Accelerating Magnetic Resonance Fingerprinting using t-Blipped Simultaneous Multi-Slice Acquisition

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Target audience: MRI physicists and engineers who are interested in quantitative MRI and accelerated acquisition.

Purpose: Magnetic resonance fingerprinting (MRF) [1] permits non-invasive quantification of multiple important properties simultaneously through a novel approach for data acquisition, post-processing and visualization. In conventional MRF, an acquisition time of approximately 10s is required for each imaging slice and this can result in long scan time, particularly when a large number of slices is required. In this work, we developed a new simultaneous multi-slice (SMS) technique to speed up MRF acquisition. Specifically, we proposed a t-blipped SMS-MRF method, which utilizes additional G_z blip encodings to provide phase modulation between the signals of simultaneously acquired slices and creates controlled-aliasing in the temporal axis. Because the blip provides controlled-aliasing in the MRF time series rather than a spatial dimension (as in blipped-CAIPI EPI) [2], we refer to the new method as t-blipped CAIPI SMS. We demonstrated, through both simulation and in vivo acquisition, the ability of t-blipped SMS-MRF technique to accelerate MRF acquisition by 2-fold (MB=2) retaining good parameter mapping at half the acquisition time.

Methods: <u>Acquisition</u>: The t-blipped SMS-MRF sequence is shown in Fig.1 (a,b). It uses a varying RF and TR train played on an IR-TrueFISP based sequence, and 40X undersampled spiral readouts. To enable SMS acquisition, it uses multi-band VERSEd [3] RF pulse and additional small G_z gradient blips of size A_{blip} and $-A_{blip}$ before and after the data acquisition window respectively. The added A_{blip} blip in t-blipped SMS-MRF introduces a phase difference between simultaneously excited slices of $2\pi\gamma A_{blip}D$ where γ is the gyromagnetic ratio, A_{blip} is the area of the gradient blip added and D is distance between the simultaneously excited slices. For the MB = 2 case that is used in this work, G_z blips are applied to create a π phase difference between the SMS slices for the even TRs, while for the odd TRs no G_z blip is applied. With this sequence, an MB=2 t-blipped SMS-MRF data at a distance of D=40 mm was acquired in vivo using a 3T Siemens Skyra with a standard Siemens 16-channel head array coil. For reference, two single-slice conventional MRF scams (10s/slice) were acquired at the same slice positions.

<u>Reconstruction</u>: Fig.1(c) shows the overall reconstruction pipeline for t-blipped SMS-MRF. First, gridding reconstruction is applied to the slice-collapsed data. Slice-SENSE is then applied using coil sensitivity estimates obtained from the slice-collapsed SMS-MRF data via an adaptive combination procedure [4]. Since the voxel aliasing in the slice and the in-plane directions are coupled, the application of SENSE [5] in the slice direction alone (i.e. slice-SENSE) would not provide a clean separation between the two imaging slices. Nonetheless, slice-SENSE provides partial separation and slice specific dictionary matching accounting for phase modulation from the G_z blips is then used to further decouple the signal and provide quantitative parameter maps estimate. After a first dictionary matching, a second dictionary matching procedure utilizing smoothed off resonance map prior, is also performed at a few localized voxels (that are automatically selected by the algorithm). This reduces minor speckled artifacts.

Results: Fig.2 shows in vivo T1 and T2 maps acquired with both conventional (one slice at a time, 10s/slice) and MB=2 t-blipped SMS-MRF (5s/slice). Fig. 3 shows the results of correlation plot comparisons from Monte Carlo simulations. In these comparisons, the x axis is always the result from a conventional MRF (10s/slice) acquisition with conventional MRF reconstruction. The y axis parameter was derived from a Monte Carlo simulation using the same initial data used for the x-axis. In the first column the y axis modeled the conventional MRF recon with 2x the noise of the original acquisition. The second column y-axis is a Monte Carlo simulation of the conventional MRF using only the first half of the time series (5s/slice). The third column is the Monte Carlo simulation of the MB=2 t-blipped SMS-MRF using all 1000 timepoints (5s/slice). In all the Monte Carlo simulations the same amount of noise was added to the data and the concordance correlation coefficients (CCC) [6] were calculated. +/- SD are plotted with error bars, which can be seen in all the cases are relatively small in comparison to the bias. From these results, it can be observed that the consistency of T1 is better than T2 in all three cases, with the 5s conventional MRF case showing the largest bias and worst stability in both T1 and T2 results. Not surprisingly the first case provides the best result.

Fig.1 SMS-MRF Acquisition & Reconstruction

Fig.2 Conventional MRF (10s/slice) — MB=2 SMS-MRF (5s/slice) — 3s/0.3s — T1 map — T2 map

Fig.3 Monte Carlo simulations
- X axis: always the result obtained from a conventional 10s/slice acquisition(unit: ms);
- Y axis: average result from a Monte-Carlo simulation using the signal from the conventional 10s/slice acquisition (unit: ms)

Discussion: In this work, we proposed the t-blipped SMS-MRF method and demonstrate its capability in accelerating MRF in an MB=2 slice-accelerated acquisition. Such technique has the potential to speed up MRF acquisition and enable more rapid quantitative parameter mapping in a clinically relevant time frame.

References: [1] Ma D, Nature'13; [2] Setsompop K, MRM'12; [2] Conolly S, JMR'88; [3] Walsh D, MRM'00; [4] Pruessmann K, MRM'99; [5] Lawrence I, Biometrics'89;