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3D MR fingerprinting with accelerated stack-of-spirals and hybrid sliding-window and GRAPPA reconstruction

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ABSTRACT

Purpose: Whole-brain high-resolution quantitative imaging is extremely encoding intensive, and its rapid and robust acquisition remains a challenge. Here we present a 3D MR fingerprinting (MRF) acquisition with a hybrid sliding-window (SW) and GRAPPA reconstruction strategy to obtain high-resolution T_1, T_2 and proton density (PD) maps with whole brain coverage in a clinically feasible timeframe.

Methods: 3D MRF data were acquired using a highly under-sampled stack-of-spirals trajectory with a steady-state precession (FISP) sequence. For data reconstruction, k_x-k_y under-sampling was mitigated using SW combination along the temporal axis. Non-uniform fast Fourier transform (NUFFT) was then applied to create Cartesian k-space data that are fully-sampled in the in-plane direction, and Cartesian GRAPPA was performed to resolve k_z under-sampling to create an alias-free SW dataset. T_1, T_2 and PD maps were then obtained using dictionary matching.

Results: Phantom study demonstrated that the proposed 3D-MRF acquisition/reconstruction method is able to produce quantitative maps that are consistent with conventional quantification techniques. Retrospectively under-sampled in vivo acquisition revealed that SW + GRAPPA substantially improves quantification accuracy over the current state-of-the-art accelerated 3D MRF. Prospectively under-sampled in vivo study showed that whole brain T_1, T_2 and PD maps with 1 mm^3 resolution could be obtained in 7.5 min.

Conclusions: 3D MRF stack-of-spirals acquisition with hybrid SW + GRAPPA reconstruction may provide a feasible approach for rapid, high-resolution quantitative whole-brain imaging.

1. Introduction

Quantitative imaging facilitates quantification of the biochemical and biophysical properties of tissues such as T_1, T_2 and proton density (PD), which have been demonstrated to be sensitive biomarkers for detecting diseases such as multiple sclerosis, epilepsy and cancer (Barbosa et al., 1994; Eis et al., 1995; Martin et al., 2015). However, due to the prohibitively long acquisition time of conventional quantitative imaging methods (e.g., multi-TI inversion-recovery for T_1 mapping and multi-TE spin echo for T_2 mapping) (Deoni, 2011), these quantification methods are rarely applied in clinical environments. A number of rapid quantitative imaging methods (Deoni et al., 2005; Dregely et al., 2016) are now available, but their reproducibility needs to be improved.

MR fingerprinting (MRF) (Ma et al., 2013) is a novel acquisition and reconstruction strategy that has shown great potential to simultaneously and efficiently obtain multiple parameter maps including T_1, T_2 and PD. A typical MRF procedure includes the following components: (i) a highly under-sampled dataset acquired with randomized TRs and Flip Angles (FAs) that create temporal and spatial incoherence, (ii) a dictionary containing the signal evolution of relevant T_1 and T_2 values obtained from extended phase graphs (EPG) (Weigel, 2015) or Bloch equation simulations (Ma et al., 2013), and (iii) a dictionary matching process where parameter maps are generated by a pixel-wise template matching between the acquired data and the dictionary.

Since the reconstructed image at each time point in MRF is heavily aliased, the use of a large number of time points (tps) is still needed to

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achieve robust quantification. This can result in relatively long acquisition time, particularly for 3D volumetric imaging. Recent studies that utilized sliding-window (SW) reconstruction (Cao et al., 2016), and sparse and/or low-rank models (Assländer et al., 2017; Davies et al., 2014; Liao et al., 2016; Mazor et al., 2016; Zhao et al., 2017, 2016) can mitigate this aliasing issue, and accelerate 2D MRF acquisition by reducing the number of acquisition time points. On the other hand, applications of Simultaneous Multi-Slice (SMS) to MRF (Jiang et al., 2016; Ye et al., 2016a, 2016b) have also improved the time-efficiency of MRF by simultaneously encoding multiple slices and accelerate the data acquisition process.

A challenge that emerges as the encoding efficiency of MRF improves and the target imaging resolution increases is the limited signal-to-noise ratio (SNR) for high resolution imaging with small voxels. Recent studies (Buonincontri and Sawiak, 2016; Ma et al., 2016b) demonstrated that 3D MRF acquisitions enjoy large SNR efficiency benefit over their 2D MRF counterparts, and could help achieve high SNR at high resolutions. However, high resolution imaging with whole-brain coverage can lead to lengthy scans which effects motion sensitivity of 3D MRF. Unlike 2D MRF, where data for each imaging slice are acquired sequentially each over a short time frame, 3D MRF acquires data for all imaging slices together over the whole acquisition period. This improves SNR efficiency but also increases motion sensitivity. To mitigate the lengthy scans at high resolutions, a recent 3D MRF work (Ma et al., 2016a) utilizes highly under-sampled stack-of-spirals acquisition that combines highly under-sampled variable density spiral with 3 × through-partition acceleration that uniformly under-samples the partitions in an interleaved fashion. This acquisition creates a dataset with incoherent aliasing across the temporal and all spatial dimensions, which can then be reconstructed using standard gridding and dictionary matching approach. Such accelerated acquisition has resulted in a 2.6-min scan time for 1.2 × 1.2 × 5 mm^3 resolution parameter mapping with 12 cm slice coverage.

