Simultaneous Multi-Slice Magnetic Resonance Fingerprinting Reconstruction using GROG+slice-GRAPPA (GsG)

Huihui Ye[1,2], Borjan Gagoski[3], Berkin Bilgic[1], Stephen F Cauley[1], Dan Ma[4], Yiping Du[2], Lawrence L Wald[1], Mark A Griswold[4], and Kawin Setsompop[1]

[1]MGH/HST Martinos Center for Biomedical Imaging, Charlestown, MA, United States, [2]Zhejiang University, Hangzhou, Zhangjiang, China, [3]Boston Children's Hospital, MA, United States, [4]Case Western Reserve University, Ohio, United States

Fig.1 SMS-MRF sequence

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

Purpose: To enable simultaneous multi-slice in magnetic resonance fingerprinting [1], we have proposed t-blipped SMS-MRF method which uses G_z blips to create TR dependent phase differences between SMS slices and slice-specific RF encoding, which utilizes different flip angle train for the different SMS slices. In this work, we propose to complement these SMS acquisition techniques with GROG+slice-GRAPPA (GsG) reconstruction, a novel k-space parallel imaging approach that can provide good unaliasing performance in the slice direction for the highly undersampled slice-collapsed MRF signal. Here we demonstrate the performance of the GsG reconstruction in conjunction with t-blipped SMS-MRF at multi-band (MB) factor of 3.

Methods: <u>Acquisition</u>: The timing diagram of the t-blipped SMS-MRF sequence is shown in Fig.1. The added A_{blip} blip will introduce a phase difference between simultaneously excited slices equals to $2\pi\gamma AD$, where γ is the gyromagnetic ratio, A is the area of the A_{blip} and D is distance between the simultaneously excited slices. For the MB = 3 case of t-blipped SMS-MRF used in this work, G_z blips are applied to create $2\pi/3$ phase difference between three simultaneously excited slices for the 2,5,8,…,998 TRs, $-2\pi/3$ phase difference between three simultaneously excited slices for the 3,6,9,…,999 TRs and no phase difference for the 1,4,7,…,1000 TRs. The slice distance factor D was set to 35mm. The acquisitions were performed on a 3T Siemens Skyra with a standard Siemens 32-channel head receive array. For reference, three single-slice conventional MRF scans (10s/slice) were acquired at the same slice positions. For training the kernels used in the GsG reconstruction, three single-slice GRE data were acquired with same three slice positions.

<u>Reconstruction</u>: Fig.2 shows our GsG reconstruction pipeline, which is modified from pseudocartesian GRAPPA algorithm [2]. First, in-plane GROG [3,4] is applied to the collapsed k-space data S to obtain gridded data SG, where the G_x and G_y GROG weights are determined from the manually collapsed GRE data. Second, slice-GRAPPA [5] kernels for 7 different patterns are calculated from the single slice GRE data, each point in SG k-space data is grouped to one of the pattern, and applied with the corresponding kernel to generate the slice-unaliased SGG k-space data (see Fig 2). In the following step, each SGG k-space data is inversely weighted by its density W which can be simply calculated by counting the numbers along the time series and divided by the total time points. After weighting, data is Fourier transformed and coil combined into image IGG in which the coil sensitivity maps are estimated from the acquired GRE data. Lastly, a dictionary matching is applied on each slice to obtain the four parameter maps.

Fig.2 GROG+slice-GRAPPA reconstruction

Results: Fig.3 shows in vivo T1, T2 and off resonance maps from conventional MRF (one slice at a time, 10s/slice), MB=3 SMS-MRF (3.33s/slice) and mixed conventional MRF and MB=3 SMS-MRF. From the results, it can be observed that the consistency between conventional MRF and accelerated MB=3 SMS-MRF is good in all the three slices. One minor difference is that WM in center slice appears noisy and over-esitimated in both T1 and T2 result. In the third column, which experiment with using data with the first 10% time points from conventional single slice MRF and later 90% time points from MB=3 SMS-MRF, provides significant improvement with results resembling that from the conventional MRF.

Discussions: In this work, we demonstrate the GsG reconstruction complies well with t-blipped SMS-MRF acquisition scheme and makes accelerating MRF three-fold faster possible. Good reconstruction is achieved with slight differences in the midline brain area for the center slice due to the incomplete separation of the slice-aliased signals. Since the signal from the first several hundred time points is more T_1 weighted due to the applied inversion pulse, we experiment retrospectively with replacing the first 10% of the time points of MB=3 SMS-MRF with conventional MRF data, which resulted in improved T_1 and T_2 consistency. Combining portions of conventional MRF with SMS-MRF acquisition to improve the robustness of the reconstruction is one of the future directions that will be considered.

Reference: [1] Ma D, Nature'13; [2] Seiberlich N, MRM'08; [3] Griswold M A, MRM'05; [4] Seiberlich N, MRM'07; [5] Setsompop K, MRM'12;