PE

During PAT reconstruction, this parameter determines the acceleration factor in the phase-encoding direction.

The max. acceleration factor in phase-encoding direction corresponds to the number of receive channels used.

Ref. lines PE

During PAT reconstruction, this parameter determines the number of reference lines in the phase-encoding direction.

The maximum number of reference lines in the phase-encoding direction corresponds to the number of lines in the phase-encoding direction. It is provided dynamically depending on the sequence and protocol parameters.

Accel. factor 3D

During 3D PAT reconstruction, this parameter determines the acceleration factor in the slice-selection direction.

The max. acceleration factor in the slice-selection direction corresponds to the number of receive channels used.



When changing the parameter **Accel. factor 3D**, slice oversampling may have to be slightly adjusted depending on the number of selected slices (adjustment is automatic via the **Scan Assistant** dialog window).

Ref. lines 3D

Determines the number of reference lines in the slice-selection direction.



This parameter may be changed only when the protocol is based on a 3D sequence that supports PAT in 3D.

The maximum number of reference lines in the slice selection direction corresponds to the number of slices of the slabs.



The maximum number of reference lines is provided dynamically according to sequence and protocol parameters.

Reordering Shift 3D

During PAT reconstruction based on the **CAIPIRINHA** algorithm, this parameter determines the shift in slice-selection direction. The max. reordering shift corresponds to the acceleration factor in the slice-selection direction minus one.

For detailed information see (→ Page 39 *PAT mode*)

Reference scan mode

The PAT reconstruction mode requires that every measurement contains reference lines for calibration.

This parameter determines the way in which the reference lines are measured.

The following options are available:

Option	Description
Integrated	The reference lines are part of the measurement procedure of the sequence. This method has the advantage of being extremely robust, for example in regions with fast motion.
Separate-GRE	GRE-based reference scan. The reference lines are measured together with the sequence, however, separately just prior to actually measuring the image data. This method is faster, e.g., for measurements with high acceleration factors and low resolution. With 3D sequences this method also supports fat saturation in the Quick saturation mode (Geometry - Saturation parameter card) . The method also supports physiologically-triggered measurements for 3D sequences. For EPI sequences, this mode reduces motion artifacts in regions with movements (e.g. breathing), especially for PAT factors > 2
Separate-EPI	EPI-based reference scan.

Option	Description
Self-calibrated	<i>For special measurements only when averaging > 1</i> Additional reference lines are not measured because the lines from the repetitions are reconstructed. The PAT factor has to be smaller or equal to the value of the Averages parameter.
tPat	<i>For special measurements only when averaging > 1 or phases > 1</i> Additional reference lines are not measured because the lines from the repetitions are reconstructed. The PAT factor has to be smaller or equal to the value of the Measurements or Phase parameters.



This parameter is not available for all PAT sequences.

CAIPIRINHA mode

Sets optimized values for the **Accel. factor PE**, **Accel. factor 3D** and **Reordering Shift 3D** parameters. Values are optimized to reach the total PAT factor set by the **Total PAT factor** parameter.

Option	Description
Free	No automatic values are set
Body Tra	Values are optimized for transversal abdomen measurement
Body Cor	Values are optimized for coronal abdomen measurement
Breast	Values are optimized for soft tissue evaluation

Total PAT factor

Sets the total PAT factor in the **CAIPIRINHA mode**.

tPAT average all frames

Determines if all temporary frames are used to calculate the sensitivity cards of tPAT reconstruction.



This parameter is available only, when the **tPAT** mode has been selected under the **Reference measurement mode** parameter.

tPAT averaged frames

Determines if all temporary frames are used to calculate the sensitivity cards of tPAT reconstruction.



This parameter is available only, when the **tPAT** mode has been selected under the **Reference measurement mode** parameter and the **tPAT average all frames** parameter is not activated.

1.3.3 Resolution - Filter Image

The screenshot shows the 'Filter Image' parameter card. It includes tabs for Routine, Contrast, Resolution, Geometry, System, Physio, Inline, and Sequence. The 'Resolution' tab is selected, and within it, the 'Filter Image' sub-tab is active. The settings are as follows:

- Image Filter:** ☒
- Intensity:** Medium
- Edge Enhancement:** 3
- Smoothing:** 3
- Unfiltered images:** ☐
- Distortion Corr.:** ☒
- Mode:** 2D
- Unfiltered images:** ☐
- Prescan Normalize:** ☐
- Normalize:** ☒ ...
- Unfiltered images:** ☐
- B1 filter:** ☐

Intensity

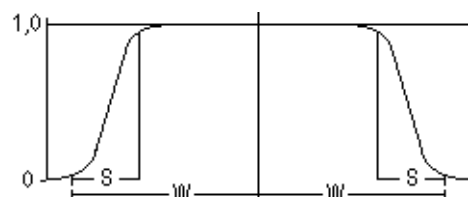
Determines to what extent the filter will be applied.



The image will be more homogeneous by increasing the filter intensity. However, image contrast may be compromised at the same time. This means that weak filters should be used whenever possible.

Slope

Shows the gradient at the flanks of the filters.



S: Slope at the flanks of the filter

W: filter width

Normalize

If you are using surface coils, the area in the vicinity of the coil will appear lighter in the images and darker in the areas farther from the coil. The signal intensity is greater in the vicinity of the coil.

Use the normalization filter to reduce the brightness of areas in the vicinity of the coil and increase the brightness in areas farther away from the coil.



Use of the normalization filter may lead to a loss of contrast and an increase in background noise.

Cut off

Determines the level of brightness below which the pixels are no longer corrected with the normalization method, but rather with a fixed value.



The threshold is given as a percentage of the maximum intensity profile. For a value of **20**, e.g., all pixels with an intensity that lies below 20% of the maximum value, a factor of 5 ($= 1/20\%$) only is used for correction.

Width

Determines the width of the filter



When you selected **Free** in the **Intensity** selection list, you can determine the increase yourself.

Unfiltered images

Determines whether unfiltered images should be saved as well.



If you reconstructed and stored unfiltered as well as filtered images in Inline, all other inline functions can no longer be accessed.
Filtered images are always shown in the Inline display.

Prescan normalize

This filter corrects for signal intensity decays caused by the coil profiles.

It works the similar way as the **Normalize** filter (→ Page 46 *Normalize*) but the data used for homogenization are acquired through an adjustment measurement.

Option	Description
Normal	This is the default mode, which will correct for signal intensity decays caused by the coil profiles.
Broad range	The Normal mode utilizes a signal threshold, which is used to avoid noise enhancement in regions far from the coils. In Broad range mode, the threshold is decreased, so that a wider range of the object is normalized. Possible applications are spine images, if the spine is distant from the coil.
Moderate	In Normal mode, noise in the center of the image might be enhanced too much. The Moderate mode does a progressively weakened normalization, so that the optical impression can be less noisy. However, the resulting images will show remainders of the original coils sensitivity profiles.



Use the **Normalize** filter instead of the **Prescan normalize** filter when you:

- use the Body Coil for the measurement (**Prescan normalize** is not possible for measurements with the Body Coil only)
- use other nuclei as H-nuclei for image generation.



Prescan normalization should be selected when using the endorectal coil in conjunction with a Spine or Body Matrix element.

B1 filter

B1 filter is a homomorphous filter that can be used to reduce signal differences in MR images caused by dielectric resonances at field strengths of 3T and higher.

The following filter intensities can be set if the parameter is activated:

- Weak
- Medium
- Strong

Dynamic Field Correction

Reduces eddy current induced distortions of diffusion weighted images.

The following options are available:

Option	Description
Direct	Each diffusion weighted image is registered to a corresponding undistorted reference image. If the measurement protocol does not contain reference images, additional scans are done at the beginning of the data acquisition. This option is recommended for diffusion weighted images with a sufficient SNR.
Adjust	A number of dedicated adjustment scans is done at the beginning of the data acquisition. The actual imaging scans are registered to these adjustment scans. After the registration, the distortion correction parameters are checked for validity. If the pixel relocation exceeds a certain threshold, the correction will be considered invalid for the respective scan. This option is recommended for diffusion weighted images with a low SNR.

Distortion Corr.

Activates 2D or 3D distortion correction. This compensates for the pillow-shaped distortions at the edge of the image. These distortions occur in images with a large FoV or eccentric slices (Offcenter).

The following options are available:

Option	Description
2D	With 2D distortion correction , image distortion is corrected individually in each slice.
3D	With 3D distortion correction , the voxel in the current slice as well as those in the surrounding slices are taken into account. The correction results are more precise, but require a longer reconstruction time.

Image filter

The image filter is used to set the intensity, edge enhancement, and smoothing.



Beginning with software version VB 15A this filter is activated by default for every protocol. For changes on the default setting please contact our customer service.

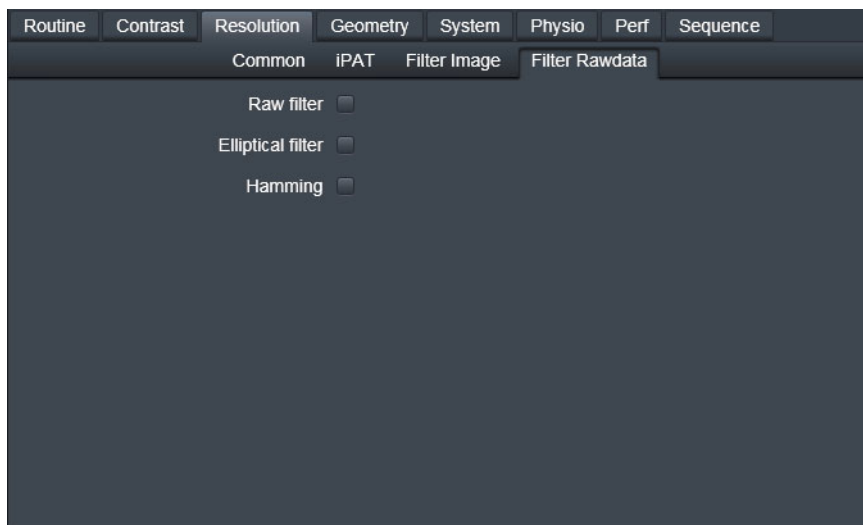
Edge enhancement

Determines the edge enhancement value of the filter.

Smoothing

Determines the limit for filter smoothing.

1.3.4 Resolution - Filter Rawdata



Raw filter

The outer lines of the raw data matrix contain the sharpness information of an image. You can weight specific lines with the raw data filter, for example, to suppress edge oscillation.

Hamming Filter

Discrete Fourier Transformation results in signal contamination within the voxel due to signals from adjacent voxels. The filter reduces this contamination.

Use the **Width** input field to set the filter width relative to the dimension of the k-space.



Use of the Hamming Filter results in an enlargement of the voxel dimension. Every voxel is actually wider than the voxel that is nominally calculated and displayed in the measurement matrix.

Elliptical filter

With the elliptical filter, you will only use the center of the raw data space (the corners are set to 0).

In this way you improve the signal-to-noise ratio up to 10% (without loss in resolution).

The following options are available:

Option	Description
In the plane	This filter is only used within the image planes.
Volume	The filter is applied to the entire volume.

POCS (Projection Onto Convex Sets)

Improves the edge sharpness for Partial Fourier sampling. Missing k-space pixels are not set to zero but are extrapolated.

The following options are available:

Option	Description
Off	No POCS.
Read slice	POCS in readout and slice direction
Read phase	POCS in readout and phase-encoding direction

1.4 Geometry

The parameter card is subdivided into several sub-cards including:

- **Common**

Here you will find all parameters pertaining to the position and size of the slices or slabs to be measured (may be different for 2D and 3D measurements).

- **Saturation**

These are the parameters relevant when planning saturation regions and/or fat / water saturation.

- **Navigator**

These are the parameters for navigator objects.

1.4.1 Geometry - Common

e.g.: Parameter card Geometry - Common (2D)

Slab group

The slabs measured within the framework of a protocol are combined into groups.

Here you can see the number of the slab group currently displayed. All slice parameters, currently seen on the **Routine** or **Geometry** card refer to this slab group.

Slabs

Determines the number of slabs in this group.

Dist. factor

Determines the gap between slices and/or slabs of a group in percentages.

At a 100% value the gap corresponds exactly to one slice and/or slab thickness. Negative values lead to overlapping.



Negative distance values cannot be entered for 3D measurements.

Position

Defines the position of the object center.

The following information is displayed when you position the mouse pointer on the field:

- **Table position**

Table position of the protocol, referenced to the whole body patient coordinate system.

- **Phase offcenter**

Shift in phase-encoding direction

- **Read offcenter**

Shift in readout direction

- **Slice shift**

Shift in slice-selection direction



The selection list is dimmed if the position matches the isocenter.



Use this key to open the **Position** dialog window for the slice selected.
(→ Page 188 *Position dialog window*)

Orientation

Indicates the position of the object in space based on the whole body patient coordinate system.



Use this key to open the **Orientation** dialog window for the slice selected.

(→ Page 187 *Orientation dialog window*)

Phase enc. dir.

The current phase-encoding direction (direction of the phase-encoding gradient) is indicated in the main orientations of the whole body patient coordinate system.

You can change the phase-encoding direction. This will swap the phase-encoding and readout direction. Using this method allows you to prevent aliasing artifacts in the phase-encoding direction or change the direction of flow and motion artifacts.



In the **Phase enc. dir.** selection list you are only offered configurations suitable to the current orientation.



Use this button to open the **Inplane Rotation** dialog window for the slice selected.

(→ Page 190 *Inplane Rotation dialog*)

Phase oversampling

Increases the phase-encoded area symmetrically at both sides of the field of view (FoV). The expanded FoV area is not shown. It is used to avoid overfolding artifacts.

Phase oversampling is shown as a percentage of the FoV in the phase-encoding direction.



Phase oversampling increases the measurement time. The signal-to-noise ratio is improved
Oversampling is always automatically performed in the readout direction so it does not lead to an increase in measurement time.

Slice oversampling

Enlarges the phase-encoding area symmetrically on both sides of the slab in the slice selection direction. This extended FoV area is not shown. It is used to avoid overfolding artifacts.

Slice oversampling is indicated as a percentage of the slab thickness.



The measurement time is prolonged through slice oversampling. The signal-to-noise ratio is improved.

Slices per slab

Determines the number of slices per slab:

Changes of the **Slices per slab** affect the following:

- Thickness of slab
- The absolute slice oversampling as percentage of the slab.

FoV read

Determines the size of the anatomical region to be displayed (extension of the measurement in the readout and phase-encoding direction) and its resolution (pixel size).



When the **Tim CT mode** is active, this parameter determines the anatomical region required during RF excitation.

FoV phase

The FoV in the phase-encoding direction (**FoV phase**) is shown as a percentage of the FoV in the readout direction (**FoV read**).

Slice thickness

Together with the number of slices, this parameter determines the extension of the measurement area in the slice selection direction.

2D measurements

In the case of 2D measurements, the slice thickness corresponds to the thickness of a slice within a slice group.

When you change the slice thickness for 2D measurements, you also change the distance between the slices.

3D measurements

For 3D measurements, the slice thickness is the thickness of a slice within a slab (partitions).

When you change the slice thickness with 3D measurements, you change the thickness of the slab as well.



Increasing the slice thickness improves the signal-to-noise ratio, but degrades the spatial resolution in the slice-selection direction.

TR (repetition time)

Determines the repetition time TR that elapses between two successive excitations. (At times an alternative designation *Repetition time* is used).

Changing the repetition time affects image contrast and measurement time.

If you would like to enter several repetition times, additional keys are superimposed for scrolling between the individual times.

Multi-slice mode

Determines the measurement modes for multi-slice mode:

- **Sequential** measurement, slice by slice
All lines (phase-encoding steps) of the first slice are measured step-by-step. This is followed by all lines of the second slice, etc.
- **Interleaved** measurement, line-by-line
All first lines (phase-encoding steps) of all interleaved slices are measured one after the other in repetition time TR. This is followed by all second lines of all interleaved slices, etc.
- **Single shot** - Special mode for fast sequences.
All lines (phase-encoding steps) of a slice after excitation are measured simultaneously. Then all lines of the second slice are measured together, etc.

Series

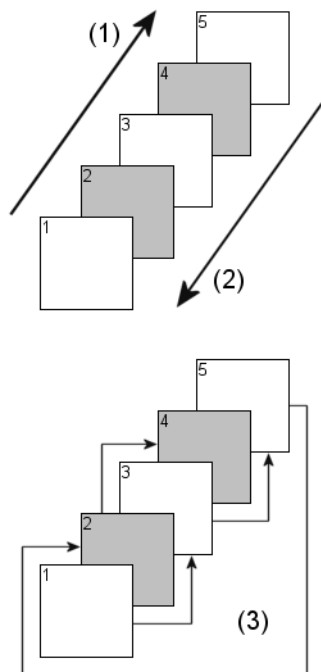
Determines the order in which the slices are processed.



The images are displayed in ascending order according to the image numbers after reconstruction, regardless of the sequence for slice processing.

The following excitation sequences are available:

1 Parameter Cards



■ Ascending (1)

The slices are excited at the beginning of the slice or slab group (beginning → end).

■ Descending (2)

The slices are excited at the end of the slice or slab group (end → beginning).

■ Interleaved (3)

■ Interleaved in A. A. (without display)

(Interleaved in breathhold interval). The slices are measured separately in the **Interleaved** mode for each breathhold interval of a multiple breathhold measurement.



Input **Interleaved in A. A.** is superposed only when you are planning a measurement in a multiple breathhold mode and selected **Breath-hold** under **Respiratory control** on the **Physio - PACE** parameter card.



You can combine the **Multi-slice mode Interleaved** and **Series Interleaved** settings for a very short TR and small slice distance to avoid cross-talk.



Determine the main orientation of the slices (e.g., sagittal-coronar-transverse) using the **MSMA** parameter.

Concatenations

Defines into how many repetition times TR the measurement of the planned slices should be divided. The system then determines across how many single sequential measurements the slices will be distributed.

Using this method, you can acquire many slices with a short repetition time (T1 weighted imaging) and prevent slice crosstalk.



When you selected a measurement in multiple breathhold mode and chose **Breath-hold** under **Respiratory control**, the number of breathhold intervals is determined via the **Concatenation** parameter.

- In the **Interleaved** multi-slice mode, the number of breathhold intervals results from the product of the parameter values **Measurements** and **Concatenations**.
- In the **Single Shot** multi-slice mode, the number of breathhold intervals is the product of the parameter values **Measurements**, **Concatenations** and **Averages**.



With triggered multislice measurements ("interleaved" excitation sequence), it is sometimes not possible to acquire all slices in one measurement. The slices missing from one measurement will then be acquired in the next measurement.



This field is active only, when the **Interleaved** or **Single Shot** option was selected in the **Multi-slice mode** on the **Geometry - Common** parameter card.

Slice group

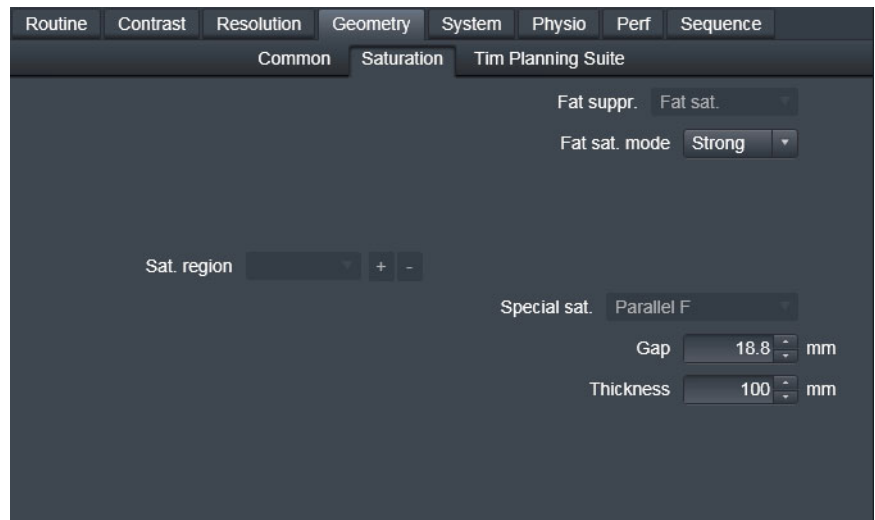
Slices measured within the framework of a protocol are combined into a group.

This parameter shows the number of the currently displayed slice group. All slice parameters that are currently seen on the **Routine** or **Geometry** task card refer to this slice group.

Slices

Determines the number of slices in this group.

1.4.2 Geometry - Saturation



Saturation regions

Saturation regions are areas whose signals are saturated by special RF pulses so as to avoid motion artifacts.

Standard and tracking saturation regions

Standard saturation regions are numbered and may be positioned as required.

