MR Fingerprinting Using FISP

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Target audience: Those interested in developing novel methods in quantitative imaging, pulse sequence design, and fast imaging.

Purpose: The purpose of this work is to achieve rapid quantification of multiple relaxation parameters that is insensitive to main field inhomogneities within MR Fingerprinting (MRF)[1] framework. Previously, both bSSFP and QUEST have been used to demonstrate the efficiency of MRF in estimating multiple relaxation parameters simultaneously[1,2]. Here we demonstrate that similar quantification of T_1 and T_2 is also possible using a sequence with unbalanced gradient moments, which gives the sequence immunity to the B_0 inhomogeneity, and potentially increases the ability to add sensitivity to other parameters such as diffusion and perfusion.

Methods: Inversion Recovery Fast Imaging with Steady State Precession (FISP) with the variable density spiral readout was used in this study. The FISP sequence is similar to FLASH (Fast Low Angle Shot) without the RF spoiling. In this case, only the unbalanced gradient dephases the transverse magnetization. Thus other than T_2 or T_2^* decay, no other mechanism destroys the transverse magnetization in FISP sequence. It is well known in conventional MR that a FISP sequence can generate different contrasts by varying the flip angle and repetition time. To generate unique signal shapes for different tissue types in MRF, the flip angle and repetition time were varied from one TR to the next as shown in Figure 1. With each TR, the unbalanced gradient achieved 2π dephasing within one voxel to make the acquisition insensitive to the inhomogeneous B_0. A variable-density spiral trajectory using minimum-time gradient design[3] was used to acquire the data. The spiral trajectory requires 6 interleaves to fully sample the inner 20x20 region, and 48 interleaves to fully sample the outer 256x256 region of k-space. One spiral interleaf was used in each TR, and the trajectory was rotated by 7.5° every TR. Acquired data were reconstructed using NUFFT[4]. A dictionary containing the signal evolutions with a range of T_1 (10~5000 ms), and T_2 (5~500 ms) was simulated by the extended phase graph (EPG) algorithm[5] using the acquisition parameters shown in Figure. 1. While the Bloch simulation can also be used to calculate the dictionary, EPG provides a faster way to simulate the expected signal without the need to consider multiple spins in a Bloch simulation. All studies were performed on a Siemens Magnetom Skyra 3T (Siemens AG Medical Solutions, Erlangen, Germany) with a 12 channel head receiver array. Data shown here were from an acquisition with 1000 time points, which yield a total acquisition of less than 15 seconds for one slice of 256 x 256 matrix size. A template-matching algorithm was used to extract T_1 and T_2 values by matching a dictionary entry to the acquired signal evolution. To evaluate the performance of MRF-FISP, a phantom study with 10 cylindrical tubes with a wide range of T_1 and T_2 values was performed to compare the result of MRF-FISP to the result of the traditional spin-echo T_1 and T_2 quantification methods. *In vivo* experiments were IRB compliant and performed after informed written consent. The mean values of T_1 and T_2 obtained from white matter (WM), gray matter (GM) were calculated.

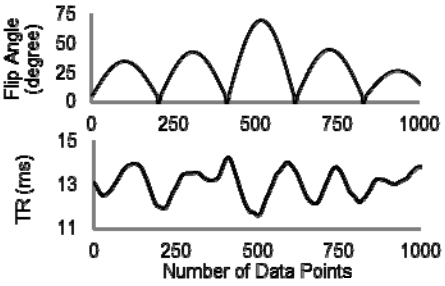

Fig. 1. An example of varied flip angles (0~75°), repetition times (11.5~14.5ms) used in the FISP-based MRF sequence.

