

# Application Guide & Release Notes

**Multi-Band EPI C2P**

**Release 015a**  
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Center for Magnetic  
Resonance Research

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# Conditions of Use

This package is provided to support collaborative research projects between the University of Minnesota and users of Siemens MRI equipment, in accordance with a current C2P agreement.

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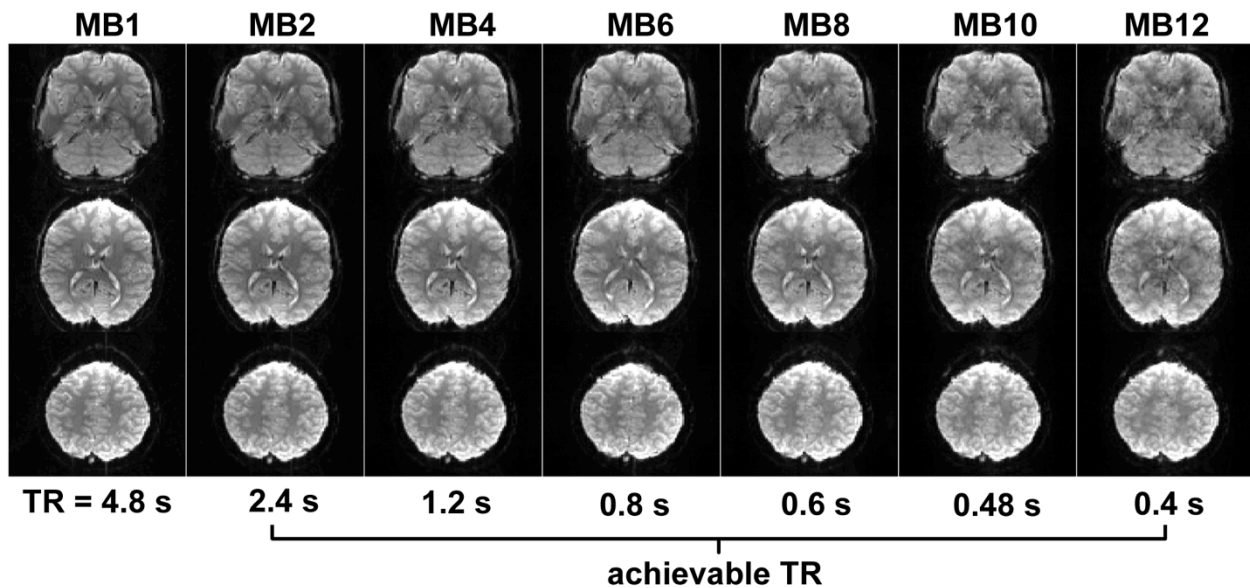
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# Overview

Multi-banded RF pulses can be used to accelerate volume coverage along the slice direction by simultaneously exciting and acquiring multiple slices and subsequently unaliasing them using parallel imaging principles and the spatial information available in multi-channel RF array coils.

This allows for a direct reduction in the volume  $T_R$  by the number of simultaneously excited slices (i.e., the multiband (MB) factor or the slice acceleration factor). For example, the figure below shows the minimum achievable  $T_R$  for a 64-slice, 2 mm isotropic resolution GRE-EPI acquisition using various MB factors:



Such a significant reduction in minimum  $T_R$  is very useful in studies of the brain. In particular, the ability to sample more rapidly while preserving whole-brain coverage is of great benefit to resting-state fMRI. It is also useful to reduce the otherwise long total scan times required for diffusion-weighted imaging techniques such as HARDI and DSI.

# Sequence Description

The pulse sequences in this package are based on the product ep2d\_bold, ep2d\_se, and ep2d\_diff sequences from Siemens.

Multi-banded RF pulses are calculated by the sequence using linear combinations of the same RF pulses used in the product sequences. To improve the MB unaliasing performance, partial FoV shifts are applied using gradient blips along the slice direction during the EPI readout. The optimum shift factor is selected automatically by the sequence.

More detailed information about the pulse sequence and image reconstruction implementation can be found in the following references:

Moeller S, Yacoub E, Olman CA, Auerbach EJ, Strupp J, Harel N, Uğurbil K. Multiband multislice GE-EPI at 7 tesla, with 16-fold acceleration using partial parallel imaging with application to high spatial and temporal whole-brain fMRI. *Magn Reson Med*. 2010;63(5):1144–1153. [[PubMed](#)]

Setsompop K, Gagoski BA, Polimeni JR, Witzel T, Wedeen VJ, Wald LL. Blipped-controlled aliasing in parallel imaging for simultaneous multislice echo planar imaging with reduced g-factor penalty. *Magn Reson Med*. 2012;67(5):1210–1224. [[PubMed](#)]