Parallel or tracking saturation regions are always linked to a slice or slab group. As a result, it is not possible to change the position and orientation of these saturation regions. Instead, the position of these regions is automatically adjusted by the system whenever you move or rotate the slice or slab group.

The position and orientation of parallel or tracking saturation regions are always linked to a slice or slab group. The system automatically adjusts these regions as soon as you shift or rotate the respective slice or slab group.

Prior to each measurement, **tracking saturation regions** are excited at a given distance either in front or behind the slice and at the thickness specified, that is, they track the current slice to be measured within the slice group.

Parallel saturation regions are positioned either on one side or on both sides parallel to the slice group. These sat regions do not travel with the slice, but are rather located at the distance specified either in front or in back of both sides of the slice group.

Saturation mode

Determines how often the saturation pulses are being sent:

Mode	Description
Standard	A saturation pulse is sent prior to each measurement in the Standard saturation mode.
Quick	Only the RF pulses actually required for saturation are sent in the Quick saturation mode. The frequency of sending sat. pulses is added to the run time.

Selecting the **Quick** saturation mode lets you reduce the measurement time with fat/water saturation and regional saturation (regular and parallel saturation regions).



To obtain shorter measurement times, select the **Quick** mode, e.g., for breathhold studies.

Saturation region

This parameter shows you the number of saturation region displayed. Via the **Thickness**, **Orientation** and **Position** parameters, you determine the position of the saturation regions.

You add a new saturation region to the measurement protocol by using the **Plus** button next to the **Sat. region** selection list. You delete the current saturation region by using the **Minus** button.

Thickness

Determines the expansion of the saturation region in millimeters.

Shape

Sets the shape (profile) of the saturation region.

Option	Description
Standard	Symmetric saturation shape with moderate edge sharpness. Corresponds to the saturation shape used in previous software versions.
Asymmetric	Asymmetric saturation shape with one sharp edge. This sharp edge can be positioned closer to the anatomy of interest. The sharp edge is indicated in the GSP.



Available only for a few sequences.

Position

Defines the position of the object center.

The following information is displayed when you position the mouse pointer on the field:

- **Table position**
Table position of the protocol, referenced to the whole body patient coordinate system.
- **Phase offcenter**
Shift in phase-encoding direction
- **Read offcenter**
Shift in readout direction
- **Slice shift**
Shift in slice-selection direction



The selection list is dimmed if the position matches the isocenter.



Use this key to open the **Position** dialog window for the slice selected.
(→ Page 188 *Position dialog window*)

Orientation

Indicates the position of the object in space based on the whole body patient coordinate system.



Use this key to open the **Orientation** dialog window for the slice selected.

(→ Page 187 *Orientation dialog window*)

Lipid Suppr.

Suppresses the signal from fat protons in a targeted way.

The following options are available:

Option	Description
Fat sat.	Suppresses the fat signal and has no effect on TE, TR is greatly prolonged. This extends the measurement time as well.
Water excit. normal	Suppresses the fat signal, effects moderate extension of TE and TR.
Water excit. fast	Suppresses the fat signal and causes slight extension of TE and TR. The effect on fat saturation is slightly less than in Water excit. normal mode.
Q-fat sat.	Suppresses the fat signal. This mode is only available when selecting Quick in the Saturation mode selection list.
SPAIR	Prior to image saturation, the fat signal is suppressed via a frequency-selective adiabatic inversion pulse. However, this option is only available with certain sequences for 1.5 T and 3 T systems.
None	Does not suppress the fat portion in the MR signal.



To shorten the measurement time in connection with fat sat, select **Quick** Mode in the **Saturation Mode** parameter.

Fat Sat. mode

Determines the extent of fat suppression.

Water suppr.

Suppresses the signal of water protons in a targeted manner.

The following options are available:

Option	Description
Water sat.	Suppresses the water signal, has no effect on TE, TR is greatly prolonged. This extends the measurement time as well.
Fat excit.	Suppresses the water signal and has a moderate effect on TE and TR. This leads to a slightly longer measurement time.
None	Does not suppress the water portion in the MR signal.

When you select **Quick** setting in the **Saturation mode** parameter in connection with fat saturation, you are able to shorten the measurement time.

Restore magn.

Accelerates restoring the longitudinal magnetization. This increases the signal for T2 weighted acquisitions (even if short repetition times are used).

Special sat.

Establishes *exactly one* parallel or tracking saturation region.



Special sats. may be used if there is one slice/slab group only.



Tracking saturation regions cannot be planned in Quick mode.

The information whether the tracking saturation region is located in front or behind the slice or slice group, is shown in the main orientation of the slice group:

- For **transverse** main orientation: **H** (in front)/**F** (in back)
- For **sagittal** main orientation: **L** (in front)/**R** (in back)
- For **coronar** main orientation: **P** (in front)/**A** (in back)

In this case *in front* means that the saturation region is tracking in front, while *back* means that the saturation region is tracking in back.

Gap

Determines the distance to the associated slice and/or slab group.

1.4.3 Geometry - Navigator

Navigator Objects

You can define navigator objects for special navigator sequences, for example, to measure respiratory movement.

Navigator

Determines the type of currently displayed navigator objects. All parameters that you can currently see on the **Geometry - Navigator** card refer to this navigator object.

You position the navigator exactly on the subphrenic space. For optimal positioning use coronar as well as transverse images.

Position

This parameter defines the position of the object center.

The following information is displayed when you position the mouse pointer on the field:

- **Table position**
Table position of the protocol, referenced to the whole body patient coordinate system.
- **Phase offcenter**
Shift in phase-encoding direction

■ **Read offcenter**

Shift in readout direction

■ **Slice shift**

Shift in slice-selection direction



The selection list is dimmed if the position matches the isocenter.



Use this key to open the **Position** dialog window for the slice selected.
(→ Page 188 *Position dialog window*)

Orientation

Indicates the position of the object in space based on the whole body patient coordinate system.



Use this key to open the **Orientation** dialog window for the slice selected.
(→ Page 187 *Orientation dialog window*)

Rotation

Determines the angle used to rotate the navigator object. The angle refers to the slice plane determined in the **Orientation** parameter.

Only 90° or 0° are possible as angle of rotation for navigator objects. The 90° angle corresponds to swapping the readout direction with the phase-encoding direction.

Base size phase

Determines the expansion of the navigator object in the phase-encoding direction.

Base size read

Determines the expansion of the navigator object in the readout direction.

Thickness

Determines the expansion of the navigator object in millimeters.

1.4.4 Geometry - Tim Planning Suite

e.g.: Geometry - Tim Planning Suite (Set-n-Go)

Large examination regions cannot be covered by a normal field of view (FoV) without distortions. However, you can divide large measurement regions into several smaller regions at different table positions that fit fully into the isocenter of the MAGNETOM. The individual images can then be composed into a single overall image.

In order to facilitate planning and evaluating multi-slice measurements, group the individual measurements or combine them in a Set-n-Go protocol. Make the required settings on the **Geometry Tim Planning Suite** parameter card.

Set-n-Go protocol

Indicates whether the measurement protocol is part of a Set-n-Go protocol.

Notes:

- Distortion correction is a prerequisite for Set-n-Go protocols. The **Distortion Corr.** parameter is automatically set to **2D**.
- The **ISO** or **FIX** mode has to be selected on the **Positioning mode** parameter under the **System - Miscellaneous** parameter card.

Measurement step

Defines the step of the Set-n-Go protocol whose parameters can currently be edited.

Table position

Determines the table position where the protocol will be measured. The zero point is defined by the initial table position of the first measurement of a series block.

The selection list defines the direction of movement.

- **H:** In the head direction
- **F:** In the foot direction

The input field defines the distance in mm.

Table position memory

Displays all table positions already used for the current series block. You can choose a table position from the list and apply it to your protocol.

Inline Composing

Indicates that the images of the steps or the protocol of a composing group can be composed into a complete image.



Inline Composing can be enabled only, when **2D** or **3D** is activated in the **Distortion Corr.** field.

Composing function

Establishes the methods used to compose the images.

The following options are available:

Option	Description
Spine	This algorithm uses the bone structures in the images as a basis. For example, it generates images for the measurement and evaluation of scoliosis, kyphosis, and pelvic obliquity.
Angio	This algorithm uses the vessel structures of the images as a basis. This allows for overall display of the vessels.
Adaptive	This algorithm is based on elastic matching. It especially corrects B0 induced inhomogeneities in image areas beyond the magnetic homogeneity volume.
Diffusion	This algorithm corrects the phase encoding direction shifts caused by different adjustment parameters of the steps of a set-n-go protocol. Used for axial whole body diffusion set-n-go measurements.

Composing Group

Determines to which composing group the protocol belongs.

You set this parameter when you use **Inline Composing** to compose the images of all protocols of a composing group into an overall image.

Last step

The chronologically last measurement of a Composing Group has to be identified as the Last Step. For this purpose you activate this checkbox.

The subsequent protocols belong to a new Composing Group, even if they have the same group number.



Protocols of a Composing Group not completed with a *Last Step* flag are identified by a post-processing icon that has been crossed out.

Normalize

This filter reduces image intensity variation in whole body diffusion measurements.

Used for composed whole body diffusion measurements.

1.4.5 Geometry - Tim CT

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
Common AutoAlign Saturation Tim Planning Suite Tim CT							
Tim CT mode On							
Range start F 0 mm							
Total FoV H >> F 697.2 mm							
Slices 14							
Slice thickness 7.0 mm							
Dist. factor 20 %							
FoV read 430 mm							
FoV phase 71.9 %							
Segments 16							
Table Speed 8.1 mm/s							

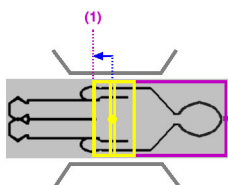
Tim CT mode

Activates the TimCT mode.

An extended measurement region is determined in the TimCT mode, which is measured in continuous table move.

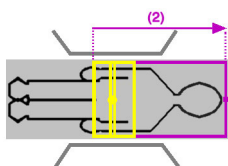
Range start

Defines the start position of the measurement region (1) (measured in the Whole Body Patient Coordinate System).



Total FoV

Determines the total length of the measurement region (2).



2D measurements**Slices**

Determines the number of slices in this group.

Slice thickness

Determines the extension of the measurement area in the slice selection direction together with the number of slices.

In the case of 2D measurements, the slice thickness corresponds to the thickness of a slice within a slice group.

When you change the slice thickness for 2D measurements, you also change the distance between the slices.

3D measurements

For 3D measurements, the slice thickness is the thickness of a slice within a slab (partitions).

When you change the slice thickness with 3D measurements, you change the thickness of the slab as well.



Increasing the slice thickness improves the signal-to-noise ratio, but degrades the spatial resolution in the slice-selection direction.

Dist. factor

Determines the gap between slices and/or slabs of a group in percentages.

At a 100% value the gap corresponds exactly to one slice and/or slab thickness. Negative values lead to overlapping.



Negative distance values cannot be entered for 3D measurements.

FoV read

Determines the size of the anatomical region to be displayed (extension of the measurement in the readout and phase-encoding direction) and its resolution (pixel size).



When the **Tim CT mode** is active, this parameter determines the anatomical region required during RF excitation.

FoV phase

The FoV in the phase-encoding direction (**FoV phase**) is shown as a percentage of the FoV in the readout direction (**FoV read**).

Segments

Defines the number of rows in the k-space that are measured for an image during a TR interval.



Relevant to physiologically-triggered measurements.

Perform CTM adjustments

Enables additional adjustment after TimCT overview measurements.

For each TimCT measurement, adjustment data have to be available for the table move covered during the measurement. If the adjustment data are not at all or only partially available, the system performs an automatic adjustment immediately before the measurement.

After the localizer measurement, adjustment is performed across the entire table range of the localizer.



For subsequent measurements *within* this area, no additional adjustments are performed.



Do not use the **Table Positioning** buttons during the **TimCT** measurement.

Table speed

Shows the table movement speed.

Recon. Mode

Determines how the images are saved.

The following options are available:

Option	Description
Total FoV	The measurement results are saved as an overall image.
Frames	The measurement results are saved as several individual images. These images fit into one image segment each.
Total FoV and individual images	The measurement results are saved as an overall image. In addition, it is also divided and stored as several individual images.

Variable resolution

Enables you to increase the resolution in the phase-encoding and slice-selection direction to the maximum permissible value in part of the examination region, independent of the values for the **Phase resolution** and **Slice resolution** parameters.

(→ Page 31 *Resolution - Common*)

The following options are available:

Option	Description
Off	Variable resolution
End of exam region	Increased resolution at the end of the examination region



If the setting is not **Off**, the reconstructed images display variable levels of resolution. In addition, the image series from the respective areas of the examination region are generated with the higher resolution only.

1.4.6 Geometry - Inversion

Graph. Sel. Inversion

Activates the graphical planning of the inversion, if the value is > 0 .

TI

Determines the inversion time for the graphical inversion.

The value range is 0 to 10000 ms. The default value is 700 ms.



This parameter is only active if **Graph. Sel. Inversion** is set to a value > 0 .

Thickness

Determines the slice thickness for the graphical inversion in millimeters.

The value range is 0 to 150 mm. The default value is 50 mm.



This parameter is only active if **Graph. Sel. Inversion** is set to a value > 0 .

Position

Defines the position of the object center.

The following information is displayed when you position the mouse pointer on the field:

- **Table position**

Table position of the protocol, referenced to the whole body patient coordinate system.

- **Phase offcenter**

Shift in phase-encoding direction

- **Read offcenter**

Shift in readout direction

- **Slice shift**

Shift in slice-selection direction



The selection list is dimmed if the position matches the isocenter.



Use this key to open the **Position** dialog window for the slice selected.
(→ Page 188 *Position dialog window*)

Orientation

Determines the orientation of the object for graphical inversion.

The following options are available:

- sagittal
- coronar
- transverse

1.4.7 Geometry - AutoAlign

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
Common AutoAlign Saturation Tim Planning Suite Tim CT							
Slice group		1		+		-	
Position		R35.4 P2		...			
Orientation		S > C-10		...			
Phase enc. dir.		A >> P		...			
AutoAlign		Head > E		...			
Initial Position		R35.4 P2		...			
R		35.4		mm			
P		2.2		mm			
H		0.0		mm			
Initial Orientation		S > C		...			
		-10.6		deg			
> T		0.0		deg			
Initial Rotation		0.00		deg			



Please refer to the **Routine** parameter card for information about parameters not mentioned here.

Initial Position

Determines the initial offset of the position of the slice plane with respect to the calculated AutoAlign matrix.

Initial Orientation

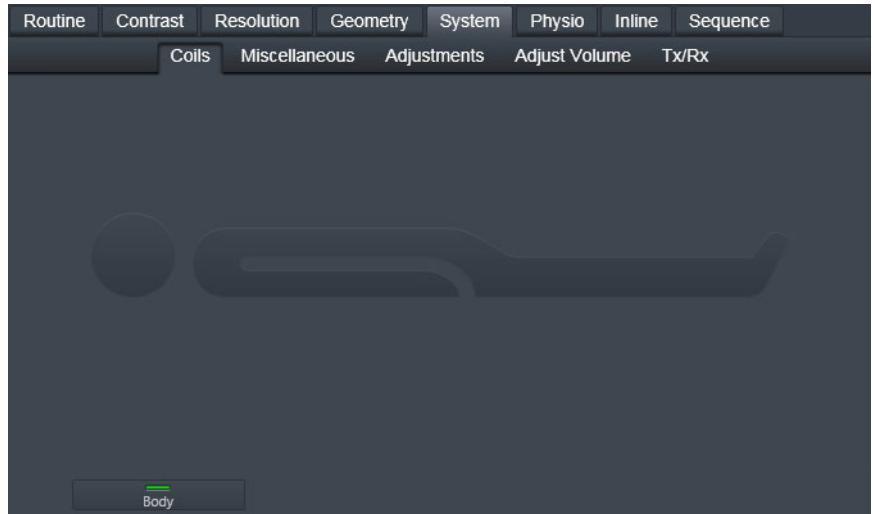
Determines the initial offset of the orientation of the slice plane with respect to the calculated AutoAlign matrix.

Initial Rotation

Determines the initial offset of the rotation of the slice plane with respect to the calculated AutoAlign matrix.

1.5 System

1.5.1 System - Coils



Here you find the positions of the coils connected and their position to the patient.

- **Coil elements with unknown positions** are displayed in the upper area of the parameter card.
- **Coil elements with known positions** are displayed in the lower area of the parameter card. These coil elements are also visible in the GSP.

The figure illustrates the position of the patient:

- Head left: Head first
- Head right: Feet first

All connected coil elements are shown on the parameter card as buttons without overlaps (maximum 64 coil elements). The user can select or deselect them for the measurement.

Several fully identical coils (e.g., Body Array coils) may be connected to the system. The coils are uniquely identified and differentiated by the software. To superpose the coil name, the name of the coil element and the coil socket number, keep the mouse pointer briefly on the appropriate button.

The *Coil Operator Manual* provides you with a detailed description of the coils and their implementation.

Coil memory

Coil selection is linked to table position. As a result, consecutive protocols with similar table positions automatically accept previously edited and completed predecessor protocols when opened.

You can also switch off coil memory:

- ◆ For that purpose deselect **Queue > Coil memory**.

Automatic coil selection

When this setting is activated, the coils in the vicinity are automatically selected when opening a protocol automatically.

The algorithm is based on a cuboid-shaped envelope across all slices of the protocol. All coils in the area of this envelope are selected. Other parameters are kept constant whenever possible.



The maximum number of coils used is limited by the number of system channels.
For large measurement regions on systems with a low number of channels, it may happen that automatic coil selection does not supply the most optimal results.

You can switch off automatic coil selection as well:

- ◆ Deselect **Queue > Auto Coil select**.



To ensure that automatic coil selection functions smoothly when using several Body Matrix Coils, the following has to be observed with respect to the numbers assigned to the coil sockets: Coils closer to the magnet have to be connected to a socket with a lower number.

Copying with copy reference

When you copy using copy reference, the target protocol inherits the coil configuration of the source protocol. This new coil configuration is stored at the respective table position.

Local coils

Matrix and array coils consist of several elements which you may select independently of one another.

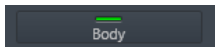
Depending on the examination region relevant to your diagnostic problem, you may activate different numbers of coil elements.



To superpose the coil name, the name of the coil element and the coil socket number, keep the mouse pointer briefly on the appropriate button.

Body coil

All local coils will be deactivated if you want to perform a measurement with the Body Coil.



Activates the Body Coil.



When you deselect the Body Coil again, you activate all previously active local coils and coil elements.



Select the coil elements that are inside the region under examination. Otherwise, image quality may be adversely affected.

Coil elements and iPAT acceleration factor

The number of coil elements or modes corresponds to the max. iPAT acceleration factor.

After the coil elements have been deselected and the acceleration factor set is technically no longer feasible, the acceleration factor is automatically set to the lowest value possible (adjustment using the **Scan Assistant** dialog window).

1.5.2 System - Miscellaneous

The screenshot displays the 'System - Miscellaneous' tab within a software interface. The top navigation bar includes tabs for Routine, Contrast, Resolution, Geometry, System (selected), Physio, Inline, and Sequence. Below this, the 'Miscellaneous' sub-tab is active, showing settings for Coils, Adjustments, Adjust Volume, and Tx/Rx. Key parameters include: Positioning mode set to 'REF', Table position set to 'H' with a value of '4 mm', Coil Combine Mode set to 'Adaptive Cor', Save uncombined checkbox, Matrix Optimization set to 'Off', Coil Focus set to 'Flat', MSMA set to 'S - C - T', Sagittal set to 'R >> L', Coronal set to 'A >> P', Transversal set to 'F >> H', and Coil Select Mode set to 'On - Coil Mei'.

This is where you set the table position. You can perform the measurement at the current table position or you can define a different position.

You are able to define the numbering for the reconstructed images in the selection list for image numbering.

Positioning mode

Determines how the table position of the protocol will be determined or which reference images should be loaded for the protocol.

The following options are available:

Option	Description
FIX	The table position is determined by the protocol, suitable reference images are being searched for.
REF	The table position of the protocol is determined by the focused reference image.
ISO	Both the table positions of the reference image and protocol are independent. The common center of all positioned slices indicates the table position. Distortion-corrected reference images (image type DIS2D / DIS3D) have to be used in this mode.

A detailed description of the dependencies between the positioning mode, table position, and reference images is included in

Table position

Determines the table position where the protocol will be measured. The zero point is defined by the initial table position of the first measurement of a series slab.

The selection list defines the direction of movement.

- **H:** In the head direction
- **F:** In the foot direction

The input field defines the distance in mm.

Table position memory

The list displays all table positions already used for the current series block. You can choose a table position from the list and apply it to your protocol.

Image numbering

Determines the image numbering. MSMA (Multi Slice Multi-Angle) is used to establish the primary sequence according to orientation.

