

syngo MR XA31

Addendum – MR Reference Handbook

Legend

	Indicates a hint
	Provides information on how to avoid operating errors or information emphasizing important details
	Indicates the solution to a problem
	Provides troubleshooting information or answers to frequently asked questions
■	Indicates a list item
✓	Indicates a prerequisite
	A condition that has to be fulfilled before starting a particular operation
◆	Indicates a single-step operation
1 2 3	Indicates steps within operating sequences
<i>Italic</i>	Used for references and for table or figure titles
→	Used to identify a link to related information as well as previous or next steps
Bold	Used to identify window titles, menu items, function names, buttons, and keys, for example, the Save button
	Used for on-screen output of the system including code-related elements or commands
Orange	Used to emphasize particularly important sections of the text
Courier	Identifies inputs you need to provide
Menu > Menu Item	Used for the navigation to a certain submenu entry
<variable>	Identifies variables or parameters, for example, within a string

⚠ CAUTION**CAUTION**

Used with the safety alert symbol, indicates a hazardous situation which, if not avoided, could result in minor or moderate injury or material damage.

CAUTION consists of the following elements:

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

⚠ WARNING**WARNING**

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

WARNING consists of the following elements:

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

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1 Introduction

This operator manual is an addendum to the Numaris/X software operator manuals.

This manual may include descriptions covering standard as well as optional software features. Due to sales rights restrictions in certain regions and service availability, we cannot guarantee that all products or features included in this manual are available through the Siemens Healthineers sales organization worldwide.



The graphics, figures, and medical images used in this documentation are examples only. Their actual display and design may be different on your system. In particular, the screenshots may show the color design of an older user interface.

References to "Siemens Service" include service personnel authorized by Siemens.



All components of the complete operator manual may include safety information that must be adhered to. The intended use of the system is stated in the operator manual MR System and Coils.

2 Keyboard shortcuts

As an alternative to using the mouse you can use keyboard shortcuts for directly accessing a variety of software functions.

The functionality of keyboard shortcuts varies depending on the mouse focus. Ensure that the focus is on the correct element by clicking it. The listing of shortcuts is structured accordingly.

Keyboard shortcuts that require you to press and hold more than one key simultaneously are indicated by this sign: "+".



Please note that many Microsoft shortcuts will also work with Numaris/X.

2.1 General shortcuts

This section provides an overview on shortcuts available in all workflows.

Basic shortcuts

F1	Open Online Help.
Esc	Cancel active function in segment, deselect all segments, all tools (Cancel). Return to the default mouse interaction.
Del	Delete selected item.
Alt + Tab	Switch to another window or application.
Ctrl + A	Select all segments.
Ctrl + C	Copy selected object.
Ctrl + X	Cut selected object.
Ctrl + V	Paste object.

Recording a video with Camtasia

	F 9	Start recording.
	F 9	Pause recording.
	F 10	Stop recording.

For more information, see: [Operator Manual MR System Administration](#).

Expert-i

Ctrl + Alt + Q	End collaboration from the connected workplace (client side)
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For more information, see: [Operator Manual MR System Administration](#).

2.2 Measurement shortcuts

This section provides an overview on shortcuts available during the measurement.

For more information, see: [Operator Manual MR Examination and Review](#).

2.2.1 Program control

Tab	Go to the next button or program step within the queue.
Shift + Tab	Go to the previous button or program step within the queue.
Up Arrow/Down Arrow/	Select the previous or next program step within the queue.
Ctrl + Spacebar	Toggle the selection.
Page Up/Page Down	Selection side up/down.

Up Arrow	Preselect the previous or next program step within the queue.
Shift + Up Arrow	Select the previous or next program steps consecutively upward or downward within the queue.
Shift + Down Arrow	
Home/End	Select the first or last program step within the queue.
Shift + Del	Remove all queue entries (Clear All , only possible if queue is not running).
F3	Stop
F12	Start next measurement (Continue) Depending on workflow status or active dialogs, Continue may apply to multiple functions simultaneously. In this case Continue is automatically assigned to the function with the highest priority: <ul style="list-style-type: none">• Close the Exam Paused dialog box during measurements with/without contrast agent and perform the next measurement (Continue of the program scheduler)
Ctrl + C	Copy program step.
Ctrl + X	Cut program step.
Ctrl + V	Paste program step.
Ctrl + S	Save program or protocols (Save As).
Ctrl + Insert	Append a measurement pause to the end of the queue (Append Pause).

Alt + Up Arrow	Move the selected step up or down within the queue (Move Up , Move Down).
Alt + Down Arrow	
Alt + Return	Open the Step Properties dialog box for the selected step (Properties).
Ctrl + Shift + F3	Start measurement of the opened protocol step (Scan).

2.2.2 Planning segments in the GSP

Ctrl + A	Select all planning segments.
Ctrl + B	Shift to image plane.
Ctrl + G	Switch Group Graphics on/off.
Ctrl + T	Change between individual sub-steps in a Set-n-Go protocol.
Ctrl + 1	Rotate selected object so that it is oriented perpendicular to the reference plane (Perpendicular).
Ctrl + 2	Shift the centers of all slice and slab groups into the defined reference image plane (Shift to image plane).
Ctrl + 3	Shift the selected slice or slab group against or in slice-selection direction (Stack- , Stack+).
Ctrl + 4	
Ctrl + 5	Move the slice group by half the distance between slices (Gap- , Gap+).
Ctrl + 6	
Ctrl + 7	Shift the selected slice or slab group in Z direction (FoV- , FoV+).
Ctrl + 8	

Up Arrow/Down Arrow	Scroll to previous or next slice according to display order.
Numerical keypad 1/2	
Left Arrow/Right Arrow	Display previous or next series in the reference segment if such a series exists. When the first (last) loaded series is reached, the last (first) loaded series is displayed (Series+ , Series-).
Numerical keypad 4/5	
Page Up/Page Down	Scroll a predefined number of images up or down, according to display order.
Home/End	Go to first image or last image.
Spacebar	Start, stop, continue playback of the movie.
H	Show or hide reference lines.
I	Scroll through images.
L	Evaluate point of interest (Pixel Coordinates).
O	Rotate image with left mouse button.
T	Show or hide image text.
W	Adjust window level and width.
Z	Zoom and pan image.

Numerical keypad

9	The image is displayed by automatically calculating a window width and window center value (Auto Windowing).
	Increase window center.
	Decrease window center.
	Increase window width.

Numerical keypad

Decrease window width.

2.2.3 Parameter cards

Ctrl + Right Arrow	Go to the next parameter card.
Ctrl + Left Arrow	Go to the previous parameter card.
Ctrl + Shift + Right Arrow	Go to the next parameter subtask card.
Ctrl + Shift + Left Arrow	Go to the previous subtask card.
Tab	Go to the next parameter.
Shift + Tab	Go to the previous parameter.
Up Arrow	Increase numerical value.
Down Arrow	Decrease numerical value.
Return or Tab (go to the next parameter)	Accept numerical value.
Up Arrow/Right Arrow	Scroll to next parameter in the parameter set.
Down Arrow/Left Arrow	Scroll to previous parameter in the parameter set.
Return or Spacebar	Select/clear check box.
Return	Expand/collapse selection list.
Arrow keys or Home to first input or End to the last input	Select entry from selection list.

Return or Esc	Apply entry from selection list.
or Tab (go to the next parameter)	
Return or Spacebar	Select button (for example, for coil selection).

2.2.4 Inline Display

Return or Spacebar	Apply function of the icon with focus.
F12	<p>Start next measurement (Continue)</p> <p>Depending on workflow status or active dialogs, Continue may apply to multiple functions simultaneously. In this case Continue is automatically assigned to the function with the highest priority:</p> <ul style="list-style-type: none"> Start the breath-hold measurement (Scan Breathhold function of the Inline Display) End the current measurement and start the next one in the queue (Stop & Continue function of the Inline Display)

2.3 Dot Cockpit shortcuts

This section provides an overview of shortcuts available in the **Dot Cockpit**.

2.3.1 General

F2	Rename directories, regions, or examinations.
Ctrl + Shift + D	Open the Dot Cockpit (only on the Examination screen).

2.3.2 Program Editor

Ctrl + O	Open program.
Ctrl + N	Create new program.
Ctrl + S	Save program.
Ctrl + Plus	Zoom in.
Ctrl + Minus	Zoom out.
Ctrl + 0	Reset zoom.
Alt + Return	Open the Step Properties dialog box for the selected step.

2.3.3 Siemens tree and user trees

Ctrl + A	Select all lower levels of the selected tree item.
Ctrl + F	Find
Ctrl + H	Collapse all, except selected.
Ctrl + N	Add directory.
Ctrl + O	Expand/collapse.
Ctrl + P	Print
Alt + Return	Open the Directory Properties dialog box for the selected region, examination, or measurement program.

2.4 Postprocessing shortcuts

This section provides an overview on shortcuts available in MR View&GO.

2.4.1 Basic shortcuts

F11	Maximize image area (full screen) on/off.
Ctrl + mouse click	Select multiple objects.
Shift + mouse click	Select multiple objects in sequence.

2.4.2 Navigation

Numerical keypad or keyboard	Stack display mode	Stripe display mode
 	Up Arrow/Down Arrow Scroll to the next/previous slice in space.	Move one segment up/down.
 	Page Up/Page Down Move a predefined number of images forwards/backwards (for calculated 2D images the slice spacing is taken into account).	Go to the next/previous page.
 	Right Arrow/Left Arrow Navigate in time points or data sets, if applicable.	Move one segment left/right.

Keyboard

	Arrow keys	In TimeCurve , navigate to the next point on the result curve or navigate to the next curve.
	Home	Go to first image (stack or stripe).
	End	Go to last image (stack or stripe).

Keyboard

	I	Scroll images.
Scroll		
	U	Activate or deactivate scrolling with skipping.
	Shift + I	Activate or deactivate performance mode for scrolling without skipping.
	Spacebar	Start/Stop movie.
Movie		
	R	Activate 3D Reference Point .
3D Reference point		
	Alt	Move the mouse pointer on a point of the image (pathology). Click the pathology while pressing the key. The images in all segments are panned so that the 3D reference point is displayed in the center of each segment.
	O	Rotate image.
Rotate		

2.4.3 Common tools

	T	Switch the image text on/off.
Full Text		

	G	Switch display of graphics on/off.
Hide Graphics		
	H	Switch display of reference lines on/off.
Hide Lines		
	E	Send selected image to the film sheet.
Print Image		
	A	Send all images of selected stacks to the film sheet.
Print Stack		
	S	Create a snapshot for findings (of selected segments).
Snapshot to Finding		
	Ctrl + Alt + A	Close the case, save and send the results (to the archive).
Save and Send		
	Ctrl + Alt + S	Close the case and save results locally.
Save and Pause		

2.4.4 Image optimization

	F5 - F8	Apply Windowing Presets.
	F 10	Invert grayscale or color values.
	Z	Zoom/Pan images
	Alt	Press and hold the key to deactivate the current tool temporarily and enable Zoom/Pan .
	W	Adjust Windowing level and width (with left mouse button).
	S	The image is displayed by automatically calculating a window width and window center value.
	P	Quick punch (3D view: MIP, VRT, MinIP)

	Q	Remove Clip Plane and Clip Box from selected segments.
		
	Esc	Hide the handles by pressing the key. To display the handles again, click a line of a plane. Press the key a second time to deactivate the clip plane/slab.

Color LUTs

	Shift + F5 - F8	Apply Color LUT presets.
MR Color LUT		
	F 9	Toggle through all Color LUTs.
	F 10	Invert the grayscale.

2.4.5 Image evaluation

	D	Measure a straight distance.
Distance Line		
	C	Measure a circular ROI.
ROI Circle		
	L	Activate pixel lens.
Pixel Lens		

	M	Place a marker on point of interest.
	V	Measure a spherical VOI.
	Ctrl + Return	Enter a line break in an annotation text.

2.4.6 Switch display type

	1	Switch to 2D display.
	2	Switch to MPR.
	3	Switch to MPR Thick.
	4	Switch to MIP.
	5	Switch to MIP Thin.
	6	Switch to MinIP Thin.

	7	Switch to VRT.
	8	Switch to VRT Thin.

2.4.7 Series panel

F11	Hide or show the Series panel.
Ctrl + scroll wheel	Change the font size.
F2	Rename results.

2.5 Patient Browser

	Ctrl + F	Put cursor into the search field.
	Ctrl + E	Open the Export Data dialog box (with selected data).
	Ctrl + R	Start DICOM Query & Retrieve .

 Open	Ctrl + O	Open selected data.
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3 Pulse Sequences

3.1 Overview of pulse sequences

The MR system is equipped with pulse sequences that have been optimized to enable you to make adjustments to meet your clinical requirements.

The sequences cover a broad range of parameters and allow for flexible timing, with the exception of flow-compensated spin-echo sequences, which have a slightly limited parameter range.

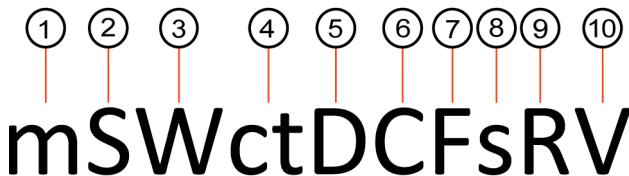
The sequences available on your system depend on how it is configured and which licenses are installed.

3.1.1 Sequence variants

The sequence variants are displayed in the protocol info line of the parameter cards and in the image text.

The variant comprises:

- The sequence type (for example, SE for spin echo)
- The expansions based on the parameters selected



- (1) Sequence mode
- (2) Sequence type
- (3) WARP mode
- (4) Continuous table move
- (5) Dimension
- (6) Number of contrasts
- (7) Flow compensation
- (8) Number of segments or combined echoes
- (9) Excitation pulse
- (10) Velocity encoding

3.1.1.1 On-screen display

The sequence variants are displayed in different ways.

- In the image text, the **complete** sequence variant name is displayed (for example, fl3d1r_tf).
- On the parameter card, only the **abbreviation** of the sequence variant is shown (sequence code), for example, fl_r.



To display the complete sequence variant name, move the mouse pointer over the sequence code.

3.1.2 Sequence variant components

3.1.2.1 Sequence mode (m)

Abbreviation	Definition
q	Quiet mode
f	Fast mode

3.1.2.2 Sequence type (S)

Abbreviation	Definition
ci	CISS (constructive interference in steady state)
csi	Chemical shift imaging
de	DESS (dual echo steady state)
D	Diffusion-weighted imaging
epfid	EPI-FID
epir	EPI spin echo with inversion recovery
epse	EPI spin echo

Abbreviation	Definition
fi	FISP (fast imaging with steady-state precession), gradient-echo sequence without RF spoiling
fid	Free induction decay
fl	FLASH (fast low angle shot), gradient-echo sequence with active RF spoiling
h	HASTE (half-Fourier single-shot turbo spin-echo)
hir	HASTE with inversion recovery
ir	Spin echo with inversion recovery
me	MEDIC (multi-echo data image combination)
ps	PSIF (time-reversed FISP)
re	RESOLVE (readout segmentation of long variable echo trains), multi-shot, diffusion-weighted EPI
se	Spin echo
spc	SPACE (sampling perfection with application-optimized contrast using different flip angle evolutions)
svs	Single-voxel spectroscopy
swi	Susceptibility-weighted imaging
tfi	TrueFISP
tfl	TurboFLASH
tgir	Turbo gradient spin echo with inversion recovery
tgse	Turbo gradient spin echo
tir	Turbo spin echo with inversion recovery
tirB	Turbo spin echo with inversion recovery and BLADE trajectory
tirBR	Turbo spin echo with inversion recovery, BLADE trajectory and “restore pulse”

Abbreviation	Definition
tirR	Turbo spin echo with inversion recovery and "restore pulse"
tse	Turbo spin echo
tseB	Turbo spin echo with BLADE trajectory
tseBR	Turbo spin echo with BLADE trajectory and "restore pulse"
tseR	Turbo spin echo with "restore pulse"

3.1.2.3 WARP mode (W)¹⁾

Abbreviation	Definition
W	Basic <i>syngo</i> WARP mode: for high bandwidth optimization
V	VAT (view angle tilting): to reduce in-plane susceptibility distortions
S	SEMAC (slice encoding for metal artifact correction): to reduce through-plane susceptibility distortions

3.1.2.4 Dimension (D)

Abbreviation	Definition
1d	One-dimensional data acquisition
2d	Two-dimensional data acquisition
3d	Three-dimensional data acquisition

1) For a detailed description, see: Operator Manual Diagnostic MR Imaging

3.1.2.5 Contrast (C)

Abbreviation	Definition
1, 2, ..., 16, ...	Number of reconstructed images with different contrasts

3.1.2.6 Flow compensation (F)

Abbreviation	Definition
r	Flow compensation in the readout and slice selection direction
rr	Flow compensation in the readout direction only
rs	Flow compensation in the slice direction only
rd	Interleaved acquisition with alternating rephased and dephased measurements
–	No flow compensation; only displayed if another character follows
pc	Flow-sensitive gradients for phase-contrast angiography

3.1.2.7 Number of segments or combined echoes (s)

Abbreviation	Definition
2, 3, ..., 15, ...	Number of segments in the k-space for segmented sequences: EPI factor × Turbo factor × segments
2, 3, 4, 5, ...	MEDIC sequences: number of combined echoes
–	If the number of segments = 1 and the number of combined echoes = 1 (only displayed if another character follows)

3.1.2.8 Excitation pulse (R)

Abbreviation	Definition
ns	Non-selective excitation
t10, t20, ..., t100	TONE pulse; number indicates the value of the TONE ramp parameter (in percent)
z	syngo ZOOMit: Zoomed excitation ²⁾

3.1.2.9 Velocity encoding (V)

Abbreviation	Definition
v2, v100 .. v300	Velocity encoding; number indicates the value of the velocity encoding in cm/s
rl	Right to left
lr	Left to right
ap	Anterior to posterior
pa	Posterior to anterior
fh	Feet to head
hf	Head to feet
in	Through plane, into page
out	Through plane, out of page

3.1.3 Sequence nomenclature

The sequence nomenclature refers to the sequence names used in the *syngo* MR database. In the **Dot Cockpit**, they are referred to as **Default Sequences**.

2) For a detailed description, see: Operator Manual Diagnostic MR Imaging

3.1.3.1 Sequence nomenclature (I)

Abbreviation	Definition
AALScout	AutoAlign localizer
BEAT	For cardiovascular MR imaging
CISS	Constructive interference in steady state
CSI	Chemical shift imaging
CV	For cardiovascular MR imaging
DESS	Dual echo steady state
EPI	Echo-planar imaging
Fast	Sequence with short echo spacing
FastView	Localizer for large body regions
FID	Free induction decay
FLASH	Fast low angle shot
GRE	Gradient-echo sequence ³⁾
HASTE	Half-Fourier single-shot TSE
MEDIC	Multi-echo data image combination
PETRA	Pointwise encoding time reduction with radial acquisition
PSIF	Time-reversed FISP sequence (FISP = fast imaging with steady-state precession)
Quiet_DWI	For quiet diffusion-weighted imaging
RESOLVE	Readout segmentation of long variable echo trains
SE	Spin-echo sequence
SPACE	For SPACE applications

3) RF spoiling can be activated with gradient-echo sequences. FLASH contrast is generated when RF spoiling is switched on, FISP contrast when RF spoiling is switched off

Abbreviation	Definition
SVS	Single-voxel spectroscopy
TurboFLASH	-
TGSE	Turbo gradient spin-echo
TrueFISP	FISP = fast imaging with steady-state precession
TSE	Turbo SE
TWIST	Sequence with high temporal resolution

3.1.3.2 Sequence nomenclature (II)

Abbreviation	Definition
_ASL	For perfusion imaging (ASL = arterial spin labeling)
_B1Map	For B1 mapping
_BOLD	For BOLD imaging (BOLD = blood oxygen level dependency)
_CB	For determining the contrast bolus
_CE	For contrast-enhanced angiography
_Diff	For diffusion contrast
_Dixon	Sequence using the Dixon technique
_Edit	Spectroscopy sequence for spectral editing ⁴⁾
_EPI	For echo-planar imaging
_FID	Free induction decay, for example, EPI_FID: gradient-echo variant of EPI sequence
_Field_Mapping	For generating a field map for BOLD postprocessing
_FreqScout	Frequency adjustment sequence for TrueFISP measurements

4) Only available at systems with a field strength of 3 T

Abbreviation	Definition
_FQ	For flow quantification
_Histo	Spectroscopy sequence for fat and iron quantification in the liver
_Interactive	For interactive real-time imaging
_Map	For myocardial mapping
_MC	Multicontrast sequence
_MRE	Sequence for MR Elastography
_NAV	Sequence with navigator
_PACE	Sequence with prospective motion correction
_PC	For phase-contrast angiography
_Peri_TOF	Time-of-flight sequence, optimized for peripheral angiography
_PHS	Phase imaging sequence
_Proj	For acquisition of projection data
_r	With flow compensation
_RD	Rephased-dephased angiography sequence
_SE	Spin-echo sequence, for example, EPI_SE: spin-echo variant of EPI sequence
_SEG	Segmented sequence
_Semi_LASER	Semi-LASER variant
_STEAM	Spectroscopy sequence for STEAM technique (STEAM = stimulated echo acquisition method)
_Therm	Temperature-sensitive sequence
_TOF	For time-of-flight (inflow angiography)
_VIBE	Volume-interpolated breath-hold examination

Abbreviation	Definition
..b..	Bandwidth per pixel; the value follows in hertz, for example, SE_15b130
..r..	With flow compensation, see also _r
.2D	For two-dimensional imaging
.3D	For three-dimensional imaging
.._15..	Echo time, for example, 15 ms

3.1.4 Spectroscopy sequence nomenclature

In the image texts and series names of spectroscopy sequences, specific abbreviations are used.

3.1.4.1 Image texts

Abbreviation	Definition
_w	Weighted (spectra scaled based on coil weighting)
_p	Phase-corrected (phase correction with prescan)
_pw	Phase-corrected, weighted
_pwc	Phase-corrected, weighted, combined (combination of all coil channels)
_upw	Unphased, weighted

3.1.4.2 Series names

Abbreviation	Definition
_ave	Single averages
_ref	Reference scan spectrum

Abbreviation	Definition
_ECC	Eddy-current corrected (with reference scan)
_noECC	Not eddy-current corrected
_uc	Uncombined
_pw	Phase-corrected, weighted
_upw	Unphased, weighted

3.2 Description of pulse sequences 1.5 T

3.2.1 AALScout

A modified FLASH3D_VIBE sequence is used for AutoAlign scout measurements in AutoAlign programs and Dot Engines. The algorithm uses bone markers (L = landmark-based) for automatic slice positioning.



The sequence parameters cannot be changed, with the exception of the selected coils and the iPAT factor.

3.2.1.1 Use

The sequence must precede any examination with AutoAlign. The slice position of subsequent measurement protocols is automatically adjusted with AutoAlign.

3.2.2 BEAT (Angio QISS)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.2.2.1 Use

For displaying the arteries of the peripheral vasculature.

3.2.2.2 Essential parameters

Magnetization preparation	Slice-sel. SR
Saturation regions	Yes
Special saturation	Tracking H/F
TI	Yes
ECG	None/Trigger
Trigger device	ECG/Pulse/Ext
Trigger delay	Yes (100 ms)
Dimension	2D

3.2.2.3 Parameters

Averages	Yes
Flip angle mode	Constant
Fat-Water Contrast	Standard/Fat saturation
Acceleration mode	None/GRAPPA/mSENSE
Reference scans	Integrated/GRE-Separate
Phase partial Fourier	Off, 7/8, 6/8, 5/8, 4/8
Set-n-Go protocol	Yes
Inline composing	Yes
Respiratory control	Off/Breath-hold
Define	Shots/Segment

Segments variable	No
TE variable	Yes
Asymmetric echo	Yes
Bandwidth variable	Yes
Sequence type	TrueFISP/GRE
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper

3.2.3 BEAT (Angio TOF)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.2.3.1 Use

3D display of vessels.

3.2.3.2 Essential parameters

Dimension	3D
Sequence type	GRE
Special saturation	Tracking H/Tracking F
Flow direction	F>>H/H>>F
Excitation	TONE
Tone ramp	20%–100%
Flow compensation	On, Read, Slice/Read, Read/Phase

3.2.3.3 Parameters

Fat-Water Contrast	Standard/Fat saturation/Water excitation
Acceleration mode	None/GRAPPA/mSENSE/CS
Reference scans	Integrated/GRE-Separate
Phase partial Fourier	Off, 7/8, 6/8, 5/8, 4/8
Interpolation	1–2 floating values
RF spoiling	On
Phase encoding rewinder	On/Off
Define	Segment
Segments variable	Yes
TE variable	Yes
Asymmetric echo	Yes
Bandwidth variable	Yes
RF pulse type	Normal/Low SAR
Gradient mode	Fast/Normal/Whisper

3.2.4 BEAT (Cine)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.2.4.1 Use

For imaging cardiac function.

3.2.4.2 Essential parameters

Cine	On
------	----

3.2.4.3 Parameters

Averages	Yes
Magnetization preparation	TI Scout (TrueFISP only)
Fat-Water Contrast	Standard
Reconstruction mode	Magnitude, Magn./Phase
Acceleration mode	None/GRAPPA/mSENSE/CS (True-FISP only)
Reference scans	Integrated/GRE-Separate/T-PAT
Phase partial Fourier	Off, 7/8, 6/8, 5/8, 4/8
Trajectory	Cartesian/Radial ⁵⁾
Saturation regions	Yes (GRE only)
ECG	None/Trigger/Retro
Trigger device	ECG/Pulse/Ext
Arrhythmia detection	None/By time
Adaptive triggering	Yes ⁶⁾
TruFi delta freq.	-300 – +300
Respiratory control	Off/Breath-hold
Inline evaluation	None/Ventricular Function/Restart InlineVF ⁷⁾
Tagging	None (TrueFISP) Grid/Line (GRE)

5) Only if Dimension = 2D is selected

6) Only if Multi-slice mode = Single-shot is selected

7) Only if Dimension = 2D is selected

Optimization	Min. TE/TR
Define	Shots/Segment
Segments variable	Yes
TE variable	No ⁸⁾
Asymmetric echo	Yes
Flow compensation	None (TrueFISP) None; On; Read; Slice/Read; Read/Phase (GRE)
Dimension	2D/3D
Sequence type	TrueFISP/GRE
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
RF spoiling	Off (TrueFISP) On (GRE)

3.2.5 BEAT (Dynamic)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.2.5.1 Use

For dynamic imaging of the heart.

8) TE is automatically set to the minimum and cannot be changed

3.2.5.2 Essential parameters

Magnetization preparation	Non-sel. IR/Non-sel. SR/Non-sel. SR Perf
TI	Yes
Multi-slice mode	Single-shot
Define	Shots
Shots per slice	1

3.2.5.3 Parameters

Flip angle mode	Constant (TrueFISP/GRE) Variable (GRE only)
Fat-Water Contrast	Standard/Fat saturation/Fat water excitation/SPAIR
Measurements	1–512
Acceleration mode	None/GRAPPA/mSENSE
Reference scans	Integrated/GRE-Separate/T-PAT
Phase partial Fourier	Off, 7/8, 6/8, 5/8
Trajectory	Cartesian/Radial
ECG	None/Trigger
Trigger device	ECG/Pulse/Ext
Adaptive triggering	Yes
TruFi delta freq.	-300 – +300
Respiratory control	Off/Breath-hold
Inline evaluation	Off/Time Course Evaluation/Time Course Filtered

Motion correction	Yes
Proton density images	Yes
TE variable	Yes
Asymmetric echo	Yes
Flow compensation	None (TrueFISP) None, On, Read, Slice/Read, Read/Phase (GRE)
Dimension	2D/3D
Sequence type	TrueFISP/GRE
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
RF spoiling	Off (TrueFISP) On (GRE)

3.2.6 BEAT (Static)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.2.6.1 Use

For localization, tissue characterization, and morphologic imaging of the heart.

Essential parameters	Magnetization preparation	None/Slice-sel. IR/Non-sel. IR/Non-sel. T2-IR/T2 Prep. Adiab.
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3.2.6.2 Parameters

Averages	Yes
Contrasts	1–32
TI	Yes
T2 Prep. Duration	Yes
Flip angle mode	Constant (TrueFISP/GRE) Variable (GRE only)
Fat-Water Contrast	Standard/Fat saturation/Fat water excitation/SPAIR
Dark Blood	Yes
Reconstruction mode	Magnitude, Magn./Phase, Magnitude/Real
Acceleration mode	None/GRAPPA/mSENSE
Reference scans	Integrated/GRE-Separate/T-PAT
Phase partial Fourier	Off, 7/8, 6/8, 5/8, 4/8
Trajectory	Cartesian/Radial
Multi-slice mode	Sequential, Single-shot
Saturation regions	Yes
ECG	None/Trigger
Trigger device	ECG/Pulse/Ext
Adaptive triggering	Yes ⁹⁾
TruFi delta freq.	-300 – +300
Respiratory control	Off/Breath-hold
Inline evaluation	None

9) Only if Multi-slice mode = Single-shot is selected

Motion correction	Yes ¹⁰⁾
Tagging	None
Define	Shots/Segment
Segments variable	Yes
TE variable	Yes
Asymmetric echo	Yes
Flow compensation	None (TrueFISP) None, On, Read, Slice/Read, Read/Phase (GRE)
Dimension	2D/3D
Sequence type	TrueFISP/GRE
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
RF spoiling	Off (TrueFISP) On (GRE)

3.2.7 BEAT_EPI

Single-shot sequence. Can be combined with inversion recovery or saturation recovery preparation pulses.

3.2.7.1

Sequence type	Define	Shot per slice	Magn. preparation	1 st Signal/Mode
GRE EPI	Shots	1	IR/SR/SR perf	ECG/Trigger

10) Only if Multi-slice mode = Single-shot and Magnetization preparation = Non-selective IR are selected

3.2.7.2 Saturation Recovery (SR) or Saturation Recovery Perfusion (SR perf)?

- SR: Rectangular saturation pulse (normally 90 degrees)
- SR perf: Echo train with three saturation pulses (90 degrees each) as well as different time intervals and gradient spoilers. More robust with respect to magnetic field inhomogeneities, however, with a higher SAR.

3.2.7.3 Use

- For measuring First Pass perfusion.
- For sequential multislice applications.

3.2.7.4 Parameters

Segments	Fixed ¹¹⁾
TE variable	No ¹²⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, SR, Selective, Non-selective
Reconstruction mode	Magnitude
Fat suppression	Yes
Asymmetric echo	Yes
Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	Yes
Dimension	2D/3D
RF pulse type	Fast/Normal

11) Max. number of segments depends on the number of lines

12) TE is automatically set to the minimum and cannot be changed

RF spoiling	On
Gradient mode	Fast/Normal/Whisper
PAT	Integrated/tPAT

3.2.8 BEAT_FQ

Flow sequence with variable flow encoding. The sequence measures a flow-compensated and a flow-encoded scan. Phase sharing enables more frequent sampling of the center raw data lines during pulsating flow.

Possible online reconstructions:

- Magnitude image
- Phase image
- Magnitude sum image

3.2.8.1 Use flow quantification

- For displaying and quantifying blood flow. Through-plane measurements for flow quantification and in-plane measurements for flow display.
- Triggered, retrospective gating possible, for displaying and quantifying blood flow during complete heart cycle coverage. Particularly suitable for patients with arrhythmias.
- Enables flow measurement in breath-hold technique using phase sharing.

3.2.8.2 Use phase-contrast angiography

- Peripheral angiography, for example, for acquiring large fluctuations in flow velocity (multivenc application)
- Localizer for 3D phase-contrast measurements
- Neuro applications, for example, for displaying arterial vessel systems

You can set the following applications on the **Angio** parameter card:

- Multivenc applications: Variable velocity encoding in one spatial direction
- Single-venc applications: Same velocity encoding in three spatial directions
- Mixed venc applications: Free selection of direction and velocity for 3 encodings

3.2.8.3 Parameters

Segments	Variable
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Asymmetric echo	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	2D/3D
Elliptical scanning ¹³⁾	Yes
Slice resolution ¹⁴⁾	Yes
Excitation pulse	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper

13) Only if Dimension = 3D is selected

14) Only if Dimension = 3D is selected

Venc cm/s	1–999
PAT	Integrated

3.2.9 BEAT_Interactive

The BEAT_Interactive sequence is used for interactive real-time imaging. The sequence is based on the BEAT sequence and inherits most of the parameter settings from it.

The BEAT_Interactive sequence has the capability to acquire multiple slices that can be measured in a predefined order and will be displayed in the **Inline Display**.

During the measurement, all slice parameters can be changed via graphic slice positioning and the parameter cards. (Prerequisite: Sequence is started via the **Copy&Go** button in the toolbar of the program control.)

The slice positions can be saved during imaging and subsequently transferred to a protocol in the wait queue.

3.2.9.1 Use (sequence type TrueFISP)

Fast sequence with a high signal-to-noise ratio. This sequence is very suitable for cardiac and abdominal applications.

3.2.9.2 Use (sequence type GRE)

Slower sequence with a lower SAR than TrueFISP. This sequence is very suitable for interventional imaging; susceptibility effects enable a good view of biopsy needles.

3.2.9.3 Parameters (sequence type TrueFISP)

TE variable	No ¹⁵⁾
Contrasts	1
Bandwidth variable	Yes

15) TE is automatically set to the minimum and cannot be changed

Magnetization Preparation	Yes
Reconstruction mode	Magnitude
Saturation regions	Regular
Phase partial Fourier	Yes
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
Trajectory	Cartesian
Slices	1

3.2.9.4 Parameters (sequence type GRE)

TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization Preparation	Yes
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular
Phase partial Fourier	Yes

Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	Yes/None
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
Trajectory	Radial
Slices	1

3.2.10 BEAT_Map

The MyoMaps sequence, BEAT_Map supports inline T1, T2 and T2* mapping of the heart. The sequence is based on the *syngo BEAT* sequence and therefore inherits the parameters and functionality of the latter. Images can be acquired with TrueFISP or GRE contrast.

3.2.10.1 Use

For generating parametric maps of the heart. For a detailed description, see: Operator Manual Diagnostic MR Imaging.

3.2.10.2 Parameters

Segments	Variable ¹⁶⁾
TE variable	No ¹⁷⁾
Contrasts	1–32

16) Max. number of segments depends on the number of lines. T1 and T2 mapping are single-shot techniques.

17) TE is automatically set to the minimum and cannot be changed

Bandwidth variable	Yes
Magnetization preparation	Non-selective, IR, T2 preparation
Reconstruction mode	Magnitude/Phase
Fat suppression	Yes
Phase partial Fourier	Yes
Sequence type	GRE/TrueFISP
Asymmetric echo	Yes
Multi-slice mode	Sequential
Flow compensation	Yes ¹⁸⁾
Dimension	2D
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
Trajectory	Cartesian
iPAT	Yes
Respiratory control	Breath-hold ¹⁹⁾
Optimization	Min. TE/TR

3.2.11 CISS

3D gradient-echo sequence for T2 imaging with a large flip angle. TE and TR are permanently set to a minimum value to ensure best possible image quality.

18) TrueFISP is essentially flow-compensated from one RF pulse to the next. GRE can be combined with flow compensation.

19) Multiple breath-hold possible, depending on protocol setup

3.2.11.1 Use

Can be used in neurology, where CSF provides contrast: cochlea, labyrinth, cranial nerves, optic nerve tract, spinal canal, etc.

3.2.11.2 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Water excitation
Phase partial Fourier	Yes
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D/3D
Elliptical scanning ²⁰⁾	Yes
Slice resolution ²¹⁾	Yes
Slice partial Fourier ²²⁾	Yes
Excitation pulses ²³⁾	Slab-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper

20) Only if Dimension = 3D is selected

21) Only if Dimension = 3D is selected

22) Only if Dimension = 3D is selected

23) Only if Dimension = 3D is selected

3.2.12 CSI_FID

FID variant for chemical shift imaging.

3.2.12.1 Parameters

TE variable	No ²⁴⁾
Bandwidth variable	Yes
Averaging mode	Short term/Long term
Dimension	2D/3D
Triggering	ECG/Respiratory
k-space weighting	Full/Elliptical/Weighted
Multiple measurements	Yes
Multinuclear support	Yes

3.2.13 CSI_SE

Spin-echo sequence for chemical shift imaging.

3.2.13.1 Use

- Localization with three orthogonal slices
- 90°–180°–180°
- Measured signal: Full spin echo

3.2.13.2 Parameters

TE variable	Yes
Bandwidth variable	Yes

24) TE is automatically set to the minimum and cannot be changed

Spectral fat suppression	Yes
Saturation regions	Regular
Averaging mode	Short term/Long term
Dimension	2D/3D
k-space weighting	Full/Elliptical/Weighted
Excitation of VOI	Yes
Multiple measurements	Yes
Fully excited VOI	Yes

3.2.14 CSI_STEAM

STEAM chemical shift imaging sequence.

3.2.14.1 Use

- Localization with three orthogonal slices
- 90°–90°–90°
- Measured signal: Stimulated echo
- Short TEs possible
- Only half of the spin-echo signal

3.2.14.2 Parameters

TE variable	Yes
Mixing time (TM) variable	Yes
Bandwidth variable	Yes
Averaging mode	Short term/Long term
Dimension	2D/3D

k-space weighting	Full/Elliptical/Weighted
Excitation of VOI	Yes
Multiple measurements	Yes

3.2.15 CV_NAV

Combination of cardiovascular sequence (type TrueFISP or GRE, Cine Off) and the prospective measurement of a navigator echo.

3.2.15.1 Use

- For displaying the coronary arteries with free breathing.
- For displaying the renal arteries in NATIVE TrueFISP protocols (Prerequisite: NATIVE license is available).

3.2.15.2 Parameters

Segments	Variable ²⁵⁾
TE variable	No ²⁶⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, SR, Selective, Non-selective
Reconstruction mode	Magnitude/Real
Fat suppression	Yes
Saturation regions	Regular/Parallel
Inversion regions ²⁷⁾	Up to 4 (with different TI)
Phase partial Fourier	Yes

25) Max. number of segments depends on the number of lines

26) TE is automatically set to the minimum and cannot be changed

27) With NATIVE license

Asymmetric echo	Yes
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None ²⁸⁾
Dimension	2D/3D
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Respiratory control	Gate & Follow/Gate/Monitor only/Off

3.2.16 DESS

3D gradient-echo sequence.

3.2.16.1 Use

Primarily in orthopedic imaging with good contrast between synovial fluid and cartilage.

3.2.16.2 Recommendations

To saturate fat at a short TR, activate a non-selective excitation pulse beforehand.

28) TrueFISP is essentially flow-compensated from one RF pulse to the next

3.2.16.3 Parameters

TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Water excitation
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Readout
Dimension	3D
Elliptical scanning ²⁹⁾	Yes
Slice resolution ³⁰⁾	Yes
Slice partial Fourier ³¹⁾	Yes
Excitation pulses ³²⁾	Slab-selective/Non-selective
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes

29) Only if Dimension = 3D is selected

30) Only if Dimension = 3D is selected

31) Only if Dimension = 3D is selected

32) Only if Dimension = 3D is selected

3.2.17 EPI SEG FID

Segmented FID EPI sequence. Faster than gradient-echo sequences, fewer off-resonance effects than with the single-shot FID EPI sequence.

3.2.17.1 Use

T2*-weighted 2D/3D imaging in the head.

3.2.17.2 Parameters

EPI factor	1–127
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D/3D
RF pulse type	Normal
RF spoiling	On/Off

Gradient mode	Fast/Normal
Respiratory control	Breath-hold ³³⁾

3.2.18 EPI SEG PHS

Segmented EPI sequence with RF and gradient-free periods for specific applications.



No protocols are provided in the Siemens protocol tree for this sequence. The sequence is to be found in the **Default Sequences** list on the **Default** tab of the **Dot Cockpit Program Editor**.

3.2.18.1 Use

You can use the EPI SEG PHS sequence to synchronize external hardware with the scanner behavior.

3.2.18.2 Parameters

EPI factor ³⁴⁾	1–127
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	None
Reconstruction mode	Magnitude, Magn./Phase
Fat-Water Contrast	Standard/Fat saturation/Fast fat saturation
Saturation regions	Standard/Quick
Multislice mode	Interleaved/Sequential

33) Multi-breath-hold possible, depending on protocol setup

34) Parameter cannot be freely set, depends on base and phase resolution

Flow compensation	On, Read, Slice, Slice/Read, Read/Phase, Read/Phase
Dimension	2D/3D
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On/Off
Phase-encoding rewinder	On/Off
Gradient mode	Fast/Normal/Whisper

3.2.19 EPI_SEG_SE

Segmented spin-echo EPI sequence. Faster than spin-echo sequences, fewer off-resonance effects than with a single-shot spin-echo EPI sequence.

3.2.19.1 Use

Fast T2-weighted 2D/3D imaging in the head.

3.2.19.2 Parameters

EPI factor	1–127
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes

Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D/3D
RF pulse type	Normal
RF spoiling	Off
Gradient mode	Fast/Normal
Respiratory control	Breath-hold ³⁵⁾

3.2.20 EPI SEG Therm

Segmented, temperature-sensitive EPI sequence.

With an EPI factor of 1, the sequence behaves like a GRE sequence.

3.2.20.1 Use

MR thermometry is used to analyze temporal changes in the complex phase of image data based on large temperature changes of $\geq 15^{\circ}\text{C}$ ($\geq 27^{\circ}\text{F}$) in soft tissue. When interpreted by a trained physician, the application may be useful as part of an interventional procedure and/or for assessing a course of treatment.

For additional information on MR thermometry, see: Operator Manual Diagnostic MR Imaging.

3.2.20.2 Parameters

EPI factor	1–13
Contrasts	1

35) Multiple breath-hold possible, depending on protocol setup

Reconstruction mode	Magnitude/Phase
Asymmetric echo	Off
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D/3D
Excitation pulses	Slice-selective
RF pulse type	Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
Trajectory	Cartesian
Slices	1–20

3.2.21 EPI2D_ASL

Single-shot FID EPI sequence.

3.2.21.1 Use

For perfusion imaging in the head. Perfusion-weighted images and rCBF images are obtained by this method.

3.2.21.2 Parameters

EPI factor ³⁶⁾	1–128
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.

36) Parameter cannot be freely set, depends on base and phase resolution

Magnetization preparation	ASL
Reconstruction mode	Magnitude
Fat suppression	Fat saturation (strong/weak)
Saturation regions	PICORE Q2T, PCASL ³⁷⁾
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal
RF spoiling	Off
Gradient mode	Fast/Normal
Online reconstruction	Perfusion-weighted images, relCBF
Flow limit	0–100 cm/s
Bolus duration	Variable ³⁸⁾
iPAT	Yes
Quality check	On/Off/On - extended

3.2.22 EPI2D_BOLD

Single-shot FID EPI sequence.

37) Parameter “Perfusion mode”

38) Parameter depends on TR

3.2.22.1 Use

For BOLD imaging in the head, t-test evaluation is performed in real time during the measurement. The calculated t-test images are shown continuously in the **Inline Display**.

3.2.22.2 Parameters

EPI factor ³⁹⁾	1–128
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal
iPAT	Yes
Simultaneous multislice (SMS)	Yes

39) Parameter cannot be freely set, depends on base and phase resolution

3.2.23 EPI2D_Diff

Single-shot spin-echo EPI sequence.

You can set diffusion-specific parameters on the **Diff** parameter card:

- Direction(s) of the diffusion-sensitive axis(es) (diffusion mode)
- Number and magnitude of b-values
- Reconstruction mode (ADC image, Trace images)

3.2.23.1 Use

For diffusion imaging, for example, for examining strokes.

3.2.23.2 Recommendations

To minimize image distortions due to susceptibility, select a bandwidth that enables use of minimum echo spacing.

3.2.23.3 Parameters

EPI factor ⁴⁰⁾	1–256
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes

40) Parameter cannot be freely set, depends on base and phase resolution

Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Excitation pulses	ZOOMit
Gradient mode	Fast/Normal
b-value [s/mm ²]	0–10000
Increment bipolar [s/mm ²]	50
Increment monopolar 0–200 [s/mm ²]	10
Increment monopolar 200–10000 [s/mm ²]	50
Diffusion mode	Read/Slice/Phase/Orthogonal/3D-Diagonal/1-Scan Trace/3-Scan Trace/4-Scan Trace/MDWW/q-Space/Free ⁴¹⁾
Online reconstruction	<ul style="list-style-type: none"> • DW and ADC image • FA image • TRACE • colored FA image
iPAT	Yes
Simultaneous multislice (SMS)	Yes
Respiratory control	Trigger/Breath-hold ⁴²⁾
Echo spacing variable	Yes

41) Only accessible with DTI license and custom diffusion vector set file

42) Multi-breath-hold possible, depending on protocol setup

Optimization	Min. TE
SliceAdjust	Yes
Phase correction	Internal/External

3.2.24 EPI2D_FID

Single-shot FID EPI sequence.

3.2.24.1 Use

For perfusion imaging in the head. You can activate online reconstruction of the following images on the **Perf** parameter card:

- Time to Peak (TTP)
- Global Bolus Plot (GBP)
- Percentage of Baseline at Peak (PBP)
- relative Cerebral Blood Volume (relCBV)
- relative Cerebral Blood Flow (relCBF)
- relative Mean Transit Time (relMTT)

3.2.24.2 Recommendations

To minimize image distortions through susceptibility, select a bandwidth that enables use of minimum echo spacing.

3.2.24.3 Parameters

EPI factor ⁴³⁾	1–256
TE variable	Yes
Contrasts	1

43) Parameter cannot be freely set, depends on base and phase resolution

Bandwidth variable	Min.–max.
Magnetization preparation	No
Reconstruction mode	Magnitude
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal
RF spoiling	Off
Gradient mode	Fast/Normal
Online reconstruction	<ul style="list-style-type: none"> • TTP • GBP • PBP • relCBV • relCBF • relMTT
iPAT	Yes

3.2.25 EPI2D_PACE

Identical to EPI2D_BOLD but with prospective 3D motion correction.



If you switch off motion correction, the entire function including prospective correction is deactivated.

3.2.25.1 Parameters

EPI factor ⁴⁴⁾	1–128
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal
RF spoiling	Off
Gradient mode	Fast/Normal
iPAT	Yes

44) Parameter cannot be freely set, depends on base and phase resolution

3.2.26 EPI2D_SE

Single-shot spin-echo EPI sequence.

3.2.26.1 Use

To examine T2-weighted lesions.

3.2.26.2 Recommendations

The CSF signal in the head can be suppressed by activating an inversion pulse with a long inversion time.

3.2.26.3 Parameters

EPI factor	1–256 ⁴⁵⁾
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D

45) Parameter cannot be freely set, depends on base and phase resolution

RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal
iPAT	Yes

3.2.27 EPI2D_SE_MRE

Single-shot spin-echo EPI sequence for MR Elastography (MRE). This sequence acquires information about the periodic movement of the tissue caused by an external source (elastography hardware) via motion-encoding gradients (MEG).

The EPI2D_SE_MRE sequence offers acquisition of multiple slices in a single, short breath-hold and is more robust against signal dephasing effects, especially at 3 T.

3.2.27.1 Use

The MRE technique generates images of the relative stiffness by imaging the propagation of the pressure waves in the human tissue.

3.2.27.2 Recommendations

Fractional MRE should only be used for patients with a very short T2* relaxation time whose resulting signal is too low. If you use Fractional MRE, the MEG duration is reduced to a fraction of the full wave period. It is automatically activated by reducing the TE time to a minimum value (in the range below the gray area).

3.2.27.3 Parameters

EPI factor	1–128 ⁴⁶⁾
TR variable	Yes

46) Parameter cannot be freely set, depends on base and phase resolution

TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Fat-Water Contrast	Standard/Fat saturation/SPAIR/ Water excitation
Fat saturation	Strong/Weak
Dimension	2D
Bandwidth variable	Yes
Special saturation	Parallel H/Parallel F
iPAT	Yes
Phase partial Fourier	Yes
Gradient mode	Fast/Normal

3.2.28 Fast_TSE

Optimized TSE sequence with shorter echo spacing.

Advantages:

- Shorter measurement times
- Possible reduction of streaking artifacts, especially for BLADE imaging

3.2.28.1 Use

Used only for conventional TSE and BLADE imaging in abdominal imaging.

3.2.28.2 Parameters

Turbo factor	1–129
TE variable	Yes

Contrasts	1–3
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ⁴⁷⁾
Fat suppression	Fat saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ⁴⁸⁾
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None/Readout/Slice
Dimension	2D
RF pulse type	Fast/Normal/Optimized
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Respiratory control	Trigger/Breath-hold ⁴⁹⁾
BLADE Trajectory	Yes
Restore	Yes

3.2.29 FastView

Gradient-echo sequence.

47) Can only be selected if Magn. Preparation = IR has been selected

48) Parameter cannot be freely set, depends on selected TE

49) Multiple breath-hold possible, depending on protocol setup

3.2.29.1 Use

For localizer images of large body regions with transverse slices and continuous table move.

3.2.29.2 Parameters

Matrix	96
Slice thickness	5 mm
TE/TR	2.19 ms/3.31 ms
FOV	480 mm × 87.5%
Table speed	36 mm/s

3.2.30 FID

The FID sequence has no localization built into the sequence and localizes only by the sensitive volume of the coil.

3.2.30.1 Use

You can select an adiabatic RF pulse for the FID sequence (on the **Contrast/Common** parameter card) to support adiabatic excitation for multinuclear spectroscopy.

- Useful for multinuclear spectroscopy with surface coils
- AHP (adiabatic half passage) or BIR-4 (B1-insensitive rotation) pulses can be used for excitation
- AHP: to generate uniform 90° excitation
- BIR-4: variable flip angle excitation from adiabatic plane-rotation pulses
- Advantage: less sensitive to B1 variations

3.2.30.2 Parameters

TE variable	No ⁵⁰⁾
Bandwidth variable	Yes
Phase cycling	Yes
Triggering	ECG/Respiratory
Multiple measurements	Yes
Multinuclear support	Yes

3.2.31 FLASH_PC

FLASH sequence.

Possible online reconstructions:

- Magnitude image
- Phase image
- Magnitude sum image

3.2.31.1 Use 2D

- Peripheral angiography, for example, for acquiring large fluctuations in flow velocity (multivenc application).
- Also as a localizer for 3D phase-contrast measurements.

3.2.31.2 Use 3D

Neuro applications, for example, for displaying arterial vessel systems.

50) TE is automatically set to the minimum and cannot be changed

You can set the following applications on the **Angio** parameter card:

- Multivenc applications: Variable velocity encoding in one spatial direction
- Single-venc applications: Same velocity encoding in three spatial directions
- Mixed venc applications: Free selection of direction and velocity for three encodings

3.2.31.3 Parameters

Segments	1–25
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Asymmetric echo	Yes
Averaging mode	Off/Weak/Strong
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	2D/3D
Elliptical scanning ⁵¹⁾	Yes
Slice resolution ⁵²⁾	Yes
Excitation pulses	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On

51) Only if Dimension = 3D is selected

52) Only if Dimension = 3D is selected

Gradient mode	Fast/Normal/Whisper
Venc cm/s	1–999

3.2.32 FLASH_Perি_TOF

2D FLASH sequence.

3.2.32.1 Use

- Peripheral angiography.
- ECG-triggered measurement of vessels in the legs at a high heart rate or in the kidneys, arms, and carotid arteries.

3.2.32.2 Recommendations

Perform data acquisition during the systole to obtain the maximum signal and to avoid pulsation artifacts.

3.2.32.3 Parameters

Segments	1–23
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Off/Allowed
Averaging mode	Short term/Long term

Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	2D
Excitation pulses	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper

3.2.33 FLASH_TOF

FLASH sequence.

3.2.33.1 Use

- Inflow angiography with 2D or 3D acquisition.
- 3D display of intracranial vessels in sequential slice acquisition.
- Display of the coronary arteries using 3D technique in sequential slice acquisition.
- Application for 2D time-of-flight examinations.

3.2.33.2 Recommendations

For three-dimensional applications, select the TONE pulse (depending on flow velocity) to counteract the saturation effect of blood flowing through the slab.

3.2.33.3 Parameters

TE variable	Yes
Contrasts	1
Bandwidth variable	Yes

Reconstruction mode	Magnitude
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Allowed
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	2D/3D
Elliptical scanning ⁵³⁾	Yes
Slice resolution ⁵⁴⁾	Yes
Slice partial Fourier ⁵⁵⁾	Yes
Excitation pulses	Slab-selective
RF pulse type	Normal ⁵⁶⁾
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
iPAT	Yes

3.2.34 FLASH3D_CE

Gradient-echo sequence.

53) Only if Dimension = 3D is selected

54) Only if Dimension = 3D is selected

55) Only if Dimension = 3D is selected

56) If Dimension = 3D is selected, TONE pulses are used, which can be optimized for different flow velocities via the TONE ramp parameter

3.2.34.1 Use

- Optimized for CE angiography
- Angiography of the carotid, thoracic, and pulmonary arteries
- Basis for Care Bolus and Test Bolus protocols for determining arrival of contrast agent
- Multistep angiography for display of peripheral vessels

3.2.34.2 Recommendations

- To suppress background signal, select fat suppression (fat saturation or water excitation).
- An IR pulse can be used instead of the fat suppression pulse. In this case, set the inversion time to suppress fat.

3.2.34.3 Parameters

Segments	1–127
TE variable	Yes ⁵⁷⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization Preparation	IR ⁵⁸⁾
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
Phase partial Fourier	Yes
Asymmetric echo	Allowed
Averaging mode	Short term

57) Sequence allows a freely-selectable TE, an automatic minimal TE, or an automatic minimal TE and TR

58) If segments >1 (segmented TurboFLASH)

Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D/3D
Elliptical scanning ⁵⁹⁾	Yes ⁶⁰⁾
Slice resolution ⁶¹⁾	Yes
Slice partial Fourier ⁶²⁾	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On
Phase encoding rewinder	Yes
Gradient mode	Fast/Normal/Whisper
3D reordering	Standard/User-defined TTC
Time to center ⁶³⁾	Yes
iPAT	Yes
iPAT ²	Yes

3.2.35 FLASH3D_RD

Magnitude contrast gradient-echo sequence.

3.2.35.1 Use

For displaying the arteries of the leg with a 3D measurement.

59) Only if Dimension = 3D is selected

60) Not available if iPAT is activated

61) Only if Dimension = 3D is selected

62) Only if Dimension = 3D is selected

63) Freely selectable if 3D reordering is set to "User-defined TTC"

3.2.35.2 Parameters

TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	3D
Elliptical scanning	Yes
Slice resolution	Yes
Slice partial Fourier	Yes
Excitation pulses	Slab-selective
RF pulse type	Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper

3.2.36 FLASH3D_VIBE

3D FLASH sequence.

3.2.36.1 Use

For contrast-enhanced examinations, in particular of the abdomen and pelvis.
Support of radiotherapy planning with respiratory self-gating.

3.2.36.2 Recommendations

To suppress the fat signal, select Dixon, fat saturation, or water excitation.

3.2.36.3 Parameters

TE variable	Yes ⁶⁴⁾
Contrasts	1–12
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Dixon	Yes
LiverLab ⁶⁵⁾	Yes
Saturation regions	Regular/Parallel
Phase partial Fourier	Yes
Asymmetric echo	Off/Weak/Strong
Averaging mode	Short term/Long term
Flow compensation	None
Dimension	3D
Elliptical scanning ⁶⁶⁾	Yes
Slice resolution ⁶⁷⁾	Yes

64) Sequence allows a freely-selectable TE, an automatic minimal TE, or an automatic TE set to the “in-phase” or “opposed phase” time

65) Depends on the Dixon and Dixon evaluation options

66) Only if Dimension = 3D is selected

Slice partial Fourier ⁶⁸⁾	Yes
Excitation pulses	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
3D reordering	Standard/User-defined TTC
iPAT	Yes
iPAT ²	Yes
CAIPIRINHA ⁶⁹⁾	Yes
Respiratory control	Breath-hold
Readout mode	Monopolar/Bipolar
Liver registration	Yes
MapIt	Yes
Motion scan	Yes ⁷⁰⁾
Number of bins	2–10 ⁷¹⁾

3.2.37 GRE

Gradient-echo sequence.

3.2.37.1 Use

- Abdominal in-phase/opposed phase imaging in one measurement
- 3D FLASH sequence for T1-weighted ortho imaging and neuro imaging

67) Only if Dimension = 3D is selected

68) Only if Dimension = 3D is selected

69) CAIPIRINHA is a generalization of iPAT² allowing undersampling on a sheared grid (→ Page 426 *Acceleration mode (parameter)*)

70) Only if Trajectory = Radial is selected

71) only if Motion scan is selected

- Fast 3D sequence for contrast enhancement studies (for example, dynamic breast diagnostics)
- Susceptibility-weighted imaging (SWI)
- Evaluation of metastases and lymph nodes in the thorax, abdomen, and pelvis (whole-body imaging)

3.2.37.2 Recommendations

- Quick parallel saturation: Enables saturation of inflowing blood without significantly increasing measurement time
- Quick fat saturation: Enables fat saturation without significantly increasing measurement time
- Water excitation: Enables fat suppression with still acceptable TR increase.
Disadvantage: TE is prolonged

3.2.37.3 Parameters

Segments	1–127
TE variable	Yes
Contrasts	1–12
Bandwidth variable	Yes
Magnetization Preparation	IR, SR ⁷²⁾
Reconstruction mode	Magnitude/Phase
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term/Long term

72) If segments >1 (segmented TurboFLASH)

Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes/None/Readout/Slice/Slice&Read-out
Dimension	2D/3D
Elliptical scanning ⁷³⁾	Yes
Slice resolution ⁷⁴⁾	Yes
Slice partial Fourier ⁷⁵⁾	Yes
Excitation pulses ⁷⁶⁾	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes ⁷⁷⁾
Grid/Line tagging	Yes
iPAT	Yes
iPAT ²	Yes
Respiratory control	Breath-hold ⁷⁸⁾
Readout mode	Monopolar/Bipolar
Acoustic noise reduction	Yes
SWI	Yes
Maplt	Yes
BM Motion correction	Yes

73) Only if Dimension = 3D is selected

74) Only if Dimension = 3D is selected

75) Only if Dimension = 3D is selected

76) Only if Dimension = 3D is selected

77) If segments >1 (segmented TurboFLASH)

78) Multi-breath-hold possible, depending on protocol setup

3.2.38 GRE_Field_Mapping

2D gradient-echo sequence that generates images at two different echo times. The first TE is variable, the second TE is fixed relative to the first TE. The different echo times correspond to the in-phase conditions of fat and water protons.

3.2.38.1 Use

When phase images are selected, you obtain a single-phase differential image that can be used as a “field map” during BOLD postprocessing. The information is required when overlaying anatomical images generated with other techniques, for example, SE or MPRAGE.

Prerequisites for using BOLD postprocessing:

- The phase range of -PI to +PI corresponds to image pixel values of -4095 to +4095
- Image geometry and slice orientation have to be identical to the EPI images
- The sequence has to be applied prior to the corresponding EPI measurement

3.2.38.2 Parameters

TE variable	Yes
Contrasts	2
Bandwidth variable	Yes
Reconstruction mode	Magnitude/Phase
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term/Long term

Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes
Dimension	2D
RF pulse type	Fast/Normal
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper

3.2.39 GRE_MRE

Gradient-echo-based sequence for MR Elastography (MRE). This sequence acquires information about the periodic movement of the tissue caused by an external source (elastography hardware) via motion-encoding gradients (MEG).

3.2.39.1 Use

The MRE technique generates images of the relative stiffness by imaging the propagation of the pressure waves in the human tissue.

3.2.39.2 Recommendations

- Rapid MRE reduces the acquisition time and thus the necessary breath-hold duration for the patient. This increases patient comfort, and image artifacts due to breathing movements of the patient can be mitigated. Rapid MRE is activated by reducing the TR time.
- Fractional MRE should only be used for patients with a very short T2* relaxation time whose resulting signal is too low. If you use Fractional MRE, the MEG duration is reduced to a fraction of the full wave period. It is automatically activated by reducing the TE time to a minimum value (in the range below the gray area).

3.2.39.3 Parameters

TR variable	50 ms (standard mode) 25 ms (rapid mode)
TE variable	Yes
Dimension	2D
Bandwidth variable	Yes
Respiratory control	Breath-hold
Special saturation	Parallel H/Parallel H/F (standard mode) Off (rapid mode)
iPAT	Yes
Orientation	Transversal
Phase partial Fourier	Yes
Base resolution	128
Normalize	Prescan
Flow compensation	On
Gradient mode	Fast/Normal

3.2.40 GRE_PHS

Gradient-echo sequence with RF and gradient-free periods for specific applications.



No protocols are provided in the Siemens protocol tree for this sequence. The sequence is to be found in the **Default Sequences** list on the **Default** tab of the **Dot Cockpit Program Editor**.

3.2.40.1 Use

You can use the GRE_PHS sequence to synchronize external hardware with the scanner behavior.

3.2.40.2 Parameters

TE variable	No
Contrasts	1–20
Bandwidth variable	Yes
Magnetization preparation	None
Reconstruction mode	Magnitude, Magn./Phase
Fat-Water Contrast	Standard/Fat saturation
Saturation regions	Parallel
Phase partial Fourier	Yes
Asymmetric echo	Off/Weak/Strong
Averaging mode	Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	On, Slice/Read
Dimension	2D/3D
Elliptical scanning ⁷⁹⁾	Yes
Slice resolution ⁸⁰⁾	Yes
Slice partial Fourier ⁸¹⁾	Yes
Excitation pulses ⁸²⁾	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR

79) Only if Dimension = 3D is selected

80) Only if Dimension = 3D is selected

81) Only if Dimension = 3D is selected

82) Only if Dimension = 3D is selected

RF spoiling	On/Off
Phase-encoding rewinder	On/Off
Gradient mode	Fast/Normal/Whisper

3.2.41 GRE_Proj

Gradient-echo-based projection imaging sequence.

