syngo MR XA60

Addendum – MR Reference Handbook

SIEMENS Healthineers

Legend

	Indicates a hint Provides information on how to avoid operating errors or information emphasizing important details
	Indicates the solution to a problem Provides troubleshooting information or answers to frequently asked questions
■	Indicates a list item
✓	Indicates a prerequisite A condition that has to be fulfilled before starting a particular operation
◆	Indicates a single-step operation
1 2 3	Indicates steps within operating sequences
Italic	Used for references and for table or figure titles
➔	Used to identify a link to related information as well as previous or next steps
Bold	Used to identify window titles, menu items, function names, buttons, and keys, for example, the Save button 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

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.

1.1 myExam Companion

myExam Companion is a new philosophy to operate MRI, providing built-in expertise and automation for any user and clinical question. With its capabilities to help users generate consistent, comprehensive results, myExam Companion is an advancement of the Dot workflow technology of Siemens Healthineers.

The following terms will be introduced with *syngo* MR XA40:

≤ *syngo* MR XA31	≥ *syngo* MR XA40
–	myExam Companion
–	myExam 3D Camera

≤ *syngo* MR XA31	≥ *syngo* MR XA40
–	myExam Autopilot

The following terms will be replaced with the introduction of *syngo* MR XA40:

≤ *syngo* MR XA31	≥ *syngo* MR XA40
Dot Engine	myExam Assist (For details see below)
Dot Engines	myExam Assist programs
Dot Cockpit	myExam Cockpit
Dot Cockpit Explorer	myExam Cockpit Explorer
Dot Cockpit Program Editor	myExam Cockpit Program Editor
Dot add-in/Dot AddIn	myExam add-in
DotAddIn Configuration	myExam Add-In Configuration
Dot Add-In Configurator	myExam Add-In Configurator
Dot View	Assist View

The Dot Engine names will be replaced with the introduction of *syngo* MR XA40. The following is a non-exhaustive list of examples:

≤ *syngo* MR XA31	≥ *syngo* MR XA40
Abdomen Dot Engine	myExam Abdomen Assist
Angio Dot Engine	myExam Angio Assist
Biopsy Dot Engine	myExam Biopsy Assist
Brain Dot Engine	myExam Brain Assist
Breast Dot Engine	myExam Breast Assist
Cardiac Dot Engine	myExam Cardiac Assist
C-Spine Dot Engine	myExam C-Spine Assist
Hip Dot Engine	myExam Hip Assist

≤ *syngo* MR XA31	≥ *syngo* MR XA40
Knee Dot Engine	myExam Knee Assist
LiverLab Dot Engine	myExam LiverLab Assist
L-Spine Dot Engine	myExam L-Spine Assist
Prostate Dot Engine	myExam Prostate Assist
RT Dot Engine	myExam RT Assist
Shoulder Dot Engine	myExam Shoulder Assist
Spine Dot Engine	myExam Spine Assist
T-Spine Dot Engine	myExam T-Spine Assist
Whole-Body Dot Engine	myExam Whole-Body Assist

In the user interface, for example, in the protocol trees, the myExam Assist names are listed without the prefix myExam.

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** **Ctrl** + **X** **Ctrl** + **V**	Copy selected object. Cut selected object. 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)

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 **Down Arrow**	Preselect the previous or next program step within the queue.
Shift + **Up Arrow** **Shift** + **Down Arrow**	Select the previous or next program steps consecutively upward or downward within the queue.
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.
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** **Alt** + **Down Arrow**	Move the selected step up or down within the queue (**Move Up**, **Move Down**).

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** **Ctrl** + **4**	Shift the selected slice or slab group against or in slice-selection direction (**Stack-**, **Stack+**).
Ctrl + **5** **Ctrl** + **6**	Move the slice group by half the distance between slices (**Gap-**, **Gap+**).
Ctrl + **7** **Ctrl** + **8**	Shift the selected slice or slab group in Z direction (**FoV-**, **FoV+**).
Up Arrow/Down Arrow **Numerical keypad 1/2**	Scroll to previous or next slice according to display order.
Left Arrow/Right Arrow **Numerical keypad 4/5**	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-**).

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 auto-matically calculating a window width and window center value (**Auto Windowing**).
	Increase window center.
	Decrease window center.
	Increase window width.
	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** or **Tab** (go to the next parameter)	Apply entry from selection list.
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	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: • 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 myExam Cockpit shortcuts

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

2.3.1 General

F2	Rename directories, regions, or examinations.
Ctrl + **Shift** + **D**	Open the **myExam 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).
 **Scroll**	**I**	Scroll images.
	U	Activate or deactivate scrolling with skipping.
	Shift + I	Activate or deactivate performance mode for scrolling without skipping.

	Keyboard	
 **Movie**	**Spacebar**	Start/Stop movie.
 **3D Reference point**	**R**	Activate **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.
 **Rotate**	**O**	Rotate image.

2.4.3 Common tools

 **Full Text**	**T**	Switch the image text on/off.
 **Hide Graphics**	**G**	Switch display of graphics on/off.
 **Hide Lines**	**H**	Switch display of reference lines on/off.

 **Print Image**	**E**	Send selected image to the film sheet.
 **Print Stack**	**A**	Send all images of selected stacks to the film sheet.
 **Snapshot**	**S**	Create a snapshot of selected segments.
 **Magnifier**	**Ctrl + M**	Magnify a section of an image.
 **Save Presentation**	**Alt + S**	Save the image presentation of a segment manually.
 **Save and Send**	**Ctrl + Alt + A**	Close the case, save and send the results (to the archive).
 **Save and Pause**	**Ctrl + Alt + S**	Close the case and save results locally.

2.4.4 Image optimization

 **MR Presets**	**F5 - F8**	Apply Windowing Presets.

 **Invert**	**F 10**	Invert grayscale or color values.
 **Zoom/Pan**	**Z**	Zoom/Pan images
	Alt	Press and hold the key to deactivate the current tool temporarily and enable **Zoom/Pan**.
 **Windowing**	**W**	Adjust Windowing level and width (with left mouse button).
 **Auto Windowing**	**Numerical keypad 9**	The image is displayed by automatically calculating a window width and window center value.
 **Punch**	**P**	Quick punch (3D view: MIP, VRT, MinIP)
 **Clip Plane**  **Clip Box**	**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		
 **MR Color LUT**	**Shift + F5** - **F8**	Apply Color LUT presets.
	F 9	Toggle through all Color LUTs.
	F 10	Invert the grayscale.

2.4.5 Image evaluation

 **Distance Line**	**D**	Measure a straight distance.
 **ROI Circle**	**C**	Measure a circular ROI.
 **Pixel Lens**	**L**	Activate pixel lens.
 **Marker**	**M**	Place a marker on point of interest.
 **VOI Sphere**	**V**	Measure a spherical VOI.
	Ctrl + Return	Enter a line break in an annotation text.

2.4.6 Switch display type

 **2D**	**1**	Switch to 2D display.
 **MPR**	**2**	Switch to MPR.
 **MPR Thick**	**3**	Switch to MPR Thick.
 **MIP**	**4**	Switch to MIP.
 **MIP Thin**	**5**	Switch to MIP Thin.
 **MinIP Thin**	**6**	Switch to MinIP Thin.
 **VRT**	**7**	Switch to VRT.
 **VRT Thin**	**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

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

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.

The conical flask indicates a research protocol, not suitable for clinical use.

Possible reasons:

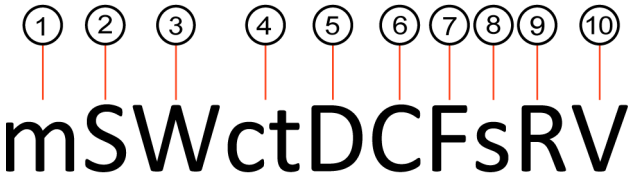
- Sequences not released for clinical use
- Licenses not released for clinical use, for example, full pTx functionality
- Configurations not released for clinical use, for example, 16 Tx array

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

Abbreviation	Definition
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
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
hir	HASTE with inversion recovery
ir	Spin echo with inversion recovery
me	MEDIC (multi-echo data image combination)
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)
swi	Susceptibility-weighted imaging

Abbreviation	Definition
tfi	TrueFISP
tfl	TurboFLASH
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”
tirR	Turbo spin echo with inversion recovery and “restore pulse”
tse	Turbo spin echo
tseB	Turbo spin echo with BLADE trajectory
tseBN	Turbo spin echo with BLADE trajectory and “normal echo mode”
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 *syngo* 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

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

3.1.2.4 Dimension (D)

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

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)

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

Abbreviation	Definition
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 **myExam Cockpit**, they are referred to as **Default Sequences**.

3.1.3.1 Sequence nomenclature (I)

Abbreviation	Definition
AALScout	AutoAlign localizer
BEAT	For MR angiography
CISS	Constructive interference in steady state
CSI	Chemical shift imaging
DESS	Dual echo steady state
EPI	Echo-planar imaging
FID	Free induction decay
FLASH	Fast low angle shot
GRE	Gradient-echo sequence[2)]
MEDIC	Multi-echo data image combination
PETRA	Pointwise encoding time reduction with radial acquisition
Quiet_DWI	For quiet diffusion-weighted imaging
RESOLVE	Readout segmentation of long variable echo trains
SE	Spin-echo sequence

2) 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
SPACE	For SPACE applications
TurboFLASH	-
TrueFISP	FISP = fast imaging with steady-state precession
TSE	Turbo SE

3.1.3.2 Sequence nomenclature (II)

Abbreviation	Definition
_B1Map	For B1 mapping
_BOLD	For BOLD imaging (BOLD = blood oxygen level dependency)
_CB	For determining the contrast bolus
_Diff	For diffusion contrast
_Dixon	Sequence using the Dixon technique
_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
_MC	Multicontrast sequence
_PACE	Sequence with prospective motion correction
_PC	For phase-contrast angiography
_r	With flow compensation
_SE	Spin-echo sequence, for example, EPI_SE: spin-echo variant of EPI sequence
_SEG	Segmented sequence

Abbreviation	Definition
_VIBE	Volume-interpolated breath-hold examination
..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

Abbreviation	Definition
_ref	Reference scan spectrum
_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

3.2.1 AALScout

A modified FLASH3D_VIBE sequence is used for AutoAlign scout measurements in AutoAlign programs. 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

The BEAT sequence is a multifunctional sequence designed for various MR 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 case: non-contrast-enhanced 3D TOF MRA

3D display of vessels.

3.2.2.2 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 BLADE

Turbo spin-echo sequence with BLADE data acquisition.

For diffusion imaging, 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)

3.2.3.1 Use

- For T1,T2, and PD imaging with reduced motion sensitivity.
- For diffusion imaging, especially for cholesteatoma imaging.

BLADE reduces motion artifacts but may result in lower contrast, lower resolution, and longer acquisition times than, for example, single-shot diffusion-weighted EPI or RESOLVE.

3.2.3.2 Parameters

Turbo factor	9–65
TE variable	Yes[3)]
Contrasts	1
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Multi-slice mode	Interleaved/Sequential
Flow compensation	None/Readout/Slice
Dimension	2D
Fast Mode	Yes
RF pulse type	Fast/Normal/Low SAR/Optimized[4)]
Gradient mode	Fast/Normal/Whisper/Performance[5)]
Dark blood	Yes
iPAT	Yes

3) Only for diffusion imaging

4) May be selected only if Fast Mode has been selected

5) Only available for XT, XR, W60, and T60 gradients

Simultaneous multislice (SMS)	Yes[6)]
SliceAdjust	Yes
Respiratory control	Trigger/Breath-hold[7)]
Flip Angle Mode	Constant/Hyperecho
BLADE Trajectory	Yes
Restore	Yes
Acoustic noise reduction	Yes
Motion correction	Yes

3.2.4 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.

3.2.4.1 Use

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

3.2.4.2 Parameters

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

6) Only for diffusion imaging

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

Averaging mode	Short term
Multi-slice mode	Sequential
Flow compensation	None
Dimension	2D/3D
Elliptical scanning[8)]	Yes
Slice resolution[9)]	Yes
Slice partial Fourier[10)]	Yes
Excitation pulses[11)]	Slab-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper

3.2.5 CSI_FID

FID variant for chemical shift imaging.

3.2.5.1 Parameters

TE variable	No[12)]
Bandwidth variable	Yes
Averaging mode	Short term/Long term
Dimension	2D/3D
Triggering	ECG/Respiratory

8) Only if Dimension = 3D is selected

9) Only if Dimension = 3D is selected

10) Only if Dimension = 3D is selected

11) Only if Dimension = 3D is selected

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

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

3.2.6 DESS

3D gradient-echo sequence.

3.2.6.1 Use

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

3.2.6.2 Recommendations

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

3.2.6.3 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[13)]	Yes
Slice resolution[14)]	Yes
Slice partial Fourier[15)]	Yes
Excitation pulses[16)]	Slab-selective/Non-selective
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes

3.2.7 EPI2D_BOLD

Single-shot FID EPI sequence.