Example:

*Using setting **S - C - T**, the reconstructed images are numbered in the following sequence:*

- *All sagittal images*
- *All coronar images*
- *All transverse images*

In the **sagittal**, **coronar**, and **transverse** selection lists, you can set the secondary sequence. This sequence determines whether the images are numbered in ascending or descending order. The patient coordinates inform about the order (L, R, P, A, H, F). The conventions of the DICOM patient coordinate system apply.

- **Sagittal R >> L or L >> R, Med >> Lat or Lat >> Med**

The sagittal images are numbered in ascending (**R >> L** from right to left or **L >> R** from left to right).

For sagittal slice the images can also be numbered according to their distance from the isocenter (**Med >> Lat** or **Lat >> Med**).

Sorting is performed according to the sagittal position of the slices

in the LPH *whole body patient* coordinate system.

- **Coronar A >> P or P >> A**

With respect to their position, coronar images are numbered in either ascending order (**A >> P** from anterior to posterior or in descending order **P >> A** from posterior to anterior).

- **Transverse F >> H or H >> F**

With respect to their position, transverse images are numbered in either ascending order (**F >> H** from foot to head or in descending order **H >> F** from head to foot).



In every case, the images are numbered by slice groups.



When you activated the **Inherit image numbering** setting of the **queue** menu, the settings for image numbering via protocols are inherited as soon as they are opened for editing.
This applies only to sequential protocols with the same or similar table position.
The inherit mode cannot be switched off.

Save uncombined

Determines whether, in addition to the combined images of an array coil, the output images of the individual coil elements are to be saved.



It is not possible to combine this parameter with the **Adaptive combine** mode under the **Coil Combine Mode** parameter.

Coil combine mode

Determines the algorithm used to combine the signals of several receive coils into one measurement.

The following algorithms are available:

- **Sum of squares**
- **Adaptive Combine**



Adaptive Combine improves the results for most protocols.



It is not possible to combine this parameter with the **Adaptive combine** mode under the **Save uncombined** parameter.

Matrix Optimization

Tim-system coils have built-in mode information. This parameter reads this information to optimize the coil matrix.

Option	Description
Off	No matrix optimization
Performance	Coil modes with compressed information content are calculated. This increases image reconstruction speed due to a lower effective number of required channels.
Cardiac	Coil modes with CP-like properties are calculated from the BodyMatrix channels. This creates channels with more homogeneous spatial sensitivities for improved image quality in cardiac applications.



This parameter **only** works with coils that have built-in mode information!

Coil Focus

Sets the coil focus for some special Coils

Option	Description
Flat	No special coil focus
Center	The outer coil elements of BodyMatrix and SpineMatrix coils are ignored for image reconstruction. This avoids picking up signal from outside the region of homogeneity



Only a limited set of coils are enabled for this feature, for example
 - Body18
 - Spine32

AutoAlign

The **AutoAlign** parameters are found on the **System - Miscellaneous** parameter card in spectroscopy protocols only.

For a detailed description, please refer to the **Routine** parameter card.
(→ Page 8 *AutoAlign*)

Coil Select Mode

Allows a protocol-specific setting for

- **Automatic coil selection**
(→ Page 80 *Automatic coil selection*)
- **Coil memory**
(→ Page 80 *Coil memory*)



Note that **Auto Coil Select** and **Coil memory** are alternating.

Option	Description
Default	Accepts the global system settings for: ■ Auto Coil Select ■ Coil memory
Auto Coil Select on	Activates Auto Coil Select for the <i>respective</i> protocol. In the Coil Coverage dialog window which is accessible via the button next to the parameter field, the sensitivity of the mechanism can be adapted by involving fewer or more coils for a given FOV. Possible settings are: ■ Minimal ■ Standard (default) ■ Generous (involves additional coils located at the edge of the FOV)
Auto Coil select off	Deactivates Auto Coil Select for the <i>respective</i> protocol. Global system settings for Coil memory are accepted.
Coil Memory on	Activates Coil memory for the <i>respective</i> protocol.
Coil Memory off	Deactivates Coil memory for the <i>respective</i> protocol. Global system settings for Auto Coil Select are accepted.
All off	Deactivates both Auto Coil Select and Coil memory .

1.5.3 System - Adjustments

These parameter card includes the settings for system adjustment.



Routine operations do not require changes in adjustment parameters. They should be adjusted in exceptional cases and by highly experienced users only.

The screenshot shows the 'System' tab selected in the top navigation bar. Below it, the 'Adjustments' sub-tab is active. The interface includes the following controls:

- B0 Shim mode:** A dropdown menu currently set to 'Standard'.
- B1 Shim mode:** A dropdown menu currently set to 'TrueForm'.
- Adjustment Tolerance:** A dropdown menu currently set to 'Auto'.
- Adjust with body coil:** An unchecked checkbox.
- Confirm freq. adjustment:** A checked checkbox.
- Only after freq. change:** An unchecked checkbox.
- Assume Dominant Fat:** A checked checkbox.
- Assume Silicone:** An unchecked checkbox.

B0 Shim mode

For the 3D-shim, several modes are offered in the protocol. The range of options depends on the measurement sequence.



Each protocol is preset to the shim mode required for optimum image quality.

Tune-up	Adjustment measurements and evaluations are not performed. The system uses the values set during system tune-up by Siemens Service. This setting is sufficient for standard imaging protocols without special requirements.
Standard	Adjustment measurements and evaluation are performed in the standard mode. This mode is suitable for imaging protocols with special requirements, for example, for fat saturation or EPI.
Advanced	Adjustment measurements and evaluation are performed in the advanced mode. This mode is used mainly for spectroscopy protocols. The advanced mode is both time-consuming and only necessary for measurements that place the greatest demand on the homogeneity of the magnetic field.
Cardiac	Adjustment measurements and evaluation are performed in the cardiac mode. This mode is suitable for imaging protocols with special requirements due to the beating heart.
Standard Neck	Adjustment measurements and evaluation are performed in the Standard mode, with additional optimizations for the neck region. This mode is suitable for imaging protocols with special requirements for fat saturation of the neck. Since adjustments are based solely on signal from the neck coil, this coil needs to be selected in the protocol.
Foot/Ankle	Adjustment measurement and evaluation are optimized for Foot/Ankle exams.
Brain	Adjustment measurement and evaluation are optimized for brain spectroscopy.
Breast	Adjustment measurement and evaluation are optimized for breast and breast spectroscopy.
Prostate	Adjustment measurement and evaluation are optimized for prostate spectroscopy.
Abdomen	Adjustment measurement and evaluation are optimized for abdominal exams.



It is also possible to use the manual interactive shimming method, independent of this protocol setting.



Only use the shim modes in their designated anatomical regions. The adjustment FoV and other settings are exclusively adapted to the given anatomical region.

Adj. water suppr.

Performs water suppression adjustment

For spectroscopy measurements, special RF pulse trains are used that suppress the water signal.

Adjust with body coil

Performs adjustment with the body coil.

Usually, all adjustments are made by using the coil elements established in the respective protocol. In addition, it is possible to receive with the body coil only. This means that new adjustments are omitted when changing the selection of coil elements.



For measurements with the transmit coils, it is not possible to perform adjustments using the body coil.

Confirm freq. adjustment

Defines whether the **Confirm Frequency Adjustment** dialog box appears before every measurement.

You can pause the system to confirm or change the resonance frequency calculated by the adjustment.

Only after freq. change

The **Confirm Frequency Adjustment** dialog box only appears, if the resonance frequency was changed due to inline adjustment.

Assume Dominant Fat

The **Assume Dominant Fat** option optimizes measurements of patients having dominant fat tissue.

Assume Silicone

Adjustment in silicone mode.

The **Assume Silicone** option optimizes measurements of patients having silicone implants.

TxRef [Nucleus]/Ref.

Shows a list of reference amplitudes for the selected primary or secondary nucleus.

It is possible to change the values for the reference amplitude.



All values changed manually are marked by an exclamation mark ("!").

Adjustment Tolerance

Defines the adjustment tolerance.

The adjustment results can be used as default values for similar table positions. The options for **Adjustment Tolerance** are:

Option	Description
None	Adjustment results are only used again at the identical table position.
Maximum	Adjustment results are used as well on similar table positions.
Auto (None)	The adjustment tolerance is determined automatically by the system. "None" is selected.
Auto (Maximum)	The adjustment tolerance is determined automatically by the system. "Maximum" is selected.

1.5.4 System - Adjust Volume

These parameter card includes the settings for system adjustment.



Routine operations do not require changes in adjustment parameters. They should be adjusted in exceptional cases and by highly experienced users only.

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
		Coils	Miscellaneous	Adjustments	Adjust Volume	Tx/Rx	
Position	L0.0 P43.5 H3.9		...				
Orientation	Transversal		...				
Rotation	90.00		deg				
R >> L	340		mm				
A >> P	340		mm				
F >> H	163		mm				
Reset							

Adjust volume

Geometry of the adjustment volume

1.5.5 System - Tx/Rx

These parameter card includes the settings for system adjustment.



Routine operations do not require changes in adjustment parameters. They should be adjusted in exceptional cases and by highly experienced users only.

This parameter card shows the results of the last automatic and successful adjustment.

Frequency 1H

Displays the system frequency.

Ref. amplitude 1H

Displays the reference amplitude.

Correction factor

Displays the correction factor for water suppression.

Puls/Amplitude

Displays the amplitude of the RF pulses used in the protocol. You are able to overwrite the automatically computed settings.



All pulse amplitudes are automatically calculated based on the reference amplitude and, if necessary, the correction factor.

Gain

Sets the sensitivity of the receiver.

The recommended receiver gain is automatically calculated by the system.

Imag. Scale. Cor.

Sets an additional modification factor, which adjusts the grayscale range of the images, after channel combination and before sending them to the database.

1.6 Physio

1.6.1 Physio - Signal 1



Physio - Signal 1 parameter card in the ECG/Trigger mode

Adjust the special measurement parameters for physiologically triggered measurements to avoid motion artifacts caused by the heartbeat or respiration.

Assign also retrospectively acquired image data to physiological signal curves.



Prior to setting the measurement parameters, we recommend to reset the long-time statistics in the **Physiological Display** window to obtain the most current value for the **Average cycle** parameter.

1st Signal/Mode

Determines the physiological signal applied and the measurement mode for physiologically triggered measurements.

Option	Description
ECG signal	ECG triggering is especially suitable for measurements of the chest and heart. The ECG signal is detected on the skin surface with electrodes. The signal shows the action potential of the heart as a curve. The R-wave in the QRS complex is used as the trigger point for the measurement.
Pulse signal	Use pulse triggering especially to suppress motion or flow artifacts generated by pulsing blood or CSF. Take the pulse signal, for example, from the middle finger of the patient with the pulse sensor. The first pulse wave ("premature pulse wave") is used for triggering. This wave corresponds to the systolic blood pressure.
External signal	Use an external triggering signal, for example, for functional measurements to trigger measurement of a series. Input an external, digital triggering signal via the PMU strip at the foot end of the patient table. The rising edge of the signal is used to start the measurement.
Respiratory signal	Respiratory triggering avoids motion artifacts caused by the patient's breathing. The respiratory signal is obtained with the respiratory belt. The cyclic expansion and contraction of the thorax generates the respiratory curve.
ECG/Retro, Pulse/Retro, Ext/Retro	Some special sequences offer retrospective gating . The measurement is performed with triggering. Instead, the acquired image data are retrospectively sorted and subsequently correlated with the characteristics of a physiological signal. Apply retrospective gating to ECG signal curves, pulse signal curves, and external trigger signal curves.

Average cycle

Displays the average time between two trigger events.

The value of the average cycle is used to compute the system acquisition window:

Signal	Calculation
ECG, Pulse, External	System acquisition window = Average cycle - 2 x standard deviation
Respiratory signal	System acquisition window = Average cycle / 2 - standard deviation

Captured cycle

Computes the acquisition window again from the current average cycle with this button.

The button displays the value of the average cycle used for the calculation.

Acquisition window

Determines the data acquisition time (the time used after the trigger pulse for a measurement following a physiologically-triggered pulse). This defines the scan acquisition window.

The size of the acquisition window, the delay time, number of phases and repetition time calculates automatically a number of cardiac sequences.

Keep the mouse pointer over the **Acquisition window** input field, to display the value recommended by the system.



Determine the acquisition window approx. 10% shorter than the average signal period (average cycle).

Trigger pulse

Determines which trigger events releases a measurement (1 = every trigger, 2 = every second trigger, etc.).



Active only for the ECG, pulse, and external trigger signals.

Trigger delay

Acquire images anywhere within the signal cycle by entering a delay time into the **Trigger delay** input field for the **ECG/Trigger** signal.

The value entered corresponds to a delay time (gray bar) between the trigger signal and the start of the measurement.



Active only for the ECG, pulse, and external trigger signals.

TR (repetition time)

Determines the repetition time **TR** that elapses between two successive excitations.

Changing the repetition time affects image contrast and measurement time.

Entering several repetition times, superimposes additional keys for scrolling between the individual times.

Concatenations

Defines into how many repetition times TR the measurement of the planned slices are divided. The system determines across how many single sequential measurements the slices are distributed.

Using this method, you can acquire many slices with a short repetition time (T1 weighted imaging) and prevent slice crosstalk.



The number of breathhold intervals is determined via the **Concatenation** parameter, if a measurement in multiple breathhold mode uses the input **Breath-hold** under **Respiratory Control**.

- In the **Interleaved** multi-slice mode, the number of breathhold intervals results from the product of the parameter values **Measurements** and **Concatenations**.
- In the **Single Shot** multi-slice mode, the number of breathhold intervals is the product of the parameter values **Measurements**, **Concatenations** and **Averages**.



Sometimes it takes two measurements to acquire all slices, using the triggered multislice measurements ("interleaved" excitation sequence).



Only active, if the **Interleaved** or **Single Shot** option is selected in the **Multi-slice mode** on the **Geometry - Common** parameter card.

Flow sensitivity

Determines the flow sensitivity of the sequence by modifying the flow-spoiling gradient.

Can be used to adjust a syngo NATIVE SPACE acquisition to the expected blood flow conditions.

Option	Description
Default	The default spoiler settings of the SPACE sequence are used.
Weak	Weak flow spoiler gradients are used.
Medium	Medium flow spoiler gradients are used.
Strong	Strong flow spoiler gradients are used.



Available only for SPACE sequences.



Available only if the parameter **NATIVE** is set to **3D mode** or **TD scout**.

Segments

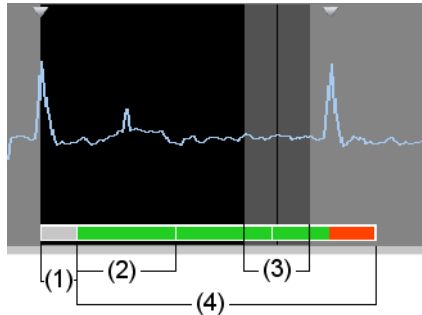
Defines the number of rows in the k-space that are measured for an image during a TR interval.



Relevant to physiologically-triggered measurements.

Displaying the time domain

Displays the physiological signal as well as the time domains resulting from the parameters set.



- (1) Displays the delay time
- (2) Displays the repetition time
- (3) Displays twice the standard deviation
- (4) Displays the measurement acquisition window



If the measurement acquisition time set exceeds the time between two trigger events, the acquisition window overlaps (overlap is displayed in red) the following trigger section.

Phases

Determines the number of phases of the heart beat or the number of respiratory phases you want to require for, e.g., multi-slice/multi-phase measurements of the heart.



The number of heart phases or respiratory phases depends on the selected repetition time TR. Always observe the limits.

Arrhythmia detection

Determines the mode for automatically detecting of arrhythmia.

Some sequences include an automatic detection of arrhythmia. This detection is based on a time-controlled recognition of additional systoles (**By time**).

Trigger window

Establishes the size of the acceptance window, if extra systolic detection is activated.



Only active for arrhythmia detection according to time.

Threshold

Determines the time when the measurement is triggered within the respiratory cycle. When the respiratory curve reaches this threshold value, the signal is triggered.

The threshold value is expressed as a percentage of the respiratory curve. 100% corresponds to the maximum expansion of the rib cage.



Only displayed for **Respiratory triggering**.

Calculated phases

Determines the number of reconstructed images per heart interval.



Displayed if you select a **Retro** mode in the **1st Signal/Mode** selection list.

Resp. phase

Determines whether **inspiration** or **expiration** is used for triggering.

Target RR

Establishes the patient's average heart rate for the system. Based on this parameter, arrhythmia is detected with some sequences and the data acquired with arrhythmia are discarded. The value should correspond to the average heart rate of the patient.



Not available for CV-NAV sequences.



The value of this parameter effects the **Segments** parameter.

NATIVE

Generates arterial and venous images without contrast agent.

Option	Description
Off	The NATIVE functionality is not used.
3D Mode	Used for 3D non-contrast enhanced angiography. Typically, two ECG-triggered data sets are acquired (in systole and diastole). The Parameters TD peak flow and TD min flow must be set properly. Resulting angiographic images are computed via Inline subtraction.
TD scout	Used to determine suitable TD values. In this mode, a series of thick-slab projection images with different trigger delays is acquired from the slab of interest. The timing can be adjusted with the two parameters TD first and TD increment .



Available only for SPACE sequences.



Available only if the parameter **1st Signal/Mode** is set to **ECG/Trigger**, **Pulse/Trigger** or **Ext./Trigger**.

TD peak flow

Defines the trigger delay for the first acquisition.

After the trigger (R-wave), the system waits for the defined delay time before the measurement starts.

A typical TD value that provides good results is obtained by subtracting approximately 30ms from the peak flow time within the cardiac cycle.



Available if **NATIVE** is set to **3D Mode**.

TD min flow

Defines the trigger delay for the second acquisition.

After the trigger (R-wave), the system waits for the defined delay time before the measurement starts.

A typical TD value that provides good results is 0ms.



Available if **NATIVE** is set to **3D Mode**.

TD first

Defines the trigger delay for the first acquisition of a series of TD scout acquisitions.

After the trigger (R-wave), the system waits for the defined delay time before the measurement starts.



Available if **NATIVE** is set to **TD scout**.

TD increment

Defines the trigger delay increment for a series of TD scout acquisitions.
The trigger delay increases from one measurement to the next.



Available if **NATIVE** is set to **TD scout**.

Measurements

Determines how often a measurement is performed.



In the context of **NATIVE**:

These measurements are carried out at different trigger delays.
Typically, two measurements are done in **3D mode**, and a series of multiple measurements are done for a **TD scout**.

Adaptive Triggering

Adapts the acquisition time to the current heart rate.

The parameter **Trigger Lock Time** sets the minimal acquisition time.



This parameter is only available for the **1st Signal/Mode** parameter in the following modes: **ECG signal**, **Pulse signal**, **Respiratory signal**, **External signal**.

Trigger Lock Time

Sets the minimal acquisition time for **Adaptive Triggering**.



This parameter is only available for the **1st Signal/Mode** parameter in the following modes: **ECG signal**, **Pulse signal**, **Respiratory signal**, **External signal**.

1.6.2 Physio - Cardiac

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
				Cardiac	PACE		
				FoV read 340 mm			
				FoV phase 78.1 %			
				Phase resolution 65 %			
Magn. preparation				Slice-sel. IR			
				TI 160 ms			
Fat suppr.				None			
				Dark blood ☒			
Dark blood thickness				400 %			
Slice-sel. IR thickness				200 %			
				Trajectory Cartesian			

Displays parameters relevant for a cardiac examination. Available only if the current measurement protocol is based on a sequence which supports physiologically triggered acquisitions.

Tagging

Combines CINE imaging with tagging pulses to generate images with a grid or line pattern superimposed on the region being scanned. When used in heart examinations, the tags deform with the myocardium during the cardiac cycle.

Option	Description
Grid tag	Results in images with a grid pattern superimposed on the region being scanned. Used to visualize regional and global cardiac wall motion e.g. in short-axis views of the heart.
Line tag	Results in images with a line pattern superimposed on the region being scanned. Used to visualize cardiac wall motion e.g. in long-axis views of the heart.
None	No tags applied.

Distance

Determines the distance between tags.

Angle

Defines the angle between line tags and the phase-encoding direction.

Magn. preparation

Determines whether an RF pulse is transmitted prior to each measurement to affect contrast (during inversion recovery (IR) and saturation recovery (SR)).

Send the inversion pulse as slice-selective or non-selective. Consider whether your current sequence is an inversion recovery sequence (IR) or a saturation recovery sequence (SR).