You can use projection data to calculate the position of one or more coils within the scanner. The Siemens software does not calculate the position. You need to calculate the position separately.



No protocols are provided in the Siemens protocol tree for this sequence. The sequence is to be found in the **Default Sequences** list on the **Default** tab of the **Dot Cockpit Program Editor**.

3.2.41.1 Use

The GRE_Proj sequence is used to acquire MR signals from any set of tracking coils. Up to four readout projections and at least six tracking coils are supported.

Using the Access-i remote control, the raw magnitude projection data can be made available for 3rd party clients (see: Operator Manual MR System Administration).

3.2.41.2 Parameters

TE variable	No
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	None
Reconstruction mode	Magnitude

Measurements	1–250
Dimension	1D
Gradient mode	Normal/Whisper
Tracking	Yes
Background suppression	Yes
Tracking flip angle	Yes

3.2.42 GRE_Wave

Gradient-echo sequence with Wave-CAIPI acceleration.

3.2.42.1 Use

For routine brain imaging with SWI contrast. For a detailed description, see: Operator Manual Diagnostic MR Imaging.

3.2.42.2 Recommendations

- To avoid aliasing artifacts, acquire images in transverse orientation.
- Acquisitions with higher acceleration factors are more susceptible to image quality degradation due to subject motion. Therefore, acceleration should not exceed 2×3 for 32-channel or 64-channel coils or 2×2 for 20-channel coils.
- An external reference scan is mandatory and automatically set.
- Interpolation is not provided.
- The acoustic noise produced by Wave-CAIPI is higher than with conventional imaging with the GRE sequence. In addition, acoustic noise reduction is not offered for Wave-CAIPI.

3.2.42.3 Parameters

TE variable	Yes
Contrasts	1–2
Bandwidth variable	Yes
Reconstruction mode	Magnitude, Magn./Phase
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel/Tracking
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes
Dimension	3D
Slice resolution ⁸³⁾	Yes
Excitation pulses ⁸⁴⁾	Slab-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
iPAT	Yes
iPAT ²	Yes
Readout mode	Monopolar
SWI	Yes
MapIt	Yes
Acceleration mode	Wave-CAPI (fixed)

83) Only if Dimension = 3D is selected

84) Only if Dimension = 3D is selected

3.2.43 HASTE

Single-shot TSE sequence.

3.2.43.1 Use

- T2 weighting for neuro applications, used, for example, with uncooperative patients
- T2 weighting for breath-hold studies in the abdomen without motion artifacts
- Cholangiography imaging when using very long echo times (~1 s)
- Myelography imaging when using very long echo times (~1 s)
- Dark blood imaging for examining cardiac anatomy
- Evaluation of metastases and lymph nodes in the thorax, abdomen, and pelvis (wholebody imaging)

3.2.43.2 Parameters

Turbo factor	1–512 ⁸⁵⁾
TE variable	Yes
Contrasts	1–4
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ⁸⁶⁾
Fat suppression	Fat saturation/Water saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ⁸⁷⁾

85) Parameter cannot be freely set, depends on base and phase resolution

86) May be selected only if Magn. Preparation = IR has been selected

Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	None/Readout/Slice
Dimension	2D/3D
Slice resolution ⁸⁸⁾	Yes
Slice partial Fourier ⁸⁹⁾	Yes
RF pulse type	Fast/Normal/Optimized ⁹⁰⁾
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Respiratory control	Trigger/Breath-hold ⁹¹⁾

3.2.44 HASTE_Diff

Single-shot TSE sequence with diffusion preparation.

3.2.44.1 Use

You can set diffusion-specific parameters on the **Diff** parameter card:

- Direction of the diffusion-sensitive axis (diffusion mode)
- Magnitude of the b-value



Only one diffusion direction and one b-value are supported.

87) Parameter cannot be freely set, depends on selected TE

88) Only if Dimension = 3D is selected

89) Only if Dimension = 3D is selected

90) If Dimension = 3D, only RF pulse type Normal is supported

91) Multi-breath-hold possible, depending on protocol setup

3.2.44.2 Recommendations

If SAR is exceeded, either the flip angle of the refocusing pulse can be reduced and/or RF pulse type **Optimized** can be selected. A smaller flip angle (for example, approx. 150°) does not have a noticeable effect on image contrast.

3.2.44.3 Parameters

Turbo factor	1–512 ⁹²⁾
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	None
Dimension	2D
RF pulse type	Fast/Normal/Optimized
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
b-value [s/mm ²]	0–1000 ⁹³⁾ 0–800 ⁹⁴⁾

92) Parameter cannot be freely set, depends on base and phase resolution

Increment [s/mm ²]	10
Online reconstruction	DW image only

3.2.45 HASTE_Interactive

The HASTE_Interactive sequence is used for interactive real-time imaging. The sequence is based on the HASTE sequence and inherits most of the parameter settings from it.

The HASTE_Interactive sequence has the capability to acquire multiple slices that can be measured in a predefined order and will be displayed in the **Inline Display**.

During the measurement, all slice parameters can be changed via graphic slice positioning and the parameter cards. (Prerequisite: Sequence is started via the **Copy&Go** button in the toolbar of the program control.)

The slice positions can be saved during imaging and subsequently transferred to a protocol in the wait queue.

3.2.45.1 Use

Interactive T2-weighted imaging

3.2.45.2 Parameters

Turbo factor	1–512 ⁹⁵⁾
TE variable	Yes
Contrasts	1–4
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude

93) If Diffusion mode = 3D-Diagonal is selected

94) If Diffusion mode = Read, Slice, or Phase is selected

95) Parameter cannot be freely set, depends on base and phase resolution

Fat suppression	Fat saturation/Water saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ⁹⁶⁾
Multi-slice mode	Single-shot
Flow compensation	None
Dimension	2D
RF pulse type	Fast/Normal/Optimized
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Respiratory control	Trigger/Breath-hold ⁹⁷⁾

3.2.46 MEDIC

MEDIC sequence (Multi-echo Data Image Combination), gradient-echo sequence with flow compensation. When combined echoes = 1, the sequence behaves like a FLASH sequence with flow compensation.

3.2.46.1 Use

- T2*-weighted imaging with a high signal-to-noise ratio for the spine (especially transverse cervical and thoracic spine) and ortho (knee and shoulder) imaging
- T2*-weighted 3D imaging of the cervical spine with a small flip angle and adjusted TR

96) Parameter cannot be freely set, depends on selected TE

97) Multi-breath-hold possible, depending on protocol setup

3.2.46.2 Parameters

Combined echoes	1–12
TE variable	Yes
Contrasts	1
IR Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes
Dimension	2D/3D
Elliptical scanning ⁹⁸⁾	Yes
Slice resolution ⁹⁹⁾	Yes
Slice partial Fourier ¹⁰⁰⁾	Yes
Excitation pulses ¹⁰¹⁾	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On/Off

98) Only if Dimension = 3D is selected

99) Only if Dimension = 3D is selected

100) Only if Dimension = 3D is selected

101) Only if Dimension = 3D is selected

Gradient mode	Fast/Normal/Whisper
iPAT	Yes

3.2.47 PETRA

The PETRA sequence provides a way of acquiring ultra-short TE images with substantially less noise from gradient switching than in conventional imaging. PETRA is a further development of the gradient-echo sequence (GRE).

3.2.47.1 Use

T1-weighted 3D isotropic images of the head. PETRA can be used as an alternative to MPRAGE with the benefit of significant lower noise and hence increased patient comfort.

3.2.47.2 Recommendations

- Perform measurements as close to the isocenter as possible.
- The sequence is non-selective. Please use a FOV large enough to cover the entire acquisition area.

3.2.47.3 Parameters under *syngo*

Parameter	Parameter card	Comment
Segments	Sequence/Part 1	If a fat saturation/water saturation pulse is selected, the number of repetitions acquired with each fat saturation/water saturation can be set with the parameter Segments
TI	Contrast/Common	If an inversion pulse is selected, TI determines the duration between the inversion pulse and the beginning of the acquired repetitions

Parameter	Parameter card	Comment
Turbo factor	Sequence/Part 1	If an inversion pulse is selected, Turbo Factor determines the number of repetitions between two inversion pulses
TR	Contrast/Common	If an inversion pulse is selected, the repetition time of the single repetitions is set to its minimum value. The repetition time corresponds to the time between two inversion pulses
Radial views	Resolution/Common	The number of radial views can be changed on the resolution card

3.2.47.4 Parameters

Segments	2–100
TE variable	Yes
Bandwidth variable	Yes
Magnetization preparation	IR
Fat suppression	Fat saturation/Water saturation
Saturation regions	Regular/Parallel
Phase partial Fourier	Yes
Dimension	3D
Acoustic noise reduction	Yes

3.2.48 PSIF

Steady-state gradient-echo sequence.

With steady-state sequences, echo time TE and repetition time TR are set to fixed minimum values to ensure the best possible image quality. In the case of the PSIF sequence, this applies to TE only. TR is a freely-adjustable parameter.

PSIF offers flow compensation in the slice or readout direction but is highly sensitive to motion artifacts. At a large flip angle, heavily T2-weighted images are generated.

3.2.48.1 Use

- T2-weighted imaging with 3D PSIF with flow compensation in the readout direction, for CSF or spine diagnostics.
- T2-weighted imaging with 2D or 3D PSIF with flow compensation in the slice selection direction, for breath-hold studies of the abdomen (dark blood T2 weighting in the liver).

3.2.48.2 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Water excitation
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Readout/Slice
Dimension	2D/3D
Elliptical scanning ¹⁰²⁾	Yes
Slice resolution ¹⁰³⁾	Yes

102) Only if Dimension = 3D is selected

103) Only if Dimension = 3D is selected

Slice partial Fourier ¹⁰⁴⁾	Yes
Excitation pulses ¹⁰⁵⁾	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes
Diffusion weighting	Yes

3.2.49 Quiet_DWI

Quiet multi-shot, diffusion-weighted, readout-segmented EPI sequence.

3.2.49.1 Use

For quiet diffusion-weighted imaging of the brain.

3.2.49.2 Recommendations

To increase the effect of noise reduction, raise the echo spacing value on the **Sequence/Part 1** parameter card.

3.2.49.3 Parameters

EPI factor ¹⁰⁶⁾	1–256
TE variable	No ¹⁰⁷⁾
Contrasts	2
Bandwidth variable	No ¹⁰⁸⁾

104) Only if Dimension = 3D is selected

105) Only if Dimension = 3D is selected

106) Parameter cannot be freely set, depends on base and phase resolution

107) Parameter cannot be freely set, depends on other parameters

108) Parameter cannot be freely set, depends on other parameters

Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
b-value	0–10000
Online reconstruction	<ul style="list-style-type: none"> • DW and ADC image • FA image • TRACE • colored FA image
iPAT	Yes
Simultaneous multislice (SMS)	Yes
Readout segments	Yes
Reacquisition mode	On/Off
Echo spacing variable	Yes
Optimization	Min. TE/TR

3.2.50 RESOLVE

Multi-shot, diffusion-weighted, readout-segmented EPI sequence.

During diffusion preparation, multi-shot DWI is sensitive to brain motion caused by CSF pulsation. This leads to non-linear phase errors that vary from shot to shot. The effect of these phase errors can be minimized by using a readout-segmented EPI readout in conjunction with 2D navigator phase correction and navigator-based reacquisition.

3.2.50.1 Use

For better image quality in neuro imaging than with standard single-shot EPI sequence.

3.2.50.2 Recommendations

- For a given spatial resolution: Reduce the minimum echo spacing (and the associated artifacts) by increasing the number of "Readout segments".
- For a fixed echo spacing: Increase the available spatial resolution by increasing the number of "Readout segments".

3.2.50.3 Parameters

EPI factor ¹⁰⁹⁾	1–256
TE variable	No ¹¹⁰⁾
Contrasts	2
Bandwidth variable	No ¹¹¹⁾
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR

109) Parameter cannot be freely set, depends on base and phase resolution

110) Parameter cannot be freely set, depends on other parameters

111) Parameter cannot be freely set, depends on other parameters

Saturation regions	Regular/Parallel
MTC	Yes
Readout partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
b-value	0–10000
Online reconstruction	<ul style="list-style-type: none"> • DW and ADC image • FA image • TRACE • colored FA image
iPAT	Yes
Simultaneous multislice (SMS)	Yes
Readout segments	Yes
Reacquisition mode	On/Off
Echo spacing variable	Yes
Optimization	Min. TE/TR

3.2.51 SE

Spin-echo sequence without flow compensation. The temporal sequence depends on the parameters selected.

3.2.51.1 Use

- As a single-contrast sequence especially well suited for T1-weighted imaging regardless of the body region selected.
- Dark blood imaging for examining cardiac anatomy by adding dark blood preparation.

3.2.51.2 Parameters

TE variable	Yes
Contrasts	1–2
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ¹¹²⁾
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Off/Allowed
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes

112) May be selected only if Magn. Preparation = IR has been selected

Blood suppression	On/Off
Acoustic noise reduction	Yes

3.2.52 SE_15b130

Classic spin-echo sequence without flow compensation. The temporal sequence is fixed, that is, independent of the parameters selected.

3.2.52.1 Use

For T1-weighted imaging.

3.2.52.2 Parameters

TE variable	Yes
Contrasts	1
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ¹¹³⁾
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D

113) May be selected only if Magn. preparation = IR has been selected

RF pulse type	Normal
Gradient mode	Normal

3.2.53 SE_17rb130

Flow-compensated spin-echo sequence. The temporal sequence is fixed, that is, independent of the parameters selected.

3.2.53.1 Use

For postgadolinium applications in the head.

3.2.53.2 Parameters

TE variable	No
Contrasts	1
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ¹¹⁴⁾
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes
Dimension	2D

114) May be selected only if Magn. preparation = IR has been selected

RF pulse type	Normal
Gradient mode	Normal

3.2.54 SE_MC

Multic_contrast sequence with up to 32 contrasts. The sequence design is derived from the TSE technique. Since stimulated echoes contribute to the signal with TSE, the second echo makes a larger signal contribution than the first echo. The temporal sequence depends on the parameters selected.

3.2.54.1 Use

For acquiring T2 relaxation curves.

3.2.54.2 Recommendations

Do **not** use the first echo in the calculation for T2 image reconstruction.

3.2.54.3 Parameters

TE variable	Yes
Contrasts	1–32
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ¹¹⁵⁾
Fat suppression	Fat saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term

115) May be selected only if Magn. Preparation = IR has been selected

Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
Maplt	Yes

3.2.55 SEMAC

The slice encoding for metal artifact correction sequence is a TSE variant for imaging patients with full joint replacements (metal implant) and corrects in-plane and through-plane distortions. SEMAC offers alternate acceleration techniques such as GRAPPA and Compressed Sensing (CS).

3.2.55.1 Use

Metal implant imaging of joints with PD, T1, T2, and STIR contrast.



Please adhere to all safety instructions regarding implants. For a detailed description, see: Operator Manual MR System and Coils.

3.2.55.2 Parameters

Turbo factor	10–599
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR

Saturation regions	Regular/Parallel
Elliptical scanning	Yes ¹¹⁶⁾
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
iPAT	Yes
Compressed Sensing	Yes
SEMAC	15–32
SAR Optimization	Yes
Fat suppression	Fat saturation/SPAIR

3.2.56 SPACE

The SPACE sequence is a variant of the 3D Turbo spin-echo sequence optimized for 3D data acquisition, T1/T2/PD weighting and dark fluid contrast. Significant SAR reduction with the variable flip angle technique. This allows for very high turbo factors (>100) and high sampling efficiencies. As a result, you obtain high-resolution isotropic images that allow free reformatting in all planes.

3.2.56.1 Use

- PD weighting with/without fat saturation and T1 weighting for orthopedic applications
- Basis for non-CE MR angiography protocols with NATIVE SPACE (prerequisite: NATIVE license is available)
- T1, T2, Flair, and double inversion recovery contrast for brain imaging
- T2 weighting for spine imaging
- T2 weighting and MRCP for body imaging

¹¹⁶⁾ only with Compressed Sensing (CS)

3.2.56.2 Parameters

Turbo factor	10–599
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, DIR, T2 prep. IR, Non-sel. T2 prep. IR
Reconstruction mode	Magnitude/Real ¹¹⁷⁾
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ¹¹⁸⁾
Flow compensation	None/Readout
Dimension	3D
Elliptical scanning	Yes
Slice resolution	Yes
Slice partial Fourier	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
iPAT ²	Yes

117) May be selected only if Magn. Preparation = IR has been selected

118) Parameter cannot be freely set, depends on selected TE

Compressed Sensing	Yes
CAIPIRINHA ¹¹⁹⁾	Yes
Respiratory control	Trigger/Breath-hold
Restore	Yes
NATIVE ¹²⁰⁾	Off/TD scout/3D mode
Flow sensitivity ¹²¹⁾	Default/Weak/Medium/Strong
Blood suppression	Body region/Free

3.2.57 SPACE_NAV

Combination of the SPACE sequence and prospective measurement of a navigator echo.

3.2.57.1 Use

- Assessment of the arterial vessel wall
- In regions affected by respiratory motion, such as the thoracic aorta

3.2.57.2 Parameters

Turbo factor	10–599
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, DIR
Reconstruction mode	Magnitude/Real ¹²²⁾

119) CAIPIRINHA is a generalization of iPAT² allowing undersampling on a sheared grid (→ Page 426 Acceleration mode (parameter))

120) With NATIVE license; “NATIVE” available only for ECG or pulse trigger, “Flow sensitivity” available only if NATIVE is not off

121) With NATIVE license; “NATIVE” available only for ECG or pulse trigger, “Flow sensitivity” available only if NATIVE is not off

122) May be selected only if Magn. Preparation = IR has been selected

Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ¹²³⁾
Flow compensation	None/Readout
Dimension	3D
Elliptical scanning	Yes
Slice resolution	Yes
Slice partial Fourier	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
iPAT ²	Yes
Respiratory control	Gate & Follow/Gate/Monitor only/Off
Restore	Yes

3.2.58 SVS_SE

Spin-echo sequence for single-voxel spectroscopy.

123) Parameter cannot be freely set, depends on selected TE

3.2.58.1 Use

- Localization with three orthogonal slices
- $90^\circ-180^\circ-180^\circ$
- Measured signal: Full spin echo

3.2.58.2 Parameters

TE variable	Yes
Bandwidth variable	Yes
Spectral fat suppression	Yes
Saturation regions	Regular
Phase cycling	Yes
Triggering	ECG/Respiratory
Excitation of VOI	Yes
Multiple measurements	Yes
Water reference scan	Yes

3.2.59 SVS_STEAM

STEAM single-voxel spectroscopy sequence.

3.2.59.1 Use

- Localization with three orthogonal slices
- $90^\circ-90^\circ-90^\circ$
- Measured signal: Stimulated echo
- Short TEs possible
- Only half of the spin-echo signal

3.2.59.2 Parameters

TE variable	Yes
Mixing time (TM) variable	Yes
Bandwidth variable	Yes
Phase cycling	Yes
Excitation of VOI	Yes
Multiple measurements	Yes
Water reference scan	Yes

3.2.60 SVS_STEAM_Histo

Five-echo STEAM single-voxel spectroscopy sequence based on the SVS_STEAM sequence.

Advantages

- All data acquired in one breath-hold
- Accurate fat evaluation due to integrated T2 correction
- Estimation of water R2 relaxivity, which correlates with the amount of iron in the liver

3.2.60.1 Use

T2-corrected fat and iron quantification in the liver. For a detailed description, see: Operator Manual Diagnostic MR Imaging.

3.2.60.2 Parameters

TE variable	Yes
Mixing time (TM) variable	Yes
Phase cycling	Yes

Triggering	No
Excitation of VOI	Yes
Multiple measurements	5 (fixed)

3.2.61 TGSE

Ultrafast turbo gradient spin-echo sequence for high resolution imaging or extremely short measurement times.

At an EPI factor of 1 and a turbo factor >1, the sequence behaves like a TSE sequence. At a turbo factor of 1 and an EPI factor >1, the sequence behaves like a segmented EPI sequence.



Increasing the EPI factor increases the sequence's sensitivity to susceptibility, therefore distortion artifacts may increase.

3.2.61.1 Use

- T2 weighting for high-resolution neuro or ortho imaging in an acceptable measurement time (recommended EPI factor at a high turbo factor ≤ 3).
- Inversion recovery neuro imaging with magnitude or real value image display.

3.2.61.2 Recommendations

If SAR is exceeded, either the flip angle of the refocusing pulse can be reduced and/or RF pulse type **Low SAR** can be selected. A smaller flip angle (for example, approx. 150°) does not have a noticeable effect on image contrast.

3.2.61.3 Parameters

Turbo factor	1–65
EPI factor	1–21

TE variable	Yes ¹²⁴⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ¹²⁵⁾
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel
MTC	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
Respiratory control	Breath-hold ¹²⁶⁾

3.2.62 TGSE_ASL

Segmented turbo gradient spin-echo sequence for high resolution imaging or extremely short measurement times.

At an EPI factor of 1 and a turbo factor >1, the sequence behaves like a TSE sequence. At a turbo factor of 1 and an EPI factor >1, the sequence behaves like a segmented EPI sequence.

124) Only if turbo factor = 1

125) May be selected only if Magn. Preparation = IR has been selected

126) Multi-breath-hold possible, depending on protocol setup



Increasing the EPI factor increases the sequence's susceptibility, therefore distortion artifacts may increase.

3.2.62.1 Use

For perfusion imaging in the head. Perfusion-weighted images and relCBF images are obtained. With multi-TI measurements, also images of the bolus arrival time (BAT) can be obtained.

3.2.62.2 Recommendations

To minimize image distortions due to susceptibility, select a bandwidth that enables use of minimum echo spacing.

3.2.62.3 Parameters

Turbo factor	1–65
EPI factor	1–127
TE variable	No ¹²⁷⁾
Bandwidth variable	Yes
Magnetization preparation	ASL
Reconstruction mode	Magnitude
Fat suppression	Fat saturation
Saturation regions	FAIR Q2T, PCASL, None ¹²⁸⁾
Averaging mode	Long term
Flow compensation	None
Dimension	3D

127) TE is automatically set to the minimum value and cannot be changed

128) Parameter "Perfusion mode"

RF pulse type	Normal
Gradient mode	Fast/Normal
Online reconstruction	Perfusion-weighted images, relCBF images, BAT images ¹²⁹⁾
Bolus duration ¹³⁰⁾	Variable
Inversion array size ¹³¹⁾	Min. 1

3.2.63 TrueFISP

TrueFISP steady-state gradient-echo sequence.

3.2.63.1 Use

- T2 weighting for neuro applications, used, for example, with uncooperative patients.
- T2 weighting for breath-hold studies in the abdomen without motion artifacts.

3.2.63.2 Recommendations

Minimize TR by selecting a high readout bandwidth to avoid interference streaks in the image.

3.2.63.3 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, SR

129) Only available for multi-TI measurements

130) Parameter depends on TI and inversion array size

131) Maximum depends on TR and TI

Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	None ¹³²⁾
Dimension	2D/3D
Elliptical scanning ¹³³⁾	Yes
Slice resolution ¹³⁴⁾	Yes
Slice partial Fourier ¹³⁵⁾	Yes
Excitation pulses ¹³⁶⁾	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes
iPAT ² ¹³⁷⁾	Yes
Respiratory control	Breath-hold ¹³⁸⁾

132) TrueFISP is essentially flow-compensated from one RF pulse to the next

133) Only if Dimension = 3D is selected

134) Only if Dimension = 3D is selected

135) Only if Dimension = 3D is selected

136) Only if Dimension = 3D is selected

137) Only if Dimension = 3D is selected

138) Multi-breath-hold possible, depending on protocol setup

3.2.64 TrueFISP_FreqScout

TrueFISP sequence. Several images with an identical geometry but different offset frequency are acquired. The distance between the frequency shifts and the number of images are controlled via the parameters **Trufi delta freq.** and **Measurements**. The offset frequencies are included in the image text. A visual analysis in the image area of **MR View&GO** determines the optimal frequency. It is entered in subsequent measurements for the **Trufi delta freq.** parameter.

3.2.64.1 Use

With TrueFISP protocols in particular, it may be necessary to adjust the offset frequency based on the image to move the typical TrueFISP stripe artifacts out of the region of interest.

3.2.64.2 Parameters

Segments	Variable
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential/Single measurement
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
iPAT	Yes

3.2.65 TSE

Turbo spin-echo sequence offering a large range of applications.

3.2.65.1 Use

- T1, T2 weighting and Flair contrast for brain and spine imaging
- T1, PD, T2, and STIR imaging for orthopedic applications
- T2 and STIR weighting for body imaging with breath-hold or 2D PACE

3.2.65.2 Parameters

Turbo factor	1–129 ¹³⁹⁾
TE variable	Yes
Contrasts	1–3
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ¹⁴⁰⁾
Fat suppression	Fat saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ¹⁴¹⁾
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None/Readout/Slice
Dimension	2D/3D
Slice resolution ¹⁴²⁾	Yes

139) At a turbo factor of 1, the sequence behaves like a spin-echo sequence

140) May be selected only if Magn. Preparation = IR has been selected

141) Parameter cannot be freely set, depends on selected TE

Slice partial Fourier ¹⁴³⁾	Yes
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Simultaneous multislice (SMS)	Yes
SliceAdjust	Yes
Respiratory control	Trigger/Breath-hold ¹⁴⁴⁾
BLADE Trajectory	Yes
Restore	Yes
Acoustic noise reduction	Yes
WARP	Yes
VAT ¹⁴⁵⁾	0–100%
SEMAC ¹⁴⁶⁾	6–32
BM Motion correction	Yes

3.2.66 TSE_Dixon

TSE Dixon is a water-fat separation technique based on the 2D TSE sequence. The Dixon technique can be used as an alternative to fat saturation.

Unlike conventional SE or TSE sequences, the TSE_Dixon sequence acquires an opposed phase gradient echo in addition to the original in-phase spin-echo. The echoes are obtained at the instant when the phase shift between water and lipid is “-π” and “0” respectively. After a linear combination of the images with phase correction, water and fat selective images can be computed.

142) Only if Dimension = 3D is selected

143) Only if Dimension = 3D is selected

144) Multi-breath-hold possible, depending on protocol setup

145) Only if WARP is selected

146) Only if WARP is selected

Advantages:

- Up to four contrasts are possible within one measurement (in-phase, opposed phase, water, and fat images)
- Less sensitive to B0 and B1 inhomogeneities
- Improved outcome with MR Conditional implants



Please adhere to all safety instructions regarding implants. For a detailed description, see: Operator Manual MR System and Coils.

On the **Contrast/Common** parameter card, from the **Fat-Water Contrast** list: **Dixon** determines whether fat and water images are displayed separately. These additional parameters can be accessed with the [...] button to the right of the **Fat-Water Contrast** parameter.

Original Echoes	The original in-phase and opposed phase images are 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

3.2.66.1 Use

- T1, T2, and PD weighting
- Compatible with multi-coil acquisition and iPAT (GRAPPA)

3.2.66.2 Image examples

(1)



(2)



(4)



(3)



- (1) reliable fat saturation
- (2) with MR Conditional implants
- (3) fat image
- (4) water image

3.2.66.3 Parameters

Turbo factor	1–129
TE variable	Yes

Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude
Saturation regions	Regular/Parallel
MTC	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None/Readout/Slice
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Simultaneous multislice (SMS)	Yes
Respiratory control	Trigger
Restore	Yes

3.2.67 TSE_MDME

Turbo spin-echo sequence variant that allows you to acquire multicontrast data with multiple delay times (**MD**) after a preparation pulse and multi-echo times (**ME**).

3.2.67.1 Use

The sequence generates magnitude and phase images that can be used as input data for the postprocessing application SyMRI® of SyntheticMR AB to generate synthetic images and to perform myelin mapping.



In order to use this sequence, a license for SyMRI® must be obtained from SyntheticMR AB (available, for example, on syngo.via OpenApps or directly from SyntheticMR AB). This sequence must not be used in combination with any other software application.

Parameters	Turbo factor	5
TE variable	Yes	
Contrasts	2	
Repetitions	4 – 17	
Bandwidth variable	Yes	
Magnetization preparation	IR ¹⁴⁷⁾	
Reconstruction mode	Magnitude/Phase	
Saturation regions	Regular/Parallel	
Averaging mode	Short term/Long term	
Multi-slice mode	Interleaved	
Flow compensation	None/Readout/Slice	
RF pulse type	Fast/Normal/Low SAR	
Gradient mode	Fast/Normal/Whisper	
iPAT	Yes	
Restore	Yes	

3.2.68 TurboFLASH

Single-shot TurboFLASH sequence.

147) Parameter cannot be deselected

3.2.68.1 Use

- 3D TurboFLASH (= MPRAGE) for fast T1-weighted volume measurements of the head.
- 3D TurboFLASH with double inversion contrast (= MP2RAGE) for homogenous T1-weighted head imaging with high CNR and optionally T1 mapping. Activated by setting two IR contrasts.
- 2D TurboFLASH with dark blood preparation for low resolution imaging of the cardiac anatomy.
- 2D TurboFLASH combined with saturation recovery preparation for contrast enhancement studies.
- 2D TurboFLASH to determine the transit time of a test bolus as preparation for CE angiography.



The 3D TurboFLASH MP2RAGE protocols are optimized for consistent T1 mapping in the range of biological T1 values in the human tissue. Mapping of T1 values that exceed the range between 400 ms and 1800 ms becomes increasingly imprecise. T1 maps are shown with a color bar that displays the color mapping between 0 and 2000 ms according to the current window levels. Computed T1 maps, however, may contain values between 0 and 4095 ms, thus exceeding the range of the color bar.

3.2.68.2 Recommendations

To prevent saturation effects, use the **Long Term** averaging mode. All slices will then be measured sequentially for one averaging before the next averaging measures the series of slices again.

3.2.68.3 Inline quality assessment for 3D TurboFLASH measurements of the head

The Inline quality assessment provides an overall image quality rating of 3D MPRAGE brain scans optimized for brain imaging. The approach is based on a careful analysis of the air background noise distribution. The background noise appears corrupted in the presence of patient-related artifacts and renders the method primarily sensitive to subject motion. A landmark-based method is used to detect the presence of aliasing artifacts. The image quality of 3D MPRAGE volumes is rated as either "high", "to be confirmed" or "not assessed" (see section "Outputs" below). It is enabled by the **Morpho** add-in. A default protocol is available in the Siemens protocol tree (\SIEMENS\head\library\3D).

3.2.68.4 Parameters

Slice thickness	≤ 3 mm
Row and column spacing	≤ 2 mm
iPAT acceleration factor	≤ 3
In-plane matrix size	$\geq 96 \times 96$
Number of slices	≥ 64
Orientations	<p>Sagittal (phase-encoding direction):</p> <ul style="list-style-type: none"> • A>>P • P>>A <p>Coronal (phase-encoding direction):</p> <ul style="list-style-type: none"> • R>>L • L>>R

3.2.68.5 Note

In selective excitation, aliasing artifact detection is not performed. The functionality is disabled if a "Head" coil is not selected.

3.2.68.6 Outputs

The overall quality rating is displayed in the image text of the original series.

Image quality

High	For a high-quality scan
Not assessed	If quality assessment is not performed (that is, inconsistent protocol parameters, error detected during processing)
To be confirmed	If quality criteria are not fulfilled (for example, motion, aliasing artifacts, and other image degradations)

3.2.68.7 Parameters

TE variable	Min.
Contrasts	1
IR Contrasts	2^{148}
Bandwidth variable	Yes
Magnetization preparation	IR,SR
Reconstruction mode	Magnitude/Real ¹⁴⁹⁾
Fat suppression	Water excitation
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	None

148) May be selected only if Magn. Preparation = IR or SR has been selected

149) May be selected only if Magn. Preparation = IR has been selected

Dimension	2D/3D
Elliptical scanning ¹⁵⁰⁾	Yes ¹⁵¹⁾
Slice resolution ¹⁵²⁾	Yes
Slice partial Fourier ¹⁵³⁾	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
3D reordering	Standard/User-defined TTC
iPAT	Yes
Respiratory control	Trigger/Breath-hold ¹⁵⁴⁾
MapIt	Yes
BM Motion correction	Yes

3.2.69 TurboFLASH_CB

2D single-shot TurboFLASH sequence.

3.2.69.1 Use

Optimized for determining arrival of bolus as preparation for contrast-enhanced angiography.

150) Only if Dimension = 3D is selected

151) Freely selectable if 3D reordering is activated

152) Only if Dimension = 3D is selected

153) Only if Dimension = 3D is selected

154) Multi-breath-hold possible, depending on protocol setup

3.2.69.2 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Magnetization Preparation	IR, SR
Reconstruction mode	Magnitude/Real ¹⁵⁵⁾
Fat suppression	Water excitation
Phase partial Fourier	Yes
Asymmetric echo	Off/Allowed
Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	None
Dimension	2D
Excitation pulses	Slice-selective
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes

3.2.70 TWIST

3D gradient-echo sequence that allows a higher temporal resolution than a standard gradient-echo sequence.

155) May be selected only if Magn. Preparation = IR or SR has been selected

3.2.70.1 Use

For evaluating dynamic processes with high spatial and temporal resolution.

3.2.70.2 Recommendations

On the **Angio/Common** parameter card: The parameter **Central region A** specifies the size of the central k-space and the parameter **Sampling density B** indicates the sampling density in the peripheral region. To increase temporal resolution, reduce one of the two parameters.

3.2.70.3 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Phase partial Fourier	Yes
Asymmetric echo	Off/Weak/Strong
Averaging mode	Short term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	3D
Elliptical scanning ¹⁵⁶⁾	Yes
Slice resolution ¹⁵⁷⁾	Yes
Slice partial Fourier ¹⁵⁸⁾	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR

156) Only if Dimension = 3D is selected

157) Only if Dimension = 3D is selected

158) Only if Dimension = 3D is selected

RF spoiling	On
Gradient mode	Fast/Normal/Whisper
iPAT	Yes
iPAT ²	Yes
Central region A	4–100%
Sampling density B	0–50%
Temporal interpolation	Yes
Time stamp in image	Yes

3.3 Description of pulse sequences 3 T

3.3.1 AALScout

A modified FLASH3D_VIBE sequence is used for AutoAlign scout measurements in AutoAlign programs and Dot Engines. The algorithm uses bone markers (L = landmark-based) for automatic slice positioning.



The sequence parameters cannot be changed, with the exception of the selected coils and the iPAT factor.

3.3.1.1 Use

The sequence must precede any examination with AutoAlign. The slice position of subsequent measurement protocols is automatically adjusted with AutoAlign.

3.3.2 BEAT (Angio QISS)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.3.2.1 Use

For displaying the arteries of the peripheral vasculature.

3.3.2.2 Essential parameters

Magnetization preparation	Slice-sel. SR
Saturation regions	Yes
Special saturation	Tracking H/F
TI	Yes
ECG	None/Trigger
Trigger device	ECG/Pulse/Ext
Trigger delay	Yes (100 ms)
Dimension	2D

3.3.2.3 Parameters

Averages	Yes
Flip angle mode	Constant
Fat-Water Contrast	Standard/Fat saturation
Acceleration mode	None/GRAPPA/mSENSE
Reference scans	Integrated/GRE-Separate
Phase partial Fourier	Off, 7/8, 6/8, 5/8, 4/8

Set-n-Go protocol	Yes
Inline composing	Yes
Respiratory control	Off/Breath-hold
Define	Shots/Segment
Segments variable	No
TE variable	Yes
Asymmetric echo	Yes
Bandwidth variable	Yes
Sequence type	TrueFISP/GRE
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ¹⁵⁹⁾

3.3.3 BEAT (Angio TOF)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.3.3.1 Use

3D display of vessels.

3.3.3.2 Essential parameters

Dimension	3D
Sequence type	GRE
Special saturation	Tracking H/Tracking F

159) Only available for XT and XR gradients

Flow direction	F>>H/H>>F
Excitation	TONE
Tone ramp	20%–100%
Flow compensation	On, Read, Slice/Read, Read/Phase

3.3.3.3 Parameters

Fat-Water Contrast	Standard/Fat saturation/Water excitation
Acceleration mode	None/GRAPPA/mSENSE/CS
Reference scans	Integrated/GRE-Separate
Phase partial Fourier	Off, 7/8, 6/8, 5/8, 4/8
Interpolation	1–2 floating values
RF spoiling	On
Phase encoding rewinder	On/Off
Define	Segment
Segments variable	Yes
TE variable	Yes
Asymmetric echo	Yes
Bandwidth variable	Yes
RF pulse type	Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ¹⁶⁰⁾

160) Only available for XT and XR gradients

3.3.4 BEAT (Cine)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.3.4.1 Use

For imaging cardiac function.

3.3.4.2 Essential parameters

Cine	On
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3.3.4.3 Parameters

Averages	Yes
Magnetization preparation	TI Scout (TrueFISP only)
Fat-Water Contrast	Standard
Reconstruction mode	Magnitude, Magn./Phase
Acceleration mode	None/GRAPPA/mSENSE/CS (True-FISP only)
Reference scans	Integrated/GRE-Separate/T-PAT
Phase partial Fourier	Off, 7/8, 6/8, 5/8, 4/8
Trajectory	Cartesian/Radial ¹⁶¹⁾
Saturation regions	Yes (GRE only)
ECG	None/Trigger/Retro
Trigger device	ECG/Pulse/Ext
Arrhythmia detection	None/By time

161) Only if Dimension = 2D is selected

Adaptive triggering	Yes ¹⁶²⁾
TruFI delta freq.	-300 – +300
Respiratory control	Off/Breath-hold
Inline evaluation	None/Ventricular Function/Restart InlineVF ¹⁶³⁾
Tagging	None (TrueFISP) Grid/Line (GRE)
Optimization	Min. TE/TR
Define	Shots/Segment
Segments variable	Yes
TE variable	No ¹⁶⁴⁾
Asymmetric echo	Yes
Flow compensation	None (TrueFISP) None; On; Read; Slice/Read; Read/Phase (GRE)
Dimension	2D/3D
Sequence type	TrueFISP/GRE
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ¹⁶⁵⁾
RF spoiling	Off (TrueFISP) On (GRE)

162) Only if Multi-slice mode = Single-shot is selected

163) Only if Dimension = 2D is selected

164) TE is automatically set to the minimum and cannot be changed

165) Only available for XT and XR gradients

3.3.5 BEAT (Dynamic)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.3.5.1 Use

For dynamic imaging of the heart.

3.3.5.2 Essential parameters

Magnetization preparation	Non-sel. IR/Non-sel. SR/Non-sel. SR Perf
TI	Yes
Multi-slice mode	Single-shot
Define	Shots
Shots per slice	1

3.3.5.3 Parameters

Flip angle mode	Constant (TrueFISP/GRE) Variable (GRE only)
Fat-Water Contrast	Standard/Fat saturation/Fat water excitation/SPAIR
Measurements	1–512
Acceleration mode	None/GRAPPA/mSENSE
Reference scans	Integrated/GRE-Separate/T-PAT
Phase partial Fourier	Off, 7/8, 6/8, 5/8
Trajectory	Cartesian/Radial

ECG	None/Trigger
Trigger device	ECG/Pulse/Ext
Adaptive triggering	Yes
TruFI delta freq.	-300 – +300
Respiratory control	Off/Breath-hold
Inline evaluation	Off/Time Course Evaluation/Time Course Filtered
Motion correction	Yes
Proton density images	Yes
TE variable	Yes
Asymmetric echo	Yes
Flow compensation	None (TrueFISP) None, On, Read, Slice/Read, Read/Phase (GRE)
Dimension	2D/3D
Sequence type	TrueFISP/GRE
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ¹⁶⁶⁾
RF spoiling	Off (TrueFISP) On (GRE)

166) Only available for XT and XR gradients

3.3.6 BEAT (Static)

The BEAT sequence is a multifunctional sequence designed for cardiovascular imaging applications. It can be used either with GRE or TrueFISP contrast, can be combined with different triggering devices (ECG, pulse, external), and offers a large range of parameter combinations.

3.3.6.1 Use

For localization, tissue characterization, and morphologic imaging of the heart.

3.3.6.2 Essential parameters

Magnetization preparation	None/Slice-sel. IR/Non-sel. IR/Non-sel. T2-IR/T2 Prep. Adiab.
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3.3.6.3 Parameters

Averages	Yes
Contrasts	1–32
TI	Yes
T2 prep. duration	Yes
Flip angle mode	Constant (TrueFISP/GRE) Variable (GRE only)
Fat-Water Contrast	Standard/Fat saturation/Fat water excitation/SPAIR
Dark Blood	Yes
Reconstruction mode	Magnitude, Magn./Phase, Magnitude/Real
Acceleration mode	None/GRAPPA/mSENSE
Reference scans	Integrated/GRE-Separate/T-PAT

Phase partial Fourier	Off, 7/8, 6/8, 5/8, 4/8
Trajectory	Cartesian/Radial
Multi-slice mode	Sequential, Single-shot
Saturation regions	Yes
ECG	None/Trigger
Trigger device	ECG/Pulse/Ext
Adaptive triggering	Yes ¹⁶⁷⁾
TruFi delta freq.	-300 – +300
Respiratory control	Off/Breath-hold
Inline evaluation	None
Motion correction	Yes ¹⁶⁸⁾
Tagging	None
Define	Shots/Segment
Segments variable	Yes
TE variable	Yes
Asymmetric echo	Yes
Flow compensation	None (TrueFISP) None, On, Read, Slice/Read, Read/Phase (GRE)
Dimension	2D/3D
Sequence type	TrueFISP/GRE
RF pulse type	Fast/Normal/Low SAR

167) Only if Multi-slice mode = Single-shot is selected

168) Only if Multi-slice mode = Single-shot and Magnetization preparation = Non-selective IR are selected

Gradient mode	Fast/Normal/Whisper/Performance ¹⁶⁹⁾
RF spoiling	Off (TrueFISP) On (GRE)

3.3.7 BEAT_EPI

Single-shot sequence. Can be combined with inversion recovery or saturation recovery preparation pulses.

3.3.7.1

Sequence type	Define	Shot per slice	Magn. preparation	1 st Signal/Mode
GRE EPI	Shots	1	IR/SR/SR perf	ECG/Trigger

3.3.7.2 Saturation Recovery (SR) or Saturation Recovery Perfusion (SR perf)?

- SR: Rectangular saturation pulse (normally 90 degrees)
- SR perf: Echo train with three saturation pulses (90 degrees each) as well as different time intervals and gradient spoilers. More robust with respect to magnetic field inhomogeneities, however, with a higher SAR.

3.3.7.3 Use

- For measuring First Pass perfusion.
- For sequential multislice applications.

169) Only available for XT and XR gradients

3.3.7.4 Parameters

Segments	Fixed ¹⁷⁰⁾
TE variable	No ¹⁷¹⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, SR, Selective, Non-selective
Reconstruction mode	Magnitude
Fat suppression	Yes
Asymmetric echo	Yes
Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	Yes
Dimension	2D/3D
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper/Performance ¹⁷²⁾
PAT	Integrated/tPAT

3.3.8 BEAT_FQ

Flow sequence with variable flow encoding. The sequence measures a flow-compensated and a flow-encoded scan. Phase sharing enables more frequent sampling of the center raw data lines during pulsating flow.

170) Max. number of segments depends on the number of lines

171) TE is automatically set to the minimum and cannot be changed

172) Only available for XT and XR gradients

Possible online reconstructions:

- Magnitude image
- Phase image
- Magnitude sum image

3.3.8.1 Use flow quantification

- For displaying and quantifying blood flow. Through-plane measurements for flow quantification and in-plane measurements for flow display.
- Triggered, retrospective gating possible, for displaying and quantifying blood flow during complete heart cycle coverage. Particularly suitable for patients with arrhythmias.
- Enables flow measurement in breath-hold technique using phase sharing.

3.3.8.2 Use phase-contrast angiography

- Peripheral angiography, for example, for acquiring large fluctuations in flow velocity (multivenc application)
- Localizer for 3D phase-contrast measurements
- Neuro applications, for example, for displaying arterial vessel systems

You can set the following applications on the **Angio** parameter card:

- Multivenc applications: Variable velocity encoding in one spatial direction
- Single-venc applications: Same velocity encoding in three spatial directions
- Mixed venc applications: Free selection of direction and velocity for 3 encodings

3.3.8.3 Parameters

Segments	Variable
TE variable	Yes
Contrasts	1

Bandwidth variable	Yes
Reconstruction mode	Magnitude
Asymmetric echo	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	2D/3D
Elliptical scanning ¹⁷³⁾	Yes
Slice resolution ¹⁷⁴⁾	Yes
Excitation pulse	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
Venc cm/s	1–999
PAT	Integrated

3.3.9 BEAT_Interactive

The BEAT_Interactive sequence is used for interactive real-time imaging. The sequence is based on the BEAT sequence and inherits most of the parameter settings from it.

The BEAT_Interactive sequence has the capability to acquire multiple slices that can be measured in a predefined order and will be displayed in the **Inline Display**.

During the measurement, all slice parameters can be changed via graphic slice positioning and the parameter cards. (Prerequisite: Sequence is started via the **Copy&Go** button in the toolbar of the program control.)

173) Only if Dimension = 3D is selected

174) Only if Dimension = 3D is selected

The slice positions can be saved during imaging and subsequently transferred to a protocol in the wait queue.

3.3.9.1 Use (sequence type TrueFISP)

Fast sequence with a high signal-to-noise ratio. This sequence is very suitable for cardiac and abdominal applications.

3.3.9.2 Use (sequence type GRE)

Slower sequence with a lower SAR than TrueFISP. This sequence is very suitable for interventional imaging; susceptibility effects enable a good view of biopsy needles.

3.3.9.3 Parameters (sequence type TrueFISP)

TE variable	No ¹⁷⁵⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization Preparation	Yes
Reconstruction mode	Magnitude
Saturation regions	Regular
Phase partial Fourier	Yes
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
RF spoiling	Off

175) TE is automatically set to the minimum and cannot be changed

Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
Trajectory	Cartesian
Slices	1

3.3.9.4 Parameters (sequence type GRE)

TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization Preparation	Yes
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular
Phase partial Fourier	Yes
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	Yes/None
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper/Performance ¹⁷⁶⁾
Dark blood	Yes

176) Only available for XT and XR gradients

Trajectory	Radial
Slices	1

3.3.10 BEAT_Map

The MyoMaps sequence, BEAT_Map supports inline T1, T2 and T2* mapping of the heart. The sequence is based on the *syngo* BEAT sequence and therefore inherits the parameters and functionality of the latter. Images can be acquired with TrueFISP or GRE contrast.

3.3.10.1 Use

For generating parametric maps of the heart. For a detailed description, see: Operator Manual Diagnostic MR Imaging.

3.3.10.2 Parameters

Segments	Variable ¹⁷⁷⁾
TE variable	No ¹⁷⁸⁾
Contrasts	1–32
Bandwidth variable	Yes
Magnetization preparation	Non-selective, IR, T2 preparation
Reconstruction mode	Magnitude/Phase
Fat suppression	Yes
Phase partial Fourier	Yes
Sequence type	GRE/TrueFISP
Asymmetric echo	Yes
Multi-slice mode	Sequential

177) Max. number of segments depends on the number of lines. T1 and T2 mapping are single-shot techniques.

178) TE is automatically set to the minimum and cannot be changed

Flow compensation	Yes ¹⁷⁹⁾
Dimension	2D
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper/Performance ¹⁸⁰⁾
Dark blood	Yes
Trajectory	Cartesian
iPAT	Yes
Respiratory control	Breath-hold ¹⁸¹⁾
Optimization	Min. TE/TR

3.3.11 CISS

3D gradient-echo sequence for T2 imaging with a large flip angle. TE and TR are permanently set to a minimum value to ensure best possible image quality.

3.3.11.1 Use

Can be used in neurology, where CSF provides contrast: cochlea, labyrinth, cranial nerves, optic nerve tract, spinal canal, etc.

3.3.11.2 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude

179) TrueFISP is essentially flow-compensated from one RF pulse to the next. GRE can be combined with flow compensation.

180) Only available for XT and XR gradients

181) Multiple breath-hold possible, depending on protocol setup

Fat suppression	Water excitation
Phase partial Fourier	Yes
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D/3D
Elliptical scanning ¹⁸²⁾	Yes
Slice resolution ¹⁸³⁾	Yes
Slice partial Fourier ¹⁸⁴⁾	Yes
Excitation pulses ¹⁸⁵⁾	Slab-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper

3.3.12 CSI_FID

FID variant for chemical shift imaging.

3.3.12.1 Parameters

TE variable	No ¹⁸⁶⁾
Bandwidth variable	Yes
Averaging mode	Short term/Long term
Dimension	2D/3D

182) Only if Dimension = 3D is selected

183) Only if Dimension = 3D is selected

184) Only if Dimension = 3D is selected

185) Only if Dimension = 3D is selected

186) TE is automatically set to the minimum and cannot be changed

Triggering	ECG/Respiratory
k-space weighting	Full/Elliptical/Weighted
Multiple measurements	Yes
Multinuclear support	Yes

3.3.13 CSI_SE

Spin-echo sequence for chemical shift imaging.

3.3.13.1 Use

- Localization with three orthogonal slices
- 90°–180°–180°
- Measured signal: Full spin echo

3.3.13.2 Parameters

TE variable	Yes
Bandwidth variable	Yes
Spectral fat suppression	Yes
Saturation regions	Regular
Averaging mode	Short term/Long term
Dimension	2D/3D
k-space weighting	Full/Elliptical/Weighted
Excitation of VOI	Yes
Multiple measurements	Yes
Fully excited VOI	Yes

3.3.14 CSI_Semi_LASER

Semi-LASER variant for chemical shift imaging.

3.3.14.1 Use

- Localization with three orthogonal slices
- $90^\circ-180^\circ-180^\circ-180^\circ-180^\circ$
- 180° pulses are adiabatic full-passage pulses and used in pairs
- Measured signal: Full spin echo

3.3.14.2 Parameters

TE variable	Yes
Bandwidth variable	Yes
Saturation regions	Regular
Averaging mode	Short term/Long term
Dimension	2D/3D
k-space weighting	Full/Elliptical/Weighted
Excitation of VOI	Yes
Multiple measurements	Yes

3.3.15 CSI_STEAM

STEAM chemical shift imaging sequence.

3.3.15.1 Use

- Localization with three orthogonal slices
- $90^\circ-90^\circ-90^\circ$

- Measured signal: Stimulated echo
- Short TEs possible
- Only half of the spin-echo signal

3.3.15.2 Parameters

TE variable	Yes
Mixing time (TM) variable	Yes
Bandwidth variable	Yes
Averaging mode	Short term/Long term
Dimension	2D/3D
k-space weighting	Full/Elliptical/Weighted
Excitation of VOI	Yes
Multiple measurements	Yes

3.3.16 CV_NAV

Combination of cardiovascular sequence (type TrueFISP or GRE, Cine Off) and the prospective measurement of a navigator echo.

3.3.16.1 Use

- For displaying the coronary arteries with free breathing.
- For displaying the renal arteries in NATIVE TrueFISP protocols (Prerequisite: NATIVE license is available).

3.3.16.2 Parameters

Segments	Variable ¹⁸⁷⁾
TE variable	No ¹⁸⁸⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, SR, Selective, Non-selective
Reconstruction mode	Magnitude/Real
Fat suppression	Yes
Saturation regions	Regular/Parallel
Inversion regions ¹⁸⁹⁾	Up to 4 (with different TI)
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None ¹⁹⁰⁾
Dimension	2D/3D
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper/Performance ¹⁹¹⁾
Dark blood	Yes

187) Max. number of segments depends on the number of lines

188) TE is automatically set to the minimum and cannot be changed

189) With NATIVE license

190) TrueFISP is essentially flow-compensated from one RF pulse to the next

191) Only available for XT and XR gradients

iPAT	Yes
Respiratory control	Gate & Follow/Gate/Monitor only/Off

3.3.17 DESS

3D gradient-echo sequence.

3.3.17.1 Use

Primarily in orthopedic imaging with good contrast between synovial fluid and cartilage.

3.3.17.2 Recommendations

To saturate fat at a short TR, activate a non-selective excitation pulse beforehand.

3.3.17.3 Parameters

TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Water excitation
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Readout
Dimension	3D

Elliptical scanning ¹⁹²⁾	Yes
Slice resolution ¹⁹³⁾	Yes
Slice partial Fourier ¹⁹⁴⁾	Yes
Excitation pulses ¹⁹⁵⁾	Slab-selective/Non-selective
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes

3.3.18 EPI_SEG_FID

Segmented FID EPI sequence. Faster than gradient-echo sequences, fewer off-resonance effects than with the single-shot FID EPI sequence.

3.3.18.1 Use

T2*-weighted 2D/3D imaging in the head.

3.3.18.2 Parameters

EPI factor	1–127
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation

192) Only if Dimension = 3D is selected

193) Only if Dimension = 3D is selected

194) Only if Dimension = 3D is selected

195) Only if Dimension = 3D is selected

Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D/3D
RF pulse type	Normal
RF spoiling	On/Off
Gradient mode	Fast/Normal
Respiratory control	Breath-hold ¹⁹⁶⁾

3.3.19 EPI_SEG_PHS

Segmented EPI sequence with RF and gradient-free periods for specific applications.



No protocols are provided in the Siemens protocol tree for this sequence. The sequence is to be found in the **Default Sequences** list on the **Default** tab of the **Dot Cockpit Program Editor**.

3.3.19.1 Use

You can use the EPI_SEG_PHS sequence to synchronize external hardware with the scanner behavior.

196) Multi-breath-hold possible, depending on protocol setup

3.3.19.2 Parameters

EPI factor ¹⁹⁷⁾	1–127
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	None
Reconstruction mode	Magnitude, Magn./Phase
Fat-Water Contrast	Standard/Fat saturation/Fast fat saturation
Saturation regions	Standard/Quick
Multislice mode	Interleaved/Sequential
Flow compensation	On, Read, Slice, Slice/Read, Read/Phase, Read/Phase
Dimension	2D/3D
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On/Off
Phase-encoding rewinder	On/Off
Gradient mode	Fast/Normal/Whisper

3.3.20 EPI SEG SE

Segmented spin-echo EPI sequence. Faster than spin-echo sequences, fewer off-resonance effects than with a single-shot spin-echo EPI sequence.

3.3.20.1 Use

Fast T2-weighted 2D/3D imaging in the head.

197) Parameter cannot be freely set, depends on base and phase resolution

3.3.20.2 Parameters

EPI factor	1–127
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D/3D
RF pulse type	Normal
RF spoiling	Off
Gradient mode	Fast/Normal
Respiratory control	Breath-hold ¹⁹⁸⁾

3.3.21 EPI SEG Therm

Segmented, temperature-sensitive EPI sequence.

With an EPI factor of 1, the sequence behaves like a GRE sequence.

198) Multiple breath-hold possible, depending on protocol setup

3.3.21.1 Use

MR thermometry is used to analyze temporal changes in the complex phase of image data based on large temperature changes of $\geq 15^{\circ}\text{C}$ ($\geq 27^{\circ}\text{F}$) in soft tissue. When interpreted by a trained physician, the application may be useful as part of an interventional procedure and/or for assessing a course of treatment.

For additional information on MR thermometry, see: Operator Manual Diagnostic MR Imaging.

3.3.21.2 Parameters

EPI factor	1–13
Contrasts	1
Reconstruction mode	Magnitude/Phase
Asymmetric echo	Off
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D/3D
Excitation pulses	Slice-selective
RF pulse type	Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper/Performance ¹⁹⁹⁾
Trajectory	Cartesian
Slices	1–20

199) Only available for XT and XR gradients

3.3.22 EPI2D_ASL

Single-shot FID EPI sequence.

3.3.22.1 Use

For perfusion imaging in the head. Perfusion-weighted images and rCBF images are obtained by this method.

3.3.22.2 Parameters

EPI factor ²⁰⁰⁾	1–128
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	ASL
Reconstruction mode	Magnitude
Fat suppression	Fat saturation (strong/weak)
Saturation regions	PICORE Q2T, PCASL ²⁰¹⁾
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Performance ²⁰²⁾

200) Parameter cannot be freely set, depends on base and phase resolution

201) Parameter “Perfusion mode”

202) Only available for XT and XR gradients

Online reconstruction	Perfusion-weighted images, relCBF
Flow limit	0–100 cm/s
Bolus duration	Variable ²⁰³⁾
iPAT	Yes
Quality check	On/Off/On - extended

3.3.23 EPI2D_BOLD

Single-shot FID EPI sequence.

3.3.23.1 Use

For BOLD imaging in the head, t-test evaluation is performed in real time during the measurement. The calculated t-test images are shown continuously in the **Inline Display**.

3.3.23.2 Parameters

EPI factor ²⁰⁴⁾	1–128
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term

203) Parameter depends on TR

204) Parameter cannot be freely set, depends on base and phase resolution

Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Excitation pulses	ZOOMit ²⁰⁵⁾
Gradient mode	Fast/Normal/Performance ²⁰⁶⁾
iPAT	Yes
Simultaneous multislice (SMS)	Yes

3.3.24 EPI2D_Diff

Single-shot spin-echo EPI sequence.

You can set diffusion-specific parameters on the **Diff** parameter card:

- Direction(s) of the diffusion-sensitive axis(es) (diffusion mode)
- Number and magnitude of b-values
- Reconstruction mode (ADC image, Trace images)

3.3.24.1 Use

For diffusion imaging, for example, for examining strokes.

3.3.24.2 Recommendations

To minimize image distortions due to susceptibility, select a bandwidth that enables use of minimum echo spacing.

205) Only available for systems with TimTX TrueShape option

206) Only available for XT and XR gradients

3.3.24.3 Parameters

EPI factor ²⁰⁷⁾	1–256
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Excitation pulses	ZOOMit
Gradient mode	Fast/Normal/Performance ²⁰⁸⁾
b-value [s/mm ²]	0–10000
Increment bipolar [s/mm ²]	50
Increment monopolar 0–200 [s/mm ²]	10

207) Parameter cannot be freely set, depends on base and phase resolution

208) Only available for XT and XR gradients

Increment monopolar 200–10000 [s/mm ²]	50
Diffusion mode	Read/Slice/Phase/Orthogonal/3D-Diagonal/1-Scan Trace/3-Scan Trace/4-Scan Trace/MDWW/q-Space/Free ²⁰⁹⁾
Online reconstruction	<ul style="list-style-type: none"> • DW and ADC image • FA image • TRACE • colored FA image
iPAT	Yes
Simultaneous multislice (SMS)	Yes
Respiratory control	Trigger/Breath-hold ²¹⁰⁾
Echo spacing variable	Yes
Optimization	Min. TE
SliceAdjust	Yes
Phase correction	Internal/External

3.3.25 EPI2D_FID

Single-shot FID EPI sequence.

3.3.25.1 Use

For perfusion imaging in the head. You can activate online reconstruction of the following images on the **Perf** parameter card:

- Time to Peak (TTP)
- Global Bolus Plot (GBP)

209) Only accessible with DTI license and custom diffusion vector set file

210) Multi-breath-hold possible, depending on protocol setup

- Percentage of Baseline at Peak (PBP)
- relative Cerebral Blood Volume (relCBV)
- relative Cerebral Blood Flow (relCBF)
- relative Mean Transit Time (relMTT)

3.3.25.2 Recommendations

To minimize image distortions through susceptibility, select a bandwidth that enables use of minimum echo spacing.

3.3.25.3 Parameters

EPI factor ²¹¹⁾	1–256
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	No
Reconstruction mode	Magnitude
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal

211) Parameter cannot be freely set, depends on base and phase resolution

RF spoiling	Off
Excitation pulses	ZOOMit ²¹²⁾
Gradient mode	Fast/Normal/Performance ²¹³⁾
Online reconstruction	<ul style="list-style-type: none"> • TTP • GBP • PBP • relCBV • relCBF • relMTT
iPAT	Yes

3.3.26 EPI2D_PACE

Identical to EPI2D_BOLD but with prospective 3D motion correction.



If you switch off motion correction, the entire function including prospective correction is deactivated.

3.3.26.1 Parameters

EPI factor ²¹⁴⁾	1–128
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation

212) Only available for systems with TimTX TrueShape option

213) Only available for XT and XR gradients

214) Parameter cannot be freely set, depends on base and phase resolution

Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Performance ²¹⁵⁾
iPAT	Yes

3.3.27 EPI2D_SE

Single-shot spin-echo EPI sequence.

3.3.27.1 Use

To examine T2-weighted lesions.

3.3.27.2 Recommendations

The CSF signal in the head can be suppressed by activating an inversion pulse with a long inversion time.

215) Only available for XT and XR gradients

3.3.27.3 Parameters

EPI factor	1–256 ²¹⁶⁾
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Performance ²¹⁷⁾
iPAT	Yes

216) Parameter cannot be freely set, depends on base and phase resolution

217) Only available for XT and XR gradients

3.3.28 EPI2D_SE_MRE

Single-shot spin-echo EPI sequence for MR Elastography (MRE). This sequence acquires information about the periodic movement of the tissue caused by an external source (elastography hardware) via motion-encoding gradients (MEG).

The EPI2D_SE_MRE sequence offers acquisition of multiple slices in a single, short breath-hold and is more robust against signal dephasing effects, especially at 3 T.

3.3.28.1 Use

The MRE technique generates images of the relative stiffness by imaging the propagation of the pressure waves in the human tissue.

3.3.28.2 Recommendations

Fractional MRE should only be used for patients with a very short T2* relaxation time whose resulting signal is too low. If you use Fractional MRE, the MEG duration is reduced to a fraction of the full wave period. It is automatically activated by reducing the TE time to a minimum value (in the range below the gray area).

