LOWER BOUND SIGNAL-TO-NOISE RATIOS AND SAMPLING DURATIONS FOR ACCURATE AND PRECISE T1 AND T2 MAPPING WITH MAGNETIC RESONANCE FINGERPRINTING

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Introduction: Magnetic resonance fingerprinting (MRF)[1] is a new technique for quantitatively characterizing multiple tissue parameters. MRF generates a unique signal evolution for each tissue by pseudo-randomly varying the acquisition parameters hundreds of times[1]. Recent studies have successfully shown its high accuracy for measuring tissues parameters, but the acquisition conditions may require a large number of consecutive TRs (N_{TR}, i.e. single-shot images). Furthermore, the accuracy and precision of MRF have not been fully investigated over a wide range of signal-to-noise ratios (SNR). The ***objective*** of this study was to provide a lower-bound SNR and N_{TR} required to maintain high precision and accuracy for both T_1 and T_2 measurements by MRF using Bloch equation simulations[2].

Methods: *Dictionary Design* – Based on the pseudorandom inversion recovery balanced steady-state free precession (pIR-bSSFP) sequence and a quasi-sinusoidal flip angle (FA) scheme proposed by Ma *et al.*[1] a dictionary was built to contain signal evolutions with a range of T_1 (100ms to 3000ms, 10ms step) and T_2 (10ms to 300ms, 5ms step) using Bloch equation simulations . We investigated the accuracy and precision of T_1 and T_2 estimates by MRF for a range of tissues ($T_{1,True}$ from 250ms to 2801ms, 150ms steps; $T_{2,True}$ from 46ms to 246ms, 30ms steps) over a range of SNRs (SNR=[5,10,15,30]) with a different number of consecutive TRs, N_{TR}=[100,150, 250, 400, 500]. *Noise Simulations* – The pIR-bSSFP signal, S(t), was simulated for each tissue under the assumption of perfect signal sampling (no motion, flow, off-resonance, B_1 inhomogeneity or undersampling artifacts). Complex Gaussian white noise was added to the simulated signals to generate noisy signals. The standard deviation (σ) of the real and imaginary components of the noise was controlled by fixing the SNR then scaling each S(t) such that SNR=mean(S(t))/($\sqrt{2}\sigma$). This method maintains a constant SNR across all tissue types, rather than a constant noise level. A template-matching algorithm was used to find the dictionary signal with the highest dot product value and the corresponding estimated T_1 and T_2 values ($T_{i,MRF}$). This process of adding noise and template matching was repeated 250 times for each tissue to generate statistics about the T_1 and T_2 estimates over a range of SNR and N_{TR}. A total of 990,000 signals were simulated. The histograms of the T_1 and T_2 estimates were used to calculate the ***accuracy*** ($T_{i,Bias}$=median($T_{i,MRF}$)-$T_{i,True,}$ i=[1,2]) and ***precision*** ($T_{i,95\%-CI}$) for each tissue. These results were then used to define the lower bound SNR and N_{TR} required to maintain ***high normalized accuracy*** ($T_{i,Bias}/T_i \leq 5\%$) and ***high normalized precision*** ($\frac{1}{2} \cdot T_{i,95\%-CI}/\text{median}(T_i) \leq 10\%$). Subtracting the accuracy (Δ***bias***) and precision (Δ***precision***) T_2 maps from the T_1 maps compared T_1 and T_2 estimates for each sampling condition.

Results: Figure 1 shows the normalized accuracy maps and Figure 2 shows the normalized precision maps for the T_1 and T_2 estimates for a subset of the simulated conditions. To achieve ***high normalized accuracy for T_1-mapping*** SNR≥10 and N_{TR}≥100 (or SNR≥5 and N_{TR}≥400) is required. To ***achieve high normalized accuracy for T_2-mapping*** SNR≥10 and N_{TR}≥150 is required. To achieve ***high normalized precision for T_1-mapping*** SNR≥10 and N_{TR}≥100 (or SNR≥5 and N_{TR}≥400 or SNR≥10 and N_{TR}≥250) is required. To achieve ***high normalized precision for T_2-mapping*** SNR≥15 and N_{TR}≥100 is required (or SNR≥10 and N_{TR}≥250 is required). By imposing that the high normalized accuracy and high normalized precision conditions are satisfied for all tissues, then SNR⩾5 with N_{TR}⩾400 (data not shown; or SNR≥15 with N_{TR}≥150) was the approximate lower-bound acquisition condition.