Option	Description
Slice sel./slab sel. (IR or SR)	Performs the measurements slice by slice.
Non-sel. (IR or SR)	The RF pulses stimulate the entire volume independent of the current slice position or measurement sequence.
T2 preparation	A special preparation pulse is transmitted for the entire volume to enhance T2 contrast. The preparation pulse suppresses signals from tissue with short T2 times. On the Contrast parameter card you can determine the duration of the preparation pulse in the T2 Prep. duration field.
TI Scout	This scout generates a series of images with different inversion time. Based on this series, you can determine the most suitable inversion time and enter the value in the TI parameter.
T2 sel IR	A special inversion preparation pulse is transmitted for the entire volume. This pulse effects that only tissue with a long T2-time (fluids) is fully inverted. Tissue with short T2 is only inverted in part. In a subsequent excitation, it is possible to display it with a higher signal (e.g. for protocols with dark fluid contrast).
None:	No inversion pulse is sent.



If you select the **None** option in the **Magn. preparation** list, the **TI** parameter on the **Contrast - Common** card is usually not offered.

TI (Inversion time)

Determines an additional T1 contrast added with spin preparation. A 180° RF pulse is used (inversion pulse) to invert the spins.

■ **For inversion recover sequences:**

TI is the time between sending the inversion pulse and the excitation pulse of the subsequent measurement (e.g., a spin-echo pulse sequence). Depending on the TI, certain signals are suppressed (e.g., fat) and additional T1 contrast is applied to the signal.

■ **For Turbo FLASH sequences:**

TI describes the time between sending the inversion pulse and reading out the echo signal, sorted in the center of the raw data matrix (this echo determines the contrast).

Fat suppr.

Suppresses the signal from fat protons in a targeted way.

Option	Description
Fat sat.	Suppresses the fat signal and has no effect on TE, TR is greatly prolonged. This extends the measurement time as well.
Water excit. normal	Suppresses the fat signal, effects moderate extension of TE and TR.
Water excit. fast	Suppresses the fat signal and causes slight extension of TE and TR. The effect on fat saturation is slightly less than in Water excit. normal mode.
Q-fat sat.	Suppresses the fat signal. This mode is only available if Quick mode is selected in the Saturation mode .
SPAIR	Prior to image saturation, the fat signal is suppressed via a frequency-selective adiabatic inversion pulse. T this option is only available with certain sequences for 1.5 T and 3 T systems.
None	Does not suppress the fat portion in the MR signal.



To shorten the measurement time in connection with fat sat select the **Quick** Mode in the **Saturation Mode** parameter.

Dark Blood

Determines if a non-selective preparation pulse (which saturates the blood) is selected for cardiac sequences. Displays the heart muscle exceptionally well and the blood appears dark in the image.

Dark blood thickness

Determines the thickness of the saturation slab used to reduce the intensity of the blood. Expresses the thickness as a percentage of the slice thickness.

Dark blood flip angle

Determines the flip angle of the preparation pulse for saturating the blood.



The default value is 200.

Slice-sel. IR thickness

Determines the thickness of the slice selective IR pulse when performing STIR imaging of the heart, given as a % of the protocol slice thickness (e.g. the default value of 200% means that the slice thickness of the STIR pulse is twice that of the acquired slice).



This parameter should be changed to higher values, e.g. 280 % when imaging patients with faster heart-rates.

FoV read

Determines the size of the displayed anatomical region (extension of the measurement in the readout and phase-encoding direction) and its resolution (pixel size).



Determines the anatomical region required during RF excitation if the **Tim CT mode** is active.

FoV phase

Displays the FoV in the phase-encoding direction (**FoV phase**) as a percentage of the FoV in the readout direction (**FoV read**).

Phase resolution

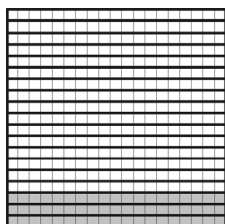
Determines the resolution of the slices in the phase-encoding direction. Provides the parameter in percentages referenced to the basic resolution.

Cine

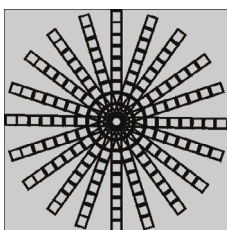
Indicates a Cine sequence for the display of dynamic processes.

Trajectory

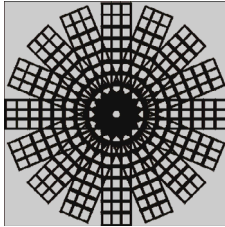
Defines the geometric shape sampled in the k-space.



Cartesian: The k-space is sampled as a matrix of rows and columns. The k-space is built up line by line, for example, from the bottom left to the top right.



Radial: The k-space is read out in individual lines, forming a star.



BLADE: Data are acquired in so-called blades. Every blade comprises parallel phase-encoding lines. The individual blades are rotated in order to cover a circle in the raw data space.



The number of lines per blade is determined in the **Turbo Factor** parameter on the **Sequence - Part 2** parameter card.

View sharing

Defines whether k-space data already acquired in a measurement should be reused, for example to obtain higher temporal resolution.

The following options are available:

Option	Description
Off	No data sharing across measurements.
Shared phases	In a CINE acquisition, k-space data are shared across subsequent (cardiac) phases.
TWIST	In a dynamic acquisition, data from the outer k-space region are shared across multiple measurements.

1.6.3 Physio - PACE

The screenshot shows the 'Physio - PACE' parameter card. It features a top navigation bar with tabs: Routine, Contrast, Resolution, Geometry, System, Physio (selected), Inline, and Sequence. Below this is a sub-navigation bar with 'Signal1', 'Cardiac', and 'PACE' (selected). The main area contains several controls: 'Resp. control' set to 'Gate & Follow', 'Scout mode' checked, a 'Tracking' button with '+' and '-' icons, 'Scout duration' at 19 s, 'Scout TR' at 100 ms, 'Chronologic posi' set to 'Before echo', 'RF pulse type' set to 'Crossed', 'Accept window ±' at 4.0 mm, 'Accept position (green)' at 128.0 mm, 'Resp. Motion Adaptation' checked, 'Search window ±' at 32.0 mm, 'Search position (red)' at 128.0 mm, and 'Concatenations' set to 1.

Displays the parameters for suppressing respiratory artifacts.

Resp. control

Determines the method used for suppressing respiratory artifacts.

Respiratory control mode	Description
Off	Switches the navigator control off.
Breath-hold	Slices of one concatenation are measured as soon as you press the Scan Breathhold button in the Inline display. The number of manual starts required for the complete measurement equals the number of concatenations set. For some sequence types, e.g. <i>TimCT Oncology</i> , the duration of a breath-hold scan can be set in the Breath-hold duration parameter. (→ Page 119 <i>Breath-hold duration</i>) The Inline display provides an icon to continue the scan to the end of the measurement.
Gate	The image data are only accepted if the diaphragm position is within the acceptance window.

Respiratory control mode	Description
Gate & Follow	If the navigator result is within the acceptance window, the positions of the slices to be measured are offset in accordance with the navigator result and the measurement is resumed with the next iteration of the loop structure. Otherwise, the current loop is repeated.
Trigger	Acquires a block of image data after a learning period of approximately 5 respiratory phases, once the measured diaphragm position indicates the end of the expiration phase. Respiratory triggering reduces motion artifacts by synchronizing measurement of the image data with the respiratory cycle of the patient.
Monitor only	Calculates and displays the navigator signals in the usual way, they are not used to control the measurement.

Scout mode

Determines a preparation phase which only measures the navigator signal. Check whether or not the navigator records the respiratory signal as required.

Scout duration

Determines the duration of the preparation phase.



Active only, if the **Scout mode** parameter is activated.

Scout TR

Determines the repetition time of the navigator pulse.

1 Parameter Cards

Accept window $\pm$

Determines one mode of the selection list under **Resp. control**.

Respiratory control mode	Effect of the Accept window $\pm$ parameter
Gate Gate & Follow	Acquires the image data as soon as the deviation of the diaphragm position (relative to the reference position) is less than the value specified in the Accept window $\pm$.
Trigger	Determines the vertical width of the yellow acceptance window shown in the Inline display. The trigger algorithm determines the end of expiration as soon as the sequence of measured diaphragm positions (green curve) falls within the acceptance window. The acceptance window is not displayed while the patient is breathing in.

Accept. position (green)

Determines the requested center position of the accept window.



Displayed only for respiratory control **Gate** or **Gate & Follow**.

Scout type

Defines the scout type used for the navigator.

Option	Description
Liver dome scout	Selects a navigator which tracks the diaphragm edge. This navigator is positioned manually by the operator on the edge of the diaphragm in the coronal reference image.
Phase scout	Selects a navigator which detects tiny fluctuations of the B0 field induced by the breathing of the patient. ■ If Position navigator is Automatic: The navigator box is positioned without operator interaction and is not visible in the GSP. ■ If Position navigator is Manual: The navigator box should be positioned within the homogeneous liver parenchyma. For a detailed description of the optimal navigator positioning refer to the <i>Operator Manual - Body</i>.

Search window ±

Enter the size in millimeters for the **Search window ±** for **Gate** or **Gate & Follow**.

Displays the search window as a red box surrounding the tolerance center in the **Inline Display**.

Search position (red)

Enter the center position of the search window in millimeters in the **Search position (red)** input field for **Gate** or **Gate & Follow**.

Tracking factor

Determines the correlation between diaphragm movement and the resulting shift in anatomy.



This parameter is superposed if you set the **Gate & Follow** under **Resp. Control**.

Chronologic position

Determines the time when triggering the navigator signal in the **Gate** or **Gate & Follow** respiratory control mode.



If the **Gate & Follow** respiratory control mode and the chronological position **before & after** of the echo train of the image are selected, the slice follow algorithm of the information is based on the first navigator signal and the gating algorithm on a combination of the first and second navigator.

RF pulse type

Determines the length and envelope of the RF excitation pulse.

Option	Description
Fast	Short RF excitation pulse which could cause cross-talk between the slices / slabs. We recommend this setting only for rapid measurements with distance factors that are not too small, e.g., for respiratory breathhold techniques.
Normal	RF excitation pulse with a good slice profile allows measurements with a small distance factors and little cross-talk.
Low SAR	Extended RF excitation pulse with good slice profile and reduced specific absorption rate. You can select this setting for SAR reduction (it reduces the measurement performance).
Optimized	Optimized RF excitation pulse to reduce slice cross-talk.

Position accept window

✓ Respiratory control is set to **Trigger**

Determines whether the system automatically sets the center of the acceptance window during a learning phase, or whether you enter it manually in the **Accept position** input field.

Trigger pulse

Determines which trigger events release a measurement (1 = every trigger, 2 = every second trigger, etc.).



Active only for the ECG, pulse, and external trigger signals.

Card. trig. per resp. cycle

Determines the number of cardiac trigger pulses per respiratory cycle.



During double triggering, this parameter is superimposed in place of **Slices per resp. cycle**.

Concatenations

Defines into how many repetition times TR the measurement of the planned slices are divided. The system determines across how many single sequential measurements the slices are distributed.

This method acquires many slices with a short repetition time (T1 weighted imaging) and prevent slice crosstalk.



Determine the number of breathhold intervals via the **Concatenation** parameter by selecting a measurement in multiple breathhold mode and select **Breath-hold** under **Respiratory Control**.

- In the **Interleaved** multi-slice mode, the number of breathhold intervals results from the product of the parameter values **Measurements** and **Concatenations**.
- In the **Single Shot** multi-slice mode, the number of breathhold intervals is the product of the parameter values **Measurements**, **Concatenations** and **Averages**.



Sometimes it takes two measurements to acquire all slices, using the triggered multislice measurements ("interleaved" excitation sequence).



Select the **Interleaved** or **Single Shot** option in the **Multi-slice mode** on the **Geometry - Common** parameter card to activate the field.

Store profile images

Displays the temporal change of the navigator signal graphically in the **Inline Display**. These images are saved in a separate series.

Accept. Position

Determines the center of the acceptance window for **Trigger**. 0% of the center position corresponds to the center position at the end of expiration during the learning phase and 100% correspond to the center position at the end of inspiration during the learning phase.

Slices per resp. cycle

Determines the number of slices acquired per respiratory cycle.



Displayed only during **haste**, **trufi** and **tfl** sequences.

Resp. Motion Adaptation

Determines whether the position of the accept window adjusts to the changes in amplitude of the respiratory curve. This prevents, for example, a shallower respiratory curve leading to infinite measurements.



Active only if the **Gate & Follow** or **Gate** mode is selected under the **Resp. control** parameter.

Breath-hold duration

Determines a patient specific duration of one breath-hold for certain sequence types (e.g. *TimCT Oncology*) as an alternative to the duration of one concatenation.

Select acquisition window

Manual: Displays the parameter **Acquisition window**. The system sets the acquisition duration per respiratory cycle equal to or less than the Acquisition window specified by the user (by adapting the number of concatenations in a 2D measurement, or by limiting the parameter range of other parameters (e.g. Slice Turbo factor for SPACE)).

Automatic: The system determines the acquisition window patient adaptive during the learning phase of the navigator triggered measurement and adapts appropriate parameters (e.g. number of concatenations) at run time.

Acquisition window

(→ Page 97 Acquisition window)



Available only if the parameter **Select acquisition window** is set to **Manual**.

Position navigator

Manual: Selects the FLASH navigator used in previous software versions. The operator positions the navigator manually on the edge of the diaphragm in the coronal localizer.

Automatic: Selects a new navigator, which tracks the patients breathing cycle, if it is crudely positioned in the vicinity of the lungs. The system positions the navigator automatically.

1.7 Angio

1.7.1 Angio - Common

Routine Contrast Resolution Geometry System Physio **Angio** Sequence

Common Inline MIP Composing

TONE ramp 70 %

Flow direction F >> H

Flip angle 18 deg

MTC ☐

Measurements 1

3D centric reordering ☒

e.g.: Angio - Common (Time-of-Flight angiography)

Routine Contrast Resolution Geometry System Physio **Angio** Sequence

Common Inline Cardiac MIP Composing

Flow mode Free

Encodings 3

Velocity enc. (cm/s) Direction

150	Through
100	Through
100	Through

Rephased images ☒

Magnitude images ☒

Magnitude sum ☐

Phase images ☒

e.g.: Angio - Common (Time-of-Flight angiography and flow quantification)

Available only if the sequence used as the basis for the current measurement protocol supports the following examinations:

- Time-of-flight angiography
- Contrast-enhanced angiography
- Phase contrast angiography (2D and 3D)
- Flow quantification

Time-of-flight angiography

In time-of-flight angiography sequences, unsaturated spins flow into the slice or volume to generate especially high signal intensity.

Contrast-enhanced angiography

Contrast-enhanced angiography (**Contrast Enhanced Angiography**) takes advantage of the fact that the contrast agent (gadolinium compound) shortens T1 in blood.

Phase contrast angiography and flow quantification

2D phase contrast angiography is used to display vessels within large measurement volumes.

With **3D phase contrast angiography**, you can further process the entire measured data volume with the MIP technique.

Flip angle

Determines the extent the RF pulse deflects the longitudinal magnetization from the Z-direction of the magnetic field. The flip angle directly affects image contrast.

For spin echo sequences, enhance the T1 contrast by reducing the flip angle.

TONE ramp

Adjusts the form of the RF excitation pulse to the velocity and direction of the blood flow (slow, medium, fast) to avoid saturation effects of blood when passing through a slab.

Specifies the ratio of the respective flip angle at the two edges of the slab in percent.



TONE-Technique = **T**ilted **O**ptimized **N**onsaturating **E**xcitation

Flow direction

Determines the direction of blood flow. The direction always refers to the patient coordinate system.



A change of the directions, can automatically position the tracking sat regions on the side of the slab from where the arterial blood exits.

MTC (magnetization transfer)

Determines whether the signal of tissue with a high portion of macro molecules is weakened by a special RF excitation pulse.



Activate the **MTC** checkbox to obtain better contrast in images for e.g., vessel examinations.

3D centric reordering

Determines whether the center of the raw data space is measured as quickly as possible after contrast agent inflow with contrast-enhanced 3D angiography. This ensures optimal contrast of the arterial vessels.

Time to center

Determines the measurement time required to reach the center of the k-space.

This information is required for timing the contrast agent bolus in contrast agent enhanced angiography.

Flow mode

Determines the flow encoding mode:

Option	Description
Single vel.	One flow sensitivity (flow sensitivity encoding): Measures the velocity of the blood in 3 spatial directions with one flow sensitivity. This mode provides vessel display independent of the direction of flow.
Single dir.	One direction for several flow sensitivities: Measures the blood flow as a function of several flow sensitivities, however, in one spatial direction only. This mode is used to acquire large variations in flow velocities (e.g., in the area of peripheral arteries).
Free	Allows for freely-selectable flow sensitivities and spatial directions.

Encodings

Determines the number of distinguished flow sensitivities.

Velocity enc.

Determines the different flow sensitivities.

Direction

Determines the location of the flow-sensitive axis for the different flow sensitivities.

Select a setting (with the **Through plane** option), where e.g., the flow sensitive axis is located vertically to the image plane. Only the flow vertically to the image plane will be acquired.

Rephased images

Determines whether flow-phased images (magnitude images) are reconstructed.

Magnitude images

Determines whether a set of magnitude images is reconstructed (1 image per flow direction or flow sensitivity).

Magnitude sum

Determines whether a magnitude sum is reconstructed from the magnitude image of a slice.

Phase images

Determines whether a set of phase images is reconstructed (1 image per flow direction or flow sensitivity).

MIP images

Defines whether MIP images (maximum intensity projection) are reconstructed from all magnitude sum images of a measurement.

This procedure is used primarily for MR angiography. As a result, blood vessels appear lighter than the rest of the image.

Std.Dev. images

Defines whether the standard deviations from the magnitude sums are calculated in order to reconstruct an image.

Central region A

Determines the size of the k-space center that is acquired with full sampling density.

This value is provided as a percentage of the total number of sample points that will be acquired.



This parameter is only active when **TWIST** is selected under the **View sharing** parameter.

Sampling density B

Determines the sampling density used to sample the individual temporal phases in the outer k-space.



This parameter is only active when **TWIST** is selected under the **View sharing** parameter.

Dynamic recon. mode

Determines in which way the k-space is dynamically reconstructed for several measurements.

Option	Description
Forward share	Data acquired in the outer k-space region are transferred to the <i>preceding</i> images.
Backward share	Data acquired in the outer k-space region are forwarded to the <i>following</i> images.
Symmetric Share	Data acquired in the outer k-space region are transferred to both the <i>preceding</i> and <i>following</i> images in symmetric fashion.



This parameter is only active when **TWIST** is selected under the **View sharing** parameter.

Temporal interpolation of MIP series

Determines the linear interpolation of the images. The number of MIP images is increased by an interpolation factor.



This parameter is only active when **TWIST** is selected under the **View sharing** parameter.

Temporal resolution / Virt. temporal resolution

Displays the time between two consecutive MIP images of the reconstructed 3D image series.

This value is the "virtual" temporal resolution resulting from the time between two measurements and the interpolation factor set under **Temporal interpolation of the MIP series**.

With an interpolation factor greater than 1, the parameter is described as **Virt. temporal resolution**.



This parameter is only active when **TWIST** is selected under the **View sharing** parameter.

Burn time-to-center

Determines if the value from the **time to k-space center** is burned into the pixel data of the image to display this information in the **Exam** task card.



This parameter is only active when **TWIST** is selected under the **View sharing** parameter.

1.7.2 Angio - Inline

Displays the parameters for dynamic image evaluation of angio examinations.

Motion Correction

This parameter registers the post-contrast minuend(s) to the pre-contrast subtrahend. It is available for the **fl3d_ce** sequence (3D mode) in the context of subtraction.

Option	Description
None	No motion correction selected
Angio Standard	Rigid-body registration algorithm
Angio Advanced	Locally adaptive algorithm



The original 3D datasets are always stored in addition to any processed results. The diagnosis may not be performed on motion corrected or subtracted images only. The original images have to be considered for diagnosis, too.

The parameter card **Angio - Inline** corresponds to the **Inline - Common** parameter card.
(→ Page 145 *Inline - Common*)

1.7.3 Angio - MIP

The parameter card **Angio - MIP** corresponds to the **Inline - MIP** parameter card.
(→ Page 161 *Inline - Composing*)

1.7.4 Angio - Composing

The parameter card **Angio - Composing** corresponds to the **Inline - Composing** parameter card.
(→ Page 161 *Inline - Composing*)

1.8 BOLD

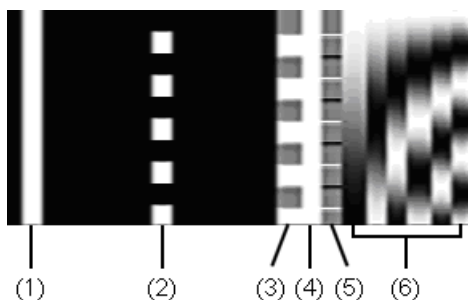
Routine	Contrast	Resolution	Geometry	System	Physio	BOLD	Sequence
GLM Statistics ☒				Motion correction ☒			
Dynamic t-maps ☐							
Ignore meas. at start 0				Spatial filter ☐			
Ignore after transition 0							
Model transition states ☒				Measurements 60			
Temp. highpass filter ☒				Delay in TR 0 ms			
Threshold 4.00				Multiple series Off			
Paradigm size 20							
Meas[1] Baseline							
Meas[2] Baseline							

BOLD (Blood Oxygenation Level Dependent Contrast) imaging displays the change in the oxygenation state of blood. Generally, T2*-weighted EPI sequences are used for this purpose.

