Plug-n-Play Magnetic Resonance Fingerprinting (PnP- MRF)

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Target Audience: MR researchers interested in relaxometry and further applications.

Introduction: Magnetic Resonance Fingerprinting (MRF) is a recently reported strategy to generate quantitative MR multi-parametric maps simultaneously [1]. MRF significantly reduces MR acquisition time for generating quantitative maps by using pseudorandom Repetition Time (TR) and Flip Angle (FA) combinations, thus generating unique signal evolutions for each tissue type for organs such as brain. The current work PnP MRF is a novel technique which is based on MRF and provides an opportunity to MR researchers who do not have access to pulse sequence designing to use this comprehensive framework on clinical scanner using readily available pulse sequence. The other utility of the proposed scheme is the fast simulation of the signal evolution using analytical equation which is required to build the dictionary, only with a minimum of forty eight observations. **Theory:** Mirrored Fast Imaging with Steady State Free Precession (Mirrored FISP) or PSIF is a Steady State Free Precession (SSFP) sequence with significantly short acquisition time and it is tolerant to T_2^* effects. The echo intensity of PSIF sequence can be obtained using analytical equations $S_{echo} = M_0 \tan\frac{\propto}{2}[1 - r(1 - E_1 Cos \propto)]$ 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], and α is flip angle, E_1 and E_2 are longitudinal and transverse relaxation times given by $E_1 = e^{\frac{-TR}{T1}}$ ms and $E_2 = e^{\frac{-TR}{T2}}$ ms respectively, M_0 is equilibrium magnetisation and S_{echo} is the echo intensity. 3D plots were generated for tissue types of organ such as brain for contrast as a function of TR/FA combination, a difference plot was generated to pick forty eight optimised TR/FA combinations. PnP MRF formulation also lends itself with both Bloch and EPG simulations. **Methods:** PSIF sequence was simulated using above mentioned analytical equation with ranges of FA and TR values varying from 31° to 68° and 11 ms to 13 ms respectively. A data driven model was built by considering ranges of TR/FA and tissue contrast between Grey Matter (GM), White Matter (WM) and Cerebrospinal Fluid (CSF). 3D plots were generated for different T_1 and T_2 values of brain tissues using a range of TR and FA combinations, ranges of TR and FA were taken between 0 to 100 ms and 0° to 90° respectively. A difference plot was generated for GM and WM for tissue contrast as a function of TR/FA combinations and the difference plot was used to pick forty eight optimum TR/FA combinations. TR/FA combinations were extracted from the plot by thresholding the difference plot to achieve optimum contrast to noise ratio (CNR). A dictionary was generated for different TR/FA combinations taken from data driven model for a range of T_1 and T_2 values, T_1 ranged between 300 and 5000 ms and T_2 ranged between 50 and 2200 ms. Six datasets each with forty eight MR brain images were acquired on Siemens Avanto 1.5T scanner using PSIF sequence with random FA and TR values, with ranges of FA and TR values varying from 31° to 68° and 11 ms to 13 ms respectively and minimum Echo Time (min TE) acquisition was performed which resulted in for a total acquisition time of five minutes for each dataset. Each entry in dictionary was used to match with the acquired signal evolution from the scanned data to localise different brain tissues and hence to obtain parametric maps for the same. The matching was performed by vector dot product between the acquired signal evolution from the scanner and all the dictionary entries and maximum value of the dot product was considered as the optimal match. **Results:** Data driven model was simulated for contrast of GM, WM and CSF as a function of TR/FA to obtain 3D plot as shown in Figure-1a, b and c respectively. Contrast between GM and WM as a function of TR/FA was simulated to obtain optimum combination of TR/FA as shown in Figure-1d. The acquired signal evolution curve for the TR and FA combinations and its corresponding match with the dictionary can be seen in Figure-2 and they match well with significantly small standard deviation. The MRF generated T_1 and T_2 maps for brain tissues are as shown in Figure-3. The T_1 and T_2 values for different brain tissues generated using MRF are in close agreement with previously reported ranges as can been seen from Table-1. **Discussion and Conclusion:** PnP MRF for the first time implements MRF using clinical scanner which do not have access to pulse sequence designing based on the data driven model. PnP MRF provides opportunity to MR researchers who do not have access to pulse sequence designing to use comprehensive framework like MRF on clinical scanner using readily available pulse sequence. Optimisation of PnP MRF has been achieved by choosing the optimum acquisition parameter to attain maximum contrast between GM and WM. Also the optimisation has been achieved with respect to number of MR images required. **Future works:** PnP MRF has been implemented using readily available PSIF sequence alone (no GRAPPA, no Partial Fourier) and significant optimisation in scan time can be achieved by making use of GRAPPA and partial Fourier acquisition. Radiologists are accustomed to read T_1, T_2 and Proton Density weighted images and as a future work PnP MRF can be modelled to obtain such images in addition to parametric images. **References:** [1] Ma D et al. *Nature*. 2013; 495(7440):187–92. [2] Hanicke W et al. *Magn. Reson. Med*. 2002; 10:2357.

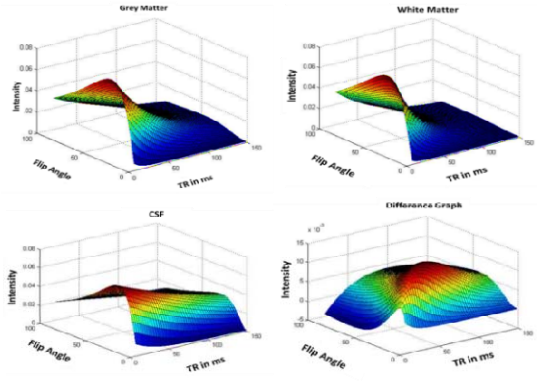

Figure-1: 3D plot showing signal intensity for a) Grey matter, b) White matter c) CSF and d) difference plot for Grey matter and White matter

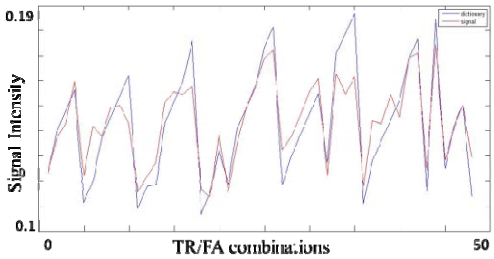

Figure-2: Acquired signal evolution for different TR/FA combinations and its match obtained from dictionary

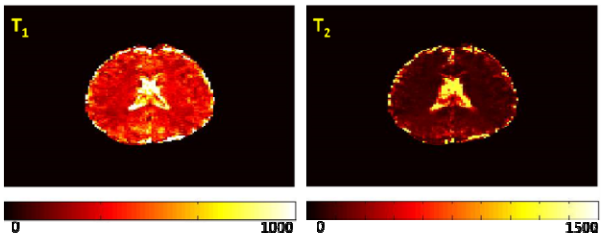

Figure-3: T_1 map and d) T_2 map generated using PnP MRF

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 PnP MRF and previously reported values for the tissue types of brain