3.2.7.1 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**.

3.2.7.2 Parameters

EPI factor[17)]	1–128
TE variable	Yes
Contrasts	1
Bandwidth variable	Min.–max.

13) Only if Dimension = 3D is selected

14) Only if Dimension = 3D is selected

15) Only if Dimension = 3D is selected

16) Only if Dimension = 3D is selected

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

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/Performance[18)]
iPAT	Yes
Simultaneous multislice (SMS)	Yes

3.2.8 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)

3.2.8.1 Use

For diffusion imaging, for example, for examining strokes.

18) Only available for XT, XR, W60, and T60 gradients

3.2.8.2 Recommendations

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

3.2.8.3 Parameters

EPI factor[19)]	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
Gradient mode	Fast/Normal/Performance[20)]
b-value [s/mm^2]	0–10000 or 0–16000[21)]

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

20) Only available for XT, XR, W60, and T60 gradients

21) Depending on the MR system

Increment bipolar [s/mm^2]	50
Increment monopolar 0–200 [s/mm^2]	10
Increment monopolar above 200 [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[22)]
Online reconstruction	• DW and ADC image • FA image • TRACE • colored FA image
iPAT	Yes
Simultaneous multislice (SMS)	Yes
Respiratory control	Trigger/Breath-hold[23)]
Echo spacing variable	Yes
Optimization	Min. TE
SliceAdjust	Yes
Phase correction	Internal/External
Deep Resolve	Gain

3.2.9 EPI2D_PACE

Identical to EPI2D_BOLD but with prospective 3D motion correction.

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

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

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

3.2.9.1 Parameters

EPI factor[24)]	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/Performance[25)]
iPAT	Yes

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

25) Only available for XT, XR, W60, and T60 gradients

3.2.10 EPI2D_SE

Single-shot spin-echo EPI sequence.

3.2.10.1 Use

To examine T2-weighted lesions.

3.2.10.2 Recommendations

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

3.2.10.3 Parameters

EPI factor	1–256[26)]
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

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

Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Performance[27)]
iPAT	Yes

3.2.11 FID

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

3.2.11.1 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

3.2.11.2 Parameters

TE variable	No[28)]
Bandwidth variable	Yes
Phase cycling	Yes

27) Only available for XT, XR, W60, and T60 gradients

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

Triggering	ECG/Respiratory
Multiple measurements	Yes
Multinuclear support	Yes

3.2.12 FLASH_PC

FLASH sequence.

Possible online reconstructions:

- Magnitude image
- Phase image
- Magnitude sum image

3.2.12.1 Use case: 2D

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

3.2.12.2 Use case: 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

3.2.12.3 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[29)]	Yes
Slice resolution[30)]	Yes
Excitation pulses	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On
Gradient mode	Fast/Normal/Whisper
Venc cm/s	1–999

29) Only if Dimension = 3D is selected

30) Only if Dimension = 3D is selected

3.2.13 GRE

Gradient-echo sequence.

3.2.13.1 Use

- Abdominal in-phase/opposed phase imaging in one measurement
- 3D FLASH sequence for T1-weighted ortho imaging and neuro imaging
- Susceptibility-weighted imaging (SWI)
- Evaluation of metastases and lymph nodes in the thorax, abdomen, and pelvis (whole-body imaging)

3.2.13.2 Recommendations

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

3.2.13.3 Parameters

Segments	1–127
TE variable	Yes
Contrasts	1–12
Bandwidth variable	Yes
Magnetization Preparation	IR, SR[31)]
Reconstruction mode	Magnitude/Phase
Fat suppression	Fat saturation/Water excitation

31) If segments >1 (segmented TurboFLASH)

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/None/Readout/Slice/Slice&Read-out
Dimension	2D/3D
Elliptical scanning[32)]	Yes
Slice resolution[33)]	Yes
Slice partial Fourier[34)]	Yes
Excitation pulses[35)]	Slab-selective/Non-selective
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper/Performance[36)]
Dark blood	Yes[37)]
Grid/Line tagging	Yes
iPAT	Yes
iPAT^2	Yes

32) Only if Dimension = 3D is selected

33) Only if Dimension = 3D is selected

34) Only if Dimension = 3D is selected

35) Only if Dimension = 3D is selected

36) Only available for XT, XR, W60, and T60 gradients

37) If segments >1 (segmented TurboFLASH)

Respiratory control	Breath-hold[38)]
Readout mode	Monopolar/Bipolar
Acoustic noise reduction	Yes
SWI	Yes
BM Motion correction	Yes
Denoising Mode	Swift Brain

3.2.14 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.

3.2.14.1 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

3.2.14.2 Parameters

TE variable	Yes
Contrasts	2
Bandwidth variable	Yes

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

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

3.2.15 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.

3.2.15.1 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

3.2.15.2 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[39)]	Yes
Slice resolution[40)]	Yes
Slice partial Fourier[41)]	Yes
Excitation pulses[42)]	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	On/Off

39) Only if Dimension = 3D is selected

40) Only if Dimension = 3D is selected

41) Only if Dimension = 3D is selected

42) Only if Dimension = 3D is selected

Gradient mode	Fast/Normal/Whisper
iPAT	Yes

3.2.16 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).

3.2.16.1 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.

3.2.16.2 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.
- Note that PETRA may result in lower contrast and lower SNR than MPRAGE.

3.2.16.3 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**

Parameter	Parameter card	Comment
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

3.2.16.4 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

3.2.17 Quiet_DWI

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

3.2.17.1 Use

For quiet diffusion-weighted imaging of the brain.

3.2.17.2 Recommendations

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

3.2.17.3 Parameters

EPI factor[43)]	1–256
TE variable	No[44)]
Contrasts	2
Bandwidth variable	No[45)]
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

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

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

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

Flow compensation	None
Dimension	2D
RF pulse type	Normal/Low SAR
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
b-value	0–10000 or 0–16000[46)]
Online reconstruction	• 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

3.2.18 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.

46) Depending on the MR system

3.2.18.1 Use

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

3.2.18.2 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”.
- RESOLVE reduces geometric distortions and signal voids and produces better image quality but results in longer acquisition times than single-shot diffusion-weighted EPI.

3.2.18.3 Parameters

EPI factor[47)]	1–256
TE variable	No[48)]
Contrasts	2
Bandwidth variable	No[49)]
Magnetization preparation	IR
Reconstruction mode	Magnitude
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Readout partial Fourier	Yes

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

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

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

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[50)]
b-value	0–10000 or 0–16000[51)]
Online reconstruction	• 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

3.2.19 SE

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

50) Only available for XT, XR, W60, and T60 gradients

51) Depending on the MR system

3.2.19.1 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.

3.2.19.2 Parameters

TE variable	Yes
Contrasts	1–2
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real[52)]
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[53)]

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

53) Only available for XT, XR, W60, and T60 gradients

Dark blood	Yes
Blood suppression	On/Off
Acoustic noise reduction	Yes
Deep Resolve	Gain/Sharp

3.2.20 SE_MC

Multicontrast 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.

3.2.20.1 Use

For acquiring T2 relaxation curves.

3.2.20.2 Recommendations

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

3.2.20.3 Parameters

TE variable	Yes
Contrasts	1–32
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real[54)]
Fat suppression	Fat saturation/SPAIR
Saturation regions	Regular/Parallel

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

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[55)]
Dark blood	Yes

3.2.21 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.

3.2.21.1 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

55) Only available for XT, XR, W60, and T60 gradients

3.2.21.2 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[56)]
Fat suppression	Fat saturation/Water excitation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes
Phase partial Fourier	Yes[57)]
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/Performance[58)]
Dark blood	Yes
iPAT	Yes

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

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

58) Only available for XT, XR, W60, and T60 gradients

iPAT[2]	Yes
Compressed Sensing	Yes
CAIPIRINHA[59)]	Yes
Respiratory control	Trigger/Breath-hold
Restore	Yes
NATIVE[60)]	Off/TD scout/3D mode
Flow sensitivity[61)]	Default/Weak/Medium/Strong
Blood suppression	Body region/Free

3.2.22 TrueFISP

TrueFISP steady-state gradient-echo sequence.

3.2.22.1 Use

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

3.2.22.2 Recommendations

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

59) CAIPIRINHA is a generalization of iPAT[2] allowing undersampling on a sheared grid (→ Page 189 *Acceleration mode (parameter)*)

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

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

3.2.22.3 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[62)]
Dimension	2D/3D
Elliptical scanning[63)]	Yes
Slice resolution[64)]	Yes
Slice partial Fourier[65)]	Yes
Excitation pulses[66)]	Slab-selective
RF pulse type	Fast/Normal
RF spoiling	Off
Gradient mode	Fast/Normal/Whisper
iPAT	Yes

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

63) Only if Dimension = 3D is selected

64) Only if Dimension = 3D is selected

65) Only if Dimension = 3D is selected

66) Only if Dimension = 3D is selected

iPAT[2 67)]	Yes
Respiratory control	Breath-hold[68)]

3.2.23 TSE

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

3.2.23.1 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

3.2.23.2 Parameters

Turbo factor	1–129[69)]
TE variable	Yes
Contrasts	1–3
Bandwidth variable	Yes
Magnetization preparation	IR
Reconstruction mode	Magnitude/Real[70)]
Fat suppression	Fat saturation/SPAIR
Saturation regions	Regular/Parallel
MTC	Yes

67) Only if Dimension = 3D is selected

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

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

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

Phase partial Fourier	Yes[71)]
Averaging mode	Short term/Long term
Multi-slice mode	Interleaved/Sequential
Flow compensation	None/Readout/Slice
Dimension	2D/3D
Slice resolution[72)]	Yes
Slice partial Fourier[73)]	Yes
Fast Mode	Yes
RF pulse type	Fast/Normal/Low SAR/Optimized[74)]
Gradient mode	Fast/Normal/Whisper/Perform-ance[75)]
Dark blood	Yes
iPAT	Yes
Simultaneous multislice (SMS)	Yes
SliceAdjust	Yes
Respiratory control	Trigger/Breath-hold[76)]
Flip Angle Mode	Constant/Hyperecho
Restore	Yes
Acoustic noise reduction	Yes

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

72) Only if Dimension = 3D is selected

73) Only if Dimension = 3D is selected

74) May be selected only if Fast Mode has been selected

75) Only available for XT, XR, W60, and T60 gradients

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

BM Motion correction	Yes
Deep Resolve	Gain/Sharp/Boost

3.2.24 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.

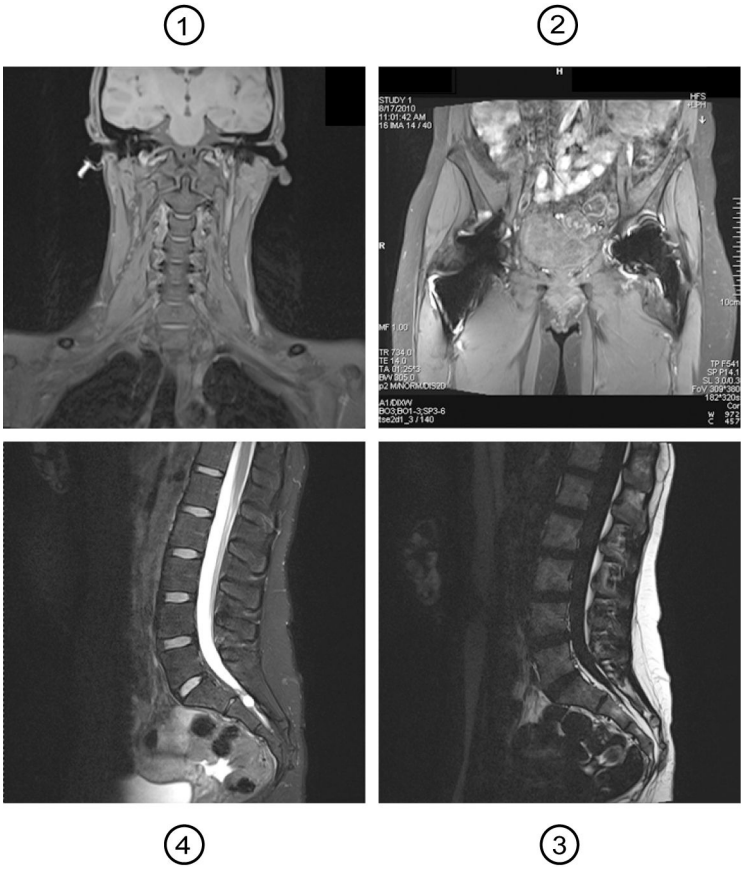
Original Echoes	The original in-phase and opposed phase images are reconstructed
Water	The Dixon method is performed, and an image is reconstructed that contains the water signal only
Fat	The Dixon method is performed, and an image is reconstructed that contains the fat signal only

3.2.24.1 Use

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

Note that TSE_Dixon water images may have lower SNR than with standard fat saturation. For example, for brain parenchyma, a T2 TSE sequence with fat saturation is faster and provides better image quality than TSE_Dixon.