GLM Statistics

Determines whether the data are acquired with the GLM statistics mode (GLM = General Linear Model).

The General Linear Model enables a comprehensive statistical analysis of fMRI data. The measurement data are modeled using a variety of functions, for example the hemodynamic response function.



Design matrix of a GLM evaluation

- (1) Display of all measurements used for evaluation.
white = measurements used
black = measurements not used
- (2) Paradigm - Active/Baseline
- (3) Paradigm convoluted with HRF (Model transition state = on)
- (4) Offset component
- (5) Evolution of paradigm over time
- (6) Model function for modelling oscillations over time



If the parameter is deactivated, all images are saved without analysis.

Dynamic t-maps

Determines whether t-maps are stored during the measurement. This is required, for example, for an Inline evaluation on the **Neuro 3D** task card.

A "StartfMRI" series is also created at the start of the measurement.

Starting ignore meas.

Determines the number of initial measurements (not used for evaluation) to avoid start-up artifacts.

Ignore after transition

Determines the number of measurements which are ignored after changing the stimulation.

Model transition states

Determines to include the hemodynamic response function of the brain in the computation.

The paradigm is linked to the hemodynamic response function of the brain to obtain a sensible model of the activity over time curve.



Add **Ignore after transition parameter** is = 0, the first temporal derivation of this model, to the design matrix to show the time offset between the measured data and the model, since slices of a series are acquired during different points in time.

Temp. highpass filter

Determines whether low frequency oscillations over time are eliminated via a high-pass filter. The number of components of the high-pass filter is determined automatically.

Threshold

Determines whether a pixel from t-test images has enough intensity to be used for reconstructing overlay images.



This threshold does not apply for reconstructing pure t-test images.

Paradigm size

Determines the number of measurements per paradigm. An input is generated in the paradigm table for each measurement.

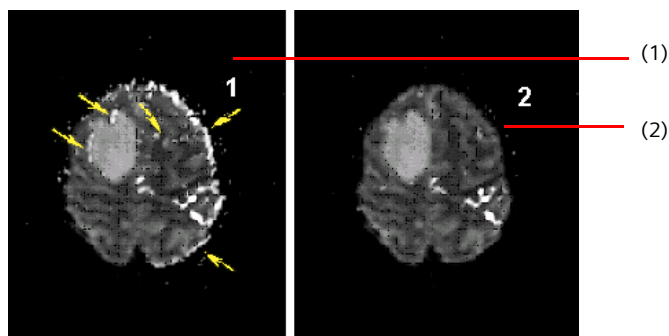
Paradigm table

Settings for all measurements within a paradigm:

Adjustment	Description
Active	Performs the measurement <i>with</i> stimulation.
Baseline	Performs the measurement <i>without</i> stimulation.

Motion correction

Determines whether motion correction is performed.



- (1) Displays patient movement.
- (2) 3D motion correction reduces the relative motion between measured data sets.

The motion correction is displayed in the image text.



The images of the first repetition exclusively contain the comment "Reference volume for motion correction".

Interpolation

Determines the interpolation method for motion correction.

- **Linear:** Linear Interpolation. The fastest method for real-time post-processing.
- **3D K-space:** Interpolation in the Fourier space. Best quality method for real-time post-processing.



Activate **Motion Correction** to display the parameter.

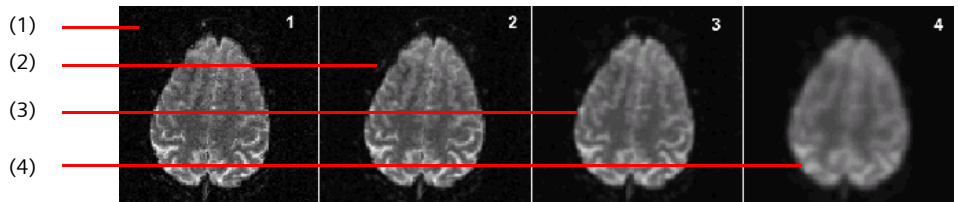
Spatial filter

Activates a low pass filter for smoothing images.

The spatial filter leads to an increase in the signal-to-noise ratio at the expense of spatial resolution.

Filter width

Determines the width of the Gaussian filter. It defines the filter strength.



- (1) No filtering
- (2) Weak (2.0)
- (3) Medium (1.0)
- (4) Strong (0.5)



Enable the **Spatial filter** checkbox to display the parameter.

Measurements

Determines how often a measurement is performed.

Delay in TR

Determines the time between two subsequent measurements. The parameter is relevant for all ep2d sequences.



The delay time set applies to all measurements.

Multiple series

Determines whether the images for each measurement cycle are stored in their own series.

If the parameter is activated, a separate series is generated for each measurement.

1.9 Diff

1.9.1 Diff - Neuro / Diff - Body

Routine	Contrast	Resolution	Geometry	System	Physio	Diff	Sequence
Neuro Body Composing							
Diffusion mode				3-Scan Trace			
Diff. directions				3			
Diffusion Scheme				Bipolar			
Diff. weightings				2			
b-Value				Averages			
0				3			
1000				3			
Noise level				40			
				Diff. weighted images			
				Trace weighted images			
				ADC maps			
				FA maps			
				Mosaic			
				Tensor			

Routine	Contrast	Resolution	Geometry	System	Physio	Diff	Sequence
Neuro Body Composing							
Diffusion mode				3-Scan Trace			
Diff. directions				3			
Diffusion Scheme				Bipolar			
Diff. weightings				2			
b-Value				Averages			
0				3			
1000				3			
Noise level				40			
				Diff. weighted images			
				Trace weighted images			
				ADC maps			
				Exponential ADC Maps			
				FA maps			
				Invert Gray Scale			
				Calculated Image			
				b-Value >= 0 s/mm ²			

Diffusion mode

Describes the measurement method and the diffusion-sensitive orientation.

1-Scan Trace	Requires only one measurement per image. Advantage: shorter acquisition time than in the 3-Scan Trace .
3-Scan Trace	Requires three measurements per image. Advantage: shorter echo time and improved SNR than in the 1-Scan Trace . One diffusion-weighted image per slice position and b-value is calculated. The diffusion weighting depends on the trace of the diffusion sensor (mean value of the diagonal elements Dxx, Dyy, and Dzz).
4-Scan Trace	Same as 3-Scan Trace but requires four measurements per image. Advantage: shorter echo time and improved SNR as compared to the 3-Scan Trace .
Orthogonal	Requires three images per slice position and b value (when $b \neq 0$), one image each in diffusion weighting in the slice, read-out and phase-encoding direction. For b-value $b = 0$, only one image per slice position is acquired.
Slice	Acquires one image per slice position and b-value, diffusion weighting is in the slice-selection direction.
Phases	Acquires one image per slice position and b-value, diffusion weighting is in the phase-encoding direction.
Read	Acquires one image per slice position and b-value, diffusion weighting is in the readout direction.
MDDW	MDDW (Multi-directional diffusion weighting). Acquires one diffusion-weighted image per slice position, per b-value, and (for $b > 0$) per diffusion encoding direction. Defines the number of directions with the Diff. Directions parameter.
3D Diagonal	Acquires one image per slice position and b-value, diffusion weighting is in the direction of the spatial diagonal
Free	User-defined diffusion direction set. If "Free" is selected, a button is displayed next to the parameter field for importing the settings from a corresponding file. (%CustomerSeq%\DiffusionVectorSets*.dvs).

Diff. directions

Determines the number of diffusion-encoding directions. Possible directions are **6, 10, 12, 20, 30, 64** or **256**.

The image text of diffusion-weighted images shows the b-value and the diffusion direction.

Example: **b1000#3**

Definition: b = 1000 s/mm², third direction of 6, 10, 12, 20, 30, 64 or 256



Editable if **Diffusion mode** is MDDW or Free.



If **Diffusion mode** "Free" is selected, a button is displayed next to the parameter field for exporting the settings to the file.

Diffusion Scheme

Bipolar	Double refocused spin echo diffusion encoding that minimizes distortions
Monopolar	Single refocused spin echo diffusion encoding that allows for shorter TE and thus increased SNR

Diff. weightings

Determines the number of diffusion-weightings that are acquired during a measurement.

Define the individual weightings in the **b-value** input field prior to the measurement (up to 16 b values).

b-value

The nominal b value is a measure of diffusion-weighting. It is provided in s/mm^2 .

The greater the value, the stronger the diffusion weighting. The b-value increases with the intensity, duration, and time interval of the diffusion-sensitive gradient pulses.

b value = 0 corresponds to one T2*-weighted image.

The number of possible b values is defined by the **Diff. weightings** parameter.

b-value >=

Specifies the minimum b-value used in ADC calculations.

This function may be useful for diffusion-weighted imaging of the abdomen. It supports calculation of images that are insensitive of vascular capillary perfusion.

Averages

Defines the number of averages per b-value.

In protocols with multiple b-values an individual number of averages may be selected for scans with different diffusion weightings (b-values).

Images with lower diffusion weighting exhibit inherently more signal than those with higher diffusion weighting. Hence the efficiency of the protocol can be improved by selecting less averages for the lower diffusion weighted images without compromising the signal to noise ratio of the highly diffusion weighted images.



For diffusion modes other than MDDW or Free, the system automatically ensures that the number of averages of higher b-values always exceeds the number of averages of lower b-values.

Diff. weighted Images

Determines if original images with diffusion weighting are reconstructed. These images contain T1, T2, and diffusion-weighted portions.

Performs diffusion weighting in the direction set with the **Diffusion mode** parameter (e.g., if **Slice** in the slice-selection direction applies).

Trace weighted Images

Determines if an isotropic diffusion-weighted image is reconstructed. In this type of image, diffusion-weighting is applied in all three spatial directions.



Whether or not this parameter is available depends on the setting of the **Diffusion mode** parameter.

ADC maps

Determines whether ADC maps are reconstructed where averaging is performed with different b-values.

ADC Maps (**A**pparent **D**iffusion **C**oefficient) show the diffusion coefficient as grayscale values. The grayscales are derived from measurements with different diffusion weighting (b-values). ADC Maps are free of T1 and T2 contributions.



Active only, if at least two b-values are set.

Exponential ADC maps

Determines whether an exponential ADC map is reconstructed.



Exponential ADC maps may eliminate T2 shine through artifacts.

FA maps

Determines whether FA maps (**F**ractional **A**nisotropy Maps) are reconstructed.

FA maps show isotropic diffusion characteristics as dark, while anisotropic diffusion characteristics are shown as bright.

Mosaic

Determines whether the acquired MDDW data are saved as a mosaic image or individually.

Tensor

Determines whether diffusion tensor data are saved in the database. This enables diffusion weighting in the **Neuro 3D** task card.

Invert gray scale

Selects inverted (PET-like) display of the diffusion trace weighted images.

Calculated image

Determines whether a virtual (b-value) image is calculated. The b-value for calculation is set in **Calculated bValue**.

Calculated bValue

Sets the b-value for the **Calculated image**.

Noise level

Determines the intensity at which pixels for reconstructing ADC maps are used.

Diff. moment

Defines the strength of diffusion weighting. It is the amplitude multiplied by the duration of the diffusion gradient.



Used only for the **psif** sequence.

1.9.2 Diff - Composing

The parameter card **Diff - Composing** corresponds to the **Inline - Composing** parameter card.

(→ Page 161 *Inline - Composing*)

1.10 Perf

Routine	Contrast	Resolution	Geometry	System	Physio	Perf	Sequence
						GBP ☒ PBP ☒ TTP ☒ relCBV ☐ relCBF ☐ relIMTT ☐ relCBVCorr ☐	Motion correction ☐ Spatial filter ☐
Measurements						60	

Defines the parameters for perfusion measurements.

One method of MR perfusion imaging is to determine the signal change in images as a function of time while injecting intravenous contrast agent. Generally, T2*-weighted EPI sequences with a gadolinium contrast agent are used for this purpose.

GBP (Global Bolus Plot)

Determines whether a global time-density curve is determined for evaluating the bolus passage.



15 measurements are minimum to activate the parameter.

PBP (Percentage of Baseline at Peak Map)

Determines whether a percental signal image is reconstructed for every slice. This image shows the signal change of the bolus peak relative to the base line.

The brighter an image area, the less contrast agent arrived on-site.



15 measurements are minimum to activate the parameter.

TTP (Time-to-Peak-Map)

Determines whether a time-to-peak image is reconstructed for every slice. The pixel intensity value in the image shows the time that expired until the signal peak was reached.

The brighter an area in the grayscale image, the more time expired until the signal peak was reached.



For the **Perf** card 15 measurements are minimum to activate the parameter.



For the **Inline - Soft Tissue** card 2 measurements are minimum to activate the parameter.



In colored perfusion images, the TTP display depends on the selected color palette.

relMTT (relative Mean Transit Time)

Determines whether a relative MTT map is reconstructed. This inline calculation is based on the local AIF method.

relCBF (relative Cerebral Blood Flow)

Determines whether a relative CBF map is reconstructed. This inline calculation is based on the local AIF method.

relCBV (relative Cerebral Blood Volume)

Determines whether a relative CBV map is reconstructed. This inline calculation is based on the local AIF method.

relCBVCorr

Determines whether a T1 corrected relative CBV map is reconstructed. This inline calculation is based on the local AIF method.

Local AIF method (no visible parameter)

The local AIF (arterial input function) method determines the incoming flow of contrast agent for a reference volume around every voxel.

This method reduces artifacts due to arterial flow differences between different regions.

In contrast to this the global AIF method determines the incoming flow of contrast agent at one reference point for all voxels.

Original images

With perfusion measurements, original images are *always* reconstructed and saved. Use them for additional post-processing.

Starting ignore meas

Determines the number of initial measurements that were not used for evaluation to avoid start-up artifacts.

Measurements

Determines how often a measurement is performed.

Motion Correction

(→ Page 181 *Motion correction*)

Spatial filter

(→ Page 133 *Spatial filter*)

1.11 Inline

1.11.1 Inline - Common

The screenshot shows the 'Inline - Common' parameter card. The top navigation bar includes tabs for Routine, Contrast, Resolution, Geometry, System, Physio, Inline, and Sequence. The 'Inline' tab is selected. Below it, the 'Common' sub-tab is active. The interface contains several settings: 'Subtract' (checked), 'StdDev' (checked), 'Save images' (checked), 'Std-Dev-Sag' (unchecked), 'Autoscaling' (unchecked), 'Std-Dev-Cor' (unchecked), 'Scaling factor' (1), 'Std-Dev-Tra' (unchecked), 'Offset' (0), 'Std-Dev-Time' (unchecked), 'Subtrahend' (1), 'Subtraction indices' (empty), 'Motion Correction' (None), 'Subtraction group' (1), and 'Measurements' (50). 'Save original images' is checked.

Defines parameters for dynamic image evaluation.



With measurement protocols for angio examinations, the **Inline** parameter card as well as the **Angio - Inline** subtask card are shown.

Subtract

Defines whether a subtraction evaluation is performed with a series of the current measurement. In this way, images are generated that e.g., show the changes after contrast agent administration.



CAUTION

Use of subtracted images for diagnostic purposes!

Fine anatomical structures are lost; incorrect diagnosis

- ◆ Always use both for diagnostic purposes, the subtracted images as well as the original images.

If the measurement is performed only once, the measured series is used for subtraction with a series from other protocols (cross-protocol subtraction):

- If the protocol is marked as a contrast agent measurement by a syringe icon, the series last buffered on the image reconstruction system will be subtracted from the current series.
- If the protocol is not marked with the syringe icon, the current series will be loaded into the buffer of the image reconstruction system and subtracted from the series of a subsequent protocol.



In the case of Set-n-Go protocols, the relationship is between the steps of the same indices.

Save images

Determines whether the result images of subtraction are stored automatically.



Enable the **Subtract** checkbox to superpose the parameter.

Autoscaling

Determines whether the display range of the computed subtraction values is adjusted automatically.



Enable the **Subtract** checkbox to superpose the parameter.

Scaling factor

Determines the factor for scaling the display area of the computed subtraction factor.



Enable the **Autoscaling** checkbox to display the parameter.

Offset

Determines the offset for the lower and upper thresholds of the display range for the computed subtraction values.



Enable the **Autoscaling** checkbox to display the parameter.

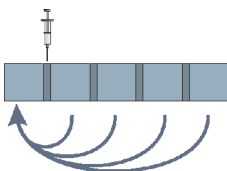
Subtrahend

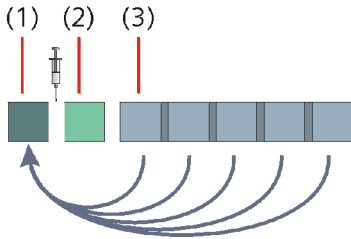


Select the **Subtrahend** check box to display the parameter.

Subtraction of series within a multiple measurement protocol:

This parameter typically defines the native series of the multiple measurement protocol. This native series is subtracted from the post-contrast series.





Subtraction of series from different protocols:

The value '-1' means that the first matching series is used as the native series. This native series is subtracted from the post-contrast series.

- (1) Native measurement protocol
- (2) Neither native nor post-contrast measurement protocol (for example high resolution examination)
- (3) Multiple measurement protocol of post-contrast series

The protocol (1) is subtracted from the series of the protocol (3).



In this example the check box **Subtract** must be selected for both, the native and the post-contrast protocol.

Subtraction indices



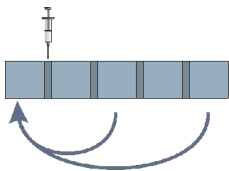
This is a parameter for subtractions within a multiple measurement protocol.

This parameter defines the post-contrast series of the multiple measurement protocol. The native series, that is defined by the parameter **Subtrahend**, is subtracted from these post-contrast series.

Example of a subtraction within a multiple measurement protocol with the following settings:

- **Measurements** = 5
- **Subtrahend** = 1
- **Subtraction indices** = 3,5

The 1st series is subtracted from the series 3 and 5.



Subtraction groups

Defines subtraction groups. The post-contrast images of this group are subtracted from the pre-contrast images of this group.

Different subtraction groups are necessary, if several pre-contrast and post-contrast protocols are measured at the same table position.

Otherwise the images of the last pre-contrast protocol would be used for subtraction.

Measurements

Determines how often a measurement is performed.

Std-Dev-Sag / Std-Dev-Cor / Std-Dev-Tra

Determine whether standard deviation images with sagittal, coronar, and transverse orientation are reconstructed from slabs measured with the current protocol. You see the scatter of the pixel values in the respective orientation.



Active only for a 3D measurement with at least 4 slices in the slabs.

Std-Dev-Time

Standard deviation result images are measured in the orientation of the slice groups and/or slabs are reconstructed from the slices groups and/or slabs of the actual protocol, if the **Std-Dev-Time** checkbox is activated. You see the scatter of the pixel values within the measurement period. Both multiple phases and multiple measurements can be evaluated.

Save original images

Determines whether the unprocessed images are stored in the database as well.



Can be deactivated only if one of the following parameters is active: **Subtraction**, **MIP**, **StdDev**, **Liver registration**, **T1-map** or **T2-map**.

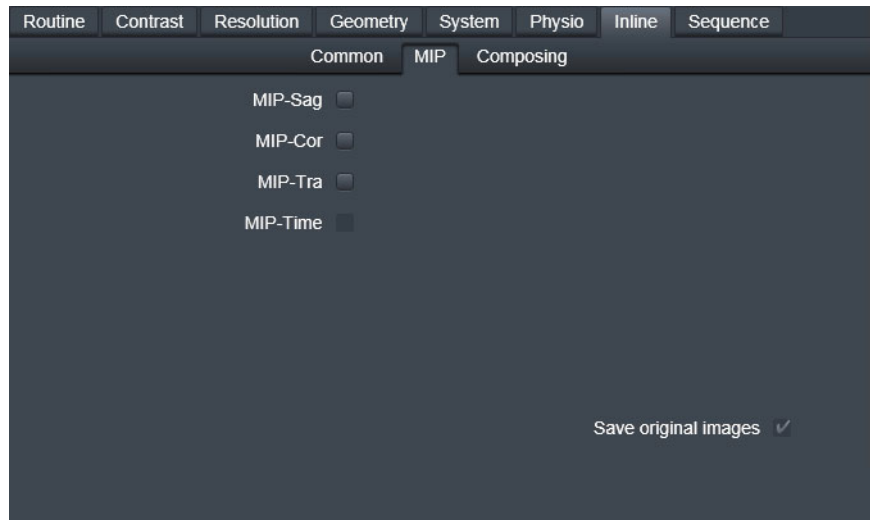
Liver registration

Activates a 3D liver registration.