Xu J, Moeller S, Auerbach EJ, Strupp J, Smith SM, Feinberg DA, Yacoub E, Uğurbil K. Evaluation of slice accelerations using multiband echo planar imaging at 3T. *Neuroimage*. 2013 Dec;83:991-1001. [[PubMed](#)]

Auerbach EJ, Xu J, Yacoub E, Moeller S, Uğurbil K. Multiband accelerated spin-echo echo planar imaging with reduced peak RF power using time-shifted RF pulses. *Magn Reson Med*. 2013 May;69(5):1261-7. [[PubMed](#)]

Sotiropoulos SN, Moeller S, Jbabdi S, Xu J, Andersson JL, Auerbach EJ, Yacoub E, Feinberg D, Setsompop K, Wald LL, Behrens TEJ, Uğurbil K, Lenglet C. Effects of image reconstruction on fiber orientation mapping from multichannel diffusion MRI: Reducing the noise floor using SENSE. *Magn Reson Med*. 2013;70(6):1682-1689. [[PubMed](#)]

Cauley SF, Polimeni JR, Bhat H, Wald LL, Setsompop K. Interslice leakage artifact reduction technique for simultaneous multislice acquisitions. *Magn Reson Med*. 2014 Jul;72(1):93-102. [[PubMed](#)]

Setsompop K, Cohen-Adad J, Gagoski BA, Raij T, Yendiki A, Keil B, Wedeen VJ, Wald LL. Improving diffusion MRI using simultaneous multi-slice echo planar imaging. *NeuroImage*. 2012 Oct 15;63(1):569-80. [\[PubMed\]](#)

# Hardware and Software Requirements

Versions of the multi-band accelerated sequences are currently provided for multiple Siemens software versions, supporting various system types. It may additionally be possible to use the sequences with other systems not listed (e.g. 1.5T systems), but compatibility and coil performance has not been tested.

- VB17A:** MAGNETOM Trio, a Tim System 3T, MAGNETOM Verio 3T, MAGNETOM 7T/9.4T/10.5T/11.7T
- VB19A:** MAGNETOM Trio, a Tim System 3T
- VB20P:** Biograph mMR

The **32-channel Head** coil is highly recommended for 3T. The 12-channel **Head Matrix** is not recommended, but it can be used for acceptable image quality at low acceleration factors. For 7T, the **Nova Medical 32-channel** head coil is recommended.

- VD11D:** MAGNETOM ConnectomA/S 3T
- VD13A-SP4:** MAGNETOM Skyra 3T
- VD13B:** MAGNETOM Skyra<sup>fit</sup> 3T
- VD13C-SP2:** MAGNETOM Skyra 3T with TimTX TrueShape (pTX) option
- VD13D:** MAGNETOM Prisma/Prisma<sup>fit</sup> 3T
- VE11A:** MAGNETOM Skyra 3T
- VE11B:** MAGNETOM Prisma 3T
- VE11C:** MAGNETOM Skyra/Prisma 3T

The **32-channel Head** coil is highly recommended. The **Head/Neck 20** coil can be used, but image quality will be diminished at higher acceleration factors.

The **Head/Neck 64** coil can also be used, but imaging performance in the brain is typically not improved over the 32-channel coil while reconstruction time is substantially longer. Enabling “**Matrix Optimization**” on the System/Miscellaneous card can improve reconstruction time when using the Head/Neck 64 coil.

# Installation Procedure

**Important note:** Starting with versions **VE11C**, **VB19A**, and **VB20P**, the host uses McAfee Embedded Control (Solidifier) security software. It is necessary to switch Embedded Control into UPDATE mode before installing any custom sequences. Please see the `Embedded_Control_Mode.pdf` document included in this archive for instructions on how to switch the Embedded Control mode.

1. Login as “Advanced User”. *If the Advanced User account is not enabled or you do not know the password, contact Local Service.*
2. If the system has Embedded Control installed, start the `MrEmbeddedControlGui` and switch the Embedded Control system into UPDATE mode. *If you do not know the Administrator account name or password, contact Local Service.*
3. Extract the .zip file to a temporary directory.
4. Run the installer program. The installer will automatically restart various processes and reboot the imager if necessary to unlock shared objects.
5. If the installer reports any error, please power cycle the system and try again.
6. If a sample protocol is available for your system, it will appear at the end of the USER tree in the Exam Explorer. If a sample protocol is not available, create a default protocol in Exam Explorer by selecting Insert Sequence, USER, then `cmrr_mbep2d_*` for the desired sequence variant.
7. If the system has Embedded Control installed, re-enable host security and switch the Embedded Control system into the ENABLED mode.



# Usage

These sequences are based on the Siemens product ep2d\_\* family of sequences; most of the protocol parameters are the same.