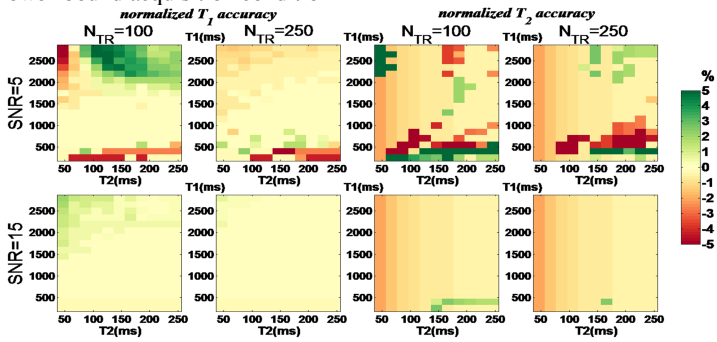

Figure 1. Maps of ***normalized accuracy*** for estimating T_1 (left two columns) and T_2 (right two columns) across a wide range of tissues and sampling conditions.

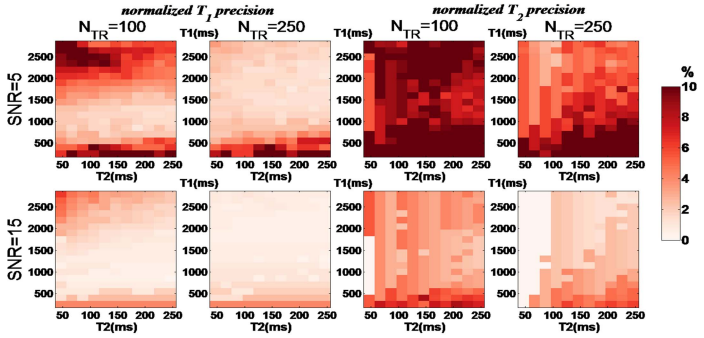

Figure 2. Maps of ***normalized precision*** for estimating T_1 (left two columns) and T_2 (right two columns) across a wide range of tissues and sampling conditions.

By evaluating Δbias and Δprecision for all tissues and all sampling conditions, we conclude that MRF is nearly equivalent for T_1 and T_2 measurements (average Δbias=-1.0±0.3%; average Δprecision=-2.5±1.8%).

Discussion and Conclusion: The results show that the pIR-bSSFP MRF scheme evaluated herein provides nearly equivalent T_1 and T_2 accuracy. The normalized precision maps indicate that higher SNR and longer N_{TR} are needed to achieve acceptable T_2 precision compared to T_1 precision. As such, under the condition of perfect sampling, Bloch equation simulations using this specific MRF scheme define that the lower-bound acquisition requirement for both high normalized accuracy and high normalized precision for both T_1 and T_2 is SNR⩾5 and N_{TR}⩾400 (or SNR≥15 with N_{TR}≥150). Note, that other MRF sampling schemes will have different performance and each needs to be carefully evaluated. Moving forward the reported accuracy and precision maps can be used to infer the necessary SNR and N_{TR} to meet a target accuracy and precision for a specific tissue (e.g. myocardium or white/gray matter). These results indicate that MRF can potentially use very rapid acquisitions (N_{TR}<1000 as originally proposed) while maintaining acceptable accuracy and precision if SNR is sufficiently high.

Reference: 1. Ma *et al*. *Nature*, vol.495, pp. 187-192, 2013. 2. http://mrsrl.stanford.edu/~brian/bloch/