Only available if a value larger than **2** is stated in the **Measurement** parameter.

1.11.2 Inline - MIP



MIP-Sag / MIP-Cor / MIP-Tra

Determines whether MIP images with sagittal, coronar or transverse orientation are reconstructed from the measured slabs of the actual protocol.



Active only for a 3D measurement with at least 4 slices in the slabs.

MIP-Time

Determines whether MIP images are reconstructed in the orientation of the measured slice groups and/or slab from the slice groups and/or slabs measured of the actual protocol. In the calculation, the highest pixel value along the time axis is taken into account.



Active only if at least one repetition measurement is made (parameter **Averages** > 1) or at least two phases were measured for triggered measurements.

Save original images

Determines whether the unprocessed images are stored in the database as well.



Can be deactivated only if one of the following parameters is active: **Subtraction**, **MIP**, **StdDev**, **Liver registration**, **T1-map** or **T2-map**.

Radial MIP

Determine whether radial MIP views are reconstructed from the measured slab of the actual protocol.

Number of radial views

Sets the number of views for radial MIP views.

Axis of radial views

Determines the rotation axis of radial MIP views.

1.11.3 Inline - Soft Tissue

The screenshot shows the 'Soft Tissue' parameter card. The top navigation bar includes tabs for Routine, Contrast, Resolution, Geometry, System, Physio, Inline, and Sequence. The sub-navigation bar includes Common, Inline, MIP, Soft Tissue (selected), Composing, and MapIt. The 'Soft Tissue' tab contains the following settings:

- Wash - In: ☒
- Color table: Perfusion
- First measurement: 1
- Last measurement: 2
- Highest value: ☒
- TTP: ☒
- Color table: RedGreen
- PEI: ☒
- Color table: Perfusion
- MIP - time: ☒
- Color table: GreenRed
- Measurements: 6
- Pause after: 25.0 s

Wash - In

Determines whether signal changes are activated at the beginning of the dynamic measurement sequence.

Color table

Determines the color table for displaying different image values.

First measurement

Determines which measurement is used as the first measurement of a sequence.

Last measurement

Determines which measurement is used as the last measurement of a sequence.

Highest value

Determines whether, in place of the last measurement, the highest value between the first and last measurement is used for reconstructing the wash - in parameter image.

TTP (Time-to-Peak-Map)

Determines whether a time-to-peak image is reconstructed for every slice. The pixel intensity value in the image shows the time that expired until the signal peak was reached.

The brighter an area in the grayscale image, the more time expired until the signal peak was reached.



For the **Perf** card, 15 measurements are minimum to activate the parameter.



For the **Inline - Soft Tissue** card, 2 measurements are minimum to activate the parameter.



In colored perfusion images, the TTP display depends on the color palette selected.

PEI (Positive Enhancement Integral)

Determines whether an image of the positive enhancement integral is reconstructed.



Positive enhancement interval (PEI): Area under a signal intensity time curve

MIP time

Determines whether MIP images are reconstructed in the orientation of the measured slice groups and/or slabs from the slice groups and/or slabs measured of the actual protocol. In the calculation, the highest pixel value along the time axis is taken into account.



Active only if at least repetition measurement is made (parameter **Averages** > 1) or at least two phases were measured for triggered measurements.

Measurements

Determines how often a measurement is performed.

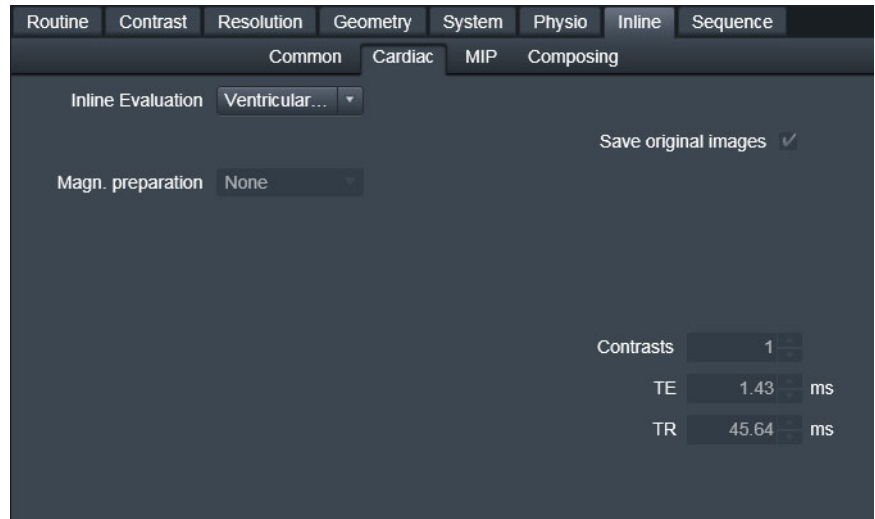
Pause after meas.

Determines (during dynamic measurements) a delay time between the individual measurements. Separately determine the pause for each measurement.



Up to 64 individual pauses are possible. In most cases, setting the same pause time for all measurements or setting the pause time to zero is best. Beginning with 65 pauses, only a general pause time is possible.

1.11.4 Inline - Cardiac



Inline evaluation

Determines whether inline evaluations are performed in physiologically triggered acquisitions.

Option	Description
None	No inline evaluation.
Ventricular Function	Activates Inline ventricular function analysis. Performs a segmentation of the left ventricle in short-axis images of the heart. Uses the images acquired in the current protocol step and in previous protocol steps in which Ventricular Function was enabled. Evaluation begins once all slices in the current protocol step have been acquired and at least two parallel short-axis slices are available. Displays the resulting contour lines as graphic overlays in the image. The contours can be edited in Argus. For automatic base plane detection Ventricular Function can be enabled on the standard long-axis views (2-, 3-, 4-chamber). Slices which are repeated or added in subsequent protocol steps are used to perform a new evaluation.
Restart InlineVF	Performs an InlineVF analysis using <i>only</i> the images acquired in the current protocol step. Minimum requirements are two parallel short-axis slices.

1 Parameter Cards

Option	Description
T1 Map	Calculation of a T1 map from a series of images acquired following magnetization preparation with a non-selective inversion pulse. The estimated T1 values are encoded in the intensity of each pixel. The number of magnetization preparation pulses can be varied, in addition to the duration, in beats, of the sampling and recovery periods following each preparation pulse.
T2 Map	Calculation of a T2 map from a series of images acquired following magnetization preparation with a T2 preparation pulse. The estimated T2 values are encoded in the intensity of each pixel. The number of T2 preparation pulses can be varied, in addition to the duration of the recovery period, in beats, following data acquisition.
T2* Map	Calculation of T2* map from a series of images acquired using a multi-echo gradient echo sequence. The estimated T2* values are encoded in the intensity of each pixel. The number of echoes is controlled by the number of Contrasts .



Availability of the following parameter values depends on the mapping type selected.

Magn. preparation

Determines whether magnetization preparation is performed prior to data acquisition in order to affect image contrast.

Option	Description
Non-sel. IR	Data acquisition is preceded by a non-selective inversion pulse, thus inverting the magnetization in the entire volume.
Non-sel. IR T1 map	Non-sel. IR pulses optimized for the T1 mapping application with an improved inversion efficiency for the operating range of interest.
T2 prep.	A preparation pulse is applied to the entire volume to enhance T2 contrast.

Option	Description
T2 prep. adiabatic	This option works similar to T2 prep. Compared to the T2 prep. option these are the main differences: ■ Preparation module is more B1-insensitive ■ Leads to better image homogeneity ■ Requires more RF power

No. of preps.

Determines the number of preparation pulses.

Sampling duration

Defines the number of images (samples) acquired with different inversion times following a preparation pulse.

T2 prep. duration

Defines the duration of the T2 preparation pulse train.

Recovery duration

Defines the recovery duration following each acquisition.

Contrasts

Determines the number of images generated with different T2* weighting within a measurement (number of image contrasts).

Motion correction

Corrects for in-plane motion between successive images acquired with single-shot acquisition techniques.

TE (echo time)

Determines the echo time (TE) that elapses between the RF excitation pulse and the pulse for the echo to be measured.

TR (repetition time)

Determines the repetition time TR that elapses between two successive excitations.

Changing the repetition time affects image contrast and measurement time.

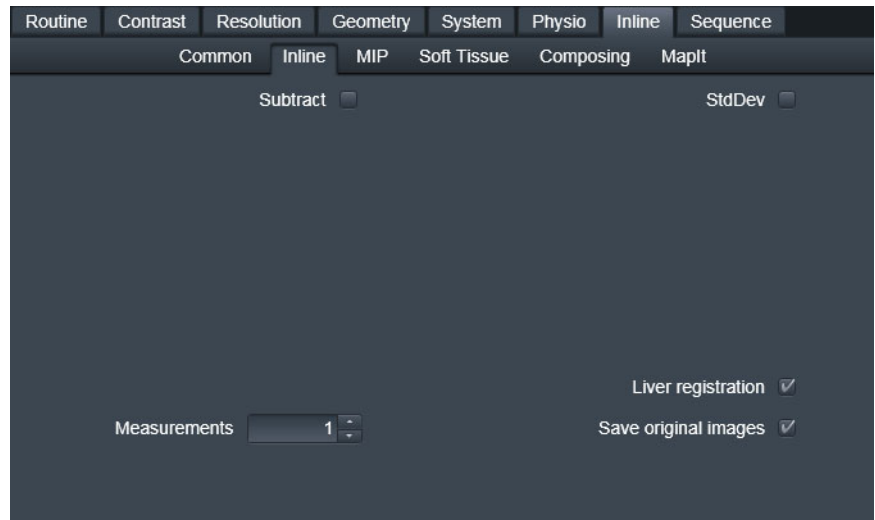
Motion correction

The (standard) motion correction corrects for patient movement in the image plane that occurs between the acquisition of two echo trains.

Save original images

Determines whether the unprocessed images are stored in the database as well.

1.11.5 Inline - Inline



The screenshot shows the 'Inline' tab in the syngo MR E11 software. The 'Subtract' checkbox is checked, and the 'StdDev' checkbox is unchecked. The 'Measurements' dropdown is set to '1'. The 'Liver registration' and 'Save original images' checkboxes are checked.

Subtract

Activates Inline subtraction which is performed on identical protocols. The measurement defined as subtrahend (without contrast agent) will be subtracted from all measurements following the subtrahend.

If activated, the subtraction specific parameters are displayed.

(→ Page 145 *Inline - Common*)



For Inline subtraction within a protocol, the number of measurements must be > 1.



CAUTION

Use of subtracted images for diagnostic purposes!

Fine anatomical structures are lost; incorrect diagnosis

- ◆ Always use both for diagnostic purposes, the subtracted images as well as the original images.

Measurements

Determines how often a measurement is performed.

Liver segmentation

Activates 3D liver segmentation based on the water or fat-sat images from the screening DIXON for quantitative liver evaluation.

Liver registration

Activates a 3D liver registration.



Only available if a value larger than **2** is stated in the **Measurement** parameter.

Save original images

Determines whether the unprocessed images are stored in the database as well.



Can be deactivated only if one of the following parameters is active: **Subtraction**, **MIP**, **StdDev**, **Liver registration**, **T1-map** or **T2-map**.

1.11.6 Inline - Composing

The screenshot shows the 'Composing' parameter card within a software interface. The top navigation bar includes tabs for Routine, Contrast, Resolution, Geometry, System, Physio, Inline, and Sequence. Below this, the 'Composing' tab is selected, showing sub-tabs for Common, Cardiac, MIP, and Composing. The 'Composing' sub-tab is active, displaying the following settings:

- Distortion Corr.** ☒
- Mode** 2D (dropdown menu)
- Unfiltered images** ☐
- Inline Composing** ☒
- Normalize** Strong (dropdown menu)
- Composing Function** Adaptive (dropdown menu)
- Composing Group** 1 (numeric input with up/down arrows)
- Last Step** ☐
- Series Description** (text input field)

Defines for Inline composing.

Combine several protocols to composing groups. As a result, the images of a protocol are automatically combined into an overall image.

Inline Composing

Indicates that the images of the steps or the protocol of a composing group are composed into a complete image.



Inline Composing is enabled only, if **2D** or **3D** is activated in the **Distortion Corr.** field.

Composing Function

Establishes the methods used to compose the images.

Option	Description
Spine	This algorithm uses the bone structures in the images as a basis. For example, it generates images for the measurement and evaluation of scoliosis, kyphosis, and pelvic obliquity.
Angio	This algorithm uses the vessel structures of the images as a basis. This allows for overall display of the vessels.
Adaptive	This algorithm is based on elastic matching. It especially corrects B0 induced inhomogeneities in image areas beyond the magnetic homogeneity volume.

Composing Group

Determines to which composing group the protocol belongs.

Used to compose the images of all protocols of a composing group into an overall image.

Last step

Determines the chronologically last measurement of a Composing Group as the Last Step.

The subsequent protocols belong to a new Composing Group, even if they have the same group number.

Protocols of a Composing Group not completed with a *Last Step* flag are identified by a post-processing icon that has been crossed out.



Distortion Corr.

Activates 2D or 3D distortion correction. This compensates for the pillow-shaped distortions at the edge of the image. These distortions occur in images with a large FoV or eccentric slices (Offcenter).

Option	Description
2D	Corrects image distortion with 2D distortion correction , individually in each slice.
3D	Takes the voxel (with 3D distortion correction) in the current slice as well as those in the surrounding slices into account. The correction results are more precise, but require a longer reconstruction time.

Unfiltered images

Determines whether unfiltered images are saved as well.



All other inline functions can no longer be accessed, if unfiltered as well as filtered images are reconstructed and stored in Inline. Filtered images are always shown in the Inline display.

1.11.7 Inline - MapIt

The screenshot shows the 'MapIt' parameter card. It features a dark-themed interface with a top navigation bar containing tabs: Routine, Contrast, Resolution, Geometry, System, Physio, Inline, and Sequence. Below this is a sub-navigation bar with tabs: Common, Inline, MIP, Soft Tissue, Composing, and MapIt. The 'MapIt' tab is selected. The main area contains several parameters: 'MapIt' is a dropdown menu set to 'T1 map'; 'Noise threshold' is a numeric input set to '15'; 'Auto angle calculation' is a toggle switch set to 'On'; 'T1 estimate' is a numeric input set to '1000' with a unit of 'ms'; 'Flip angle 1' is a numeric input set to '5' with a unit of 'deg'; 'Measurements' is a numeric input set to '2'; 'Contrasts' is a numeric input set to '1'; 'TE' is a numeric input set to '1.26' with a unit of 'ms'; and 'TR' is a numeric input set to '20.00' with a unit of 'ms'. At the bottom right, there is a 'Save original images' checkbox which is checked.

The parameters are only valid for the currently selected step.

MapIt

Determines whether inline parametric maps are calculated.

Option	Description
None	No parametric maps are calculated.
T1 map	Activates the Inline computation of T1 maps. The Measurement parameter is set to the value 2 and cannot be changed. The Contrasts parameter is set to the value 1 and cannot be changed.
T2 map	Activates the Inline computation of T2 maps. The Contrasts parameter is set to value 2 . It can assume a value from 2 to 12 . The Measurement parameter is set to the value 1 and cannot be changed.
T2* map	Activates the Inline computation of T2* maps. The Contrasts parameter is set to value 2 . It can assume a value from 2 to 12 . The Measurement parameter is set to the value 1 and cannot be changed.
R2 map	Activates the Inline computation of R2 maps. The Contrasts parameter is set to value 2 . It can assume a value from 2 to 12 . The Measurement parameter is set to the value 1 and cannot be changed.

Option	Description
R2* map	Activates the Inline computation of R2* maps. The Contrasts parameter is set to value 2 . It can assume a value from 2 to 12 . The Measurement parameter is set to the value 1 and cannot be changed.



Different options are available depending on the sequence.

Auto angle calculation

Activates automatic calculation for the two flip angles for T1 cards.



Available only, if the **T1 map.** mode is selected under the **Parametric map** parameter.

T1 estimate

An estimated value for T1 is required for automatically calculating the flip angle.



Only available if the **Auto angle calculation** parameter is activated.

Flip angle

✓ **T1 map** mode in the **MapIt** parameter

Determines the individual flip angle for each measurement for estimating T1 maps.



This parameter is editable only if the **Auto angle calculation** parameter is deactivated.

✓ Another mode is selected in the **MapIt** parameter

Indicates the flip angle used.

Measurements

Determines how often a measurement is performed.

Contrasts

Determines the number of images generated with different T2 (e.g., se-tse sequences) or T2*-weighting (**gre** sequences) within a measurement (number of image contrasts).



Available only for a few sequences.



Define an echo time for each contrast.

TE (echo time)

Determines the echo time (TE) that elapses between the RF excitation pulse and the pulse for the echo to be measured.



Not active for all sequences.



Enter several echo times for multi-echo sequences. Scroll through the echo times below the field names by using the arrow keys. When changing a given echo time, the following echo times are adjusted accordingly.

TR (repetition time)

Determines the repetition time TR that elapses between two successive excitations. (At times an alternative designation *Repetition time* is used).

Changing the repetition time affects image contrast and measurement time.

Entering several repetition times, additional keys are superimposed for scrolling between the individual times.

Noise threshold

Determines the threshold of ignored measurement values to suppresses noise.

Save original images

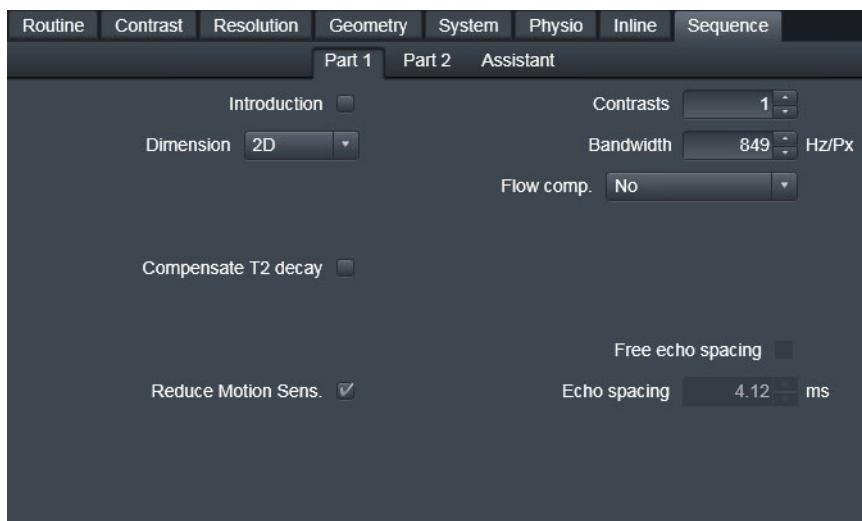
Determines whether the unprocessed images are stored in the database as well.



Can be deactivated only if one of the following parameters is active: **Subtraction**, **MIP**, **StdDev**, **Liver registration**, **T1-map** or **T2-map**.

1.12 Sequence

1.12.1 Sequence - Part 1



The screenshot shows the 'Sequence' parameter card in an MRI software interface. The 'Sequence' tab is selected, and the 'Part 1' sub-tab is active. The parameters are as follows:

- Introduction:** ☐
- Dimension:** 2D (dropdown menu)
- Contrasts:** 1 (spinner)
- Bandwidth:** 849 Hz/Px (spinner)
- Flow comp.:** No (dropdown menu)
- Compensate T2 decay:** ☐
- Free echo spacing:** ☐
- Reduce Motion Sens.:** ☒
- Echo spacing:** 4.12 ms (spinner)

Defines parameters specific to a sequence type.

Different sequence types are available for examinations:

- Gradient echo sequences (GRE, FLASH, Turboflash, True FISP, MEDIC, PSIF, CISS, DESS)
- Spin echo sequences (se)
- Turbo spin echo sequences (tse)
- HASTE sequences
- Single-shot EPI sequences
- Segmented epi sequences (ep_seg_fid, ep_seg_se)

The protocol info line above the parameter card includes an abbreviation which helps you recognize the sequence of the current protocol.

Introduction

Determines whether the patient is made aware that the measurement has started by the short knocking noise made by the gradient system.

Dimension

Indicates whether a 2D or 3D measurement is planned.



If you switch from 2D to 3D, the slice group parameters on the different parameter cards change into slab group parameters.



Hidden or inactive for sequences where this dimension cannot be changed.

Elliptical scanning

Determines whether the corners of the k-space that contribute only minimally toward resolution are ignored during data acquisition.

Reduces the measurement time by up to 25% for 3D sequences without compromising resolution.

Phase stabilization

Avoids phase errors generated by e.g., respiration.

Phase stabilization improves image quality especially for gradient-echo sequences.

Compensate T2 decay

Avoids negative effects of T2 decay while acquiring long echo trains.