The most important changes appear on the following measurement cards:

## Routine Card

The image shows a software interface for configuring MRI sequence parameters. The parameters are organized into two columns. The left column includes: Slice group (1), Slices (72), Dist. factor (0%), Position (Isocenter), Orientation (Transversal), Phase enc. dir. (A >> P), AutoAlign (---), and Phase oversampling (0%). The right column includes: FoV read (192 mm), FoV phase (100.0%), Slice thickness (2.00 mm), TR (818 ms), TE (31 ms), Multi-band accel. factor (8), Filter (None), and Coil elements (HEA,HEP). At the bottom, there is a horizontal slider for the Multi-band accel. factor, ranging from 2 to 12, with a green marker at 8. Below the slider is a row of tabs: Routine, Contrast, Resolution, Geometry, System, Physio, BOLD, and Sequence.

**Multi-band accel. factor:** This parameter is only editable if the number of slices is greater than 1. The number of slices must be an integer multiple of the multi-band acceleration factor. The maximum acceleration factor is 16 (BOLD/SE) or 8 (diffusion) in the current release if iPAT is not used, otherwise the product of the MB accel. factor and the iPAT factor may not exceed 18. Note that image quality is not likely to be acceptable at the highest allowed acceleration factors for most protocols.

**Slices:** The number of slices must be an integer multiple of the multi-band acceleration factor. It may be necessary to reset the multi-band accel.

factor to 1 in order to select an arbitrary number of slices; a new multi-band accel. factor can then be re-selected.

**Averages:** Online averaging has been disabled due to incompatibility with the online reconstruction.

**Dist. factor:** There must be a minimum gap of 100% of the slice thickness between adjacent bands in the RF pulse. Therefore, in a case where the number of bands is equal to the number of slices, a minimum distance factor of 100% will be required. In the usual case where slices  $\gg$  bands, however, a distance factor of 0% can be used.

## Contrast/Common Card

The image shows a software interface for MRI sequence configuration. It features two tabs: 'Common' and 'Dynamic', with 'Dynamic' currently selected. The interface contains several control elements:

- TR:** A numeric input field set to 3650, followed by a unit 'ms'.
- TE:** A numeric input field set to 95, followed by a unit 'ms'.
- Fat suppression:** A dropdown menu currently set to 'Fat sat.'.
- Grad. rev. fat suppression:** A dropdown menu currently set to 'Disabled'.
- MTC:** A checkbox that is currently unchecked, with a red square icon to its left.
- Magn. preparation:** A dropdown menu currently set to 'None'.
- Flip angle:** A numeric input field set to 78, followed by a unit 'deg'.
- TR Slider:** A horizontal green slider bar at the bottom, with numerical markers at 3650, 3646, and 30000.

At the bottom of the interface, there is a row of seven tabs: 'Routine', 'Contrast', 'Resolution', 'Geometry', 'System', 'Physio', and 'Sequence'. The 'Contrast' tab is currently selected.

**Grad rev. fat suppr. (SE/diffusion only):** If enabled, the polarity of the slice select gradients will be reversed between excitation and refocusing. This can provide effective fat suppression at no cost in time or SAR. It can also result in signal losses in areas of B0 inhomogeneity. Typically it is most useful at 3T.

## Resolution/iPAT Card

The screenshot displays the 'Resolution/iPAT Card' interface with the following settings:

- PAT mode:** GRAPPA (dropdown menu)
- Accel. factor PE:** 2 (spin box)
- Ref. lines PE:** 24 (spin box)
- Matrix Coil Mode:** Auto (Triple) (dropdown menu)
- Reference scan mode:** GRE (dropdown menu)

At the bottom, there is a slider for 'Accel. factor PE' ranging from 2 to 4, with a green bar indicating the current value of 2.

The interface includes tabs at the top: 'Common', 'iPAT', and 'Filter'. At the bottom, there are navigation tabs: 'Routine', 'Contrast', 'Resolution', 'Geometry', 'System', 'Physio', 'Diff', and 'Sequence'.

**Reference scan mode:** If iPAT is enabled, the reference scan acquisition scheme can be selected here. “Single-shot” EPI (Siemens default for accel. factor 2) is the fastest but limits the number of reference lines. “Segmented” EPI (Siemens default for accel. factor >2) allows for more reference lines, but increases motion sensitivity. “GRE” offers high SNR and is insensitive to motion, but may result in other artifacts (this option is currently experimental).

## Sequence/Special Card

The screenshot shows the 'Special' tab of the 'Sequence/Special Card' interface. The 'Excite pulse duration' is set to 2560 us. The 'Physio recording' is set to 'Off'. The 'Single-band images' checkbox is unchecked. The 'Online multi-band recon.' is set to 'Online'. The 'FFT scale factor' is set to 1.00. The 'Triggering scheme' is set to 'Standard'. A progress bar at the bottom indicates the 'Excite pulse duration' is currently at 2560, with a range from 600 to 16380. The interface is divided into sections: Part 1, Part 2, and Special. The bottom navigation bar includes: Routine, Contrast, Resolution, Geometry, System, Physio, BOLD, and Sequence.