3.3.28.3 Parameters

EPI factor	1–128 ²¹⁸⁾
TR variable	Yes
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.
Fat-Water Contrast	Standard/Fat saturation/SPAIR/ Water excitation
Fat saturation	Strong/Weak

218) Parameter cannot be freely set, depends on base and phase resolution

Dimension	2D
Bandwidth variable	Yes
Special saturation	Parallel H/Parallel F
iPAT	Yes
Phase partial Fourier	Yes
Gradient mode	Fast/Normal

3.3.29 Fast_TSE

Optimized TSE sequence with shorter echo spacing.

Advantages:

- Shorter measurement times
- Possible reduction of streaking artifacts, especially for BLADE imaging

3.3.29.1 Use

Used only for conventional TSE and BLADE imaging in abdominal imaging.

3.3.29.2 Parameters

Turbo factor	1–129
TE variable	Yes
Contrasts	1–3
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ²¹⁹⁾
Fat suppression	Fat saturation/SPAIR

219) Can only be selected if Magn. Preparation = IR has been selected

Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ²²⁰⁾
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None/Readout/Slice
Dimension	2D
RF pulse type	Fast/Normal/Optimized
Gradient mode	Fast/Normal/Whisper/Performance ²²¹⁾
Dark blood	Yes
iPAT	Yes
Respiratory control	Trigger/Breath-hold ²²²⁾
Hyperecho	Yes
BLADE Trajectory	Yes
Restore	Yes

3.3.30 FastView

Gradient-echo sequence.

3.3.30.1 Use

For localizer images of large body regions with transverse slices and continuous table move.

220) Parameter cannot be freely set, depends on selected TE

221) Only available for XT and XR gradients

222) Multiple breath-hold possible, depending on protocol setup

3.3.30.2 Parameters

Matrix	96
Slice thickness	5 mm
TE/TR	1.44 ms/2.56 ms
FOV	480 mm × 87.5%
Table speed	46 mm/s

3.3.31 FID

The FID sequence has no localization built into the sequence and localizes only by the sensitive volume of the coil.

3.3.31.1 Use

You can select an adiabatic RF pulse for the FID sequence (on the **Contrast/Common** parameter card) to support adiabatic excitation for multinuclear spectroscopy.

- Useful for multinuclear spectroscopy with surface coils
- AHP (adiabatic half passage) or BIR-4 (B1-insensitive rotation) pulses can be used for excitation
- AHP: to generate uniform 90° excitation
- BIR-4: variable flip angle excitation from adiabatic plane-rotation pulses
- Advantage: less sensitive to B1 variations

3.3.31.2 Parameters

TE variable	No ²²³⁾
Bandwidth variable	Yes
Phase cycling	Yes

223) TE is automatically set to the minimum and cannot be changed

Triggering	ECG/Respiratory
Multiple measurements	Yes
Multinuclear support	Yes

3.3.32 FLASH_PC

FLASH sequence.

Possible online reconstructions:

- Magnitude image
- Phase image
- Magnitude sum image

3.3.32.1 Use 2D

- Peripheral angiography, for example, for acquiring large fluctuations in flow velocity (multivenc application).
- Also as a localizer for 3D phase-contrast measurements.

3.3.32.2 Use 3D

Neuro applications, for example, for displaying arterial vessel systems.

You can set the following applications on the **Angio** parameter card:

- Multivenc applications: Variable velocity encoding in one spatial direction
- Single-venc applications: Same velocity encoding in three spatial directions
- Mixed venc applications: Free selection of direction and velocity for three encodings

3.3.32.3 Parameters

Segments	1–25
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Asymmetric echo	Yes
Averaging mode	Off/Weak/Strong
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	2D/3D
Elliptical scanning ²²⁴⁾	Yes
Slice resolution ²²⁵⁾	Yes
Excitation pulses	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
Venc cm/s	1–999

3.3.33 FLASH_Perি_TOF

2D FLASH sequence.

224) Only if Dimension = 3D is selected

225) Only if Dimension = 3D is selected

3.3.33.1 Use

- Peripheral angiography.
- ECG-triggered measurement of vessels in the legs at a high heart rate or in the kidneys, arms, and carotid arteries.

3.3.33.2 Recommendations

Perform data acquisition during the systole to obtain the maximum signal and to avoid pulsation artifacts.

3.3.33.3 Parameters

Segments	1–23
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Off/Allowed
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	2D
Excitation pulses	Slab-selective
RF pulse type	Fast/Normal

RF spoiling	On
Gradient mode	Fast/Normal/Whisper

3.3.34 FLASH_TOF

FLASH sequence.

3.3.34.1 Use

- Inflow angiography with 2D or 3D acquisition.
- 3D display of intracranial vessels in sequential slice acquisition.
- Display of the coronary arteries using 3D technique in sequential slice acquisition.
- Application for 2D time-of-flight examinations.

3.3.34.2 Recommendations

For three-dimensional applications, select the TONE pulse (depending on flow velocity) to counteract the saturation effect of blood flowing through the slab.

3.3.34.3 Parameters

TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Allowed

Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	2D/3D
Elliptical scanning ²²⁶⁾	Yes
Slice resolution ²²⁷⁾	Yes
Slice partial Fourier ²²⁸⁾	Yes
Excitation pulses	Slab-selective
RF pulse type	Normal ²²⁹⁾
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
iPAT	Yes

3.3.35 FLASH3D_CE

Gradient-echo sequence.

3.3.35.1 Use

- Optimized for CE angiography
- Angiography of the carotid, thoracic, and pulmonary arteries
- Basis for Care Bolus and Test Bolus protocols for determining arrival of contrast agent
- Multistep angiography for display of peripheral vessels

226) Only if Dimension = 3D is selected

227) Only if Dimension = 3D is selected

228) Only if Dimension = 3D is selected

229) If Dimension = 3D is selected, TONE pulses are used, which can be optimized for different flow velocities via the TONE ramp parameter

3.3.35.2 Recommendations

- To suppress background signal, select fat suppression (fat saturation or water excitation).
- An IR pulse can be used instead of the fat suppression pulse. In this case, set the inversion time to suppress fat.

3.3.35.3 Parameters

Segments	1–127
TE variable	Yes ²³⁰⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization Preparation	IR ²³¹⁾
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
Phase partial Fourier	Yes
Asymmetric echo	Allowed
Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D/3D
Elliptical scanning ²³²⁾	Yes ²³³⁾
Slice resolution ²³⁴⁾	Yes

230) Sequence allows a freely-selectable TE, an automatic minimal TE, or an automatic minimal TE and TR

231) If segments >1 (segmented TurboFLASH)

232) Only if Dimension = 3D is selected

233) Not available if iPAT is activated

234) Only if Dimension = 3D is selected

Slice partial Fourier ²³⁵⁾	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On
Phase encoding rewinder	Yes
Gradient mode	Fast/Normal/Whisper
3D reordering	Standard/User-defined TTC
Time to center ²³⁶⁾	Yes
iPAT	Yes
iPAT ²	Yes

3.3.36 FLASH3D_RD

Magnitude contrast gradient-echo sequence.

3.3.36.1 Use

For displaying the arteries of the leg with a 3D measurement.

3.3.36.2 Parameters

TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel

235) Only if Dimension = 3D is selected

236) Freely selectable if 3D reordering is set to "User-defined TTC"

MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Yes
Dimension	3D
Elliptical scanning	Yes
Slice resolution	Yes
Slice partial Fourier	Yes
Excitation pulses	Slab-selective
RF pulse type	Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper

3.3.37 FLASH3D_VIBE

3D FLASH sequence.

3.3.37.1 Use

For contrast-enhanced examinations, in particular of the abdomen and pelvis.

Support of radiotherapy planning with respiratory self-gating.

3.3.37.2 Recommendations

To suppress the fat signal, select Dixon, fat saturation, or water excitation.

3.3.37.3 Parameters

TE variable	Yes ²³⁷⁾
Contrasts	1–12
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Dixon	Yes
LiverLab ²³⁸⁾	Yes
Saturation regions	Regular/Parallel
Phase partial Fourier	Yes
Asymmetric echo	Off/Weak/Strong
Averaging mode	Short term/Long term
Flow compensation	None
Dimension	3D
Elliptical scanning ²³⁹⁾	Yes
Slice resolution ²⁴⁰⁾	Yes
Slice partial Fourier ²⁴¹⁾	Yes
Excitation pulses	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On

237) Sequence allows a freely-selectable TE, an automatic minimal TE, or an automatic TE set to the “in-phase” or “opposed phase” time

238) Depends on the Dixon and Dixon evaluation options

239) Only if Dimension = 3D is selected

240) Only if Dimension = 3D is selected

241) Only if Dimension = 3D is selected

Gradient mode	Fast/Normal/Whisper/Performance ²⁴²⁾
3D reordering	Standard/User-defined TTC
iPAT	Yes
iPAT ²	Yes
CAIPIRINHA ²⁴³⁾	Yes
Respiratory control	Breath-hold
Readout mode	Monopolar/Bipolar
Liver registration	Yes
MapIt	Yes
Motion scan	Yes ²⁴⁴⁾
Number of bins	2–10 ²⁴⁵⁾

3.3.38 GRE

Gradient-echo sequence.

3.3.38.1 Use

- Abdominal in-phase/opposed phase imaging in one measurement
- 3D FLASH sequence for T1-weighted ortho imaging and neuro imaging
- Fast 3D sequence for contrast enhancement studies (for example, dynamic breast diagnostics)

242) Only available for XT and XR gradients

243) CAIPIRINHA is a generalization of iPAT² allowing undersampling on a sheared grid (→ Page 426 *Acceleration mode (parameter)*)

244) Only if Trajectory = Radial is selected

245) only if Motion scan is selected

- Susceptibility-weighted imaging (SWI)
- Evaluation of metastases and lymph nodes in the thorax, abdomen, and pelvis (whole-body imaging)

3.3.38.2 Recommendations

- Quick parallel saturation: Enables saturation of inflowing blood without significantly increasing measurement time
- Quick fat saturation: Enables fat saturation without significantly increasing measurement time
- Water excitation: Enables fat suppression with still acceptable TR increase.
Disadvantage: TE is prolonged

3.3.38.3 Parameters

Segments	1–127
TE variable	Yes
Contrasts	1–12
Bandwidth variable	Yes
Magnetization Preparation	IR, SR ²⁴⁶⁾
Reconstruction mode	Magnitude/Phase
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential

246) If segments >1 (segmented TurboFLASH)

Flow compensation	Yes/None/Readout/Slice/Slice&Read-out
Dimension	2D/3D
Elliptical scanning ²⁴⁷⁾	Yes
Slice resolution ²⁴⁸⁾	Yes
Slice partial Fourier ²⁴⁹⁾	Yes
Excitation pulses ²⁵⁰⁾	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper/Performance ²⁵¹⁾
Dark blood	Yes ²⁵²⁾
Grid/Line tagging	Yes
iPAT	Yes
iPAT ²	Yes
Respiratory control	Breath-hold ²⁵³⁾
Readout mode	Monopolar/Bipolar
Acoustic noise reduction	Yes
SWI	Yes
MapIt	Yes
BM Motion correction	Yes

247) Only if Dimension = 3D is selected

248) Only if Dimension = 3D is selected

249) Only if Dimension = 3D is selected

250) Only if Dimension = 3D is selected

251) Only available for XT and XR gradients

252) If segments >1 (segmented TurboFLASH)

253) Multi-breath-hold possible, depending on protocol setup

3.3.39 GRE_Field_Mapping

2D gradient-echo sequence that generates images at two different echo times. The first TE is variable, the second TE is fixed relative to the first TE. The different echo times correspond to the in-phase conditions of fat and water protons.

3.3.39.1 Use

When phase images are selected, you obtain a single-phase differential image that can be used as a “field map” during BOLD postprocessing. The information is required when overlaying anatomical images generated with other techniques, for example, SE or MPRAGE.

Prerequisites for using BOLD postprocessing:

- The phase range of -PI to +PI corresponds to image pixel values of -4095 to +4095
- Image geometry and slice orientation have to be identical to the EPI images
- The sequence has to be applied prior to the corresponding EPI measurement

3.3.39.2 Parameters

TE variable	Yes
Contrasts	2
Bandwidth variable	Yes
Reconstruction mode	Magnitude/Phase
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel/Tracking
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term/Long term

Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes
Dimension	2D
RF pulse type	Fast/Normal
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper

3.3.40 GRE_MRE

Gradient-echo-based sequence for MR Elastography (MRE). This sequence acquires information about the periodic movement of the tissue caused by an external source (elastography hardware) via motion-encoding gradients (MEG).

3.3.40.1 Use

The MRE technique generates images of the relative stiffness by imaging the propagation of the pressure waves in the human tissue.

3.3.40.2 Recommendations

- Rapid MRE reduces the acquisition time and thus the necessary breath-hold duration for the patient. This increases patient comfort, and image artifacts due to breathing movements of the patient can be mitigated. Rapid MRE is activated by reducing the TR time.
- Fractional MRE should only be used for patients with a very short T2* relaxation time whose resulting signal is too low. If you use Fractional MRE, the MEG duration is reduced to a fraction of the full wave period. It is automatically activated by reducing the TE time to a minimum value (in the range below the gray area).

3.3.40.3 Parameters

TR variable	50 ms (standard mode) 25 ms (rapid mode)
TE variable	Yes
Dimension	2D
Bandwidth variable	Yes
Respiratory control	Breath-hold
Special saturation	Parallel H/Parallel H/F (standard mode) Off (rapid mode)
iPAT	Yes
Orientation	Transversal
Phase partial Fourier	Yes
Base resolution	128
Normalize	Prescan
Flow compensation	On
Gradient mode	Fast/Normal

3.3.41 GRE_PHS

Gradient-echo sequence with RF and gradient-free periods for specific applications.



No protocols are provided in the Siemens protocol tree for this sequence. The sequence is to be found in the **Default Sequences** list on the **Default** tab of the **Dot Cockpit Program Editor**.

3.3.41.1 Use

You can use the GRE_PHS sequence to synchronize external hardware with the scanner behavior.

3.3.41.2 Parameters

TE variable	No
Contrasts	1–20
Bandwidth variable	Yes
Magnetization preparation	None
Reconstruction mode	Magnitude, Magn./Phase
Fat-Water Contrast	Standard/Fat saturation
Saturation regions	Parallel
Phase partial Fourier	Yes
Asymmetric echo	Off/Weak/Strong
Averaging mode	Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	On, Slice/Read
Dimension	2D/3D
Elliptical scanning ²⁵⁴⁾	Yes
Slice resolution ²⁵⁵⁾	Yes
Slice partial Fourier ²⁵⁶⁾	Yes
Excitation pulses ²⁵⁷⁾	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR

254) Only if Dimension = 3D is selected

255) Only if Dimension = 3D is selected

256) Only if Dimension = 3D is selected

257) Only if Dimension = 3D is selected

RF spoiling	On/Off
Phase-encoding rewinder	On/Off
Gradient mode	Fast/Normal/Whisper

3.3.42 GRE_Proj

Gradient-echo-based projection imaging sequence.

You can use projection data to calculate the position of one or more coils within the scanner. The Siemens software does not calculate the position. You need to calculate the position separately.



No protocols are provided in the Siemens protocol tree for this sequence. The sequence is to be found in the **Default Sequences** list on the **Default** tab of the **Dot Cockpit Program Editor**.

3.3.42.1 Use

The GRE_Proj sequence is used to acquire MR signals from any set of tracking coils. Up to four readout projections and at least six tracking coils are supported.

Using the Access-i remote control, the raw magnitude projection data can be made available for 3rd party clients (see: Operator Manual MR System Administration).

3.3.42.2 Parameters

TE variable	No
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	None
Reconstruction mode	Magnitude

Measurements	1–250
Dimension	1D
Gradient mode	Normal/Whisper
Tracking	Yes
Background suppression	Yes
Tracking flip angle	Yes

3.3.43 GRE_Wave

Gradient-echo sequence with Wave-CAIPI acceleration.

3.3.43.1 Use

For routine brain imaging with SWI contrast. For a detailed description, see: Operator Manual Diagnostic MR Imaging.

3.3.43.2 Recommendations

- To avoid aliasing artifacts, acquire images in transverse orientation.
- Acquisitions with higher acceleration factors are more susceptible to image quality degradation due to subject motion. Therefore, acceleration should not exceed 2×3 for 32-channel or 64-channel coils or 2×2 for 20-channel coils.
- An external reference scan is mandatory and automatically set.
- Interpolation is not provided.
- The acoustic noise produced by Wave-CAIPI is higher than with conventional imaging with the GRE sequence. In addition, acoustic noise reduction is not offered for Wave-CAIPI.

3.3.43.3 Parameters

TE variable	Yes
Contrasts	1–2
Bandwidth variable	Yes
Reconstruction mode	Magnitude, Magn./Phase
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel/Tracking
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes
Dimension	3D
Slice resolution ²⁵⁸⁾	Yes
Excitation pulses ²⁵⁹⁾	Slab-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On
Gradient mode	Fast/Normal/Whisper/Performance ²⁶⁰⁾
iPAT	Yes
iPAT ²	Yes
Readout mode	Monopolar
SWI	Yes
Maplt	Yes
Acceleration mode	Wave-CAPI (fixed)

258) Only if Dimension = 3D is selected

259) Only if Dimension = 3D is selected

260) Only available for XT and XR gradients

3.3.44 HASTE

Single-shot TSE sequence.

3.3.44.1 Use

- T2 weighting for neuro applications, used, for example, with uncooperative patients
- T2 weighting for breath-hold studies in the abdomen without motion artifacts
- Cholangiography imaging when using very long echo times (~1 s)
- Myelography imaging when using very long echo times (~1 s)
- Dark blood imaging for examining cardiac anatomy
- Evaluation of metastases and lymph nodes in the thorax, abdomen, and pelvis (wholebody imaging)

3.3.44.2 Parameters

Turbo factor	1–512 ²⁶¹⁾
TE variable	Yes
Contrasts	1–4
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ²⁶²⁾
Fat suppression	Fat saturation/Water saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ²⁶³⁾

261) Parameter cannot be freely set, depends on base and phase resolution

262) May be selected only if Magn. Preparation = IR has been selected

Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	None/Readout/Slice
Dimension	2D/3D
Slice resolution ²⁶⁴⁾	Yes
Slice partial Fourier ²⁶⁵⁾	Yes
RF pulse type	Fast/Normal/Optimized ²⁶⁶⁾
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Respiratory control	Trigger/Breath-hold ²⁶⁷⁾

3.3.45 HASTE_Interactive

The HASTE_Interactive sequence is used for interactive real-time imaging. The sequence is based on the HASTE sequence and inherits most of the parameter settings from it.

The HASTE_Interactive sequence has the capability to acquire multiple slices that can be measured in a predefined order and will be displayed in the **Inline Display**.

During the measurement, all slice parameters can be changed via graphic slice positioning and the parameter cards. (Prerequisite: Sequence is started via the **Copy&Go** button in the toolbar of the program control.)

The slice positions can be saved during imaging and subsequently transferred to a protocol in the wait queue.

263) Parameter cannot be freely set, depends on selected TE

264) Only if Dimension = 3D is selected

265) Only if Dimension = 3D is selected

266) If Dimension = 3D, only RF pulse type Normal is supported

267) Multi-breath-hold possible, depending on protocol setup

3.3.45.1 Use

Interactive T2-weighted imaging

3.3.45.2 Parameters

Turbo factor	1–512 ²⁶⁸⁾
TE variable	Yes
Contrasts	1–4
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ²⁶⁹⁾
Multi-slice mode	Single-shot
Flow compensation	None
Dimension	2D
RF pulse type	Fast/Normal/Optimized
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Respiratory control	Trigger/Breath-hold ²⁷⁰⁾

268) Parameter cannot be freely set, depends on base and phase resolution

269) Parameter cannot be freely set, depends on selected TE

270) Multi-breath-hold possible, depending on protocol setup

3.3.46 MEDIC

MEDIC sequence (Multi-echo Data Image Combination), gradient-echo sequence with flow compensation. When combined echoes = 1, the sequence behaves like a FLASH sequence with flow compensation.

3.3.46.1 Use

- T2*-weighted imaging with a high signal-to-noise ratio for the spine (especially transverse cervical and thoracic spine) and ortho (knee and shoulder) imaging
- T2*-weighted 3D imaging of the cervical spine with a small flip angle and adjusted TR

3.3.46.2 Parameters

Combined echoes	1–12
TE variable	Yes
Contrasts	1
IR Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes
Dimension	2D/3D

Elliptical scanning ²⁷¹⁾	Yes
Slice resolution ²⁷²⁾	Yes
Slice partial Fourier ²⁷³⁾	Yes
Excitation pulses ²⁷⁴⁾	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes

3.3.47 PETRA

The PETRA sequence provides a way of acquiring ultra-short TE images with substantially less noise from gradient switching than in conventional imaging. PETRA is a further development of the gradient-echo sequence (GRE).

3.3.47.1 Use

T1-weighted 3D isotropic images of the head. PETRA can be used as an alternative to MPRAGE with the benefit of significant lower noise and hence increased patient comfort.

3.3.47.2 Recommendations

- Perform measurements as close to the isocenter as possible.
- The sequence is non-selective. Please use a FOV large enough to cover the entire acquisition area.

271) Only if Dimension = 3D is selected

272) Only if Dimension = 3D is selected

273) Only if Dimension = 3D is selected

274) Only if Dimension = 3D is selected

3.3.47.3 Parameters under *syngo*

Parameter	Parameter card	Comment
Segments	Sequence/Part 1	If a fat saturation/water saturation pulse is selected, the number of repetitions acquired with each fat saturation/water saturation can be set with the parameter Segments
TI	Contrast/Common	If an inversion pulse is selected, TI determines the duration between the inversion pulse and the beginning of the acquired repetitions
Turbo factor	Sequence/Part 1	If an inversion pulse is selected, Turbo Factor determines the number of repetitions between two inversion pulses
TR	Contrast/Common	If an inversion pulse is selected, the repetition time of the single repetitions is set to its minimum value. The repetition time corresponds to the time between two inversion pulses
Radial views	Resolution/Common	The number of radial views can be changed on the resolution card

3.3.47.4 Parameters

Segments	2–100
TE variable	Yes
Bandwidth variable	Yes
Magnetization preparation	IR
Fat suppression	Fat saturation/Water saturation

Saturation regions	Regular/Parallel
Phase partial Fourier	Yes
Dimension	3D
Acoustic noise reduction	Yes

3.3.48 PSIF

Steady-state gradient-echo sequence.

With steady-state sequences, echo time TE and repetition time TR are set to fixed minimum values to ensure the best possible image quality. In the case of the PSIF sequence, this applies to TE only. TR is a freely-adjustable parameter.

PSIF offers flow compensation in the slice or readout direction but is highly sensitive to motion artifacts. At a large flip angle, heavily T2-weighted images are generated.

3.3.48.1 Use

- T2-weighted imaging with 3D PSIF with flow compensation in the readout direction, for CSF or spine diagnostics.
- T2-weighted imaging with 2D or 3D PSIF with flow compensation in the slice selection direction, for breath-hold studies of the abdomen (dark blood T2 weighting in the liver).

3.3.48.2 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Fat suppression	Water excitation
Phase partial Fourier	Yes

Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	Readout/Slice
Dimension	2D/3D
Elliptical scanning ²⁷⁵⁾	Yes
Slice resolution ²⁷⁶⁾	Yes
Slice partial Fourier ²⁷⁷⁾	Yes
Excitation pulses ²⁷⁸⁾	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes
Diffusion weighting	Yes

3.3.49 Quiet_DWI

Quiet multi-shot, diffusion-weighted, readout-segmented EPI sequence.

3.3.49.1 Use

For quiet diffusion-weighted imaging of the brain.

3.3.49.2 Recommendations

To increase the effect of noise reduction, raise the echo spacing value on the **Sequence/Part 1** parameter card.

275) Only if Dimension = 3D is selected

276) Only if Dimension = 3D is selected

277) Only if Dimension = 3D is selected

278) Only if Dimension = 3D is selected

3.3.49.3 Parameters

EPI factor ²⁷⁹⁾	1–256
TE variable	No ²⁸⁰⁾
Contrasts	2
Bandwidth variable	No ²⁸¹⁾
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
b-value	0–10000
Online reconstruction	<ul style="list-style-type: none"> • DW and ADC image • FA image • TRACE • colored FA image

279) Parameter cannot be freely set, depends on base and phase resolution

280) Parameter cannot be freely set, depends on other parameters

281) Parameter cannot be freely set, depends on other parameters

iPAT	Yes
Simultaneous multislice (SMS)	Yes
Readout segments	Yes
Reacquisition mode	On/Off
Echo spacing variable	Yes
Optimization	Min. TE/TR

3.3.50 RESOLVE

Multi-shot, diffusion-weighted, readout-segmented EPI sequence.

During diffusion preparation, multi-shot DWI is sensitive to brain motion caused by CSF pulsation. This leads to non-linear phase errors that vary from shot to shot. The effect of these phase errors can be minimized by using a readout-segmented EPI readout in conjunction with 2D navigator phase correction and navigator-based reacquisition.

3.3.50.1 Use

For better image quality in neuro imaging than with standard single-shot EPI sequence.

3.3.50.2 Recommendations

- For a given spatial resolution: Reduce the minimum echo spacing (and the associated artifacts) by increasing the number of "Readout segments".
- For a fixed echo spacing: Increase the available spatial resolution by increasing the number of "Readout segments".

3.3.50.3 Parameters

EPI factor ²⁸²⁾	1–256
TE variable	No ²⁸³⁾
Contrasts	2
Bandwidth variable	No ²⁸⁴⁾
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Readout partial Fourier	Yes
Averaging mode	Long term
Multi-slice mode	Interleaved
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper/Performance ²⁸⁵⁾
b-value	0–10000

282) Parameter cannot be freely set, depends on base and phase resolution

283) Parameter cannot be freely set, depends on other parameters

284) Parameter cannot be freely set, depends on other parameters

285) Only available for XT and XR gradients

Online reconstruction	<ul style="list-style-type: none"> • DW and ADC image • FA image • TRACE • colored FA image
iPAT	Yes
Simultaneous multislice (SMS)	Yes
Readout segments	Yes
Reacquisition mode	On/Off
Echo spacing variable	Yes
Optimization	Min. TE/TR

3.3.51 SE

Spin-echo sequence without flow compensation. The temporal sequence depends on the parameters selected.

3.3.51.1 Use

- As a single-contrast sequence especially well suited for T1-weighted imaging regardless of the body region selected.
- Dark blood imaging for examining cardiac anatomy by adding dark blood preparation.

3.3.51.2 Parameters

TE variable	Yes
Contrasts	1–2
Bandwidth variable	Yes
Magnetization preparation	IR

Reconstruction mode	Magnitude/Real ²⁸⁶⁾
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Asymmetric echo	Off/Allowed
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ²⁸⁷⁾
Dark blood	Yes
Blood suppression	On/Off
Acoustic noise reduction	Yes

3.3.52 SE_15b130

Classic spin-echo sequence without flow compensation. The temporal sequence is fixed, that is, independent of the parameters selected.

3.3.52.1 Use

For T1-weighted imaging.

286) May be selected only if Magn. Preparation = IR has been selected

287) Only available for XT and XR gradients

3.3.52.2 Parameters

TE variable	Yes
Contrasts	1
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ²⁸⁸⁾
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D
RF pulse type	Normal
Gradient mode	Normal

3.3.53 SE_17rb130

Flow-compensated spin-echo sequence. The temporal sequence is fixed, that is, independent of the parameters selected.

3.3.53.1 Use

For postgadolinium applications in the head.

288) May be selected only if Magn. preparation = IR has been selected

3.3.53.2 Parameters

TE variable	No
Contrasts	1
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ²⁸⁹⁾
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	Yes
Dimension	2D
RF pulse type	Normal
Gradient mode	Normal

3.3.54 SE_MC

Multic_contrast sequence with up to 32 contrasts. The sequence design is derived from the TSE technique. Since stimulated echoes contribute to the signal with TSE, the second echo makes a larger signal contribution than the first echo. The temporal sequence depends on the parameters selected.

3.3.54.1 Use

For acquiring T2 relaxation curves.

289) May be selected only if Magn. preparation = IR has been selected

3.3.54.2 Recommendations

Do **not** use the first echo in the calculation for T2 image reconstruction.

3.3.54.3 Parameters

TE variable	Yes
Contrasts	1–32
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ²⁹⁰⁾
Fat suppression	Fat saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ²⁹¹⁾
Dark blood	Yes
MapIt	Yes

290) May be selected only if Magn. Preparation = IR has been selected

291) Only available for XT and XR gradients

3.3.55 SEMAC

The slice encoding for metal artifact correction sequence is a TSE variant for imaging patients with full joint replacements (metal implant) and corrects in-plane and through-plane distortions. SEMAC offers alternate acceleration techniques such as GRAPPA and Compressed Sensing (CS).

3.3.55.1 Use

Metal implant imaging of joints with PD, T1, T2, and STIR contrast.



Please adhere to all safety instructions regarding implants. For a detailed description, see: Operator Manual MR System and Coils.

3.3.55.2 Parameters

Turbo factor	10–599
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR
Saturation regions	Regular/Parallel
Elliptical scanning	Yes ²⁹²⁾
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ²⁹³⁾
iPAT	Yes
Compressed Sensing	Yes
SEMAC	15–32

292) only with Compressed Sensing (CS)

293) Only available for XT and XR gradients

SAR Optimization	Yes
Fat suppression	Fat saturation/SPAIR

3.3.56 SPACE

The SPACE sequence is a variant of the 3D Turbo spin-echo sequence optimized for 3D data acquisition, T1/T2/PD weighting and dark fluid contrast. Significant SAR reduction with the variable flip angle technique. This allows for very high turbo factors (>100) and high sampling efficiencies. As a result, you obtain high-resolution isotropic images that allow free reformatting in all planes.

3.3.56.1 Use

- PD weighting with/without fat saturation and T1 weighting for orthopedic applications
- Basis for non-CE MR angiography protocols with NATIVE SPACE (prerequisite: NATIVE license is available)
- T1, T2, Flair, and double inversion recovery contrast for brain imaging
- T2 weighting for spine imaging
- T2 weighting and MRCP for body imaging

3.3.56.2 Parameters

Turbo factor	10–599
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, DIR, T2 prep. IR, Non-sel. T2 prep. IR
Reconstruction mode	Magnitude/Real ²⁹⁴⁾

294) May be selected only if Magn. Preparation = IR has been selected

Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ²⁹⁵⁾
Flow compensation	None/Readout
Dimension	3D
Elliptical scanning	Yes
Slice resolution	Yes
Slice partial Fourier	Yes
Excitation pulses	Slab-selective/Non-selective/ZOOMit ²⁹⁶⁾
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ²⁹⁷⁾
Dark blood	Yes
iPAT	Yes
iPAT ²	Yes
Compressed Sensing	Yes
CAIPIRINHA ²⁹⁸⁾	Yes
Respiratory control	Trigger/Breath-hold
Restore	Yes
NATIVE ²⁹⁹⁾	Off/TD scout/3D mode

295) Parameter cannot be freely set, depends on selected TE

296) Only available for systems with TimTX TrueShape option

297) Only available for XT and XR gradients

298) CAIPIRINHA is a generalization of iPAT² allowing undersampling on a sheared grid (→ Page 426 *Acceleration mode (parameter)*)

299) With NATIVE license; "NATIVE" available only for ECG or pulse trigger, "Flow sensitivity" available only if NATIVE is not off

Flow sensitivity ³⁰⁰⁾	Default/Weak/Medium/Strong
Blood suppression	Body region/Free

3.3.57 SPACE_NAV

Combination of the SPACE sequence and prospective measurement of a navigator echo.

3.3.57.1 Use

- Assessment of the arterial vessel wall
- In regions affected by respiratory motion, such as the thoracic aorta

3.3.57.2 Parameters

Turbo factor	10–599
TE variable	Yes
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, DIR
Reconstruction mode	Magnitude/Real ³⁰¹⁾
Fat suppression	Fat saturation/Water excitation
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ³⁰²⁾
Flow compensation	None/Readout
Dimension	3D

300) With NATIVE license; "NATIVE" available only for ECG or pulse trigger, "Flow sensitivity" available only if NATIVE is not off

301) May be selected only if Magn. Preparation = IR has been selected

302) Parameter cannot be freely set, depends on selected TE

Elliptical scanning	Yes
Slice resolution	Yes
Slice partial Fourier	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ³⁰³⁾
Dark blood	Yes
iPAT	Yes
iPAT ²	Yes
Respiratory control	Gate & Follow/Gate/Monitor only/Off
Restore	Yes

3.3.58 SVS_Edit

The SVS>Edit sequence is used for spectral editing. The sequence is based on the SVS_SE sequence from which it inherits most of its parameter settings.

3.3.58.1 Use

Detection and relative quantification of *J*-coupled metabolites in the brain with single-voxel spectroscopy.

3.3.58.2 Parameters

TE variable	Yes
Bandwidth variable	Yes
Water suppression	Yes

303) Only available for XT and XR gradients

Saturation regions	Regular
Phase cycling	Yes
Excitation of VOI	Yes
Water reference scan	Yes
Edit Frequency	Yes
Edit Bandwidth	Yes
Edit Mirror Frequency	Yes

3.3.59 SVS_SE

Spin-echo sequence for single-voxel spectroscopy.

3.3.59.1 Use

- Localization with three orthogonal slices
- 90°–180°–180°
- Measured signal: Full spin echo

3.3.59.2 Parameters

TE variable	Yes
Bandwidth variable	Yes
Spectral fat suppression	Yes
Saturation regions	Regular
Phase cycling	Yes
Triggering	ECG/Respiratory
Excitation of VOI	Yes

Multiple measurements	Yes
Water reference scan	Yes

3.3.60 SVS_STEAM

STEAM single-voxel spectroscopy sequence.

3.3.60.1 Use

- Localization with three orthogonal slices
- $90^\circ-90^\circ-90^\circ$
- Measured signal: Stimulated echo
- Short TEs possible
- Only half of the spin-echo signal

3.3.60.2 Parameters

TE variable	Yes
Mixing time (TM) variable	Yes
Bandwidth variable	Yes
Phase cycling	Yes
Excitation of VOI	Yes
Multiple measurements	Yes
Water reference scan	Yes

3.3.61 SVS_STEAM_Histo

Five-echo STEAM single-voxel spectroscopy sequence based on the SVS_STEAM sequence.

Advantages

- All data acquired in one breath-hold
- Accurate fat evaluation due to integrated T2 correction
- Estimation of water R2 relaxivity, which correlates with the amount of iron in the liver

3.3.61.1 Use

T2-corrected fat and iron quantification in the liver. For a detailed description, see: Operator Manual Diagnostic MR Imaging.

3.3.61.2 Parameters

TE variable	Yes
Mixing time (TM) variable	Yes
Phase cycling	Yes
Triggering	No
Excitation of VOI	Yes
Multiple measurements	5 (fixed)

3.3.62 TGSE

Ultrafast turbo gradient spin-echo sequence for high resolution imaging or extremely short measurement times.

At an EPI factor of 1 and a turbo factor >1, the sequence behaves like a TSE sequence. At a turbo factor of 1 and an EPI factor >1, the sequence behaves like a segmented EPI sequence.



Increasing the EPI factor increases the sequence's sensitivity to susceptibility, therefore distortion artifacts may increase.

3.3.62.1 Use

- T2 weighting for high-resolution neuro or ortho imaging in an acceptable measurement time (recommended EPI factor at a high turbo factor ≤ 3).
- Inversion recovery neuro imaging with magnitude or real value image display.

3.3.62.2 Recommendations

If SAR is exceeded, either the flip angle of the refocusing pulse can be reduced and/or RF pulse type **Low SAR** can be selected. A smaller flip angle (for example, approx. 150°) does not have a noticeable effect on image contrast.

3.3.62.3 Parameters

Turbo factor	1–65
EPI factor	1–21
TE variable	Yes ³⁰⁴⁾
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ³⁰⁵⁾
Fat suppression	Fat saturation
Saturation regions	Regular/Parallel
MTC	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	2D

304) Only if turbo factor = 1

305) May be selected only if Magn. Preparation = IR has been selected

RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ³⁰⁶⁾
Dark blood	Yes
Respiratory control	Breath-hold ³⁰⁷⁾

3.3.63 TGSE_ASL

Segmented turbo gradient spin-echo sequence for high resolution imaging or extremely short measurement times.

At an EPI factor of 1 and a turbo factor >1, the sequence behaves like a TSE sequence. At a turbo factor of 1 and an EPI factor >1, the sequence behaves like a segmented EPI sequence.



Increasing the EPI factor increases the sequence's susceptibility, therefore distortion artifacts may increase.

3.3.63.1 Use

For perfusion imaging in the head. Perfusion-weighted images and relCBF images are obtained. With multi-TI measurements, also images of the bolus arrival time (BAT) can be obtained.

3.3.63.2 Recommendations

To minimize image distortions due to susceptibility, select a bandwidth that enables use of minimum echo spacing.

306) Only available for XT and XR gradients

307) Multi-breath-hold possible, depending on protocol setup

3.3.63.3 Parameters

Turbo factor	1–65
EPI factor	1–127
TE variable	No ³⁰⁸⁾
Bandwidth variable	Yes
Magnetization preparation	ASL
Reconstruction mode	Magnitude
Fat suppression	Fat saturation
Saturation regions	FAIR Q2T, PCASL, None ³⁰⁹⁾
Averaging mode	Long term
Flow compensation	None
Dimension	3D
RF pulse type	Normal
Gradient mode	Fast/Normal/Performance ³¹⁰⁾
Online reconstruction	Perfusion-weighted images, relCBF images, BAT images ³¹¹⁾
Bolus duration ³¹²⁾	Variable
Inversion array size ³¹³⁾	Min. 1

3.3.64 TrueFISP

TrueFISP steady-state gradient-echo sequence.

308) TE is automatically set to the minimum value and cannot be changed

309) Parameter "Perfusion mode"

310) Only available for XT and XR gradients

311) Only available for multi-TI measurements

312) Parameter depends on TI and inversion array size

313) Maximum depends on TR and TI

3.3.64.1 Use

- T2 weighting for neuro applications, used, for example, with uncooperative patients.
- T2 weighting for breath-hold studies in the abdomen without motion artifacts.

3.3.64.2 Recommendations

Minimize TR by selecting a high readout bandwidth to avoid interference streaks in the image.

3.3.64.3 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR, SR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential
Flow compensation	None ³¹⁴⁾
Dimension	2D/3D
Elliptical scanning ³¹⁵⁾	Yes
Slice resolution ³¹⁶⁾	Yes

314) TrueFISP is essentially flow-compensated from one RF pulse to the next

315) Only if Dimension = 3D is selected

316) Only if Dimension = 3D is selected

Slice partial Fourier ³¹⁷⁾	Yes
Excitation pulses ³¹⁸⁾	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes
iPAT ^{2 319)}	Yes
Respiratory control	Breath-hold ³²⁰⁾

3.3.65 TrueFISP_FreqScout

TrueFISP sequence. Several images with an identical geometry but different offset frequency are acquired. The distance between the frequency shifts and the number of images are controlled via the parameters **Trufi delta freq.** and **Measurements**. The offset frequencies are included in the image text. A visual analysis in the image area of **MR View&GO** determines the optimal frequency. It is entered in subsequent measurements for the **Trufi delta freq.** parameter.

3.3.65.1 Use

With TrueFISP protocols in particular, it may be necessary to adjust the offset frequency based on the image to move the typical TrueFISP stripe artifacts out of the region of interest.

3.3.65.2 Parameters

Segments	Variable
TE variable	Yes
Contrasts	1

317) Only if Dimension = 3D is selected

318) Only if Dimension = 3D is selected

319) Only if Dimension = 3D is selected

320) Multi-breath-hold possible, depending on protocol setup

Bandwidth variable	Yes
Reconstruction mode	Magnitude
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Sequential/Single measurement
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ³²¹⁾
iPAT	Yes

3.3.66 TSE

Turbo spin-echo sequence offering a large range of applications.

3.3.66.1 Use

- T1, T2 weighting and Flair contrast for brain and spine imaging
- T1, PD, T2, and STIR imaging for orthopedic applications
- T2 and STIR weighting for body imaging with breath-hold or 2D PACE

3.3.66.2 Parameters

Turbo factor	1–129 ³²²⁾
TE variable	Yes
Contrasts	1–3

321) Only available for XT and XR gradients

322) At a turbo factor of 1, the sequence behaves like a spin-echo sequence

Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real ³²³⁾
Fat suppression	Fat saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes ³²⁴⁾
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None/Readout/Slice
Dimension	2D/3D
Slice resolution ³²⁵⁾	Yes
Slice partial Fourier ³²⁶⁾	Yes
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper/Performance ³²⁷⁾
Dark blood	Yes
iPAT	Yes
Simultaneous multislice (SMS)	Yes
SliceAdjust	Yes
Respiratory control	Trigger/Breath-hold ³²⁸⁾
Hyperecho	Yes

323) May be selected only if Magn. Preparation = IR has been selected

324) Parameter cannot be freely set, depends on selected TE

325) Only if Dimension = 3D is selected

326) Only if Dimension = 3D is selected

327) Only available for XT and XR gradients

328) Multi-breath-hold possible, depending on protocol setup

BLADE Trajectory	Yes
Restore	Yes
Acoustic noise reduction	Yes
WARP	Yes
VAT ³²⁹⁾	0–100%
SEMAC ³³⁰⁾	6–32
BM Motion correction	Yes

3.3.67 TSE_Dixon

TSE Dixon is a water-fat separation technique based on the 2D TSE sequence. The Dixon technique can be used as an alternative to fat saturation.

Unlike conventional SE or TSE sequences, the TSE_Dixon sequence acquires an opposed phase gradient echo in addition to the original in-phase spin echo. The echoes are obtained at the instant when the phase shift between water and lipid is “-π” and “0” respectively. After a linear combination of the images with phase correction, water and fat selective images can be computed.

Advantages:

- Up to four contrasts are possible within one measurement (in-phase, opposed phase, water, and fat images)
- Less sensitive to B0 and B1 inhomogeneities
- Improved outcome with MR Conditional implants



Please adhere to all safety instructions regarding implants. For a detailed description, see: Operator Manual MR System and Coils.

On the **Contrast/Common** parameter card, from the **Fat-Water Contrast** list: **Dixon** determines whether fat and water images are displayed separately. These additional parameters can be accessed with the [...] button to the right of the **Fat-Water Contrast** parameter.

329) Only if WARP is selected

330) Only if WARP is selected

Original Echoes	The original in-phase and opposed phase images are 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

3.3.67.1 Use

- T1, T2, and PD weighting
- Compatible with multi-coil acquisition and iPAT (GRAPPA)

3.3.67.2 Image examples

(1)



(2)



(4)



(3)



- (1) reliable fat saturation
- (2) with MR Conditional implants
- (3) fat image
- (4) water image

3.3.67.3 Parameters

Turbo factor	1–129
TE variable	Yes

Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude
Saturation regions	Regular/Parallel
MTC	Yes
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None/Readout/Slice
Dimension	2D
RF pulse type	Fast/Normal/Low SAR
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
iPAT	Yes
Simultaneous multislice (SMS)	Yes
Respiratory control	Trigger
Hyperecho	Yes
Restore	Yes

3.3.68 TSE_MDME

Turbo spin-echo sequence variant that allows you to acquire multicontrast data with multiple delay times (**MD**) after a preparation pulse and multi-echo times (**ME**).

3.3.68.1 Use

The sequence generates magnitude and phase images that can be used as input data for the postprocessing application SyMRI® of SyntheticMR AB to generate synthetic images and to perform myelin mapping.



In order to use this sequence, a license for SyMRI® must be obtained from SyntheticMR AB (available, for example, on syngo.via OpenApps or directly from SyntheticMR AB). This sequence must not be used in combination with any other software application.

Parameters	Turbo factor	5
TE variable	Yes	
Contrasts	2	
Repetitions	4 – 17	
Bandwidth variable	Yes	
Magnetization preparation	IR ³³¹⁾	
Reconstruction mode	Magnitude/Phase	
Saturation regions	Regular/Parallel	
Averaging mode	Short term/Long term	
Multi-slice mode	Interleaved	
Flow compensation	None/Readout/Slice	
RF pulse type	Fast/Normal/Low SAR	
Gradient mode	Fast/Normal/Whisper/Performance ³³²⁾	
iPAT	Yes	
Restore	Yes	

331) Parameter cannot be deselected

332) Only available for XT and XR gradients

3.3.69 TurboFLASH

Single-shot TurboFLASH sequence.

3.3.69.1 Use

- 3D TurboFLASH (= MPRAGE) for fast T1-weighted volume measurements of the head.
- 3D TurboFLASH with double inversion contrast (= MP2RAGE) for homogenous T1-weighted head imaging with high CNR and optionally T1 mapping. Activated by setting two IR contrasts.
- 2D TurboFLASH with dark blood preparation for low resolution imaging of the cardiac anatomy.
- 2D TurboFLASH combined with saturation recovery preparation for contrast enhancement studies.
- 2D TurboFLASH to determine the transit time of a test bolus as preparation for CE angiography.



The 3D TurboFLASH MP2RAGE protocols are optimized for consistent T1 mapping in the range of biological T1 values in the human tissue. Mapping of T1 values that exceed the range between 400 ms and 1800 ms becomes increasingly imprecise. T1 maps are shown with a color bar that displays the color mapping between 0 and 2000 ms according to the current window levels. Computed T1 maps, however, may contain values between 0 and 4095 ms, thus exceeding the range of the color bar.

3.3.69.2 Recommendations

To prevent saturation effects, use the **Long Term** averaging mode. All slices will then be measured sequentially for one averaging before the next averaging measures the series of slices again.

3.3.69.3 Inline quality assessment for 3D TurboFLASH measurements of the head

The Inline quality assessment provides an overall image quality rating of 3D MPRAGE brain scans optimized for brain imaging. The approach is based on a careful analysis of the air background noise distribution. The background noise appears corrupted in the presence of patient-related artifacts and renders the method primarily sensitive to subject motion. A landmark-based method is used to detect the presence of aliasing artifacts. The image quality of 3D MPRAGE volumes is rated as either "high", "to be confirmed" or "not assessed" (see section "Outputs" below). It is enabled by the **Morpho** add-in. A default protocol is available in the Siemens protocol tree (\SIEMENS\head\library\3D).

3.3.69.4 Parameters

Slice thickness	≤ 3 mm
Row and column spacing	≤ 2 mm
iPAT acceleration factor	≤ 3
In-plane matrix size	$\geq 96 \times 96$
Number of slices	≥ 64
Orientations	<p>Sagittal (phase-encoding direction):</p> <ul style="list-style-type: none"> • A>>P • P>>A <p>Coronal (phase-encoding direction):</p> <ul style="list-style-type: none"> • R>>L • L>>R

3.3.69.5 Note

In selective excitation, aliasing artifact detection is not performed. The functionality is disabled if a "Head" coil is not selected.

3.3.69.6 Outputs

The overall quality rating is displayed in the image text of the original series.

Image quality

High	For a high-quality scan
Not assessed	If quality assessment is not performed (that is, inconsistent protocol parameters, error detected during processing)
To be confirmed	If quality criteria are not fulfilled (for example, motion, aliasing artifacts, and other image degradations)

3.3.69.7 Parameters

TE variable	Min.
Contrasts	1
IR Contrasts	$2^{333})$
Bandwidth variable	Yes
Magnetization preparation	IR,SR
Reconstruction mode	Magnitude/Real ³³⁴⁾
Fat suppression	Water excitation
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	None

333) May be selected only if Magn. Preparation = IR or SR has been selected

334) May be selected only if Magn. Preparation = IR has been selected

Dimension	2D/3D
Elliptical scanning ³³⁵⁾	Yes ³³⁶⁾
Slice resolution ³³⁷⁾	Yes
Slice partial Fourier ³³⁸⁾	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper/Performance ³³⁹⁾
Dark blood	Yes
3D reordering	Standard/User-defined TTC
iPAT	Yes
Respiratory control	Trigger/Breath-hold ³⁴⁰⁾
MapIt	Yes
BM Motion correction	Yes

3.3.70 TurboFLASH_CB

2D single-shot TurboFLASH sequence.

3.3.70.1 Use

Optimized for determining arrival of bolus as preparation for contrast-enhanced angiography.

335) Only if Dimension = 3D is selected

336) Freely selectable if 3D reordering is activated

337) Only if Dimension = 3D is selected

338) Only if Dimension = 3D is selected

339) Only available for XT and XR gradients

340) Multi-breath-hold possible, depending on protocol setup

3.3.70.2 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Magnetization Preparation	IR, SR
Reconstruction mode	Magnitude/Real ³⁴¹⁾
Fat suppression	Water excitation
Phase partial Fourier	Yes
Asymmetric echo	Off/Allowed
Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	None
Dimension	2D
Excitation pulses	Slice-selective
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper/Performance ³⁴²⁾
Dark blood	Yes

3.3.71 TWIST

3D gradient-echo sequence that allows a higher temporal resolution than a standard gradient-echo sequence.

341) May be selected only if Magn. Preparation = IR or SR has been selected

342) Only available for XT and XR gradients

3.3.71.1 Use

For evaluating dynamic processes with high spatial and temporal resolution.

3.3.71.2 Recommendations

On the **Angio/Common** parameter card: The parameter **Central region A** specifies the size of the central k-space and the parameter **Sampling density B** indicates the sampling density in the peripheral region. To increase temporal resolution, reduce one of the two parameters.

3.3.71.3 Parameters

TE variable	Min.
Contrasts	1
Bandwidth variable	Yes
Reconstruction mode	Magnitude
Phase partial Fourier	Yes
Asymmetric echo	Off/Weak/Strong
Averaging mode	Short term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None
Dimension	3D
Elliptical scanning ³⁴³⁾	Yes
Slice resolution ³⁴⁴⁾	Yes
Slice partial Fourier ³⁴⁵⁾	Yes
Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR

343) Only if Dimension = 3D is selected

344) Only if Dimension = 3D is selected

345) Only if Dimension = 3D is selected

RF spoiling	On
Gradient mode	Fast/Normal/Whisper
iPAT	Yes
iPAT ²	Yes
Central region A	4–100%
Sampling density B	0–50%
Temporal interpolation	Yes
Time stamp in image	Yes

4 Measurement Parameters

4.1 General information

Siemens Service has set up routine measurement programs on your system that require minimal interactions on your part. Usually, you need to change just a few parameters prior to measurement.

The best time for you to adjust the measurement parameters of your first protocol is directly after graphic slice positioning, when your protocol is still open.

The parameter cards of the **Examination** screen contain all protocol measurement parameters, sorted by main topics. The parameter card stack is arranged from left to right to provide easy access to the cards most frequently used and processed.

- (→ Page 261 *Routine parameter card*)
- (→ Page 269 *Contrast parameter cards*)
- (→ Page 282 *Resolution parameter cards*)
- (→ Page 290 *Geometry parameter cards*)
- (→ Page 304 *System parameter cards*)
- (→ Page 315 *Physio parameter cards*)
- (→ Page 325 *Angio parameter cards*)
- (→ Page 329 *BOLD parameter card*)
- (→ Page 331 *Diff parameter card*)
- (→ Page 334 *Perf parameter card*)
- (→ Page 336 *Inline parameter cards*)
- (→ Page 349 *Sequence parameter cards*)
- (→ Page 360 *FastView parameter card*)

During routine measurements, it is usually enough to check the parameters of the **Routine** parameter card to change the field of view or other parameters that require frequent modification.

For more specialized diagnostic problems and special anatomical conditions, go to the **Contrast**, **Resolution**, **Geometry**, and **System** parameter cards. These allow you to adjust the measurement parameters to your requirements.

Depending on the sequence used for measurement, other sequence and application-specific parameter cards will be displayed.



Not all parameters are available for all sequences.

The availability of a parameter depends on the sequence, the installed licenses, and the settings of other parameters.



When a parameter option in a selection list is displayed in angle brackets <....>, other parameters must also be changed to activate the option.

Numeric values are marked red in this case.

Values marked green can be adjusted without changing any other parameter.

4.2 Routine parameter card

The **Routine** parameter card includes all important parameters of your measurement protocols. You can check and modify them during measurement preparations.

The **Routine** parameter card shows different parameters depending on whether your measurement protocol includes 2D or 3D measurements.

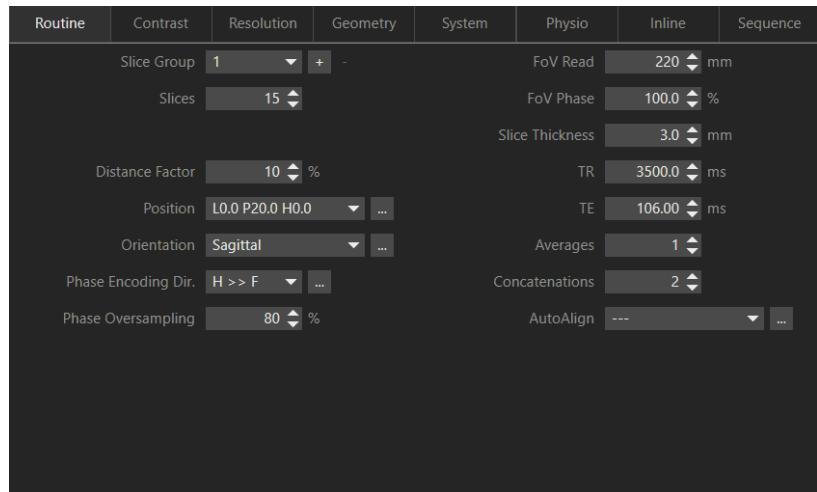
(→ Page 262 *Routine parameter card*)

(→ Page 266 *Routine parameter card - Spectroscopy SVS*)

(→ Page 267 *Routine parameter card - Spectroscopy CSI*)

4.2.1 Routine parameter card

4.2.1.1 Slice parameters for 2D measurements



Example

Slice Group	Number of the slice group currently displayed (→ Page 388 <i>Slice Group (parameter)</i>)
Slices	Number of slices in this slice group (→ Page 389 <i>Slices (parameter)</i>)
Distance Factor	Slice distance in this slice group (→ Page 389 <i>Distance Factor (parameter)</i>)
Position	Position of the slice group (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of the slice group (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)

Phase Encoding Dir.	Phase-encoding direction (→ Page 391 <i>Phase Encoding Dir. (parameter)</i>) The angle of slice rotation can also be set in a dialog box. (→ Page 366 <i>Inplane Rotation dialog box</i>)
Phase Oversampling	Expands the FOV in the phase-encoding direction (→ Page 392 <i>Phase Oversampling (parameter)</i>)
Slice Thickness	Thickness of the individual slices (→ Page 390 <i>Slice Thickness (parameter)</i>)

4.2.1.2 Slab parameters for 3D measurements

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
Slab Group	1	+ -		FoV Read	200	mm	
Slabs	1			FoV Phase	100.0	%	
Slices per Slab	52			Slice Thickness	0.8	mm	
Distance Factor	50	%		TR	8000.0	ms	
Position	Isocenter	...		TE	245.00	ms	
Orientation	Coronal	...		Averages	1		
Phase Encoding Dir.	F >> H	...		Concatenations	1		
Phase Oversampling	100	%		AutoAlign	---		
Slice Oversampling	15.4	%					

Example

Slab Group	Number of the slab group currently displayed (→ Page 393 <i>Slab Group (parameter)</i>)
Slabs	Number of slabs in this group (→ Page 393 <i>Slabs (parameter)</i>)

Slices per Slab	Number of slices (partitions) per slab (→ Page 394 <i>Slices per Slab (parameter)</i>)
Distance Factor	Distance of slabs in the slab group (→ Page 389 <i>Distance Factor (parameter)</i>)
Position	Position of slab group (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of the slab group (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Phase Encoding Dir.	Phase-encoding direction (→ Page 391 <i>Phase Encoding Dir. (parameter)</i>) The angle of slice rotation can also be set in a dialog box. (→ Page 366 <i>Inplane Rotation dialog box</i>)
Phase Oversampling	Expand the FOV in the phase-encoding direction (→ Page 392 <i>Phase Oversampling (parameter)</i>)
Slice Oversampling	Expand the FOV in the slice-selection direction (→ Page 392 <i>Slice Oversampling (parameter)</i>)
Slice Thickness	Slice thickness (partitions) of the slabs (→ Page 390 <i>Slice Thickness (parameter)</i>)

4.2.1.3 Parameters for image resolution and contrast

FoV Read	Field of view in readout direction (→ Page 394 <i>FoV Read, FoV Phase (parameter)</i>)
FoV Phase	Field of view in phase-encoding direction (→ Page 394 <i>FoV Read, FoV Phase (parameter)</i>)

TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)
TE	Echo time (→ Page 396 <i>TE (parameter)</i>)
Averages	Number of averages in a measurement (→ Page 397 <i>Averages (parameter)</i>)
Filter	Display of the selected filter You can set the filters on the Resolution/Filter parameter card.

4.2.1.4 Parameters for monitoring the excitation sequence

Concatenations	Display of the selected concatenations (→ Page 397 <i>Concatenations (parameter)</i>)
Breath-holds	Number of breath-holds Displayed instead of Concatenations when Resp. Control option Breath-hold is selected. (→ Page 397 <i>Concatenations (parameter)</i>)

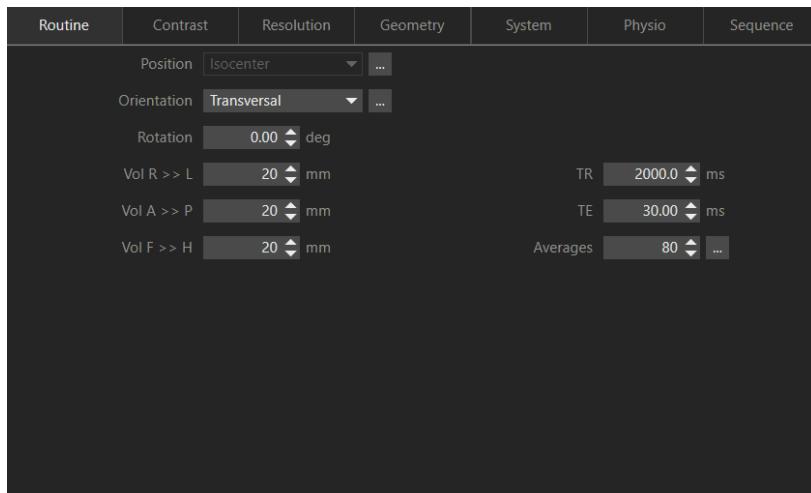
4.2.1.5 AutoAlign

AutoAlign	Adjust the AutoAlign orientation (→ Page 398 <i>AutoAlign (parameter)</i>) (→ Page 367 <i>AutoAlign dialog box</i>)
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4.2.1.6 Coils

Coil Elements	Display of the selected coils and coil elements You set the coils on the System/Coils parameter card.
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4.2.2 Routine parameter card - Spectroscopy SVS



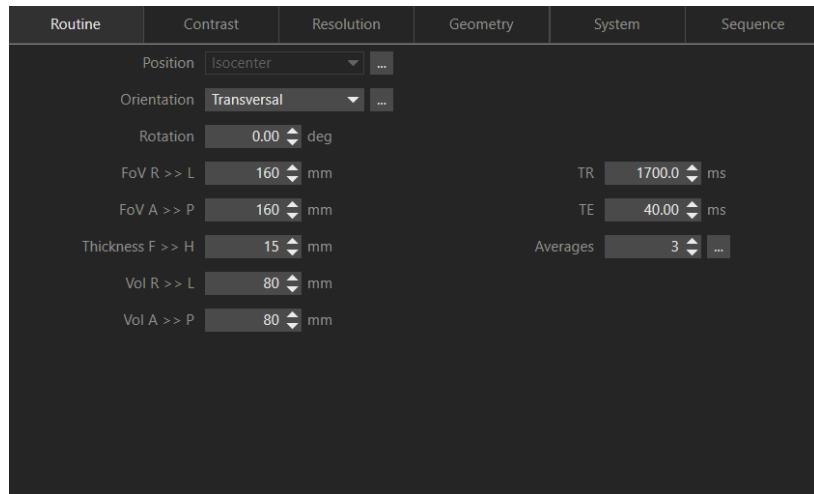
Example

For a Spectroscopy SVS measurement protocol, the following parameters are shown on the **Routine** parameter card:

Position	Position of the measurement volume (VOI) (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of the measurement volume (VOI) (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)

Rotation	"In-plane" angle of rotation (→ Page 399 <i>Rotation (parameter)</i>)
Vol ...	Extent of the measurement volume (VOI) (→ Page 399 <i>VOI parameters</i>)
TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)
TE	Echo time (→ Page 396 <i>TE (parameter)</i>)
Averages	Number of averages in a measurement (→ Page 397 <i>Averages (parameter)</i>)
Coil Elements	Display of the selected coils and coil elements You set the coils on the System/Coils parameter card.

4.2.3 Routine parameter card - Spectroscopy CSI



Example

For a Spectroscopy CSI measurement protocol, the following parameters are shown on the **Routine** parameter card depending on the dimension (2D or 3D measurement):

Position	Common position of the CSI slice and VOI (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Common orientation of the CSI slice and VOI (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Rotation	Common "in-plane" rotation of the CSI slice and VOI (→ Page 399 <i>Rotation (parameter)</i>)
FoV ...	Size of Field of View (→ Page 400 <i>FOV parameters</i>)
Thickness ...	CSI slice thickness (→ Page 400 <i>Thickness .. parameters</i>)
Vol ...	Extent of the VOI (→ Page 400 <i>VOI parameters - Spectroscopy</i>)
Slices	For 2D CSI measurements: Number of slices in this slice group (→ Page 389 <i>Slices (parameter)</i>)
TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)
TE	Echo time (→ Page 396 <i>TE (parameter)</i>)

Averages	Number of averages in a measurement (→ Page 397 <i>Averages (parameter)</i>)
Coil Elements	Displays the selected coils and coil elements You set the coils on the System/Coils parameter card.