Reordering

Determines the acquisition sequence of raw data lines.

■ Linear

The k-space is stepped through linearly.

■ Centric

The first measured raw data lines are sorted into the center of the k-space.



In the **Centric** mode, you achieve good fat saturation with single shot sequences, because the center of the k-space is measured early on after the fat sat pulse.

Asymmetric echo

Enables echo asymmetry in the readout direction. It is used to reduce the echo time. The maximum asymmetry not to be exceeded is defined in the sequence.

Option	Description
Allowed	An asymmetric echo is used automatically, if necessary. If the echo time is long enough, the echo remains centered.
Weak	A weak asymmetric echo is used.
Strong	A strong asymmetric echo is used. Truncation artifacts can occur.
Half echo	A completely asymmetric echo is used. Extremely short echo times below 1 ms can be obtained (only available for UTE sequences).



You can display the asymmetry of the echo in a tooltip.

Contrasts

Determines the number of images generated with different T2 (e.g., se-tse sequences) or T2* weighting (**gre** sequences) within a measurement (number of image contrasts).



Available only for a few sequences.



Define an echo time for each contrast.

Bandwidth

Determines the fat-water-pixel offset and the signal-to-noise ratio.

In some sequences it is possible to assign a readout bandwidth to each contrast.

Value for bandwidth in image text compared to protocol parameter:

For two reasons, the MR scan is performed with a bandwidth value that can slightly differ from the value entered in the parameter card:

First, the bandwidth is internally converted to the dwell time which must be a multiple of the ADC sampling time type. The basis for the scan is 100 nsec and not the bandwidth itself. The real bandwidth used internally is always some fractional value within the rastered values as used in the parameter card. The data in the image text is provided with an accuracy of 1 Hz while the increments in the parameter card are sequence-specific and can be much larger.

Second, the dwell time can be different for each frame. The image text should not be a copy of the protocol parameter but reflect the actual value of each frame.

Flow comp.

Prevents signal loss and smearing caused by moving spins. Additional gradient pulses are switched with a suitable time duration and amplitude.

Specify flow compensation separately for each contrast.

Option	Description
Yes	Compensation in readout and slice encoding direction, as well as in phase-encoding direction for some sequences (e.g., tfl, CV).
Read	Compensation in readout direction only
Slice	Compensation in slice-selection direction only
No	No flow compensation

Readout mode

Determines the read-out mode for gradient echo sequences (GRE).

Mode	Description
Bipolar	The MR signals of the different contrasts are alternately read out with a positive or negative gradient. This enables narrower echo spacing than in the monopolar mode. The fat-water shift alternates from contrast to contrast.
Monopolar	The MR signals of all contrasts are read out with a positive gradient. Echo spacing is greater than in the bipolar mode. The fat-water shift is identical in all contrasts.

Optimization

Used for time optimization.

Mode	Description
Min. TE	The time for TE is optimized to the minimum.
Min. TR	The time for TR is optimized to the minimum.
Min. TR TE	The times for TE and TR are optimized to the minimum.
Min. echo spacing	Echo spacing is optimized to the minimum.
In phase	Determine the shortest time interval in which fat and water are in phase.
Opposed phase	Determine the shortest time interval in which fat and water are out-of phase.
None	Time optimization is not performed.



It is no longer possible to change the optimized parameters manually.

Allowed delay

Establishes the maximum permissible delay time after completing the measurement.

The delay time is used to reduce the specific absorption rate (SAR). The required delay time is automatically calculated by the system and ranges between 0 seconds and the maximum delay time.

Free echo spacing

Determines whether you can determine the echo spacing in the **Echo spacing** input field.

Echo spacing

Determines the spacing between the echoes in the pulse train, e.g., for Turbo spin echo (TSE) or EPI sequences.

Smaller echo spacing effects a more compact sequence timing and reduces image artifacts. This means better resolution in the phase-encoding direction for TSE sequences or lower susceptibility distortion for EPI sequences.



High echo spacing can lead to susceptibility distortion for EPI sequences.



If acoustic noise reduction is activated for a TSE sequence, extending the echo spacing increases the noise reducing effect.

Sequence type

Establishes the type of sequence.

Type	Description
Gre	The sequence measures with the gradient echo method.
Trufi	The sequence measures with the TrueFisp method.

Reduced motion sens.

Determines if modified phase-encoding gradients are used. Stabilizes the sequence against slight motions which normally lead to segmentation artifacts.

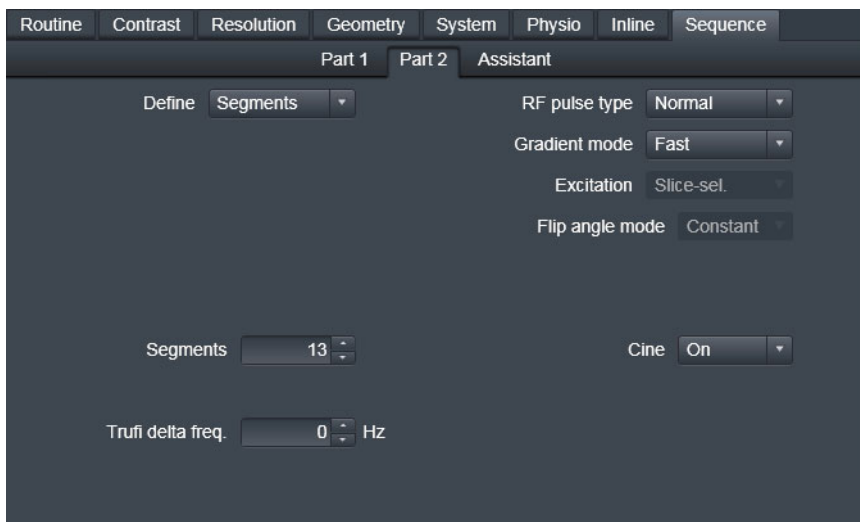


Only available for tse sequences.

Adiabatic-mode

Determines whether a non-sensitive B_1 excitation pulse (adiabatic pulse) is used to reduce the signal variations via the field of view.

1.12.2 Sequence - Part 2



The screenshot shows the 'Sequence - Part 2' interface. At the top, there are tabs for 'Routine', 'Contrast', 'Resolution', 'Geometry', 'System', 'Physio', 'Inline', and 'Sequence'. Below these, there are sub-tabs for 'Part 1', 'Part 2', and 'Assistant'. The 'Part 2' sub-tab is selected. The interface contains several controls: a 'Define Segments' dropdown menu, 'RF pulse type' set to 'Normal', 'Gradient mode' set to 'Fast', 'Excitation' set to 'Slice-sel.', 'Flip angle mode' set to 'Constant', 'Segments' set to '13', 'Cine' set to 'On', and 'Trufi delta freq.' set to '0 Hz'.

Define

The **Echo trains/Turbo factor** parameters or **Shots/Segment** parameters are reconstructed as a function of one another.

Determines which of the two parameters is freely selectable.

Option	Description
Echo trains	Determines that the Turbo factor is computed according to the desired number of echo trains per slice.
Turbo factor	Determines that the number of echo trains per slice are computed on the basis of the Turbo factor.
Shots	Determines that the segment size is computed according to the desired number of shots per slice.
Segment	Determines that the number of shots per slice is computed on the basis of the segment size.

Turbo factor

Determines the number of refocused spin echoes per RF excitation pulse that contribute to an image. It therefore determines the gain in measurement time as compared to a conventional spin echo sequence with comparable parameters.



If the **BLADE** mode is selected in the parameter card **Resolution - Common** or **Physio - Cardiac** in the **Trajectory** parameter, the turbo factor determines the lines per blade.

Slice turbo factor

Defines the number of slices measured with an echo train.



Only active if the echo train is long enough to measure several slices and if the **Echo trains** mode was selected in the **Define** selection list.
(→ Page 176 *Define*)

Echo trains per slice

Defines the number of echo trains a slice is measured with.

Echo train duration

Proves whether the echo train is long enough for a sensible measurement.

EPI factor

Determines the number of refocused gradient echoes per RF excitation pulse that contribute toward an image.



For single-shot EPI sequences, the number of lines to be measured is used as the EPI factor.

Segments

Defines the number of rows in the k-space measured for an image during a TR interval.



Especially relevant to physiologically-triggered measurements.

Combined echoes

Determines the number of echoes of a measurement that are combined into an image (e.g., for a MEDIC sequence).

You obtain flow-compensated T2*-images with a high signal-to-noise ratio.

Trufi delta freq.

Used to move banding artifacts to nonrelevant image areas.



Only active for **TrueFisp** sequences.

Reacquisition mode

Defines whether acquisition is automatically repeated to improve image quality when data are corrupted (for example by motion)

Option	Description
On	Reacquisition mode is activated
Off	Reacquisition mode is deactivated



Available only for a few sequences.

RF Pulse Type

Determines the length and envelope of the RF excitation pulse.

Option	Description
Fast	Short RF excitation pulse, can cause cross-talk between the slices / slabs. Use this setting only for rapid measurements with distance factors that are not too small, e.g., for respiratory breathhold techniques.
Normal	RF excitation pulse with a good slice profile allows measurements with a small distance factors and little cross-talk.
Low SAR	Extended RF excitation pulse with good slice profile and reduced specific absorption rate. Use this setting for SAR reduction to reduce measurement performance.
Optimized	Optimized RF excitation pulse to reduce slice cross-talk.

Gradient mode

Determines the rise time and maximum gradient strength that is used to switch gradients during the course of the sequence.

Possible settings depending on the gradient system:

Option	Description
Fast	Gradient rise time and strength are fully utilized. This mode may cause peripheral nerve stimulation in the patient.
Normal	This setting represents a good compromise between performance and noise development.
Whisper	Ensures rather quiet gradients at an acceptable performance level.

Adjusting the gradient mode with the stimulation monitor, the setting is identified by an asterisk *, e.g., **Fast***. The gradient rise times are adjusted automatically to prevent them from exceeding the stimulation limit.

You can modify the mode by changing **Fast*** to **Fast**.

Excitation

Determines how the RF excitation pulse is sent.

Option	Description
slice-sel	RF excitation is selective in through-plane direction, a single slice is excited.
slab-sel	RF excitation is selective in through-plane direction, a single slab is excited.
non-sel	RF excitation is done for the whole FoV This option may lead to aliasing artifacts in the slice-selection direction.
slab-sel PE	RF excitation is selective in phase encoding direction, a single slab is excited. Compared to slab-sel this option leads to different behavior regarding aliasing artifacts.

Flip angle mode

Provides for a more precisely defined flip angle of the refocusing pulse in the echo train.

Option	Description
Constant	The flip angle of the refocusing pulse remains constant across the entire echo train. (→ Page 20 <i>Flip angle</i>)
Hyperecho	The flip angles of the refocusing pulse vary across the echo train when generating a so-called hyper echo. Enables T2 weighted contrast with a high signal-to-noise ratio, and is optimized for SAR.
Variable	The flip angles of the refocusing pulse increase across the echo train. Enables optimum FLASH contrast. Used for cardiovascular sequences, for example.
T1 var	The flip angles of the refocusing pulse vary across the echo train. Enables T1 weighted imaging with short echo times and is optimized for SAR.
T2 var	The flip angles of the refocusing pulse vary across the echo train. Enables very long echo trains for fast T2 weighted measurements, and is optimized for SAR.
PD var	The flip angles of the refocusing pulse vary across the echo train. Particularly suited to proton density measurements, and optimized for SAR.

RF spoiling

Destroys the remaining phase coherence of the spins. Used for gradient echo sequences to produce FLASH contrast.

Incr. Gradient Spoiling

Increases the gradient spoiling to improve image quality.



Increasing the gradient spoiling may increase **TR** (e.g. for VIBE sequence) and/or **Echo spacing** (e.g. for TFL sequence).

Cine

Indicates a Cine sequence for the display of dynamic processes.

Motion correction

Indicates whether a BLADE motion correction is performed. The motion correction corrects for patient movement in the image plane that occurs between the acquisition of two echo trains.

Option	Description
On	Corrects patient motions in the image plane.
Off	Motion correction is not performed.
On+Off	Two image series are reconstructed, one with motion correction and one without motion correction.



Active only if you select the **BLADE** mode in the **Trajectory** field on the parameter card **Resolution - Common**.

Shots per slice

Number of shots necessary for a slice/slab to completely fill the k-space.



Active only if the **Define** parameter is set to **Shots**.

Stereotactic

Reduces image artifacts caused by the use of stereotactic frames.



Activate if a stereotactic frame is used.

Acoustic noise reduction

Activates the acoustic noise reduction to increase patient comfort during the examination. The effects on contrast and image quality will only be marginal.



Available only for a few sequences.

Phase Correction

Defines whether the sequence performs a phase correction.



In most cases the mode **Auto** will provide best results!

Option	Description
On	Phase correction is performed
Off	No phase correction
Auto	Whether or not a phase correction is performed, depends on the type of the system and the type of the protocol.



This parameter should only be adapted by experienced users!

WARP

This parameter reduces susceptibility artefacts if the patient has MR conditional implants.

The sequence uses high bandwidth rf-pulses to reduce artefacts caused by off-resonance effects occurring in the vicinity of MR conditional implants.



Please adhere to all safety instructions regarding implants.
(→ Operator Manual - MR System)



Available only for a few sequences.

VAT

Off-resonance effects (for example from MR conditional implants) may lead to severe image distortions: image signal may be displaced by many pixels in the frequency encoding direction.

The VAT-technique (View Angle Tilting) reduces such distortions by applying additional frequency encoding gradients.

- 0% = off
- 100% = maximal effect



This parameter may lead to image blurring, especially of object edges.

Blurring can be reduced by

- high readout bandwidth
- thin slices
- reduced VAT



This parameter is available only if **WARP** is activated.

SEMAC

Specifies the number of additional encoding steps to correct for distortions caused by orthopedic metal implants and to improve image quality, in particular in the presence of full hip or knee joint replacements.

If set to a value > 0 , the SEMAC sequence (slice encoding for metal artifact correction) is used to resolve through-plane distortions.

If set to "0", no phase encoding is performed.



While applying SEMAC, the scan time is prolonged by the number of SEMAC encoding steps. As the signal to noise ratio is also increased, measures such as parallel imaging, partial Fourier, reduced number of averages and reduced phase oversampling can be applied to shorten the imaging time again.



This parameter is available only if **WARP** is activated.

1.12.3 Sequence - Assistant



Mode

Defines the strategy to avoid SAR limit exceeding. Therefore the system manipulates the selected parameter.

Option	Description
Off	No SAR assistant functionality
TR	TR is increased by the system to avoid exceeding the SAR limit
Min flip angle	Flip angle is reduced by the system to avoid exceeding the SAR limit

Min flip angle

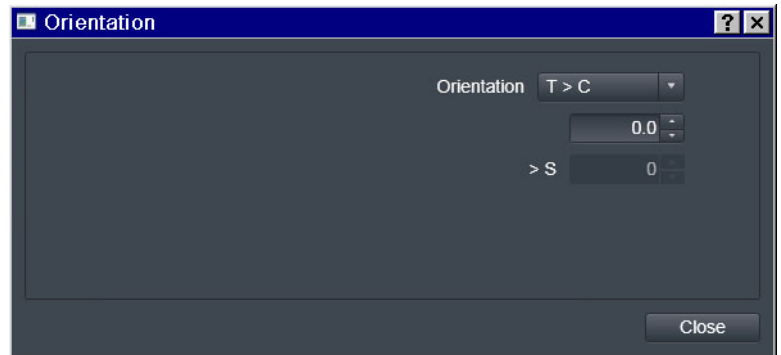
Sets the allowed minimum value for the flip angle.

Max. TR

Sets the allowed maximum value for the TR.

1.13 Dialog windows

1.13.1 Orientation dialog window

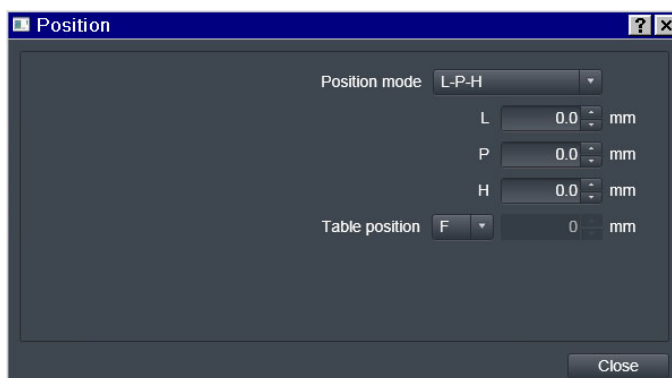


Orientation

Determines the orientation of the slice and/or slab referenced to the *Whole Body Patient Coordinate System*.

- Selection list, left:
Determines the direction of the tilt
- Input field, center
Determines the flip angle (for single oblique slices)
- Input field, right:
Determines the flip angle for the third orientation plane (for double-oblique slices)

1.13.2 Position dialog window



Position mode

Determines the direction for shifting the center of the object out of the magnet isocenter.

- In the **L-P-H** mode, enter the offset based on the *Whole Body Patient Coordinate System*:

L – to the left

P – to posterior

H – towards the head

A negative value moves in the opposite direction (right, anterior, and feet).

- Enter the shift of the slice from the planned isocenter in the gradient direction in the **Offcenter-Shift** mode:

Phase – in the phase-encoding direction

Read – in the readout direction

Shift – in the slice-selection direction



During volume positioning (e.g., VOI, adjustment volume), *always* work in **L-P-H** mode. The **Position mode** selection list is *not* available.



The selected position mode is maintained after the current positioning. Opening the **Position** dialog window the next time (even from another protocol), the position mode previously selected is still applied.

L	3.9	mm
P	10.9	mm
H	0.2	mm

Determining the direction for shifting the center of the object out of the magnet isocenter.

Table position

Determines the table position where the protocol is measured. The zero point is defined by the initial table position of the first measurement of a series block.

The selection list defines the direction of movement.

- **H:** In the head direction
- **F:** In the foot direction

The input field defines the distance in mm.

1.13.3 Inplane Rotation dialog

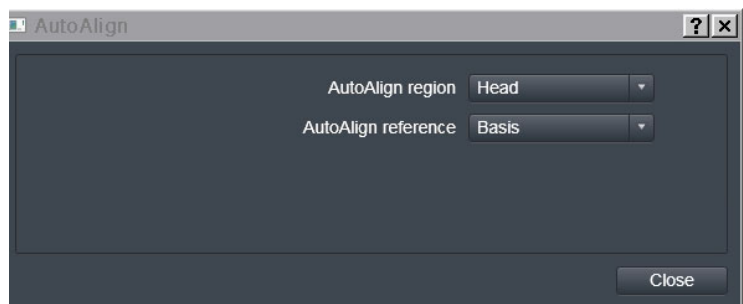


If activating the **Auto** checkbox, the rotation in the slice plane is automatically calculated if the **Rotation** input window is dimmed.



The **Auto** checkbox is available only if **Coronar** is not selected in the **Orientation** parameter.

1.13.4 AutoAlign dialog



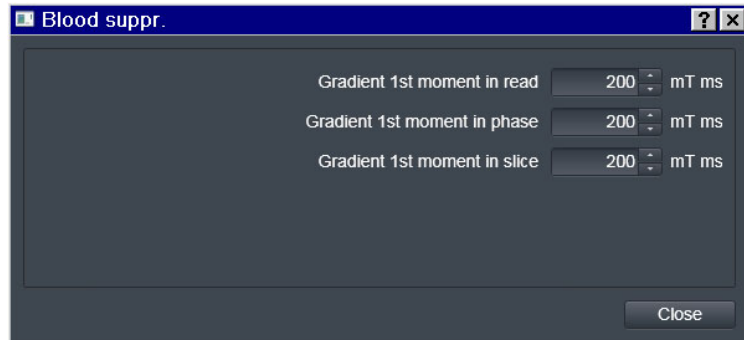
AutoAlign region

Defines the anatomical region for **AutoAlign**, e.g., Head, Spine, Knee.

AutoAlign reference

At least one AutoAlign reference is predefined for every anatomical region. Usually, there are several predefined references for the head region.

1.13.5 Blood Suppression parameters dialog



gradient moment in read

Sets the gradient moment (first order) in read direction for blood suppression.



The tooltip shows the resulting b value.

gradient moment in phase

Sets the gradient moment (first order) in phase direction for blood suppression.



The tooltip shows the resulting b value.

gradient moment in slice

Sets the gradient moment (first order) in slice direction for blood suppression.



The tooltip shows the resulting b value.