**Excite pulse duration:** The required RF pulse voltage increases linearly with the multi-band acceleration factor. Here the pulse length of the excitation RF pulse can be manipulated manually at the cost of  $T_E$  and bandwidth.

Verify on the System/Transmitter/Receiver card that the voltage of all pulses, especially those with names similar to “MBExc” and “MBRef” (SE/diffusion only) are below the system maximum value. Otherwise, the pulse(s) will be clipped and the flip angle(s) will be less than expected. A warning message will pop up on the host if this occurs.

**Refocus pulse duration (*SE/diffusion only*):** This parameter will appear arrayed beneath the Excite pulse duration parameter in SE or diffusion sequences. It allows for manually controlling the duration of the refocusing pulse(s) only.

**Single-band images:** Select this checkbox to send the single-band reference images to the database in a separate series (e.g. for quality

control). NOTE: this option is not compatible with FMRI post-processing and motion correction (the single-band images will be quietly discarded in this case).

**MB LeakBlock kernel:** Select this checkbox to replace the default slice-GRAPPA kernel optimization with LeakBlock kernel optimization (ref. *MRM* 2014;72:93-102). This approach is designed to minimize inter-slice correlations, but may come at the cost of somewhat higher overall noise and within-slice artifacts. NOTE: this option may cause the reconstruction of the first image to be delayed due to increased initial computational requirements.

**MB dual kernel:** Select this checkbox to calculate separate kernels for odd and even lines (ref. *NeuroImage* 2012;63:569-580). This approach is designed to reduce ghosting, but it has not been carefully vetted. It is provided for experimental use.

**MB RF phase scramble:** Select this checkbox to optimize inter-band phase offsets in the RF pulse shape to reduce the required peak RF power (ref. *Proc. ISMRM* 2012, #2209). Overall SAR is unchanged. This option is currently only defined for MB acceleration factors 3-8.

**Time-shifted MB RF (SE/diffusion only):** Select this checkbox to temporally offset the bands in the RF pulse shape to reduce the required peak RF power (ref. *MRM* 2013;69:1261-7). Overall SAR is unchanged. For SE and monopolar diffusion, the “aligned- $T_E$ ” scheme described in the reference is used. Refer to the tooltip for specific shift offset information.

**SENSE1 coil combine:** Select this checkbox to use a SENSE R=1 algorithm for SNR-optimized coil combination (ref. *MRM* 2013;70(6):1682-9). Coil combine mode “sum of squares” must also be selected on the System/Miscellaneous card.

**Invert RO/PE polarity:** Select this checkbox to automatically apply a 180-degree in-plane rotation to the acquisition parameters (e.g. to use for eddy current correction in post-processing).

**Sparse TR acq.:** Select this checkbox to disable readout and phase encoding gradients for selected measurements, e.g. to allow for “silent” periods during auditory scans (while maintaining RF steady state). Note: the on/off periods must be defined using the **Triggering scheme** option; *this checkbox will only appear if a triggering paradigm is active.*

**PF omits higher k-space (BOLD only):** When phase partial Fourier is active, select this checkbox to fully acquire the early k-space lines (before the k-space center) and omit the latest lines. This option can be used to reduce minimum  $T_R$  when long  $T_E$  is used. This is the opposite of the product (default) approach, which always omits the early k-space in order to reduce minimum  $T_E$ .

**Disable freq. update:** This option will disable dynamic transmitter frequency updating, which is intended to correct for frequency drift over the course of long scans (caused by e.g. gradient heating). This update adds a 20 ms dead period at the end of every  $T_R$ . Image drift in the phase encoding direction will still be corrected in post-processing if this option is selected.

**Online multi-band recon.:** *Online* will reconstruct the multi-band accelerated images in ICE and send them to the database. *Aliased* will send the aliased images directly to the database without reconstruction (for debugging). *None* is equivalent to EmptyIcE (e.g. for later reconstruction offline).

If the optional remote reconstruction service is configured, the option to enable it will be found here.

**FFT scale factor:** This parameter may be used to adjust the image brightness, i.e. to optimize dynamic range. Note that on VD11D and newer platforms 16-bit DICOM format is used.

**Physio. recording:** Control recording of physiological signals (cardiac, respiration, ECG, external) to text or encoded DICOM files. Text files will be stored in C:\MedCom\Log\Physio\ on the host computer (MRC). *Legacy* uses the classic CPmuSequence/IdeaCmdTool logging facility (this is the only option available on VAXx/VBxx systems and VD11x; it is known to be

unreliable on VD11x/VD13x/VE11x). *DICOM* and *File* use the new online/ICE logging available since VD13A, which is recommended for use when available. *File* writes the log data to individual text files for each signal (this option was named *Online* in previous versions). *DICOM* embeds these logs in a special DICOM “image” stored in the database (sample Matlab code for reading the special DICOM files is provided in the [GitHub repository](#)). *Multiple* enables both *Legacy* and *File* options (not recommended for routine use).

