Accuracy Analysis for MR Fingerprinting

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Purpose: Magnetic resonance fingerprinting (MRF) is a novel technique, which enables simultaneous multi-parameter mapping and tissue classification by varying different acquisition parameters, such as flip angle and repetition time, to generate unique signal evolution for each tissue type [1]. Although the derivation of the parameter maps from the signal evolution is usually done by matching the measured signal to an entry of a pre-calculated dictionary, in general the mapping is a non-linear and non-convex problem. This means that for a measured signal evolution there may be several good matches that are not necessarily close to the true solution, which may lead to inaccuracies in the reconstructed parameter maps, depending on the signal SNR and the resolution (the degree of detail) of the dictionary. In this work, we demonstrate a comprehensive accuracy analysis exemplified on a bSSFP-based MRF sequence, which allows predicting the accuracy of MRF in different parameter ranges and defining confidence areas for the performance of MRF.

Methods: The following two aspects are considered in the MRF accuracy analysis: i) Quantitative resolution of the dictionary and ii) sensitivity to noise. The MRF dictionary is constructed by computing the signal evolution for the selected MRF sequence and a discrete set of tissue parameter values. If a tissue parameter value of a measured signal is not an element of the dictionary, it is desirable that the reconstructed parameter value is the next available dictionary element closest to the true one. To evaluate the accuracy related to the dictionary resolution, a set of test signals (T1 ranging from 200 to 3000ms, 20 ms steps, T2 ranging from 20 to 300 ms, 2 ms steps, and B0 from 0 to 100Hz, 1Hz steps) is computed using Bloch simulations for a selected MRF sequence shown in Fig.1 , using 250 values of (TR;α) over time. A dictionary with reduced resolution (ΔT1 = 40ms, ΔT2 = 4ms, ΔB0 = 2Hz) is constructed for MRF reconstruction, such that the test signals either exactly match or are located between two dictionary values. Fo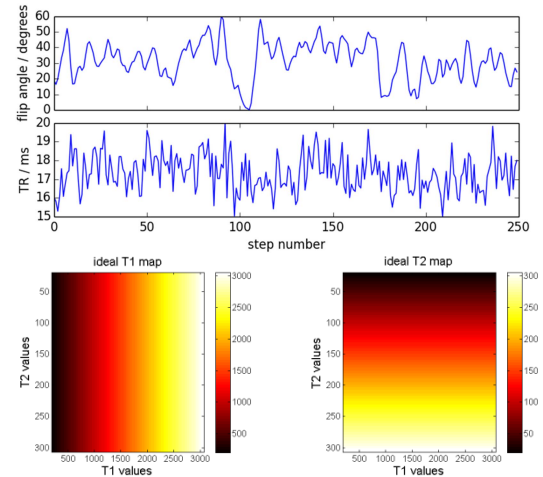r the noise sensitivity analysis, Gaussian noise is added to the real and imaginary part of the simulated ideal signal evolutions before reconstruction to simulate different SNR values. An SNR=75 was chosen as a typical value observed in phantom measurements. To probe the sensitivity of the MRF reconstruction to noise, the SNR was reduced to 10 for a second set of simulations.

Fig. 1 Top: Flip angle and TR patterns for the MRF sequence Bottom: T1 and T2 variations used in the analysis

Results and Discussion: If the exact B0 value is contained in the dictionary, a perfect B0 match is obtained; otherwise, the next closest available B0 value is correctly selected leading to a maximal reconstruction error of half the dictionary resolution, even if the exact T1 and T2 of the test signal are not available in the dictionary. The accuracy in the T1 and T2 maps, however, strongly depends on the accurate match of B0. The T1 and T2 error maps for B0 = 0 are shown in Fig. 2. In case that the exact B0 is available in the dictionary, T1 mapping shows a monotonic behavior over a large range (exact match if the T1 value is available and maximal error of ΔT1/2 otherwise), while T2 maps are monotonic for small values, but show small underestimation for high T2 values (Fig.2
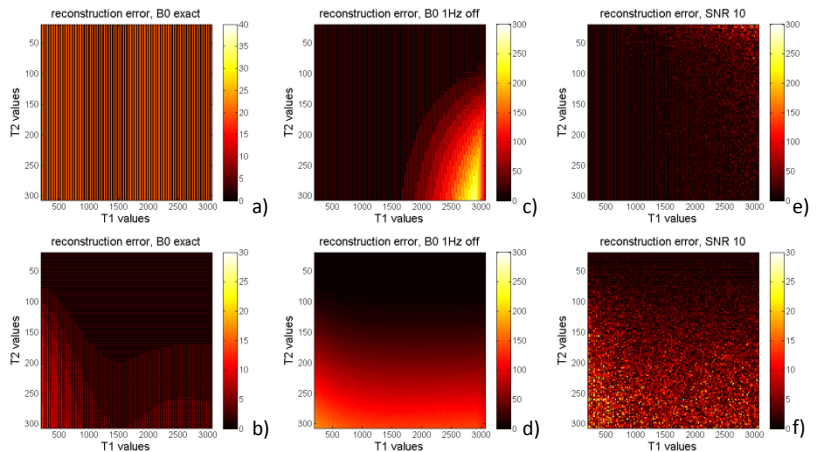

Fig. 2 Reconstruction error for T1(top) and T2 (bottom) in case of exact B0 match (a,b), offset of 1Hz in B0 (c,d), and large amount of noise (SNR = 10) (e,f). Limited dictionary resolution in B0 may lead to significant reconstruction error for large T2, while the influence of noise is benign.

a,b). Even in cases of small reconstruction errors in B0 (e.g. 1 Hz) due to limited dictionary resolution, however, T2 values may be highly underestimated for T2>100ms. T1 maps remain perfect for a large range, but also show some error for high T1 and high T2 (Fig.2 c,d). For other B0 values, the error maps show slightly different patterns but with the same general trend. The reconstruction error distribution is specific to the MRF sequence and can show very different behavior depending on the TR and α patterns. The matching is very robust with respect to noise, SNR=75 leads to noise-free maps, while the reconstruction error in the maps is below 10% over the entire range of the simulation for SNR=10.

Conclusions: MRF is a promising approach for quantitative MRI. However, the mapping accuracy can largely vary over different parameter ranges. The predominant source of inaccuracies is the high sensitivity of the bSSFP-based MRF sequences to B0 variations leading to large changes in the signal evolution even for small changes in B0. For the selected sequence and dictionary resolution, a confidence region can be defined approximately as T1 < 1500 and T2 < 100ms in which the considered MRF sequence provides accurate parameter maps. In order to assure accurate mapping for larger ranges of T1 and T2 values, it is required to use a high sampling density in B0 for constructing the MRF dictionary. The proposed analysis can be used for comparing different MRF sequences and as an input to sequence optimization.

References: Ma D et al. Nature. 2013; 495:187-192