MR Fingerprinting (MRF): a Novel Quantitative Approach to MRI

Introduction: Conventional MRI attempts to generate pure "weighted" images that depend only on one or two parameters of interest. Much of the MR pulse sequence development at ISMRM is directed at generating a constant signal level over time to acquire a weighted image as quickly as possible, It is well known that this is difficult to achieve (e.g. pure T2 weighting in a fast spin echo sequence) and is limited in the presence of motion or phase changes. Here we propose a new concept for MRI based on recent advances in Compressed Sensing which we call MR fingerprinting (MRF). MRF is based on a change in perspective: instead of providing a constant signal level over time, we use a sequence that attempts to generate a different signal evolution for each tissue with different relaxation parameters. We then use a pattern recognition based reconstruction to derive quantitative estimates of the underlying relaxation parameters. This is analogous to matching fingerprints (MR signal) to a database (dictionary), and by extension retrieving a host of additional personal information such as identity, address, phone number, etc. (T_1, T_2, diffusion coefficient, etc.). Here we show that these estimates are independent of B_0 and B_1 variations using a sequence with very low SAR. We initially demonstrate this MRF concept by generating quantitative MR images in a clinically feasible time.

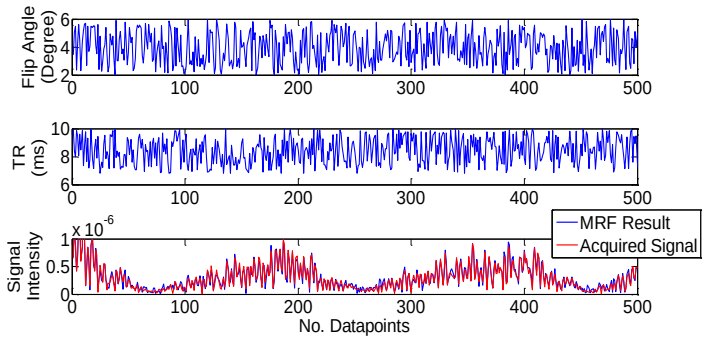

Figure 1: Flip angle (a) and TR (b) were randomly varied from one TR to the next in random the TrueFISP sequence. An example time course (c) from reconstructed images shows oscillating signal evolution.

Methods: The goal of an MRF sequence is to provide a unique signal evolution in each tissue type by varying the basic sequence parameters. One example of this type of sequence is to use random TrueFISP, which was chosen for the first demonstration of MRF due to extensive existing knowledge about the evolution of the TrueFISP signal evolution. Figure 1 demonstrates a sequence where 500 data points for each pixel were acquired. For each data point, we randomly varied the TR (range: 6.8-10ms) and flip angle (range: 2-6 degrees), and an inversion pulse was added every 200 TRs. Using such a sequence, the signal varies wildly from one TR to the next (see Figure 1C). To determine the relaxation parameters, pattern recognition of the signal time course is completed using Orthogonal Matching Pursuit (OMP) [2,3], which can resolve the correct signal and obtain multiple parameters simultaneously. OMP involves building a dictionary that contains all expected signal evolutions based on the designed sequence parameters (TR, TE, flip angle, B_0) by using a Bloch simulation. This method was evaluated in a phantom study, where 10 cylindrical phantoms constructed with varying concentrations of $GdCl_3$ (Aldrich) and agarose (Sigma) to yield T_1 and T_2 values ranging from 67 to 1700 ms and 30 to 300 ms, respectively. The phantom was scanned using a 1.5T Siemens Espree (Siemens Medical Solutions). Around 15000 characteristic parameter sets (T_1 from 50 to 2000 ms, T_2 from 20 to 400 ms, and off-resonance from -40 to 40Hz) were used to simulate possible signal time courses using Bloch simulations of the spin evolution, and were stored in the dictionary. OMP was then used to select the elements from the dictionary that best represent the acquired signals, yielding the corresponding T_1, T_2, proton density, and off-resonance maps. As a gold standard comparison, a standard spin-echo sequence was performed to quantify T_1 and T_2 separately (T_1 quantification: 13 TRs ranging from 50 to 5000ms, TE = 8.5 ms; T_2 quantification: 15 echoes with TE=15-225 ms with 15ms increment). T_1 and T_2 maps of the spin echo sequences were obtained by fitting the time courses on a pixel-by-pixel basis using a three-parameter nonlinear least squares fit. Square regions of interest (ROI) were chosen from each of the cylinders and the mean MRF values were compared with the values from the standard measurements.