**Triggering scheme (*BOLD/SE only*):** This parameter, and the arrayed parameters below it, can be used to control the sending of the external trigger signal (EXT\_TRIG) per slice, per volume, and/or controlled by a custom paradigm. Refer to the tooltips for details. The paradigm definition is similar to that of the BOLD card. If scheme “standard” is selected, the external trigger will be sent once at the start of each repetition (same behavior as the product sequences).

# Important Issues (not bugs)

***This release will expire on 6 December 2017!***

Please refer to <https://github.com/CMRR-C2P/MB> for the latest information.

- Only diffusion modes “MDDW” and “Free” are compatible with multi-band. The other modes have been disabled. The MDDW license is therefore required to insert the MB diffusion sequence.
- It is not possible to use fMRI post-processing and/or motion correction and also save the single-band reference images. If both are selected, the ICE program will silently discard the single-band reference images. It is generally not recommended to use these post-processing steps since they slow down the online reconstruction and can very easily be performed offline (often with better results).
- Demanding diffusion acquisitions with high b values may fail with gradient duty cycle errors if the highest gradient amplitudes are requested on the same axis over several consecutive  $T_{RS}$ . This can be avoided by using e.g. a randomized vector table (in “Free” mode) to distribute the gradient demand more evenly over time. (This also applies to the product diffusion sequence.)
- Monopolar+ and bipolar+ diffusion schemes are not available. Unfortunately, Siemens does not make the code to enable these modes available for customer sequences.
- Reconstruction is sometimes slow, especially with iPAT enabled. This is unavoidable due to the complexity of the unaliasing calculations, but it is something that we continually aim to improve. It is recommended to have the fastest available MRIR/MARS from Siemens. Using the [remote reconstruction service](#) can offer dramatic performance improvements, approaching real time.



# Known Bugs

Please refer to <https://github.com/CMRR-C2P/MB> to read and submit bug reports.

# Version Changes

## Release 015a, 11 April 2017

- Stability improvements for GPU reconstructions.
- Support multi-echo acquisitions when using “online” physiology logging.
- Triggering fix for “Sparse TR” mode.
- Added version check and file integrity verification to install script.

## Release 015, 3 March 2017

- The SMS license is now required to enable slice acceleration on versions VE11C and newer.
- Added new option to embed “Online” physiology log data in a special DICOM file (VD13x/VE11x and newer versions).
- The scale of respiratory traces should no longer change during an acquisition when using “Online” physiology logging.
- ECG traces should now be stored at the highest temporal resolution (400 Hz) when using “Online” physiology logging.
- “Learning phase” physiology samples will no longer be stored when using “Online” physiology logging.
- Inactive/unused signal sources will not produce log files when using “Online” physiology logging.
- If a K10 GPU is detected in the MaRS, both logical devices will be used properly for improved reconstruction performance.
- The excitation pulse voltage is now displayed correctly on VD13x/VE11x.
- Various “common” ICE errors will now cause friendly/informative popup messages to appear on the host.
- The installation script will report an error if an encrypted file is encountered (this can occur inadvertently when extracting .zip archives to NTFS volumes on macOS systems).
- Additional triggering paradigm options added.

## Release 014, 20 July 2016

- VE11C version added.
- Multi-echo support fully enabled.

- GPU support for accelerated image reconstruction enabled for VE11x versions.
- Maximum allowed MB factor limit raised from 4 to 8 for diffusion variant; maximum combined MBxiPAT factor limit raised from 12 to 18 for all variants.
- Partial GPU support added for systems with K10 GPUs.
- “Sparse  $T_R$ ” acquisition option added to allow for the prescription of “quiet” periods during a scan, e.g. for auditory studies.
- Protocol option added to disable frequency feedback, e.g. for timing-dependent studies.
- Dual kernel reconstruction option added for evaluation.
- Fixed UI and protocol conversion issues related to hidden “SB fake slice bands” option.
- Image reconstruction stability improved for very small matrix sizes.

#### Release 013a, 7 January 2016

- Fixed bug in VB17A/VB19A/VB20P diffusion variant which prevented existing protocols from being loaded without being “fixed” and reset to default parameters.

#### Release 013, 14 December 2015

- VE11A/VE11B versions added.
  - Note: GPU support is currently not available for VE11A/VE11B versions.
- VD13x/VE11x: New ‘Online’ physiology logging option. This should be much more reliable than the scheme used in previous versions (still available as ‘Legacy’ mode). Example MATLAB code for reading the new file format is available in the [GitHub repository](#).
- New protocols created with this version will now default to using the LeakBlock kernel.

