Pulse Sequence Optimization for Improved MRF Scan Efficiency

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TARGET AUDIENCE: Clinicians and MR scientists interested in quantitative parameter mapping and Magnetic Resonance Fingerprinting.

PURPOSE: To introduce a flexible framework for efficient MR Fingerprinting (MRF) pulse sequence design. Previous work has shown that MRF can map several parameters simultaneously including T_1, T_2, and spin density[1,2]. However, not all sequences are equally effective at encoding unique signal evolutions over time. Additionally, specific sequences may be better suited for certain expected parameter ranges or sampling patterns. This work introduces a flexible framework for pulse sequence optimization that can be applied to any MRF scan, including highly undersampled acquisitions, by simulating the MRI signal encoding, gridding, and pattern recognition directly in the optimization. The method was validated in a phantom study by designing a sequence for mapping T_1, T_2, and M_0 in under 3s. **METHODS:** The goal of this sequence design framework was to optimally select the varied sequence parameters (250 flip angles and TRs) for MRF with a FISP-based readout[2]. The optimization used a genetic algorithm to select sequence parameters using a cost function that minimized error in parameter quantification during a simulated MRF experiment. Thus, a numerical phantom was generated with physiological T_1 (300-2500ms) and T_2 (20-150ms) values for the optimization algorithm. MRI signal encoding and gridding was performed on each iteration of the optimization. The phantom was sampled along one interleaf of a variable density spiral (acceleration factor R=48) that was rotated with each successive image, and images were gridded using the NUFFT[4]. The dictionary was created using a Bloch simulation, and the signal time course from each pixel was matched to the dictionary. The sum of the mean relative errors in the estimated T_1 and T_2 maps was used as the cost function. The optimization consisted of a two-step process. The purpose of Step 1 was to find a suitable initial guess. In this step, the sequence was initialized with pseudorandom TRs and flip angles created by a Perlin noise function[5]. An inversion pulse with T_I=20.64ms was inserted before the first readout to improve T_1 sensitivity. The genetic algorithm in MATLAB was used to choose parameters defining the Perlin distribution that yielded an improved set of TRs and flip angles. Specifically, three variables were used that controlled the degree of interpolation, the number of octaves, and the duration of relaxation pauses with no RF excitation. Once suitable starting parameters were found, the sequence was refined in Step 2 where the individual flip angles, TRs, and the T_I were optimized as independent variables in the genetic algorithm. The random initial guess and the final optimized sequence are shown in Figure 1 along with the first 250 parameters of the original unoptimized MRF sequence presented in [2]. A phantom containing T_1 and T_2 values known from a spin echo experiment was imaged on a 3T scanner with a 16-channel brain coil using MRF with (1) random TRs and flip angles, (2) the original MRF sequence from [2], and (3) the optimized MRF sequence. **RESULTS:** Images from the phantom study are shown in Figure 2. The sequence with randomly chosen flip angles and TRs produced artifacts in the T_1, T_2, and M_0 maps due to undersampling and failed pattern matching. The original MRF sequence produced an accurate T_1 map but artifacts in the T_2 map, which was expected since the original sequence was not optimized for such a short scan time. The highest quality T_1, T_2, and M_0 maps were obtained with the optimized sequence. Figure 3 compares the T_1 and T_2 measurements obtained by MRF with those from spin echo. Both the conventional unoptimized and the optimized MRF sequences resulted in T_1 values that were highly correlated with the standard values ($R^2 > 0.99$). The T_2 measurements from the optimized sequence were much closer to the standard values ($R^2 = 0.99$) compared to the unoptimized sequence ($R^2 = 0.76$). **DISCUSSION:** The results indicate that pulse sequence optimization can reduce scan time for MRF by reducing errors in parameter quantification. By increasing the encoding efficiency, shorter signal evolutions are required for accurate parameter mapping, which may be especially useful in applications which require a reduced scan time. The optimization framework is flexible and easily generalized to other MRF sequence types, and could be used to increase the sensitivity of MRF to additional tissue properties. Different digital phantoms can be used to tailor the sequence for different applications, other k-space sampling patterns or acceleration factors can be employed, or new cost functions can be used to more heavily weight T_1 or T_2 or to include additional parameters. **CONCLUSION:** A general method for optimizing MRF pulse sequences has been introduced. The method was validated by improving scan efficiency for mapping T_1, T_2, and M_0 within 3s.

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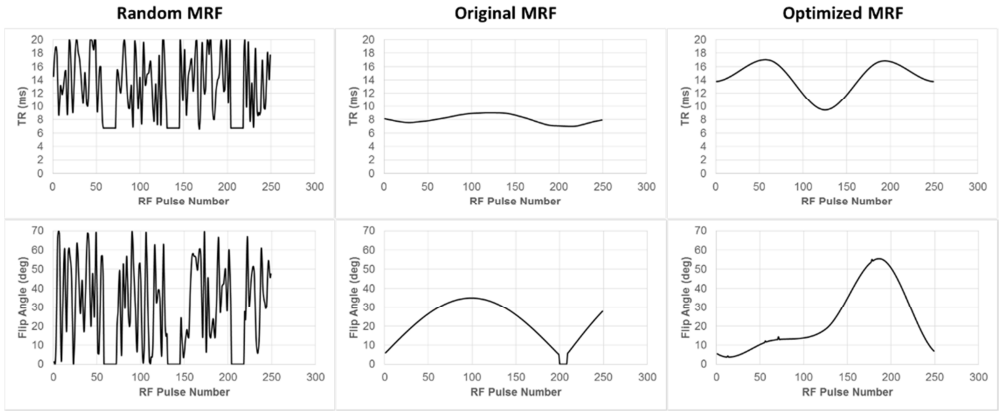

***Figure 1**. Flip angles and repetition times are shown for the random initial sequence, original MRF sequence, and optimized MRF sequence.*

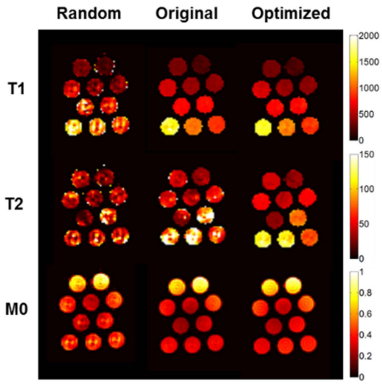

***Figure 2**. T_1, T_2, and M_0 maps acquired using the random, original, and optimized MRF sequences.*

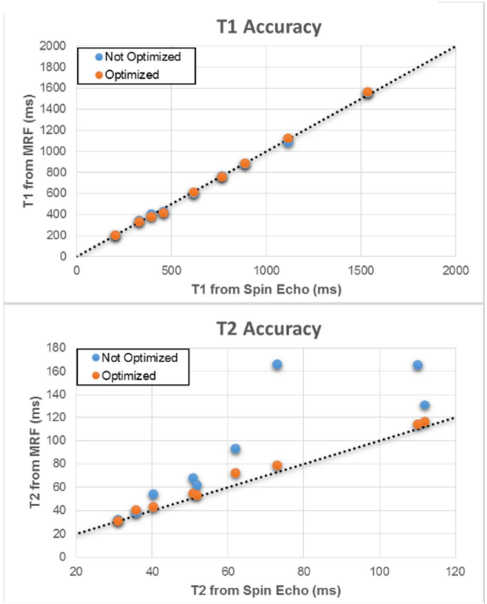

***Figure 3**. T_1 and T_2 measurements from the original and optimized MRF sequences are compared with standard values from a spin echo experiment.*