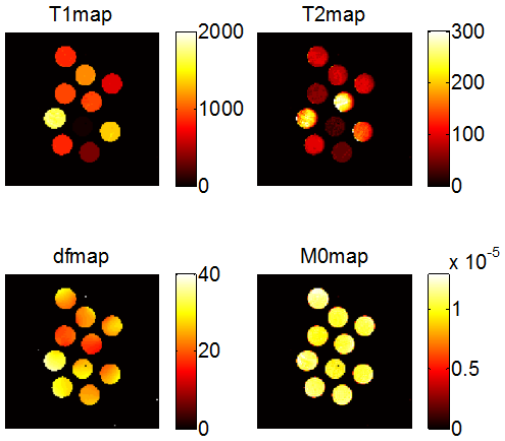

Figure 2: T_1, T_2, M_0 and off-resonance maps generated from the MRF phantom experiment.

Results and Discussion: Figure 1C shows the signal time course from one pixel of the reconstructed MRF series and its corresponding dictionary match. The T_1, T_2, M_0, and off-resonance maps generated from MRF are shown in Figure 2. In Figure 3, T_1 and T_2 values obtained from MRF methods are compared with the values from standard spin-echo sequence measurements. As can be seen in Figure 3, Both T_1 and T_2 values are in good agreement with the traditional measurement even though the MRF sequence used only very low flip angles. In addition, we simultaneously obtained a map of off-resonance. The concept of MRF uses a completely different approach to experimental design in MRI, where the sequence design is optimized not towards yielding individual images with various weightings, but rather towards generating unique signal timecourses that can be matched with a compressed sensing approach to the corresponding parameters to yield the underlying tissue parameters. The method is robust as long as the designed sequence provides unique signal evolution curves for different tissues, and the chosen reconstruction method is able to generate the required parameter maps. In addition, because a single preparation is avoided, the equilibrium signal state is never reached, which allows for continuous scanning to assess measure multiple parameters at once. Also, since the reconstruction is probabilistic, MRF may be less susceptible to motion. The presented sequence design is but one of the infinite sequence designs possible and to be explored, that could yield quantification of any of the various parameters which affect the MR signal without errors due to B_0, B_1 and other effects.

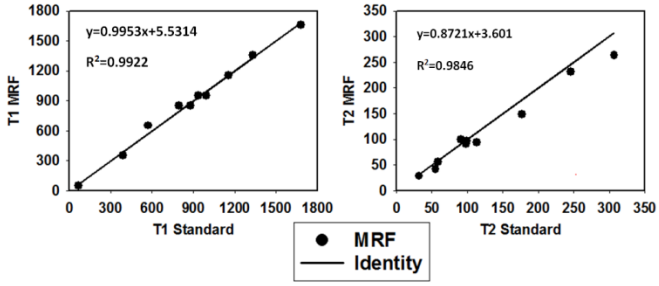

Figure 3: T_1 (left) and T_2 (right) values from MRF are compared with values measured from standard spin-echo sequences

Reference: [1] Schmitt et al. Magn Reson Med. 2004, 51:661-667; [2] Tropp J el al. IEEE Trans Inf Theory 2007, 53:4655-4666. [3]Doneva et al. Magn Reson Med. 2010, 64:1114-1120. **Acknowledgements**: The authors would like to acknowledge funding from Siemens Medical Solutions and NIH grants 1RO1HL094557, 5K99EB011527, and 1KL2RR024990.