3.2.24.2 Image examples



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

3.2.24.3 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
Flip Angle Mode	Constant/Hyperecho
Restore	Yes
Deep Resolve	Gain/Sharp

3.2.25 TurboFLASH

Single-shot TurboFLASH sequence.

3.2.25.1 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.

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.

3.2.25.2 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.

3.2.25.3 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** myExam add-in. A default protocol is available in the Siemens protocol tree (\\SIEMENS\head\library\3D).

3.2.25.4 Parameters

Slice thickness	≤ 3 mm
Row and column spacing	≤ 2 mm
iPAT acceleration factor	≤ 3
In-plane matrix size	≥ 96 × 96
Number of slices	≥ 64
Orientations	Sagittal (phase-encoding direction): • A>>P • P>>A Coronal (phase-encoding direction): • R>>L • L>>R

3.2.25.5 Note

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

3.2.25.6 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)

Image quality	
To be confirmed	If quality criteria are not fulfilled (for example, motion, aliasing artifacts, and other image degradations)

3.2.25.7 Parameters

TE variable	Min.
Contrasts	1
IR Contrasts	2[77)]
Bandwidth variable	Yes
Magnetization preparation	IR,SR
Reconstruction mode	Magnitude/Real[78)]
Fat suppression	Water excitation
Phase partial Fourier	Yes
Asymmetric echo	Yes
Averaging mode	Long term
Multi-slice mode	Single-shot
Flow compensation	None
Dimension	2D/3D
Elliptical scanning[79)]	Yes[80)]
Slice resolution[81)]	Yes
Slice partial Fourier[82)]	Yes

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

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

79) Only if Dimension = 3D is selected

80) Freely selectable if 3D reordering is activated

81) Only if Dimension = 3D is selected

Excitation pulses	Slab-selective/Non-selective
RF pulse type	Fast/Normal
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper/Performance[83)]
Dark blood	Yes
3D reordering	Standard/User-defined TTC
iPAT	Yes
Respiratory control	Trigger/Breath-hold[84)]
BM Motion correction	Yes

3.2.26 UTE

The ultrashort echo time (UTE) sequence is utilizing a 3D radial center-out readout designed to measure signal at ultrashort echo times. The sequence consists of a short non-selective hard RF pulse followed by a transmit/receive switch time and a 100% asymmetric FID acquisition from the k-space center to the surface of a sphere. In order to achieve the shortest possible echo time, data acquisition already starts during ramp-up of the readout gradient. K-space is sampled using a 3D radial trajectory

3.2.26.1 Use

X-Nuclei data acquisition.

3.2.26.2 Parameters

TE variable	Yes
Contrasts	1–32

82) Only if Dimension = 3D is selected

83) Only available for XT, XR, W60, and T60 gradients

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

Bandwidth variable	Yes
Magnetization Preparation	Yes
Reconstruction mode	Magnitude, Phase, Magn./Phase
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	3D
RF pulse type	Fast/Normal/Low SAR
RF spoiling	On/Off
Gradient mode	Fast/Normal/Whisper
Dark blood	Yes
Trajectory	Radial

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 87 *Routine parameter card*)
- (→ Page 92 *Contrast parameter cards*)
- (→ Page 99 *Resolution parameter cards*)
- (→ Page 105 *Geometry parameter cards*)
- (→ Page 114 *System parameter cards*)
- (→ Page 120 *Physio parameter cards*)
- (→ Page 126 *Flow parameter card*)
- (→ Page 127 *BOLD parameter card*)
- (→ Page 129 *Diff parameter card*)
- (→ Page 131 *Inline parameter cards*)
- (→ Page 135 *Sequence parameter cards*)

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 88 *Routine parameter card*)

(→ Page 91 *Routine parameter card - Spectroscopy CSI*)

4.2.1 Routine parameter card

4.2.1.1 Slice parameters for 2D measurements

Slice Group	Number of the slice group currently displayed (➔ Page 154 *Slice Group (parameter)*)
Slices	Number of slices in this slice group (➔ Page 155 *Slices (parameter)*)
Distance Factor	Slice distance in this slice group (➔ Page 156 *Distance Factor (parameter)*)
Position	Position of the slice group (➔ Page 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of the slice group (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Phase Encoding Dir.	Phase-encoding direction (➔ Page 158 *Phase Encoding Dir. (parameter)*) The angle of slice rotation can also be set in a dialog box. (➔ Page 144 *Inplane Rotation dialog box*)
Phase Oversampling	Expands the FOV in the phase-encoding direction (➔ Page 158 *Phase Oversampling (parameter)*)
Slice Thickness	Thickness of the individual slices (➔ Page 156 *Slice Thickness (parameter)*)

4.2.1.2 Slab parameters for 3D measurements

Slab Group	Number of the slab group currently displayed (➔ Page 159 *Slab Group (parameter)*)
Slabs	Number of slabs in this group (➔ Page 160 *Slabs (parameter)*)
Slices per Slab	Number of slices (partitions) per slab (➔ Page 160 *Slices per Slab (parameter)*)
Distance Factor	Distance of slabs in the slab group (➔ Page 156 *Distance Factor (parameter)*)
Position	Position of slab group (➔ Page 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of the slab group (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Phase Encoding Dir.	Phase-encoding direction (➔ Page 158 *Phase Encoding Dir. (parameter)*) The angle of slice rotation can also be set in a dialog box. (➔ Page 144 *Inplane Rotation dialog box*)
Phase Oversampling	Expand the FOV in the phase-encoding direction (➔ Page 158 *Phase Oversampling (parameter)*)
Slice Oversampling	Expand the FOV in the slice-selection direction (➔ Page 159 *Slice Oversampling (parameter)*)
Slice Thickness	Slice thickness (partitions) of the slabs (➔ Page 156 *Slice Thickness (parameter)*)

4.2.1.3 Parameters for image resolution and contrast

FoV Read	Field of view in readout direction (➔ Page 161 *FoV Read, FoV Phase (parameter)*)
FoV Phase	Field of view in phase-encoding direction (➔ Page 161 *FoV Read, FoV Phase (parameter)*)
TR	Repetition time (➔ Page 163 *TR (parameter)*)
TE	Echo time (➔ Page 163 *TE (parameter)*)
Averages	Number of averages in a measurement (➔ Page 163 *Averages (parameter)*)
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 164 *Concatenations (parameter)*)
Breath-holds	Number of breath-holds Displayed instead of **Concatenations** when **Resp. Control** option **Breath-hold** is selected. (➔ Page 164 *Concatenations (parameter)*)

4.2.1.5 AutoAlign

AutoAlign	Adjust the **AutoAlign** orientation (➔ Page 165 *AutoAlign (parameter)*) (➔ Page 144 *AutoAlign dialog box*)

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.

4.2.2 Routine parameter card - Spectroscopy CSI

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 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Common orientation of the CSI slice and VOI (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Rotation	Common "in-plane" rotation of the CSI slice and VOI (➔ Page 166 *Rotation (parameter)*)
FoV ...	Size of Field of View (➔ Page 167 *FOV parameters*)
Thickness ...	CSI slice thickness (➔ Page 167 *Thickness .. parameters*)

Vol ...	Extent of the VOI (➔ Page 167 *VOI parameters - Spectroscopy*)
Slices	For 2D CSI measurements: Number of slices in this slice group (➔ Page 155 *Slices (parameter)*)
TR	Repetition time (➔ Page 163 *TR (parameter)*)
TE	Echo time (➔ Page 163 *TE (parameter)*)
Averages	Number of averages in a measurement (➔ Page 163 *Averages (parameter)*)
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 93 *Contrast/Common parameter card*)

  (➔ Page 96 *Contrast/Common parameter card - Spectroscopy*)

- The **Dynamic** subcard allows you to set parameters for dynamic image evaluation.

  (➔ Page 97 *Contrast/Dynamic parameter card*)

- The **Angio** subcard allows you to set parameters for time-of-flight angiography (TOF).

  (→ Page 98 *Contrast/Angio parameter card*)

4.3.1 Contrast/Common parameter card

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 163 *TR (parameter)*)
TE	Echo time (→ Page 163 *TE (parameter)*)
TD	Time after delay (diffusion time)
Flip Angle Mode	Change of the refocusing flip angle along the echo train (→ Page 261 *Flip Angle Mode (parameter)*) (→ Page 151 *Organ under Examination dialog box*)
Flip Angle	Flip angle (→ Page 168 *Flip Angle (parameter)*)

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 168 *Magn. Preparation (parameter)*) (➔ Page 152 *Inversion Pulse Settings dialog box*)
IR Contrast, SR Contrast	Enable multiple contrasts with different times for inversion recovery (IR) or saturation recovery (SR) (➔ Page 152 *Inversion Pulse Settings dialog box*)
T2 Prep. Duration	Duration of the T2 preparation pulse (➔ Page 170 *T2 prep. Duration (parameter)*)
TI	Inversion time (➔ Page 170 *TI (parameter)*)

4.3.1.3 Signal increase

Wrap-up Magn.	Accelerated relaxation of longitudinal magnetization or destruction of remaining magnetization (➔ Page 171 *Wrap-up Magn. (parameter)*)

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 171 *Fat-Water Contrast (parameter)*) (➔ Page 147 *Fat Suppression Optimization dialog box*) (➔ Page 148 *Dixon dialog box*)
Dark Blood	Display blood dark in the image (➔ Page 223 *Dark Blood (parameter)*) (➔ Page 146 *Dark Blood Pulse Settings dialog box*)
Blood Suppression	Provide presets for blood suppression (➔ Page 174 *Blood Suppression (parameter)*) (➔ Page 146 *Blood Suppression dialog box*)
MTC	Magnetization transfer (➔ Page 174 *MTC (parameter)*)
MTC Mode	Apply multiple MTC pulses before acquisition. Only available for the EPI2D_SE_MS sequence and if **MTC** is selected. (➔ Page 175 *MTC Mode (parameter)*)
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 175 *Lines Per Shot (parameter)*)
Freeze Suppr. Tissue	Automatic calculation of TI based on TR (➔ Page 175 *Freeze Suppr. Tissue (parameter)*)
Minimize Inflow	Minimize the effect of inflowing body fluid. (➔ Page 176 *Minimize Inflow (parameter)*)

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 **Fast Fat Saturation** or **Fast Water Saturation**.

4.3.1.5 Miscellaneous

Reordering	Acquisition sequence of raw data (➔ Page 251 *Reordering (parameter)*)
Original echoes	Save the unprocessed images in the database as well.

4.3.2 Contrast/Common parameter card - Spectroscopy

For a spectroscopy measurement protocol, the following parameters are shown on the **Contrast** parameter card:

TR	Repetition time (➔ Page 163 *TR (parameter)*)
TE	Echo time (➔ Page 163 *TE (parameter)*)
TM	Mix time (STEAM sequences only) (➔ Page 176 *TM (parameter)*)
Pulse Type	Radio frequency pulse type. Only available in FID sequence with multinuclear license. (➔ Page 259 *RF Pulse Type (parameter)*)
Pulse Duration	Duration of excitation RF pulse. Only available in FID sequence with multinuclear license.
Flip Angle	Flip angle of excitation pulse (➔ Page 168 *Flip Angle (parameter)*)

Preparation Scans	Preliminary measurements (➔ Page 245 *Preparation Scans (parameter)*)
Averages	Number of averages in a measurement (➔ Page 163 *Averages (parameter)*) (➔ Page 145 *Averaging Details dialog box*)
Water Suppression	Suppression of the water signal (➔ Page 176 *Water Suppression (parameter)*)
Water Suppr. BW	Bandwidth of the RF pulses for water suppression (➔ Page 177 *Water Suppr. BW (parameter)*)

4.3.3 Contrast/Dynamic parameter card

The **Dynamic** subcard allows you to set parameters for dynamic image evaluation.

Dynamic Mode	Selection of the dynamic mode (➔ Page 167 *Dynamic Mode (parameter)*)
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
Phases	Number of Compressed Sensing GRASP-VIBE phases (GRASP = Golden-Angle Radial Sparse Parallel MRI)
Duration	Duration for the dynamic phases
Reconstructed Volumes	Number of reconstructed volumes for the corresponding Compressed Sensing GRASP-VIBE phase
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 168 *Flip Angle (parameter)*)
Measurements	Number of measurements (➔ Page 177 *Measurements (parameter)*)
Pause after Meas.	Pause between measurements (➔ Page 178 *Pause after Meas. (parameter)*)
Delay in TR	Time between consecutive volumes for all ep2d sequences (➔ Page 180 *Delay in TR (parameter)*)
Multiple Series	Save every measurement as a separate series. (➔ Page 180 *Multiple Series (parameter)*)
3D Reordering	Center of raw data space is measured as quickly as possible (➔ Page 229 *3D Reordering (parameter)*)
Reordering	Acquisition sequence of raw data (➔ Page 251 *Reordering (parameter)*)
Preview	Switch on/off the reconstruction for the dynamic Compressed Sensing GRASP-VIBE preview
Reconstruction	Selection of the Compressed Sensing GRASP-VIBE reconstruction mode

4.3.4 Contrast/Angio parameter card

The **Contrast**/**Angio** parameter card allows you to adjust specific parameters for time-of-flight angiography (TOF).