#### Release 012d, 14 December 2015

- VD13C/D: The pop up message indicating clipped RF pulses was not being displayed; this has been fixed.
- VD13A/B/C/D: Eliminated some harmless but severe-looking error messages that could appear in the logs at the start of sequence execution (particularly with physiology logging enabled).

Release 012c, 13 October 2015

- A pop up message will now be displayed on the host at runtime to clearly indicate when the sequence has expired; protocols will still be visible and editable after expiration.
- VD13x: Corrected 10  $\mu$ s per  $T_R$  timing error when real-time frequency feedback is enabled.
- VD13x/VD11D: If online motion correction is enabled, 16-bit DICOM encoding (“high dynamic range”) will be disabled due to incompatibility with the Siemens online motion correction routines. Using the online motion correction is not recommended.
- If magnitude+phase reconstruction is selected, a new option to force enabling of the Maxwell correction is available. Otherwise, by default, Maxwell correction is disabled for phase image reconstructions.
- Minimum  $T_E$  has been slightly reduced for diffusion acquisitions (allows for replicating the HCP/Lifespan 3T protocol exactly on Prisma systems).
- The maximum number of repetitions allowed is no longer affected by the number of receiver coils selected (e.g. the Head/Neck 64).
- Fixed preparation failure when selecting a GRE iPAT reference scan in combination with time-shifted RF pulses.
- The default RF time shift has been adjusted to match the published 7T HCP protocol (for 5.12 ms excitation pulse, 1.92 ms shift).
- On Tx-Array systems, the clipped RF pulse check has been disabled since it can not be made compatible with amplitude correction factors (CP\_mode.ini)  $\neq 1$  on arbitrary transmit channels.
- Due to poor performance, GPU acceleration will be automatically disabled if a Tesla K8, K10, or similar device is detected.
- If the remote reconstruction service is configured, an option is now available to save images directly to disk on the server for real-time processing with minimal latency.
- Fixed reconstruction failure for multi-echo, single-band acquisitions.
- Various UI fixes for multi-echo protocols (generally improved handling of arrayed  $T_E$  values).
- Fixed reconstruction error for multi-echo + multi-band acquisitions when using GPU acceleration on VD13x.
- Reduced ICE log chatter...

#### Release 012b, 18 May 2015

- VD13D: On systems with dual GPUs, reconstruction should no longer occasionally fail with kernel errors.

#### Release 012, 19 November 2014

- An option has been added to use LeakBlock (aka Split slice-GRAPPA, ref. Cauley *MRM* 2014;72:93-102) kernel optimization in place of the default slice-GRAPPA kernel. This option may offer reduced leakage artifacts (inter-slice crosstalk) at the cost of overall reduced SNR, increased within-slice aliasing artifacts, and increased reconstruction time.
- The slice acquisition timing reported in the DICOM files (e.g. MosaicRefAcqTimes in the shadow header) should now be physically correct for all repetitions as well as for the single-band reference. *This time it should really be true...*
- The default CAIPIRINHA PE shift has been changed from FoV/3 to FoV/4 for iPAT R=2 protocols to improve unaliasing performance.
- When time-shifted RF pulses are being used in combination with iPAT using the GRE reference scan option, the reference scan acquisition should now be shorter and offer improved performance.
- The single-band reference images are now always acquired with linear slice order to reduce the possibility of banding artifacts that may appear during interleaved acquisitions (the MB acquisition is unchanged).
- Minimum allowed  $T_R$  may be shorter for certain protocols, especially on systems with  $>40$  mT/m body gradient sets (Prisma, Connectom).
- An internal hard limit on maximum allowed RF pulse bandwidth has been removed. This will allow for more coverage in the slice direction, but  $B_1$  transmit homogeneity over large bandwidths has not been carefully evaluated on all systems (warnings will be written to the trace log when the expected limit is exceeded).
- The popup message that appears when the requested RF flip angle cannot be achieved due to insufficient RF peak power should no longer appear repeatedly if a SAR or stimulation change proposal is being calculated by the system.
- VD13: Image reconstruction should no longer fail at the end of a scan (with no data loss) if SENSE1 coil combination is used with DTI postprocessing enabled.

- Image reconstruction should no longer fail at the start of a scan if an Image Numbering scheme (defined on System/Miscellaneous card) other than the default is used.
- VD13: When the “log physiology to file” option is selected, the EXT\_2 signal will now also be logged.
- An option to use RF spoiling is now available (possibly useful for extremely short  $T_R$ ).
- Optional flow compensation in the slice direction is now available in the BOLD variant.
- The “free echo spacing” option is no longer disabled.
- Other bug fixes and UI performance improvements.