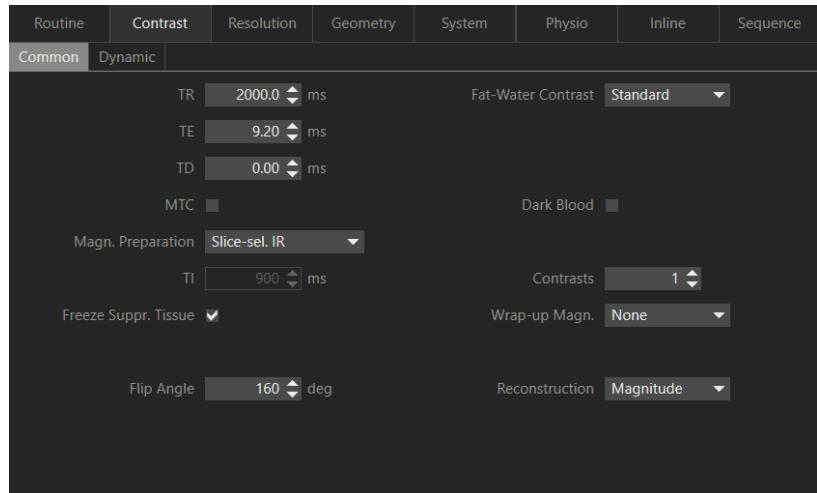
4.3 Contrast parameter cards

The **Contrast** parameter cards include all parameters you can use to influence image contrast for an MR measurement.

The **Contrast** parameter card is divided into the following subcards:

- The **Common** subcard allows you to adjust the sequence parameters.
(→ Page 270 *Contrast/Common parameter card*)
(→ Page 274 *Contrast/Common parameter card - Spectroscopy*)
- The **Dynamic** subcard allows you to set parameters for dynamic image evaluation.
(→ Page 276 *Contrast/Dynamic or Angio/Dynamic parameter card*)
- The **ASL** subcard allows you to adjust parameters for perfusion sequences.
(→ Page 278 *Contrast/ASL parameter card*)

4.3.1 Contrast/Common parameter card



Example

4.3.1.1 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.

TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)
TE	Echo time (→ Page 396 <i>TE (parameter)</i>)
TD	Time after delay (perfusion/diffusion time)

Flip Angle Mode	Change of the refocusing flip angle along the echo train (→ Page 512 <i>Flip Angle Mode (parameter)</i>) (→ Page 381 <i>Organ under Examination dialog box</i>)
Flip Angle	Flip angle (→ Page 401 <i>Flip Angle (parameter)</i>)

4.3.1.2 Spin preparation

The actual measurement is preceded by an RF pulse (spin preparation) when you want to change the contrast or suppress certain signals (for example, for an inversion recovery sequence).

Magn. Preparation	Magnetization preparation (→ Page 401 <i>Magn. Preparation (parameter)</i>) (→ Page 382 <i>Inversion Pulse Settings dialog box</i>)
IR Contrast, SR Contrast	Enable multiple contrasts with different times for inversion recovery (IR) or saturation recovery (SR) (→ Page 382 <i>Inversion Pulse Settings dialog box</i>)
T2 Prep. Duration	Duration of the T2 preparation pulse (→ Page 403 <i>T2 prep. Duration (parameter)</i>)
TI	Inversion time (→ Page 404 <i>TI (parameter)</i>)

4.3.1.3 Signal increase

Wrap-up Magn.	Accelerated relaxation of longitudinal magnetization or destruction of remaining magnetization (→ Page 404 <i>Wrap-up Magn. (parameter)</i>)
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4.3.1.4 Signal suppression

The MR signal comprises the sum of signals from water and fat protons. Artifacts can be produced by the chemical shift. Motion artifacts can be displayed more intensely, which negatively impacts contrast.

Signal suppression may reduce or prevent these effects.

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

Fat-Water Contrast	Suppression of the fat or water signal (→ Page 405 <i>Fat-Water Contrast (parameter)</i>) (→ Page 373 <i>Fat Suppression Optimization dialog box</i>) (→ Page 374 <i>Dixon dialog box</i>)
Dark Blood	Display blood dark in the image (→ Page 465 <i>Dark Blood (parameter)</i>) (→ Page 370 <i>Dark Blood Pulse Settings dialog box</i>)
Blood Suppression	Provide presets for blood suppression (→ Page 408 <i>Blood Suppression (parameter)</i>) (→ Page 371 <i>Blood Suppression dialog box</i>)
MTC	Magnetization transfer (→ Page 408 <i>MTC (parameter)</i>)
SWI	Activate the reconstruction of susceptibility-weighted images. It highlights susceptibility constants in brain tissue.
Lines per Shot	Rows acquired in a single shot (→ Page 408 <i>Lines Per Shot (parameter)</i>)

Freeze Suppr. Tissue	Automatic calculation of TI based on TR (→ Page 409 <i>Freeze Suppr. Tissue (parameter)</i>)
Minimize Inflow	Minimize the effect of inflowing body fluid. (→ Page 409 <i>Minimize Inflow (parameter)</i>)

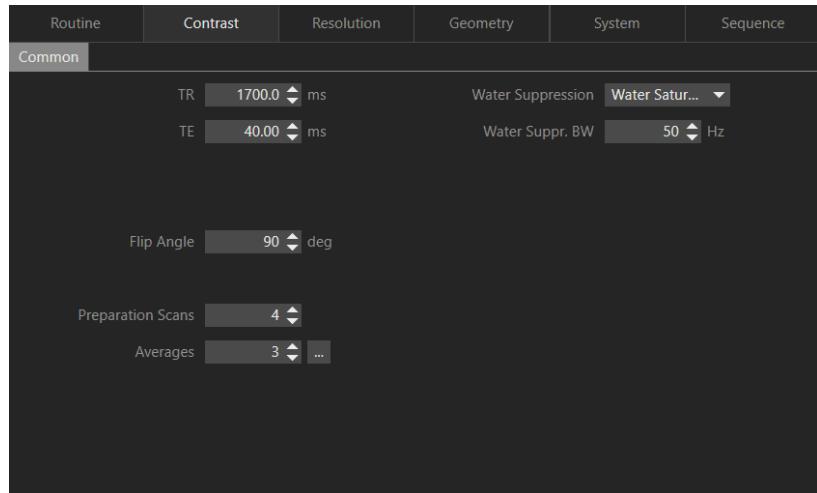


For some types of sequences, the **Geometry/Saturation** parameter card contains the **Saturation Mode** parameter. If you have selected the **Quick** option for this parameter, the settings for fat and water saturation will change to **Q-fat sat.** or **Q-water sat.**

4.3.1.5 Miscellaneous

Reordering	Acquisition sequence of raw data (→ Page 503 <i>Reordering (parameter)</i>)
Original echoes	Save the unprocessed images in the database as well.

4.3.2 Contrast/Common parameter card - Spectroscopy



Example

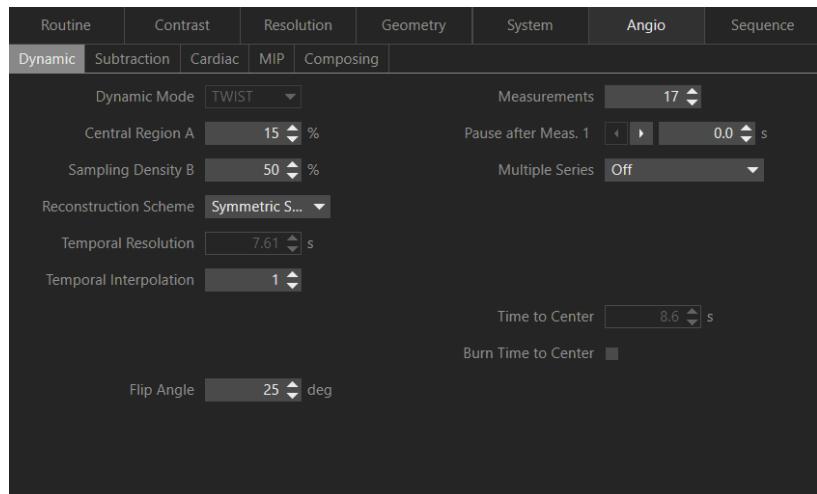
For a spectroscopy measurement protocol, the following parameters are shown on the **Contrast** parameter card:

TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)
TE	Echo time (→ Page 396 <i>TE (parameter)</i>)
TM	Mix time (STEAM sequences only) (→ Page 409 <i>TM (parameter)</i>)
Pulse Type	Radio frequency pulse type. Only available in FID sequence with multinuclear license. (→ Page 510 <i>RF Pulse Type (parameter)</i>)
Pulse Duration	Duration of excitation RF pulse. Only available in FID sequence with multinuclear license.
Flip Angle	Flip angle of excitation pulse (→ Page 401 <i>Flip Angle (parameter)</i>)

Preparation Scans	Preliminary measurements (→ Page 498 <i>Preparation Scans (parameter)</i>)
Averages	Number of averages in a measurement (→ Page 397 <i>Averages (parameter)</i>) (→ Page 369 <i>Averaging Details dialog box</i>)
Water Suppression	Suppression of the water signal (→ Page 410 <i>Water Suppression (parameter)</i>)
Water Suppr. BW	Bandwidth of the RF pulses for water suppression (→ Page 411 <i>Water Suppr. BW (parameter)</i>)
Spectral Suppr.	Mode for spectral signal suppression (for SE sequences only) (→ Page 411 <i>Spectral Suppr. (parameter)</i>)
Lipid Suppr. BW	Bandwidth of the fat suppression pulse (for SE sequences only) (→ Page 411 <i>Lipid Suppr. BW (parameter)</i>)
Lipid s. Delta Pos.	Spectral shift of the fat suppression pulse (for SE sequences only) (→ Page 412 <i>Lipid s. Delta pos. (parameter)</i>)
Water s. BW	Bandwidth of the water suppression pulse (for SE sequences only) (→ Page 412 <i>Water s. BW (parameter)</i>)
Water s. Delta Pos.	Spectral shift of the water suppression pulse (for SE sequences only) (→ Page 412 <i>Water s. Delta Pos. (parameter)</i>)
Edit Frequency	Spectral editing (for SVS_Edit sequence only): Position of the spectral editing pulses

Edit Bandwidth	Spectral editing (for SVS_Edit sequence only): Bandwidth of the spectral editing pulses
Edit Mirror Frequency	Spectral editing (for SVS_Edit sequence only): Mirror frequency of the spectral editing pulses For a detailed description of spectral editing, see: Operator Manual Diagnostic MR Imaging

4.3.3 Contrast/Dynamic or Angio/Dynamic parameter card



Example

The **Dynamic** subcard allows you to set parameters for dynamic image evaluation.

Dynamic Mode	Selection of the dynamic mode (→ Page 401 <i>Dynamic Mode (parameter)</i>)
Liver Workflow	Switch on/off liver workflow including liver auto bolus detection option and dynamic phase labeling
Liver auto bolus detection	Switch on/off liver auto bolus detection

Central Region A	Size of the k-space center with full resolution (→ Page 418 <i>Central Region A (parameter)</i>)
Phases	Number of Compressed Sensing GRASP-VIBE phases (GRASP=Golden-Angle Radial Sparse Parallel MRI)
Sampling Density B	Resolution of outer k-space area (→ Page 418 <i>Sampling Density B (parameter)</i>)
Duration	Duration for the dynamic phases
Reconstruction Scheme	Method for dynamic reconstruction of the k-space (→ Page 471 <i>Reconstruction Scheme (parameter)</i>)
Temporal Resolution / Virt. Temporal Resolution	Time between two MIP images in sequence (→ Page 475 <i>Temporal Resolution/Virt. Temporal Resolution (parameter)</i>)
Reconstructed Volumes	Number of reconstructed volumes for the corresponding Compressed Sensing GRASP-VIBE phase
Temporal Interpolation	Linear interpolation of the image data (→ Page 475 <i>Temporal Interpolation (parameter)</i>)
Delay After Bolus	The reconstruction of the reconstructed volumes for the arterial phase will start after this time after bolus detection.
Flip Angle	Flip angle (→ Page 401 <i>Flip Angle (parameter)</i>)
Measurements	Number of measurements (→ Page 412 <i>Measurements (parameter)</i>)
Pause after Meas.	Pause between measurements (→ Page 413 <i>Pause after Meas. (parameter)</i>)
Delay in TR	Time between consecutive volumes for all ep2d sequences (→ Page 414 <i>Delay in TR (parameter)</i>)

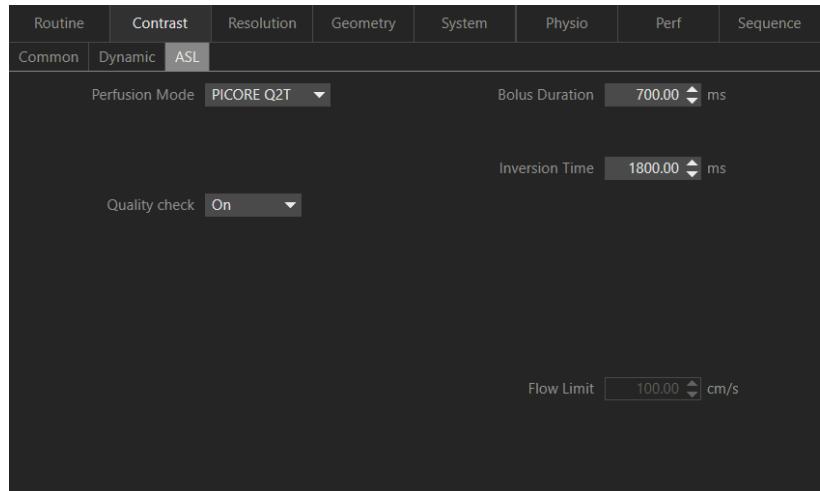
Multiple Series	Save every measurement as a separate series. (→ Page 415 <i>Multiple Series (parameter)</i>)
3D Reordering	Center of raw data space is measured as quickly as possible (→ Page 473 <i>3D Reordering (parameter)</i>)
Time to Center	Time until k-space center is reached (→ Page 474 <i>Time to Center (parameter)</i>)
Reordering	Acquisition sequence of raw data (→ Page 503 <i>Reordering (parameter)</i>)
Preview	Switch on/off the reconstruction for the dynamic Compressed Sensing GRASP-VIBE preview
Burn Time to Center	Writes the value of Time to center of k-space in the image text (→ Page 474 <i>Burn Time to Center (parameter)</i>)
Reconstruction	Selection of the Compressed Sensing GRASP-VIBE reconstruction mode

4.3.4 Contrast/ASL parameter card

Arterial Spin Labeling (ASL) is supported to measure cerebral perfusion and relative cerebral blood flow (relCBF).

Perfusion Mode	ASL perfusion preparation (→ Page 415 <i>Perfusion Mode (parameter)</i>)
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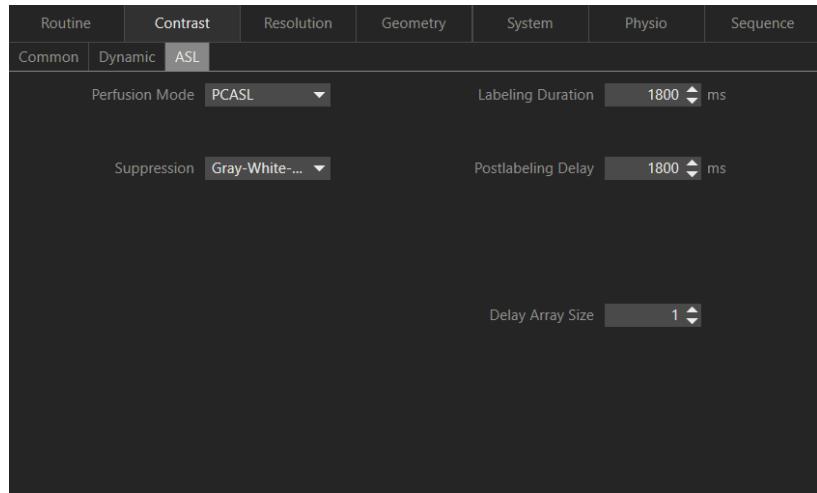
4.3.4.1 Pulsed Arterial Spin Labeling (PASL)



Example

Quality check	Activate the inline image quality check (→ Page 416 <i>Quality check (parameter)</i>)
Bolus Duration	Duration after labeling/control pulse in which blood can enter the imaging volume
Inversion Time	Duration between labeling/control pulse and start of image acquisition
Flow Limit	Weakening of the signal from major arteries (2D sequence only) (→ Page 416 <i>Flow Limit (parameter)</i>)
Inversion Array Size	Size of inversion array to be measured in the sequence (3D sequence only)

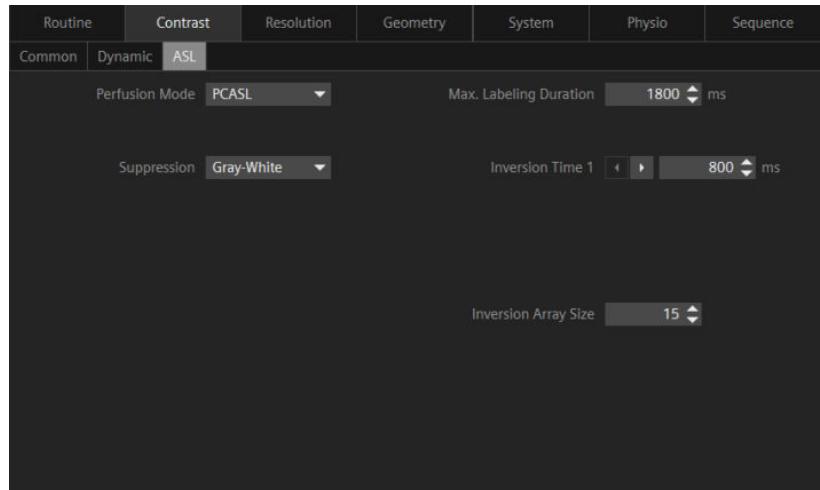
4.3.4.2 Pseudo-Continuous Arterial Spin Labeling (PCASL)



Example

Suppression	Background suppression reduces the signal from tissue spins but preserves the perfusion signal
Labeling Duration	Duration of the pseudo-continuous labeling pulse train
Postlabeling Delay	Duration(s) between end of labeling train and start of image acquisition
Delay Array Size	Number of different postlabeling delay times to be measured by the sequence

4.3.4.3 Multiple-TI Arterial Spin Labeling (Multi-TI ASL)



Example

The displayed parameters depend on the selected **Perfusion Mode** parameter.

Perfusion Mode	Displayed parameters	
FAIR Q2T	Bolus Duration	Maximum duration between the labeling/control pulse and the bolus termination pulses
	Inversion Time	Duration between labeling/control pulse and start of image acquisition
	Inversion Array Size	Number of different inversion times to be measured by the sequence
PCASL	Max. Labeling Duration	Maximum duration of the pseudo-continuous labeling pulse train
	Inversion Time	Duration between start of labeling train and start of image acquisition (inversion time = labeling duration + postlabeling delay)
	Inversion Array Size	Number of different inversion times to be measured by the sequence

4.4 Resolution parameter cards

The image resolution lets you determine the size and the level of detail shown by the images calculated from raw data. However, please remember, the higher the image resolution, the longer the acquisition time.

The **Resolution** parameter card is divided into the following subcards:

- The **Common** subcard allows you to adjust parameters affecting image resolution.
(→ Page 282 *Resolution/Common parameter card*)
(→ Page 285 *Resolution/Common parameter card - Spectroscopy*)
- The **Acceleration** subcard allows you to adjust parameters for the acceleration mode.
(→ Page 287 *Resolution/Acceleration parameter card*)
- The **Filter** subcard allows you to adjust parameters for filtering of raw data.
(→ Page 289 *Resolution/Filter parameter card*)

4.4.1 Resolution/Common parameter card

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
Common	Acceleration	Filter					
FoV Read	180	mm					
FoV Phase	100.0	%					
Slice Thickness	3.0	mm					
Base Resolution	256						
Phase Resolution	85	%					
Interpolation <input checked="" type="checkbox"/>							

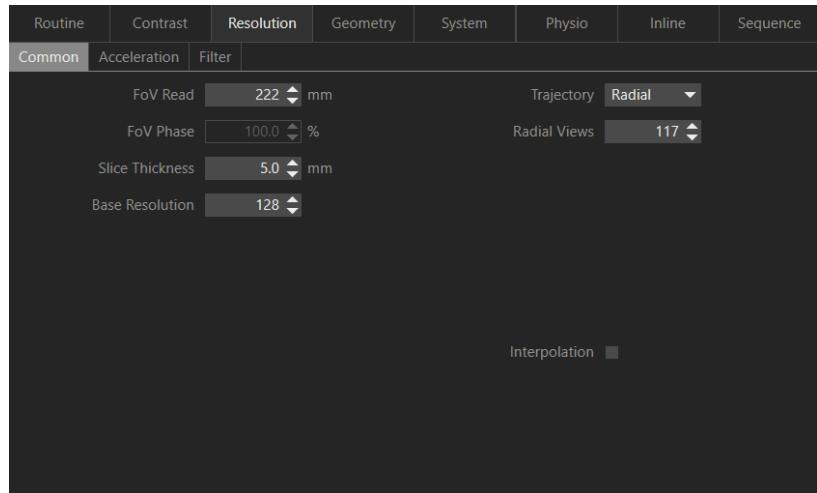
Example

All parameters affecting image resolution are located on the **Resolution/Common** parameter card.

The **Resolution/Common** parameter card differs for 2D and 3D measurements.

FoV Read	Field of View (FOV) in the readout direction (→ Page 394 <i>FoV Read, FoV Phase (parameter)</i>)
FoV Phase	Field of view (FOV) in the phase-encoding direction (→ Page 394 <i>FoV Read, FoV Phase (parameter)</i>)
Slice Thickness	Thickness of the individual slices or slice thickness (partitions) of the slabs (→ Page 390 <i>Slice Thickness (parameter)</i>)
Base Resolution	Number of readout steps (→ Page 416 <i>Base Resolution (parameter)</i>)
Phase Resolution	Ratio of phase-encoding to readout steps (→ Page 417 <i>Phase Resolution (parameter)</i>)
Slice Resolution	Resolution ratio in slice selection direction (→ Page 419 <i>Slice Resolution (parameter)</i>)
Interpolation	Double the size of the image matrix by interpolation. (→ Page 423 <i>Interpolation (parameter)</i>)

4.4.1.1 Cartesian/Radial/Spiral measurements

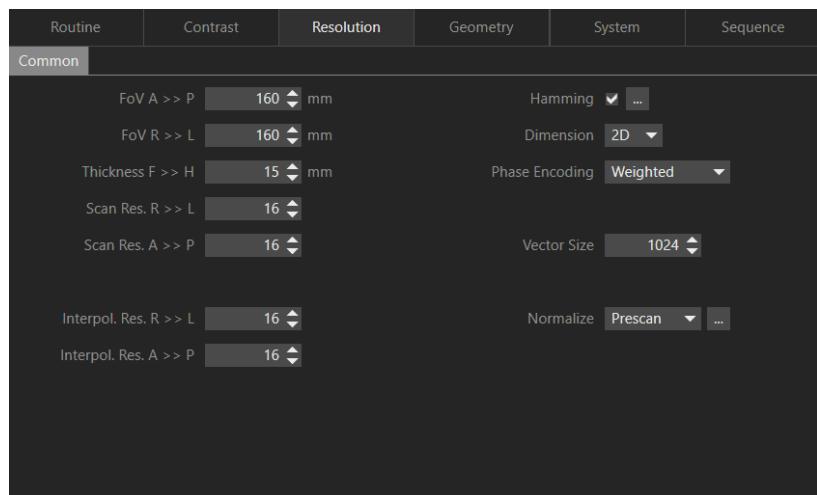


Example

Trajectory	Geometric form of k-space sampling (→ Page 420 <i>Trajectory (parameter)</i>)
Radial Views	Number of radial lines for k-space sampling (→ Page 421 <i>Radial Views (parameter)</i>)
BLADE Coverage	Number of radial blades for k-space sampling (→ Page 422 <i>BLADE Coverage (parameter)</i>)
Radial Interleaves	Number of required TR intervals (→ Page 422 <i>Radial Interleaves (parameter)</i>)
Spiral Interleaves	Number of interleaves for spiral sequences (→ Page 423 <i>Spiral Interleaves (parameter)</i>)

Motion Scan	Acquire respiratory self-gated data Only available if the Trajectory is defined as Radial .
Number of Bins	Defines the number of respiratory states into which the acquired radial views are grouped. A minimum of two bins is required and up to ten bins are allowed. Only available if the Motion Scan check box is selected.

4.4.2 Resolution/Common parameter card - Spectroscopy

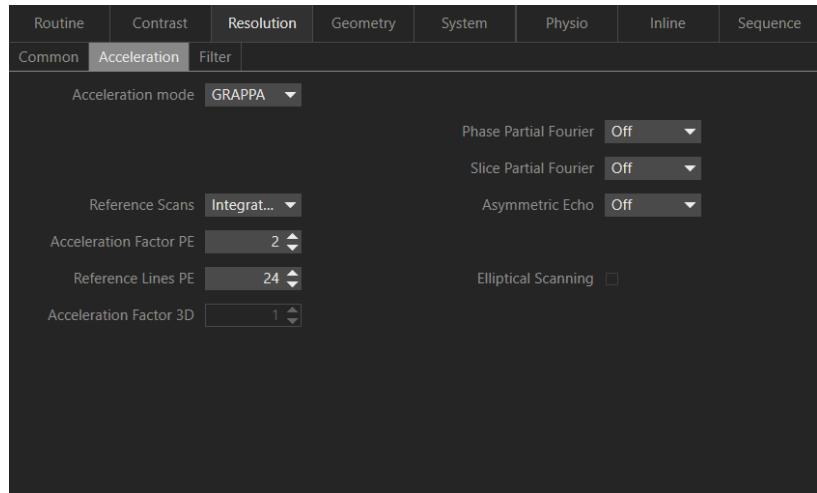


Example

For a spectroscopy measurement protocol, the following parameters are shown on the **Resolution/Common** parameter card depending on the measurement method (SVS or CSI) and the dimension (2D or 3D measurement):

FoV ...	Size of Field of View (→ Page 400 <i>FOV parameters</i>)
Thickness ...	CSI slice thickness (→ Page 400 <i>Thickness .. parameters</i>)
Scan Res. ...	Number of phase- encoding steps in the spatial directions of the slice/slab (→ Page 424 <i>Scan Res. (parameters)</i>)
Interpol. Res. ...	Number of reconstructed spectra in the spatial directions of the slice/slab (→ Page 425 <i>Interpol. Res. (parameters)</i>)
Hamming	Activate the Hamming filter (→ Page 425 <i>Hamming (parameter)</i>) (→ Page 378 <i>Filter Hamming dialog box</i>)
Dimension	Set 2D or 3D measurement. (→ Page 502 <i>Dimension (parameter)</i>)
Phase Encoding	Selection of a phase encoding type (→ Page 502 <i>Phase Encoding (parameter)</i>)
Vector Size	Number of data points (resolution) in spectral direction (→ Page 424 <i>Vector Size (parameter)</i>)
Normalize	Normalization filter (→ Page 431 <i>Normalize (parameter)</i>) (→ Page 379 <i>Normalize Filter Settings dialog box</i>)

4.4.3 Resolution/Acceleration parameter card



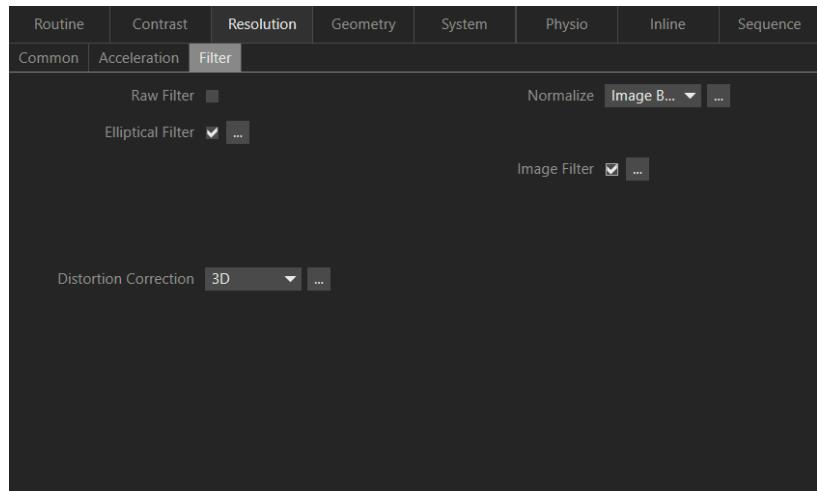
Example

Acceleration mode	Acceleration mode (→ Page 426 <i>Acceleration mode (parameter)</i>) (→ Page 385 <i>CS Reconstruction dialog box</i>)
Total Factor	Total acceleration factor (→ Page 428 <i>Total Factor (parameter)</i>)
Reference Scans	Measurement method of the reference lines (→ Page 429 <i>Reference Scans (parameter)</i>)
Acceleration Factor PE	Acceleration factor in the phase-encoding direction (→ Page 427 <i>Acceleration Factor PE (parameter)</i>)
Reference Lines PE	Number of reference lines in the phase-encoding direction (→ Page 428 <i>Reference Lines PE (parameter)</i>)
Accel. Factor 3D	Acceleration factor in the slice-selection direction (→ Page 428 <i>Accel. Factor 3D (parameter)</i>)

SMS Factor	Number of simultaneously excited slices for simultaneous multi slice (SMS) imaging. Higher factors require high density coils to separate the signals from slices.
Ref. Lines 3D	Number of reference lines in the slice selection direction (→ Page 428 <i>Ref. Lines 3D (parameter)</i>)
FOV shift factor	FOV shift factor
Reordering shift 3D	Set the reordering shift for CAIPIRINHA mode. (→ Page 426 <i>Acceleration mode (parameter)</i>)
Phase Partial Fourier	Asymmetric sampling of k-space in the phase-encoding direction (→ Page 417 <i>Phase Partial Fourier (parameter)</i>)
Slice Partial Fourier	Asymmetric sampling of k-space in the slice selection direction (→ Page 419 <i>Slice Partial Fourier (parameter)</i>)
Asymmetric Echo	Asymmetry of echo in the readout direction (→ Page 504 <i>Asymmetric Echo (parameter)</i>)
Readout partial Fourier	Reduce the number of shots that are required to generate an image.
Elliptical Scanning	Elliptical k-space sampling (→ Page 503 <i>Elliptical Scanning (parameter)</i>)
Readout Segments	Number of segments in the readout direction for multi-shot, readout-segmented sequences

CAIPIRINHA mode	Set optimized values to reach a total PAT factor. (→ Page 430 <i>CAIPIRINHA mode (parameter)</i>)
Advanced Reconstruction	Advanced reconstruction options (for TSE sequence only). (→ Page 430 <i>Advanced Reconstruction (parameter)</i>) (→ Page 386 <i>Deep Resolve dialog box</i>)

4.4.4 Resolution/Filter parameter card



Example

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. (→ Page 376 <i>Filter Raw dialog box</i>)
Elliptical Filter	With the elliptical filter, you only use the center of the raw data space. (→ Page 375 <i>Filter Elliptical dialog box</i>)

Distortion Correction	Activate 2D or 3D distortion correction (→ Page 433 <i>Distortion Correction (parameter)</i>) (→ Page 372 <i>Distortion Correction dialog box</i>)
Normalize	Normalization filter (→ Page 431 <i>Normalize (parameter)</i>) (→ Page 379 <i>Normalize Filter Settings dialog box</i>)
POCS	Projection Onto Convex Sets: It improves edge sharpness during partial Fourier sampling. (→ Page 425 <i>POCS (parameter)</i>)
Image Filter	Set filters for edge enhancement and smoothing (→ Page 377 <i>Image Filter Settings dialog box</i>)

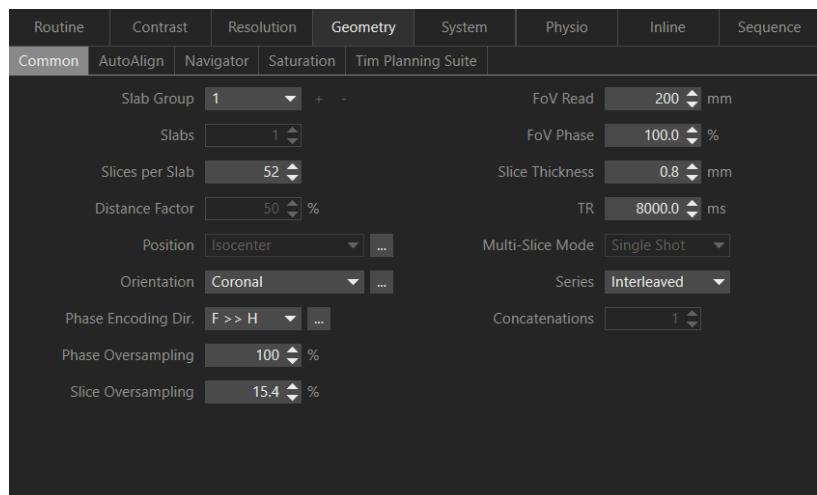
4.5 Geometry parameter cards

The **Geometry** parameter card is divided into the following subcards:

- The **Common** subcard allows you to adjust parameters pertaining to the position and size of the slices or slabs to be measured (may be different for 2D and 3D measurements).
 - (→ Page 291 *Geometry/Common parameter card*)
 - (→ Page 295 *Geometry/Common parameter card - Spectroscopy SVS*)
 - (→ Page 296 *Geometry/Common parameter card - Spectroscopy CSI*)
- The **AutoAlign** subcard allows you to adjust parameters for automatic alignment.
 - (→ Page 298 *Geometry/AutoAlign parameter card*)
- The **Navigator** subcard allows you to adjust parameters for navigator objects.
 - (→ Page 299 *Geometry/Navigator parameter card*)

- The **Tim Planning Suite** subcard allows you to adjust parameters for planning and evaluating multi-slice measurements.
(→ Page 300 *Geometry/Tim Planning Suite parameter card*)
- The **Saturation** subcard allows you to adjust the parameters that are relevant for planning saturation regions and/or fat saturation or water saturation.
(→ Page 302 *Geometry/Saturation parameter card*)

4.5.1 Geometry/Common parameter card



Example

The **Routine** examination mode is used to plan the position and orientation of slice and slab groups, using the positioning toolbar and the mouse.

If these tools do not meet the needs of your special task, additional options are available on the **Geometry/Common** parameter card.

The **Geometry/Common** parameter card differs for 2D and 3D measurements.

4.5.1.1 Slice parameters for 2D measurements

Slice Group	Number of the slice group currently displayed (→ Page 388 <i>Slice Group (parameter)</i>)
Slices	Number of slices in this slice group (→ Page 389 <i>Slices (parameter)</i>)
Distance Factor	Slice distance in this slice group (→ Page 389 <i>Distance Factor (parameter)</i>)
Slice Thickness	Thickness of the individual slices (→ Page 390 <i>Slice Thickness (parameter)</i>)
Position	Position of the slice group (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of the slice group (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Phase Encoding Dir.	Phase-encoding direction (→ Page 391 <i>Phase Encoding Dir. (parameter)</i>) The angle of slice rotation can also be set in a dialog box. (→ Page 366 <i>Inplane Rotation dialog box</i>)
Phase Oversampling	Expands the FOV in the phase-encoding direction (→ Page 392 <i>Phase Oversampling (parameter)</i>)

4.5.1.2 Slab parameters for 3D measurements

Slab Group	Number of the slab group currently displayed (→ Page 393 <i>Slab Group (parameter)</i>)
Slabs	Number of slabs in this group (→ Page 393 <i>Slabs (parameter)</i>)
Slices per Slab	Number of slices (partitions) per slab (→ Page 394 <i>Slices per Slab (parameter)</i>)
Distance Factor	Distance of slabs in the slab group (→ Page 389 <i>Distance Factor (parameter)</i>)
Slice Thickness	Slice thickness (partitions) of the slabs (→ Page 390 <i>Slice Thickness (parameter)</i>)
Position	Position of slab group (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of the slab group (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Phase Encoding Dir.	Phase-encoding direction (→ Page 391 <i>Phase Encoding Dir. (parameter)</i>) The angle of slice rotation can also be set in a dialog box. (→ Page 366 <i>Inplane Rotation dialog box</i>)
Phase Oversampling	Expand the FOV in the phase-encoding direction. (→ Page 392 <i>Phase Oversampling (parameter)</i>)
Slice Oversampling	Expand the FOV in the slice-selection direction. (→ Page 392 <i>Slice Oversampling (parameter)</i>)

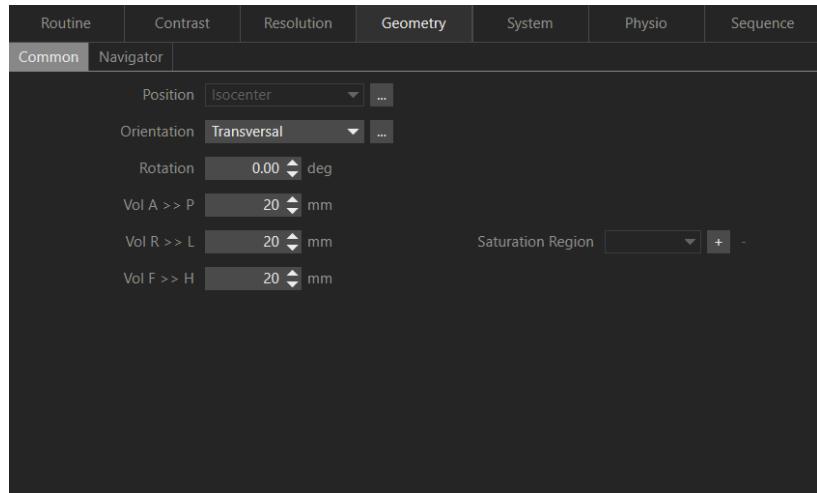
4.5.1.3 Parameters for extending the measuring range

FoV Read	Field of View (FOV) in the readout direction (→ Page 394 <i>FoV Read, FoV Phase (parameter)</i>)
FoV Phase	Field of view (FOV) in the phase-encoding direction (→ Page 394 <i>FoV Read, FoV Phase (parameter)</i>)
TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)

4.5.1.4 Parameters for monitoring the excitation sequence

Multi-Slice Mode	Method for multislice measurements (→ Page 433 <i>Multi-Slice Mode (parameter)</i>)
Series	Excitation sequence of slices (→ Page 434 <i>Series (parameter)</i>)
Concatenations	Number of concatenations (→ Page 397 <i>Concatenations (parameter)</i>)

4.5.2 Geometry/Common parameter card - Spectroscopy SVS



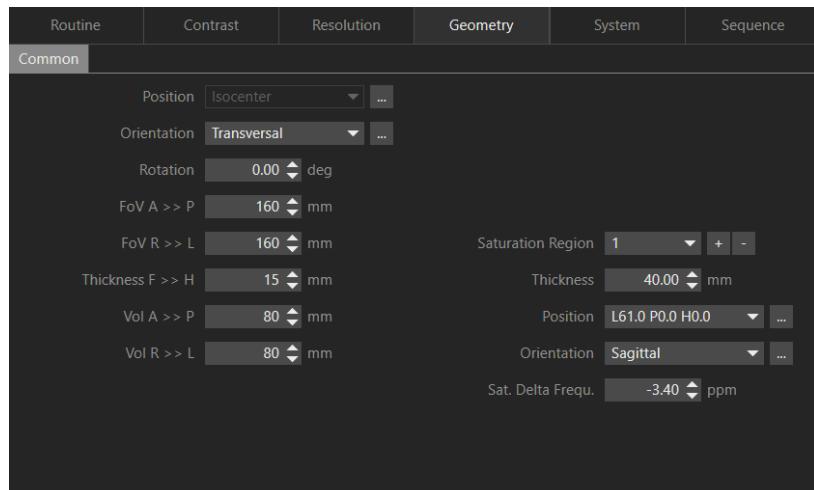
Example

For an SVS measurement protocol, the following parameters are shown on the **Geometry/Common** parameter card:

Position	Position of the measurement volume (VOI) (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of the measurement volume (VOI) (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Rotation	"In-plane" angle of rotation (→ Page 399 <i>Rotation (parameter)</i>)
Vol R ...	Extent of the measurement volume (VOI) (→ Page 399 <i>VOI parameters</i>)
Saturation Region	Number of the currently selected saturation region (→ Page 441 <i>Saturation Region (parameter)</i>)

Thickness	Thickness of the currently selected saturation region (→ Page 441 <i>Saturation Region (parameter)</i>)
Position	Position of the currently selected saturation region (→ Page 441 <i>Saturation Region (parameter)</i>)
Orientation	Orientation of the currently selected saturation region (→ Page 441 <i>Saturation Region (parameter)</i>)
Sat. Delta Frequ.	Frequency shift of the saturation pulse (→ Page 436 <i>Sat. Delta Frequ. (parameter)</i>)

4.5.3 Geometry/Common parameter card - Spectroscopy CSI



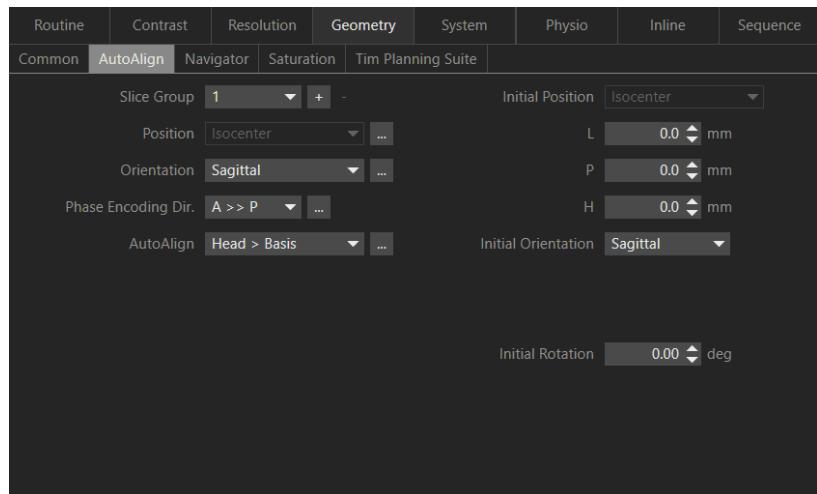
Example

For a CSI measurement protocol, the following parameters are shown on the **Geometry/Common** parameter card depending on the dimension (2D or 3D measurement):

Position	Common position of the CSI slice and VOI (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Common orientation of the CSI slice and VOI (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Rotation	Common "in-plane" rotation of the CSI slice and VOI (→ Page 399 <i>Rotation (parameter)</i>)
FoV ...	Size of Field of View (→ Page 400 <i>FOV parameters</i>)
Thickness ...	CSI slice thickness (→ Page 400 <i>Thickness .. parameters</i>)
Vol ...	Extent of the VOI (→ Page 400 <i>VOI parameters - Spectroscopy</i>)
Fully Excited VOI	Complete excitation of all metabolites within the VOI. Only available for csi_se sequences. (→ Page 436 <i>Fully Excited VOI (parameter)</i>)
Saturation Region	Number of the currently selected saturation region (→ Page 441 <i>Saturation Region (parameter)</i>)
Thickness	Thickness of the currently selected saturation region (→ Page 441 <i>Saturation Region (parameter)</i>)
Position	Position of the currently selected saturation region (→ Page 441 <i>Saturation Region (parameter)</i>)

Orientation	Orientation of the currently selected saturation region (→ Page 441 <i>Saturation Region (parameter)</i>)
Sat. Delta Frequ.	Frequency shift of the saturation pulse (→ Page 436 <i>Sat. Delta Frequ. (parameter)</i>)

4.5.4 Geometry/AutoAlign parameter card



Example

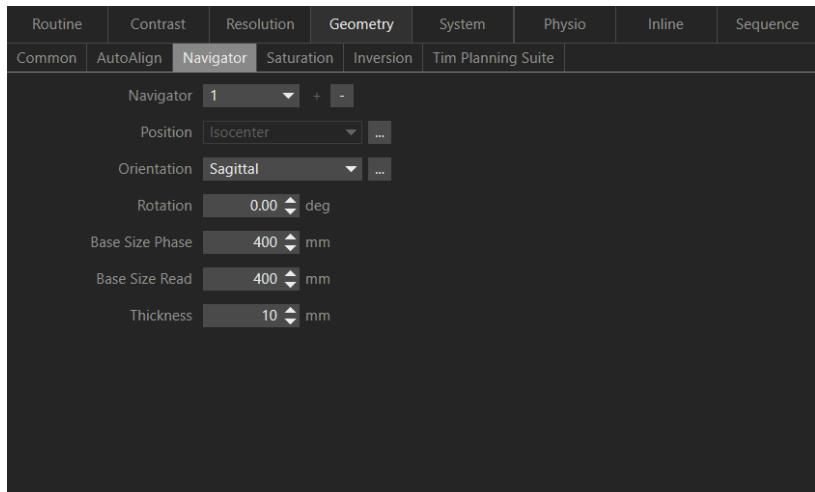
Initial Position	Initial offset of the position of the slice plane with respect to the calculated AutoAlign matrix
Initial Orientation	Initial offset of the orientation of the slice plane with respect to the calculated AutoAlign matrix
Initial Rotation	Initial offset of the rotation of the slice plane with respect to the calculated AutoAlign matrix

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



Initial Rotation is limited to certain AutoAlign algorithms, for example, **Head**.

4.5.5 Geometry/Navigator parameter card



Example

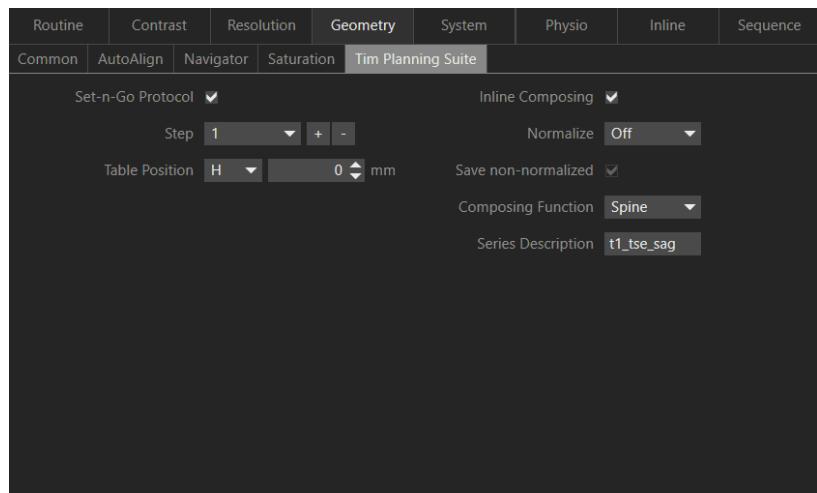
The **Geometry/Navigator** parameter card contains the parameters that have to be set to run a protocol with the Navigator.

You can use the Navigator technique to record respiratory movement.

Navigator	Selection of the Navigator object (→ Page 437 <i>Navigator (parameter)</i>)
Position	Position of the navigator object in the patient coordinate system (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)

Orientation	Orientation of the navigator object in the patient coordinate system (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Rotation	Angle by which the navigator object is rotated in the slice plane defined by the orientation (→ Page 399 <i>Rotation (parameter)</i>)
Base Size Phase	Extent of the navigator object in the phase-encoding direction
Base Size Read	Extent of the navigator object in the readout direction
Thickness	Thickness of the navigator slice

4.5.6 Geometry/Tim Planning Suite parameter card



Example

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. The individual images can then be composed into a single overall image/volume.

To aid planning and evaluating multi-slice measurements, group the individual measurements or combine them in a Set-n-Go protocol. Use the **Geometry/Tim Planning Suite** parameter card for the required settings.

4.5.6.1 Set-n-Go protocols

Set-n-Go Protocol	The measurement protocol is part of a Set-n-Go protocol (→ Page 437 <i>Set-n-Go Protocol (parameter)</i>)
Step	Measurement step of the Set-n-Go protocol whose parameters can currently be edited
Table Position	Set the table position (→ Page 437 <i>Table Position (parameter)</i>)
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.

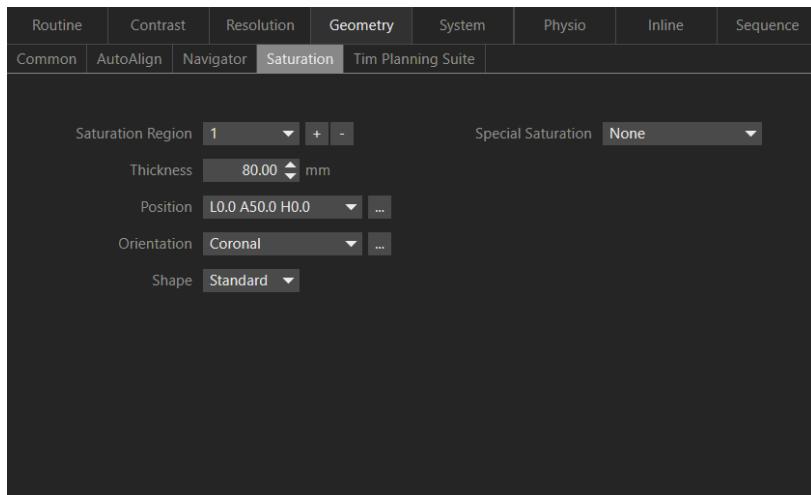
4.5.6.2 Inline Composing

Inline Composing	Compose images into a complete image/volume (→ Page 437 <i>Inline Composing (parameter)</i>)
Normalize	Normalization filter strength (→ Page 379 <i>Normalize Filter Settings dialog box</i>)
Composing Function	Method of composing (→ Page 438 <i>Composing Function (parameter)</i>)
Series Description	Enter a series description

4.5.6.3 Composing groups

Composing Group	Assignment to a composing group (→ Page 438 <i>Composing Group (parameter)</i>)
Last Step	Close the composing group. (→ Page 439 <i>Last Step (parameter)</i>)

4.5.7 Geometry/Saturation parameter card



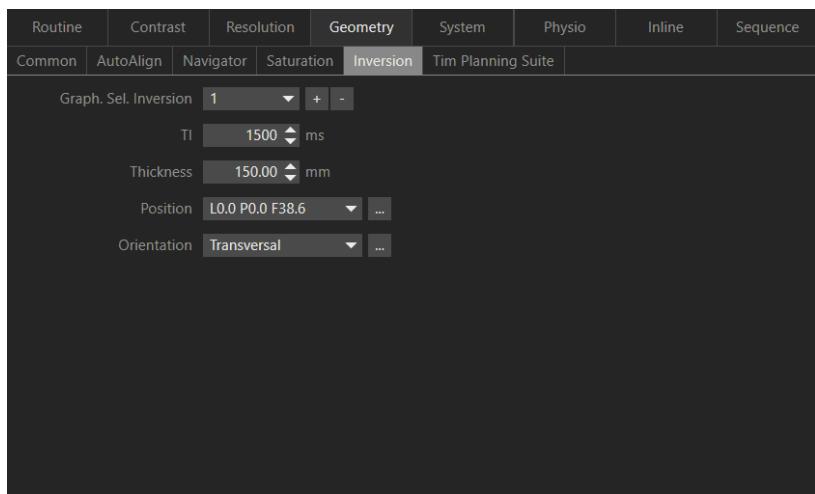
Example

The **Geometry/Saturation** card contains all parameters relevant for planning saturation regions as well as fat or water saturation.

Saturation Region	Number of the saturation slice displayed (→ Page 441 <i>Saturation Region (parameter)</i>)
Thickness	Thickness of the saturation slice
Shape	Shape (profile) of the saturation region (→ Page 443 <i>Shape (parameter)</i>)

Position	Position of this saturation slice (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of this saturation slice (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Special Saturation	Parallel or tracking saturation regions (→ Page 443 <i>Special Saturation (parameter)</i>)
Gap	Distance of the special sat from the associated slice and/or slab group
Thickness	Thickness of the gap

4.5.8 Geometry/Inversion parameter card



Example

The **Geometry/Inversion** parameter card is used for the graphical planning of slice-selective inversion, e.g., TIRM sequences.

Graph. Sel. Inversion	Graphical planning of the inversion, if the value is > 0
TI	Inversion time for the graphical inversion It is only active if Graph. Sel. Inversion is set to a value > 0.
Thickness	Slice thickness for the graphical inversion It is only active if Graph. Sel. Inversion is set to a value > 0.
Position	Position of the object center (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of the object (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)

4.6 System parameter cards

The **System** parameter card is divided into the following subcards:

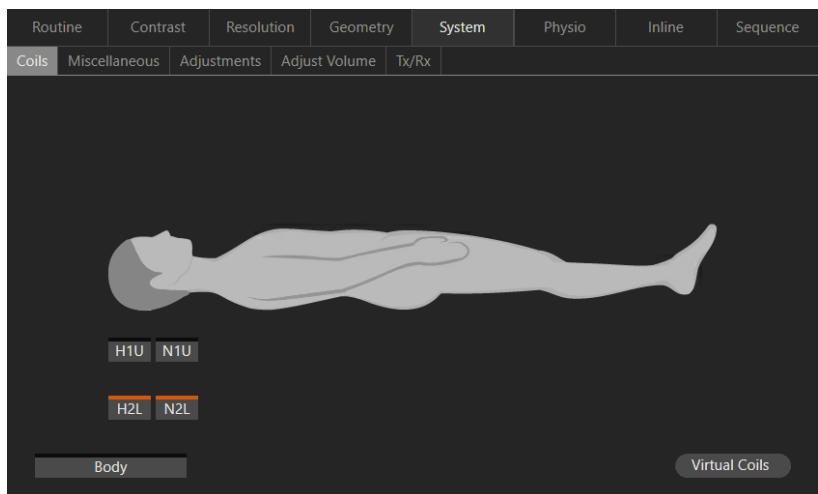
- The **Coils** subcard shows the stylized patient, the approximate position of the coils, and the selection of coils used for measurement.
(→ Page 305 *System/Coils parameter card*)
- The **Adjustments** subcard allows you to adjust coil selection and specify the adjustment settings.
(→ Page 307 *System/Adjustments parameter card*)
- The **Adjust Volume** subcard allows you to define the adjustment volume.
(→ Page 309 *System/Adjust Volume parameter card*)
- The **Tx/Rx** subcard allows you to view and adjust transmitter/receiver settings.
(→ Page 310 *System/TxRx parameter card*)

- The **pTx** subcard allows you to set the B1 shim mode.
(→ Page 312 *System/pTx parameter card*)
- The **Miscellaneous** subcard allows you to set automatic coil selection, to change specific settings for the coils, and to adjust miscellaneous settings.
(→ Page 313 *System/Miscellaneous parameter card*)

4.6.1 System/Coils parameter card



The **System/Coils** parameter card is only displayed if coils have been assigned to the current protocol.



Example (depends on the connected coils)

This subcard shows the stylized patient and the positions of the coils connected.

The upper area of the parameter displays the coils with positions not (yet) known, the lower area of the parameter card displays the coils with known positions. These coil elements are shown in the GSP as well.

The figure also illustrates the position of the patient:

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

The body coil shows the table position relative to the patient.

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

Several fully identical coils (for example, 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, move the mouse pointer briefly on the appropriate button.

The Operator Manual MR System and Coils provides you with a detailed description of the coils and how they are used.

4.6.1.1 Coils

Local coils	Selection of array coils (→ Page 444 <i>Local coils (parameter)</i>)
Body coil	Selection of the body coil (→ Page 444 <i>Body coil (parameter)</i>)
Virtual Coils	Selection of virtual coils (→ Page 384 <i>Virtual Coils dialog box</i>) The Virtual Coils button is only available in the Dot Cockpit , it is not shown on the Examination screen.



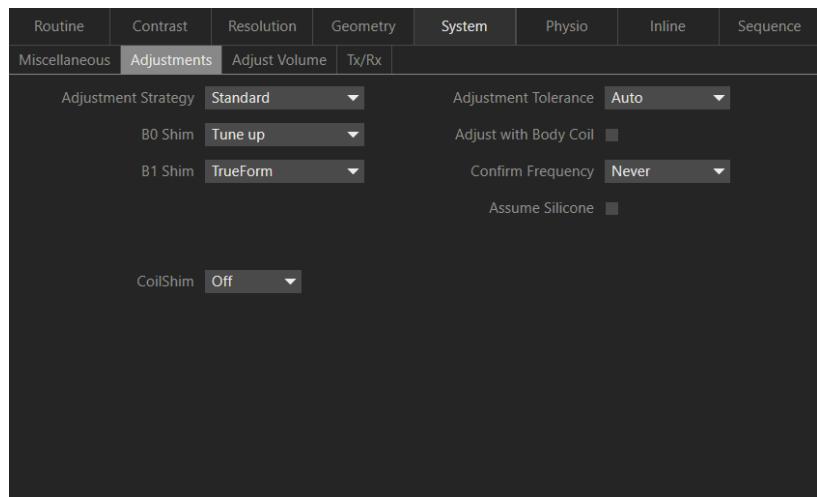
Select the coil elements that are inside the region under examination. Otherwise, image quality may be adversely affected.

4.6.1.2 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.

4.6.2 System/Adjustments parameter card



Example

The **System/Adjustments** parameter card is used to view adjustment settings that apply to the measurement protocol currently open. The adjustments may be changed as required.

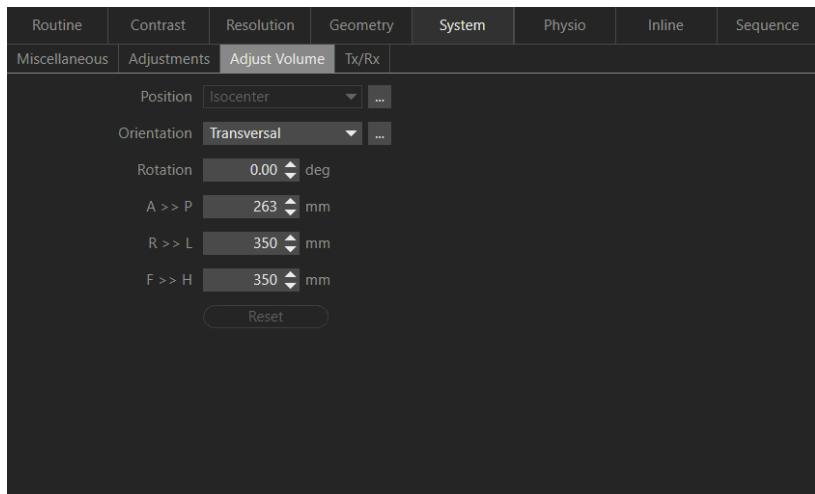


Routine measurements do not require changes in adjustment parameters. They should be adjusted in exceptional cases and by highly experienced users only.

Adjustment Strategy	Adjustment strategy (→ Page 444 <i>Adjustment Strategy (parameter)</i>) (→ Page 368 <i>Adjustment Strategy dialog box</i>)
B0 Shim	Set the B0 shim mode. (→ Page 445 <i>B0 Shim (parameter)</i>)
B1 Shim	Set the B1 shim mode. (→ Page 447 <i>B1 Shim (parameter)</i>)
Local Shim	Include the local shim functionality. Additional shim currents in dedicated coils are used. This parameter is only visible if the coil plugged in is a local shim coil.
CoilShim	Improve image quality in the c-spine and in the neck (→ Page 447 <i>CoilShim (parameter)</i>)
Adjustment Tolerance	Predefine adjustment tolerance regarding similar table positions. (→ Page 448 <i>Adjustment Tolerance (parameter)</i>)
Adjust with Body Coil	Perform adjustment with the body coil. (→ Page 448 <i>Adjust with Body Coil (parameter)</i>)
Confirm Frequency	Define when the Confirm Frequency Adjustment dialog box will appear. (→ Page 451 <i>Confirm Frequency (parameter)</i>)
Assume Silicone	Optimize measurements of patients having silicone implants. If the check box has been selected, the system automatically adjusts the frequency to the water peak.
Adj. Water Suppr.	For spectroscopy measurements, special RF pulse trains are used that suppress the water signal.

Assume Dominant Fat	Optimize measurements of patients having dominant fat tissue.
Manual Adjustments	<p>Perform a manual adjustment</p> <p>For detailed information, see: Operator Manual MR Examination and Review.</p>

4.6.3 System/Adjust Volume parameter card



Example

With **Adjust Volume** enabled, the adjustment volume is automatically calculated by the system on the basis of the slices to be measured.