Flow Direction	Direction of blood flow (➔ Page 229 *Flow Direction (parameter)*)
TONE Ramp	Inflow velocity of blood (➔ Page 228 *TONE Ramp (parameter)*)

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 99 *Resolution/Common parameter card*)

  (➔ Page 101 *Resolution/Common parameter card - Spectroscopy*)

- The **Acceleration** subcard allows you to adjust parameters for the acceleration mode.

  (➔ Page 102 *Resolution/Acceleration parameter card*)

- The **Filter** subcard allows you to adjust parameters for filtering of raw data.

  (➔ Page 104 *Resolution/Filter parameter card*)

4.4.1 Resolution/Common parameter card

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 161 *FoV Read, FoV Phase (parameter)*)
FoV Phase	Field of view (FOV) in the phase-encoding direction (➔ Page 161 *FoV Read, FoV Phase (parameter)*)
Slice Thickness	Thickness of the individual slices or slice thickness (partitions) of the slabs (➔ Page 156 *Slice Thickness (parameter)*)
Base Resolution	Number of readout steps (➔ Page 180 *Base Resolution (parameter)*)
Phase Resolution	Ratio of phase-encoding to readout steps (➔ Page 181 *Phase Resolution (parameter)*)
Slice Resolution	Resolution ratio in slice selection direction (➔ Page 182 *Slice Resolution (parameter)*)
Interpolation	Double the size of the image matrix by interpolation. (➔ Page 186 *Interpolation (parameter)*)

4.4.1.1 Cartesian/Radial/Spiral measurements

Trajectory	Geometric form of k-space sampling (➔ Page 183 *Trajectory (parameter)*)
Radial Views	Number of radial lines for k-space sampling (➔ Page 184 *Radial Views (parameter)*)
BLADE Coverage	Number of radial blades for k-space sampling (➔ Page 185 *BLADE Coverage (parameter)*)
Radial Interleaves	Number of required TR intervals (➔ Page 185 *Radial Interleaves (parameter)*)

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

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 167 *FOV parameters*)
Thickness ...	CSI slice thickness (➔ Page 167 *Thickness .. parameters*)
Scan Res. ...	Number of phase- encoding steps in the spatial directions of the slice/slab (➔ Page 187 *Scan Res. (parameters)*)
Interpol. Res. ...	Number of reconstructed spectra in the spatial directions of the slice/slab (➔ Page 188 *Interpol. Res. (parameters)*)
Hamming	Activate the Hamming filter (➔ Page 188 *Hamming (parameter)*) (➔ Page 150 *Filter Hamming dialog box*)
Dimension	Set 2D or 3D measurement. (➔ Page 249 *Dimension (parameter)*)

Phase Encoding	Selection of a phase encoding type (➔ Page 249 *Phase Encoding (parameter)*)
Vector Size	Number of data points (resolution) in spectral direction (➔ Page 187 *Vector Size (parameter)*)
Normalize	Normalization filter (➔ Page 193 *Normalize (parameter)*) (➔ Page 150 *Normalize Filter Settings dialog box*)

4.4.3 Resolution/Acceleration parameter card

Acceleration mode	Acceleration mode (➔ Page 189 *Acceleration mode (parameter)*) (➔ Page 153 *CS Reconstruction dialog box*)
Total Factor	Total acceleration factor (➔ Page 191 *Total Factor (parameter)*)
Reference Scans	Measurement method of the reference lines (➔ Page 192 *Reference Scans (parameter)*)
Acceleration Factor PE	Acceleration factor in the phase-encoding direction (➔ Page 190 *Acceleration Factor PE (parameter)*)
Reference Lines PE	Number of reference lines in the phase-encoding direction (➔ Page 191 *Reference Lines PE (parameter)*)
Accel. Factor 3D	Acceleration factor in the slice-selection direction (➔ Page 191 *Accel. Factor 3D (parameter)*)

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 191 *Ref. Lines 3D (parameter)*)
FOV shift factor	FOV shift factor
Reordering shift 3D	Set the reordering shift for CAIPIRINHA mode. (➔ Page 189 *Acceleration mode (parameter)*)
Phase Partial Fourier	Asymmetric sampling of k-space in the phase-encoding direction (➔ Page 182 *Phase Partial Fourier (parameter)*)
Slice Partial Fourier	Asymmetric sampling of k-space in the slice selection direction (➔ Page 183 *Slice Partial Fourier (parameter)*)
Asymmetric Echo	Asymmetry of echo in the readout direction (➔ Page 251 *Asymmetric Echo (parameter)*)
Readout partial Fourier	Reduce the number of shots that are required to generate an image.
Elliptical Scanning	Elliptical k-space sampling (➔ Page 250 *Elliptical Scanning (parameter)*)
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 193 *CAIPIRINHA mode (parameter)*)
Deep Resolve	Deep learning reconstruction options (➔ Page 153 *Deep Resolve dialog box*)

4.4.4 Resolution/Filter parameter card

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 148 *Filter Raw dialog box*)
Elliptical Filter	With the elliptical filter, you only use the center of the raw data space. (➔ Page 148 *Filter Elliptical dialog box*)
Distortion Correction	Activate 2D or 3D distortion correction (➔ Page 196 *Distortion Correction (parameter)*) (➔ Page 147 *Distortion Correction dialog box*)
Static Field Correction	Activate static-field correction. Only available for sequences of the EPI2D_* family. (➔ Page 196 *Static Field Correction (parameter)*)
Normalize	Normalization filter (➔ Page 193 *Normalize (parameter)*) (➔ Page 150 *Normalize Filter Settings dialog box*)
POCS	Projection Onto Convex Sets: It improves edge sharpness during partial Fourier sampling. (➔ Page 188 *POCS (parameter)*)
Image Filter	Set filters for edge enhancement and smoothing (➔ Page 149 *Image Filter Settings dialog box*)

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 105 *Geometry/Common parameter card*)

  (→ Page 109 *Geometry/Common parameter card - Spectroscopy SVS*)

  (→ Page 110 *Geometry/Common parameter card - Spectroscopy CSI*)

- The **AutoAlign** subcard allows you to adjust parameters for automatic alignment.

  (→ Page 111 *Geometry/AutoAlign parameter card*)

- The **Navigator** subcard allows you to adjust parameters for navigator objects.

  (→ Page 111 *Geometry/Navigator 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 112 *Geometry/Saturation parameter card*)

4.5.1 Geometry/Common parameter card

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 154 *Slice Group (parameter)*)
Slices	Number of slices in this slice group (➔ Page 155 *Slices (parameter)*)
Distance Factor	Slice distance in this slice group (➔ Page 156 *Distance Factor (parameter)*)
Slice Thickness	Thickness of the individual slices (➔ Page 156 *Slice Thickness (parameter)*)
Position	Position of the slice group (➔ Page 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of the slice group (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Phase Encoding Dir.	Phase-encoding direction (➔ Page 158 *Phase Encoding Dir. (parameter)*) The angle of slice rotation can also be set in a dialog box. (➔ Page 144 *Inplane Rotation dialog box*)
Phase Oversampling	Expands the FOV in the phase-encoding direction (➔ Page 158 *Phase Oversampling (parameter)*)

4.5.1.2 Slab parameters for 3D measurements

Slab Group	Number of the slab group currently displayed (➔ Page 159 *Slab Group (parameter)*)
Slabs	Number of slabs in this group (➔ Page 160 *Slabs (parameter)*)
Slices per Slab	Number of slices (partitions) per slab (➔ Page 160 *Slices per Slab (parameter)*)
Distance Factor	Distance of slabs in the slab group (➔ Page 156 *Distance Factor (parameter)*)
Slice Thickness	Slice thickness (partitions) of the slabs (➔ Page 156 *Slice Thickness (parameter)*)
Position	Position of slab group (➔ Page 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of the slab group (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Phase Encoding Dir.	Phase-encoding direction (➔ Page 158 *Phase Encoding Dir. (parameter)*) The angle of slice rotation can also be set in a dialog box. (➔ Page 144 *Inplane Rotation dialog box*)
Phase Oversampling	Expand the FOV in the phase-encoding direction. (➔ Page 158 *Phase Oversampling (parameter)*)
Slice Oversampling	Expand the FOV in the slice-selection direction. (➔ Page 159 *Slice Oversampling (parameter)*)

4.5.1.3 Parameters for extending the measuring range

FoV Read	Field of View (FOV) in the readout direction (➔ Page 161 *FoV Read, FoV Phase (parameter)*)
FoV Phase	Field of view (FOV) in the phase-encoding direction (➔ Page 161 *FoV Read, FoV Phase (parameter)*)
TR	Repetition time (➔ Page 163 *TR (parameter)*)

4.5.1.4 Parameters for monitoring the excitation sequence

Multi-Slice Mode	Method for multislice measurements (➔ Page 197 *Multi-Slice Mode (parameter)*)
Series	Excitation sequence of slices (➔ Page 197 *Series (parameter)*)
Concatenations	Number of concatenations (➔ Page 164 *Concatenations (parameter)*)

4.5.2 Geometry/Common parameter card - Spectroscopy SVS

For an SVS measurement protocol, the following parameters are shown on the **Geometry**/**Common** parameter card:

Position	Position of the measurement volume (VOI) (➔ Page 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of the measurement volume (VOI) (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Rotation	"In-plane" angle of rotation (➔ Page 166 *Rotation (parameter)*)
Vol R ...	Extent of the measurement volume (VOI) (➔ Page 166 *VOI parameters*)
Saturation Region	Number of the currently selected saturation region (➔ Page 202 *Saturation Region (parameter)*)
Thickness	Thickness of the currently selected saturation region (➔ Page 202 *Saturation Region (parameter)*)
Position	Position of the currently selected saturation region (➔ Page 202 *Saturation Region (parameter)*)
Orientation	Orientation of the currently selected saturation region (➔ Page 202 *Saturation Region (parameter)*)
Sat. Delta Frequ.	Frequency shift of the saturation pulse (➔ Page 199 *Sat. Delta Frequ. (parameter)*)

4.5.3 Geometry/Common parameter card - Spectroscopy CSI

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 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Common orientation of the CSI slice and VOI (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Rotation	Common "in-plane" rotation of the CSI slice and VOI (➔ Page 166 *Rotation (parameter)*)
FoV ...	Size of Field of View (➔ Page 167 *FOV parameters*)
Thickness ...	CSI slice thickness (➔ Page 167 *Thickness .. parameters*)
VoI ...	Extent of the VOI (➔ Page 167 *VOI parameters - Spectroscopy*)
Fully Excited VOI	Complete excitation of all metabolites within the VOI. Only available for csi_se sequences. (➔ Page 199 *Fully Excited VOI (parameter)*)
Saturation Region	Number of the currently selected saturation region (➔ Page 202 *Saturation Region (parameter)*)
Thickness	Thickness of the currently selected saturation region (➔ Page 202 *Saturation Region (parameter)*)

Position	Position of the currently selected saturation region (➔ Page 202 *Saturation Region (parameter)*)
Orientation	Orientation of the currently selected saturation region (➔ Page 202 *Saturation Region (parameter)*)
Sat. Delta Frequ.	Frequency shift of the saturation pulse (➔ Page 199 *Sat. Delta Frequ. (parameter)*)

4.5.4 Geometry/AutoAlign parameter card

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

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 200 *Navigator (parameter)*)
Position	Position of the navigator object in the patient coordinate system (➔ Page 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of the navigator object in the patient coordinate system (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Rotation	Angle by which the navigator object is rotated in the slice plane defined by the orientation (➔ Page 166 *Rotation (parameter)*)
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/Saturation parameter card

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 202 *Saturation Region (parameter)*)
Thickness	Thickness of the saturation slice
Shape	Shape (profile) of the saturation region (➔ Page 204 *Shape (parameter)*)

Position	Position of this saturation slice (➔ Page 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of this saturation slice (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Special Saturation	Parallel or tracking saturation regions (➔ Page 204 *Special Saturation (parameter)*)
Gap	Distance of the special sat from the associated slice and/or slab group
Thickness	Thickness of the gap

4.5.7 Geometry/Inversion parameter card

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 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of the object (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)

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 115 *System/Coils parameter card*)

- The **Adjustments** subcard allows you to adjust coil selection and specify the adjustment settings.

