Acquisition and Processing Pipeline for Multi-Contrast fMRI Multi-Echo SMS (MESMS) GE-EPI at 7T

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Target Audience: MR Scientists and Neuroscientists with an interest in fMRI at Ultra High Fields and Simultaneous Multi Slice acquisitions

Purpose: Multi-echo (ME) acquisition has recently been shown to be a robust and reliable method for extracting valuable information for both task-driven and resting-state fMRI data [1-3]. Nonetheless, ME-EPI acquisition can cause a decrease in temporal sampling rate. With recent technological development in pulse sequence and coil array design, it is possible to acquire multiple EPI imaging slices in one single shot with simultaneous multiple slice (SMS) approach and Blipped-CAIPI controlled aliasing [4-6]. Multi-echo-SMS (MESMS) EPI was recently proposed [7], by combining SMS with ME-EPI acquisition, to provide improved temporal sampling efficiency. The method was demonstrated at 7T [8] and also at 3T with Blipped-CAIPI [7] for resting-state data acquisition. Another active area of fMRI development is in exploring the use of phase information via Quantitative Susceptibility Mapping (QSM) [9-11] to provide an additional contrast mechanism and to help identify physiological sources of the BOLD response. In this work, we demonstrate the first high-resolution ME-SMS acquisition with Blipped-CAIPI at 7T. We also incorporate a fast pipeline for phase and QSM processing of the multi-echo high-temporal-sampling-rate data (~20s per echo volume) to enable this large dataset to be processed in a reasonable time frame. The acquisition and processing method used in this work should aid in the exploration of three interrelated functional contrasts (T2*-weighted, quantitative T2* and QSM) at high temporal and spatial resolutions.

Methods: Data were acquired on a 7T whole-body MR system (Siemens Healthcare Sector, Erlangen, Germany) with a custom made 32-element phased array head coil and a gradient system achieving maximum amplitude of 70mT/m. A healthy volunteer was scanned in accordance with local IRB requirements. One 3× slice accelerated multi-echo dataset of the whole brain consisting of 180 time points was acquired using the following parameters: 2mm isotropic voxel size, 3× slice acceleration, 3× in plane acceleration, FoV=200×200mm^2, TR=2040ms, TE = [15ms, 35ms, 54ms, 74ms], no Partial Fourier, BW=2380Hz/px, echo spacing = 0,55. For maximal SNR with SMS imaging, a blipped-CAIPI phase shift of FOV/2 was employed. Fat suppression was achieved using a spectral saturation pulse. Image reconstruction was performed offline using Matlab (Mathworks, Natick, MA). Single-coil images were reconstructed with in-plane GRAPPA and slice-GRAPPA [12] from which magnitude images were combined using sum of squares combination. Raw phase images were processed using Laplacian [13] unwrapping and SHARP [14] filtering coil-by-coil, and combined by averaging the resulting maps across coils [15]. Phase jumps between Multiband slice groups were corrected for by calculating and applying constant phase offsets. Susceptibility maps for each time point were computed using magnitude-weighted L2 regularization with fast reconstruction (~0.9 sec per volume) that employs a preconditioned conjugate gradient solver [16]. The phase and QSM calculation for all TEs within one time point takes a total time of 14s for the unwrapping, 55s for the SHARP background removal and 3s for the QSM calculation.

