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CMRR - Center for Magnetic Resonance Research Software for Siemens MRI Scanners

Technology No. 20180139

The Center for Magnetic Resonance Research (CMRR) at the University of Minnesota develops magnetic resonance imaging, spectroscopy methodologies and instrumentation to non-invasively acquire structural, functional and biochemical information from humans. These capabilities are used to study the function of organs in healthy and diseased states. CMRR has developed pulse sequence software that runs on Siemens platforms that is available for researchers.

Process to Obtain a CMRR License

- To begin the licensing process, email CMRR. Initial contact information for specific licenses are provided under each software.
- Obtain authorization from your Siemens Regional Collaboration Manager for the specific software you would like to license. Please make sure you complete the entire licensing process.
- CMRR will send you an Authorization Code.
- Select the license from this web page and complete the license agreement. You will be asked to enter the Authorization Code.
- CMRR will send you your account information and instructions for downloading the software. The entire licensing process may take up to two weeks to process.

Available Licenses

Multiband EPI (GE-fMRI and SE diffusion) 6 Months

This sequence package contains binaries for multiband slice accelerated EPI with controlled aliasing. Only the sequence binary files for Siemens software versions VB17/VD11, along with the relevant ICE reconstruction, will be provided. The binaries will expire every 6 months, at which time the recipient will be provided with an updated or similar version with a new expiration date.
>>>Contact **Essa Yacoub**.

Multiband EPI (GE-fMRI and SE diffusion) Human Connectome Version

This sequence package contains binaries for multiband slice accelerated EPI with controlled aliasing. Only the sequence binary files for Siemens software versions VB17/VD11, along with the relevant ICE reconstruction, will be provided. This version of the software will not be updated and is the version of the software used by the NIH sponsored Human Connectome Project.
>>>Contact **Essa Yacoub**.

Spectroscopy Package

The spectroscopy package contains spectroscopic and shimming sequences, and the accompanying reconstructions developed at the CMRR. The following sequences are included: LASER (semi-LASER, MEGA-semi-LASER), PRESS (MEGA-PRESS), STEAM, FAST(EST)MAP. The sequence code is transferred as compiled code and cannot be modified by the licensee. If you are interested in obtaining the spectroscopy package, please follow instructions on CMRR's Spectroscopy web page.

Single Slice MASE

The single slice multiecho adiabatic spin echo (MASE) imaging sequence designed to produce accurate T2 measurements at high fields. The sequence will be transferred as compiled code and will operate only on Siemens 1.5, 3T and 7T systems.
>>>Contact **Edward J. Auerbach**.

FAIR ASST

This sequence package contains binary files for one variant of FAIR (Flow-sensitive Alternating Inversion Recovery) arterial spin labeling (ASL) imaging approach: FAIR ASST (FAIR with Active Suppression of Superior Tagging). This variant has incorporated configurable modules, such as QUIPSS II, Q2TIPS, and intravascular spin suppression using flow-encoding crush gradients, to satisfy different study needs. For example, with turning off these and ASST modules, FAIR ASST will become a standard FAIR sequence. This sequence also supports the use of HSN adiabatic RF pulses (e.g. N>= 4) to minimize the peak power for the adiabatic inversion RF pulses, which can facilitate perfusion imaging at ultra high fields, such as 7T. This method was first developed at UT Southwestern Medical Center and further improved/upgraded at CMRR. Currently, only the sequence binary files for Siemens software version VB17 is provided.
>>>Contact **Xiufeng Li**.

OPTIMAL FAIR

This sequence package contains binary files for one variant of FAIR (Flow-sensitive Alternating Inversion Recovery) arterial spin labeling (ASL) imaging approach: OPTIMAL FAIR (Orthogonally Positioned Tagging Imaging Method for Arterial Labeling with FAIR). With OPTIMAL FAIR technique, oblique coronal imaging slices with high in-plane resolution can be placed perpendicular to the longitudinal axis of the hippocampus along the A–P direction. This reduces partial volume effects and increases resolution, allowing the detection of finer details of the A–P differences in perfusion parameters, thus enabling reliable studies of these perfusion differences in both normal and compromised or diseased hippocampus. This variant has incorporated configurable modules, such as QUIPSS II, Q2TIPS, and intravascular spin suppression using flow-encoding crush gradients, to satisfy different study needs. With turning off these modules, OPTIMAL FAIR will become a standard FAIR sequence. This sequence also supports the use of HSN adiabatic RF pulses (e.g. N>= 4) to minimize the peak power for the adiabatic inversions, which can facilitate

perfusion imaging at ultra high fields, such as 7T. This method was first developed at UT Southwestern Medical Center and further improved/upgraded at CMRR. Currently, only the sequence binary files for Siemens software version VB17 is provided.
>>>Contact **Xiufeng Li**.

MB-EPI PCASL

This sequence package contains binary files for PCASL (pseudo-continuous arterial spin labeling (ASL)) imaging approach using multi-band echo planar imaging readout (MB-EPI): MB-EPI PCASL. High-resolution perfusion imaging is highly desirable in both neuroscience research and clinical applications to reduce partial volume effects on gray matter (GM) and white matter (WM) cerebral blood flow quantification, to improve the ability to assess perfusion abnormality in sub-cortical brain structures, e.g. the hippocampus, and identify small brain lesions. MB-EPI PCASL method provides a novel alternative for high-resolution whole-brain non-contrast enhanced perfusion imaging by reducing imaging acquisition time and increasing perfusion signal-to-noise ratio efficiency. The current version of this MB-EPI PCASL C2P sequence only supports Siemens scanners using the platform VB17, and the version that supports other platforms, e.g. Prisma, will be provided later.
>>>Contact **Xiufeng Li**.

Multi Slice Adiabatic $T_{1?}$, $T_{2?}$ and RAFFn Relaxation Mapping Sequences

This sequence package contains the binary files for Multi slice adiabatic $T_{1?}$, $T_{2?}$ and RAFFn relaxation mapping sequences with segmented GRE readout and parallel imaging. The current version of this sequence only supports Siemens scanners using the platform VB17.
>>>Contact **Shalom Michaeli**.

Time of Flight Angiography

This sequence package contains the MR sequence to realize Time of Flight Angiography acquisitions featuring specific methods to limit or reduce SAR at high magnetic field, including implementation of the VERSE alrogithm on excitation and saturation RF pulses and sparse application of Magnetization Transfer RF pulses.
>>>Contact **Pierre-Francois Van de Moortele**.

Time Efficient Whole-brain Coverage in Magnetic Resonance Fingerprinting Using Echo-planar Imaging, Slice-interleaving and Simultaneous Multi-slice Imaging Sequence

This sequence package contains binary files that use a slice-interleaved acquisition method combined with simultaneous multi-slice imaging to provide high quality T1 and T2 maps. A slice-interleaved acquisition is shown to offer quantification precision comparable to single-slice measurements in a fraction of the measurement time.
>>>Contact **Mehmet Akcakaya**.

Gradient-Modulated PETRA

This sequence package contains binaries for the Pointwise Encoding Time Reduction with Radial Acquisition sequence with Gradient Modulation (GM-PETRA) and the image reconstruction program. In the GM-PETRA sequence, gradient modulation after hard pulse excitation and oversampling in single point imaging (SPI) acquisition are implemented. The current version of the sequence only supports Siemens software version VE11C. The online ICE reconstruction will be provided along with the sequence binaries.
>>>Contact **Naoharu Kobayashi**.

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