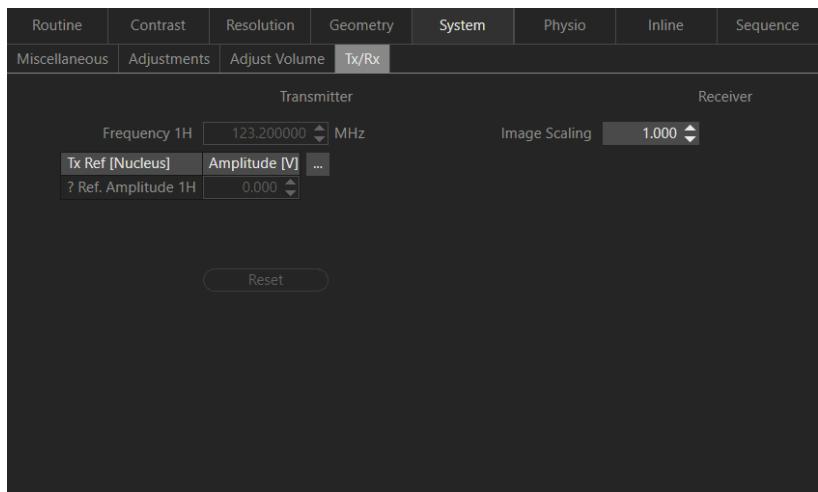
(→ Page 449 *Adjusting the volume*)



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

Position	Position of the measurement volume (VOI) (→ Page 390 <i>Position (parameter)</i>) (→ Page 362 <i>Position dialog box</i>)
Orientation	Orientation of the measurement volume (VOI) (→ Page 391 <i>Orientation (parameter)</i>) (→ Page 361 <i>Orientation dialog box</i>)
Rotation	"In-plane" angle of rotation (→ Page 399 <i>Rotation (parameter)</i>)
R >> L A >> P F >> H	Extent of the measurement volume (VOI) (→ Page 399 <i>VOI parameters</i>)
Reset	Reset parameters

4.6.4 System/TxRx parameter card



Example

The **System/Tx/Rx** parameter card lets you view adjustment settings applicable to the measurement protocol currently open. It shows the results of the last automatic and successful adjustment.

The left side of the **System/Tx/Rx** card shows the values of the last successful transmitter setting.

The right side of the parameter card shows the values for the receiver gain automatically calculated by the system.



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

4.6.4.1 Transmitter

Frequency 1H	Display of the system frequency
Tx Ref [Nucleus]	Reference amplitude for the selected primary or secondary nucleus (→ Page 448 <i>Tx Ref [Nucleus] (parameter)</i>) (→ Page 381 <i>RF Pulses dialog box</i>)
Ref. Amplitude 1H	Display of the reference amplitude
Reset	Reset parameters
Correction Factor	Display of the correction factor for water suppression

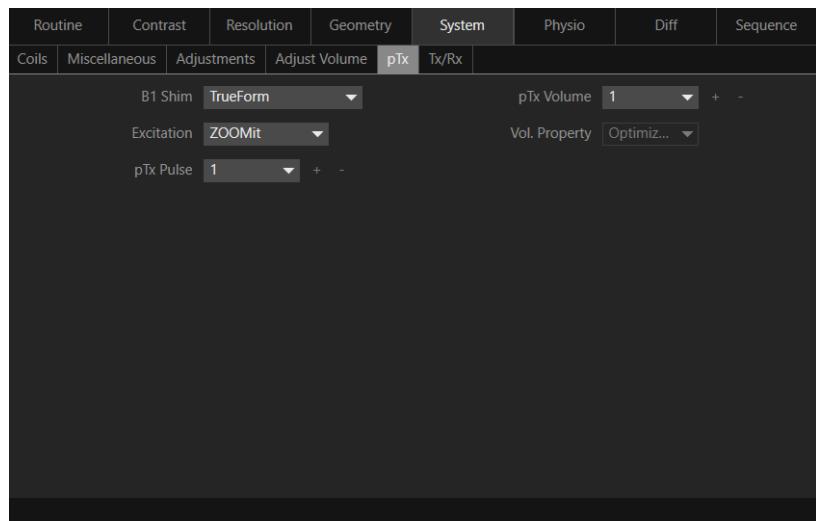


All pulse amplitudes are automatically calculated based on the reference amplitude and, if necessary, the correction factor.

4.6.4.2 Receiver

Gain	Set the sensitivity of the receiver. The recommended receiver gain is automatically calculated by the system.
Image Scaling	Set an additional modification factor, which adjusts the grayscale range of the images, after channel combination and before they are sent to the database.

4.6.5 System/pTx parameter card

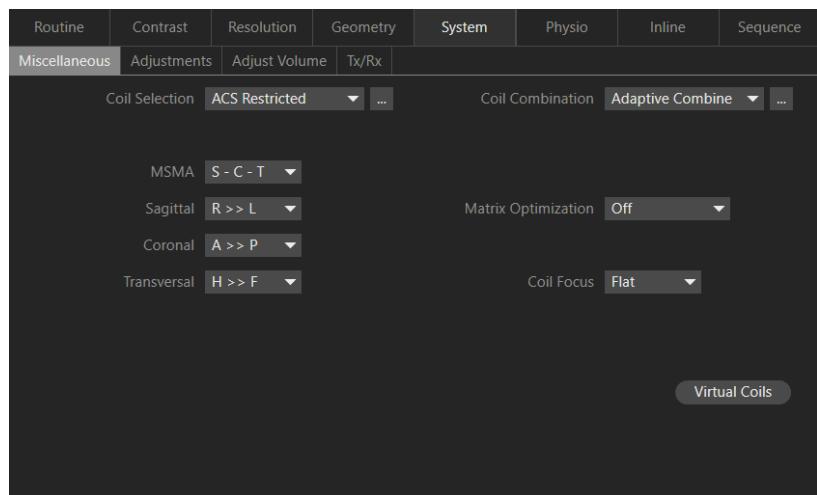


Example

B1 Shim	Set the B1 shim mode. (→ Page 447 <i>B1 Shim (parameter)</i>)
Excitation	Mode for radio-frequency pulse (→ Page 511 <i>Excitation (parameter)</i>)

pTx Acceleration	Acceleration factor from 1 (no acceleration) to a maximum of 2 The duration of the excitation RF pulse is reduced by this factor.
pTx Volume	Number of B1 shim volumes
Vol. Property	Set the usage of the pTx Volume

4.6.6 System/Miscellaneous parameter card



Example

The **System/Miscellaneous** parameter card contains a number of different settings.

4.6.6.1 Coils

Coil Selection	Protocol-specific coil selection (→ Page 453 <i>Coil Selection (parameter)</i>) (→ Page 364 <i>Coil Selection dialog box</i>)
Coil Combination	Algorithm for signal calculation (→ Page 453 <i>Coil Combination (parameter)</i>) (→ Page 365 <i>Coil Combination dialog box</i>)
Matrix Optimization	Tim System coils have built-in mode information. (→ Page 454 <i>Matrix Optimization (parameter)</i>)
Coil Focus	Coil focus for some special coils (→ Page 455 <i>Coil Focus (parameter)</i>)

4.6.6.2 Image numbering

MSMA	Primary order (→ Page 451 <i>MSMA (parameter)</i>)
Coronal, Transverse, Sagittal	Secondary order (→ Page 451 <i>MSMA (parameter)</i>)

4.6.6.3 Positioning the measurement

Table Position	Set the table position. (→ Page 437 <i>Table Position (parameter)</i>)
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.

4.7 Physio parameter cards

The **Physio** parameter card is divided into the following subcards:

- The **Signal** subcard allows you to adjust synchronizing physiological signals (ECG signal, pulse, respiration).
(→ Page 315 *Physio/Signal parameter card*)
- The **Cardiac** subcard allows you to adjust parameters relevant for cardiac examinations.
(→ Page 320 *Physio/Cardiac, Angio/Cardiac, or Inline/Cardiac parameter card*)
- The **PACE** subcard allows you to adjust parameters to suppress respiratory artifacts and for multi-breath-hold measurements.
(→ Page 323 *Physio/PACE parameter card*)

4.7.1 Physio/Signal parameter card

Physiological motion associated with the cardiac and respiratory cycles can result in image artifacts. Such artifacts are recognizable in the image as, for example, noise or blurring.

You can avoid these types of motion artifacts by synchronizing physiological signals (ECG signal, pulse, respiration) with the measurements.

Image data can also be retrospectively sorted with respect to the physiological signal curves.

The **Physio/Signal** parameter card contains different parameters depending on your selection: ECG I, pulse, external signal, or respiratory triggering.

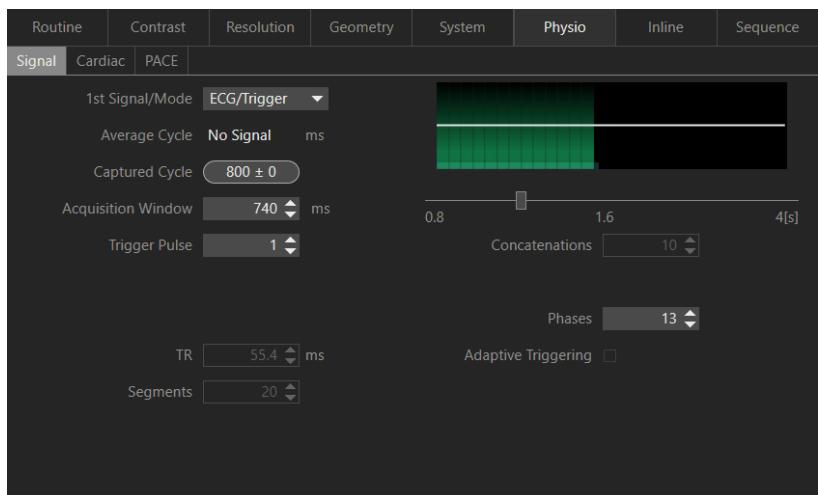


The trigger signal statistics are calculated as a moving average. Reset these statistics in the **Physiological Display** window if the trigger signal has been highly variable.

1st Signal/Mode	Select signal and measurement mode (→ Page 455 <i>1st Signal/Mode (parameter)</i>)
Concatenations	Number of concatenations (→ Page 397 <i>Concatenations (parameter)</i>)

(→ Page 464 *Display of time ranges*)

4.7.1.1 Parameters for ECG I, pulse, or external signal



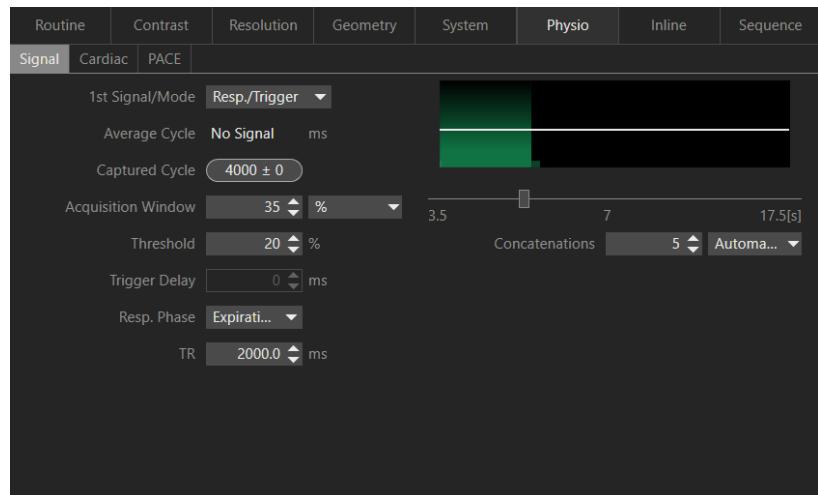
Example with ECG signal

Average Cycle	Average time between trigger events (→ Page 456 <i>Average Cycle (parameter)</i>)
Captured Cycle	Current captured average cycle (→ Page 457 <i>Captured Cycle (parameter)</i>)
Acquisition Window	Time window for data acquisition (→ Page 457 <i>Acquisition Window (parameter)</i>)
Trigger Pulse	Trigger counter (→ Page 458 <i>Trigger Pulse (parameter)</i>)

Trigger Delay	Delay time (→ Page 458 <i>Trigger Delay (parameter)</i>)
Adaptive Triggering	Real-time adaptation of the acquisition to the current heart rate. (→ Page 459 <i>Adaptive Triggering (parameter)</i>)
Trigger Lock Time	Set the minimal acquisition time for Adaptive Triggering . (→ Page 459 <i>Trigger Lock Time (parameter)</i>)
Target RR	Target RR, average heart rate (→ Page 459 <i>Target RR (parameter)</i>)
TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)
Segments	Number of lines of k-space acquired during a TR interval (→ Page 440 <i>Segments (parameter)</i>)
Phases	Number of images depicting the phases of the cardiac cycle that can be calculated using the current protocol (→ Page 460 <i>Phases (parameter)</i>)
Arrhythmia Detection	Detection of arrhythmia (→ Page 460 <i>Arrhythmia Detection (parameter)</i>)
Trigger Window	Time window for ignoring triggers that occur outside a defined time range (→ Page 460 <i>Trigger Window (parameter)</i>)
Calculated Phases	Number of images depicting the phases of the cardiac cycle that can be generated in a retrograd CINE acquisition. (→ Page 461 <i>Calculated Phases (parameter)</i>)

Flow Sensitivity	Flow sensitivity of the sequence by modifying the flow-spoiling gradient (→ Page 461 <i>Flow sensitivity (parameter)</i>)
NATIVE	Generate arterial and venous images without contrast agent. (→ Page 461 <i>NATIVE (parameter)</i>)
TD min flow	Delay time for the second acquisition (→ Page 462 <i>TD min flow (parameter)</i>)
TD peak flow	Delay time for the first acquisition (→ Page 462 <i>TD peak flow (parameter)</i>)
TD first	Delay time for the first acquisition of a series of TD scout acquisitions (→ Page 463 <i>TD first (parameter)</i>)
TD Increment	Delay increment for a series of TD scout acquisitions (→ Page 463 <i>TD increment (parameter)</i>)
Measurements	Number of measurements performed (→ Page 412 <i>Measurements (parameter)</i>)

4.7.1.2 Parameters for respiratory signal

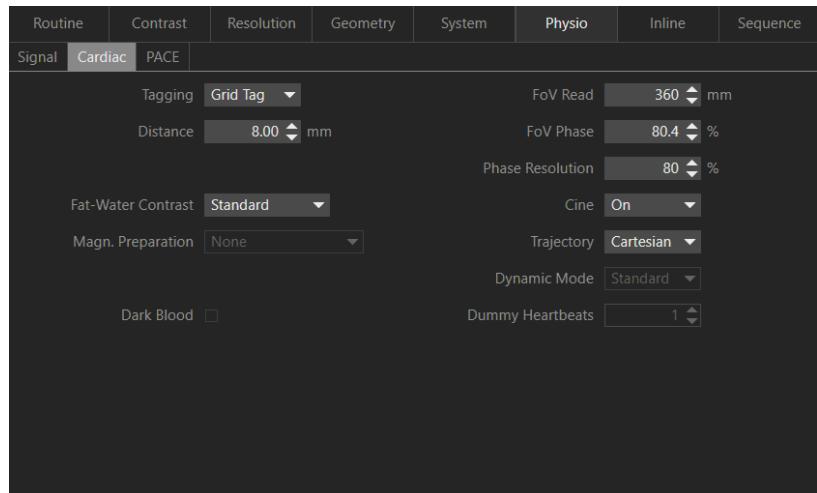


Example with respiratory signal

Average Cycle	Average time between trigger events (→ Page 456 <i>Average Cycle (parameter)</i>)
Captured Cycle	Current captured average cycle (→ Page 457 <i>Captured Cycle (parameter)</i>)
Acquisition Window	Time for data acquisition (→ Page 457 <i>Acquisition Window (parameter)</i>)
Threshold	Threshold for respiration (→ Page 463 <i>Threshold (respiration parameter)</i>)
Resp. Phase	Respiratory phase (inspiration or expiration) Here, you select whether Inspiration (breathing in) or Expiration (breathing out) will be used for triggering.
TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)

Segments	Number of rows in the k-space during a TR interval (→ Page 440 Segments (parameter))
Phases	Number of respiratory phases (→ Page 460 Phases (parameter))

4.7.2 Physio/Cardiac, Angio/Cardiac, or Inline/Cardiac parameter card



Example

The **Cardiac** subcard displays parameters relevant for a cardiac examination. It is available only if the current measurement protocol is based on a sequence that supports physiologically triggered acquisitions.



The **Physio/Cardiac** parameter card is displayed only if the current measurement protocol is based on a sequence supporting cardiac measurements.

4.7.2.1 Resolution

FoV Read	Field of view in the readout direction (→ Page 394 <i>FoV Read, FoV Phase (parameter)</i>)
FoV Phase	Field of view in the phase-encoding direction (→ Page 394 <i>FoV Read, FoV Phase (parameter)</i>)
Phase Resolution	Phase resolution (→ Page 417 <i>Phase Resolution (parameter)</i>)

4.7.2.2 Orientation lines

Tagging	Show orientation lines (→ Page 465 <i>Tagging (parameter)</i>)
Distance	Distance between tags
Angle	Angle between line tags and the phase-encoding direction If you have selected Line Tag as auxiliary lines, you can also enter the angle between the orientation lines (tags) and the phase-encoding direction.

4.7.2.3 Image contrast

Fat-Water Contrast	Suppression of the fat or water signal (→ Page 405 <i>Fat-Water Contrast (parameter)</i>) (→ Page 373 <i>Fat Suppression Optimization dialog box</i>) (→ Page 374 <i>Dixon dialog box</i>)
Magn. Preparation	Magnetization preparation (→ Page 401 <i>Magn. Preparation (parameter)</i>) (→ Page 382 <i>Inversion Pulse Settings dialog box</i>)

TI	Inversion time (→ Page 404 <i>TI (parameter)</i>)
Dark Blood	Display blood dark in the image (→ Page 465 <i>Dark Blood (parameter)</i>) (→ Page 370 <i>Dark Blood Pulse Settings dialog box</i>)
Trufi Delta Freq.	Shifts banding artifacts (→ Page 509 <i>Trufi Delta Freq. (parameter)</i>)

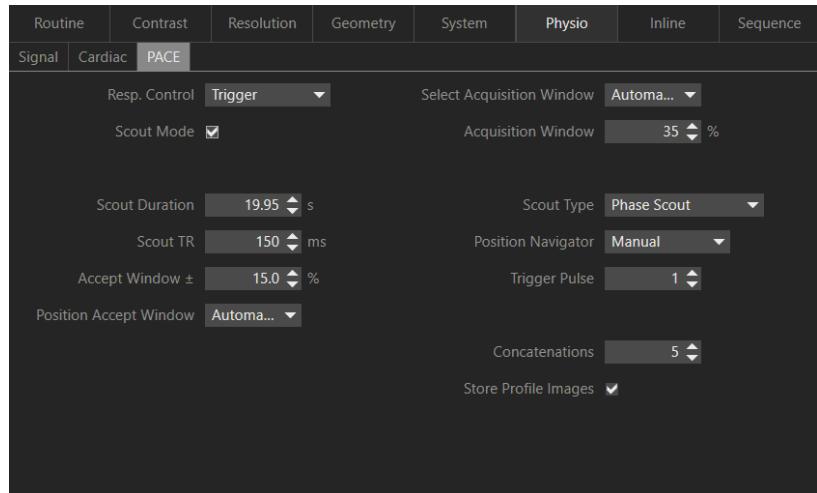
4.7.2.4 Cine measurements

Cine	Indication whether this is a Cine sequence displaying dynamic processes
Trajectory	Geometric form of k-space sampling (→ Page 420 <i>Trajectory (parameter)</i>)
Dynamic Mode	Selection of the dynamic mode (→ Page 401 <i>Dynamic Mode (parameter)</i>)
Dummy Heartbeats	Defines the number of dummy heartbeats (→ Page 470 <i>Dummy Heartbeats (parameter)</i>)

4.7.2.5 STIR imaging

Slice-sel. IR thickness	Thickness of the slice selective IR pulse (→ Page 465 <i>Slice-sel. IR thickness (parameter)</i>)
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4.7.3 Physio/PACE parameter card



Example

The **Physio/PACE** parameter card allows you to set parameters to suppress respiratory artifacts and for multi-breath-hold measurements. (PACE stands for "Prospective Acquisition CorrEction".)

Resp. Control	Respiratory control for compensation of respiratory artifacts (→ Page 466 <i>Resp. Control (parameter)</i>)
Scout Mode	Acquisition of the navigator signal (→ Page 467 <i>Scout Mode (parameter)</i>)
Scout Duration	Duration of the preparation phase The parameter is active only if the Scout Mode parameter is selected.
Scout TR	Repetition time of a navigator pulse
Scout Type	Definition of the scout type used for the navigator (→ Page 467 <i>Scout Type (parameter)</i>)

Accept Window ±	Permitted deviation from the tolerance center (→ Page 467 <i>Accept window ± (parameter)</i>)
Position Accept Window	Automatically centered position for the acceptance window for the respiratory control gate (→ Page 468 <i>Position Accept Window (parameter)</i>)
Accept Position	Centered position of the acceptance window for the respiratory control trigger (→ Page 468 <i>Accept. Position (parameter)</i>)
Search Window ±	Size of the search window (→ Page 468 <i>Search Window ± (parameter)</i>)
Select Acquisition Window	Set the method by which the acquisition window is defined. (→ Page 469 <i>Select Acquisition Window (parameter)</i>)
Acquisition Window	Time window for data acquisition (→ Page 457 <i>Acquisition Window (parameter)</i>)
Position Navigator	Set the method by which the position navigator is defined. (→ Page 469 <i>Position Navigator (parameter)</i>)
Search Position	Centering position of the search window
Tracking Factor	Relationship between diaphragm movement and anatomy (→ Page 469 <i>Tracking Factor (parameter)</i>)
Chronologic Position	Time of the navigator signal (→ Page 470 <i>Chronologic Position (parameter)</i>)
Trigger Pulse	Trigger pulse (→ Page 458 <i>Trigger Pulse (parameter)</i>)

Slices per Resp. Cycle	Number of slices acquired during a respiratory cycle. The parameter is available only for haste , trufi , and tfl sequences.
Card. Trig. per Resp. Cycle	Number of cardiac trigger pulses per respiratory cycle. Replaces Slices per resp. cycle for double triggering.
Resp. Motion Adaptation	Adjust accept window to respiratory curve. (→ Page 470 <i>Resp. Motion Adaptation (parameter)</i>)
Breath-hold duration	Determine a patient specific duration of one breath-hold for certain sequence types as an alternative to the duration of one concatenation.
Concatenations	Distribution of slices to be measured (→ Page 397 <i>Concatenations (parameter)</i>)
Store Profile Images	Store the navigator signal time curve as an image. (→ Page 469 <i>Store Profile Images (parameter)</i>)

4.8 Angio parameter cards

The **Angio** parameter card allows you to adjust specific parameters for angiography techniques.

The **Angio** parameter card is available only if the sequence used as the basis for the current measurement protocol supports the following examinations:

- **Time-of-flight angiography (TOF)**: In time-of-flight angiography sequences, unsaturated spins flow into the slice or volume to generate especially high signal intensity in the vessel.
- **Contrast-enhanced angiography (CE)** 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.

The intensity of each pixel is a measure of the velocity components at that location. Since only moving spins contribute to the signal, very thick slices can be displayed as well. The result is a projection image of all vessels in the excited slice volume.

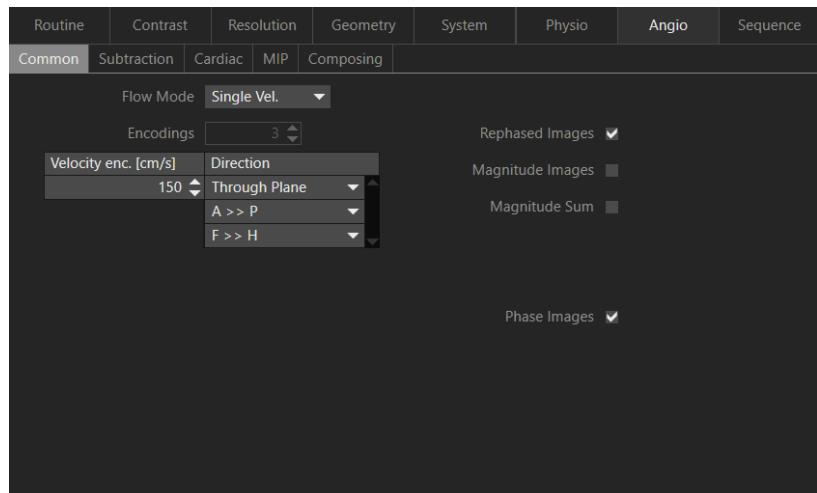
- The **3D phase contrast angiography** allows you to process the entire data volume measured using the MIP technique in order to display special projections of vessel sections.
- The MR **flow quantification technique** allows for non-invasive examination and evaluation of blood flow.

Depending on the measurement protocol, the **Angio** parameter card is divided into the following subcards:

- The **Common** subcard contains different parameters depending on whether the protocol is a magnitude angio or a contrast-enhanced angio examination.
(→ Page 327 *Angio/Common parameter card*)
- The **Dynamic** subcard allows you to set parameters for dynamic image evaluation.
(→ Page 338 *Inline/Dynamic or Angio/Dynamic parameter card*)
(→ Page 276 *Contrast/Dynamic or Angio/Dynamic parameter card*)
- The **Subtraction** subcard allows you to set subtraction parameters.
(→ Page 339 *Inline/Subtraction or Angio/Subtraction parameter card*)
- The **Cardiac** subcard allows you to adjust parameters relevant for a cardiac examinations.
(→ Page 320 *Physio/Cardiac, Angio/Cardiac, or Inline/Cardiac parameter card*)
- The **MIP** subcard allows you to adjust parameters for the calculation of MIP images.
(→ Page 341 *Inline/MIP or Angio/MIP parameter card*)

- The **Composing** subcard allows you to adjust parameters for Composed Measurement Groups.
(→ Page 344 *Inline/Composing, Diff/Composing, or Angio/Composing parameter card*)

4.8.1 Angio/Common parameter card



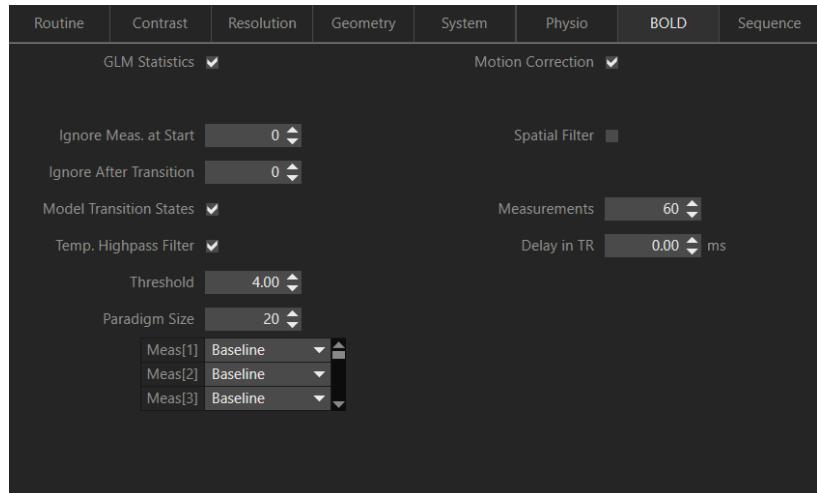
Example

The **Angio/Common** card allows you to adjust specific parameters for 2D/3D phase contrast angiography.

Flow Mode	Flow-encoding mode (→ Page 474 <i>Flow Mode (parameter)</i>)
Encodings	Number of flow sensitivities to be set for flow encoding The possible number depends on the selected Flow Mode .
Velocity enc.	Flow sensitivities for a flow encoding The possible entries depend on the selected Flow Mode .

Direction	Flow-sensitive axis (→ Page 475 <i>Direction (parameter)</i>)
Rephased Images	Flow-rephased images are reconstructed from the data of the phase-contrast angiography measurement.
Magnitude Images	Magnitude images (either per flow direction or per flow sensitivity) are reconstructed from the data of the phase-contrast angiography measurement (1 image per flow direction or flow sensitivity).
Magnitude Sum	A magnitude sum image is reconstructed from the magnitude images of a phase-contrast angiography measurement.
MIP Images	MIP images (maximum intensity projection) are reconstructed from all magnitude sum images of a measurement.
Std. Dev. Images	Standard deviations from the magnitude sums are calculated in order to reconstruct an image.
Phase Images	Phase images (either per flow direction or per flow sensitivity) are reconstructed from the data of the phase-contrast angiography measurement (1 image per flow direction or flow sensitivity).
Burn Time-to-Center	Write the value of Time to center of k-space in the image text. (→ Page 474 <i>Burn Time to Center (parameter)</i>)

4.9 BOLD parameter card



Example

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.

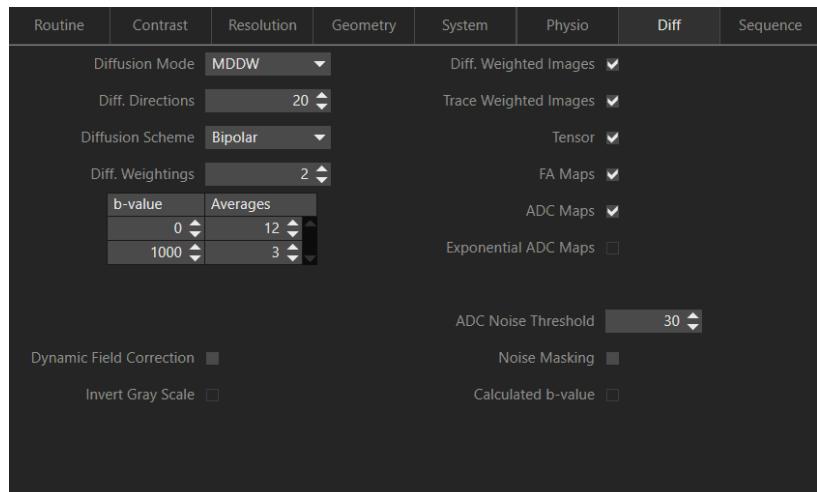


The **BOLD** parameter card is displayed only if the current measurement protocol is based on a sequence that supports BOLD measurements.

GLM Statistics	Activate the GLM method (General Linear Model). (→ Page 476 <i>GLM Statistics (parameter)</i>)
Ignore Meas. at Start	Number of initial measurements excluded from the evaluation in order to avoid start-up artifacts
Ignore After Transition	Number of measurements after the change in stimulation that are excluded from the evaluation (→ Page 477 <i>Ignore After Transition (parameter)</i>)
Model Transition States	Use of the hemodynamic response function. (→ Page 477 <i>Model Transition States (parameter)</i>)

Temp. Highpass Filter	Eliminate low-frequency oscillations over time. (→ Page 478 <i>Temp. Highpass Filter (parameter)</i>)
Threshold	Threshold value for the pixel intensity to calculate overlaid images (→ Page 478 <i>Threshold (parameter)</i>)
Paradigm Size	Number of measurements per paradigm. An input is generated in the paradigm table for each measurement.
Paradigm Size Meas[...]	Table of individual BOLD measurements indicating stimulation (active or baseline) (→ Page 478 <i>Paradigm Size (parameter)</i>)
Motion Correction	Activate motion correction. (→ Page 479 <i>Motion Correction (parameter)</i>)
Interpolation	Interpolation method used for motion correction (→ Page 480 <i>Interpolation (BOLD parameter)</i>)
Spatial Filter	Low-pass filtering for smoothing images The spatial filter increases the signal-to-noise ratio, but reduces local resolution.
Filter Width	Width of the low-pass filter (→ Page 480 <i>Filter Width (parameter)</i>)
Measurements	Number of measurements to be performed (→ Page 412 <i>Measurements (parameter)</i>)
Delay in TR	Time between consecutive measurements for all EPI sequences (→ Page 414 <i>Delay in TR (parameter)</i>)
Multiple Series	Save every measurement as a separate series. (→ Page 415 <i>Multiple Series (parameter)</i>)

4.10 Diff parameter card



Example

The parameters specific to diffusion-weighted measurements are located on the **Diff** parameter card.



The **Diff** parameter card is available only if the current measurement protocol is based on a sequence that supports diffusion-weighted measurements.

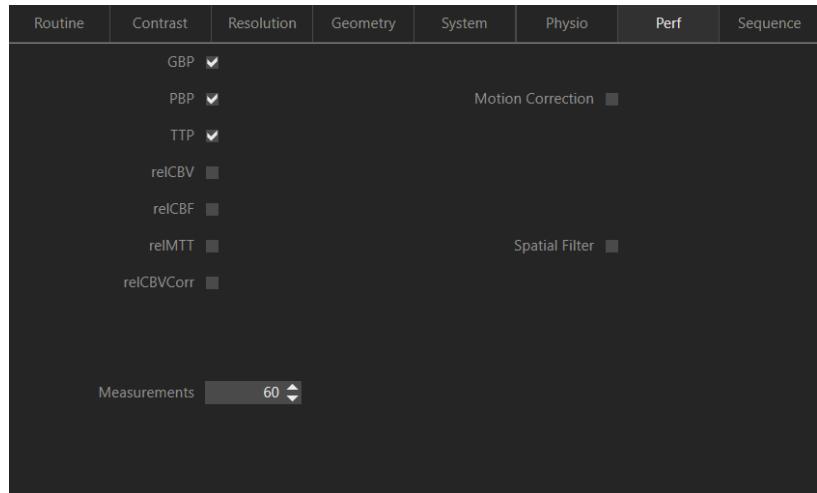
The diffusion of water molecules along a field gradient reduces the MR signal. Signal loss is not as pronounced in areas where the water molecules are not able to diffuse as quickly. **Diffusion-weighted measurements** are based on such diffusion-dependent differences in signal intensity.

Diffusion Mode	Diffusion-sensitive direction (→ Page 481 <i>Diffusion Mode (parameter)</i>)
Diff. Directions	Number of diffusion-encoding directions (can only be selected in MDDW diffusion mode) (→ Page 482 <i>Diff. Directions (parameter)</i>)
Diffusion Scheme	Set the spin echo diffusion encoding. (→ Page 483 <i>Diffusion Scheme (parameter)</i>)

Diff. Weightings	Number of diffusion-weightings that are acquired during a measurement Define the individual weightings in the b-Value input fields prior to measurement (up to 16 b values).
Averages	Number of averages per b-value (→ Page 483 <i>Averages (diffusion parameter)</i>)
b-Value	Value for diffusion weighting (→ Page 483 <i>b-Value (parameter)</i>)
Dynamic Field Correction	Reduce geometric distortions generated by eddy currents (→ Page 380 <i>Filter Dynamic Field Correction dialog box</i>)
Invert Gray Scale	Inverted (PET-like) display of the diffusion trace-weighted images
Diff. Weighted Images	Original images with diffusion weighting (→ Page 484 <i>Diff. Weighted Images (parameter)</i>)
Trace Weighted Images	Diffusion-weighted images averaged across all spatial directions (→ Page 484 <i>Trace Weighted Images (parameter)</i>)
Tensor	Calculated representation of diffusion data The diffusion tensor is stored as a file on the database to enable diffusion evaluation from the Neuro 3D advanced application.
FA Maps	FA maps (Fractional Anisotropy Maps) are reconstructed. FA maps show isotropic diffusion characteristics as dark, while anisotropic diffusion characteristics are shown as bright.
ADC Maps	Apparent Diffusion Coefficient averaged across various spatial directions (→ Page 484 <i>ADC Maps (parameter)</i>)

Exponential ADC Maps	Exponential Apparent Diffusion Coefficient (→ Page 485 <i>Exponential ADC Maps (parameter)</i>)
b-Value>=	Minimum b-value used in ADC calculations (→ Page 484 <i>b-Value >= (parameter)</i>)
Calculated Image	A virtual (b-value) image is calculated.
Calculated b-Value	A virtual (b-value) image is calculated. b-value for the virtual (b-value) image is specified.
ADC Noise Threshold	Threshold of the pixel intensity for calculating ADC maps
Noise Masking	Define whether a noise mask, which is generated from a Prescan normalize scan, will be applied to the images.
Diff. Moment	Measure for the strength of diffusion weighting. It is the amplitude multiplied by the duration of the diffusion gradient. It is only displayed for psif sequences.

4.11 Perf parameter card



Example

The parameters specific to perfusion measurements are located on the **Perf** parameter card.



You can only see the **Perf** parameter card if the current measurement protocol includes a sequence supporting 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	The GBP (Global Bolus Plot) determines the global time intensity curve. (→ Page 485 <i>GBP (parameter)</i>)
PBP	Percentage of Baseline at Peak map Calculation of signal change compared with the baseline (→ Page 485 <i>PBP (parameter)</i>)

TTP	Time to peak map (→ Page 486 <i>TTP (parameter)</i>)
relCBV	relative Cerebral Blood Volume (→ Page 487 <i>relCBV (parameter)</i>)
relCBF	relative Cerebral Blood Flow (→ Page 486 <i>relCBF (parameter)</i>)
relMTT	relative Mean Transit Time (→ Page 486 <i>relMTT (parameter)</i>)
relCBVCorr	relative Cerebral Blood Volume (T1 corrected) (→ Page 487 <i>relCBVCorr (parameter)</i>)
Starting Ignore Meas.	Number of initial measurements excluded from the evaluation in order to avoid start-up artifacts
Measurements	Number of measurements for dynamic measurement (→ Page 412 <i>Measurements (parameter)</i>)
Motion Correction	Activate motion correction. (→ Page 479 <i>Motion Correction (parameter)</i>)
Spatial Filter	Low-pass filtering for smoothing images The spatial filter increases the signal-to-noise ratio, but reduces local resolution.



For perfusion measurements, the original images are always reconstructed and stored. You can use them for additional postprocessing functions.

4.12 Inline parameter cards

The **Inline** parameter card is divided into the following subcards:

- On the **Liver** subcard, you can select a 3D liver registration.
(→ Page 337 *Inline/Liver parameter card*)
- The **Dynamic** subcard allows you to set parameters for dynamic image evaluation.
(→ Page 338 *Inline/Dynamic or Angio/Dynamic parameter card*)
- The **Subtraction** subcard allows you to set subtraction parameters.
(→ Page 339 *Inline/Subtraction or Angio/Subtraction parameter card*)
- The **Cardiac** subcard allows you to adjust parameters relevant for a cardiac examinations.
(→ Page 320 *Physio/Cardiac, Angio/Cardiac, or Inline/Cardiac parameter card*)
- The **MIP** subcard allows you to set parameters for the calculation of MIP and MPR images.
(→ Page 341 *Inline/MIP or Angio/MIP parameter card*)
- The **Soft Tissue** subcard allows you to adjust parameters relevant for soft tissue examinations.
(→ Page 343 *Inline/Soft Tissue parameter card*)
- The **Composing** subcard allows you to set parameters for Composed Measurement Groups.
(→ Page 344 *Inline/Composing, Diff/Composing, or Angio/Composing parameter card*)
- The **MapIt** subcard allows you to configure inline calculation of Parametric Maps.
(→ Page 346 *Inline/MapIt parameter card*)

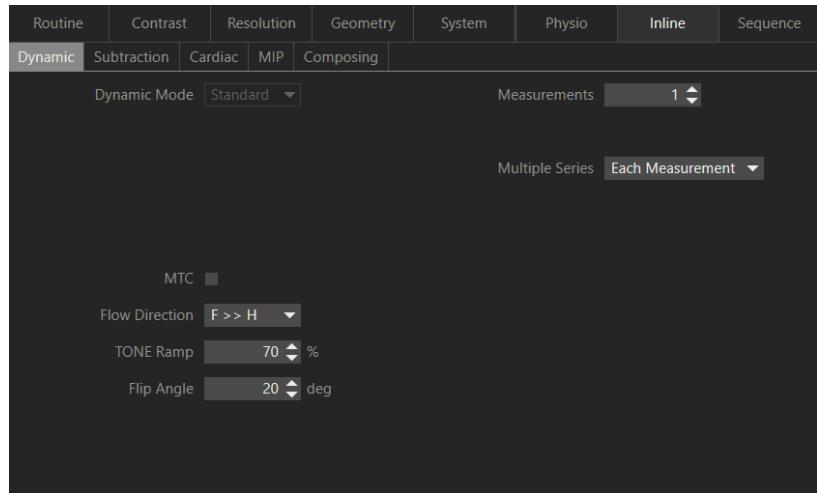
4.12.1 Inline/Liver parameter card

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
Dynamic	Liver	Subtraction	Cardiac	MIP	Soft Tissue	Composing	Maplt
<input type="checkbox"/> Liver Registration <input checked="" type="checkbox"/> Dixon Evaluation				<input checked="" type="checkbox"/> Liver Segmentation <input checked="" type="checkbox"/> Fat Fraction			
<input checked="" type="checkbox"/> Save Original Images				<input checked="" type="checkbox"/> Water Fraction <input checked="" type="checkbox"/> T2* <input checked="" type="checkbox"/> R2* <input checked="" type="checkbox"/> Report			

Example

Liver Registration	Activate 3D liver registration. (→ Page 488 <i>Liver Registration (parameter)</i>)
Liver Segmentation	Activate liver segmentation
Save Original Images	Save the unprocessed images in the database as well.

4.12.2 Inline/Dynamic or Angio/Dynamic parameter card



Example

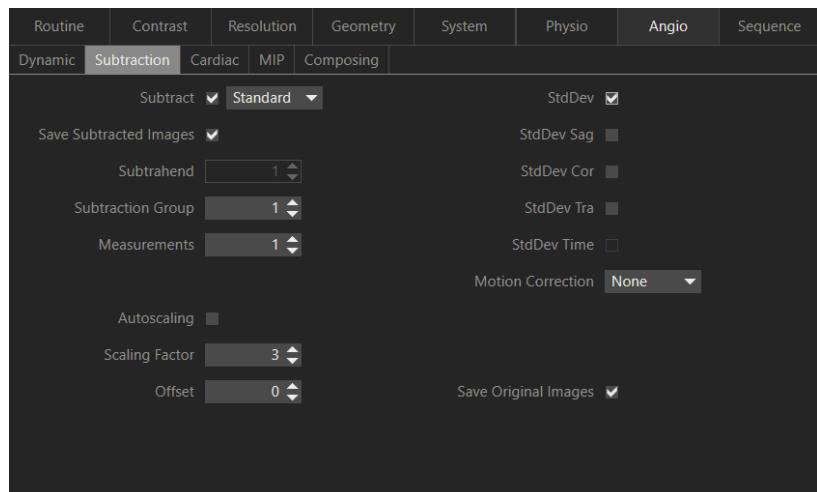
The **Inline/Dynamic or Angio/Dynamic** parameter card allows you to adjust specific parameters for time-of-flight angiography (TOF)

Dynamic Mode	Selection of the dynamic mode (→ Page 401 <i>Dynamic Mode (parameter)</i>)
MTC	Magnetization transfer contrast (→ Page 408 <i>MTC (parameter)</i>)
Flow Direction	Direction of blood flow (→ Page 471 <i>Flow Direction (parameter)</i>)
TONE Ramp	Inflow velocity of blood (→ Page 471 <i>TONE Ramp (parameter)</i>)
Flip Angle	Flip angle (→ Page 401 <i>Flip Angle (parameter)</i>)
Measurements	Number of measurements (→ Page 412 <i>Measurements (parameter)</i>)

Reconstruction Scheme	Method for dynamic reconstruction of the k-space (→ Page 471 <i>Reconstruction Scheme (parameter)</i>)
3D Reordering	Center of raw data space is measured as quickly as possible (→ Page 473 <i>3D Reordering (parameter)</i>)

(→ Page 276 *Contrast/Dynamic or Angio/Dynamic parameter card*)

4.12.3 Inline/Subtraction or Angio/Subtraction parameter card



Example

The **Subtraction** subcard allows you to set subtraction parameters.

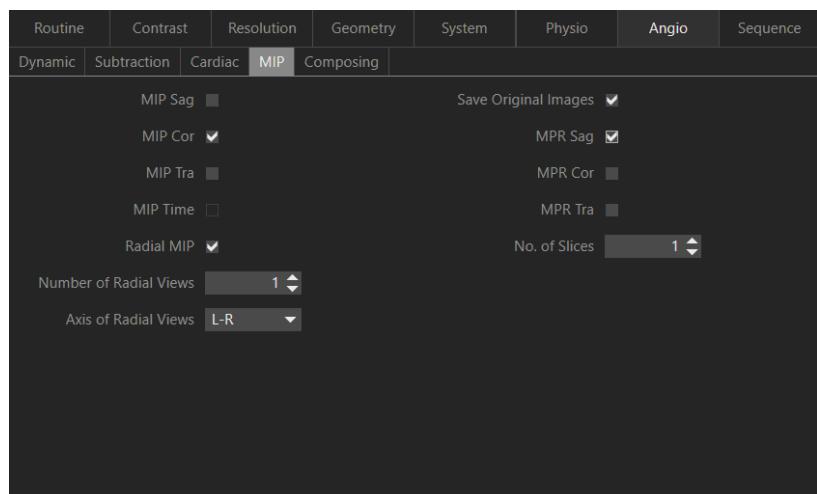


When performing Inline subtraction, please ensure that the parameters **Autoscaling**, **Scaling Factor**, and **Offset** are either **deselected** or set to **1**.

Subtract	Activate or deactivates subtraction. (→ Page 488 <i>Subtract (parameter)</i>)
Save Subtracted Images	Save result images of subtraction. The parameter is only displayed if the Subtract option is activated.
Subtrahend	Define the native series to be subtracted. (→ Page 490 <i>Subtrahend (parameter)</i>)
Subtraction Group	Definition of subtraction groups (→ Page 492 <i>Subtraction Group (parameter)</i>)
Measurements	Number of measurements for dynamic measurement (→ Page 412 <i>Measurements (parameter)</i>)
Subtraction Indices	Define the postcontrast series to be subtracted from. (→ Page 491 <i>Subtraction Indices (parameter)</i>)
Autoscaling	Automatic scaling of result images of subtraction (→ Page 489 <i>Autoscaling (parameter)</i>)
Scaling Factor	Input of a scaling factor for the result images of subtraction (→ Page 489 <i>Scaling Factor (parameter)</i>)
Offset	Input of an offset value for the result images of subtraction (→ Page 490 <i>Offset (parameter)</i>)
StdDev Sag	Calculation of standard deviation result images in the sagittal direction (→ Page 492 <i>Std-Dev-Sag (parameter)</i>)
StdDev Cor	Calculation of standard deviation result images in the coronal direction (→ Page 493 <i>Std-Dev-Cor (parameter)</i>)

StdDev Tra	Calculation of standard deviation result images in the transverse direction (→ Page 493 <i>Std-Dev-Tra (parameter)</i>)
StdDev Time	Calculation of standard deviation result images in the chronological sequence (→ Page 493 <i>Std-Dev-Time (parameter)</i>)
Liver Registration	Activate a 3D liver registration. (→ Page 488 <i>Liver Registration (parameter)</i>)
Motion Correction	Register the postcontrast minuend(s) to the pre-contrast subtrahend. (→ Page 493 <i>Motion Correction (Inline parameter)</i>)
Save Original Images	Save the unprocessed images in the database as well.

4.12.4 Inline/MIP or Angio/MIP parameter card



Example

The **Inline/MIP** or **Angio/MIP** parameter card allows you to set parameters for the calculation of radial or parallel MIP images (Maximum Intensity Projection) and parallel MPR images (Multiplanar Reconstruction).



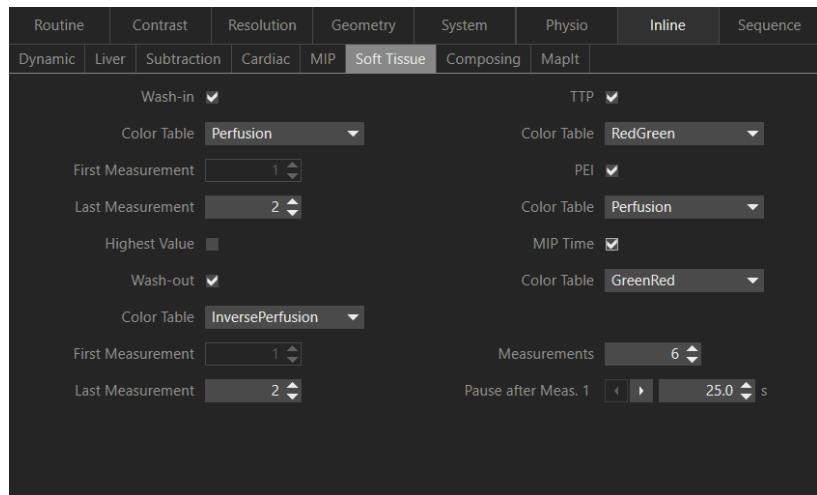
In case of measurement protocols for angiography examinations, the **Inline** parameter card is displayed as the **Angio/MIP** subcard.

MIP Sag	Calculation of MIP images in the sagittal direction
MIP Cor	Calculation of MIP images in the coronal direction
MIP Tra	Calculation of MIP images in the transverse direction
MIP Time	Calculation of MIP images in chronological sequence (→ Page 494 <i>MIP Time (parameter)</i>)
Radial MIP	Calculation of radial MIP views (→ Page 494 <i>Radial MIP (parameter)</i>)
Save Original Images	Save the unprocessed images in the database as well.
MPR Sag	Calculation of MPR images in the sagittal direction
MPR Cor	Calculation of MPR images in the coronal direction
MPR Tra	Calculation of MPR images in the transverse direction
No. of Slices	Number of slices in this slice group (→ Page 389 <i>Slices (parameter)</i>)



You can only edit the **MIP Sag/MIP Cor/MIP Tra** parameters when you are performing a 3D measurement and the number of slices in the slabs is at least 4.

4.12.5 Inline/Soft Tissue parameter card

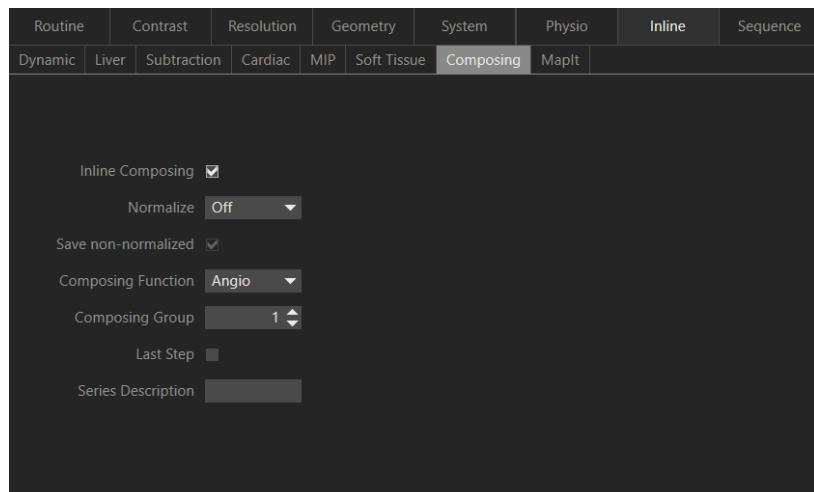


Example

Wash-In	Enable parameters for signal change in the starting range of the dynamic measurement sequence.
Color Table	Definition of color palettes to color-code the parameter maps for individual images
First Measurement	Definition of first measurement used for the wash-in/wash-out calculation within a measurement series
Last Measurement	Definition of last measurement used for the wash-in/wash-out calculation within a measurement series
Highest Value	Value from the last measurement or highest value between the first and second measurement used for calculation of the wash-in parameter image
Wash-Out	Parameter for signal change in the end range of the dynamic measurement sequence
TTP	Time to peak map (→ Page 486 <i>TTP (parameter)</i>)

PEI	Reconstruction of Positive Enhancement Integral (area under a signal - time curve)
MIP-Time	MIP images; highest pixel value along the time axis (→ Page 494 <i>MIP Time (parameter)</i>)
Measurements	Number of measurements to be performed (→ Page 412 <i>Measurements (parameter)</i>)
Pause after Meas.	Pause between individual measurements (→ Page 413 <i>Pause after Meas. (parameter)</i>)

4.12.6 Inline/Composing, Diff/Composing, or Angio/Composing parameter card



Example

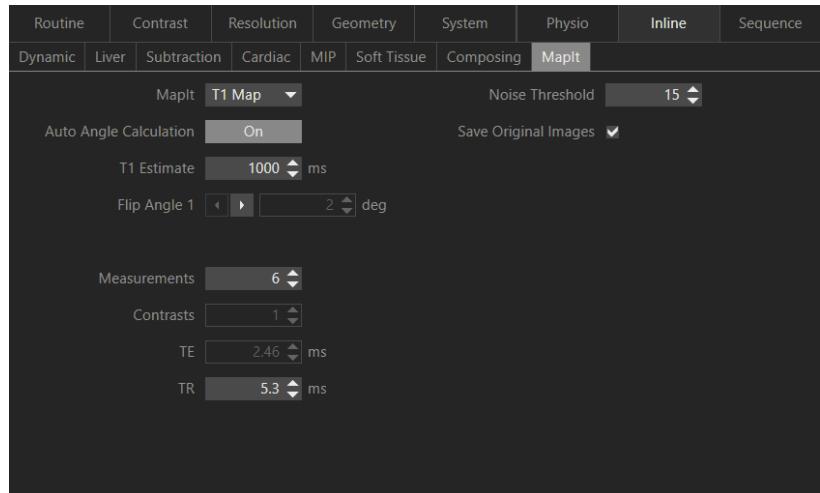
To cover examination regions where the FOV extends beyond a single table position (for example whole body/spine or peripheral MR angiography), it is necessary to perform a number of individual measurements at different table positions. The individual images are then composed into a single overall image.

In this case, Set-n-Go protocols or Composed Measurement groups are required as parentheses. The parentheses enable measurements at various table positions to be planned and evaluated easily.

You set the parameters for Composed Measurement Groups at the **Composing** parameter card.

Inline Composing	Compose images into a complete image (→ Page 437 <i>Inline Composing (parameter)</i>)
Normalize	Normalization filter strength (→ Page 379 <i>Normalize Filter Settings dialog box</i>)
Save non-normalized	Save the non-normalized images in the database as well. (→ Page 438 <i>Save non-normalized (parameter)</i>)
Composing Function	Method of composing (→ Page 438 <i>Composing Function (parameter)</i>)
Composing Group	Assignment to a composing group (→ Page 438 <i>Composing Group (parameter)</i>)
Last Step	Closes the composing group (→ Page 439 <i>Last Step (parameter)</i>)
Series Description	Enter a series description

4.12.7 Inline/MapIt parameter card



Example

MapIT	Inline calculation of Parametric Maps (→ Page 494 <i>MapIt (parameter)</i>)
Auto Angle Calculation	Automatic calculation of the flip angles for T1 maps
T1 Estimate	Estimated value for T1 (→ Page 495 <i>T1 Estimate (parameter)</i>)
Flip Angle	First flip angle for T1 maps or displays flip angle used (→ Page 496 <i>Flip Angle (MapIt parameter)</i>)
Noise Threshold	Threshold below which measurement values are ignored. This suppresses noise.
Save Original Images	Save the unprocessed images in the database as well.
Measurements	Number of measurements to be performed (→ Page 412 <i>Measurements (parameter)</i>)

Contrasts	Number of contrasts (→ Page 496 <i>Contrasts (parameter)</i>)
TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)
TE	Echo time (→ Page 396 <i>TE (parameter)</i>)



The parameters are only valid for the currently selected step.

4.12.8 Inline/Cardiac parameter card

Routine	Contrast	Resolution	Geometry	System	Physio	Inline	Sequence
Subtraction	Cardiac	Composing					
Inline Evaluation T1 Map				Motion Correction Standard			
Magn. Preparation Non-sel. IR T1map							
No. of Preps 2							
Sampling Duration 1 5 Beats				Contrasts 1			
Recovery Duration 1 3 Beats				TE 1.12 ms			
				TR 280.6 ms			

Example

Inline Evaluation	Inline evaluations are performed in physiologically triggered acquisitions. (→ Page 496 <i>Inline Evaluation (parameter)</i>)
Magn. Preparation	Magnetization preparation is performed prior to data acquisition in order to influence image contrast. (→ Page 498 <i>Magn. Preparation (Inline parameter)</i>) (→ Page 382 <i>Inversion Pulse Settings dialog box</i>)
No. of preps.	Number of preparation pulses
Sampling duration	Number of heartbeats during which image data is acquired following a magnetization preparation pulse. The number depends on No. of preps.
T2 prep. duration	Duration of the T2 preparation pulse train
Recovery duration	Number of recovery heartbeats during which no images are acquired. A preparation pulse is applied, data is acquired and before the next preparation pulse is applied, a recovery time elapses in which no images are acquired.
Motion correction	Correction for in-plane motion between successive images acquired with single-shot acquisition techniques The (standard) motion correction corrects for patient movement in the image plane that occurs between the acquisition of two echo trains.
Proton Density Images	Number of proton density weighted images (→ Page 488 <i>Proton Density Images (parameter)</i>)
Save Original Images	Save the unprocessed images in the database as well. (→ Page 488 <i>Save Original Images (parameter)</i>)

Contrasts	Number of contrasts (→ Page 496 <i>Contrasts (parameter)</i>)
TE	Echo time (→ Page 396 <i>TE (parameter)</i>)
TR	Repetition time (→ Page 396 <i>TR (parameter)</i>)

4.13 Sequence parameter cards

Your system provides a number of different sequence types for measurements:

- 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)

Depending on the type of sequence associated with the measurement protocol, different display and input fields appear on the subcards of the **Sequence** parameter card.



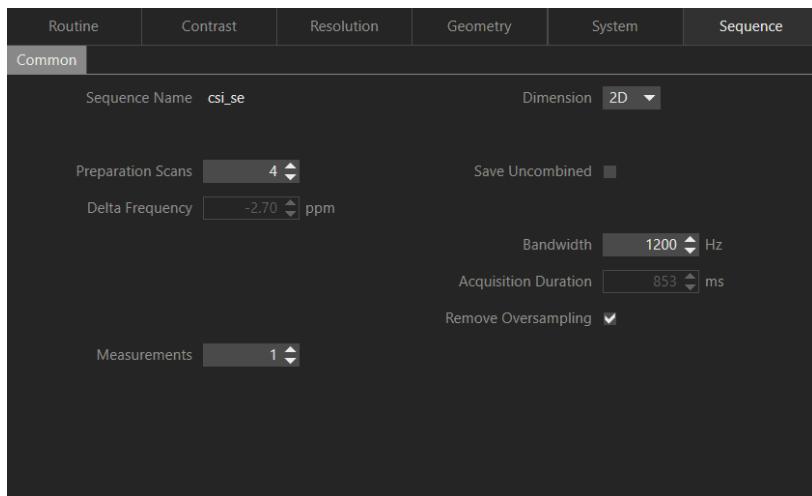
A tooltip including the name and type of sequence used will be displayed if you move the mouse pointer over the **Sequence Name** field.

The **Sequence** parameter card is divided into the following subcards:

- The **Common** subcard allows you to adjust sequence parameters for spectroscopy.
(→ Page 350 *Sequence/Common parameter card - Spectroscopy*)

- The **Part 1** and **Part 2** subcards allow you to adjust further sequence parameters.
 (→ Page 352 *Sequence/Part 1 parameter card*)
 (→ Page 354 *Sequence/Part 2 parameter card*)
- The **Nuclei** subcard allows you to adjust parameters for CSI measurements.
 (→ Page 357 *Sequence/Nuclei parameter card - Spectroscopy CSI*)

4.13.1 Sequence/Common parameter card - Spectroscopy



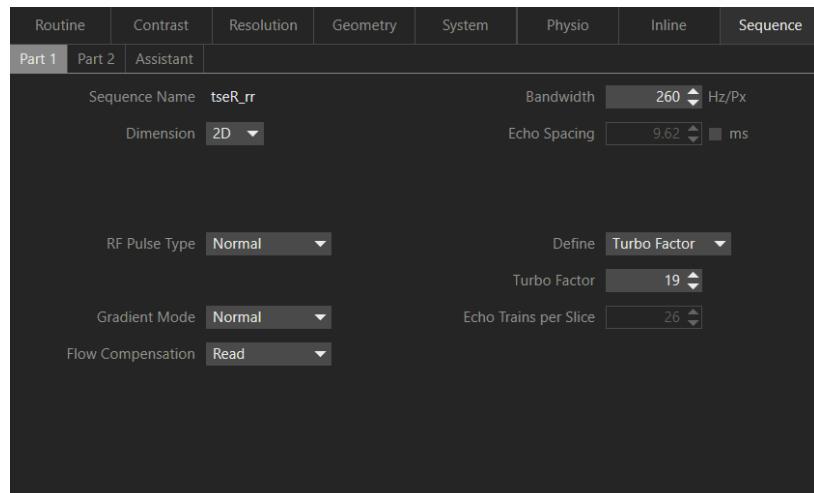
Example

The following parameters can be set depending on the measurement method (SVS or CSI):

Sequence Name	Display of the sequence name
Preparation Scans	Preliminary measurements (→ Page 498 <i>Preparation Scans (parameter)</i>)
Delta Frequency	Frequency shift for slice selection (→ Page 498 <i>Delta Frequency (parameter)</i>)

Measurements	Number of measurements (→ Page 412 Measurements (parameter))
Pause after Meas.	Pause between measurements (→ Page 413 Pause after Meas. (parameter))
Phase Cycling	Selection of a phase cycle to eliminate interference signals (→ Page 499 Phase Cycling (parameter))
Phase Encoding	Selection of a phase encoding type (→ Page 502 Phase Encoding (parameter))
Freq. Corr. Accumulation	Internal frequency correction to minimize motion artifacts (→ Page 500 Freq. Corr. Accumulation (parameter))
Ref. Scan Mode	Reference scan for eddy current correction (→ Page 500 Ref. Scan Mode (parameter))
No. of ref. scans	Number of averages acquired during the reference scan (→ Page 501 No. of ref. scans (parameter))
Dimension	Set 2D or 3D measurement. (→ Page 502 Dimension (parameter))
Save Uncombined	Save the output images of the individual coil elements.
Bandwidth	ADC bandwidth for data acquisition (→ Page 499 ADC Bandwidth (parameter))
Acquisition Duration	Readout duration (→ Page 499 Acquisition Duration (parameter))
Remove Oversampling	Oversampling data is removed. (→ Page 500 Remove Oversampling (parameter))

4.13.2 Sequence/Part 1 parameter card

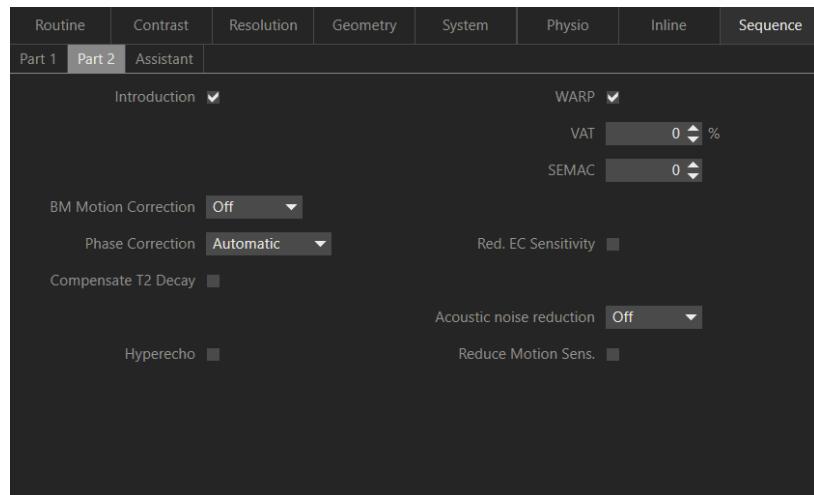


Example

Sequence Name	Display of the sequence name
Dimension	Set 2D or 3D measurement. (→ Page 502 <i>Dimension (parameter)</i>)
Elliptical scanning	Elliptical k-space sampling (→ Page 503 <i>Elliptical Scanning (parameter)</i>)
Phase Stabilization	Prevent phase errors and improves image quality. (→ Page 503 <i>Phase Stabilization (parameter)</i>)
Reordering	Acquisition sequence of raw data (→ Page 503 <i>Reordering (parameter)</i>)
Excitation	Mode for radio-frequency pulse (→ Page 511 <i>Excitation (parameter)</i>)
RF Pulse Type	Radio frequency pulse type (→ Page 510 <i>RF Pulse Type (parameter)</i>)

Gradient Mode	Mode used by the gradient system (→ Page 511 <i>Gradient Mode (parameter)</i>)
Flow Compensation	Flow compensation for moving spins (→ Page 505 <i>Flow Compensation (parameter)</i>)
Bandwidth	ADC bandwidth for data acquisition (→ Page 499 <i>ADC Bandwidth (parameter)</i>)
Echo Spacing	Interval between two echoes (→ Page 506 <i>Echo Spacing (parameter)</i>)
Turbo Factor	Number of echoes per echo train (→ Page 508 <i>Turbo Factor (parameter)</i>)
Readout Mode	Readout mode for GRE sequences (→ Page 506 <i>Readout Mode (parameter)</i>)
Sequence Type	Type of sequence (→ Page 508 <i>Sequence Type (parameter)</i>)
Adiabatic	Use a B_1 -insensitive excitation pulse (adiabatic pulse) in order to reduce the signal variation across the field of view.

