Optimization of acquisition parameters for Magnetic Resonance Fingerprinting

Amaresha Shridhar Konar[1], Rashmi R Rao[1], Shaik Imam[1], Shivaprasad Chikop[1], Sachin Anchan[1], and Sairam Geethanath[1]
[1]*Medical Imaging Research Center, Dayananda Sagar College of Engineering, Bangalore, Karnataka, India*

Target Audience: The current work is relevant to researchers working in the MR community mainly interested in exploring MRF and its applications.

Introduction: Magnetic Resonance Fingerprinting (MRF) is a novel framework that provides simultaneous quantitative MR multi- parametric maps. MRF reduces scan time by generating unique signal observations for different tissue types of the brain such as White Matter (WM), Gray Matter (GM) and Cerebrospinal Fluid (CSF) from signal evolutions obtained through pseudorandomized combinations of Repetition Time (TR) and Flip Angle/Alpha (FA/∝) [1]. Thousand measurements were used to generate the characteristic signal observations in ref [1]. The purpose of this work is to reduce the number of TR/FA combinations and to determine their optimal combinations required to generate MR parametric maps.

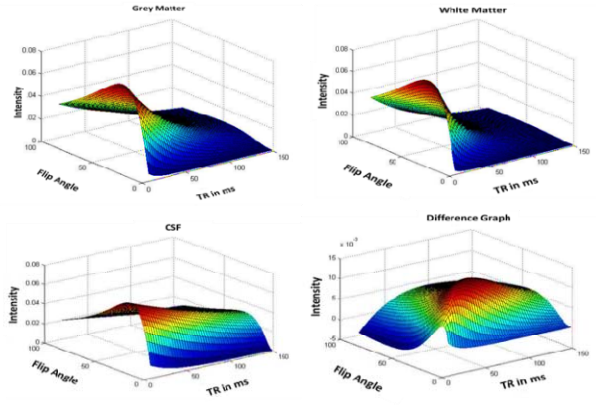

Figure 1: 3D plot showing signal intensity for a) Grey matter, b) White matter c) CSF and d) difference plot for Grey matter and White matter

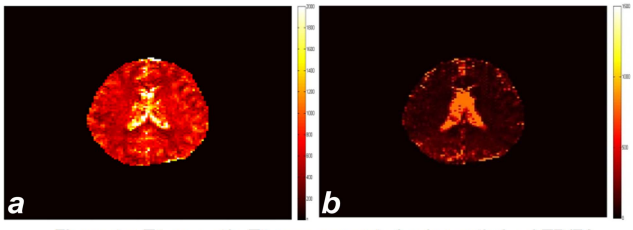

Figure 1a: T1 map, 1b: T2 map generated using optimized TR/FA

Tissue Type	T_1	T_2
CSF	4780±367	2165±58
Previously Reported	4103-5400	1800-2460
White Matter	546±63	66±7
Previously Reported	608-756	54-81
Gray Matter	1086±71	95±9
Previously Reported	998-1304	78-98

Table 1: T_1 and T_2 values obtained from MR parametric maps generated using optimized TR/FA and previously reported values for the same

Theory: Mirrored Fast Imaging with Steady State Free Precession (Mirrored FISP) or PSIF is a sequence with significantly short acquisition time and is tolerant to T_2^* effects. Echo intensities for PSIF sequence can be calculated using eq. (1) and eq. (2) $S_{echo} = M_0 \tan\frac{\propto}{2}[1 - r(1 - E_1 Cos \propto)]$ (1) where $r = \sqrt{\frac{1-E_2^2}{1-E_1^2E_2^2-2E_1(1-E_2^2)Cos\propto+(E_1^2-E_2^2)Cos^2\propto}}$ (2), where α is flip angle, E_1 and E_2 are longitudinal and transverse relaxation times given by $E_1 = e^{-TR/T1}$ and $E_2 = e^{-TR/T2}$, M_0 is equilibrium magnetization and S_{echo} is the echo intensity [2]. Minimum number of TR/FA combinations can be determined by sample size analysis.

Methods: PSIF sequence was used to generate 3D signal intensity plots for WM, GM, CSF and a plot for the difference between GM and WM were generated using eq. (1) and eq. (2). Values of FA were chosen to be varying from 2^0 to 90^0 and TR values varying from 10ms to 90ms. The signal intensity graph for the difference between GM and WM was calculated since the T_1 and T_2 values for GM and WM are very close and hence to enable maximum differentiation between these tissue types. Power and Sample size (PS) software was used to optimize the number of TR/ FA combinations to be used to obtain MR parametric maps. The statistical model was built to obtain sample space and the parameters with alpha as 0.05, expected power was assumed to be 0.8, mean and standard deviation for corresponding T_1 and T_2 values of GM and WM were taken from [1]. The values which were obtained to be 48 combinations of TR/FA were chosen from the difference 3D plot to achieve high Contrast to Noise Ratio (CNR). By applying a threshold to the difference plot, maximum values were obtained. 6 datasets with 48 images of the brain were acquired on a Siemens 1.5T Avanto scanner using PSIF sequence with minimum Evolution Time (min TE) and TR/FA values as mentioned above. The total acquisition time was five minutes for each dataset; GRAPPA and Partial Fourier were not used during data acquisition. The acquired signal observations and simulated signals were normalized and matched using a vector dot product to obtain MR parametric maps. The simulation of PSIF sequence for the dictionary was performed using the analytical eq. (1). The dictionary was built for values of T_1 in the range between 300ms and 500ms (in increments of 10ms) and T_2 values were included in the range between 50ms and 2200ms (in increments of 20ms) and this dictionary included a total of 50,976 entries. The T_1 and T_2 maps generated are shown in Figure 2.

Results: The 3D plots for GM, WM, CSF and the difference plot generated are as shown in Figure 1. The MR parametric maps (T_1 and T_2) obtained by pattern matching of the acquired signal observations with the simulated dictionary are shown in Figure 2. Mean and Standard deviation of T_1 and T_2 values for WM, GM, and CSF were calculated and tabulated as shown in Table 1. It can be observed that the values obtained lie in the range of previously reported values.

Discussion and Conclusion: Current work demonstrates that the minimum number of TR/FA combinations required to differentiate between WM and GM tissue types is 48. This reduces the number of measurements to 48 as compared to 1000 measurements reported in [1]. It has also been demonstrated that the values of these TR/FA yield MR parametric maps with acceptable CNR. It can be observed that in order to reduce acquisition time, TR/FA combinations can be chosen for minimum values of TR from the 3D plots. Also to obtain MR parametric maps with acceptable SNR can be obtained by choosing TR/FA combinations from the corresponding 3D plots GM, WM, CSF. It must also be noted that acceleration schemes such as Parallel Imaging (PI) and Partial Fourier have not been employed and inclusion of such techniques would significantly reduce acquisition time.

References: [1] Dan Ma et al., Nature 2013; 495(7440):187–92, [2] Hanicke W et al., Magnetic Resonance in Medicine, 2002, 10-2357, [3] http://biostat.mc.vanderbilt.edu/wiki/Main/PowerSampleSize