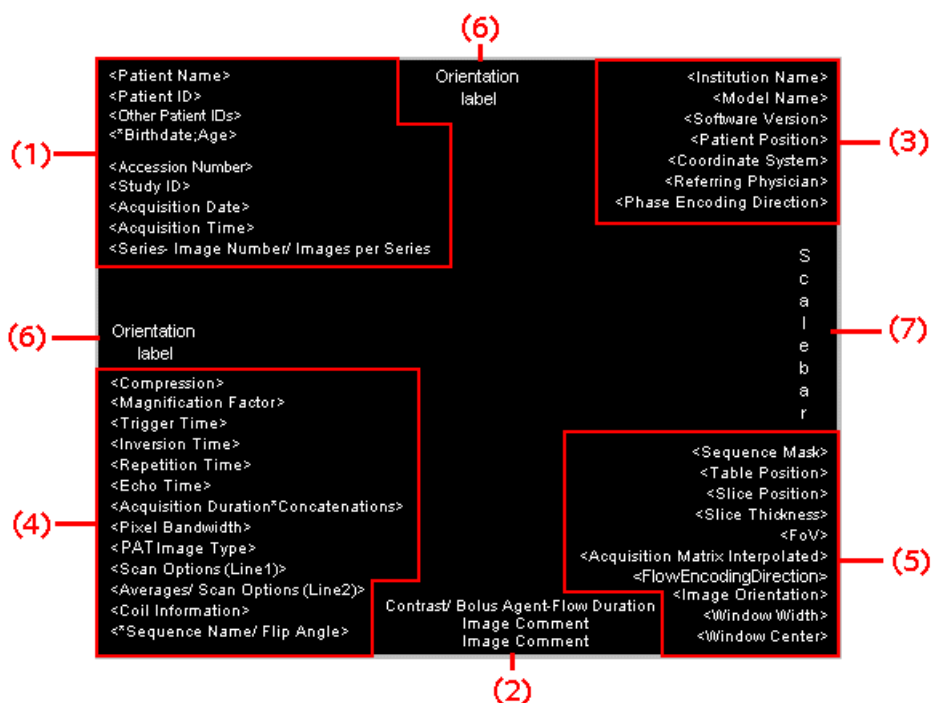
2 Image Text

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2.1 Text Information in Medical Images

Various information is shown as image text on medical images. This information is used to identify the patient and to document measurement and image parameters.

The image text is sorted by topic and positioned in the four corners of the image.



- (1) Patient and examination data
- (2) Comment lines
- (3) System-specific information
- (4) Examination and image parameters
- (5) Data regarding the MR image
- (6) Orientation mark
- (7) Scale bar

2.2 Image Text Components

Here is a list of the individual items of information in the image text components.

(1) Patient and examination data

The top left corner shows the patient and examination data.



Text lines *Other Patient IDs* and *Accession Number* are suppressed when empty. All subsequent lines are moved upward.

Image text	Example	Description
Patient name	Peter Patient	
Patient ID	02081948	
Additional patient number	0123456789	
Date of birth, age	*11/11/1970; 30Y	
Accession number	# 12345	
Examination Number	STUDY 1	
Date acquired	17.10.01	
Time acquired	13:47:46	
Series and image number and total number of images	2 IMA 5/7	Series 2, a total of 7 images in series 2, image 5 is displayed

(2) Comment lines

At the lower edge next to the measurement and image parameters, data regarding contrast agent administration as well as an image comment are provided.



The second line of the image comment is optional.

Image text	Example	Description
Contrast medium/time after injection in sec	GADOLINIUM 1.1	1.1 s after administering GADOLINIUM
Image comment	Motion: 0.27, -0.07, 1.29, -0.47, 0.11, -0.01	Motion correction parameter

(3) System-specific information

The top right corner shows the name of your hospital or practice, the system name, the software version as well as the patient position and direction of viewing.

Image text	Abbreviation	Example
Institution	-	St. Mary's, New York
System name	-	MAGNETOM Verio
Software version	-	MR B15V
Patient position (orientation and position) and viewing orientation	HFS - Head First Supine HFP - Head First Prone HFDR - Head First Decubitus Right HFDL - Head First Decubitus Left FFS - Feet First Supine FFP - Feet First Prone FFDR - Feet First Decubitus Right FFDL - Feet First Decubitus Left	
Coordinate system	LPH (patient coordinate system left-posterior-head)	+LPH

Image text	Abbreviation	Example
Referring physician		Dr. Mustermann
Phase encoding direction		→



The phase encoding direction displayed in the system-specific information *only* refers to the original series. It does *not* refer to reformatted images like MPR or MIP images.

(4) Examination and image parameters

In the bottom left corner you can see the parameters used to generate the image.

Image text	Abbreviation	Example
Rate of compression Loss of quality through compression	<i>CR (Compression Ratio)</i> How much storage space is saved (bits) 100 means that: an image that is normally 512 KB, is now only 5.12 KB This applies to lossless compression as well. <i>CQ (Compression Quality)</i> Measure for loss on resolution 100 = no loss, 0 =greatest loss on resolution <i>CQ!</i> Image is compressed, however, the numbers for CR or CQ are missing Either CR or CQ is shown.	CR 100 CQ 75 CQ!
Current zoom factor	MF	MF 1.51
Trigger time	TT in msec	TT 50
Inversion time	TI in msec	TI 50
Repetition time	TR in msec	TR 600
Echo time	TE in msec	TE 30

2 Image Text

Image text	Abbreviation	Example
Measurement duration * concatenations	TA HH:MM:SS (hours range); MM:SS (minutes range); SS:HS (seconds range)	TA 02:36 * 4
Pixel bandwidth	BW in Hertz/pixels	BW 1000.0
Image type	(→ Page 204 <i>Image Types</i>) p(x) - Grappa with acceleration factor x P(x) - Sense with acceleration factor x	p2 M/MIP
Measurement options (1st line)	RG - Respiratory Gating CG - Cardiac Gating RT - Respiratory Trigger CT - Cardiac Trigger EXT - External Trigger	RG/CT
Averages/measurement options (2nd line)	A(y) - Number of averages FS - fat saturation WS - Water saturation WE - Water excitation SAT (y) - Number of saturation regions DB - Dark blood IR - Inversion recovery SR - Saturation recovery G(x) - Grid tag with x mm grid distance or L (x) - Line tag with x mm line distance MT - MTC pulse PPF - Phase Partial Fourier	A4/FS/SAT1/MT
Coil information	(→ Page 201 <i>Abbreviations in the Image Text</i>)	NE1;SP1
Sequence name/flip angle	A * in front of the sequence name means that an original Siemens sequence was used.	*TS2_23 80

(5) Data about the MR image

The bottom right corner shows data regarding the position, orientation, and thickness of the acquired slice, about the extent (FoV), as well as the window values.



The text line *Flow Encoding Direction* is suppressed when empty. All subsequent lines are moved upward.

Image text	Abbreviation	Example
Sequence mask	D - Door open I - Interpolation R - Raw data filter E - Elliptical filter	DII
Table position (H,F)	TP H/F in mm	TP H300
Slice position (+LPH)	SP in mm	SP L8.7
Slice thickness Interpolated slice thickness	SL in mm SL i in mm	SL 4.0 SL 4.0 i
FoV (field of view)	FoV in mm	FoV 230×230
Acquisition matrix interpolated Acquisition matrix not interpolated	I - Interpolation p - partial Fourier s - swap	192p×256s 192p×256s
Image orientation	Sag, Tra, Cor	Tra>Cor(-20)>Sag(-30)
Flow-encoding direction	v(XXX)_inplane_xy - in-plane flow encoding v(XXX)_through - through-plane flow encoding XXX - flow velocity in cm/sec xy - direction, e.g., fh (feet to head)	v150_inplane_fh
Window width (contrast)	W	W -100
Window center (brightness)	C	C -200



Note that the image text only shows information on the first contrast of the measurement. Some sequences are able to measure more than one contrast. For these measurements, only information on the first contrast are available.

2.3 Abbreviations in the Image Text

The coils and coil elements used are shown in the lower left image text.

<Patient Name>	Orientation	<Institution Name>
<Patient ID>	label	<Model Name>
<Other Patient IDs>		<Software Version>
<*Birthdate;Age>		<Patient Position>
<Accession Number>		<Coordinate System>
<Study ID>		<Referring Physician>
<Acquisition Date>		<Phase Encoding Direction>
<Acquisition Time>		
<Series- Image Number/ Images per Series>		S
		c
		a
		i
		e
Orientation		b
label		a
		r
<Compression>		
<Magnification Factor>		
<Trigger Time>		
<Inversion Time>		<Sequence Mask>
<Repetition Time>		<Table Position>
<Echo Time>		<Slice Position>
<Acquisition Duration*Concatenations>		<Slice Thickness>
<Pixel Bandwidth>		<FoV>
<PAT Image Type>		<Acquisition Matrix Interpolated>
<Scan Options (Line1)>		<FlowEncodingDirection>
<Averages/ Scan Options (Line2)>		<Image Orientation>
<Coil Information>	Contrast/ Bolus Agent-Flow Duration	<Window Width>
<*Sequence Name/ Flip Angle>	Image Comment	<Window Center>
	Image Comment	

The following notation is used:

- The coils are sorted alphabetically in ascending order and separated by a semi-colon.
- The elements of the coils are sorted numerically in ascending order and separated by commas.

MAGNETOM Aera, Skyra, and Skyra24

Image text	Coil_ID	Coil name
HC1,HC3,HC5, NC1 HC2,HC4,HC6, HC7,NC2	HeadNeck_64	HeadNeck 64
HEA HEP	Head_32	Head 32

2 Image Text

Image text	Coil_ID	Coil name
H1U, N1U H2L, N2L	HeadNeck_16	Head_Upper Head_Lower
HE1, HE3, NE1 HE2, HE4, NE2	HeadNeck_20	Head Neck 20
SP1, SP2, SP3, SP4, SP5, SP6, SP7, SP8	Spine_24	Spine 24
SP1, SP2, SP3, SP4, SP5, SP6, SP7, SP8	Spine_32	Spine 32
BO1, BO2	Body_6	Body 6
BO1, BO2, BO3	Body_18	Body 18
PA1, PA2, PA3, PA4, PA5, PA6	PA_36_H PA_36_F	Peripheral Angio 36
SHL	ShoulderLarge_16	Shoulder Large 16
SHS	ShoulderSmall_16	Shoulder Small 16
FA1, FA2	FootAnkle_16	FootAnkle 16
HW1, HW2, HW3	HandWrist_16	Hand Wrist 16
FL	FlexLarge_4	Flex Large 4
FS	FlexSmall_4	Flex Small 4
L4	Loop_4	Loop 4
L7	Loop_7	Loop 7
L11	Loop_11	Loop 11
SC	SpecialPurpose_4	SpecialPurpose 4
2BL, 2BR	4Ch_BI_Breast_F 4Ch_BI_Breast_H	4Ch BI Breast F 4Ch BI Breast H
7BL, AXL, 7BR, AXR	16Ch_AI_Breast_F 16Ch_AI_Breast_H	16Ch AI Breast

Image text	Coil_ID	Coil name
BCL, BCR, BAL, BAR	Breast_18_F Breast_18_H	Breast 18
EN	Endorectal	Endorectal
PeH, PeN	Pediatric_16	Pediatric 16
15K	TxRx_Knee_15	TxRx Knee 15
K15	TxRx_15Ch_Knee	TxRx 15Ch Knee
HE	TxRx_CP_Head	TxRx CP Head
EX	TxRx_CP_Extremity	TxRx CP Extremity
BL1, BR1	2Ch_Breast_F_Sen 2Ch_Breast_H_Sen	2Ch Breast F Sen 2Ch Breast H Sen
BL2, BR2	4Ch_Breast_F_Sen 4Ch_Breast_H_Sen	4Ch Breast F Sen 4Ch Breast H Sen
BL4, BR4	8Ch_Breast_F_Sen 8Ch_Breast_H_Sen	8Ch Breast F Sen 8Ch Breast H Sen
BL5, BR5	10Ch_Breast_F_Sen 10Ch_Breast_H_Sen	10Ch Breast F Sen 10Ch Breast H Sen
BL8, BR8	16Ch_Breast_F_Sen 16Ch_Breast_H_Sen	16Ch Breast F Sen 16Ch Breast H Sen
PR	Prostate_2_F_Sen Prostate_2_H_Sen	Prostate 2 F Sen Prostate 2 H Sen
1H, 31P	31P_1H_Flex_Coil	31P/1H Flex Coil



Not all Coils are available at all system types.

2.4 Image Types

The image type is shown in the lower left image text.

<Patient Name>	Orientation	<Institution Name>
<Patient ID>	label	<Model Name>
<Other Patient IDs>		<Software Version>
<*Birthdate;Age>		<Patient Position>
<Accession Number>		<Coordinate System>
<Study ID>		<Referring Physician>
<Acquisition Date>		<Phase Encoding Direction>
<Acquisition Time>		
<Series: Image Number/ Images per Series>		S
		c
		a
		I
		e
		b
		a
		r
Orientation		
label		
<Compression>		
<Magnification Factor>		
<Trigger Time>		
<Inversion Time>		<Sequence Mask>
<Repetition Time>		<Table Position>
<Echo Time>		<Slice Position>
<Acquisition Duration*Concatenations>		<Slice Thickness>
<Pixel Bandwidth>		<FoV>
<PAT Image Type>		<Acquisition Matrix Interpolated>
<Scan Options (Line1)>		<FlowEncodingDirection>
<Averages/ Scan Options (Line2)>		<Image Orientation>
<Coil Information>	Contrast/ Bolus Agent-Flow Duration	<Window Width>
<*Sequence Name/ Flip Angle>	Image Comment	<Window Center>
	Image Comment	

An image may include more than one image type, e.g., after several post-processing steps. These are appended to one another and separated by a forward slash. If the maximum line length is exceeded, the last image types are omitted.

Example

Assuming the defined maximum length is 18 characters:

From **TYP1/TYP2/TYP3/TYP4** (19 characters)

will be truncated to **TYP1/TYP2/TYP3** (14 characters).

Abbreviation	Image type	Topic
3D EDITOR	Image resulting from 3D editor processing	3D reconstruction
3D FUSION	Fusion image	3D reconstruction
ADC	Apparent Diffusion Coefficient Map	Diffusion, Perfusion
ADD	Image resulting from an addition	Dynamic Analysis
AVERAGE	VRT image	3D reconstruction
BLACK IMAGE	Graphic image	3D reconstruction
BLACK IMAGE	Graphics and table image	Mean Curve
COMB	Combination image	Diffusion, Perfusion
COMPOSED	Composed Images	Image Composing
COR	Correlation image	Functional imaging Dynamic Analysis
CPR	Curved Cut Projection image. CPR image types: Thin CPR (Thickness < 30 mm) Normal CPR (Thickness 30 mm ... < 60 mm)	Spine Dot Engine
CPR*	Thick Curved Cut Projection image (Thickness ≥ 60 mm). Cannot be used as a reference image for position display.	Spine Dot Engine
CVxx	Filtered Images (xx stands for filter strength, integer value)	Dynamic Analysis
DIFFER	Differentiation image	Dynamic Analysis
DIFFUS	Diffusion image	Dynamic Analysis
DIS2D	2D distortion corrected image	Inline post-processing
DIS2D*	2D distortion-corrected image. Cannot be used as a reference image for positioning, because measurement is too far off-center.	Inline post-processing

2 Image Text

Abbreviation	Image type	Topic
DIS3D	3D_distortion-corrected image	Inline post-processing
DIV	Division image	Dynamic Analysis
E1	Diffusion image that shows the weighting of the eigenvector E1	Diffusion
E1-E2	Diffusion image that shows the weighting of the eigenvector ratio E1-E2	Diffusion
E1-E3	Diffusion image that shows the weighting of the eigenvector ratio E1-E3	Diffusion
E2	Diffusion image that shows the weighting of the eigenvector E2	Diffusion
E2-E3	Diffusion image that shows the weighting of the eigenvector ratio E2-E3	Diffusion
E3	Diffusion image that shows the weighting of the eigenvector E3	Diffusion
EXP	Exponential Map	Diffusion
FA	Fractional Anisotropy Map	Diffusion
FIL	Inline Image Filter	Inline post-processing
FILTERED	BOLD or perfusion image with spatial filtering	Inline post-processing
FSx_Y, FSHx_y, FMx_y, FS, FSH or FM	Offline Image Filter	Dynamic Analysis
GBP	Global time-density curve (Global Average Bolus Curve Plotted; passage of bolus)	Diffusion, Perfusion
GSP	Reference image with graphic objects	Graphic slice position
INT	Integration image	Dynamic Analysis
LIN	Barycentric Map, category "Linear"	Diffusion

Abbreviation	Image type	Topic
LOG	Logarithmic function image	Dynamic Analysis
LOW_B	Image with low diffusion weighting	Diffusion
M	Rephased image (magnitude image)	Flow quantification
MAG	Magnitude image	Phase contrast Angio
MEAN	Mean value image	Functional imaging Dynamic Analysis
MIP	Maximum Intensity Projection image	3D reconstruction Inline post-processing
MIP THIN	MIP Thin image	3D reconstruction
MIP_COR	Coronary image from MIP reconstruction	Inline post-processing
MIP_SAG	Sagittal image from MIP reconstruction	Inline post-processing
MIP_TRA	Transverse image from MIP reconstruction	Inline post-processing
MITP	Maximum Intensity Time Projection image	Diffusion, Perfusion
MOCO	BOLD or perfusion image with motion correction	Inline post-processing
MOSAIC	Mosaic image	Functional imaging
MPR	Multiplanar reconstruction image (MPR)	3D reconstruction
MPR CURVED	Curved MPR image	3D reconstruction
MPR THICK	MPR Thick image	3D reconstruction
MPR THIN	MPR Thin image	3D reconstruction
MSUM	Sum image from magnitude images of a slice	Phase contrast Angio
MULT	Multiplication image	Dynamic Analysis
ND	non-distortion corrected image	Inline post-processing

2 Image Text

Abbreviation	Image type	Topic
NORM	Image after normalization algorithm	Inline post-processing
OTHER	Converted N3/3.5 image or SC (secondary captured) image	Import/Export
P	Phase contrast image	Flow quantification
PBP	Percentage signal image (Percent-of-Baseline at Peak; bolus peak relative to baseline).	Diffusion, Perfusion
PDT1	T1-weighted proton density image	Dynamic Analysis
PDT2	T2-weighted proton density image	Dynamic Analysis
PEI	Positive Enhancement Integral image	Diffusion, Perfusion
PLAN	Barycentric Map, category "Planar"	Diffusion
POSDISP	Position display image	Position display
PROJECTION IMAGE	Projection image	Inline post-processing
R	Real image	Flow quantification
RA	Relative Anisotropy Map (relative FA)	Diffusion
RELCBF	Relative CBF image (relat. cerebr. blood flow)	Diffusion
RELCBV	Relative CBV image (relat. cerebr. blood volume)	Diffusion
RELMTT	Relative MTT image (relat. average transit time)	Diffusion, Perfusion
RESAMPLED	Zooming/panning image	3D reconstruction
RETRO	Retro-Gating image	Inline post-processing
SCM	Signal Change image	Diffusion, Perfusion
SDEV	Standard deviation image	Dynamic Analysis
SLOPE	SLOPE evaluation result	Dynamic Analysis

Abbreviation	Image type	Topic
sMRI	Structural MRI (Anatomy)	Diffusion
SPEC	Spectrum	Spectroscopy
SPHER	Barycentric Map, category "Spherical"	Diffusion
SSD	SSD reconstruction (Shaded Surface Display)	3D reconstruction
STDDEV_COR	Coronal standard deviation image	Inline post-processing
STDDEV_SAG	Sagittal standard deviation image	Inline post-processing
STDDEV_TRA	Transverse standard deviation image	Inline post-processing
SUB	Subtraction image	Dynamic Analysis
SUBTRACT	Subtraction image	3D reconstruction
T1	T1 image	Dynamic Analysis
T2	T2 image	Dynamic Analysis
TCS	Time Course of Signal	Diffusion, Perfusion
TG	Tensor graphic	Diffusion
TMIP	Temporal MIP, MIP reconstruction of time sequence of images	Inline post-processing
TMIP_COR	Coronal TMIP image	Inline post-processing
TMIP_SAG	Sagittal TMIP image	Inline post-processing
TMIP_TRA	Transverse TMIP image	Inline post-processing
TRACE	Trace weighted image	Diffusion
TSTDDEV	Temporary standard deviation image	Inline post-processing
TTEST	Student's t-test image (for BOLD images)	Functional imaging Dynamic Analysis

2 Image Text

Abbreviation	Image type	Topic
TTP	Time To Peak image	Diffusion, Perfusion
TU	The protocol parameters were automatically changed by a tool (e. g. AutoAlign Spine)	General
TU M	Protocol parameters were automatically changed by a tool (e. g. AutoAlign Spine) and then one more time manually.	General
VR	Volume Ratio Map	Diffusion
VRT	VRT (Volume Rendering Technique) image	3D reconstruction
WI	Wash In image	Diffusion, Perfusion
WO	Wash Out image	Diffusion, Perfusion