4.13.3 Sequence/Part 2 parameter card



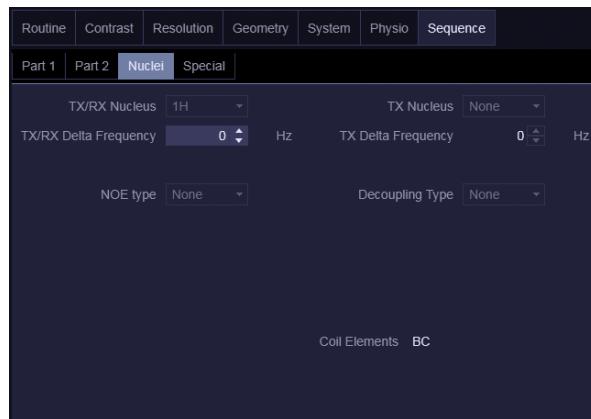
Example

Introduction	Inform the patient that measurement has started by a short knocking noise made by the gradient system.
Define	The Echo trains/Turbo factor parameters or Shots/Segment parameters are reconstructed as a function of one another. (→ Page 508 <i>Define (parameter)</i>)
Turbo Factor	Number of echoes per echo train (→ Page 508 <i>Turbo Factor (parameter)</i>)
Segments	Raw data lines in a TR (→ Page 440 <i>Segments (parameter)</i>)
Echo Train Duration	Display of duration of echo train in order to check whether the echo train is long enough for a sensible measurement
Echo Trains per Slice	Number of echo trains per slice

Slice Turbo Factor	Number of slices per echo train (→ Page 509 <i>Slice Turbo Factor (parameter)</i>)
Shots per Slice	Number of shots per slice The parameter is active only if the Define parameter is set to Shots .
EPI Factor	Number of refocused gradient echoes (→ Page 509 <i>EPI Factor (parameter)</i>)
Phase Correction	Performs a phase correction (→ Page 515 <i>Phase Correction (parameter)</i>)
Compensate T2 Decay	Prevent negative effects of T2 decay. (→ Page 503 <i>Compensation T2 Decay (parameter)</i>)
Hyperecho	The flip angle of the refocusing pulse varies across the echo train, forming a hyperecho. This mode enables T2-weighted contrast with a high signal-to-noise ratio, and is optimized for SAR.
RF Spoiling	The RF spoiler pulse is used to break down any remaining phase coherence between spins. It is used for gradient echo sequences to produce FLASH contrast.
Inc. Gradient Spoiling	Increase the gradient spoiling to improve image quality. (→ Page 513 <i>Inc. Gradient Spoiling (parameter)</i>)
BM Motion Correction	Activate motion correction with Kinetic Sensor/In-bore camera. (→ Page 513 <i>BM Motion Correction (parameter)</i>)
Phase Enc. Rewinder	Rewinds the phase encoding moment
Stereotactic	Balance stereotactic frames (→ Page 514 <i>Stereotactic (parameter)</i>)

WARP	Reduce susceptibility artifacts if the patient has MR Conditional orthopedic implants. (→ Page 514 <i>WARP (parameter)</i>)
VAT	Reduce image distortions by applying additional frequency encoding gradients. (→ Page 515 <i>VAT (parameter)</i>) Only available if WARP is selected.
SEMAC	Specify number of additional encoding steps to correct for distortions caused by MR Conditional orthopedic implants (→ Page 516 <i>SEMAC (parameter)</i>) Only available if WARP is selected.
SAR Optimization	Reduce the energy applied by the sequence but does not influence supervision of the SAR or SAR limits. (→ Page 516 <i>SAR Optimization (parameter)</i>)
Red. EC sensitivity	Reduce eddy current sensitivity
Acoustic Noise Reduction	Activate the acoustic noise reduction to increase patient comfort during the examination.
Reduce Motion Sens.	Reduce motion artifacts (→ Page 508 <i>Reduce Motion Sens. (parameter)</i>)

4.13.4 Sequence/Nuclei parameter card - Spectroscopy CSI



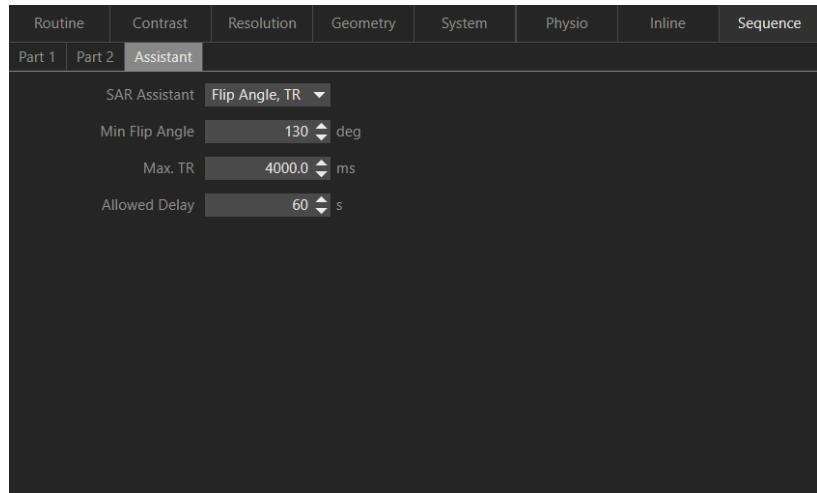
Example

The **Sequence/Nuclei** parameter card is available for CSI measurements when a ^{31}P measurement protocol is selected.

TX/RX Nucleus	Primary nucleus for the measurement For a ^{31}P MRS measurement, select the corresponding ^{31}P nucleus.
TX/RX Delta Frequency	Frequency shift for receiving the signal from the primary nucleus. The frequency shift applies to the adjustment frequency for the primary nucleus.
NOE Type	Pulse type for the ^1H saturation pulse
NOE Count	Number of ^1H saturation pulses that are transmitted during data acquisition of the ^{31}P signal
NOE Duration	Pulse duration of a ^1H saturation pulse
NOE Pause	Time interval between two ^1H saturation pulses
NOE Flip Angle	Flip angle of the ^1H saturation pulse (→ Page 517 <i>NOE Flip Angle (parameter)</i>)

TX Nucleus	¹ H nucleus as a secondary nucleus (enhances the ³¹ P signal for ³¹ P MRS measurements) During data acquisition, ¹ H saturation pulses are transmitted to strengthen the ³¹ P signal.
TX Delta Frequency	Frequency shift for sending the saturation pulse for the secondary nucleus. The frequency shift applies to the adjustment frequency for the secondary nucleus.
Decoupling Type	Mode for ¹ H decoupling (→ Page 517 <i>Decoupling Type (parameter)</i>)
Decoupling Duration	Mode for ¹ H decoupling (→ Page 517 <i>Decoupling Duration (parameter)</i>)
DC Total Duration	Proportion of decoupling duration relative to the readout duration (→ Page 518 <i>DC Total Duration (parameter)</i>)
DC Pause Fract.	Time interval between the ¹ H decoupling pulses (for ³¹ P-MRS with Waltz-4 decoupling) (→ Page 518 <i>DC Pause Fract. (parameter)</i>)
Decoupling Flip Angle	Flip angle of the ¹ H decoupling pulse (for ³¹ P-MRS) (→ Page 518 <i>Decoupling Flip Angle (parameter)</i>)
Coil Elements	Display of the selected coils and coil elements You set the coils on the System/Coils parameter card.

4.13.5 Sequence/Assistant parameter card

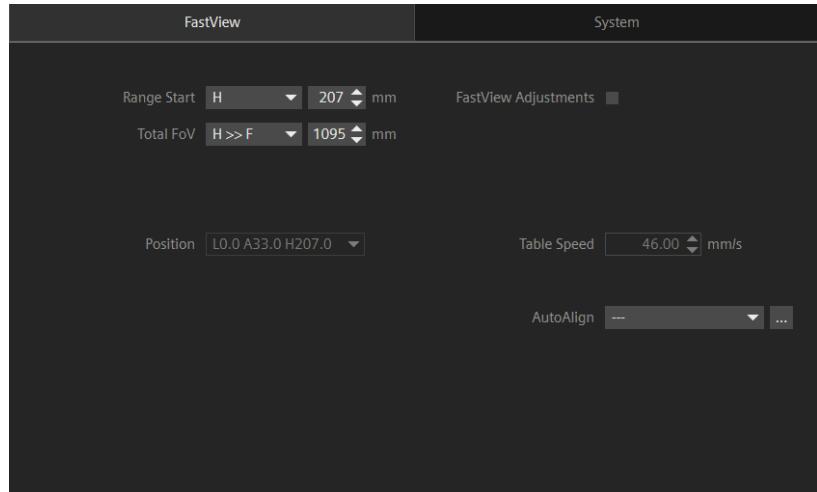


Example

This parameter card is used define the strategy to avoid the SAR limit from being exceeded.

SAR Assistant	Strategy to avoid the SAR limit from being exceeded (→ Page 519 <i>SAR Assistant (parameter)</i>)
Min Flip Angle	Allowed minimum value for the flip angle.
Max. TR	Allowed maximum value for the TR.
Allowed Delay	Maximum delay time after the end of the measurement (→ Page 505 <i>Allowed Delay (parameter)</i>)

4.14 FastView parameter card



Example

The **FastView** parameter card allows you to adjust parameters for the FastView localizer.

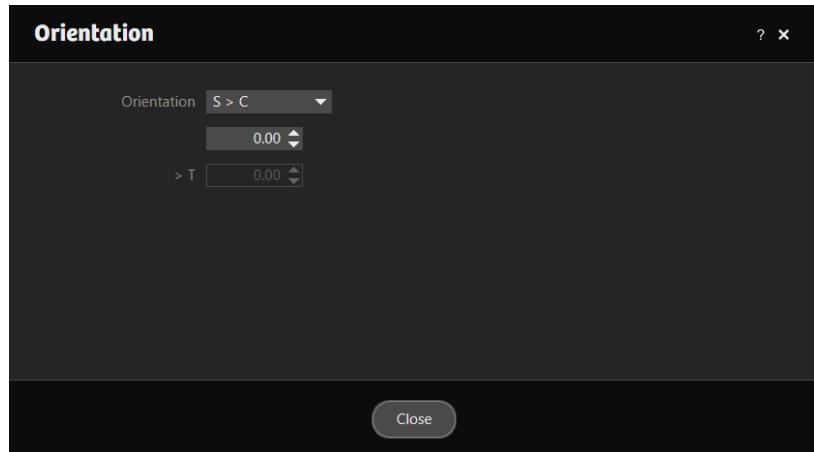
Range Start	Starting position of measurement region (→ Page 439 <i>Range Start (parameter)</i>)
Total FoV	Total length of measurement region (→ Page 440 <i>Total FoV (parameter)</i>)
Position	Display of the position of the slice group
FastView Adjustments	Perform FastView adjustments
Table Speed	Display of the table movement speed

4.15 Parameter dialog boxes

Various parameters are available on several parameter cards.

These additional parameters are accessible via the [...] button.

4.15.1 Orientation dialog box



Example

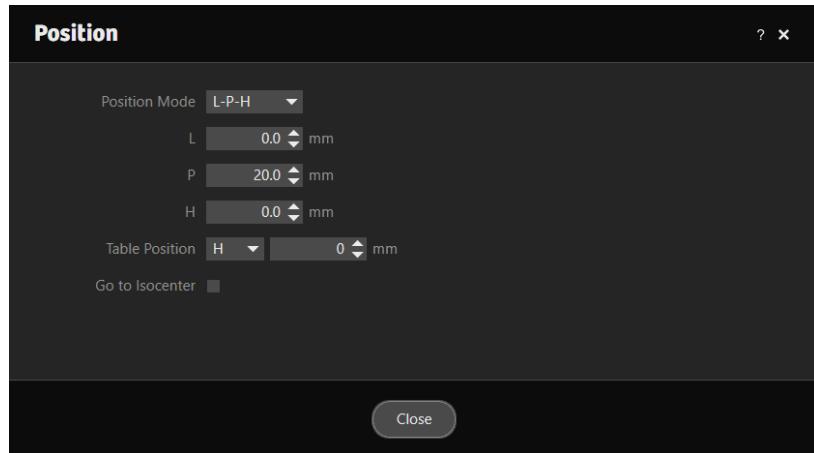
The **Orientation** determines the orientation of the slice and/or slab.

Starting from a main orientation, you can rotate or tilt the graphical object at precise angles.

The values refer to the whole body patient coordinate system.

- **Orientation:** Direction of the tilt
- Center input field: Flip angle (for single oblique slices)
- **>T:** Flip angle for the third orientation plane (for double-oblique slices)

4.15.2 Position dialog box



Example

In the **Position** dialog box, you define the shift of the object center outside the magnet isocenter.

You can position graphics objects to within one tenth of a millimeter.

The **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**: Toward 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 retained after the current positioning. The next time you open the **Position** dialog box (even from another protocol), the position mode previously selected will still be applied.

Determining the direction for shifting the center of the object out of the magnet isocenter.

The **Table Position** determines the table position at which the protocol is measured. The zero point is defined by the initial table position of the first measurement of a series block.

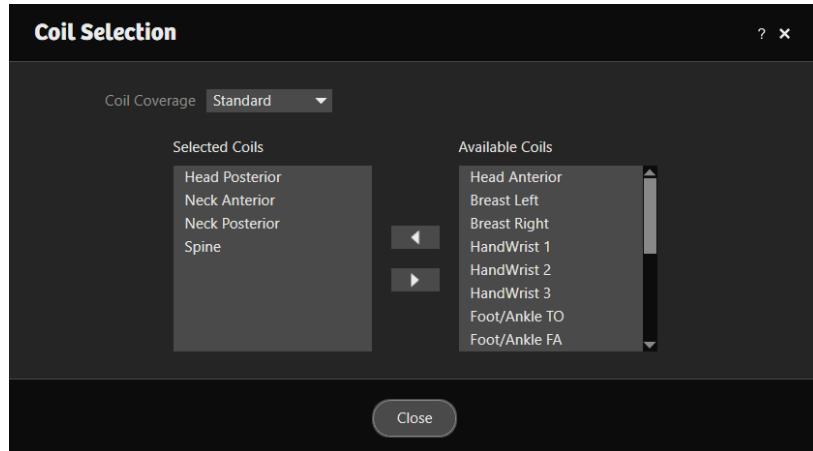
The selection list defines the direction of movement:

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

The input field defines the distance in mm.

With **Go to Isocenter**, you can specify that measurement is performed at the isocenter (irrespective the set **Positioning Mode**).

4.15.3 Coil Selection dialog box



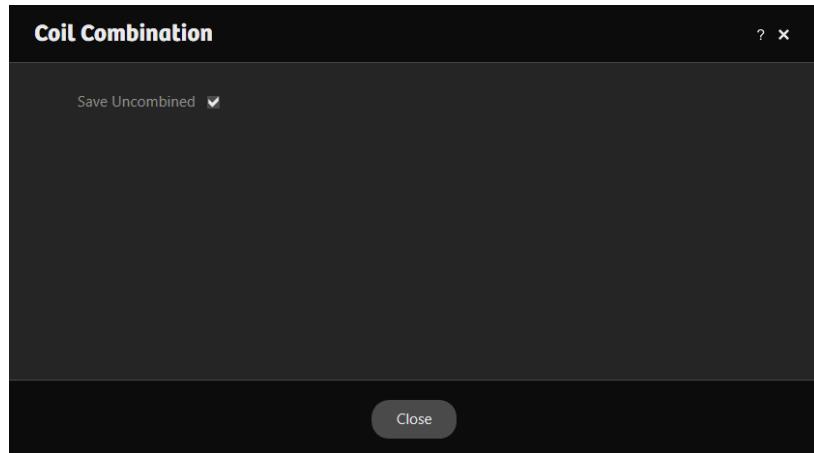
Example

With **Coil Coverage**, you can adapt the sensitivity for automatic coil selection, by involving fewer or more coils for a given FOV.

- **Standard** (default)
- **Minimal** involves a minimum set of coils located at the edge of the FOV.
- **Generous** involves additional coils located at the edge of the FOV.

For **ACS Restricted** mode, you can restrict automatic selection of coil elements to individual coils, by moving them from the **Available Coils** into the **Selected Coils** area using the arrow buttons.

4.15.4 Coil Combination dialog box



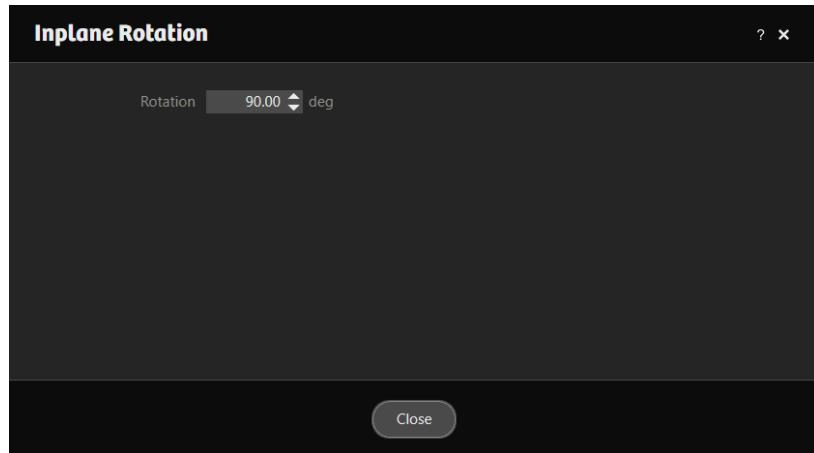
Example

The **Save Uncombined** parameter determines whether, in addition to the combined images of an array coil, the output images of the individual coil elements will be saved.



Save Uncombined mode cannot be combined with **Adaptive Combine** mode under the **Coil Combine Mode** parameter.

4.15.5 Inplane Rotation dialog box



Example

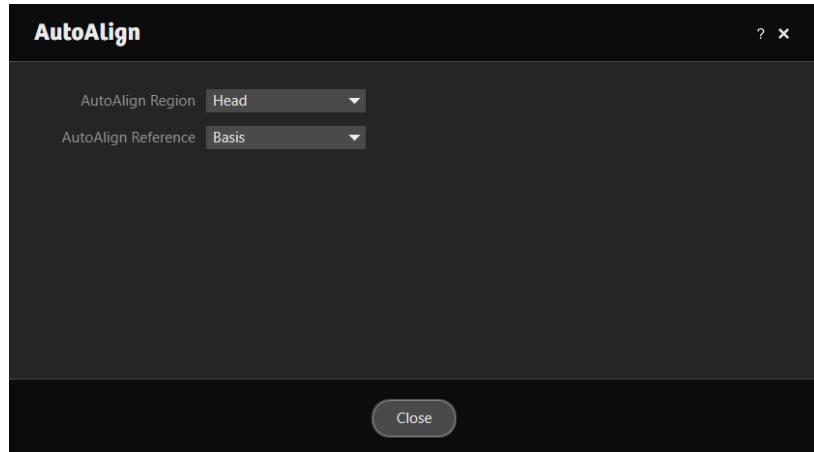
Set the **Rotation** angle in the slice plane.



The **Auto** check box is available if **Coronal** is not selected in the **Orientation** dialog box.

If the **Auto** check box is selected, the rotation in the slice plane will be calculated automatically.

4.15.6 AutoAlign dialog box

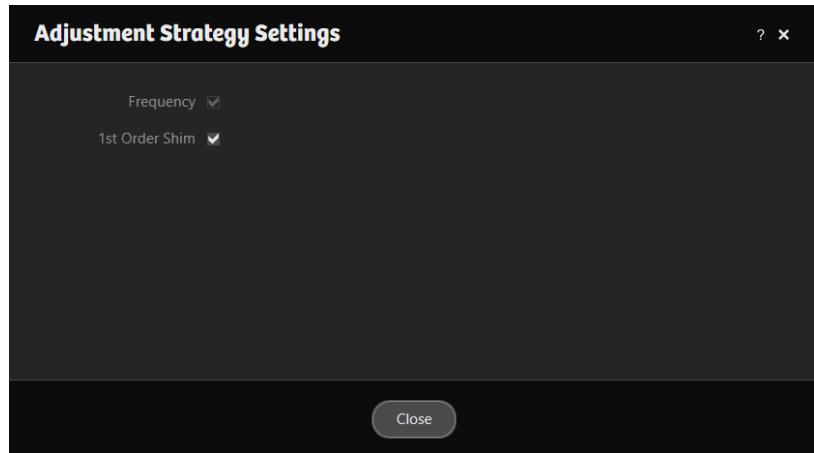


Example

Here, you can set the region, the reference, and different geometry parameters.

- The **AutoAlign Region** defines the anatomical region for **AutoAlign**, e.g., Head, Spine, Knee.
- At least one **AutoAlign Reference** is predefined for every anatomical region. Usually, there are several predefined references for the head region.

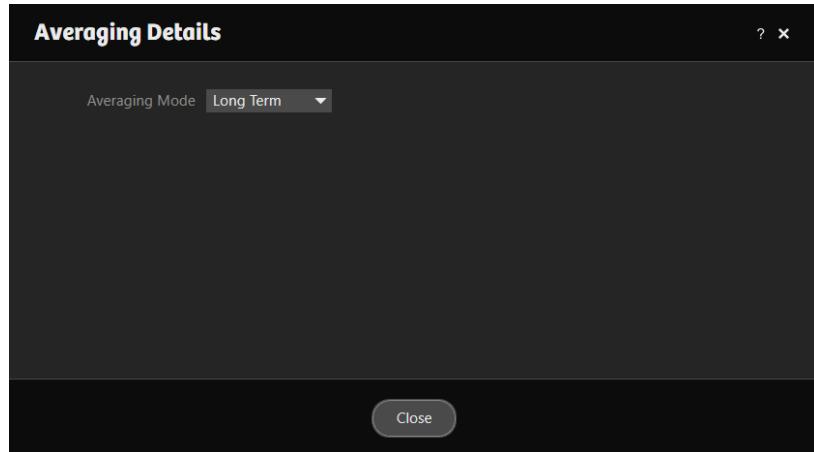
4.15.7 Adjustment Strategy dialog box



Example

- **Frequency** activates frequency adjustment to apply on a slice-by-slice basis (**SliceAdjust**).
- **1st Order Shim** activates first order shim adjustments (**SliceAdjust**)
- **TX Reference** activates TX reference adjustment to apply on a slice-by-slice basis (**SliceAdjust**).
- **pTx** activates pTx adjustment to apply on a slice-by-slice basis (**SliceAdjust**)

4.15.8 Averaging Details dialog box



Example

The **Averaging Mode** parameter defines the method for averaging the measurements:

- **Short term:** Gives a better signal-to-noise ratio while maintaining the best resolution.
- **Long term:** Gives a better signal-to-noise ratio with optimized suppression of motion artifacts.

For a spectroscopy CSI measurement protocol:

- **Short term:** Measures all averages for a point in the data matrix directly in sequence, and only then goes to the next point in the data matrix. This provides a better signal-to-noise ratio while maintaining the best resolution.
- **Long term:** Measures all points of the data matrix before the data for the next average is acquired. This results in a better signal-to-noise ratio when suppression of motion artifacts is optimized.



CSI (Chemical Shift Imaging) measurements can be terminated in **Long term** mode without having to completely discard the acquired data.

This may be necessary if there is a danger of motion artifacts.

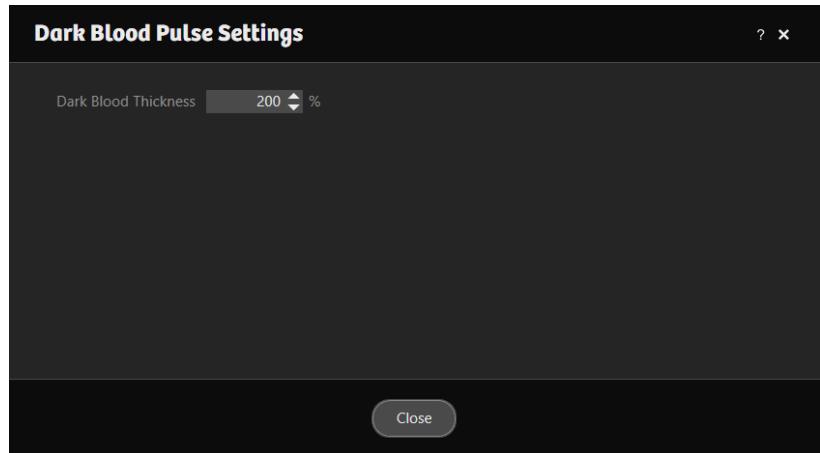
At least one average has to be acquired to enable a measurement to be terminated without complete loss of data.

The **Inline Display** provides information regarding the averaging that was just performed.

For a spectroscopy SVS measurement protocol:

- **Save Single Averages:** Determines whether single averages will be saved as well.

4.15.9 Dark Blood Pulse Settings dialog box



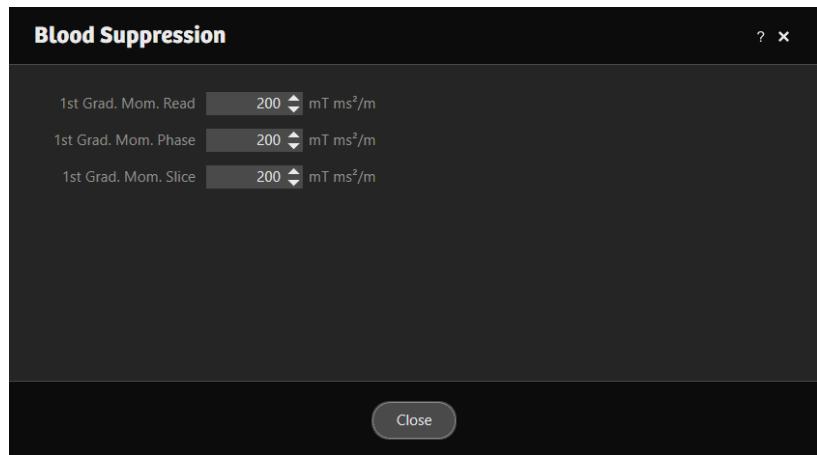
Example

The **Dark Blood Thickness** parameter sets the slice thickness of the preparation pulse to saturate the blood. The thickness is expressed as a percentage of the slice thickness.



A typical value is a slice thickness which is double that of the measurement slice.

4.15.10 Blood Suppression dialog box



Example

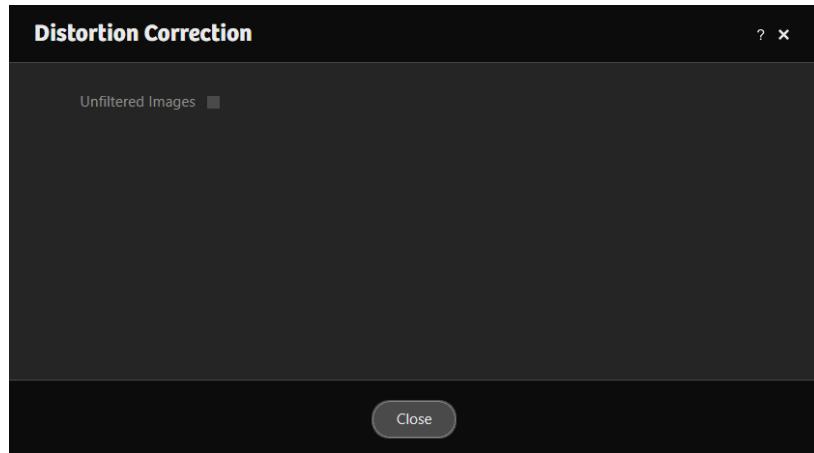
Here, you can set the b-values for the **Blood Suppression** parameter.

- **1st Grad. Mom. Read** sets the gradient moment (first order) in the read direction for blood suppression.
- **1st Grad. Mom. Phase** sets the gradient moment (first order) in the phase direction for blood suppression.
- **1st Grad. Mom. Slice** sets the gradient moment (first order) in the slice direction for blood suppression.



The tooltip shows the resulting b-value.

4.15.11 Distortion Correction dialog box



Example

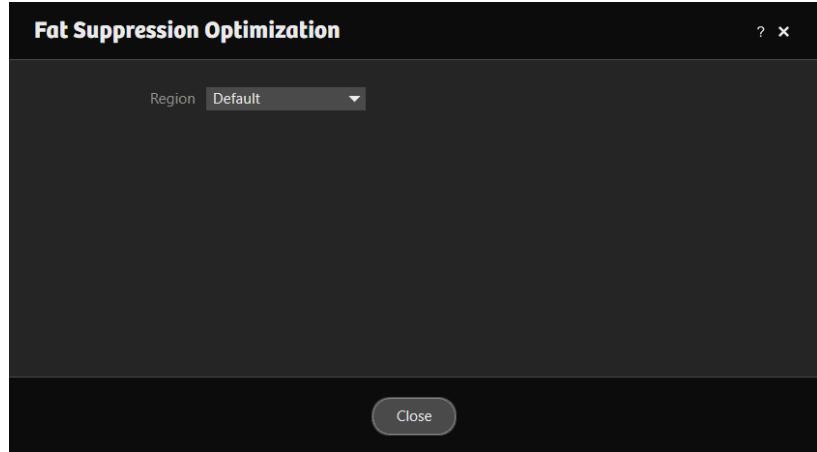
The **Unfiltered Images** parameter sets whether unfiltered images will be saved as well.



If you have 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**.

4.15.12 Fat Suppression Optimization dialog box



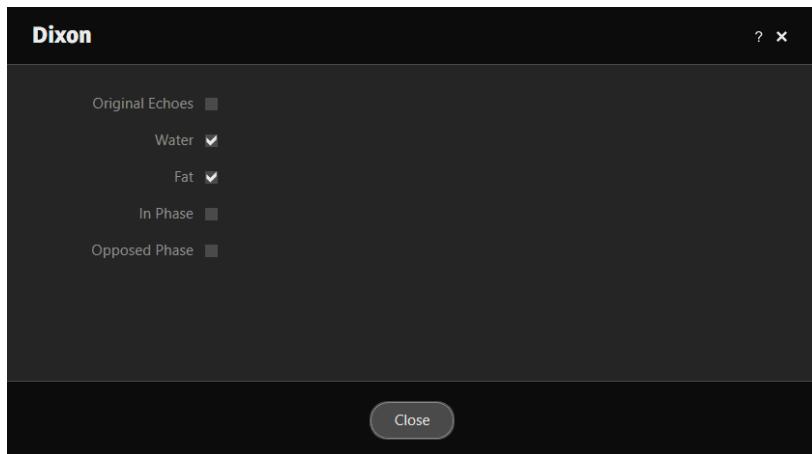
Example

- Fat saturation can be optimized region-specifically with the **Region** parameter:
 - **Default:** Standard fat saturation mode behavior
 - **Abdomen:** Fat saturation for abdomen
 - **Joint:** Fat saturation for joints
 - **C-Spine:** Fat saturation for c-spine
- **Water** controls if a water image is reconstructed.
- **Water fraction** controls if a water fraction image is reconstructed.
- **Fat** controls if a fat image is reconstructed.
- **Fat fraction** controls if a fat fraction image is reconstructed.
- **T2*** controls if a T2* image is reconstructed.
- **R2*** controls if a R2* image is reconstructed.
- **In Phase** controls if an -in-phase image is reconstructed.

- **Opposed Phase** controls if an opposed-phase image is reconstructed.
- **Report** controls if a detailed Dixon evaluation report is created in the postprocessing.

i If an entry other than **Default** for **Region** is selected, the entry in the **Fat Saturation** dialog box will be marked by an asterisk *.

4.15.13 Dixon dialog box



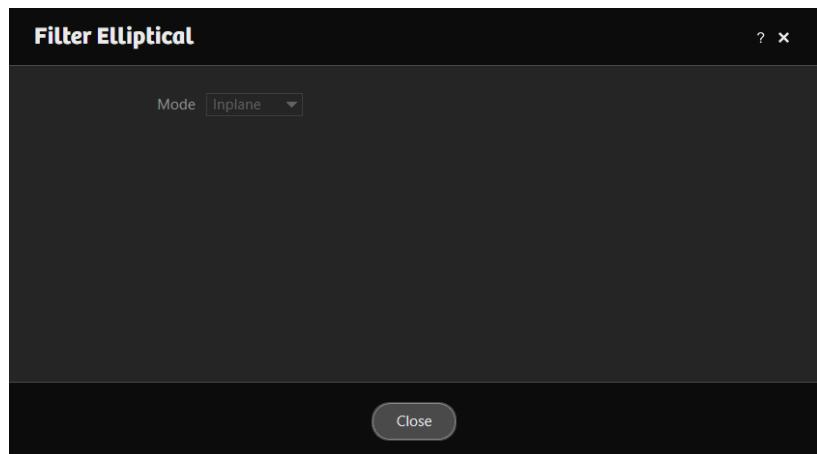
Example

Here, you can activate the detailed postprocessing options for Dixon.

- **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.

- **Fat fraction** controls if a fat fraction image is reconstructed.
- **Water fraction** controls if a water fraction image is reconstructed.
- **T2*** controls if a T2* image is reconstructed.
- **R2*** controls if a R2* image is reconstructed.
- **Report** controls if a detailed Dixon evaluation report is created in the postprocessing.

4.15.14 Filter Elliptical dialog box

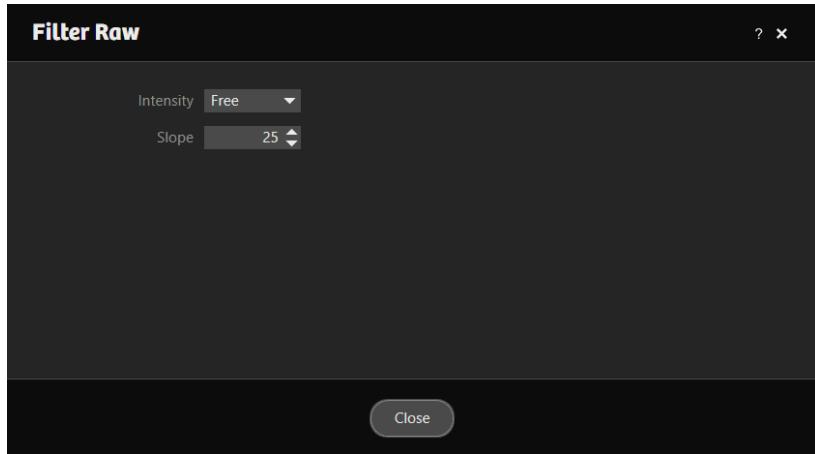


Example

The **Mode** parameter defines the usage of the elliptical filter:

- **In Plane:** The filter is only used within the image planes.
- **Volume:** The filter is applied to the entire volume.

4.15.15 Filter Raw dialog box



Example

The **Intensity** parameter determines to what extent the filter will be applied.

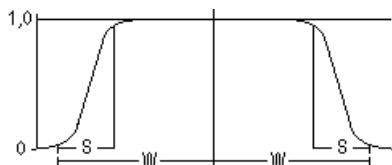
The following filter intensities can be set:

- **Weak**
- **Medium**
- **Strong**
- **Free:** Freely define the **Slope** of the filter.



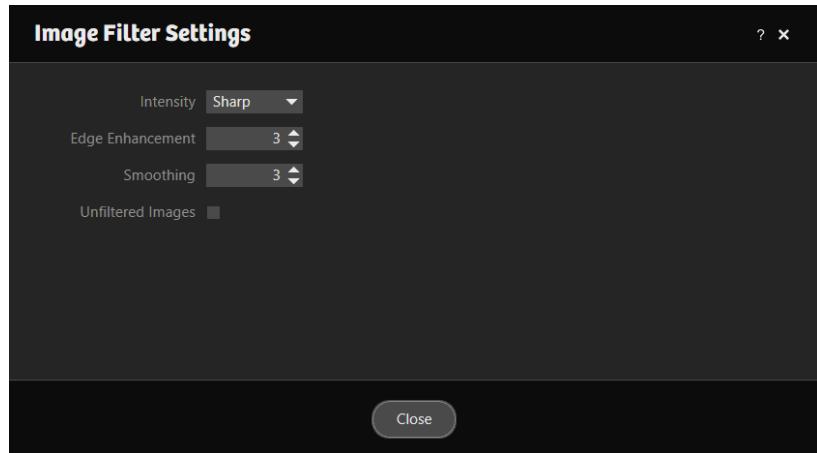
The image will be more homogeneous if the filter intensity is increased. However, image contrast may be compromised at the same time. This means that weak filters should be used whenever possible.

The **Slope** parameter shows the slope gradient at the edges of the filters.



S: Slope at the edges of the filter, **W:** Filter width

4.15.16 Image Filter Settings dialog box



Example

The **Intensity** parameter determines the extent to which the filter will be applied.

The following filter intensities can be set:

- **Weak**
- **Medium**
- **Strong**

The **Edge Enhancement** parameter determines the strength for the edge enhancement filter.

The **Smoothing** parameter determines the strength for the smoothing filter.

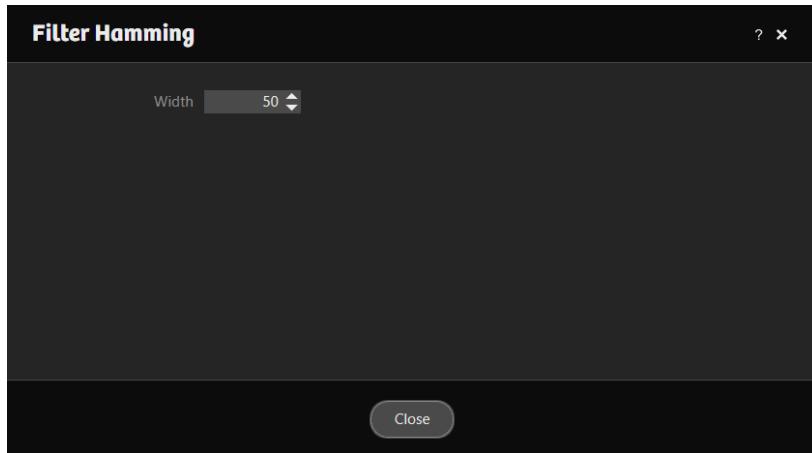
The **Unfiltered Images** parameter determines whether unfiltered images will be saved as well.



If you have 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**.

4.15.17 Filter Hamming dialog box

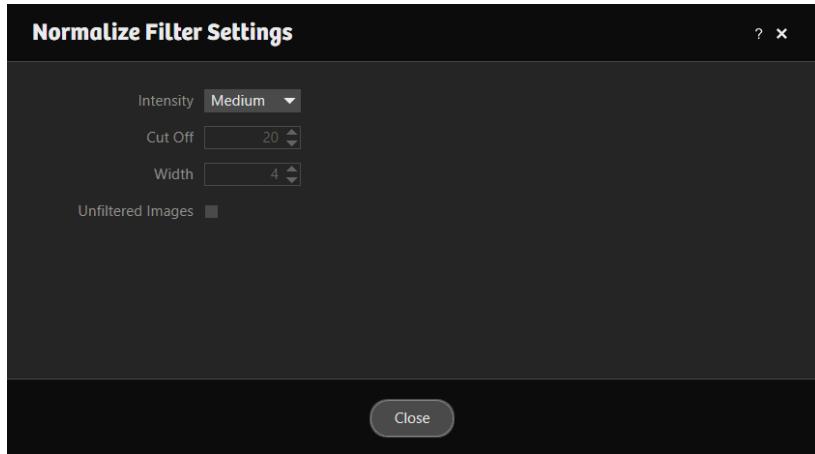


Example

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

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

4.15.18 Normalize Filter Settings dialog box



Example

The **Intensity** parameter determines the extent to which the filter will be applied.

The following filter intensities can be set:

- **Weak**
- **Medium**
- **Strong**
- **Free:** Freely define the **Cut Off** and **Width** of the filter.

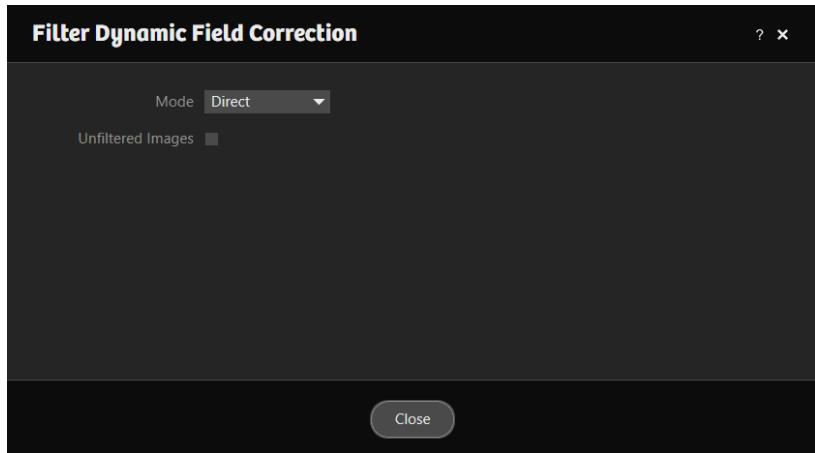
The **Unfiltered Images** parameter determines whether unfiltered images will be saved as well.



If you have 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**.

4.15.19 Filter Dynamic Field Correction dialog box



Example

The dynamic field correction filter reduces eddy current induced distortions of diffusion-weighted images.

The **Mode** parameter defines the filter mode:

- **Direct:** Each diffusion-weighted image is allocated to a corresponding undistorted reference image. If the measurement protocol does not contain reference images, additional scans are performed at the beginning of the data acquisition.

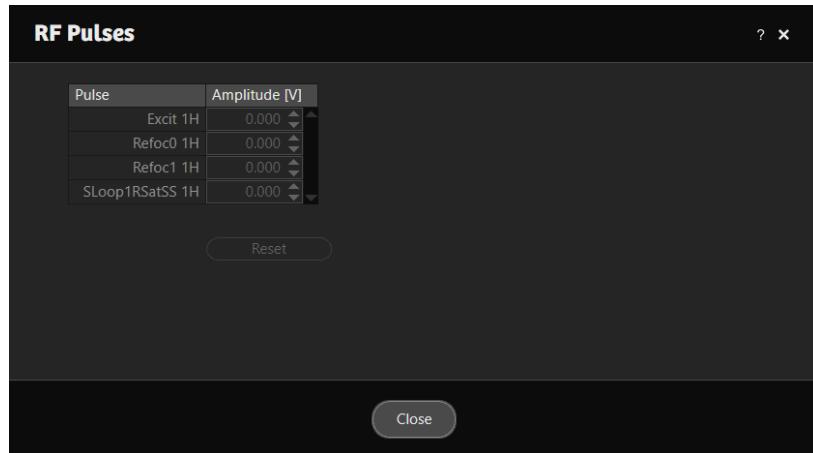
This option is recommended for diffusion-weighted images with a sufficient SNR.

- **Adjustment:** A number of dedicated adjustment scans are performed at the beginning of data acquisition. The actual imaging scans are allocated 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.

The **Unfiltered Images** parameter determines whether unfiltered images should be saved as well.

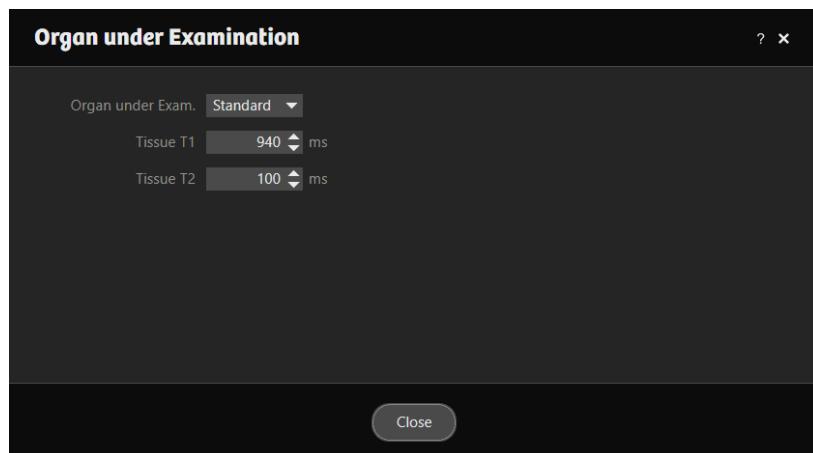
4.15.20 RF Pulses dialog box



Example

In the **RF Pulses** dialog box, you can adjust the amplitudes of the excitation pulses.

4.15.21 Organ under Examination dialog box



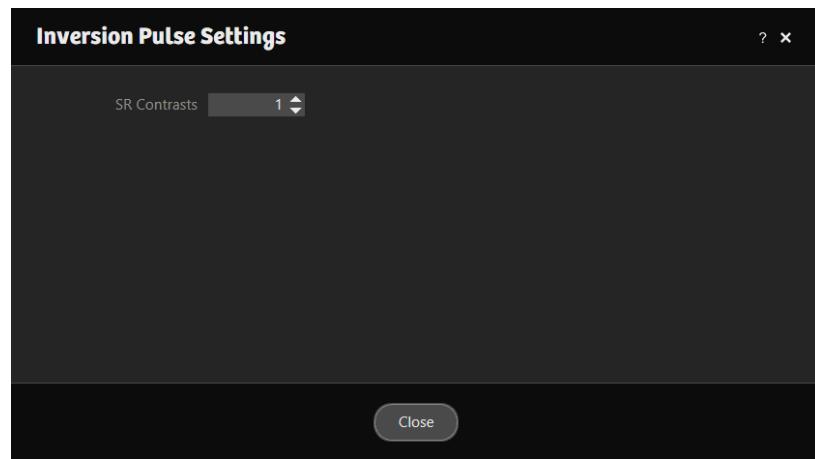
Example

Organ under Exam.: Set organ under examination

Tissue T1: Specify T1 value for the tissue of interest

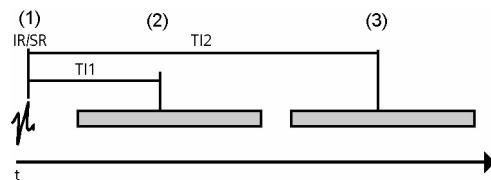
Tissue T2: Specify T2 value for the tissue of interest

4.15.22 Inversion Pulse Settings dialog box



Example

The IR Contrast or SR Contrast parameter enables multiple contrasts with different times for inversion recovery (IR) or saturation recovery (SR). It determines the number of editable contrast times.



Multiple contrast measurement

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



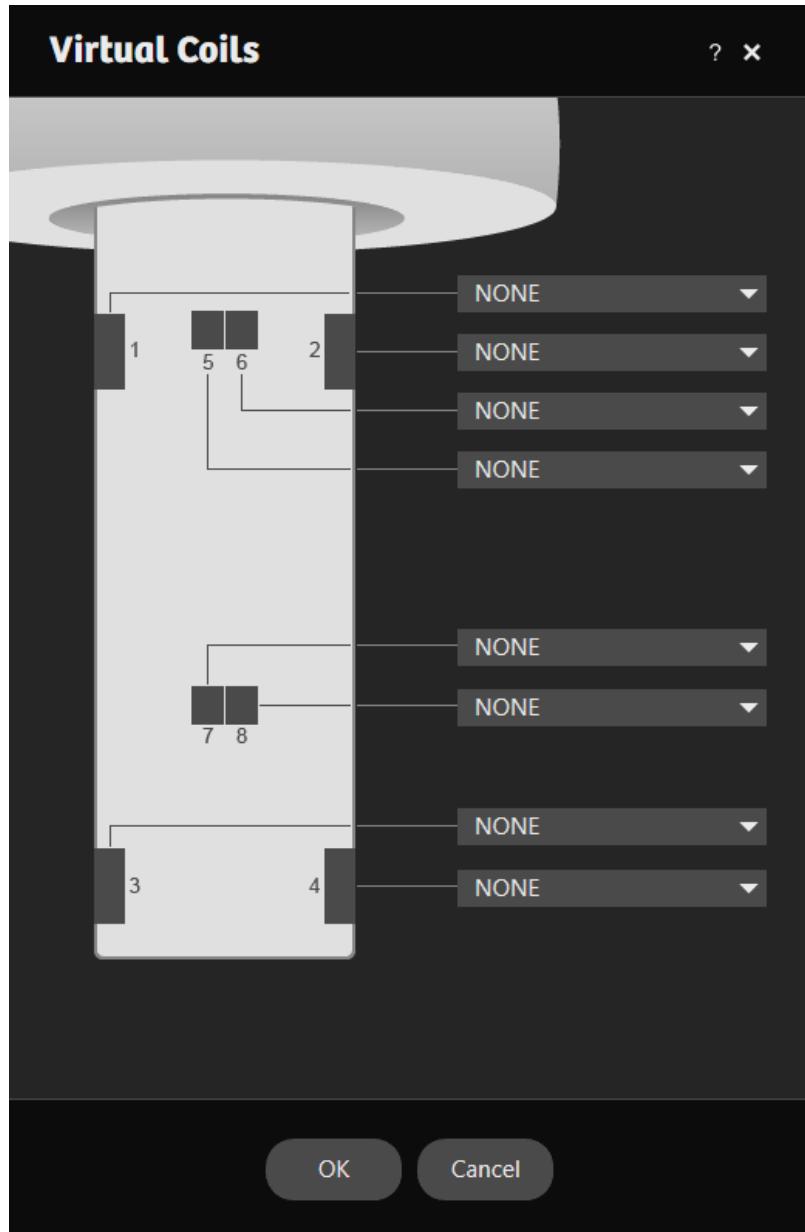
The **IR Contrasts** parameter is visible only if **Magn. Preparation** is set to **Slice-sel. IR** or **Non-sel. IR**.

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



The parameter is available only for a few sequences.

4.15.23 Virtual Coils dialog box



Example

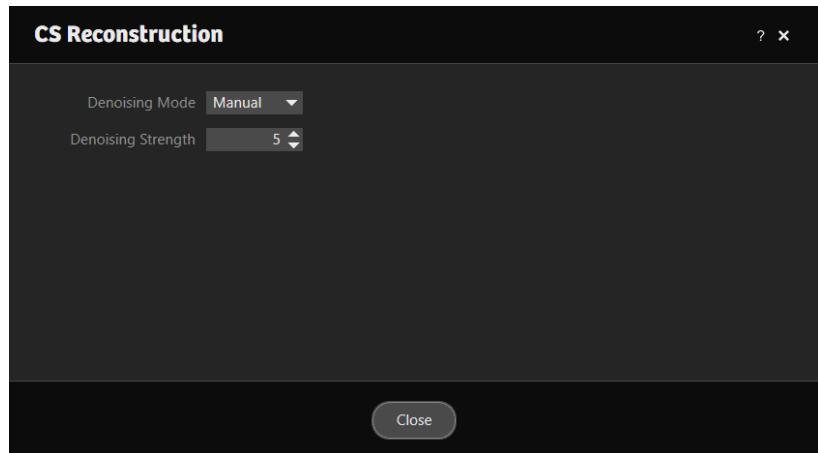
Using virtual coils, you can prepare protocols with coils that are not currently plugged into system. These coils are called virtual coils.

The **Virtual Coils** dialog box shows the stylized table and the positions of the virtual coils.

Select the coil elements that are inside the region under examination.

All supported coil plugs are offered for the simulation. An error message is shown when you select a coil combination that is not possible. Coil combinations that are theoretically possible but without relevance in practical application are not checked.

4.15.24 CS Reconstruction dialog box



Example

In the **CS Reconstruction** dialog box, you can define the denoising mode and strength for Compressed Sensing (CS) protocols.

The denoising mode determines how the denoising strength is adjusted. The denoising strength, that is, the regularization parameter in Compressed Sensing reconstruction, influences the overall image appearance. It controls the balance between noise amplification and image smoothing.

Denoising Mode:

- **Automatic:** The denoising strength changes automatically depending on the imaging protocol.
- **Manual:** The denoising strength can be set explicitly.



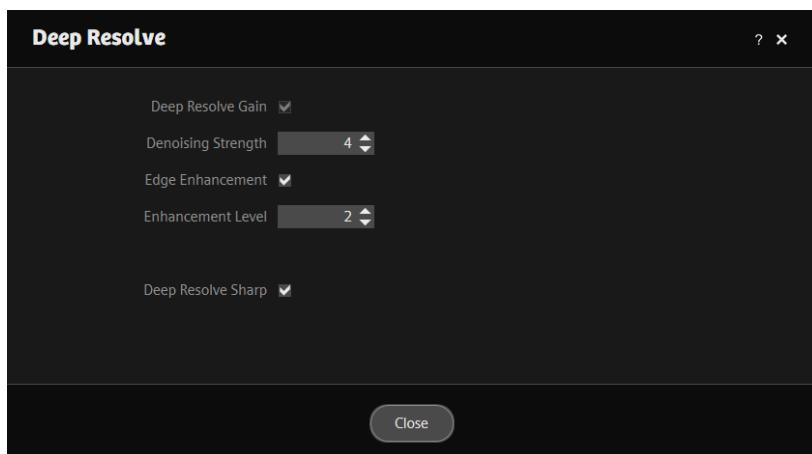
Automatic denoising mode is recommended for CS protocols.

In **Manual** denoising mode, changes to protocol parameters will not automatically update the denoising strength.

Denoising Strength:

- The lower the value, the noisier the image; the higher the value, the smoother the image.
- This parameter is only available if the **Manual** denoising mode is selected.

4.15.25 Deep Resolve dialog box



Example

Here, you can fine-tune the advanced reconstruction mode **Deep Resolve** (for TSE sequence only).

- **Deep Resolve Gain:** Apply a denoising algorithm during image reconstruction to improve the SNR of the acquired images. This check box is permanently selected.

If the denoising algorithm fails on certain image slices, for example, due to insufficient SNR, then this image will nevertheless contain the image text "DRG", but a comment is added stating that this slice could not be denoised.

- **Denoising Strength:** Set strength of denoising algorithm
- **Edge Enhancement:** Maintain image sharpness
- **Enhancement Level:** Set degree of edge enhancement
- **Deep Resolve Sharp:** Reconstruction method that increases the perceived sharpness of the images by using an improved interpolation. The degree of interpolation is still controlled by the **Phase Resolution** and **Interpolation** parameters. This means that if no interpolation is selected (**Phase Resolution** = 100 % and **Interpolation Off**), **Deep Resolve Sharp** is not active.

4.16 Parameters

This section lists most of the measurement parameters (unsorted).

All the measurement parameters are located on the parameter cards or in the parameter dialog boxes.

(→ Page 260 *General information*)

(→ Page 360 *Parameter dialog boxes*)



Not all parameters are available for all sequences.

The availability of a parameter depends on the sequence, the installed licenses, and the settings of other parameters.



When a parameter option in a selection list is displayed in angle brackets <...>, other parameters must also be changed to activate the option.

Numeric values are marked red in this case.

Values marked green can be adjusted without changing any other parameter.

4.16.1 Slice Group (parameter)

The slices of a measurement protocol are grouped together to form slice groups.

The **Slice Group** parameter shows the number of the currently displayed slice group.

All slice parameters that are currently seen on the **Routine** or **Geometry** card refer to this slice group.

4.16.1.1 Displaying the parameters of another slice group

The selection list of the field **Slice Group** shows how many slice groups are planned in the current measurement protocol.

- ◆ Select another slice group from the list to check its parameters and change them, if necessary.

4.16.1.2 Creating a new slice group

- ◆ Click the + button next to the **Slice Group** selection list to create a new slice group.

The new slice group is inserted in the selected reference image. It is slightly offset with respect to the existing outside group to avoid covering it up.

4.16.1.3 Deleting a slice group

- 1 Select a slice group.

- 2 Click the - button next to the Slice Group selection list to delete the selected slice group.

4.16.2 Slices (parameter)

The number of slices defines the extent of the examination in the slice-selection direction.

The **Slices** parameter determines the number of slices in a slice group.

The larger the number of slices to be measured, the longer the measurement time for sequential multislice measurements.

The number of slices possible with multiple slice measurements depends on the repetition time TR. This means you can only increase the number of planned slices for a constant repetition time within the range limit. If the limit is exceeded, the TR is automatically adjusted by the system.



If you use more than one slice group and move the mouse pointer over the Slices field, you will see a tooltip stating the total number of slices planned in your measurement protocol.

4.16.3 Distance Factor (parameter)

The **Distance Factor** parameter determines the gap between slices and/or slabs of a group as a percentage.

At 100%, the gap between the slices/slabs is exactly one slice/slab thickness. Negative values result in overlapping of slices.



Negative distance values must not be entered for 3D measurements.



If you move the mouse pointer over the input field, a tooltip is displayed indicating the distance between slices or slabs in millimeters.

4.16.4 Slice Thickness (parameter)

Together with the number of slices, the **Slice Thickness** determines the extent of the measurement region 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. Changing the slice thickness changes the distance between slices since the distance factor remains constant.

3D measurements: In the case of 3D measurements, the slice thickness is the thickness of the individual slices within the slabs (partitions). If you change the slice thickness for 3D measurements, the slab thickness also changes.



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

4.16.5 Position (parameter)

The **Position** 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 the phase-encoding direction
- **Read Offcenter:** Shift in the readout direction
- **Slice shift:** Shift in the slice-selection direction



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

MR Spectroscopy: For a SVS measurement, the **Position** parameter defines the position of the center of the VOI; for CSI measurement, it defines the common position of the CSI slice (or CSI slab) and the VOI.

4.16.6 Orientation (parameter)

The **Orientation** parameter indicates the position of the object in space based on the whole body patient coordinate system.

- **Sagittal**
- **Coronal**
- **Transverse**

MR Spectroscopy: For a SVS measurement, the **Orientation** parameter defines the orientation of the VOI; for a CSI measurement, it defines the common orientation of the CSI slice (or CSI slab) and the VOI.



For spectroscopy measurements of the head, always select the basic **Transverse** orientation. Since you can freely select the extent of the VOI, this does not constitute a real limitation. The basic **Transverse** orientation effects a temporal sequence for slice selection, which is proven to be the preferred method for spectroscopy applications of the head (T. Ernst, L. Chang; Magn. Reson. Med., 36; 462-468; 1996).

4.16.7 Phase Encoding Dir. (parameter)

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

With the **Phase Encoding Dir.** parameter, you can 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.



The **Phase Encoding Dir.** selection list provides only possibilities that would be useful during current orientation.

4.16.8 Phase Oversampling (parameter)

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 used to avoid aliasing artifacts that occur when excited structures are larger than the field of view (FOV) in the phase-encoding direction. Areas that are truncated are still within the sensitive range of the coils and become visible at the opposite side of the image (convoluted).



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

Phase oversampling is indicated as a percentage of the field of view (FOV) in the phase-encoding direction.

Example: With 30% phase oversampling, the measurement region increases by 15% on both sides of the FOV in phase-encoding direction.



Oversampling is performed automatically in the readout direction, since it does not extend the measurement time.

4.16.9 Slice Oversampling (parameter)

Slice oversampling increases the phase-encoded area symmetrically on both sides of the slab in the slice-selection direction.

The slices are reconstructed but not displayed in the image. Using this method prevents aliasing artifacts in the slice-selection direction in 3D measurements.

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



Slice oversampling, like phase oversampling, increases the measurement time and improves the signal-to-noise ratio.