#### Release 011a, 9 June 2014

(eja: vb17a/d7f82ea, vb19a/da328c9, vd11d/1f6d304, vd13a/de62ca8, vd13c/af3cafa, vd13d/5cd7089)

- Fixed image reconstruction preparation error when selecting GRE-based iPAT reference scan option.
- GRE-based iPAT reference scan can now be used in combination with time-shifted MB RF pulses (SE, diffusion variants).
- Fixed UI issue where diffusion mode “Free” could not be selected in new protocols under VB17A/VB19A/VD11D.
- VD13x: Fixed failure to prepare image reconstruction on systems without a CUDA GPU (48-channel MARS).
- VD13C: Corrected CUDA version; GPU support should now work properly when a GPU is present.

#### Release 011, 23 May 2014

(eja: vb17a/d9ea75d, vb19a/504763c, vd11d/483fe46, vd13a/5a1c0a3, vd13c/1b34f94, vd13d/c791fc7)

- GRE-based iPAT reference scan option added (note: segmented reference scan was used for MB+iPAT acquisitions in all previous versions).
- MB acquisitions with descending slice order should work properly.
- The slice timing info in the image shadow header under MosaicRefAcqTimes should now be accurate for all MB repetitions (previously the info for the first repetition was incorrect).
- VD13: GPU acceleration has been enabled for VD13A/C/D systems with a 64- or 128-channel MARS2 installed (only newer revisions with Tesla C2070 or better). Most scans using 32 or fewer channels

should reconstruct in real time. This unfortunately does not seem to be true for >32 channels...

- VD13: All available advanced  $B_0$  shim modes are now selectable.
- VD13A: “Tx Feedback” is now enabled by default on VD13A Skyra systems for improved stability. If you have a Skyra with an older Tx box and MB scans stop with TxK2304 errors, contact Siemens to have it upgraded, or in the meantime contact us or see the support web page for instructions on how to disable it again.

#### Release 010c, 28 March 2014

(eja: vd13a/59bad81, vd13c/1b2c8d6, vd13d/4b0f402)

- VD13C: Fixed issue preventing SE sequence from being inserted.
- VD13A: Fixed issue where diffusion mode Free could not be selected in new protocols, related diffusion UI slowness.
- VD13D: New protocols now default to gradient mode Performance if it is available (e.g. for Prisma).
- Removed non-functional diffusion modes (only MDDW and Free are supported).

#### Release 010b, 13 December 2013

(eja: seqs only all versions; vb17a/41a9b7e, vd11d/R010/dae2076, vd13a/sp2/3451f7c, vd13a/R010/fd129fc, vd13d/R010/7d45ede; added 29 Jan 2014: vb19a/6a5af2e, vd13c/2bfb96d)

- VB17A: Fixed scanner crash and reboot if a non-MB sequence was used following a MB sequence in the same session.
- VD13D: Fixed incorrect orientation labeling of slices with the “invert RO/PE” option selected.
- VD11D/VD13x: Fixed inconsistent synchronization of frequency feedback acquisition. This could result in timing errors of ~20ms per  $T_R$  and degraded image quality for certain protocols.
- If the “log physiology to file” checkbox is selected, the directory C:\MedCom\log\Physio will now be created if it does not already exist.
- iPAT reference scan for R=2 is now segmented as it was in previous versions (protocols with larger numbers of reference lines should no longer break on import).
- Descending slice order should now work properly (really).

#### Release 010a, 22 November 2013

(eja: vb17a/857e1d9 all seqs, vd11d/R010/2638d72 diff seq only)

- VB17A: Fixed display of current measurement in the status bar.

- VB17A/VD11D: Fixed inability to select diffusion mode Free.
- VB17A: RF pulse durations can now be set freely for single-band SE/diffusion protocols on UHF systems.

#### Release 010, 20 November 2013

(eja: vb17a/r206, vd11d/R010/6fea7e1, vd13a/sp2/49ca23b, vd13a/R010/5b5bc96, vd13d/R010/eacfbce)

- The number of preparation scans acquired at the start of the measurement has been reduced, notably for diffusion protocols and protocols using iPAT.
- VD13A: Transmitter feedback is now specifically disabled for Skyra systems by default. This new feature is currently causing crashes with multiband pulses; Siemens may fix it in a future hardware update.
- Gradient reversal fat suppression is now an independently selectable option. In previous versions it was automatically enabled if fat suppression modes “none” or “strong” were selected (following Siemens default behavior since VD11).
- New options have been added for sending optical trigger signals per slice or repetition.
- New options have been added to use phase scrambling and/or time-shifting approaches to reduce peak RF power.
- Clipped RF pulse warning window should no longer pop under the exam window.
- Descending slice order should now work properly.
- VB17: iPAT>2 should work now on pTX systems.
- VD13: Images should no longer jump in the phase direction.
- Copying sequence parameters from other protocols should be more reliable.
- UI responsiveness and stability should be improved.