  (➔ Page 116 *System/Adjustments parameter card*)

- The **Adjust Volume** subcard allows you to define the adjustment volume.

  (➔ Page 117 *System/Adjust Volume parameter card*)

- The **Tx/Rx** subcard allows you to view and adjust transmitter/receiver settings.

  (➔ Page 118 *System/TxRx parameter card*)

- The **pTx** subcard allows you to set the B1 shim mode.

  (➔ Page 119 *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 119 *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.

This subcard shows the stylized patient and the positions of the coils connected.

The figure also illustrates the position of the patient:

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

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	Display of array coils (➔ Page 205 *Local coils (parameter)*)
Virtual Coils	Selection of virtual coils (➔ Page 152 *Virtual Coils dialog box*) The **Virtual Coils** button is only available in the **myExam 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

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 205 *Adjustment Strategy (parameter)*) (➔ Page 145 *Adjustment Strategy dialog box*)
B0 Shim	Set the B0 shim mode. (➔ Page 206 *B0 Shim (parameter)*)
B1 Shim	Set the B1 shim mode. (➔ Page 207 *B1 Shim (parameter)*)
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.
Adjustment Tolerance	Predefine adjustment tolerance regarding similar table positions. (➔ Page 208 *Adjustment Tolerance (parameter)*)
Confirm Frequency	Define when the **Confirm Frequency Adjustment** dialog box will appear. (➔ Page 210 *Confirm Frequency (parameter)*)
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	Perform a manual adjustment For detailed information, see: Operator Manual MR Examination and Review.

4.6.3 System/Adjust Volume parameter card

With **Adjust Volume** enabled, the adjustment volume is automatically calculated by the system on the basis of the slices to be measured.

(➔ Page 208 *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 157 *Position (parameter)*) (➔ Page 143 *Position dialog box*)
Orientation	Orientation of the measurement volume (VOI) (➔ Page 157 *Orientation (parameter)*) (➔ Page 142 *Orientation dialog box*)
Rotation	"In-plane" angle of rotation (➔ Page 166 *Rotation (parameter)*)
R >> L **A >> P** **F >> H**	Extent of the measurement volume (VOI) (➔ Page 166 *VOI parameters*)
Reset	Reset parameters

4.6.4 System/TxRx parameter card

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 208 *Tx Ref [Nucleus] (parameter)*) (➔ Page 151 *RF Pulses dialog box*)
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

B1 Shim	Set the B1 shim mode. (➔ Page 207 *B1 Shim (parameter)*)
Excitation	Mode for radio-frequency pulse (➔ Page 261 *Excitation (parameter)*)
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 Pulse	Replaces a pulse in the sequence with a full pTx pulse. For example, in the TurboFLASH sequence the non-selective block excitation pulse is replaced with a kT points pulse.
pTx Volume	Number of B1 shim volumes
Vol. Property	Set the usage of the **pTx Volume**

4.6.6 System/Miscellaneous parameter card

The **System**/**Miscellaneous** parameter card contains a number of different settings.

4.6.6.1 Coils

Store Coil Selection	The coil selection defined in this step will automatically be applied to all following measurement steps that use Beat Sensor triggering.
Radial Sorting	Slices in the radial slice group are sorted in radial order
Coil Combination	Algorithm for signal calculation (➔ Page 212 *Coil Combination (parameter)*) (➔ Page 144 *Coil Combination dialog box*)

4.6.6.2 Image numbering

MSMA	Primary order (➔ Page 211 *MSMA (parameter)*)
Coronal, **Transverse**, **Sagittal**	Secondary order (➔ Page 211 *MSMA (parameter)*)

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 121 *Physio/Signal parameter card*)

- The **PACE** subcard allows you to adjust parameters to suppress respiratory artifacts and for multi-breath-hold measurements.

  (➔ Page 124 *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 213 *1st Signal/Mode (parameter)*)
Concatenations	Number of concatenations (➔ Page 164 *Concatenations (parameter)*)
Log Signals	Log physiological values and image acquisition time stamps (➔ Page 214 *Log Signals (parameter)*)

(➔ Page 222 *Display of time ranges*)

4.7.1.1 Parameters for ECG I, pulse, or external signal

Average Cycle	Average time between trigger events (➔ Page 215 *Average Cycle (parameter)*)
Captured Cycle	Current captured average cycle (➔ Page 215 *Captured Cycle (parameter)*)

Acquisition Window	Time window for data acquisition (➔ Page 215 *Acquisition Window (parameter)*)
Trigger Pulse	Trigger counter (➔ Page 216 *Trigger Pulse (parameter)*)
Trigger Delay	Delay time (➔ Page 217 *Trigger Delay (parameter)*)
Adaptive Triggering	Real-time adaptation of the acquisition to the current heart rate. (➔ Page 217 *Adaptive Triggering (parameter)*)
Trigger Lock Time	Set the minimal acquisition time for **Adaptive Triggering**. (➔ Page 217 *Trigger Lock Time (parameter)*)
Target RR	Target RR, average heart rate (➔ Page 218 *Target RR (parameter)*)
TR	Repetition time (➔ Page 163 *TR (parameter)*)
Segments	Number of lines of k-space acquired during a TR interval (➔ Page 201 *Segments (parameter)*)
Phases	Number of images depicting the phases of the cardiac cycle that can be calculated using the current protocol (➔ Page 218 *Phases (parameter)*)
Arrhythmia Detection	Detection of arrhythmia (➔ Page 218 *Arrhythmia Detection (parameter)*)
Trigger Window	Time window for ignoring triggers that occur outside a defined time range (➔ Page 219 *Trigger Window (parameter)*)

Calculated Phases	Number of images depicting the phases of the cardiac cycle that can be generated in a retrogated CINE acquisition. (➔ Page 219 *Calculated Phases (parameter)*)
Flow Sensitivity	Flow sensitivity of the sequence by modifying the flow-spoiling gradient (➔ Page 219 *Flow sensitivity (parameter)*)
NATIVE	Generate arterial and venous images without contrast agent. (➔ Page 220 *NATIVE (parameter)*)
TD min flow	Delay time for the second acquisition (➔ Page 220 *TD min flow (parameter)*)
TD peak flow	Delay time for the first acquisition (➔ Page 221 *TD peak flow (parameter)*)
TD first	Delay time for the first acquisition of a series of TD scout acquisitions (➔ Page 221 *TD first (parameter)*)
TD Increment	Delay increment for a series of TD scout acquisitions (➔ Page 221 *TD increment (parameter)*)
Measurements	Number of measurements performed (➔ Page 177 *Measurements (parameter)*)

4.7.1.2 Parameters for respiratory signal

Average Cycle	Average time between trigger events (➔ Page 215 *Average Cycle (parameter)*)
Captured Cycle	Current captured average cycle (➔ Page 215 *Captured Cycle (parameter)*)

Acquisition Window	Time for data acquisition (➔ Page 215 *Acquisition Window (parameter)*)
Threshold	Threshold for respiration (➔ Page 222 *Threshold (respiration parameter)*)
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 163 *TR (parameter)*)
Segments	Number of rows in the k-space during a TR interval (➔ Page 201 *Segments (parameter)*)
Phases	Number of respiratory phases (➔ Page 218 *Phases (parameter)*)

4.7.2 Physio/PACE parameter card

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 224 *Resp. Control (parameter)*)
Scout Mode	Acquisition of the navigator signal (➔ Page 225 *Scout Mode (parameter)*)
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 225 *Scout Type (parameter)*)
Accept Window ±	Permitted deviation from the tolerance center (→ Page 225 *Accept window ± (parameter)*)
Position Accept Window	Automatically centered position for the acceptance window for the respiratory control gate (→ Page 226 *Position Accept Window (parameter)*)
Accept Position	Centered position of the acceptance window for the respiratory control trigger (→ Page 226 *Accept. Position (parameter)*)
Search Window ±	Size of the search window (→ Page 226 *Search Window ± (parameter)*)
Select Acquisition Window	Set the method by which the acquisition window is defined. (→ Page 227 *Select Acquisition Window (parameter)*)
Acquisition Window	Time window for data acquisition (→ Page 215 *Acquisition Window (parameter)*)
Position Navigator	Set the method by which the position navigator is defined. (→ Page 227 *Position Navigator (parameter)*)
Search Position	Centering position of the search window
Tracking Factor	Relationship between diaphragm movement and anatomy (→ Page 227 *Tracking Factor (parameter)*)
Chronologic Position	Time of the navigator signal (→ Page 228 *Chronologic Position (parameter)*)
Trigger Pulse	Trigger pulse (→ Page 216 *Trigger Pulse (parameter)*)

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 228 *Resp. Motion Adaptation (parameter)*)
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 164 *Concatenations (parameter)*)
Store Profile Images	Store the navigator signal time curve as an image. (➔ Page 227 *Store Profile Images (parameter)*)

4.8 Flow parameter card

The **Flow** parameter card allows you to adjust specific parameters for 2D/3D phase contrast angiography.

- **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.

- **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.

Flow Mode	Flow-encoding mode (➔ Page 229 *Flow Mode (parameter)*)
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 flow encoding The possible entries depend on the selected **Flow Mode**.
Direction	Flow-sensitive axis (➔ Page 230 *Direction (parameter)*)
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.
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).

4.9 BOLD parameter card

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 230 *GLM Statistics (parameter)*)
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 231 *Ignore After Transition (parameter)*)
Model Transition States	Use of the hemodynamic response function. (→ Page 232 *Model Transition States (parameter)*)
Temp. Highpass Filter	Eliminate low-frequency oscillations over time. (→ Page 232 *Temp. Highpass Filter (parameter)*)
Threshold	Threshold value for the pixel intensity to calculate overlaid images (→ Page 232 *Threshold (parameter)*)
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 233 *Paradigm Size (parameter)*)
Motion Correction	Activate motion correction. (→ Page 233 *Motion Correction (parameter)*)
Interpolation	Interpolation method used for motion correction (→ Page 234 *Interpolation (BOLD parameter)*)
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 234 *Filter Width (parameter)*)
Measurements	Number of measurements to be performed (➔ Page 177 *Measurements (parameter)*)
Delay in TR	Time between consecutive measurements for all EPI sequences (➔ Page 180 *Delay in TR (parameter)*)
Multiple Series	Save every measurement as a separate series. (➔ Page 180 *Multiple Series (parameter)*)

4.10 Diff parameter card

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 235 *Diffusion Mode (parameter)*)
Diff. Directions	Number of diffusion-encoding directions (can only be selected in MDDW diffusion mode) (➔ Page 236 *Diff. Directions (parameter)*)
Diffusion Scheme	Set the spin echo diffusion encoding. (➔ Page 237 *Diffusion Scheme (parameter)*)

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 237 *Averages (diffusion parameter)*)
b-Value	Value for diffusion weighting (➔ Page 238 *b-Value (parameter)*)
Dynamic Field Correction	Reduce geometric distortions generated by eddy currents (➔ Page 151 *Filter Dynamic Field Correction dialog box*)
Invert Gray Scale	Inverted (PET-like) display of the diffusion trace-weighted images
Diff. Weighted Images	Original images with diffusion weighting (➔ Page 238 *Diff. Weighted Images (parameter)*)
Trace Weighted Images	Diffusion-weighted images averaged across all spatial directions (➔ Page 239 *Trace Weighted Images (parameter)*)
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 239 *ADC Maps (parameter)*)

Exponential ADC Maps	Exponential Apparent Diffusion Coefficient (➔ Page 239 *Exponential ADC Maps (parameter)*)
b-Value>=	Minimum b-value used in ADC calculations (➔ Page 238 *b-Value >= (parameter)*)
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 Inline parameter cards

The **Inline** parameter card is divided into the following subcards:

- The **Subtraction** subcard allows you to set subtraction parameters.

  (➔ Page 132 *Inline/Subtraction parameter card*)

- The **MIP** subcard allows you to set parameters for the calculation of MIP and MPR images.

  (➔ Page 133 *Inline/MIP parameter card*)

- The **Composing** subcard allows you to set parameters for Composed Measurement Groups.

  (➔ Page 134 *Inline/Composing parameter card*)

4.11.1 Inline/Subtraction parameter card

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 240 *Subtract (parameter)*)
Save Subtracted Images	Save result images of subtraction. The parameter is only displayed if the **Subtract** option is activated.
Measurements	Number of measurements for dynamic measurement (➔ Page 177 *Measurements (parameter)*)
Autoscaling	Automatic scaling of result images of subtraction (➔ Page 241 *Autoscaling (parameter)*)
Scaling Factor	Input of a scaling factor for the result images of subtraction (➔ Page 241 *Scaling Factor (parameter)*)
Offset	Input of an offset value for the result images of subtraction (➔ Page 241 *Offset (parameter)*)
StdDev Sag	Calculation of standard deviation result images in the sagittal direction (➔ Page 241 *Std-Dev-Sag (parameter)*)
StdDev Cor	Calculation of standard deviation result images in the coronal direction (➔ Page 242 *Std-Dev-Cor (parameter)*)

StdDev Tra	Calculation of standard deviation result images in the transverse direction (→ Page 242 *Std-Dev-Tra (parameter)*)
StdDev Time	Calculation of standard deviation result images in the chronological sequence (→ Page 242 *Std-Dev-Time (parameter)*)
Save Original Images	Save the unprocessed images in the database as well. (→ Page 240 *Save Original Images (parameter)*)

4.11.2 Inline/MIP parameter card

The **Inline**/**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).