4.16.10 Slab Group (parameter)

The slabs of a measurement protocol are grouped together to form slab groups.

The **Slab Group** parameter shows the number of the slab group currently displayed.

All slice parameters, currently seen on the **Routine** or **Geometry** card refer to this slab group.

4.16.10.1 Displaying the parameters of another slab group

In the selection list of the field **Slab Group**, you can see how many slab groups are planned for the current measurement protocol.

- ◆ Select a different slab group from the list to check its parameters and change them, if necessary.

4.16.10.2 Creating a new slab group

- ◆ Click the + button next to the selection list **Slab Group** to create a new slab group.

The new slab group will be inserted in the selected reference image. It is slightly offset from the existing outside group to avoid covering it up.

4.16.10.3 Deleting a slab group

- 1 Select a slab group.
- 2 Click the - button next to the selection list **Slab Group** to delete the selected slab group.

4.16.11 Slabs (parameter)

The **Slabs** parameter defines the number of slabs, and therefore, the extent of the measurement in the slice-selection direction.

The larger the number of slabs, the longer the measurement time for sequential multislice measurements.

The number of slabs possible with multiple slice measurements depends on the repetition time TR. As a result you are only permitted to increase the number of slabs for a constant repetition time within the range limit. If the limit is exceeded, the TR is automatically adjusted by the system.



If you use more than one slab group and move the mouse pointer over the field **Slabs**, a tooltip is displayed indicating the total number of slabs planned in your measurement protocol.

4.16.12 Slices per Slab (parameter)

Slices per Slab shows the number of slices (partitions) per slab.

Each time you change the number of slices per slab, the thickness of the slab and slice oversampling will be adjusted automatically. The thickness of the slab is calculated from the slice thickness and the number of slices. The slice oversampling is expressed as a percentage of the slab thickness.



Position the mouse pointer over the input field. A tooltip stating the resulting slab thickness in millimeters will be displayed.

4.16.13 FoV Read, FoV Phase (parameter)

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).

FoV Phase displays the FOV in the phase-encoding direction (**FoV Phase**) as a percentage of the FOV in the readout direction (**FoV Read**).

The field of view (FOV) is used to define the number of readout steps and the ratio between readout steps and phase-encoding steps. In this way, you determine the size of the anatomical region displayed and its resolution (pixel size).



The settings for the field of view (FOV) depend on the resolution ratio selected.

The pixel size is determined by both the basic resolution and the phase resolution, as well as by the FOV in the readout direction.

The basic resolution determines the number of pixels in the readout direction, and the phase resolution determines the aspect ratio of the pixels (square or rectangular).

Changing the FOV in the readout direction changes the pixel size, but not the aspect ratio.



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



For very large pixels, resolution of the reconstructed images decreases because the signal is averaged across a larger area.

4.16.13.1 Square field of view (FOV)

With the FOV phase set to 100%, the system will measure a square FOV. In other words, the same number of pixels is measured in the readout direction as in the phase-encoding direction.

4.16.13.2 Rectangular field of view (FOV)

When examining elongated parts of the body, it may be helpful to work with a rectangular field of view to reduce the measurement time.

To obtain a rectangular FOV, set the parameter FOV phase to a value less than 100%.

- **Changing the field of view in the readout direction (frequency-encoding direction)**

Changing the FOV in the readout direction also changes the FOV in the phase-encoding direction. It also changes the pixel size.

You can change the FOV in the readout direction only as a function of the phase-encoding direction. If you increase the FOV in the readout direction, the FOV is also enlarged in the phase-encoding direction. The resolution ratio remains constant.

- **Changing the field of view in the phase-encoding direction**

The gradients for encoding the phases are switched in the phase-encoding direction (FOV phase).

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 adjusted to keep the resolution ratio constant. The phase-encoding direction is indicated by an arrow in the image.



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

4.16.14 TR (parameter)

The **TR** parameter 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, additional keys are superimposed for scrolling between the individual times.

4.16.15 TE (parameter)

The echo time **TE** is the time between the RF excitation pulse and the resulting echo that is measured.



For gradient echo sequences, a tooltip shows the in-phase and opposed phase condition.

For some sequences, the echo time cannot be changed. In this case, the input field is grayed out.



You can enter several echo times for multi-echo sequences. You can then scroll through the echo times using the arrow keys. When you change one echo time, the following echo times will be adjusted accordingly.

MR Spectroscopy: The setting for the echo time is especially important for certain spectroscopy measurements (e.g., lactate measurement). A phase reversal of the lactate peak in a spin-echo measurement (at 135 ms) provides additional indications for determining lactate.

4.16.16 Averages (parameter)

The **Averages** parameter allows you to set the number of times a measurement will be repeated.

The results of repeated measurements are averaged by the system.

It improves the signal-to-noise ratio and reduces motion artifacts.



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

4.16.17 Concatenations (parameter)

The **Concatenations** parameter defines into how many repetition times TR the measurement of the planned slices will 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 breath-hold mode** and choose **Breath-hold** under **Respiratory control**, the number of breath-hold intervals is determined via the **Concatenations** parameter.

- In the **Interleaved** multi-slice mode, the number of breath-hold intervals results from the product of the parameter values **Measurements** and **Concatenations**.
- In the **Single Shot** multi-slice mode without triggering, the number of breath-hold intervals is the product of the parameter values **Measurements**, **Concatenations**, and **Averages**.



For certain measurement programs (for example, measurements based on the BEAT sequence), the parameter **Breath-holds** is displayed instead of **Concatenations** when **Resp. Control** option **Breath-hold** is selected on the **Physio/PACE** card. In that case, the number of breath-holds is controlled via the **Breath-holds** parameter.



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 concatenation.

4.16.18 AutoAlign (parameter)

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.

AutoAlign is used in two different variants:

- In **AutoAlign scout protocols**, the **AutoAlign** parameter is used to specify the anatomical region in which the AutoAlign matrices will be computed.
- **AutoAlign clinical protocols** are protocols that use only one of the AutoAlign matrices. Almost all protocols can be used as an AutoAlign clinical protocol.



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



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



The **AutoAlign** parameter may not be available if an AddIn is attached to the protocol that does not contain the AutoAlign component

4.16.18.1 Setting up an AutoAlign scout manually

- 1 Select the AutoAlign region.
- 2 Select the coils to use.
- 3 Use iPAT if available.
- 4 Select prescan normalize.
- 5 Determine your workflow properties:

Positioning mode: local range mode

Distortion Correction: 2D

Automatic coil selection: OFF

Auto load: Load images into graphical segments

Wait for user start (working man): OFF

4.16.19 Rotation (parameter)

The **Rotation** parameter 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 the angle of rotation for navigator objects. The 90° angle corresponds to swapping the readout direction with the phase-encoding direction.

For spectroscopy measurement, you can set an angle in the Rotation input field. You can rotate the VOI, the CSI slice/CSI slab about this angle in the slice plane defined by the orientation.

4.16.20 VOI parameters

The **VOI** parameters define the extent of the measurement volume (volume of interest, VOI) in the three spatial directions.

The parameter values are expressed in millimeters [mm].



The directional information in the parameter names is adjusted to match the orientation of the VOI.

Example:

- **VOI R >> L**: VOI extent in direction R >> L (from right to left).
- **VOI A >> P**: VOI extent in direction A >> P (from anterior to posterior).
- **VOI F >> H**: VOI extent in direction F >> H (from feet to head)

4.16.21 FOV parameters

The **FOV** parameters determine the size of the field of view and as a result, they determine the size of the CSI slice for a 2D CSI measurement and the size of the 3D CSI slab for a 3D CSI measurement.



You can define the thickness of a CSI slice in a 2D CSI measurement using the **Thickness** parameter. For a 3D CSI measurement, you can set both the thickness of the excited slice using the **VOI** parameter (e.g., **VOI F >> H** for transverse orientation) and the size of the range covered by the phase encoding (e.g., **FoV F >> H**).

4.16.22 Thickness .. parameters

You use the parameter **Thickness ..** (e.g., **Thickness F >> H** for a CSI slice in transverse orientation) to determine the thickness of the CSI slice for a 2D measurement.



For 2D hybrid CSI protocols, the thickness of the CSI slice also defines the extent of the VOI in the "slice-selection direction".

4.16.23 VOI parameters - Spectroscopy

The **VOI** parameters define the extent of the measurement volume (volume of interest, VOI) within the CSI slice.



Please note that the VOI must be smaller than the FOV of the CSI slice by a factor of 0.75. Otherwise, convolution artifacts cannot be ruled out.

An addition, a third **VOI** parameter is displayed for 3D CSI measurements (e.g., **VOI F >> H** for transverse orientation of the CSI slices). This parameter determines the extent of the VOI in the "slice-selection direction".

4.16.24 Dynamic Mode (parameter)

The parameter allows you to select the dynamic mode.

- **GRASP** controls availability of additional Compressed Sensing GRASP-VIBE parameters.
(GRASP = Golden-Angle Radial Sparse Parallel MRI)
- **TWIST** controls availability of additional TWIST parameters.

4.16.25 Flip Angle (parameter)

The **Flip Angle** specifies the angle by which the longitudinal (z) magnetization will be rotated into the xy plane by the RF pulse.

The flip angle directly affects image contrast.

With a 90° excitation pulse, for example, the longitudinal magnetization is rotated 90° out of the Z direction. 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.

4.16.26 Magn. Preparation (parameter)

The **Magn. Preparation** parameter determines whether an RF pulse will be transmitted prior to each measurement to influence contrast (during inversion recovery (IR) and saturation recovery (SR)).

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:

- **Slice sel. .../Slab sel. ... (IR, T2-IR, DIR, or SR):** Selective preparation is performed (slice or slab).
- **Non-sel. ... (IR, T2-IR, DIR, or SR, or SR Perf):** Non-selective preparation is performed.

The RF pulses stimulate the entire volume independently of the current slice position or measurement sequence.

- **Non-sel. IR T1map:** A non-selective adiabatic inversion preparation pulse 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.

On the **Contrast** parameter card, you can determine the duration of the preparation pulse in the **T2 Prep. Duration** field.

- **T2 prep. adiab:** This option works similar to **T2 prep.** with adiabatic pulses.

These are the main differences from the **T2 prep.** option:

- 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 saturated and hence experiences a more complete recovery during the TI time. In a subsequent excitation, it is possible to display it with a higher signal (e.g. for protocols with dark fluid contrast).

- **Non-sel. T2 prep. IR:** Similar to **Non-sel. T2-IR** but with an improved CSF suppression, in particular in the pons.

- **Non-sel. IR HighBW:** Non-selective inversion recovery pulse with high bandwidth to reduce artifacts, for example, susceptibility artifacts or artifacts due to poor shimming of the region of interest.
- **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.

4.16.27 IR Scheme (parameter)

The **IR Scheme** parameter defines whether IR pulses of different slices may be interleaved.

- **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 TI 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.



The parameter is available only for a few sequences.

4.16.28 T2 prep. Duration (parameter)

The **T2 prep. Duration** parameter defines the duration of the T2 preparation pulse train to increase T2 contrast.



The parameter is active only if the **T2 Preparation** option is selected in the **Magn. Preparation** field.

4.16.29 TI (parameter)

The inversion time **TI** parameter 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.)

4.16.30 Wrap-up Magn. (parameter)

The **Wrap-up Magn.** parameter determines how the remaining magnetization will be treated immediately after each data acquisition shot.

- **None:** No wrap-up
- **Restore:** Accelerates restoring the longitudinal magnetization. It 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.

4.16.31 Fat-Water Contrast (parameter)

The **Fat-Water Contrast** parameter controls whether the signal from fat protons or water protons will be suppressed in a targeted way.

Since the resonance frequencies of water protons and fat protons are different, it is possible to suppress the protons with frequency-selective RF pulses.

The following options are available:

- **Standard:** No fat or water saturation, fat and water are both excited
- **Fat Saturation:** Suppresses the fat signal and has no effect on TE, TR might be prolonged. This extends the measurement time as well.

Fat saturation can be optimized region-specific in the **Fat Suppression Optimization** dialog box, which is accessible via the [...] button next to the parameter field.

(→ Page 373 *Fat Suppression Optimization dialog box*)

- **Fast Fat Saturation:** Suppresses the fat signal and causes slight extension of TE and TR. The effect on fat saturation is slightly less than in **Fat Saturation** mode.
- **Water Excitation:** Excites only water spins so that any fat signal is suppressed. This causes moderate extension of TE and TR.
- **Fast Water Excitation:** Like **Water Excitation**, the effect is slightly less.
- **Q-fat sat.:** Suppresses the fat signal. This mode is available only if **Quick** was selected in the **Saturation Mode** selection list.

- **SPAIR:** Prior to image saturation, the fat signal is suppressed via a frequency-selective adiabatic inversion pulse.

SPAIR fat saturation can be optimized region-specifically in the **Fat Suppression Optimization** dialog box, which is accessible via the [...] button next to the parameter field.

(→ Page 373 *Fat Suppression Optimization dialog box*)

Possible values are:

- **Default:** Standard SPAIR mode behavior
- **Thorax:** Optimized SPAIR mode for Thorax imaging
- **Abdomen & Pelvis:** Optimized SPAIR mode for Abdomen and pelvis imaging

SPAIR and region-specific options are only available with certain sequences for 1.5 T and 3 T systems.

- **Dixon:** Enable the Dixon method to reduce motion artifacts.

Additional Dixon parameters can be set in the **Dixon** dialog box, which is accessible via the [...] button next to the parameter field.

(→ Page 374 *Dixon dialog box*)

- **Fast Dixon:** Enable single excitation to reduce motion artifacts.
- **Water Saturation:** During measurement, a water suppression pulse is transmitted to fully suppress the water signal.
- **Fast Water Saturation:** Like **Water Saturation**, but the effect is slightly less.
- **Partial Water Saturation:** Like **Water Saturation**, but the effect is slightly less.
- **Fat Excitation:** Suppresses the water signal by selectively exciting fat protons. This has only a moderate effect on TE and TR and increases the measurement time slightly.

- **Water Supresion Weak:** If this option is selected, the water signal is reduced but not fully suppressed. This allows you to include the water line in various postprocessing functions.
- **Water Suppression RF Off:** This option can be used to measure a reference raw data set if you want to perform eddy current compensation during a spectroscopy evaluation.



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



For SVS protocols, an integrated water reference measurement is available, see (→ Page 500 Ref. Scan Mode (parameter)).

To perform eddy current compensation for CSI, the CSI protocol has to be measured twice. For the first measurement, water suppression is selected (**Water Saturation** or **Water Suppresion Weak** options) to acquire the spectroscopy raw data. For the second measurement, the **Water Suppression RF Off** option is selected to acquire the reference raw data.

In addition, please note: It is not possible to acquire a raw data set for reference if the water suppression during the first measurement is not the CHESS water suppression described here, but rather the spectral signal suppression.

Switching the water saturation on or off does not affect the configuration of the water saturation adjustment.

4.16.32 Fat Saturation (parameter)

Use the **Fat Saturation** parameter to set the strength of the fat saturation pulse.

- **Weak:** Weak saturation
- **Strong:** Strong saturation

4.16.33 Blood Suppression (parameter)

The **Blood Suppression** parameter determines whether the blood signal is suppressed by weak diffusion weighting. This is done by gradient moments (first order).

- **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 box
- **None / Off:** No blood suppression

4.16.34 MTC (parameter)

In addition to the saturation of water or fat protons, another type of presaturation may be applied.

By applying a special RF pulse, magnetization transfer weakens the signal from tissue with a high macro molecular content (e.g., white/gray brain tissue). Since this effect is barely noticeable in blood, the contrast between blood and white/gray brain tissue is increased.

The **MTC** parameter determines whether the signal of tissue with a high portion of macro molecules is weakened by a special RF excitation pulse.



Select the **MTC** check box to obtain better contrast in images for e.g., vessel examinations.

4.16.35 Lines Per Shot (parameter)

The **Lines Per Shot** parameter 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 if the **Q-fat sat** or **SPAIR** mode has been selected in the **Lipid suppr.** parameter.

4.16.36 Freeze Suppr. Tissue (parameter)

When you select the **Freeze Suppr. Tissue** parameter, the system computes the T1-value of the tissue that is currently suppressed by the TR/TI combination selected and saves it. A change in the repetition time (TR) automatically adjusts the inversion time (TI) with immediate effect, so that the tissue with the saved T1-value is suppressed by the new TR/TI combination as well.

4.16.37 Minimize Inflow (parameter)

Body-fluid-suppressed head measurements may be influenced by body fluid from the neighboring slices. Since this inflow of body fluid was not inverted at the inversion time, it results in undesirable signal contributions. This signal contribution is minimized as much as possible when selecting the **Minimize Inflow** parameter.



When you activate this parameter, the maximum possible number of slices per TR may be reduced.

4.16.38 TM (parameter)

For protocols based on STEAM sequences, you can set the time interval between the 2nd and 3rd RF pulse with the **TM** parameter.

During this time, the magnetization - ultimately the object of the measurement - is oriented in the longitudinal direction and therefore only subject to T1 relaxation.

This means that the duration of the TM interval does not contribute to echo time **TE**.



The T1 weighting can be enhanced by extending the **TM** interval.

4.16.39 Water Suppression (parameter)

MR Spectroscopy: To reduce the high-intensity water signal, it should be already suppressed during data acquisition.

The following options are available:

- **Water Saturation:** During measurement, a water suppression pulse is transmitted to fully suppress the water signal.
- **Weak Water Suppr.:** If this option is selected, the water signal is reduced but not fully suppressed. This allows you to include the water line in various postprocessing functions.
- **None:** No water suppression is applied during measurement. The water suppression module is completely deactivated.
- **Only RF off:** This option can be used to measure a reference raw data set if you want to perform eddy current compensation during a spectroscopy evaluation.



To measure a reference raw data set for eddy current compensation, the protocol is measured twice: for the first measurement, water suppression is activated (**Water Saturation** or **Weak Water Suppr.** options) to acquire the spectroscopy raw data. For the second measurement, the **Only RF off** option is selected to acquire the reference raw data.

In addition, please note: It is not possible to acquire a raw data set for reference if the water suppression during the first measurement is not the CHESS water suppression described here, but rather the spectral signal suppression.

Switching the water saturation on or off does not affect the configuration of the water saturation adjustment.

4.16.40 Water Suppr. BW (parameter)

The **Water Suppr. BW** parameter defines the bandwidth of the high-frequency pulses for water suppression with spectroscopy measurements.

A value of 35 Hz is highly suitable for a magnetic field strength of 1.5 T



Due to the higher bandwidth, the water signal is suppressed more effectively. However, the effect on adjacent signals (e.g., creatine, (CH₂)) increases as well.

4.16.41 Spectral Suppr. (parameter)

In spectroscopy measurements with spin echo sequences, it is possible to suppress certain spectral signals with MEGA RF pulses within localized sequence sections.

The following options are available in the **Spectral Suppr.** selection list:

- **Lipid suppr.:** Suppression of lipid signals
- **Water suppr.:** Suppression of water signals
- **Lipid + Water suppr.:** Suppression of fats and water signals
- **None:** No spectral suppression

4.16.42 Lipid Suppr. BW (parameter)

If you have selected fat suppression or fat + water suppression for spectral signal suppression (**Spectral suppr.** parameter), use the **Lipid Suppr. BW** input field to set the bandwidth of the fat suppression pulse used.



If fat + water suppression is selected, the bandwidths of the two suppression pulses are coupled. This means that a value entered in the **Lipid Suppr. BW** input field also applies as the bandwidth for the water suppression pulse, and is automatically entered in the **Water s. BW**.

4.16.43 Lipid s. Delta pos. (parameter)

If you have selected fat suppression or fat + water suppression for spectral signal suppression (**Spectral suppr.** parameter), you can set the spectral shift of the fat suppression pulse to be used by **Lipid s. Delta pos.**.

4.16.44 Water s. BW (parameter)

If you have selected water suppression or fat + water suppression for spectral signal suppression (**Spectral suppr.** parameter), use the **Water s. BW** spin box to set the bandwidth of the water suppression pulse used.



If fat + water suppression is selected, the bandwidths of the two suppression pulses are coupled. This means that a value entered in the **Water s. BW** input field also applies as the bandwidth for the fat suppression pulse, and is automatically entered in the **Lipid suppr. BW**.

4.16.45 Water s. Delta Pos. (parameter)

If you have selected water suppression or fat + water suppression for spectral signal suppression (**Spectral suppr.** parameter), use the **Water s. Delta Pos.**, you can set the spectral shift of the water suppression pulse to be used.

4.16.46 Measurements (parameter)

The **Measurements** parameter determines how often a measurement is performed.

- **Dynamic studies:** In dynamic studies with contrast agent or in movement studies (for example, joints), you can repeat the measurements at regular intervals. Set the number of measurements in the **Measurements** spin box.

For example, you can track the inflow of the contrast agent, the activation of a region of the brain (for example, due to finger movement), or various stages of joint movement.

- **NATIVE:** These measurements are performed at different trigger delays.

Typically, two measurements are performed in **3D** mode, and a series of multiple measurements are performed for a **TD scout**.



If you perform dynamic measurements with CAIPIRINHA reconstruction, do not interrupt the measurements. Otherwise, not all images will be reconstructed.

4.16.47 Pause after Meas. (parameter)

For dynamic measurements, the **Pause after Meas.** field is used to define delay times (pause times) between individual measurements. Separately determine the pause for each measurement.



If you position and move the mouse pointer over the **Pause after Meas.** parameter name, a tooltip indicates the pause values.

If you move the mouse pointer over an input field of the spin box, a tooltip will appear stating the starting and ending time of the first 10 measurements.

4.16.47.1 Setting pauses

You separately determine the pause for each measurement:

- 1 Click the lower arrow keys to get to the pause the duration of which you want to change.
- 2 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.

4.16.48 Reconstruction (parameter)

- MR images are usually **magnitude images**. The MR signal intensity is displayed directly in these images.
- In **phase images**, the grayscale corresponds to the phase positions of the spins (between -180° and +180°). It depends on the velocity of the spins as they move in the body (e.g., velocity of blood flow). Spins with the same phase position and therefore velocity have the same gray scale value in these images.
- In **real images**, the grayscale distribution indicates the real distribution of the longitudinal magnetization after an inversion pulse.

You can select the image type that you want to reconstruct from the **Reconstruction** selection list:

- **Magnitude** - magnitude images
- **Phase** - phase images
- **Real** - real images
- **Magn./Phase** - Magnitude and phase images
- **Real/Phase** - Real and phase images



You can only select real images if an inversion pulse is used.



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

4.16.49 Delay in TR (parameter)

Delay in TR determines the time between two subsequent measurements. The parameter is relevant for all ep2d sequences.



You can only set one delay time which is the same for all measurements.

4.16.50 Multiple Series (parameter)

If you have defined multiple measurements in the **Measurements** field, use the **Multiple Series** parameter to define whether the images of each measurement should be stored in separate series.

- **Each Measurement:** A separate series is created for every measurement.
- **Each Slice:** A separate series is created for every slice.
(Not for BOLD sequences)
- **Each Slice and Measurement:** A separate series is created for every slice and every measurement.
(Not for BOLD sequences)
- **Off:** All images of a measurement are stored together in one series.

4.16.51 Perfusion Mode (parameter)

The **Perfusion Mode** parameter determines the ASL perfusion preparation.

The following options are currently available:

- **PICORE Q2T** (only for 2D ASL): The PICORE labeling scheme is used in conjunction with periodic saturation pulses (Q2T). FOCI pulses are used for inversion.
- **FAIR Q2T** (only for 3D ASL): The FAIR labeling scheme is used in conjunction with periodic saturation pulses (Q2T). FOCI pulses are used for inversion.
- **PCASL:** Pseudo-Continuous Arterial Spin Labeling is an improved version of Pulsed Arterial Spin Labeling (PASL).

With PCASL, the signal-to-noise ratio and image homogeneity will be improved. PCASL provides more robust labeling of the blood spins.

PCASL works with 2D EPI and 3D TGSE acquisitions.

PCASL can be used with standard head/neck coils in all tilted positions.

- **None** (only for 3D ASL): No labeling scheme is used. Pure M0 images are provided.

4.16.52 Quality check (parameter)

The **Quality check** parameter 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.

4.16.53 Flow Limit (parameter)

The **Flow Limit** parameter is used in ASL to limit flow in order to attenuate the signal from large arteries.



The flow limit is switched off when it is set to maximum.

4.16.54 Base Resolution (parameter)

Base Resolution specifies the number of pixels in the readout direction. It 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**.

Example of changing the number of readout steps:

Enter the value 256 for the number of readout steps.

With a phase resolution of 100% and a square FOV (FOV Phase = 100%), the result is a 256 x 256 matrix.

The size of the pixels depends on the size of the field of view (FOV) you have entered in the readout direction.

For an FOV of 256 mm in the readout direction, the pixels are 1 mm x 1 mm in size and for a 396 mm FOV in the readout direction, the pixels are 1.5 mm x 1.5 mm.

4.16.55 Phase Resolution (parameter)

Phase Resolution defines the resolution of slices in the phase-encoding direction expressed as a percentage value of 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. For example, at 75%, the pixels are rectangular, and resolution decreases.

If you reduce the FOV in the phase-encoding direction, the number of pixels has to be reduced as well to keep the resolution ratio constant. As a result, the number of phase-encoding steps is reduced.

Examples of image resolutions:

FOV readout (mm)	FOV phase [%]	Phase reso- lution [%]	Matrix size	Pixel [mm]
256	100	100	256 x 256	1 x 1
256	75	100	192 x 256	1 x 1
256	100	75	192 x 256	1.33 x 1
256	75	75	144 x 256	1.33 x 1



If you move the mouse pointer over the **Phase resolution** parameter, a tooltip will be displayed together with the matrix.

4.16.56 Phase Partial Fourier (parameter)

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

The **Phase Partial Fourier** parameter determines that the k-space is asymmetrically sampled in the slice selection direction. As a result, the measurement is reduced while the spatial resolution remains unchanged. However, the signal-to-noise ratio is reduced.

Possible settings:

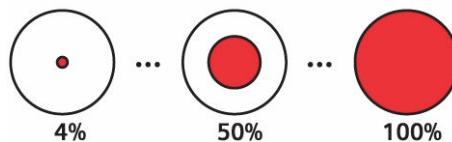
- **4/8** (Half Fourier), **5/8**, **6/8**, **7/8**: Number of phase-encoding steps that are acquired
- **Allowed**: The sequence automatically computes and uses the most optimal setting of the phase partial Fourier.
- **Off**: The entire image matrix is used.



Different modes are available depending on the sequence.

4.16.57 Central Region A (parameter)

The **Central Region A** parameter determines the size of the k-space center that is acquired with full sampling density.



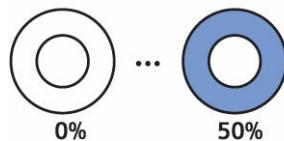
The value is expressed as a percentage of the total number of sample points that will be acquired.



The parameter is only active when **TWIST** is selected under the **View Sharing** parameter.

4.16.58 Sampling Density B (parameter)

The **Sampling Density B** parameter determines the sampling density used to sample the individual temporary phases in the outer k-space.



The value is provided as a percentage of the total number of sample points that will be acquired (0% = keyhole examination).



The parameter is only active when **TWIST** is selected under the **View Sharing** parameter.

4.16.59 Slice Resolution (parameter)

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

The **Slice Resolution** parameter defines the resolution in the slice-selection direction. The resolution ratio in the slice-selection direction is expressed as a percentage of the readout steps.

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

With slice resolution < 100%, fewer phase-encoding 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**).

4.16.60 Slice Partial Fourier (parameter)

With 3D measurements, you can change the image matrix and therefore the measurement time not only in the phase-encoding direction and readout direction but also in the slice-selection direction.

As with **Phase Partial Fourier**, with **Slice Partial Fourier** only a part of the raw data matrix in the slice-selection direction is acquired (asymmetric sampling of the k-space in slice-selection direction).

The signal-to-noise ratio is reduced, but resolution in the slice-selection direction remains the same.

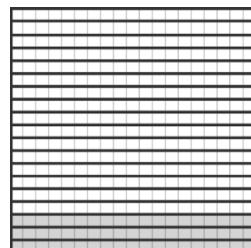
Possible settings:

- **4/8** (Half Fourier), **5/8**, **6/8**, **7/8**: Number of phase-encoding steps that are acquired
- **Allowed**: The sequence automatically computes and uses the optimal setting of the phase partial Fourier.
- **Off**: The entire image matrix is used.

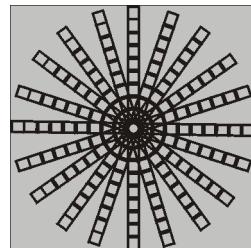
4.16.61 Trajectory (parameter)

The **Trajectory** parameter defines the geometric shape to be sampled in the k-space.

The following shapes are possible:



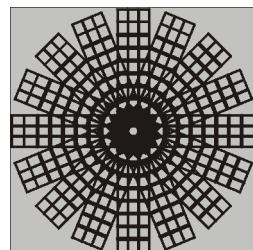
Cartesian: The k-space is sampled as a matrix of rows and columns. The k-space is built up line by line, for example, from the bottom left to the top right.



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

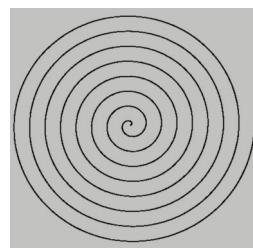
This mode is available for the CV (cardio vascular) sequence.

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.

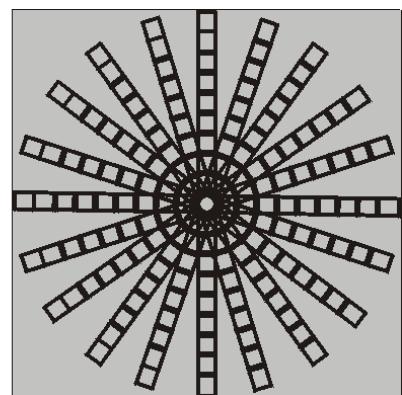
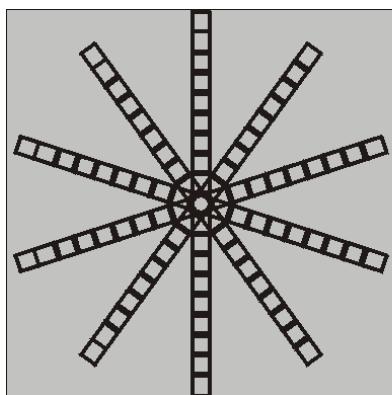
The number of lines per blade is determined in the **Turbo Factor** parameter on the **Sequence/Part 2** parameter card.



Trajectory Spiral: The k-space is sampled in a spiral pattern starting at the k-space center.

4.16.62 Radial Views (parameter)

In the case of radial sequence, the **Radial Views** parameter defines the number of radial lines to be used for k-space sampling.



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

4.16.63 BLADE Coverage (parameter)

The **BLADE Coverage** parameter calculates the number of blades of varying rotation angles for k-space sampling.

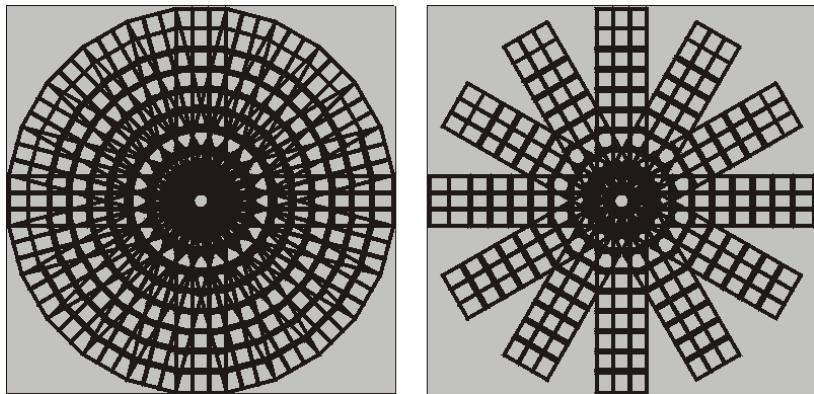
The value is indicated as a percentage.

- **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 is increased and the signal-to-noise ratio is improved.

- **Less than 100%:** Fewer blades are measured than necessary for complete coverage.

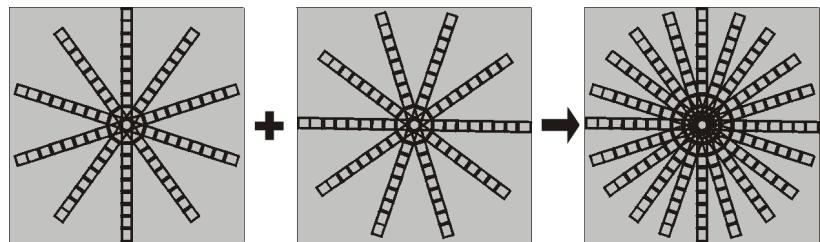
The measurement time is reduced and image quality is degraded.



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

4.16.64 Radial Interleaves (parameter)

In the **Radial Interleaves** field, you enter the number of TR intervals required to radially sample all lines of the k-space.



Example: Radial Interleaves=2: All desired lines of the k-space are sampled in two TR intervals.

4.16.65 Spiral Interleaves (parameter)

In the **Spiral Interleaves** field, you enter the number of interleaves for spiral sequences.

This parameter is only available if the trajectory **Spiral** is selected.

4.16.66 Interpolation (parameter)

Interpolation doubles the image matrix size without increasing the measurement time (for example, from a 256x256 to a 512x512 matrix).

In the context of TOF within the BEAT sequence, the **Interpolation** check box is replaced by a parameter field that offers interpolation factor values of 1.0, 1.5, and 2.0.

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, rather than the measurement matrix, is shown to the right at the lower margin 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. There is no interpolation in the slice-selection direction. If you increase the base resolution, interpolation is cleared automatically. Otherwise, the reconstruction time will increase considerably. You can select interpolation at any time.

4.16.67 Vector Size (parameter)

The **Vector Size** parameter defines the number of data points for measurement of the chemical shift and therefore also the resolution in spectroscopy measurements.

The following options are available:

- 512
- 1024
- 2048



A setting of 512 points is recommended (default setting).

4.16.68 Scan Res. (parameters)

The **Scan Res.** parameters define the number of phase-encoding steps in the two spatial directions of a CSI slice or the three spatial directions of a CSI-slab.



Unlike MR image resolution, the measurement resolution may not match powers of 2. This allows for more flexible measurement times.



The maximum number of phase-encoding steps in the first two spatial directions is 32. The number of phase-encoding steps in the third direction must not be more than 16 (for 3D CSI only).



The maximum size of a reconstructed data set is 128 MB. This is equivalent to a 3D CSI data set of, for example, $32*32*16*1024$ complex measurement points.

4.16.69 Interpol. Res. (parameters)

Using the **Interpol. Res.** parameters, you define the number of reconstructed spectra in the two spatial directions of a CSI slice, or the three spatial directions of a CSI slab.

The following rules apply:

- Interpolation resolution can be set to 8, 16, or 32.
- The number of reconstructed spectra has to be equal to or greater than the number of phase-encoding steps.
- If the number of reconstructed spectra is greater than the number of phase-encoding steps, the displayed spectra are interpolated from the measured spectra.
- The maximum size of a reconstructed data set is 128 MB.

4.16.70 Hamming (parameter)

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



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

4.16.71 POCS (parameter)

The **POCS** (Projection Onto Convex Sets) parameter improves edge sharpness for partial Fourier sampling and missing k-space points are not set to zero, but are extrapolated instead.

The following options are available:

- **Off:** No POCS
- **Read Slice:** POCS in the readout and slice direction
- **Read Phase:** POCS in the readout and phase-encoding direction

4.16.72 Acceleration mode (parameter)

The following options are available for **Acceleration mode**:

- **None:** In-plane acceleration is not used.
- **CAIPIRINHA:** In-plane acceleration with CAIPIRINHA reconstruction
- **GRAPPA:** In-plane acceleration with GRAPPA reconstruction
- **mSENSE:** In-plane acceleration with SENSE reconstruction
- **CS:** Compressed Sensing-based acceleration

The denoising mode and strength for Compressed Sensing (CS) protocols can be defined in the **CS Reconstruction** dialog box, which is accessible via the [...] button next to the parameter field.

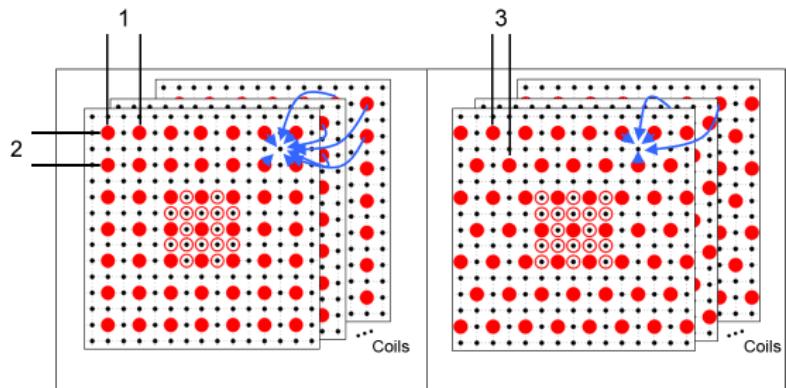
(→ Page 385 *CS Reconstruction dialog box*)

- **SMS:** Simultaneous multi slice (SMS) imaging with GRAPPA reconstruction
- **Wave-CAIPI:** Acceleration technique for susceptibility-weighted imaging (SWI). **Wave-CAIPI** combines the CAIPIRINHA acceleration method with a wave trajectory and is only available for the GRE_Wave sequence.

(→ Page 112 *GRE_Wave*)



If you perform dynamic measurements with CAIPIRINHA reconstruction, do not interrupt the measurements. Otherwise, not all images will be reconstructed.



Reduced data acquisition with GRAPPA and CAIPIRINHA

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



An **Acceleration mode** can be selected only when at least two coil elements or RF receive channels are available.

The parameter is dimmed and set to the **None** default option if there are not enough coil elements or RF receive channels.

The number of coil elements or modes have to match the number of acceleration factors given.

4.16.73 Acceleration Factor PE (parameter)

During PAT reconstruction, the **Acceleration Factor PE** parameter determines the acceleration factor in the phase-encoding direction.

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

4.16.74 Total Factor (parameter)

This parameter defines the total acceleration factor. Available in conjunction with **CAIPIRINHA** and **CS**.

4.16.75 Reference Lines PE (parameter)

During PAT reconstruction, the **Reference Lines PE** 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 arises dynamically depending on the sequence and protocol parameters.

4.16.76 Accel. Factor 3D (parameter)

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

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



When you change 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 box).

4.16.77 Ref. Lines 3D (parameter)

The **Ref. Lines 3D** parameter defines the number of reference lines in the slice-selection direction for PAT reconstruction.



The **Ref. Lines 3D** parameter can be changed only if 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.

4.16.78 Reference Scans (parameter)

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

The **Reference Scans** parameter determines the way in which the reference lines are measured.

- **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.

- **GRE/Separate:** GRE-based reference scan. The reference lines are measured together with the sequence, but separately just prior to actually measuring the image data. This method is faster, e.g., for measurements with high acceleration factors and low resolution.

In 3D sequences, this method also supports fat saturation in saturation mode **Quick (Geometry/Sat. Regions** 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.

- **TSE/Separate:** TSE-based reference scan that can be used to reduce scan time and motion artifacts. Furthermore, it can help to reduce aliasing artifacts in large body regions such as the abdomen, pelvis, thorax, and spine.

- **EPI/Separate:** EPI-based reference scan.

- **Self - calibration:** For special measurements only when averaging > 1

Additional reference lines are not measured because the lines from the repetitions are reconstructed.

The PAT factor has to be less than or equal to the value of the **Averaging** parameter.

- **TPAT:** Available in combination with cardiac cine or dynamic acquisitions. Requires that **Measurements** > 1 or cardiac **Phases** > 1.

Additional reference lines are not measured because the lines from the repetitions are reconstructed.

The PAT factor has to be less than or equal to the value of the **Measurements** or **Phases** parameter.



The **Reference Scans** parameter is **not** available for all PAT sequences.

4.16.79 CAIPIRINHA mode (parameter)

The **CAIPIRINHA mode** parameter sets optimized values for the **Accel. Factor PE**, **Accel. Factor 3D**, **Accel. Factor Center**, and **Reordering Shift 3D** parameters. Values are optimized to reach the total factor set by the **Total factor** parameter.

- **Free:** No automatic values are set
- **Body Tra:** Values are optimized for transverse abdomen measurement
- **Body Cor:** Values are optimized for coronal abdomen measurement
- **Breast:** Values are optimized for soft tissue evaluation

4.16.80 Advanced Reconstruction (parameter)

The **Advanced Reconstruction** parameter allows to select specific reconstruction options.

The following options are available:

- **Deep Resolve** (for TSE sequence only): A denoising algorithm will be applied during image reconstruction to improve the SNR of the acquired images. The denoising algorithm can be optimized in the **Deep Resolve** dialog box, which is accessible via the [...] button next to the parameter field.
(→ Page 386 *Deep Resolve dialog box*)
- **Off:** No specific reconstruction.

4.16.81 Normalize (parameter)

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.

A normalization filter reduces the brightness of areas in the vicinity of the coil and increases the brightness in areas farther away from the coil.



Use of a normalization filter may cause a loss of contrast and an increase in background noise.

With the **Normalize** parameter, you can select a normalization filter that reduces image intensity variations.

- **Off:** No normalization filter
- **Image Based:** Perform normalization based on the image content

- The **Prescan Normalize** filter corrects for signal intensity decays caused by the coil profiles.

It works in a similar way to the **Image Based** filter, but the data used for homogenization are acquired through an adjustment measurement.

- **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.

Moderate mode effects progressively weakened normalization, so that the optical impression can be less noisy.

However, the resulting images will exhibit some residual effects of the original coils sensitivity profiles.

- **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.



Use the **Image Based** filter instead of the **Prescan Normalize** filter when you:

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



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



For spectroscopy protocols, only the **Prescan Normalize** and **Off** options are available. The image based prescan is mapped to the spectroscopy data for correction. For spectroscopy, the **Prescan Normalize** option (**Normalize Filter Settings** dialog box) has no effect.

If **Prescan Normalize** is selected the prescan data is used for phase correction of the spectroscopy data.

4.16.82 Distortion Correction (parameter)

The **Distortion Correction** parameter activates 2D or 3D distortion correction. This compensates for the pin-cushion distortion at the edge of the image. These distortions occur in images with a large FOV or eccentric slices (**Offcenter**).

- **2D:** With 2D distortion correction, image distortions are individually corrected 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.

4.16.83 Multi-Slice Mode (parameter)

The **Multi-Slice Mode** parameter activates the multi-slice measurement methods.

- **Sequential:** Measurement slice by slice

All lines (phase-encoding steps) of the first slice are measured in sequence first, followed by all lines of the second slice etc.

- **Interleaved:** Measurement by lines

The first line (phase-encoding step) of all slices of a concatenation are measured first, followed by all second lines, etc.

- **Single Shot:** Special mode for fast sequences

All lines (phase-encoding steps) of a single slice are measured at once after a single excitation, followed by all lines of the second slice, etc.

The **Single Shot** multislice mode is available for very fast sequences only (e.g., epi, haste, Turboflash). These sequences do not offer any other modes.

The **Interleaved** multi-slice mode enables a reduction in measurement time. The individual lines of different slices can be excited in quicker succession within a repetition time TR without affecting the signals of adjacent lines.



The **Sequential** setting is a prerequisite for planning a tracking sat region.



If you have selected **Interleaved**, you can select the number of **Concatenations** on the **Routine**, **Geometry/Common**, and **Physio** parameter cards.

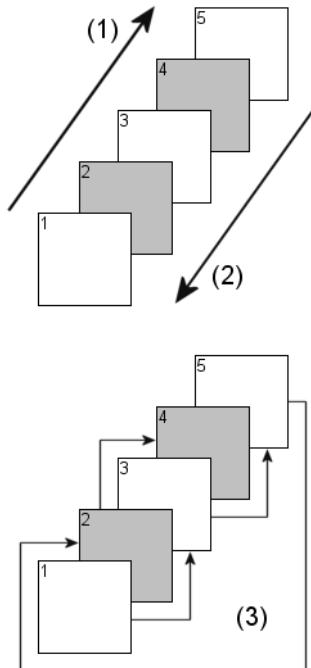
4.16.84 Series (parameter)

The **Series** parameter 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 sequences are available:



- (1) **Ascending:** The slices are excited starting at the beginning of the slice or slab group (start -> end).
- (2) **Descending:** The slices are excited starting at the end of the slice or slab group (end -> start).
- (3) **Interleaved**
 - **Interleaved in A. A.** (without display): (Interleaved in breath-hold interval). The slices are measured separately in the Interleaved mode for each breath-hold interval of a multiple breath-hold measurement.



Input Interleaved in A. A. is superposed only when you are planning a measurement in a multiple breath-hold mode and have 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-coronal-transverse) using the **MSMA** parameter.



Please note that the **Concatenations** parameter influences the acquisition order defined by the **Series** parameter. When the number of concatenations is **equal** to the number of slices the resulting acquisition order is descending, even if the **Series** parameter is set to **Interleaved**.

4.16.85 Sat. Delta Frequ. (parameter)

For spin-echo sequences, you can insert up to eight freely positionable saturation regions to further restrict the VOI.

Set the value for the frequency shift of the saturation pulses (in [ppm]) in the **Sat. Delta Frequ.** spin box.

4.16.86 Fully Excited VOI (parameter)

A CSI measurement with a spin-echo sequence allows you to minimize shift artifacts by selecting the **Fully excited VOI** option.

The actual excited VOI is enlarged with respect to the VOI displayed so that all metabolites with a maximum intensity are acquired within the displayed VOI.

Additionally, four saturation regions are positioned at the edges of the VOI to suppress the signals from the areas outside the VOI.



The automatically positioned saturation regions are displayed in the image area.



The FOV may have to be enlarged to prevent aliasing artifacts. For this purpose, the recommended minimum size of the FOV is shown when you move the mouse pointer over the VOI input field.



The **Delta frequency** parameter on the **Sequence/Common** parameter card is set at a fixed value of -2.85 ppm.

4.16.87 Navigator (parameter)

The **Navigator** parameter 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 coronal as well as transverse images.

4.16.88 Set-n-Go Protocol (parameter)

The **Set-n-Go Protocol** parameter indicates whether the measurement protocol is part of a Set-n-Go protocol.



Distortion correction is a prerequisite for Set-n-Go protocols. The **Distortion Corr.** parameter is automatically set to **2D**.

4.16.89 Table Position (parameter)

The **Table Position** parameter determines the table position at which 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.

4.16.90 Inline Composing (parameter)

The **Inline Composing** parameter 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 selected only when distortion correction (**2D** or **3D**) is selected in the **Distortion Corr.** field.

4.16.91 Composing Function (parameter)

The **Composing Function** parameter determines the algorithm to compose the images.

- **Angio:** This algorithm uses the vessel structures of the images as a basis. This permits overall display of the vessels.
- **Spine:** This algorithm uses the bone structures in the images as a basis. For example, it generates images for measurement and evaluation of scoliosis, kyphosis, and pelvic obliquity.
- **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-and-go protocol.

4.16.92 Save non-normalized (parameter)

The **Save non-normalized** parameter determines whether the non-normalized images are stored in the database as well.

4.16.93 Composing Group (parameter)

The **Composing Group** parameter 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.

4.16.94 Last Step (parameter)

The chronologically last measurement of a **Composing Group** has to be identified as the **Last Step**. For this purpose, you select this check box.

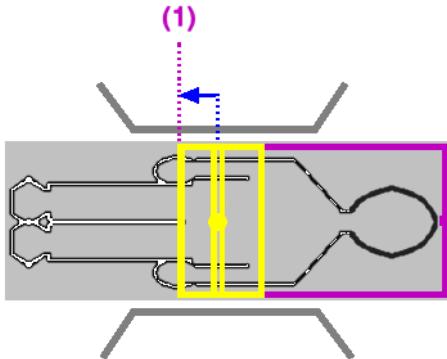
The subsequent protocols belong to a new **Composing Group**, even if they have the same group number.



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

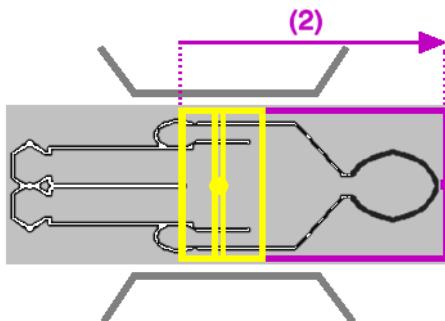
4.16.95 Range Start (parameter)

The **Range Start** parameter defines the start position of the measurement region (1) (measured in the Whole Body Patient Coordinate System).



4.16.96 Total FoV (parameter)

The **Total FoV** parameter determines the total length of the measurement region (2).



4.16.97 Segments (parameter)

The **Segments** parameter defines the number of rows in the k-space that are measured for an image during a TR interval.



The parameter is especially relevant to physiologically-triggered measurements.

4.16.98 Saturation Mode (parameter)

The **Saturation Mode** selection list is used to select how often saturation pulses will be transmitted in interleaved multislice measurement.

- **Standard:** A saturation pulse is transmitted before each slice excitation (duration about 10 ms) to reduce the maximum number of slices that can be measured within a certain repetition time TR. Remedy: increase the repetition time TR (and therefore the measurement time) to maintain a constant number of slices.
- **Quick:** Not every slice excitation is preceded by a saturation pulse. Instead, saturation pulses are applied at sequence-dependent time intervals (about 300 ms). In this way, you are able to measure more slices within a repetition time than in the **Standard** saturation mode.



Select the **Quick** mode, for example, to reduce the overall measurement time in breath-hold studies. In **Quick** mode, the quality of fat saturation varies depending on the slice position.

4.16.99 Saturation Region (parameter)

Saturation regions are areas where the signal is saturated using special RF pulses. You can use the **Saturation Region** parameter to avoid motion artifacts. Depending on the measurement protocol and the slice or slab groups planned, you can define standard, parallel, or tracking saturation regions.

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

The **Saturation Region** parameter shows you the number of saturation regions displayed.

Via the **Position**, **Orientation**, and **Thickness/Rotation** parameters, you determine the geometry of the saturation regions.

The **Gap** parameter determines the distance from the corresponding slice or slab group.

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

You may:

- Change the thickness of a saturation region
- Freely position saturation regions with **Orientation** and **Position**. Proceed in the same way as for positioning slice and slab groups.

- **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.

- **Tracking saturation regions** are excited at the specified distance "before" or "after" the slice and at the thickness set. In this way, they are "tracking" the slice currently being measured.
- **Parallel saturation regions** are positioned either on one side or on both sides parallel to the slice group. These saturation regions do not move along with the slice, but rather remain at the specified distance "before" or "after" or on both sides of the slice group.

The setting "before" or "after" the slice or slice group is displayed in the main orientation of the slice group:

- For transverse main orientation: **H** ("before") / **F** ("behind")
- For sagittal main orientation: **L** ("before") / **R** ("behind")
- For coronal main orientation: **P** ("before") / **A** ("behind")

4.16.99.1 Planning a new saturation region

- 1 Click the + button next to the **Saturation Region** field to insert a new saturation region.

Parallel or tracking saturation regions are positioned adjacent to the slice or slab group present.

- 2 Select a type from the **Special Saturation** selection list.

4.16.99.2 Deleting a saturation region

- 1 Select the saturation region you want to delete.
- 2 Then click the - button next to the **Saturation Region** field.

4.16.100 Shape (parameter)

The **Shape** parameter sets the shape (profile) of the saturation region.

- **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.



The parameter is available only for a few sequences.

4.16.101 Special Saturation (parameter)

The **Special Saturation** parameter establishes exactly one parallel or tracking saturation region.

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** ("before") / **F** ("behind")
- For **sagittal** main orientation: **L** ("before") / **R** ("behind")
- For **coronal** main orientation: **P** ("before") / **A** ("behind")



Special Saturation regions are only possible if there is only one slice or slab group.



If you have selected the **Quick** saturation mode, you will find that only one **Quick** option is offered for all parallel saturators (for example, **Q Parallel H**).

Tracking saturation regions cannot be planned in **Quick** mode.

4.16.102 Local coils (parameter)



Example

Several local coils consist of coil elements, which you may select independently of one another.

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



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

4.16.103 Body coil (parameter)

Body

Body coil



All local coils will be cleared if you want to perform a measurement with the **Body** coil.

When you cleared the **Body** coil again, you select all previously active local coils and coil elements.

4.16.104 Adjustment Strategy (parameter)

The **Adjustment Strategy** parameter allows you to select a strategy for making adjustments.

- **Standard**
- **SliceAdjust**

- **FastView**
- **Offcenter:** Dedicated adjustment strategy for off-center elbow, hand, or wrist imaging.

In this mode, the **Flip Angle** parameter on the **Contrast/Common** parameter card can be used to set not only the refocusing pulse but also the excitation pulse (for TSE-based sequences only).



Please note that **Offcenter** mode is not available for all MR systems.

4.16.105 B0 Shim (parameter)

For the 3D-shim, several modes are offered in the protocol.



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

The range of options depends on the measurement sequence.

- **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.
- **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 signals from the neck coil, this coil needs to be selected in the protocol.

- **Advanced:** Adjustment measurements and evaluation are performed in advanced mode. This mode is used mainly for spectroscopy protocols. 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.
- **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 abdomen exams.
- **Absolute:** Adjustment measurements and evaluation are performed in **Absolute** mode. The determination of absolute B0 values can improve B0 homogeneity. AbsoluteShim mode is more time consuming than **Standard** mode.



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



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

4.16.106 B1 Shim (parameter)

The **B1 Shim** parameter allows you to correct inhomogeneities of the RF excitation (B1 field).

- **TrueForm:** The B1 field is optimized for body regions, so the optimization is anatomy-specific.
- **TrueForm C:** The measurement must be performed in CP mode. This option is only available for certain protocols, for example, specific HASTE protocols.
- **Patient-specific:** RF excitation is parameterized on the basis of B1 maps of the subject. The optimization is applied to the whole volume covered by the slice group.
- **Volume-selective:** The B1 field is optimized in a specified volume according to the chosen pTx volumes.
- **Low SAR pat. spec.:** Reduces the SAR level. SAR reduction depends on the size and position of the FOV relative to the center of the magnet, and therefore requires additional scan adjustments.

4.16.107 CoilShim (parameter)

The **CoilShim** parameter improves image quality in the c-spine and in the neck.

It reduces patient-dependent signal loss and uneven fat saturation due to inhomogeneities at the shoulder/neck transition.



Please note that this parameter is not available for all MR systems.

-
- **Off:** **CoilShim** is inactive.
 - **Auto (on/off):** **CoilShim** is active.

Prerequisites:

- Plugged coils: BM Head/Neck 20 (HN20 TCS) or BM Head/Neck 64 (HN64 CS). (If no CS coil is plugged, the parameter is not available.)
- Lower neck element (**NE2/NC2**) is selected.

- The B0 shim mode of the protocol is either **Standard** or **Standard Neck**.
- The absolute table position of the protocol is within the scope of the CoilShim elements. (This does not apply if **SliceAdjust** is used.)

See: Operator Manual Diagnostic MR Imaging for details.

4.16.108 Adjust with Body Coil (parameter)

Usually, all adjustments are made by using the coil elements defined in the respective protocol. It is also possible to receive with the body coil only. This means that new adjustments are omitted when the selection of coil elements is changed.

Select the **Adjust with Body Coil** check box.



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

4.16.109 Tx Ref [Nucleus] (parameter)

The **Tx Ref [Nucleus]** display field shows a list of reference amplitudes for the selected primary or secondary nucleus.

You can enter new values for the reference amplitude.



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

You can reset your manual settings at any time: Click **Reset**.

4.16.110 Adjustment Tolerance (parameter)

If you would like to use the adjustment results for similar table positions, you can set them as default values via the **Adjustment Tolerance** field:

- **None**: Adjustment results are only used again at the identical table position.
- **Maximum**: Adjustment results are also used on similar table positions.

- **Auto (None):** The adjustment tolerance is determined automatically by the system. Currently, **None** is selected.
- **Auto (Maximum):** The adjustment tolerance is determined automatically by the system. Currently, **Maximum** is selected.

4.16.111 Adjusting the volume

Experienced users may find it necessary to adjust the adjustment volume. The volume may be adjusted with the mouse during slice positioning in the reference images, or by entering numbers.



This feature is for experienced users only! Do not change the adjustment volume suggested by the measurement protocol during routine operation.

4.16.111.1 Entering the adjustment volume orientation numerically

- 1 Select one of the main orientations for manual adjustment of the measurement volume.
– or –
Click the button next to the **Orientation** selection list.
- 2 Select the primary orientation you want to start with and the primary orientation for rotating the adjustment volume in the **Orientation** dialog box.
- 3 Enter the angle of rotation in the adjacent spin box.
- 4 For a double-oblique orientation, enter the angle of the second rotation.
- 5 Click the **Close** button to close the **Orientation** dialog box and apply your entries.

4.16.111.2 Changing the position of the adjustment volume

The current position of the center is displayed in the **Position** field. You can change this position:

- 1 Click the button next to the **Position** selection list.
- 2 Enter the position of the center of the adjustment volume in the **Position** dialog box with reference to the isocenter: **L** for Left; **P** for Posterior; **H** for Head

Position values refer to the patient coordinate system. Enter the slice offset from the magnet isocenter. The value combination **L=0, P=0, H=0** corresponds to the isocenter. Negative values such as **L=-10 (R=10)** will offset the adjustment volume in the opposite direction.
- 3 Click the **Close** button to close the **Position** dialog box and apply your entries.

4.16.111.3 Enlarging/ reducing the adjustment volume numerically

- ◆ Enter the extent of the adjustment volume in the three spatial directions.

The field designation depends on the orientation of the adjustment volume.

The following example is for a transverse adjustment volume:

A >> P: Extension of the adjustment volume in the readout direction (in this case: A >> P) in mm.

F >> H: Extension of the adjustment volume in the phase-encoding direction (in this case: F >> H) in mm.

R >> L: Extension of the adjustment volume in the slice selection direction (in this case: R >> L) in mm.

4.16.111.4 Changing the adjustment volume

- ◆ Enter the angle in the **Rotation** input field about which you want to rotate the volume.

4.16.111.5 Applying the settings

- ◆ Whenever you change the settings press the **Enter** key.
 - or –
- Click outside the input field with the mouse.

4.16.112 Confirm Frequency (parameter)

The **Confirm Frequency** defines when the **Confirm Frequency Adjustment** dialog box will appear.

- **Never:** The **Confirm Frequency Adjustment** dialog box will never appear.
- **Always:** The **Confirm Frequency Adjustment** dialog box will appear before every measurement.
- **When Changed:** The **Confirm Frequency Adjustment** dialog box will only appear if the resonance frequency was changed due to inline adjustment.

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

4.16.113 MSMA (parameter)

The **MSMA** parameter determines the image numbering. MSMA (Multi Slice Multi-Angle) is used to establish the primary sequence according to orientation.

The letters in the **MSMA** selection list indicate the views:

- **S:** Sagittal images
- **C:** Coronal images
- **T:** Transverse images

Example: **S - C - T** numbers the reconstructed images in the following order:

- All sagittal images
- All coronal images
- All transverse images

In the **Sagittal**, **Coronal**, 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 provide information about the order (L, R, A, P, H, F). The DICOM patient coordinate system conventions 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) order with regard to position.

For sagittal slices, image numbering can also be defined based on 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.

- **Coronal A >> P or P >> A:** The coronal images are numbered in ascending order with respect to their position (A >> P from anterior to posterior or P >> A from posterior to anterior).
- **Transverse F >> H or H >> F:** The transverse images are numbered in ascending order with respect to their position (F >> H from foot to head or H >> F from head to foot).



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

4.16.113.1 Application example

You are planning a measurement with 3 slice groups. You can move or rotate the slice groups without changing the numbers of the slice groups.



The number of the selected slice group is shown on the **Geometry** parameter card in the **Slice Group** selection list. The number of the slice group does not affect the numbering of reconstructed images.

After measurement, you can view the numbering of the reconstructed images in the **Position Display** of **MR View&GO**, in the image area of **MR View&GO** or in the **Patient Browser**.

The **Position Display** shows you the position and numbers of the reconstructed images.

4.16.114 Coil Combination (parameter)

The **Coil Combination** parameter 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** improves the results for most protocols.

4.16.115 Coil Selection (parameter)

The **Coil Selection** allows a protocol-specific setting for the coil selection mode:

- In **Auto Coil Select** mode, the coil selection is adapted automatically during graphical slice positioning (move/rotate) in such a way that the nearest coil elements are selected. No other measurement parameters will be changed. An automatic selection can always be changed manually.

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. Automatic coil selection may not provide the optimum results for large examination regions on systems with a low number of channels.

- **ACS All but spine** works like **Auto Coil Select** mode, except that the spine coil is excluded from automatic selection of coil elements.
- **ACS Restricted** works like **Auto Coil Select** mode, except that automatic selection of coil elements is restricted to the coils preconfigured in the **Coil Selection** dialog box.
(→ Page 364 *Coil Selection dialog box*)
- In **Manual** mode, coils must be selected manually.
- **Default:** Accepts the global system settings for **Auto Coil Select**.



To ensure that automatic coil selection functions smoothly when you are 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 must be connected to the sockets with lower numbers.



The maximum number of coils used is limited by the number of system channels.

For large measurement regions on systems with a small number of channels, automatic coil selection may not supply the optimal results.



When you copy using copy reference, the target protocol inherits the coil configuration of the source protocol. The new configuration is saved at the corresponding table position.

4.16.116 Matrix Optimization (parameter)

Tim-system coils have built-in mode information. The **Matrix Optimization** parameter reads this information to optimize the coil matrix.

