MR Fingerprinting: Rapid Simultaneous Quantification of T1, T2, Proton Density and Off-resonance using a Spiral Trajectory

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Target audience: For those who are interested in quantitative imaging, pulse sequence design and fast imaging.

Purpose: The goal of this study is to rapidly and accurately quantify multiple relaxation parameters using MR Fingerprinting (MRF) in a short acquisition time. MRF is a novel approach that permits quantification of multiple important properties of a material or tissue simultaneously. In MRF, there is no a priori required shape of the signal evolution. The only desired properties of the signal are temporal and spatial incoherence. Once this is established, the signal evolutions from different materials or tissue types can be differentiated using pattern recognition algorithms. Previously, variations in sequence parameters such as flip angle (FA) and TR, during acquisition have been used to make the signal evolution temporally incoherent [1]. This study uses a rapid spiral sampling pattern in each acquisition block to improve the spatial incoherence. The interaction between these two properties provides new opportunities to accelerate image acquisition through rejection of under-sampling errors.

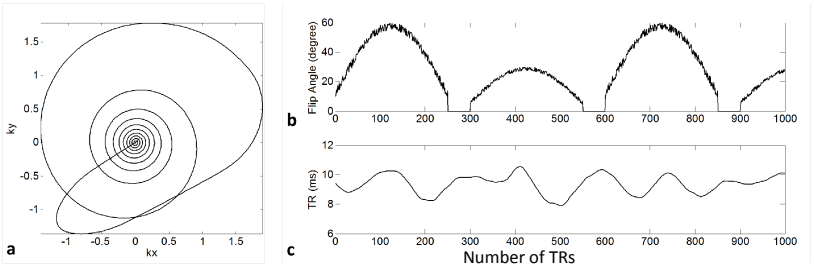

Figure 1: (a) One variable density spiral trajectory was used per TR of the MRF sequence. Flip angle (b) and TR(c) were also changed from one TR to the next.

Methods: The MRF acquisition based on an inversion recovery balanced steady state free precession (IR-bSSFP) sequence was employed. As shown in Figure 1, one variable density spiral trajectory with 5.8ms readout time was used in each acquisition block (or TR). The spiral trajectory was designed to have zero and first moment gradient compensation using minimum-time gradient design[2]. The spiral trajectory was rotated by 7.5° from one TR to the next, so that each image has a slightly different spatial encoding. This variable density trajectory requires one interleaf to sample the inner 10x10 region, while 48 interleaves are required to fully sample the outer portions of k-space. The flip angle (range 5 to 60 degree), RF phase (0° and 180°) and TR (range 7.9 to 10.8ms) were also changed from one TR to next as shown in Figure 1. Highly undersampled images were reconstructed using NUFFT, and the signal evolutions from these images were used directly to quantify T_1, T_2, M_0 and off-resonance simultaneously. Signal time courses with different sets of T_1, T_2 and off-resonance values were simulated through Bloch simulation using the above acquisition parameters and stored in a dictionary. The range of T_1 and T_2 was chosen to lie in physiologically encountered ranges: T_1 between 50 and 5000 ms, T_2 between 20 and 2000 ms and off-resonance between -300 and 300 Hz with variable step sizes. A total of 296,904 dictionary entries were generated in 195 seconds on a standard desktop computer. One dictionary entry was selected for each measured pixel location using Orthogonal Matching Pursuit (OMP)[3]. The proton density (M_0) of each pixel was calculated as the scaling factor between the measured signal and the simulated time course from the dictionary. A square field of view of 300x300 mm^2 was covered with a matrix of 128x128 pixels, yielding a total time of about 9 seconds for the complete acquisition of 1000 time points, where each time point was reconstructed from a single spiral interleaf. In vivo experiments were performed in compliance with the IRB. White matter (WM), gray matter (GM) and cerebrospinal fluid (CSF) regions of interest (ROI) were then selected from the resultant maps. The mean values of T1 and T2 obtained from each region were calculated and compared with literature values. All studies were performed at 1.5T scanner (Siemens Espree) with a 32 channel head receiver array.

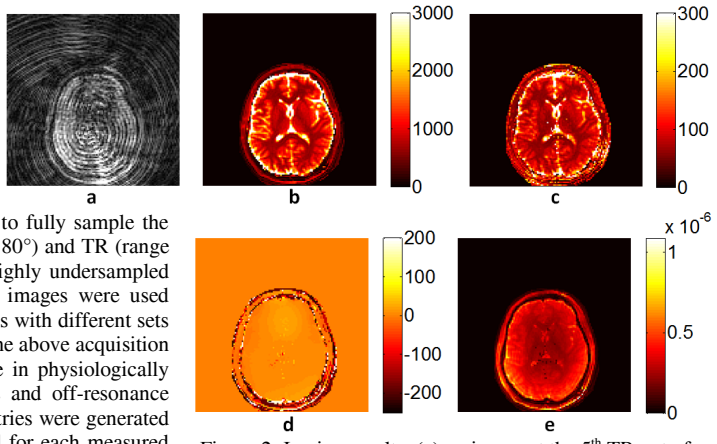

Figure 2: In vivo results: (a) an image at the 5th TR out of 1000 was reconstructed from only one spiral readout demonstrating the errors from under-sampling. The T_1 (b), T_2 (c), M_0 off-resonance (d) and M0 (e) maps show a near compete rejection of these errors.

	T1 (ms)	T2 (ms)
WM	685±33	65±4
Previously Reported	608~756	54~81
GM	1180±104	97±5.9
Previously Reported	998~1304	78~98
CSF	4880±379	550±251
Previously Reported	4103~ 5400	1800~2460

Table 1: In vivo data: Comparison of MRF results and reference values on different brain regions

Results: Figure 2 shows four maps generated from an in vivo experiment. One of the reconstructed images from highly undersampled data is also shown to demonstrate severe undersampling errors in the individual time frames of the acquisition. The mean values of T1 and T2 from three typical regions in the brain are listed in the Table 1 and are in good agreement with the literature [4-5].

Discussion: Spiral sampling allows higher acceleration factors compared with Cartesian sampling while maintaining SNR and make aliasing artifacts largely incoherent with the signal. The key assumption underlying the MRF concept is that one can generate incoherent signal evolutions from each different materials or tissues using an appropriate acquisition scheme. These unique signal evolutions can be matched to theoretical signal evolutions and subsequently yield underlying quantitative information. Pattern recognition is a probabilistic process, and the form of all predicted signal evolution is known. Therefore, as long as the errors during acquisition do not cause another fingerprint to become the most likely match, the correct quantitative identification will still be made. This concept allows MRF to generate quantitative maps even in the presence of dramatic undersampling.

Conclusion: The interaction of spatial and temporal incoherence greatly improves the acquisition efficiency of the MRF performance. A single-shot spiral acquisition allows quantitation of four parameters simultaneously within 10 seconds per slice. Further improvements are expected through the combination of MRF and parallel imaging methods, which have not been included up to this point.

Reference: [1] D.Ma et al. ISMRM2012, p. 288. [2] B.A.Hargreaves, [Online]. Available: http://www-mrsrl.stanford.edu/~brian/mintgrad/.
[3] M.Doneva, Magn Reson Med. 2010, 64:1114-1120. [4]J.Vymazal et al. Radiology. 1999, 2:489-495. [5]S.Deoni et al. Magn Reson Med. 2005, 53:237-241

Acknowledgement: The authors would like to acknowledge funding from Siemens Medical Solutions and NIH grants 5R01HL094557 and R00EB011527.