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 243 *MIP Time (parameter)*)
Radial MIP	Calculation of radial MIP views (→ Page 243 *Radial MIP (parameter)*)
Save Original Images	Save the unprocessed images in the database as well. (→ Page 240 *Save Original Images (parameter)*)
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 155 *Slices (parameter)*)

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.

4.11.3 Inline/Composing parameter card

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 200 *Inline Composing (parameter)*)
Normalize	Normalization filter strength (➔ Page 150 *Normalize Filter Settings dialog box*)
Save non-normalized	Save the non-normalized images in the database as well. (➔ Page 201 *Save non-normalized (parameter)*)
Composing Function	Method of composing (➔ Page 200 *Composing Function (parameter)*)

Composing Group	Assignment to a composing group (➔ Page 201 *Composing Group (parameter)*)
Last Step	Closes the composing group (➔ Page 201 *Last Step (parameter)*)
Series Description	Enter a series description

4.12 Sequence parameter cards

Your system provides a number of different sequence types for measurements:

- Gradient echo sequences (GRE, FLASH, Turboflash, True FISP, MEDIC, CISS, DESS)
- Spin echo sequences (se)
- Turbo spin echo sequences (tse)
- Single-shot EPI sequences

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 136 *Sequence/Common parameter card - Spectroscopy*)

- The **Part 1** and **Part 2** subcards allow you to adjust further sequence parameters.

  (➔ Page 137 *Sequence/Part 1 parameter card*)

  (➔ Page 139 *Sequence/Part 2 parameter card*)

- The **Nuclei** subcard allows you to adjust parameters for CSI measurements.

  (➔ Page 141 *Sequence/Nuclei parameter card - Spectroscopy CSI*)

- The **Assistant** subcard allows you to define the strategy to avoid the SAR limit from being exceeded.

  (➔ Page 142 *Sequence/Assistant parameter card*)

4.12.1 Sequence/Common parameter card - Spectroscopy

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 245 *Preparation Scans (parameter)*)
Delta Frequency	Frequency shift for slice selection (➔ Page 246 *Delta Frequency (parameter)*)
Measurements	Number of measurements (➔ Page 177 *Measurements (parameter)*)
Pause after Meas.	Pause between measurements (➔ Page 178 *Pause after Meas. (parameter)*)
Phase Cycling	Selection of a phase cycle to eliminate interference signals (➔ Page 246 *Phase Cycling (parameter)*)
Phase Encoding	Selection of a phase encoding type (➔ Page 249 *Phase Encoding (parameter)*)
Freq. Corr. Accumulation	Internal frequency correction to minimize motion artifacts (➔ Page 247 *Freq. Corr. Accumulation (parameter)*)

Ref. Scan Mode	Reference scan for eddy current correction (➔ Page 248 *Ref. Scan Mode (parameter)*)
No. of ref. scans	Number of averages acquired during the reference scan (➔ Page 249 *No. of ref. scans (parameter)*)
Dimension	Set 2D or 3D measurement. (➔ Page 249 *Dimension (parameter)*)
Save Uncombined	Save the output images of the individual coil elements.
Bandwidth	ADC bandwidth for data acquisition (➔ Page 247 *ADC Bandwidth (parameter)*)
Acquisition Duration	Readout duration (➔ Page 247 *Acquisition Duration (parameter)*)
Remove Oversampling	Oversampling data is removed. (➔ Page 247 *Remove Oversampling (parameter)*)
Inc. Gradient Spoiling	Increase the gradient spoiling to improve spectral quality. (➔ Page 262 *Inc. Gradient Spoiling (parameter)*)

4.12.2 Sequence/Part 1 parameter card

Sequence Name	Display of the sequence name
Dimension	Set 2D or 3D measurement. (➔ Page 249 *Dimension (parameter)*)
Elliptical scanning	Elliptical k-space sampling (➔ Page 250 *Elliptical Scanning (parameter)*)
Phase Stabilization	Prevent phase errors and improves image quality. (➔ Page 250 *Phase Stabilization (parameter)*)

Reordering	Acquisition sequence of raw data (➔ Page 251 *Reordering (parameter)*)
Excitation	Mode for radio-frequency pulse (➔ Page 261 *Excitation (parameter)*)
RF Pulse Type	Radio frequency pulse type (➔ Page 259 *RF Pulse Type (parameter)*)
Gradient Mode	Mode used by the gradient system (➔ Page 260 *Gradient Mode (parameter)*)
Flow Compensation	Flow compensation for moving spins (➔ Page 253 *Flow Compensation (parameter)*)
Bandwidth	ADC bandwidth for data acquisition (➔ Page 247 *ADC Bandwidth (parameter)*)
Echo Spacing	Interval between two echoes (➔ Page 254 *Echo Spacing (parameter)*)
Asymmetric Echo	Asymmetry of echo in the readout direction (➔ Page 251 *Asymmetric Echo (parameter)*)
Optimization	Time optimization (➔ Page 255 *Optimization (parameter)*)
Define	The **Echo trains**/**Turbo factor** parameters or **Shots**/**Segment** parameters are reconstructed as a function of one another. (➔ Page 257 *Define (parameter)*)
Turbo Factor	Number of echoes per echo train (➔ Page 258 *Turbo Factor (parameter)*)
Segments	Raw data lines in a TR (➔ Page 201 *Segments (parameter)*)

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 258 *Slice Turbo Factor (parameter)*)
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 258 *EPI Factor (parameter)*)
Readout Mode	Readout mode for GRE sequences (➔ Page 254 *Readout Mode (parameter)*)
Sequence Type	Type of sequence (➔ Page 256 *Sequence Type (parameter)*)
Adiabatic	Use a B_1-insensitive excitation pulse (adiabatic pulse) in order to reduce the signal variation across the field of view.

4.12.3 Sequence/Part 2 parameter card

Introduction	Inform the patient that measurement has started by a short knocking noise made by the gradient system.
Phase Correction	Performs a phase correction (➔ Page 263 *Phase Correction (parameter)*)
Compensate T2 Decay	Prevent negative effects of T2 decay. (➔ Page 250 *Compensation T2 Decay (parameter)*)

Flow Attenuation	Select flow attenuation gradients to reduce CSF-induced flow artifacts.
Fast Mode	Use faster RF pulses to enable shorter echo spacing.
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 262 *Inc. Gradient Spoiling (parameter)*)
BM Motion Correction	Activate motion correction with Kinetic Sensor/In-bore camera. (➔ Page 262 *BM Motion Correction (parameter)*)
Phase Enc. Rewinder	Rewinds the phase encoding moment
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 256 *Reduce Motion Sens. (parameter)*)
Phase Enc. Order	Define the order of linear reordering (➔ Page 256 *Phase Enc. Order (parameter)*)
Motion Correction	TSE and HASTE sequences: • Inplane motion correction for multi-average protocols. • (➔ Page 257 *Motion Correction (parameter for multiple averages)*) BLADE sequence: turns motion correction on or off.

4.12.4 Sequence/Nuclei parameter card - Spectroscopy CSI

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 ^{1}H saturation pulse
NOE Count	Number of ^{1}H saturation pulses that are transmitted during data acquisition of the ^{31}P signal
NOE Duration	Pulse duration of a ^{1}H saturation pulse
NOE Pause	Time interval between two ^{1}H saturation pulses
NOE Flip Angle	Flip angle of the ^{1}H saturation pulse (➔ Page 264 *NOE Flip Angle (parameter)*)
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.
Coil Elements	Display of the selected coils and coil elements You set the coils on the **System**/**Coils** parameter card.

4.12.5 Sequence/Assistant parameter card

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 264 *SAR Assistant (parameter)*)
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 253 *Allowed Delay (parameter)*)

4.13 Parameter dialog boxes

Various parameters are available on several parameter cards.

These additional parameters are accessible via the **[...]** button.

4.13.1 Orientation dialog box

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)

4.13.2 Position dialog box

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.

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**).

4.13.3 Coil Combination dialog box

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.

4.13.4 Inplane Rotation dialog box

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.

4.13.5 AutoAlign dialog box

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.

4.13.6 Adjustment Strategy dialog box

- **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**)

4.13.7 Averaging Details dialog box

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.

4.13.8 Dark Blood Pulse Settings dialog box

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.

4.13.9 Blood Suppression dialog box

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.

4.13.10 Distortion Correction dialog box

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**.

4.13.11 Fat Suppression Optimization dialog box

- 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
  - **Brain**: Fat saturation for brain
- **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.

If an entry other than **Default** for **Region** is selected, the entry in the **Fat Saturation** dialog box will be marked by an asterisk *****.

4.13.12 Dixon dialog box

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.

4.13.13 Filter Elliptical dialog box

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.

4.13.14 Filter Raw dialog box

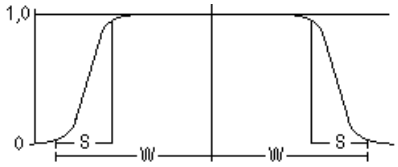
The **Intensity** parameter determines to what extent the filter will be applied.

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

4.13.15 Image Filter Settings dialog box

The **Intensity** parameter determines the extent to which the filter will be applied.

The following filter intensities can be set:

- **Sharp**
- **Medium**
- **Smooth**

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**.

4.13.16 Filter Hamming dialog box

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.

4.13.17 Normalize Filter Settings dialog box

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**.

4.13.18 Filter Dynamic Field Correction dialog box

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.

4.13.19 RF Pulses dialog box

In the **RF Pulses** dialog box, you can adjust the amplitudes of the excitation pulses.

4.13.20 Organ under Examination dialog box

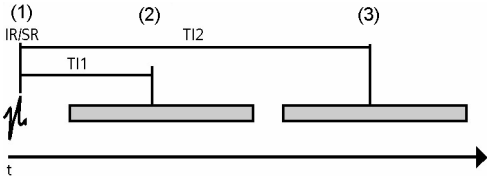
Organ under Exam.: Set organ under examination

Tissue T1: Specify T1 value for the tissue of interest

Tissue T2: Specify T2 value for the tissue of interest

4.13.21 Inversion Pulse Settings dialog box

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.

4.13.22 Virtual Coils dialog box

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.

4.13.23 CS Reconstruction dialog box

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.

4.13.24 Deep Resolve dialog box

In the **Deep Resolve** dialog box , you can select specific deep learning reconstruction options.

Denoising Mode:

- **Gain**: Apply a denoising algorithm during image reconstruction to improve the SNR of the acquired images.

  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.

- **Boost**: Deep learning image reconstruction for TSE sequence, see: Operator Manual Diagnostic MR Imaging.

- **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.

4.14 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 86 *General information*)

(→ Page 142 *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.

4.14.1 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.

4.14.1.1 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.

4.14.1.2 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.

4.14.1.3 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.

4.14.2 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.

4.14.3 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.

4.14.4 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.

4.14.5 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.

4.14.6 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).

4.14.7 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.

4.14.8 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.

4.14.9 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.

4.14.10 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.

4.14.10.1 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.

4.14.10.2 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.

4.14.10.3 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.

4.14.11 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.

4.14.12 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.

4.14.13 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.

4.14.13.1 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.

4.14.13.2 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.

4.14.14 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.

4.14.15 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.

4.14.16 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.

4.14.17 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.

4.14.18 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 a myExam add-in is attached to the protocol that does not contain the AutoAlign component

4.14.18.1 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

4.14.19 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.

4.14.20 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)

4.14.21 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**).

4.14.22 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".

4.14.23 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".

4.14.24 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)

4.14.25 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.

4.14.26 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.

4.14.27 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.

4.14.28 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.

4.14.29 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.)

4.14.30 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.

4.14.31 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 147 *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.
- **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 147 *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 148 *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 Suppresion 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.

For SVS protocols, an integrated water reference measurement is available, see (→ Page 248 *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.

4.14.32 Fat Saturation (parameter)

Use the **Fat Saturation** parameter to set the strength of the fat saturation pulse.

- **Weak**: Weak saturation
- **Strong**: Strong saturation

4.14.33 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

4.14.34 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.

4.14.35 MTC Mode (parameter)

For ms-EPI FLAIR acquisition, multiple magnetization transfer contrast (MTC) pulses can be applied before the acquisition in order to improve gray-white contrast and lesion conspicuity. This may help to obtain an image impression similar to corresponding TSE FLAIR acquisitions, which are strongly affected by MT effects.