#### Release 009a, 21 May 2013

(eja: seq/ICE VB17A r158/r157, VD11D r236/r234, VD13A-SP2 r22/r20)

- VB17: Fixed inability to load existing diffusion protocols.
- Minimum  $T_E/T_R$  should now match previous versions.

#### Release 009, 15 May 2013

(eja: VB17A r157, VD11D r234, VD13A-SP2 r20)

- First “development” release.



- Added VD13A-SP2 version.
- Dramatic image quality improvements. All images should appear significantly sharper, and MB+iPAT performance is especially improved.
- The maximum allowed MB factor has been increased from 8 to 16.
- Allowed MB\*iPAT factors have been increased to 12.
- Many user interface improvements. The user interface should be more responsive and more stable in general.
- All diffusion modes aside from MDDW and Free have been disabled. Previously the other modes were selectable but would crash image reconstruction.
- Saving single-band images in combination with FMRI postprocessing and/or motion correction will no longer crash image reconstruction (the single-band images will be discarded).
- Minimum  $T_E/T_R$ /thickness increments have been reduced.

#### Release 008, 13 February 2013

(eja: seq/ICE VB17A r121/r122; VD11D r206/r205)

- First “stable” release.
- Added options for reconstructing phase images
- MB+iPAT reconstruction improvements

#### Release 007, 21 November 2012

(eja: VB17A r113; VD11D r195)

- Reconstruction speed improvements
- Fixed occasional occurrence of intensity variations between bands in some (mostly diffusion) protocols
- VD11: Siemens product frequency feedback/update enabled
- VD11: Checkbox added to invert readout and phase encoding gradient polarity (useful for post-processing eddy current corrections)
- SENSE1: image comment now indicates whether SENSE1 has been applied
- SENSE1: susceptibility-induced signal loss reduced

#### Release 006b, 21 June 2012

(eja: VB17A r92)

- VB17: fixed cases in monopolar diffusion where spoiler gradients failed to be played out for single-band  $b=0$  reference scan

## Release 006a, 23 May 2012

(eja: VB17A r91; VD11D r154)

- Fixed memory leak which caused recon to eventually crash for long series
- VB17: fixed FFT scaling factor for SENSE1
- Minor improvements to exported physiological log data

## Release 006, 18 May 2012

(eja: VB17A r88; VD11D r151)

- Expiration date extended to 1 December 2012
- Added spin-echo EPI sequence variant
- Fixed clipped RF pulse dialog false alarms (for real this time...)
- VD11: fixed crash when physiological logging is enabled
- VB17: improved EPI ghost correction for BOLD variant
- VB17: fixed DTI recon preparation failure for certain syngo patch levels
- Limited max. MB factor to 3 for diffusion
- Removed non-working “free echo spacing” checkbox
- Misc. UI improvements

## Release 005, 6 April 2012

(eja: VB17A r75; VD11D r125)

- Image quality improvements for MB7 and MB8
- Added SENSE1 coil combination option
- Restored option to save single-band reference images to a separate series
- Fixed clipped RF pulse dialog for VB17 diffusion refocusing pulses
- Further reconstruction speed improvements

## Release 004a, 20 March 2012

(eja: VB17A r72; VD11D r111)

- Fixed incompatibility with protocols created with earlier revisions
- Reconstruction speed improvements

## Release 004, 20 March 2012

(eja: VB17A r71; VD11D r110)

- Fixed DTI recon crash when postprocessing was explicitly not selected

- Added warning dialog on host if (MB) RF pulses will be clipped
- Fixed crash when creating new DTI protocols
- Fixed gradient errors on systems with lower slew rates (e.g., Verio)
- UI responsiveness, stability improvements
- Removed “single-band images” option due to unresolved ICE crashes; will restore in a later release

#### Release 003, 27 January 2012

(eja: VB17A r64; VD11D r78)

- Reconstruction speed improvements
- MB+iPAT image quality improvements
- Added option to save single-band reference images to a separate series
- Reduced number of prep scans at start of BOLD measurement
- Adaptive coil combine now compatible with MB (VD11D only)

#### Release 002a, 4 January 2012

(eja: VB17A r60; VD11D r61)

- VB17A ICE program expiration date fixed

#### Release 002, 18 November 2011

(eja: VB17A r58; VD11D r61)

- Diffusion variant (ep2d\_diff) released
- iPAT (GRAPPA only) enabled
- Option to log physiological data to file added
- Additional FFT scale factor UI parameter added (VB17 only)
- Bug fixes

#### Release 001, 26 September 2011

(eja: VB17A r50; VD11D r36)

- Initial public release