In this work, we propose an approach to further accelerate 3D stack-of-spiral MRF using a hybrid SW and 3D GRAPPA reconstruction. Here, SW and gridding are used to remove in-plane aliasing and create a Cartesian dataset that is fully sampled in-plane. This then allows a direct application of parallel imaging through Cartesian GRAPPA (Griswold et al., 2002), to resolve k_z under-sampling and create an alias-free SW dataset for the dictionary matching process. We demonstrated that such approach can enable a 3-fold acceleration in the partition direction while reducing the number of required TRs for pattern matching by 3.6-fold (using 420 instead of 1500 TRs as in (Ma et al., 2016a)). Our phantom study demonstrated that the results obtained by the SW + GRAPPA approach are in a good agreement with conventional quantitative methods. The utility of the proposed method is then demonstrated in vivo by both retrospective and prospective under-sampling of stack-of-spirals 3D MRF acquisitions. This allows whole-brain parameter mapping at 1 mm isotropic resolution with a whole brain coverage (260 × 260 × 192 mm^3) in 7.5 min.

2. Methods

2.1. Pulse sequence development

3D slab-selective fast imaging with steady-state precession (FISP) sequence (Jiang et al., 2015; Ma et al., 2016b) and stack-of-spirals acquisition (Thedens et al., 1999) was implemented for MRF. Fig. 1(a) shows the diagram of this partition-by-partition sampled 3D FISP pulse sequence. For each partition, the sequence can be separated into 2 compartments: i) a 5 s FISP acquisition with variable TRs and FA, and ii) a 2 s wait time for signal recovery, which is also being used to efficiently acquire low-flip-angle training data for GRAPPA reconstruction. The total acquisition time for each partition is 7 s. Before acquiring 3D MRF data, a 7-s dummy scan (5-s MRF plus 2-s wait time) was employed to achieve steady-state longitudinal magnetization.

For FISP-MRF acquisition in each partition, a total of 420 time-points were acquired, with the number of time-points chosen based on our previous SW 2D MRF work (Cao et al., 2016). The TRs of the acquisition varied between 12 and 13 ms with a Perlin noise pattern, and the FAs varied sinusoidally from 5° to 80°, as shown in Fig. 1(b) and (c). TE was fixed to 2.7 ms for all time-points. Variable density spiral (VDS) k-space sampling trajectory (Kim et al., 2003), which consisted of 30 interleaves with zero-moment nulling, was utilized for acquisition (Fig. 1 (d)). Interleaves were rotated by 12° for each TR to create full-sampling for every 30 TRs. In each TR, a pair of encoding and rewinder gradients was utilized for slice-encoding at each partition, and a constant dephasing gradient was used to provide a constant phase shift required for the FISP acquisition.

Partition-segmented GRAPPA training data acquisitions were

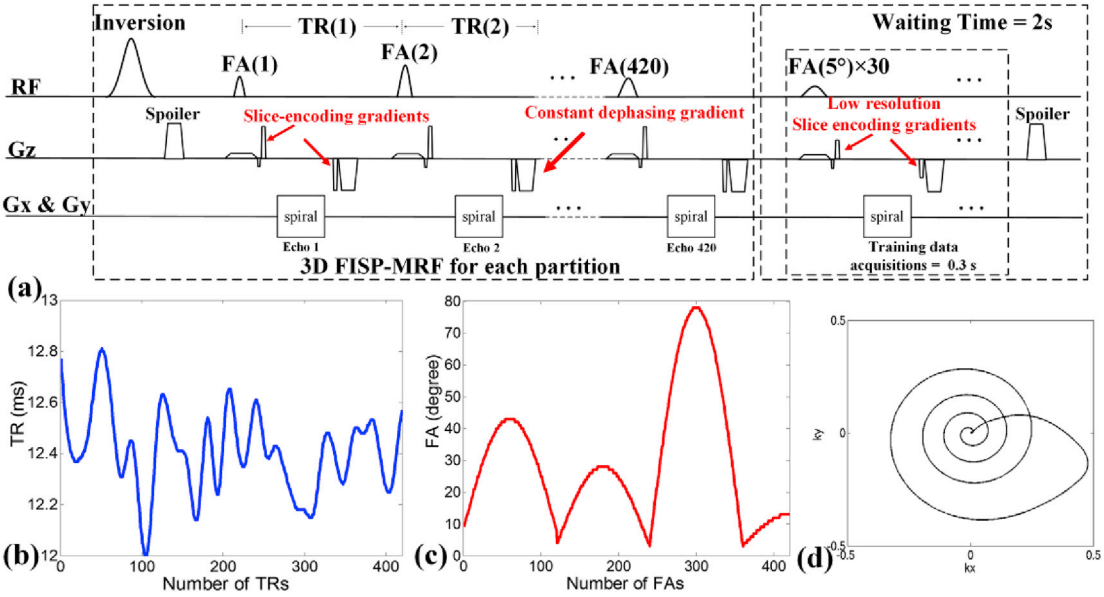

Fig. 1. **(a)** Pulse sequence of 3D-MRF with partition-segmented GRAPPA training data acquisition. The TRs and FAs of 420 time points per each partition are shown in **(b)** and **(c)**, respectively. **(d)** One interleaf of normalized variable density spiral trajectory.