- **Off:** No matrix optimization
- **Performance:** Coil modes with compressed information content are calculated.

This increases image reconstruction speed because the lower effective number of required channels is smaller.

- **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!

4.16.117 Coil Focus (parameter)

The **Coil Focus** parameter sets the coil focus for some special coils.

- **Flat:** No special coil focus
- **Center:** The outer coil elements of BodyMatrix and SpineMatrix coils are ignored for image reconstruction.

This avoids picking up signals from outside the region of homogeneity



Only a limited set of coils are enabled for this feature, for example, Body 18 or BM Spine 32.

4.16.118 1st Signal/Mode (parameter)

The **1st Signal/Mode** selection list determines the physiological signal applied and the measurement mode for physiologically triggered measurements.

The following physiological trigger signals can be selected:

- **ECG/Trigger:** The ECG signal is detected on the skin surface with electrodes. The signal shows the action potential of the heart as a curve.

The individual curve phases correspond to the respective contraction or relaxation phases of the heart. The R-wave in the QRS complex is used as the trigger point for the measurement.

ECG triggering is especially suitable for measurements of the chest and heart because such images would be blurred by the heartbeat when a standard measurement mode is used.

- **Pulse/Trigger:** Pulse triggering is especially suitable for suppressing motion and flow artifacts that result from pulsating blood or CSF.

You can 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.

- **Ext./Trigger:** You can input an external, digital triggering signal via the PMU strip at the foot end of the patient table.

You use an external triggering signal, for example, for functional measurements to trigger measurement of a series.

The rising edge of the signal is used to start the measurement.

- **Resp./Trigger:** The respiratory signal is obtained with the respiratory belt and the sensor in the spine coil. The cyclic expansion and contraction of the thorax generates the respiratory curve.

With respiratory triggering, you can avoid motion artifacts caused by the patient breathing.

- **ECG/Retro, Pulse/Retro, Ext./Retro:** Some special sequences offer retrospective gating. The measurement is performed with triggering. The acquired image data are retrospectively sorted and subsequently correlated with the characteristics of a physiological signal.

Contrary to triggering, retrospective gating allows you to measure all cardiac phases including the late diastole.

Apply retrospective gating to ECG signal curves, pulse signal curves, and external trigger signal curves.

For detailed information regarding ECG triggering, see: Operator Manual MR System and Coils.

4.16.119 Average Cycle (parameter)

The **Average Cycle** displays the average time between two trigger events.

The average cycle is recalculated and updated continually. You cannot change this value.

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

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



If **Average cycle** displays "No Signal", the sensors are not connected or they are not providing a usable signal.

4.16.120 Captured Cycle (parameter)

In order to have the acquisition window calculated from the current cycle, click the **Captured Cycle** button.

The value of the current average cycle is displayed on the button and used to calculate the acquisition window. Protocol parameters may have to be adjusted.



The **Captured Cycle** parameter is reset as soon as you edit the value for the acquisition window.

4.16.121 Acquisition Window (parameter)

The **Acquisition Window** parameter 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.

From the size of the acquisition window, the delay time, number of phases and repetition time are calculated automatically for a number of cardiac sequences.



The **Acquisition Window** parameter is available only if the parameter **Select acquisition window** is set to **Manual**.



A tooltip is displayed if you move the mouse pointer over the **Acquisition Window** input field. It shows the measurement time recommended by the system.



In ECG triggering, the **Acquisition Window** should be 10% smaller than the average signal period (average cycle).

Please also note the difference in meaning between the terms system acquisition time and measurement acquisition time:

- **System acquisition time:** Calculated by the system; difference between the average cycle and twice the standard deviation. The acquisition window cannot be larger than the system acquisition time.
- **Measurement acquisition time:** The time actually used by the system for data acquisition.

4.16.122 Trigger Pulse (parameter)

The **Trigger Pulse** input field is used to define whether to use every trigger event or only every nth event to trigger measurements.

- **Value 1** means that every trigger pulse starts a measurement.
- **Value 2** means that every second trigger pulse starts a measurement.
etc.



The parameter is available only for the ECG, pulse, and external trigger signals.

4.16.123 Trigger Delay (parameter)

After the trigger signal, the system waits for the time specified before measurement starts.

For an adult patient with a pulse of 70 beats per minute, with ECG triggering you need a delay time of 0 ms to obtain systolic images, and a delay time of 250 - 350 ms to obtain diastolic images.

The **Trigger Delay** parameter allows to acquire images at any point in the signal cycle.



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



This parameter is active only for the ECG, pulse, and external trigger signals.

4.16.124 Adaptive Triggering (parameter)

Adaptive Triggering activates real-time adaptation of the acquisition to the current heart rate.

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



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

4.16.125 Trigger Lock Time (parameter)

The **Trigger Lock Time** sets the minimum acquisition time for **Adaptive Triggering**.



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

4.16.126 Target RR (parameter)

The **Target RR** parameter establishes the patient's average heart rate for the system.

The parameter can be used to ignore triggers that occur outside a defined time window. This is a time range defined by the **Target RR** and the **Trigger Window**.

For example, for a **Target RR** of 800 ms and a **Trigger Window** of 200 ms, any triggers occurring outside the time interval of 700 to 900 ms are rejected and data acquired in such intervals rejected and re-acquired.



The **Target RR** value should correspond to the average heart rate of the patient.

4.16.127 Phases (parameter)

The **Phases** field defines how many phases of the cardiac cycle can be calculated using the current protocol.

You may use this field, i.e., for multislice/multiphase measurements of the heart.



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

4.16.128 Arrhythmia Detection (parameter)

Some sequences include an automatic detection of arrhythmia.

The **Arrhythmia Detection** is based on recognition of triggers that occur outside a specified time window (**By Time**).



If you have selected the entry **By time** for the **Arrhythmia detection** parameter, the **Trigger window** parameter will appear on the parameter card.

4.16.129 Trigger Window (parameter)

The **Trigger Window** parameter establishes the size of a time window. In combination with the **Target RR** parameter, it defines a time range for ignoring triggers that occur outside.

For example, for a **Target RR** of 800 ms and a **Trigger Window** of 200 ms, any triggers occurring outside the time interval of 700 to 900 ms are rejected and data acquired in such intervals rejected and re-acquired.



This parameter is only active for **Arrhythmia Detection - By time**.

For detailed information regarding ECG triggering, see: Operator Manual MR System and Coils.

4.16.130 Calculated Phases (parameter)

The **Calculated Phases** parameter is used to define the number of images depicting the phases of the cardiac cycle that can be generated in a retrograded CINE acquisition.

4.16.131 Flow sensitivity (parameter)

The **Flow sensitivity** parameter modifies the flow-spoiling gradient of the sequence.

It can be used to adjust a NATIVE SPACE acquisition to the expected blood flow conditions.

- **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.



The parameter is available only for SPACE sequences when the **NATIVE** is set to **3D mode** or **TD scout**.

4.16.132 NATIVE (parameter)

With **NATIVE** set, arterial and venous images without contrast agent are generated.

- **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**.



The parameter is available only for SPACE sequences if **1st Signal/Mode** is set to **ECG/Trigger**, **Pulse/Trigger**, or **Ext./Trigger**.

4.16.133 TD min flow (parameter)

The **TD min flow** parameter defines the trigger delay for the second acquisition.

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

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



The parameter is available only if **NATIVE** is set to **3D Mode**.

4.16.134 TD peak flow (parameter)

The **TD peak flow** parameter defines the trigger delay for the first acquisition.

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



The parameter is available only if **NATIVE** is set to **3D Mode**.

4.16.135 TD first (parameter)

The **TD first** parameter 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 measurement starts.



The parameter is available only if **NATIVE** is set to **TD scout**.

4.16.136 TD increment (parameter)

The **TD increment** parameter defines the trigger delay increment for a series of TD scout acquisitions.

The trigger delay increases from one measurement to the next.



The parameter is available only if **NATIVE** is set to **TD scout**.

4.16.137 Threshold (respiration parameter)

The **Threshold** parameter determines the time when 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.



Threshold is only displayed for **Respiratory triggering**.

4.16.138 Display of time ranges

The top right areas of the parameter card shows the physiological signal and the time domains resulting from the parameters set. Unlike the **Physiological Display** dialog box, a frozen image is displayed on the **Physio** parameter card.

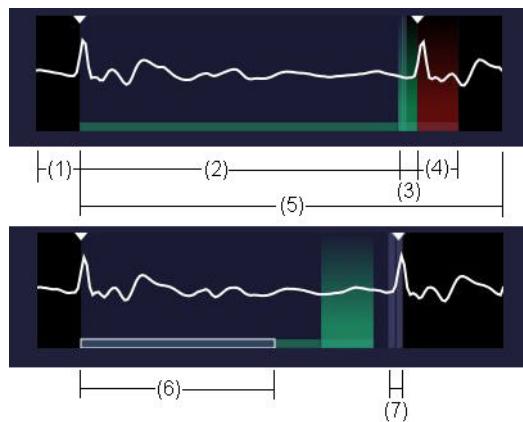
Each time range is assigned a different color:

- Green: Measurement interval and/or acquisition window
- Light blue: Measurement pauses

No data is acquired during this time. Here, saturation pulses (inversion time or dark blood) are transmitted, for example.

- Red: Trigger occurred during acquisition window

The trigger is ignored and the red bars indicate that the acquisition did not take place during the intended phase of the cardiac cycle.



Time ranges for ECG triggering

- (1) Delay time
- (2) Repetition time
- (3) Measurement interval
- (4) Trigger occurred
- (5) Measurement acquisition window
- (6) Measurement pause
- (7) Double standard deviation

4.16.139 Tagging (parameter)

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.

Possible settings:

- **Grid tag:** Results in images with a grid pattern superimposed on the region being scanned.

Used to visualize regional and global cardiac wall motion, for example, 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, for example, in long-axis views of the heart.

- **None:** No tags applied.

4.16.140 Dark Blood (parameter)

With the **Dark Blood** option, a special preparation pulse is transmitted to saturate the blood in cardiac sequences. It allows for excellent visualization of the heart muscle.

Blood appears dark in the image, hence the name "dark blood".

4.16.141 Slice-sel. IR thickness (parameter)

The **Slice-sel. IR thickness** parameter allows to control the thickness of the inversion slice in a TIRM sequence (also known as STIR sequence). This is important in high heart rate patients where the old implementation can cause a partial signal dropout, which can be mistaken as pathological finding.

The thickness is given as a percentage of the protocol slice thickness, for example, the default value of 200% means that the slice thickness of the STIR pulse is twice that of the acquired slice.



The **Slice-sel. IR thickness** parameter should be changed to higher values, for example, 280% when imaging patients with faster heart-rates.

4.16.142 Resp. Control (parameter)

The **Resp. Control** field lets you select a method for suppressing respiratory artifacts.

- **Off:** Navigator control is switched off.
- **Breath-hold:** The slices of a concatenation are measured as soon as you press the **Scan Breathhold** button on the **Inline Display**. The number of manual starts required for the complete measurement equals the number of concatenations set.

For some sequence types, the duration of a breath-hold scan can be set in the **Breath-hold duration** parameter.

The **Inline Display** also provides an icon for continuing the scan until the end of the measurement.

- **Gate:** The image data are only accepted if the diaphragm position is within the acceptance window.
- **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:** After a learning period of approximately 5 respiratory phases, a block of image data is acquired once the measured diaphragm position indicated 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:** The navigator signals are calculated and displayed in the usual way, but they are not used to control the measurement.

4.16.143 Scout Mode (parameter)

The **Scout Mode** is used to plan a preparation phase for measuring only the Navigator signal. In this way, you are able to check whether or not the navigator records the respiratory signal as required.

4.16.144 Scout Type (parameter)

The **Scout Type** parameter defines the scout type used for the navigator.

- **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, see: Operator Manual Diagnostic MR Imaging.

4.16.145 Accept window ± (parameter)

Enable **Accept window ±** if you have selected one of the modes below in conjunction with **Resp. Control**.

Respiratory control mode	Effect of the Accept window ± parameter
Gate	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 ± .
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 ± .

Respiratory control mode	Effect of the Accept window \pm parameter
Trigger	<p>Vertical width of the yellow acceptance window shown in the Inline Display</p> <p>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.</p>

4.16.146 Position Accept Window (parameter)

If the respiratory control is set to **Trigger**, the **Position Accept Window** parameter is available.

The **Position Accept Window** parameter determines whether the system will set the center of the acceptance window "automatically" (**Automatic**) during the learning phase or whether you will set it "manually" (**Manual**) as a percentage in the **Accept Position** window.

4.16.147 Accept. Position (parameter)

With the **Accept. Position** parameter, you can set the center of the acceptance window for trigger respiratory control.

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.



This parameter only appears during **Gate** or **Gate & Follow** respiratory control.

4.16.148 Search Window \pm (parameter)

For **Gate** or **Gate & Follow** respiratory control, you can enter the size of the window in millimeters in the **Search Window \pm** field.

The search window is displayed as a red box surrounding the tolerance center in the **Inline Display**.

4.16.149 Select Acquisition Window (parameter)

- **Manual:** Displays the parameter **Acquisition Window**. The system sets the acquisition duration per respiratory cycle to less than or equal to 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.

4.16.150 Position Navigator (parameter)

- **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 patient's breathing cycle, if it is crudely positioned in the vicinity of the lungs. The system positions the navigator automatically.

4.16.151 Store Profile Images (parameter)

The temporal change of the navigator signal is displayed graphically in the **Inline Display**. These images can be saved in a separate series.

4.16.152 Tracking Factor (parameter)

The **Tracking Factor** parameter is shown when you set **Gate & Follow** mode under **Resp. Control**.

The **Tracking Factor** establishes the correlation between the movement of the diaphragm and the resulting shift of the anatomy to be measured.



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

4.16.153 Chronologic Position (parameter)

The **Chronologic Position** selection list lets you select the time for triggering the navigator signal (with **Gate** or **Gate & Follow**):

- **Before echo:** Before the echo train of the image
- **After echo:** After the echo train of the image

If you have selected **Gate & Follow** under respiratory control, the **After echo train of image** option is not available.

- **Before & After:** Before and after the echo train of the image



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.

4.16.154 Resp. Motion Adaptation (parameter)

The **Resp. Motion Adaptation** parameter determines whether the position of the accept window will adjust to the changes in amplitude of the respiratory curve. This prevents, for example, a shallower respiratory curve leading to infinite measurements.



This parameter is available only when the **Gate & Follow** mode has been selected under the **Resp. Control** parameter.

4.16.155 Dummy Heartbeats (parameter)

Defines the number of dummy heartbeats played out per slice to generate steady state magnetization. During these heartbeats no data is acquired.

4.16.156 TONE Ramp (parameter)

TONE Technique = Tilted, Optimized, Nonsaturating Excitation

The **TONE Ramp** parameter 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.

This parameter specifies the ratio of the respective flip angle at the two edges of the slab as a percentage. The nominal flip angle is used at the center of the slab. For example, a flip angle of 20° and a TONE ramp value of 60% together produce an excitation profile with a flip angle that rises from 15° to 25° across the slab.

The results are an even signal distribution for the blood vessels of a slab.

4.16.157 Flow Direction (parameter)

The **Flow Direction** parameter defines the direction of blood flow to be visualized. The direction always refers to the patient coordinate system.

For example, in a mostly transverse slice you can select the **H >> F or F >> H** direction.



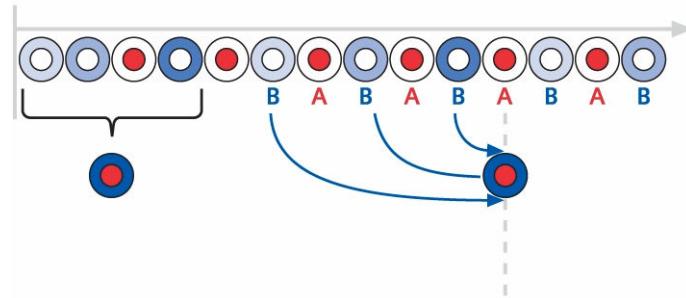
Changing the directions, can automatically position the tracking sat regions on the side of the slab from which the arterial blood exits.

4.16.158 Reconstruction Scheme (parameter)

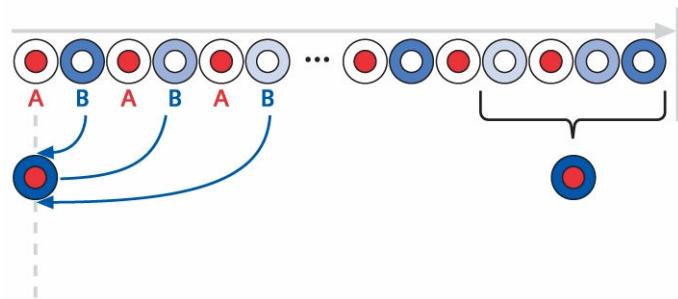
The **Reconstruction Scheme** determines how the k-space is dynamically reconstructed for multiple measurements.

- **Forward Share:** Data acquired in the outer k-space region are transferred to the following images.
- **Backward Share:** Data acquired in the outer k-space region are forwarded to the preceding images.
- **Symmetric Share:** Data acquired in the outer k-space region are transferred to both the preceding and following images in a symmetrical fashion.

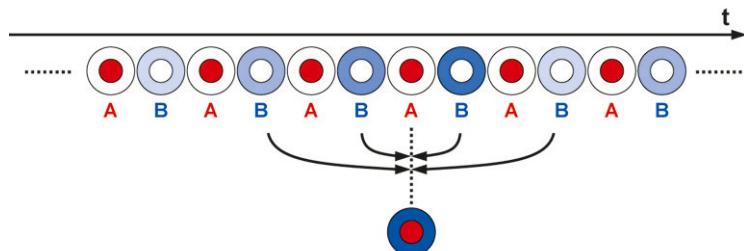
Forward Share: The complete k-space is sampled at the beginning of the measurement. The data acquired in region B is forwarded to the following images.



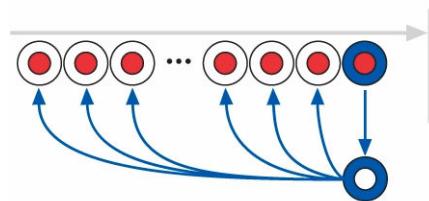
Backward Share: The complete k-space is sampled at the end of the measurement. The data acquired in region B is transferred to the preceding images.



Symmetric Share: The complete k-space is always sampled both at the beginning and at the end of the measurement.



Keyhole examination: The prerequisite for this is a sampling density $B = 0$. It requires **Backward share** as the reconstruction mode.



The parameter is only active when **TWIST** is selected under the **View Sharing** parameter.

4.16.159 3D Reordering (parameter)

The **3D Reordering** parameter determines the time to center.

- **Standard** determines that the center of the raw data space is measured as quickly as possible after contrast agent inflow.
This ensures optimal contrast of the arterial vessels.
- **User Defined TTC** allows you to set a value for the time to center.



The **3D Reordering** option is available for sequences with contrast-enhanced (**CE**) 3D angiography.

4.16.160 Time to Center (parameter)

The **Time to Center** field determines the measurement time required until the measurement has reached the k-space center.

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



The parameter is only visible for fl3d_ce and TWIST sequences.

4.16.161 Burn Time to Center (parameter)

The **Burn Time to Center** parameter determines if the value from the **time to k-space center** is burned into the pixel data of the image so that this information is displayed in the **Examination** screen.



The parameter is only active when **TWIST** is selected under the **View Sharing** parameter.

4.16.162 Flow Mode (parameter)

The **Flow Mode** selection list defines the encoding mode flow.

- **Single vel.:** One flow sensitivity (flow sensitivity encoding)

Blood flow is measured in 3 spatial directions based on a set flow sensitivity. This mode provides vessel display irrespective of the direction of flow.

- **Single dir.:** One direction for several flow sensitivities
Blood flow is measured based on multiple flow sensitivities, but in only one spatial direction. This mode is used to acquire large variations in flow velocities (e.g., in the area of peripheral arteries).
- **Free:** Permits free selection of the flow sensitivities and spatial directions.

4.16.163 Direction (parameter)

During flow encoding, the **Direction** table is used for assigning a flow sensitive axis to each flow sensitivity.

If the **Through Plane** option is selected, only the flow-sensitive axis perpendicular to the image plane will be detected.



The possible entries depend on the selected **Flow Mode**.

4.16.164 Temporal Interpolation (parameter)

The **Temporal Interpolation** parameter determines how the images are interpolated linearly. The number of MIP images is increased by an interpolation factor.



The parameter is only active when **TWIST** is selected under the **View Sharing** parameter.

4.16.165 Temporal Resolution/Virt. Temporal Resolution (parameter)

The **Temporal Resolution/Virt. Temporal Resolution** field shows 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**.

With an interpolation factor greater than 1, the parameter is called **Virt. Temporal Resolution**.



The parameter is only active when **TWIST** is selected under the **View Sharing** parameter.

4.16.166 GLM Statistics (parameter)

The **GLM Statistics** parameter determines whether the data are acquired with the GLM statistics mode (GLM = General Linear Model).



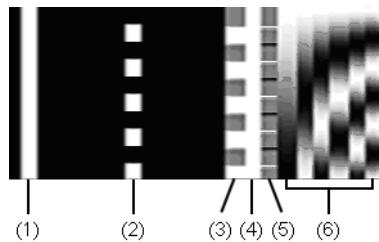
If the parameter is cleared, all images are saved without analysis.

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

Using the GLM, the signal changes are modeled using an expanded hemodynamic response function of the brain. This enables better description of the measurement data. The method provides a reliable model for the activity over time curve.

The hemodynamic response function is a curve that represents the brain's response, and therefore the resulting MR signal changes to a short, needle-shaped stimulus.

The model can also be utilized for data acquired shortly after a change in stimulation. Additionally, temporal changes between the model function and measurement data can be modeled. This is necessary because the measurement of individual slices does not take place at the same time.

**Design matrix of a GLM evaluation**

- (1) Display of all measurements used for evaluation.
white = used measurements
black = unused measurements
- (2) Paradigm - Active/Baseline
- (3) Paradigm folded with HRF (hemodynamic response function)
(Model transition state = on)
- (4) Offset component
- (5) Evolution of paradigm over time
- (6) Model function for modeling oscillations over time

The following parameter settings effect an analysis to be performed with the HRF:

- **Ignore after transition** = 0
- **Model transition states** = on
- **Temp. highpass filter** = on

4.16.167 Ignore After Transition (parameter)

The **Ignore After Transition** parameter determines the number of measurements that will be ignored after the stimulation has been changed.

Example: With **Ignore After Transition=2** and the first change in paradigm for measurement 11, measurements 1,2,11 and 12 are ignored.

4.16.168 Model Transition States (parameter)

The **Model Transition States** parameter determines that the hemodynamic response function of the brain will be included in the computation.

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



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

4.16.169 Temp. Highpass Filter (parameter)

The **Temp. Highpass Filter** parameter determines whether low frequency oscillations over time will be eliminated with a high pass filter.

The number of components of the high-pass filter is determined automatically.

The filter components are displayed in the last column of the design matrix (no. 6).

4.16.170 Threshold (parameter)

The **Threshold** input field is used to enter the threshold value for the t-test evaluation. At a certain level of intensity, pixels from the t-test images will be used to calculate overlaid images.



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

4.16.171 Paradigm Size (parameter)

The **Paradigm Size** is the table size of all measurements within a paradigm.

You make the following settings for every measurement:

- **Active:** Measurement is performed **with** stimulation.
- **Baseline:** Measurement is performed **without** stimulation.

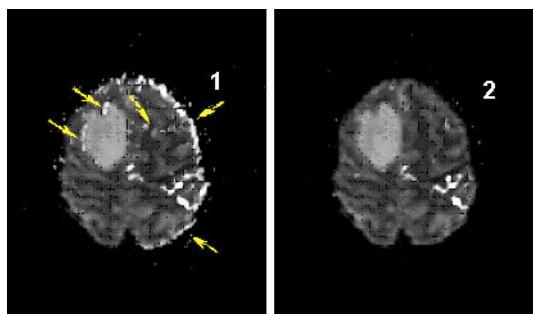


You may edit the cells in the right column of the paradigm table. Just click them with the mouse. The selection list appears and you can select one of the settings listed above.

4.16.172 Motion Correction (parameter)

When the **Motion Correction** option is selected, motion correction is performed during calculation.

In Neuro imaging, small patient movements (0.3 mm) may cause significant artifacts in the functional information. In the following figure, patient movement is marked in yellow (1). Using the 3D motion correction, you can reduce relative movements (translation and rotation) between measured volume data sets (2).



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

The motion correction is displayed in the image text.

Image type **MOCO** applies.

The comment line shows the correction parameters. The images of the first repetition have only the comment "**Reference volume for motion correction**".

Example: Motion: -3.98, -0.27, 4.04, -2.48, 3.12, -0.35

The first three values show the translation in the X, Y, Z direction (in millimeters) and the following three values show the rotation about the X, Y, Z axis (degrees).

4.16.173 Interpolation (BOLD parameter)

If the **Motion Correction** option is activated, you can select an interpolation method for motion correction in the **Interpolation** selection list:

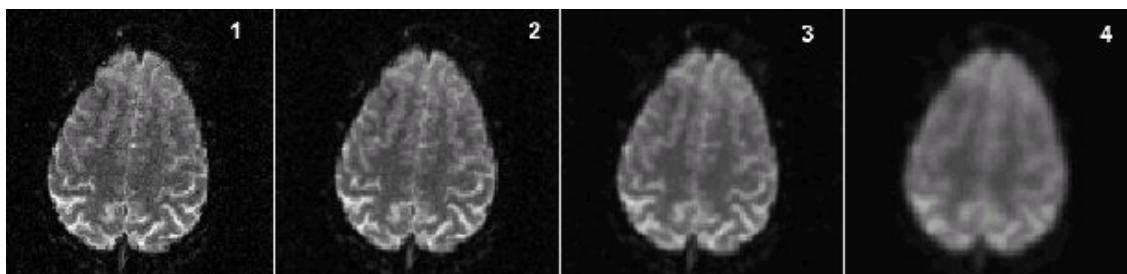
- **Linear:** Linear interpolation
Fast method of real-time post-processing
- **3D k-Space:** Interpolation in Fourier space
Good quality method of real-time postprocessing

4.16.174 Filter Width (parameter)

The **Filter Width** parameter determines the width of the Gaussian filter used. It defines the filter strength.



This parameter is active only when the **Spatial Filter** check box is selected.



Example

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

4.16.175 Diffusion Mode (parameter)

The **Diffusion Mode** parameter determines 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 better SNR than in the **3-Scan Trace**.

- **Orthogonal:** Requires three images per slice position and b value (when $b > 0$), 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** (Multi-directional diffusion weighting): Acquires one diffusion-weighted image per slice position, per b-value, per average, 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, the [...] button is displayed next to the parameter field for importing the settings from a corresponding file (%CustomerSeq%\DiffusionVectorSets*.dvs).
Please note: The folder "%CustomerSeq%" is mapped to "K:\CustomerSeq".
Allows import/export of customized diffusion directions (=diffusion vector sets, DVS).
- **q-space:** Enables the acquisition of a q-space data set. Sampling can be full or half sphere up to a maximum b-value.
- **q-Space weightings:** Number of q-space coordinates sampled along each positive coordinate axis (excluding the origin).
- **q-space max. b-value:** b-value that corresponds to the diffusion weighting of the outermost q-space coordinates.
- **q-Space coverage:**
 - **Full:** Complete q-space coverage (sampling of a spherical q-space region).
 - **Half:** Partial q-space coverage (only one half of the sphere is sampled, thus reducing the acquisition time).

4.16.176 Diff. Directions (parameter)

The **Diff. Directions** parameter 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: $b = 1000 \text{ s/mm}^2$, third direction of 6, 10, 12, 20, 30, 64 or 256



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

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

4.16.177 Diffusion Scheme (parameter)

The parameter **Diffusion Scheme** sets the spin echo diffusion encoding.

- **Bipolar:** Double refocused spin echo diffusion encoding that minimizes distortions
- **Monopolar:** Single refocused spin echo diffusion encoding that enables shorter TE and thus increased SNR



For diffusion SMS measurements, we recommend that you select the monopolar gradient mode, see **Acceleration mode**.

4.16.178 Averages (diffusion parameter)

The **Averages** parameter 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 fewer 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 equals or exceeds the number of averages of lower b-values.

4.16.179 b-Value (parameter)

The **b-Value** is a measure of diffusion weighting. It is expressed in s/mm².

The **b-Value** table is for assigning a b-value to each diffusion weighting for a diffusion-weighted measurement.

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.

4.16.180 b-Value >= (parameter)

The **b-Value >=** parameter specifies the minimum b-value used in ADC calculations.

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

4.16.181 Diff. Weighted Images (parameter)

When the **Diff. Weighted Images** option is active, you obtain original images with diffusion weighting. These images contain T1, T2, and diffusion-weighted portions.

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

4.16.182 Trace Weighted Images (parameter)

The **Trace Weighted Images** parameter determines whether 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.

4.16.183 ADC Maps (parameter)

The **ADC Maps** parameter determines whether ADC maps are reconstructed where averaging is performed with different b-values.

ADC maps (Apparent Diffusion Coefficient) 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.



The parameter is available only, if at least two b-values are set.

4.16.184 Exponential ADC Maps (parameter)

The **Exponential ADC Maps** parameter determines whether an exponential ADC map is reconstructed.



Exponential ADC maps may eliminate T2 shine-through artifacts.

4.16.185 GBP (parameter)

If you select the **GBP** (Global Bolus Plot) option, a global time-density curve will be calculated from the perfusion measurement data to enable evaluation of the bolus passage.



15 measurements are the minimum required to select the parameter.

4.16.186 PBP (parameter)

When the **PBP** (Percentage of Baseline at Peak map) option is selected, a percentage signal image is calculated for each slice of the perfusion measurement.

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 target.



15 measurements are the minimum required to select the parameter.

4.16.187 TTP (parameter)

When the **TTP** (time to peak map) option is selected, a time-to-peak image is calculated for each slice of the perfusion measurement.

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 this reason, arrival of the contrast agent is delayed.

- Gray scale value (Perfusion) = $1000 + (\text{time to peak in seconds}) \times 10$
- Gray scale value (Breast evaluation) = Time-to-peak in seconds



For the **Perf** card, 15 measurements are the minimum required to select the parameter.

For the **Inline/Soft Tissue** card, 2 measurements are the minimum required to select the parameter.



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

4.16.188 relMTT (parameter)

The **relMTT** (relative Mean Transit Time) determines whether a relative MTT map is reconstructed.



This inline calculation is based on the local AIF method.

(→ Page 487 *Local AIF method*)

4.16.189 relCBF (parameter)

The **relCBF** (relative Cerebral Blood Flow) determines whether a relative CBF map is reconstructed.



This inline calculation is based on the local AIF method.

(→ Page 487 *Local AIF method*)

4.16.190 relCBV (parameter)

The **relCBV** (relative Cerebral Blood Volume) determines whether a relative CBV map is reconstructed.



This inline calculation is based on the local AIF method.

(→ Page 487 *Local AIF method*)

4.16.191 relCBVCorr (parameter)

The **relCBVCorr** (relative Cerebral Blood Volume corrected) determines whether a T1 corrected relative CBV map is reconstructed.



This inline calculation is based on the local AIF method.

(→ Page 487 *Local AIF method*)

4.16.192 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.

Unlike the global AIF method, it determines the incoming flow of contrast agent at one reference point for all voxels.

It supports the calculation of **relCBF**, **relCBV**, and **reIMTT** maps. Additional T1 corrected **relCBVCorr** maps are provided.

4.16.193 Liver Registration (parameter)

The **Liver Registration** parameter activates a 3D liver registration.



The parameter is available only if a value greater than 2 is set in the **Measurement** parameter.

4.16.194 Proton Density Images (parameter)

The **Proton Density Images** parameter sets the number of proton density weighted images to be acquired at the start of a dynamic acquisition. These images are used for surface coil correction.



The **Proton Density Images** parameter is only available for cardiac dynamic acquisitions.

4.16.195 Save Original Images (parameter)

The **Save Original Images** parameter determines whether the unprocessed images are stored in the database as well.



The parameter can be cleared only when at least one of the following parameters is selected: **Subtraction**, **MIP**, **StdDev**, **Liver Registration**, **T1-map**, or **T2-map**.

4.16.196 Subtract (parameter)

The **Subtract** parameter activates inline subtraction, which is performed on identical protocols. The measurement defined as the subtrahend (without contrast agent) will be subtracted from all following measurements.

If selected, the parameters specific to subtraction are displayed.



For Inline subtraction within a protocol, the number of measurements must be > 1 .

4.16.197 Subtraction (parameter)

The **Subtraction** parameter defines whether a subtraction evaluation will be performed with a series of the current measurement. This generates images showing, for example, changes after contrast agent administration.

If 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.

4.16.198 Autoscaling (parameter)

If the **Autoscaling** option is selected, the subtraction result images are scaled automatically, that is, the display area of the calculated values is adjusted automatically.



The **Autoscaling** parameter is only displayed if the **Subtract** option is selected.

4.16.199 Scaling Factor (parameter)

The **Scaling Factor** input field is used for entering an individual factor for scaling the display range of the calculated subtraction values.



The **Scaling factor** parameter is displayed only if the **Subtract** option is activated and the **Autoscaling** option is activated.

4.16.200 Offset (parameter)

The **Offset** input field is used for entering an offset for the lower and upper threshold of the display range of the calculated subtraction values.



The **Offset** parameter is displayed only if the **Subtract** option is selected and the **Autoscaling** option is cleared.

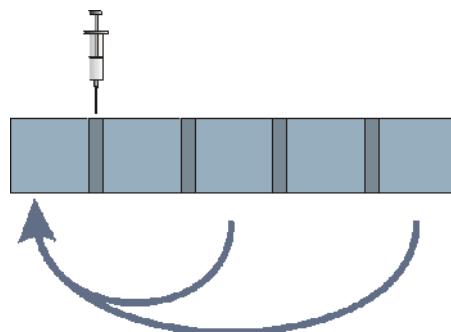
4.16.201 Subtrahend (parameter)



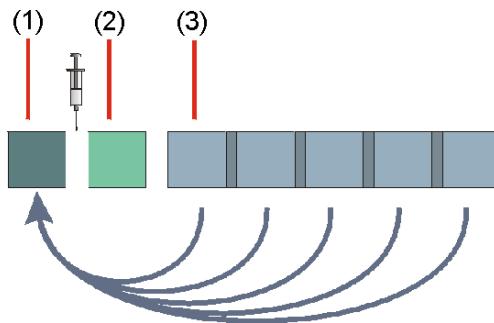
Select the **Subtrahend** check box to display the parameter.

Subtraction of series within a multiple measurement protocol:

The **Subtrahend** parameter typically defines the native series of the multiple measurement protocol. This native series is subtracted from the postcontrast 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 postcontrast series.



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

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



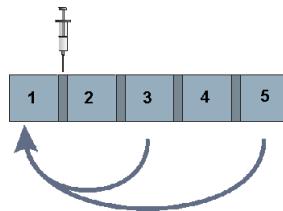
In this example, the **Subtract** check box must be selected for both the native and the postcontrast protocol.

4.16.202 Subtraction Indices (parameter)

The **Subtraction Indices** parameter defines the postcontrast series of the multiple measurement protocol. The native series, which is defined by the parameter **Subtrahend**, is subtracted from these postcontrast series.



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



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.

4.16.203 Subtraction Group (parameter)

The postcontrast images of a **Subtraction Group** are subtracted from the precontrast images of a subtraction group.

Different subtraction groups are necessary if several precontrast and postcontrast protocols are measured at the same table position. Otherwise the images of the last precontrast protocol would be used for subtraction.

4.16.204 Std-Dev-Sag (parameter)

If the **Std-Dev-Sag** option is selected, standard deviation result images with sagittal orientation are calculated from the acquired slabs of the current protocol. You can see variances in pixel values in the sagittal direction.



It is only possible to edit the **Std-Dev-Sag** parameter when you are performing a 3D measurement and the number of slices in the slabs is at least 4.

4.16.205 Std-Dev-Cor (parameter)

If the **Std-Dev-Cor** option is selected, standard deviation result images with coronal orientation are calculated from the acquired slabs of the current protocol. You can see the variance of the pixel values in the coronal direction.



It is only possible to edit the **Std-Dev-Cor** parameter if it is a 3D measurement and the number of slices in the slabs is at least 4.

4.16.206 Std-Dev-Tra (parameter)

If the **Std-Dev-Tra** option is selected, standard deviation result images with transverse orientation are calculated from the acquired slabs of the current protocol. You can see the variance of the pixel values in the transverse direction.



It is only possible to edit the **Std-Dev-Tra** parameter if it is a 3D measurement and the number of slices in the slabs is at least 4.

4.16.207 Std-Dev-Time (parameter)

If the **Std-Dev-Time** option is activated, standard deviation result images with the orientation of the acquired slice groups or slabs are calculated from the acquired slice groups or slabs of the current protocol.

You can see the scatter of the pixel values within the measurement period. Both multiple phases and multiple measurements can be evaluated.

4.16.208 Motion Correction (Inline parameter)

In Angio imaging, the **Motion Correction** parameter registers the postcontrast minuend(s) to the precontrast subtrahend. It is available for the **f13d_ce** sequence (3D mode) in the context of subtraction.

- **None:** No motion correction selected
- **Angio Standard:** Rigid-body registration algorithm
- **Angio Advanced:** Locally adaptive algorithm



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

For **Motion Correction** parameter (**Inline/Cardiac**), see: Operator Manual Diagnostic MR Imaging.

4.16.209 MIP Time (parameter)

If the **MIP-Time** option is selected, MIP images (Maximum Intensity Projection) with the orientation of the acquired slice groups or slabs are calculated from the acquired slice groups or slabs of the current protocol. In the calculation, the highest pixel value along the time axis is taken into account.



It is only possible to edit the **MIP-Time** option if there is at least one measurement repetition (parameter **Averages** > 1) or, in the case of triggered measurement, at least two phases are measured.

4.16.210 Radial MIP (parameter)

The **Radial MIP** parameter determines whether radial MIP views are reconstructed from the measured slab of the actual protocol.

- **Number of Radial Views:** Number of views for radial MIP views.
- **Axis of Radial Views:** Rotation axis of radial MIP views.

4.16.211 MapIt (parameter)

The **MapIt** parameter determines whether inline parametric maps are calculated.

- **None:** No parametric maps are calculated.

- **T1 Map:** Activates the Inline computation of T1 maps.

The **Contrasts** parameter is set to the value 1 and cannot be changed.

The **Measurement** parameter is set to the value 2 and cannot be changed.

- **T2 Map:** Activates the Inline computation of T2 maps.

The **Contrasts** parameter is set to value 2. It can have 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 have 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 have 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 have 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.

4.16.212 T1 Estimate (parameter)

You enter an estimated value for T1 in the **T1 Estimate** field. This value is required for automatically calculating the flip angle.



This parameter is only available when the **Auto angle calculation** parameter has been selected.

4.16.213 Flip Angle (MapIt parameter)

- When you selected the **T1 map** mode in the **MapIt** parameter:
This parameter determines the first flip angle for T1 maps.
- When another mode was selected in the MapIt parameter:
This parameter displays the flip angle used.



The **Flip Angle** parameter can be edited only when the **Auto Angle Calculation** parameter has been cleared.

4.16.214 Contrasts (parameter)

The **Contrasts** parameter is used to define the number of image contrasts. You can specify the number of images to be acquired with different T2 (e.g., se-tse sequences) or T2* weightings (gre sequences) in one measurement.



You must define an echo time for each contrast.



The parameter is available only for a few sequences.

4.16.215 Inline Evaluation (parameter)

The **Inline Evaluation** parameter determines whether inline evaluations are performed in physiologically triggered acquisitions.

- **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 graphical 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 only the images acquired in the current protocol step. Minimum requirements are two parallel short-axis slices.
- **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, of the sampling and recovery, in beats 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**.

4.16.216 Magn. Preparation (Inline parameter)

The **Magn. Preparation** parameter determines whether magnetization preparation is performed prior to data acquisition in order to influence image contrast.

- **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-selective inversion pulses optimized for the T1 mapping application with improved inversion efficiency for the operating range of interest.
- **T2 prep.:** A preparation pulse is applied to the entire volume to enhance T2 contrast.
- **T2 prep. adiabatic:** This option works in a similar way to **T2 prep.**

These are the main differences from the **T2 prep.** option:

- Preparation module is more B1-insensitive
- Results in better image homogeneity
- Requires more RF power

4.16.217 Preparation Scans (parameter)

The **Preparation Scans** parameter is used to set the number of preparation measurements for spectroscopy.

The result is an equilibrium magnetization for the following MR experiment.



Data acquisition is deactivated during preparation measurements.

4.16.218 Delta Frequency (parameter)

The **Delta Frequency** parameter is used to determine the signal in the spectrum for which you want to obtain an exact slice selection.

The frequency shift stated refers to the system frequency, i.e., usually the water signal.



You can use the frequency to reduce the chemical shift artifact.



If you select the **Fully excited Vol** option on the **Geometry/Common** parameter card, the **Delta Frequency** parameter is set to a fixed value and cannot be changed.

4.16.219 Phase Cycling (parameter)

The **Phase Cycling** parameter is used to set a phase cycle to eliminate interfering signals in SVS spectroscopy measurements.

- **None:** No phase cycle.
- **Auto:** Selects the phase cycle of the longest cycle that fits into the number of acquisitions
- **Two step:** Single phase cycle
- **Eight steps:** Eliminates all interference from the slice-selective pulses.
- **EXOR cycle:** 4 steps; single Exor cycle.
- **16 EXOR cycle:** 16 steps; Exor cycle that eliminates all interfering signals from the slice-selective pulses.

4.16.220 ADC Bandwidth (parameter)

The **Bandwidth** parameter defines the current ADC bandwidth during data acquisition. The bandwidth may be varied between 1 and 2 kHz.

At a magnetic field strength of 1.5 T, the typical signals of the ^1H -MRS are fully resolved at a bandwidth of 1 kHz.

4.16.221 Acquisition Duration (parameter)

Acquisition Duration displays the current readout duration in spectroscopy measurements.



The read-out time is the product of the number of measurement points (vector size) and the inverted bandwidth.

The read-out time is read-only and cannot be modified.

4.16.222 Remove Oversampling (parameter)

The **Remove Oversampling** option is selected by default. The oversampling data are removed during automatic evaluation of spectroscopy raw data. This produces a ringing effect in the time signals that does not adversely affect the frequency data.



If you do not want to evaluate measured spectroscopy data with Siemens software, it is advisable to not remove the oversampling data.

In this case, switch off the **Remove Oversampling** option.

4.16.223 Freq. Corr. Accumulation (parameter)

The ¹H-MRS SVS sequence contains internal frequency correction to minimize the motion artifacts caused by respiration.

When the **Freq. Corr. Accumulation** function is switched on, the frequency of each individual acquisition is adjusted to the frequency of the first (reference) acquisition. The corrected measurement is then accumulated.



When this parameter is selected, the **Water suppression** parameter is automatically set to **Weak water suppr..** Spectral water suppression should not be selected.

4.16.224 Ref. Scan Mode (parameter)

A reference scan is performed prior to measurement. The reference scan has no water suppression. It is used for eddy current correction.

- **Off:** No reference scan
- **Inline correction:** A reference scan is performed.

The spectra are corrected based on the reference scan.
Only the corrected spectra are saved.
- **No inline correction:** A reference scan is performed.

The following spectra are saved:
 - Reference scan
 - Uncorrected spectra
- **Save all:** A reference scan is performed.

The spectra are corrected based on the reference scan.
The following spectra are saved:
 - Reference scan
 - Uncorrected spectra
 - Corrected spectra



If the reference scan is not suitable for correction, no inline correction is executed. The reference scan and the uncorrected spectra are saved instead.



In conjunction with the parameter **Save uncombined (System/Miscellaneous parameter card)**, the following uncombined spectra are saved:

- Uncorrected spectra
- Corrected spectra (only if Save all is selected)

4.16.225 No. of ref. scans (parameter)

The **No. of ref. scans** parameter sets the number of averages acquired during the reference scan.



This parameter is only available if **Ref. scan mode** is selected.

4.16.226 Dimension (parameter)

The **Dimension** selection list is used to set a 2D or a 3D measurement.



Switching from **2D** to **3D** changes the entries on all parameter cards. They now contain slab group parameters instead of slice group parameters.



You cannot switch the dimension for all sequences. In these cases, the **Dimension** parameter is displayed dimmed or is not available.

4.16.227 Phase Encoding (parameter)

The **Phase Encoding** parameter defines the phase-encoding types used for a CSI measurement.

The following phase-encoding types (sampling schemes) are available:

- **Full:** The entire k-space defined by the number of phase-encoding steps is measured.
- **Elliptical:** Only the points located on or within the k-space ellipse are measured. This saves you about 1/4 the measurement time without significant loss of spatial resolution.
- **Weighted:** Is identical to **Elliptical** with one averaging (NA=1). If multiple averaging steps are performed (NA > 1), the central points of the k space are measured NA times and the points on the elliptical boundary at least once. For the intermediate points, the measurement frequency is determined by their radial distance from the center of the k-space.

With **Weighted**, you can use the **Hamming** filter. Set this filter on the **Resolution/Common** parameter card during measurement. This ensures optimal use of measurement time with respect to the SNR gain when acquiring multiple accumulations.

4.16.228 Elliptical Scanning (parameter)

The **Elliptical Scanning** parameter determines whether the corners of the k-space that contribute only minimally toward resolution will be ignored during data acquisition.

It reduces the measurement time by up to 25% for 3D sequences without compromising resolution.

4.16.229 Phase Stabilization (parameter)

Phase stabilization prevents phase errors caused, for example, by respiration.



The **Phase Stabilization** option is especially suitable for improving the image quality of gradient echo sequences with long echo time (**TE**).

4.16.230 Compensation T2 Decay (parameter)

The activation of **Compensation T2 Decay** avoids negative effects of the T2 decay during acquisition of long echo trains.



You can select the **Compensation T2 Decay** option for turbo echo sequences.

4.16.231 Reordering (parameter)

The **Reordering** parameter defines the acquisition sequence of the raw data lines.

- **Linear:** The k-space is stepped through linearly.
- **Centric:** The first measured raw data lines are from the center of the k-space. The fat saturation in single shot sequences is improved since the center of the k-space is measured immediately after the fat saturation pulse.

4.16.232 Asymmetric Echo (parameter)

The **Asymmetric Echo** parameter permits echo asymmetry in the readout direction. It is used to reduce the echo time. The maximum asymmetry that must not be exceeded is defined in the sequence.

- **Off:** No asymmetric echo is used.
- **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 may occur.
- **Half Echo:** A fully asymmetric echo is used.
Extremely short echo times below 1 ms can be obtained (only available for UTE sequences).



The asymmetry of the echo may result in readout artifacts.



You can display the asymmetry of the echo in a tooltip.

4.16.233 Readout Bandwidth (parameter)

The **Bandwidth** parameter 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 differing from the protocol parameter.

For two reasons, the MR scan is performed with a bandwidth value that can differ slightly 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 ns 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 real value of each frame.

4.16.234 Flow Compensation (parameter)

The **Flow Compensation** parameter prevents signal loss and smearing caused by moving spins. For this purpose, additional gradient pulses are switched with a suitable time duration and amplitude.

Some sequences enable you to specify flow compensation separately for each contrast:

- **Yes:** Compensation in the readout and slice encoding direction, as well as in the phase-encoding direction for some sequences (e.g., tfl, CV).
- **Read:** In the readout direction only
- **Slice:** In the slice-selection direction only
- **None:** No flow compensation

4.16.235 Allowed Delay (parameter)

The **Allowed Delay** parameter defines 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 from 0 seconds to the maximum delay time.

4.16.236 Free Echo Spacing (parameter)

If you select the **Free Echo Spacing** option, you can define the time interval between two echoes in the **Echo Spacing** spin box.



Excessive echo spacing may cause increased distortion in EPI sequences due to susceptibility.

4.16.237 Echo Spacing (parameter)

The **Echo Spacing** is the time interval between the echoes in the pulse train, e.g., for Turbo spin echo (TSE) or EPI sequences.

Smaller echo spacing provides 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.

4.16.238 Readout Mode (parameter)

The **Readout Mode** parameter defines the readout mode for gradient echo sequences (GRE).

- **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 monopolar mode.

However, 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 bipolar mode.
The fat-water shift is identical in all contrasts.

4.16.239 Optimization (parameter)

The **Optimization** parameter is used for time optimization.

- **None:** Time optimization is not performed.
- **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:** The shortest time interval is determined at which fat and water are in phase.
- **Opposed phase:** The shortest time interval is determined at which fat and water are out-of phase.
- **In/Opp:** The shortest time interval is determined at which fat/water are in/out phase.
- **Opp/In:** The shortest time interval is determined at which fat/water are out/in phase.
- **Equidistant:** The shortest time interval is determined at which fat and water are in equidistant phase.



If the **Optimization** if set to **Min. TE** or **Min. TR** changing a parameter might cause other parameters (for example, TR, TE, or bandwidth) to change in the background, without user notification. In the RESOLVE sequence, the **Optimization** parameter is always set to **Min. TE** or **Min. TR**.



It is not possible to change the optimized parameters manually.

4.16.240 Sequence Type (parameter)

The **Sequence Type** parameter establishes the type of sequence.

- **Gre:** The sequence measures with the gradient echo method.
- **TruFi:** The sequence measures with the TrueFisp method.

4.16.241 Reduce Motion Sens. (parameter)

The **Reduce Motion Sens.** parameter determines if modified phase-encoding gradients are used. This stabilizes the sequence against slight motions, which would normally result in segmentation artifacts.



This parameter is only available for **tse** sequences.

4.16.242 Define (parameter)

The **Echo trains/Turbo factor** parameters or **Shots/Segment** parameters are reconstructed as a function of one another.

- **Echo trains:** The turbo factor is computed according to the desired number of echo trains per slice.
- **Turbo Factor:** The number of echo trains per slice is calculated based on the turbo factor.
- **Shots:** The segment size is determined based on the desired number of shots per slice.
- **Segment:** The number of shots per slice is determined based on the segment size.

4.16.243 Turbo Factor (parameter)

The **Turbo Factor** parameter specifies the number of refocused spin-echoes per RF excitation necessary for image generation.

It therefore determines the measurement time gained as compared with a conventional spin-echo sequence with comparable parameters.



When the **Blade** mode is selected under the **Trajectory** parameter on the **Resolution/Common** or **Physio/Cardiac** parameter cards, the **Turbo Factor** determines the number of lines per blade.

4.16.244 Slice Turbo Factor (parameter)

The **Slice Turbo Factor** parameter defines the number of slices to be measured with an echo train.



The parameter is active only if the echo train is long enough to measure multiple slices, and **Echo trains** mode is selected in the **Define** field.

4.16.245 EPI Factor (parameter)

The **EPI Factor** specifies the number of refocused gradient echoes per RF excitation necessary for image generation.



For single-shot EPI sequences, the number of lines to be measured is used as the **EPI Factor**.

4.16.246 Combined Echoes (parameter)

The echoes of a multi-echo sequence can be added to improve the signal-to-noise ratio (for example MEDIC sequences).

The **Combined Echoes** method provides flow-compensated T2* images with a high signal-to-noise ratio.

MEDIC sequences exhibit a smaller chemical shift and less susceptibility artifacts than normal gradient echo sequences.

4.16.247 Trufi Delta Freq. (parameter)

Use the **Trufi Delta Freq.** parameter to move banding artifacts to areas of the image where they do not pose a problem.



This field is active only in **TrueFisp** sequences.

4.16.248 Reacquisition Mode (parameter)

The **Reacquisition Mode** parameter defines whether acquisition is automatically repeated to improve image quality when data are corrupted (for example, by motion).

- **On:** Reacquisition mode is activated.
- **Off:** Reacquisition mode is deactivated.



The parameter is available only for a few sequences.

4.16.249 RF Pulse Type (parameter)

The **RF Pulse Type** parameter defines the length and the form (envelope) of the radio frequency pulses.

- **Fast:** Short RF excitation pulse

Cross-talk may occur between the slices/slabs. This setting is recommended only for fast measurements with reasonable distance factors, for example, breath-hold techniques.

- **Normal:** RF pulse with a good slice profile

It permits measurements with small distance factors with little cross-talk.

- **Low SAR:** Extended RF pulse with a good slice profile and reduced specific absorption rate

It can be set after an SAR warning. This reduces measurement performance.

- **Optimized:** Optimized RF pulse for reducing slice cross-talk

- **Rectangular:** Standard rectangular excitation pulse for spectroscopy

- **AHP:** Adiabatic Half-Passage pulse for spectroscopy

This pulse reduces the sensitivity of the excitation to B1 inhomogeneity effects, for example, when surface coils are used. The AHP pulse only allows a 90 degree excitation.

- **BIR-4:** B1 InSensitive Rotation pulse with tanh/tan modulation for spectroscopy

This pulse reduces the sensitivity of the excitation to B1 inhomogeneity effects.

4.16.250 Gradient Mode (parameter)

The **Gradient Mode** parameter determines the rise time and maximum gradient strength that is used to switch gradients during the course of the sequence.

The possible settings depend on the gradient system:

- **Fast:** The gradient rise time and strength are fully utilized.

This mode may cause peripheral nerve stimulation in the patient.

- **Normal:** For most sequences this setting is a good compromise between performance and noise.

- **Whisper:** Lowest possible noise at acceptable system performance.

- **Performance:** This mode is available on systems with high end gradient systems. The gradient rise time and strength are fully utilized.

This mode may cause peripheral nerve stimulation in the patient.



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**.

4.16.251 Excitation (parameter)

The **Excitation** parameter determines how the RF excitation pulse is sent.

- **Slice-sel:** RF excitation is selective in the through-plane direction; a single slice is excited.
- **Slab-sel:** RF excitation is selective in the through-plane direction; a single slab is excited.
- **Non-sel:** RF excitation is performed for the whole FOV.
This option may result in aliasing artifacts in the slice-selection direction.
- **Slab-sel PE:** RF excitation is selective in phase the encoding direction; a single slab is excited.
This option causes different behavior regarding aliasing artifacts than **Slab-sel**.
- **ZOOMit:** RF excitation is performed for a reduced FOV, which can be imaged in a shorter scan time.
Excitation with **ZOOMit** is integrated in BOLD, diffusion EPI sequences, and SPACE.
- **TONE:** Activates 3D TOF mode for the BEAT sequence. If selected, the sequence uses an RF excitation pulse with a linearly increasing flip angle profile.
The **TONE** option is only available for 3D gradient-echo protocols, that is, it cannot be selected for every parameter combination.

4.16.252 Flip Angle Mode (parameter)

The **Flip Angle Mode** parameter provides a more precisely defined flip angle of the refocusing pulse in the echo train.

- **Constant:** The flip angle of the refocusing pulse remains constant across the entire echo train.
(→ Page 401 *Flip Angle (parameter)*)
- **Hyperecho:** The flip angle of the refocusing pulse varies across the echo train, forming a hyperecho.

This mode 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.

This mode enables optimum FLASH contrast. It is used for cardiovascular sequences, for example.

- **T1 var:** The flip angle of the refocusing pulse varies across the echo train.

This mode enables T1-weighted imaging with short echo times, and is optimized for SAR.

- **T2 var:** The flip angle of the refocusing pulse varies across the echo train.

This mode enables very long echo trains for fast T2-weighted measurements, and is optimized for SAR.

- **PD var:** The flip angle of the refocusing pulse varies across the echo train.

This mode is particularly suited to proton density measurements and is optimized for SAR.

4.16.253 Inc. Gradient Spoiling (parameter)

When the **Inc. Gradient Spoiling** parameter is set, the gradient spoiling is increased to improve image quality.



Increasing the gradient spoiling increases TR (e.g., for VIBE sequence) and/or **Echo spacing** (e.g., for TFL sequence).

4.16.254 BM Motion Correction (parameter)

You can use this motion correction feature for neurological imaging to reduce motion artifacts caused by movements of the patient's head. The motion correction feature is available for TurboFLASH sequences with MPRAGE contrast, TSE, and GRE sequences.



Please note that this parameter is not available for all MR systems.

- **Off:** Motion correction is switched off
- **Auto (On):** Motion correction is switched on and will be applied, if applicable.
- **Auto (Off):** Motion correction is switched on but cannot be used because at least one of the prerequisites for motion correction is not met. Refer to the parameter's tooltip for details.



The "Auto" states are dynamic and can change depending on the situation. For example, the system automatically sets **Auto(Off)** if a requirement is not met. Once this is remedied, **Auto(On)** will be automatically re-enabled.

4.16.255 Stereotactic (parameter)

The **Stereotactic** parameter reduces image artifacts caused by the use of stereotactic frames.



This parameter should be activated only when a stereotactic frame is used.

4.16.256 WARP (parameter)

The **WARP** parameter reduces susceptibility artifacts if the patient has MR Conditional orthopedic implants.

The sequence uses high-bandwidth RF pulses to reduce artifacts caused by off-resonance effects occurring in the vicinity of MR Conditional orthopedic implants.



Follow all safety instructions regarding implants. ([Operator Manual - MR System](#))



The parameter is available only for a few sequences.

4.16.257 VAT (parameter)

Off-resonance effects (for example from MR Conditional implants) may result in 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 result in 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.

4.16.258 Phase Correction (parameter)

The **Phase Correction** parameter defines whether the sequence performs a phase correction.

- **On:** Phase correction is performed
- **Off:** No phase correction
- **Automatic:** Whether or not a phase correction is performed depends on the type of system and the type of protocol.



In most cases, **Automatic** mode will provide good results!

For diffusion protocols, an external phase correction scan can be used to help reducing ghosting artifacts especially in the presence of fat (applicable, for example, for body or breast imaging).

- **External:** Phase correction is performed with an external phase correction scan.
- **Internal:** The conventional internal phase correction scan is applied.



The **Phase Correction** parameter should only be adapted by experienced users!

4.16.259 SAR Optimization (parameter)

The **SAR Optimization** parameter varies the flip angle in the SEMAC encoding direction.

- **Off:** No SAR optimization
- **On:** SAR optimization is activated
- **Automatic:** SAR optimization is always activated

4.16.260 SEMAC (parameter)

The **SEMAC** parameter (slice encoding for metal artifact correction) specifies the number of additional encoding steps to correct for distortions caused by MR Conditional orthopedic implants and to improve image quality, in particular in the presence of hip or knee joint full replacements.

- If set to a value > 0, the SEMAC sequence 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 like 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.

4.16.261 NOE Flip Angle (parameter)

With the **NOE Flip Angle** parameter, you set the flip angle of the ^1H saturation pulses. The flip angle is spatially dependent on the Heart/Liver coil. The setting should be seen as a pulse-enhancing factor and not as a calibrated flip angle.



The setting has a direct effect on the pulse tension of the ^1H saturation pulses that you can control on the **System/Tx/Rx** parameter card.



To achieve the best saturation with the ^1H saturation pulses, use the maximum possible **NOE Flip Angle**. The SAR monitor ensures that the energy absorption for the patient remains within limits.

4.16.262 Decoupling Type (parameter)

With the **Decoupling Type** parameter, you set the mode for ^1H decoupling.

- **CW:** A decoupling pulse is continuously transmitted during data acquisition. The decoupling has a narrow bandwidth in the frequency domain. The decoupling frequency should be accurately set for optimal decoupling.
- **WALTZ-4:** A series of short decoupling pulses is transmitted during data acquisition. The decoupling has a broad bandwidth in the frequency domain and does not depend to the same degree on the setting of the decoupling frequency.

4.16.263 Decoupling Duration (parameter)

With the **Decoupling Duration** parameter, you define the duration of a ^1H decoupling pulse for ^{31}P MRS measurements using **Waltz 4** decoupling.



The **Decoupling Duration** parameter can be edited only for the **Waltz 4** decoupling mode.

4.16.264 DC Total Duration (parameter)

With the **DC Total Duration** parameter, you set the proportion of decoupling duration relative to the readout duration [%].



Ideally, the decoupling duration should correspond to the readout duration (100%). Values < 100% reduce the decoupling irradiation to an appropriate time interval at the beginning of the decoupling window. This is useful in preventing a TR increase as a result of the SAR limit.

4.16.265 DC Pause Fract. (parameter)

With the **DC Pause Fract.** parameter, you define the time interval between ^1H decoupling pulses (as a percentage of decoupling duration) for ^{31}P MRS measurements using **Waltz 4** decoupling.



The **DC Pause Fract.** parameter can be edited only for the **Waltz 4** decoupling mode.

4.16.266 Decoupling Flip Angle (parameter)

Use the **Decoupling Flip Angle** parameter to set the flip angle of the ^1H decoupling pulses for a ^{31}P MRS measurement.

- With **Waltz 4** decoupling, the flip angle refers to the center 180° pulse. It should therefore be 180°.
- With **CW** decoupling, the flip angle is specified over an interval of 10 ms.

The flip angle is spatially dependent on the Heart/Liver coil. The setting should be seen as a pulse-enhancing factor and not as a calibrated flip angle.



The setting has a direct effect on the pulse tension of the ^1H decoupling pulses that you can control on the **System/Tx/Rx** parameter card.

4.16.267 SAR Assistant (parameter)

The **SAR Assistant** parameter defines the strategy to avoid exceeding the SAR limit. The system therefore manipulates the selected parameter.

- **Off:** No SAR assistant functionality
- **TR:** TR is increased by the system to avoid exceeding the SAR limit.
- **Flip Angle:** Flip angle is reduced by the system to avoid exceeding the SAR limit.
- **Flip Angle, TR:** First, the flip angle is reduced, then TR.
- **TR, Flip Angle:** First, TR is reduced, then the flip angle.

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