The following options can be selected:

- **Weak**
- **Medium**
- **Strong**

This parameter is only available for the EPI2D_SE_MS sequence and if **MTC** is selected.

4.14.36 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 **Fast Fat Saturation** or **SPAIR** mode has been selected in the **Lipid suppr.** parameter.

4.14.37 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.

4.14.38 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.

4.14.39 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.

4.14.40 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.

4.14.41 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.

4.14.42 Measurements (parameter)

The **Measurements** parameter determines how often a measurement is performed.

- **Dynamic studies**: 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 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.

4.14.43 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.

4.14.43.1 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.

4.14.44 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.

4.14.45 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.

4.14.46 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.

4.14.47 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.

4.14.48 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 resolution [%]	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.

4.14.49 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.

4.14.50 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**).

4.14.51 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.

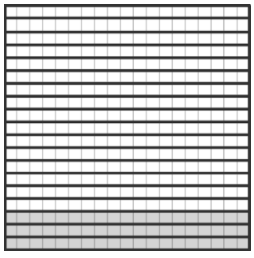
Possible settings:

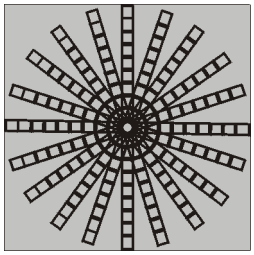
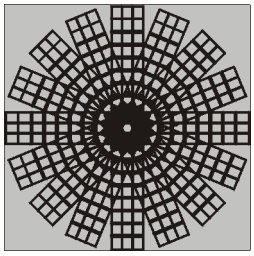
- **4/8** (Half Fourier), **5/8**, **6/8**, **7/8**: Number of phase-encoding steps that are acquired
- **Allowed**: The sequence automatically computes and uses the optimal setting of the phase partial Fourier.
- **Off**: The entire image matrix is used.

4.14.52 Trajectory (parameter)

The **Trajectory** parameter defines the geometric shape to be sampled in the k-space.

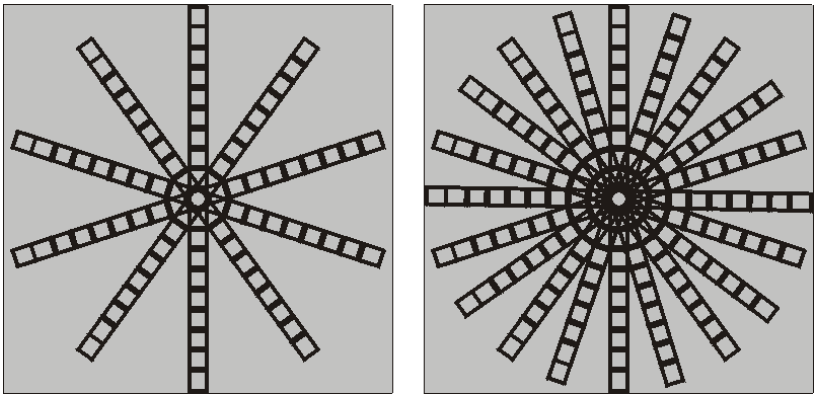
The following shapes are possible:

	**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 BEAT 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.

4.14.53 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

4.14.54 BLADE Coverage (parameter)

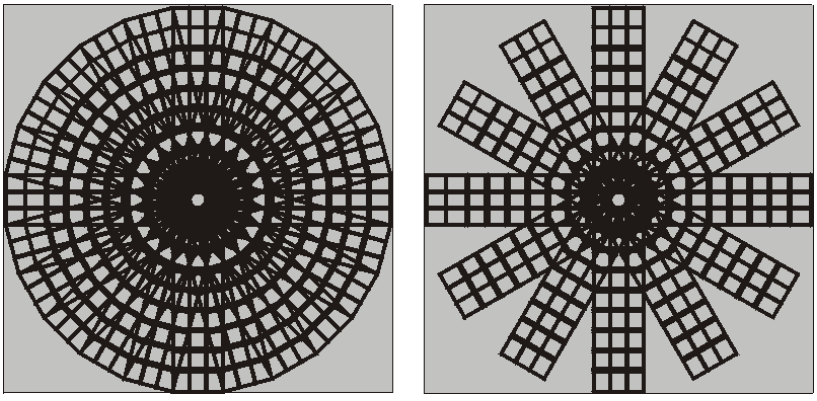
The **BLADE Coverage** parameter calculates the number of blades of varying rotation angles for k-space sampling.

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 than100%**: More blades are measured than necessary for complete coverage.

  The measurement time is increased and the signal-to-noise ratio is improved.
- **Less than100%**: Fewer blades are measured than necessary for complete coverage.

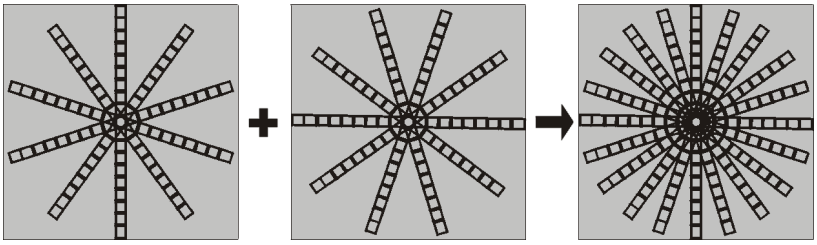
  The measurement time is reduced and image quality is degraded.



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

4.14.55 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.

4.14.56 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.

4.14.57 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).

4.14.58 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.

4.14.59 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.

4.14.60 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.

4.14.61 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

4.14.62 Acceleration mode (parameter)

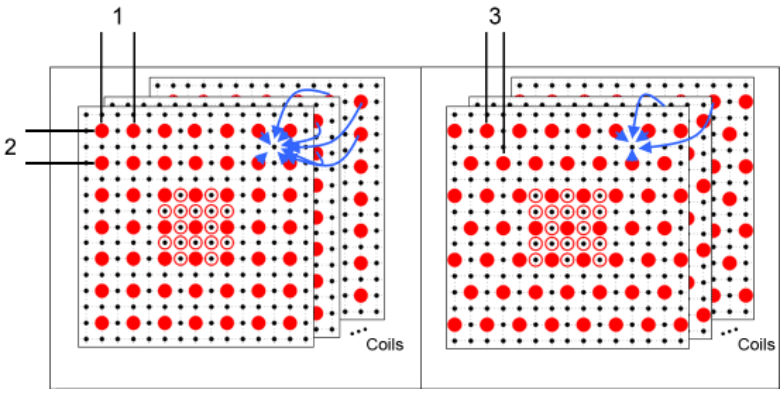
The following options are available for **Acceleration mode**:

- **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 153 *CS Reconstruction dialog box*)
- **SMS**: Simultaneous multi slice (SMS) imaging with GRAPPA reconstruction

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 = **Accel. factor PE**)
(2) Every m^{th} point in the slice-encoding direction is acquired (where m = **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.

4.14.63 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.

4.14.64 Total Factor (parameter)

This parameter defines the total acceleration factor. Available in conjunction with **CAIPIRINHA** and **CS**.

4.14.65 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.

4.14.66 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).

4.14.67 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.

4.14.68 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, for example, 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.

- **Fast GRE/Separate**: Fast GRE-based reference scan supported by the sequence EPI2D_Diff.

- **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.

4.14.69 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

4.14.70 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.

  The **B1 Filter** settings can be selected in the **Filter Bias** dialog box, which is accessible via the **[...]** button next to the parameter field.

  Possible values are:

  – **Weak**, **Medium**, and **Strong**: Different filter settings of a homomorphous filter.

  – **Deep RxE**: Deep learning filter.

    If you select the **Deep RxE** filter, clear the **Prescan Normalize** check box in the **Filter Bias** dialog box.

    The **Deep RxE** filter can result in an elevated signal in the bone, especially in combination with fat saturation techniques.

    The **Deep RxE** filter can also be used for sodium imaging, for example, with the UTE sequence. However, **Deep RxE** was mainly trained on proton data.

    For MSK and sodium imaging, consider reviewing the original images without **Deep RxE**, not only images with **Deep RxE**.

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.

4.14.71 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.

4.14.72 Static Field Correction (parameter)

The **Static Field Correction** parameter automatically triggers acquisition of a field map, which is used to correct susceptibility-induced distortions and intensity variations.

When the parameter is selected, **2D** distortion correction is activated if no distortion correction mode was previously selected. Moreover, B0 shim mode will be switched to **Absolute**.

Static Field Correction is only available for sequences of the EPI2D_* family.

See: Operator Manual Diagnostic MR Imaging for details.

4.14.73 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.

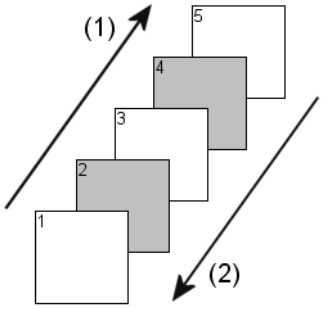
If you have selected **Interleaved**, you can select the number of **Concatenations** on the **Routine**, **Geometry**/**Common**, and **Physio** parameter cards.

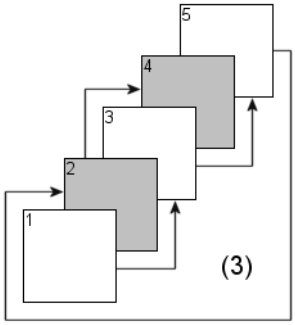
4.14.74 Series (parameter)

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 sequential, even if the **Series** parameter is set to **Interleaved**.

4.14.75 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.

4.14.76 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.

4.14.77 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.

4.14.78 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.

4.14.79 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-n-go protocol.

4.14.80 Save non-normalized (parameter)

The **Save non-normalized** parameter determines whether the non-normalized images are stored in the database as well.

4.14.81 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.

4.14.82 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.

4.14.83 Segments (parameter)

The **Segments** parameter defines the number of rows in the k-space that are measured for an image during a TR interval.

For ms-EPI acquisitions, the **Segments** parameter determines the number of shots per slice.

The parameter is especially relevant to physiologically-triggered measurements.

4.14.84 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.

4.14.85 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”)

4.14.85.1 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.

4.14.85.2 Deleting a saturation region

1 Select the saturation region you want to delete.

2 Then click the **-** button next to the **Saturation Region** field.

4.14.86 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.

4.14.87 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.

4.14.88 Local coils (parameter)

Example

Displays the selected local coils and 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.

4.14.89 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** and **SliceAdjust** modes are not available for all MR systems.

4.14.90 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.
- **Brain**: Adjustment measurement and evaluation are optimized for brain spectroscopy.
- **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.

4.14.91 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.
- **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.

4.14.92 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**.

4.14.93 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.

4.14.94 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.

4.14.94.1 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.

4.14.94.2 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.

4.14.94.3 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.

4.14.94.4 Changing the adjustment volume

- Enter the angle in the **Rotation** input field about which you want to rotate the volume.

4.14.94.5 Applying the settings

- Whenever you change the settings press the **Enter** key.

  – or –

  Click outside the input field with the mouse.

4.14.95 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.

4.14.96 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.

4.14.96.1 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.

4.14.97 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.

4.14.98 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**: Respiratory motion is captured by a respiratory cushion or, for BioMatrix systems, by the Respiratory Sensor of the BM Spine 32, BM Spine 72, or the BioMatrix Contour L coil (for future use). 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**, **Beat Sensor/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, Beat Sensor, pulse, and external trigger signal curves.

For detailed information regarding ECG triggering, see: Operator Manual MR System and Coils.

4.14.99 Log Signals (parameter)

When you select the **Log Signals** check box, all parameters recorded by the physiological sensors are stored for further offline processing. The PMU data and time stamps of the acquired images are written as plain text files to the file system and stored in the DICOM database (displayed in the **Patient Browser**).

The text files are located in the the scanner directory `%SimMeasData%\Physio_Logfiles`.

For each active PMU channel, one text file is created. In addition, two further general text files are created. The name of each file is made up of two parts. The first part refers to the acquisition time of the first image.

The second part refers to the content of the file:

- "AcquisitionInfo": the file contains the acquisition times of all images aquired by the sequence
- "PhysioTriggertimes": the file contains all trigger events sent by the scanner
- PMU channel ID, such as "PULS" or "RESP": the file contains the received signal curves; one file for each active PMU channel

4.14.100 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.

4.14.101 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.

4.14.102 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.

4.14.103 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.

4.14.104 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.

4.14.105 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**.

4.14.106 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**.

4.14.107 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.

4.14.108 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.

4.14.109 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.

4.14.110 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.

4.14.111 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 retrogated CINE acquisition.

4.14.112 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**.

4.14.113 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**.

4.14.114 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**.

4.14.115 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**.

4.14.116 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**.

4.14.117 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**.

4.14.118 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**.