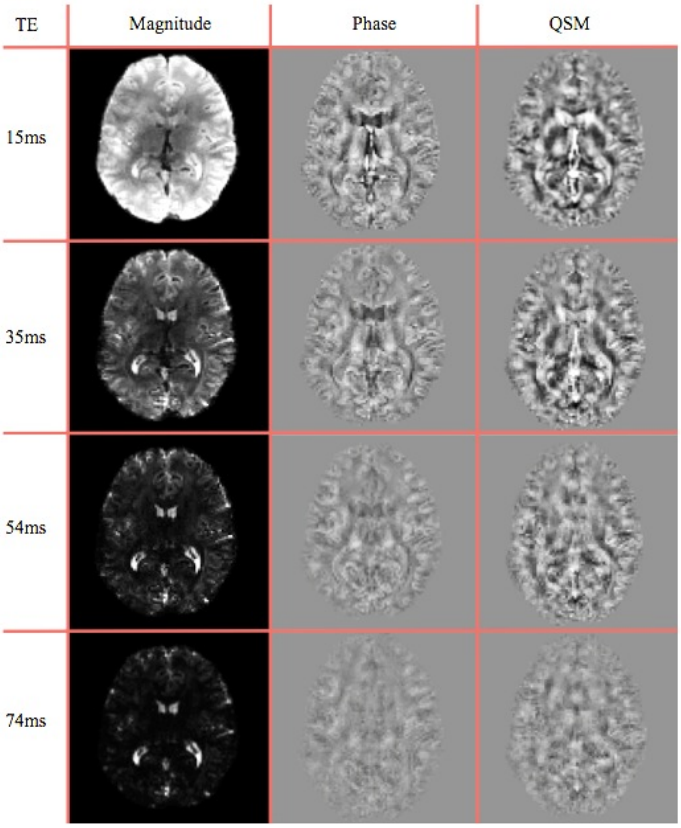

Fig 1: Subset of one time point for multi–echo contrast of Magnitude, Phase and QSM data of one slice acquired in one shot.

Results: The Magnitude, phase and QSM information were successfully obtained from the MESMS acquisition at all of the four TE values (Fig.1). As expected, the magnitude signal follows an exponential decay with TE, resulting in low signal at TE=74ms. The phase and subsequent QSM information provide additional anatomical contrast in deep gray matter structure. The phase information obtained at the first two echoes provide robust and low noise data. At the later echoes, the information is less robust and of lower contrast.

Discussion and Conclusion: This work presents a method and pipeline for acquisition and reconstruction of magnitude, phase and QSM information at multiple echoes. Data were acquired at 7 T with a high temporal sampling rate, and are expected to be a valuable for investigating the underpinnings of the BOLD response given the multiple contrasts that can be acquired simultaneously. Several techniques have been developed for filtering phase data to generate anatomical QSM maps but it is not yet clear what the optimal strategies are for functional phase data. Therefore MESMS data maybe beneficial for generating robust and stable time-resolved QSM maps for measuring functional changes by e.g. using a CNR weighted processing [1]. The different components of the BOLD response tend to evolve at different time scales. Therefore having a high temporal resolution and multiple contrasts that might potentially evolve differently both spatially and temporally can potentially help us understand and exploit the different components of the BOLD response. Furthermore, the acquired time-resolved QSM data might help quantifying blood oxygenation changes during the time course of activations and better understand the relation between local susceptibility changes and BOLD contrast [9,10]. The presented dataset is also suitable for further analysis, e.g., the calculation of proton density and quantitative T2* maps. This may be a desirable step as such maps have been previously shown to be useful in distinguishing BOLD and non-BOLD components of signal change [2,3].

The acquisition and reconstruction method proposed in this work should aid in the exploration of these interesting research area, a topic which we are currently exploring.

References: [1] Poser D et al. NeuroImage 2009; [2] Kundu P et al. NeuroImage 2012; [3] Kundu P et al. PNAS 2013; [4] Larkman DJ et al. JMRI 2001; [5] Moeller S et al. MRM 2009; [6] Setsompop K et al. MRM 2012; [7] Olafsson V et al. ISMRM 2012; [8] Boyacioglu R et al. ISMRM 2013; [9] Balla D et al. ISMRM 2012; [10] Balla D et al. ISMRM 2013; [11] Bianciardi M. HBM 2013 [12] Cauley S et al. MRM 2013 [13] Li W et al NeuroImage 2011 [14] Schweser F et al. NeuroImage 2011 [15] Wu B et al. MRM 2012 [16] Bilgic B et al. MRM 2013