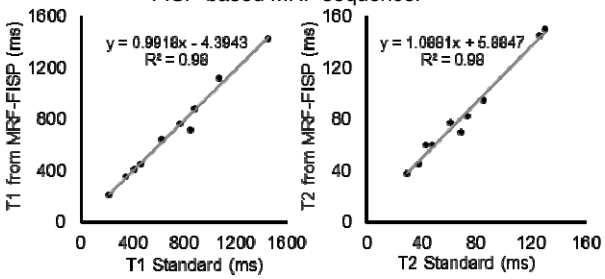

Fig. 2. The comparison of T_1 (left) and T_2 (right) values obtained from MRF-FISP and the spin-echo methods.

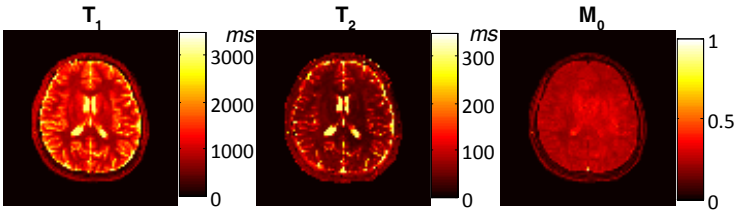

Fig. 3. T_1, T_2 and M_0 maps from human brain. T_1 and T_2 values of WM and GM are in good agreement with literature values.

Results: Figure 2 shows T_1 and T_2 values from the phantom compared to the values from the spin-echo methods. It demonstrates that MRF-FISP is in good agreement with the gold standard conventional measurements. Figure 3 shows T_1, T_2 and M_0 maps generated for an asymptomatic volunteer. The mean values of T_1 and T_2 from WM and GM are in good agreement with the literature results[6]. Figure 4 shows the estimates of T_1 and T_2 and their standard deviations for each phantom as a function of the acquisition time. With the new information added in the acquisition, MRF-FISP generated lower error with increasing acquisition time.

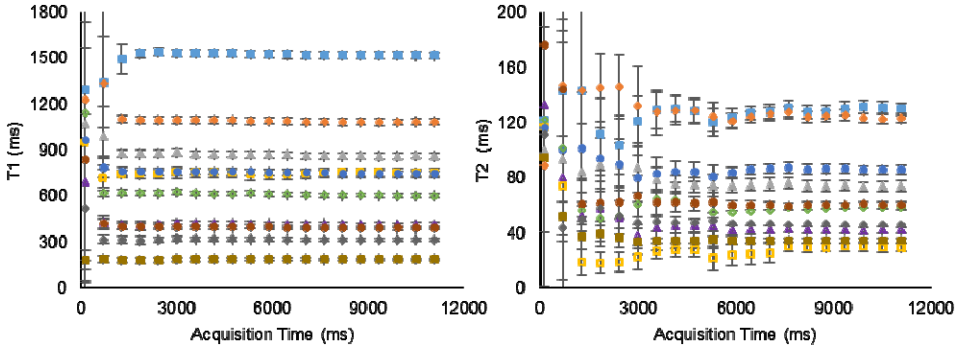

Fig. 4. Estimated T_1 and T_2 values with the standard deviations of the phantom with increasing the acquisition time in MRF-FISP acquisition. Different color represents different cylindrical phantom.

Discussion: We demonstrate an MRF acquisition with an unbalanced gradient sequence that gives accurate quantification of the relaxation parameters. With the unbalanced gradient, the sequence is less sensitive to B_0 inhomogeneities, which would help the extension of MRF applications in other organs and higher fields where obtaining a homogeneous B_0 is a challenge. It also has the potential to extend the quantification to other important parameters, such as diffusion, perfusion.

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References: 1. Ma D et al. *Nature.* 2013;495(7440):187–92. 2. Jiang Y et al. *ISMRM 2013*, prog#19. 3. Lee JH et al. *Magn. Reson. Med.* 2003;50(6):1276–85. 4. Fessler JA, Sutton BP. *IEEE Trans. Signal Process.* 2003;51(2):560–574. 5. Hennig J. *Concepts Magn. Reson.* 1991;3(3):125–143. 6. Stanisz GJ et al. *Magn. Reson. Med.* 2005;54(3):507–12.