4.14.119 Display of time ranges

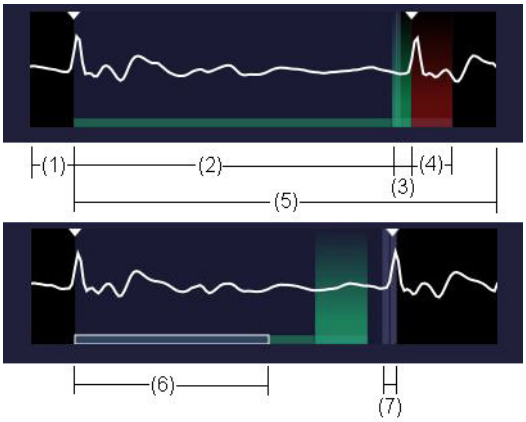
The top right areas of the parameter card shows the physiological signal and the time domains resulting from the parameters set. Unlike the **Physiological Display** dialog box, a frozen image is displayed on the **Physio** parameter card.

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 occured 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 occured
(5) Measurement acquisition window
(6) Measurement pause
(7) Double standard deviation

4.14.120 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".

4.14.121 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.

4.14.122 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.

4.14.123 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.

4.14.124 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.

4.14.125 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 **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 ± parameter
Trigger	Vertical width of the yellow acceptance window shown in the **Inline Display** The trigger algorithm determines the end of expiration as soon as the sequence of measured diaphragm positions (green curve) falls within the acceptance window. The acceptance window is not displayed while the patient is breathing in.

4.14.126 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.

4.14.127 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.

4.14.128 Search Window ± (parameter)

For **Gate** or **Gate & Follow** respiratory control, you can enter the size of the window in millimeters in the **Search Window ±** field.

The search window is displayed as a red box surrounding the tolerance center in the **Inline Display**.

4.14.129 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.

4.14.130 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.

4.14.131 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.

4.14.132 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**.

4.14.133 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.

4.14.134 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.

4.14.135 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.

4.14.136 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.

4.14.137 3D Reordering (parameter)

The **3D Reordering** parameter determines the order in which the data of the raw data space are acquired.

- **Standard** leads to a fixed value for the time to center.
- **Min. TTC** determines that the center of the raw data space is acquired as early as possible after the start of the scan.
- **User Defined TTC** allows you to set a value for the time to center.

4.14.138 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.

4.14.139 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**.

4.14.140 GLM Statistics (parameter)

The **GLM Statistics** parameter determines whether the data are acquired with the GLM statistics mode (GLM = General Linear Model).

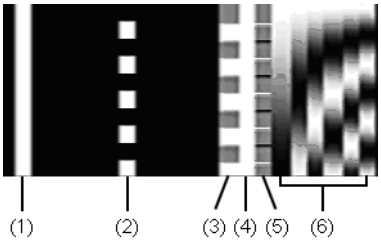
If the parameter is cleared, all images are saved without analysis.

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

4.14.141 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.

4.14.142 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.

4.14.143 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).

4.14.144 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.

4.14.145 Paradigm Size (parameter)

The **Paradigm Size** is the table size of all measurements within a paradigm.

You make the following settings for every measurement:

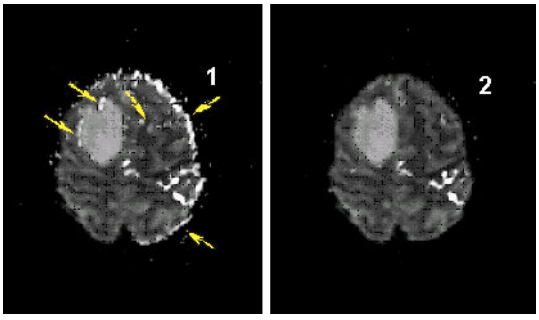
- **Active**: Measurement is performed **with** stimulation.
- **Baseline**: Measurement is performed **without** stimulation.

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.

4.14.146 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).

4.14.147 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

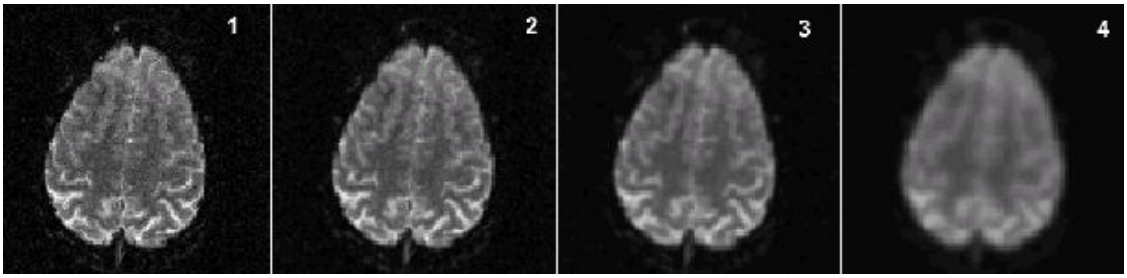
- **3D k-Space**: Interpolation in Fourier space

  Good quality method of real-time postprocessing

4.14.148 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)

4.14.149 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).

4.14.150 Diff. Directions (parameter)

The **Diff. Directions** parameter determines the number of diffusion-encoding directions.

Possible directions are **6**, **10**, **12**, **20**, **30**, **64**, **128**, or **256**.

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

Example: **b1000#3**

Definition: b = 1000 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.

4.14.151 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 recommended that you select the monopolar gradient mode, see **Acceleration mode**.

4.14.152 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.

4.14.153 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.

4.14.154 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.

4.14.155 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).

4.14.156 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.

4.14.157 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.

4.14.158 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.

4.14.159 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.

4.14.160 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: **Subtract**, **MIP**, **StdDev**, **Liver Registration**, **T1-map**, or **T2-map**.

4.14.161 Subtract (parameter)

The **Subtract** parameter activates inline subtraction, which can be used for two main applications:

- Subtraction of series within a multiple measurement protocol, that is, the number of measurements is > 1.
- Subtraction of series from different protocols, each with one measurement

The measurement defined as the subtrahend will be subtracted from all following measurements.

If the **Subtract** check box is selected, the parameters specific to subtraction are displayed.

In addition, you can select the subtraction mode from the list:

- **Standard**: Negative grayscale values are set to 0.
- **Absolute**: Absolute values of the computed result pixel values are stored in the result image.

4.14.162 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.

4.14.163 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.

4.14.164 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.

4.14.165 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.

4.14.166 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.

4.14.167 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.

4.14.168 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.

4.14.169 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.

4.14.170 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.

4.14.171 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.

4.14.172 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.
- **Time Course Evaluation**: Provides a means to process and analyze cardiac time series data sets. Generates parametric maps characterizing the intensity properties (slope of time curve) of the time series. Can be combined with surface coil correction, provided that proton-density-weighted images are obtained at the beginning of the time series.

  Motion correction can be enabled to register all images within the time series. If a pair of motion-corrected time series of the same slice are available, these in turn can be combined to generate a cross-series parametric map, which is the ratio of the two upslope maps.
- **Time Course Evaluation filtered**: Same as **Time Course Evaluation**, except that temporal smoothing of the data is performed.
- **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**.

4.14.173 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

4.14.174 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.

4.14.175 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 VoI** option on the **Geometry**/**Common** parameter card, the **Delta Frequency** parameter is set to a fixed value and cannot be changed.

4.14.176 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.

4.14.177 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 ^{1}H-MRS are fully resolved at a bandwidth of 1 kHz.

4.14.178 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.

4.14.179 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.

4.14.180 Freq. Corr. Accumulation (parameter)

The ^{1}H-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.

4.14.181 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)

4.14.182 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.

4.14.183 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.

4.14.184 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.

4.14.185 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.

4.14.186 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**).

4.14.187 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.

4.14.188 Reordering (parameter)

The **Reordering** parameter defines the order of k-space filling.

Depending on the used sequence, the **Reordering** options and their meaning can differ.

In general:

- **Linear**: The k-space is stepped through linearly.
- **Centric**: The first measured raw data lines are for 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.

BLADE sequence:

- **Linear**: For each blade, the k-space is stepped through linearly.
- **Centric**: For each blade, the central k-space lines are filled with early echoes and the peripheral k-space lines are filled with late echoes.

SPACE sequence:

- **Linear**: For each shot, the k-space is stepped through linearly in the phase-encoding direction from one edge to the other of the phase-encoding 3D plane.
- **Radial**: For each shot, the k-space is stepped through at a radius of the phase-encoding 3D plane.

4.14.189 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.

4.14.190 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.

4.14.191 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

4.14.192 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.

4.14.193 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.

4.14.194 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.

4.14.195 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.

4.14.196 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.

4.14.197 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.

4.14.198 Reduce Motion Sens. (parameter)

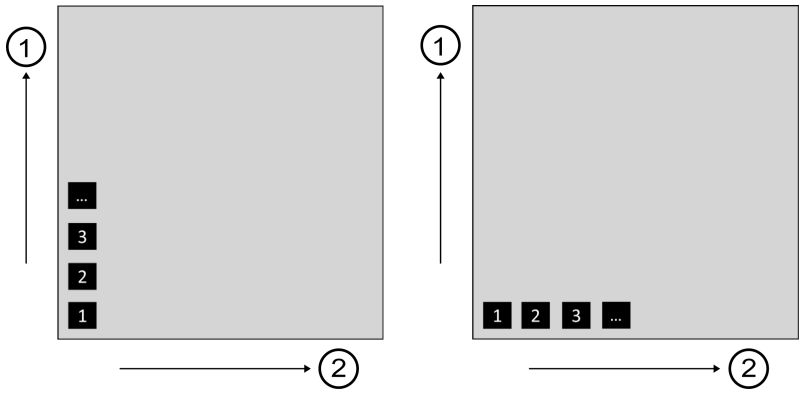
The **Reduce Motion Sens.** parameter determines if modified phase-encoding gradients are used. This stabilizes the sequence against slight motions, which would normally result in segmentation artifacts.

This parameter is only available for TSE sequences or FL3D_VIBE breast protocols.

4.14.199 Phase Enc. Order (parameter)

The **Phase Enc. Order** parameter is used to define the order of linear reordering (k-space filling).

- **Automatic**: Use the existing setup.
- **Lines in Slices**: Acquire all lines for one slice and then proceed to the next slice.
- **Slices in Lines**: Acquire one line for all slices and then proceed to the next line. This can help to reduce signal fluctuations in breast protocols without fat saturation, especially in subtraction images.



Lines in Slices (left), Slices in Lines (right)

(1) Number of lines
(2) Number of slices

4.14.200 Motion Correction (parameter for multiple averages)

You can combine averaging and motion correction for TSE and HASTE sequences to generate images with diagnostic SNR without introducing blurring as a result of organ movement between averages.

- **None**: No motion correction
- **Registration of Averages**: Inplane motion correction, only active if **Averages** is set to a value > 0.

  (➔ Page 163 *Averages (parameter)*)

4.14.201 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.

4.14.202 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.

4.14.203 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.

4.14.204 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**.

4.14.205 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.

4.14.206 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.

4.14.207 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.

4.14.208 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**.

4.14.209 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**.
- **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.

4.14.210 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 168 *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.

4.14.211 Inc. Gradient Spoiling (parameter)

When the **Inc. Gradient Spoiling** parameter is set, the gradient spoiling is increased to improve image or spectral quality.

Increasing the gradient spoiling increases TR and/or **Echo spacing** for imaging sequences.

4.14.212 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.

4.14.213 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**: Wether 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!

4.14.214 NOE Flip Angle (parameter)

With the **NOE Flip Angle** parameter, you set the flip angle of the ^{1}H 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 ^{1}H saturation pulses that you can control on the **System/Tx/Rx** parameter card.

To achieve the best saturation with the ^{1}H saturation pulses, use the maximum possible **NOE Flip Angle**. The SAR monitor ensures that the energy absorption for the patient remains within limits.

4.14.215 SAR Assistant (parameter)

The **SAR Assistant** parameter defines the strategy to avoid exceeding the SAR limit. The system therefore manipulates the selected parameter.

The **SAR Assistant** allows a combination of up to three parameters that can be changed (**Flip Angle**, **TR**, and **RF Pulse Type**). The **SAR Assistant** parameter list defines whether a parameter is used at all and in what order.

For example, the selection **Flip Angle > TR > RF Pulse Type** means that first the flip angle is reduced. If this modification does not lead to a solution, the system continues to increase TR without resetting the flip angle and then, if necessary, the RF pulse type is changed.

Modification limits:

- Flip angle: the maximum possible value for the modification corresponds to the defined minimum flip angle
- TR: the maximum possible value for the modification corresponds to the defined maximum TR

- RF pulse type:
  - a limit for the RF pulse type cannot be specified
  - the possible settings (**Fast**, **Normal**, or **Low SAR**) depend on the sequence
  - the maximum TR is also relevant for RF pulse type, that is, if the RF pulse type is changed, then TR can also be changed automatically to the maximum

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