Preparation Scheme Optimization for Abdominal MRF

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Synopsis

Motivation: The absence of cardiac triggering in abdominal Magnetic Resonance Fingerprinting allows increased flexibility in the choice and placement of preparation modules.

Goals: Investigate the extent to which the accuracy of relaxation time quantification in abdominal MRF can be increased by optimizing the design of the preparation scheme.

Approach: Evaluate a large number of randomly created sequences with respect to a CRLB cost function. Investigate the predictive power of the cost function by using a selection of the sequences for simulations and *in vivo* measurements.

Results: Relaxation time quantification accuracy correlates with the CRLB. Established preparation schemes are already close to optimal.

Impact

This work provides an improved understanding about the correlation of sequence design, reconstruction techniques and relaxation time map accuracy.

Main

Introduction

One of the major challenges in abdominal Magnetic Resonance Fingerprinting (MRF) are the high B_1^+-inhomogeneities that occur compared to measurements in the brain. The initial approach to mitigate B_1^+-related signal deviations was to simultaneously map the B_1^+ field and include it in the dictionary[1]. Today, abdominal MRF predominantly employs a sequence design developed for cardiac MRF[2]. Here, the sequence is divided into several blocks, each preceded by a magnetization preparation. This allows the use of smaller flip angles which are less prone to B_1^+-inhomogeneities. However, in cardiac MRF, the placement of these blocks is dictated by ECG triggering, whereas in abdominal MRF they can be placed more flexibly. This opens up a potential for optimization that has not been exploited so far.

Methods

The Cramer-Rao Lower Bound (CRLB) has previously been employed as a predictor of MRF relaxation time quantification accuracy[3,4]. As such, it has been used as a cost function to optimize flip angles and relaxation times in iterative algorithms. However, since the placement and especially the selection of preparation modules is a discrete problem and even an iterative algorithm does not guarantee convergence to a global optimum, we decided to cover the optimization space with a brute-force approach in this case. The idea is to compute the CRLB for a large number of randomly created sequences, select a few promising candidates and evaluate these in simulations and *in vivo* experiments. The sequences consist of a variable number of blocks (between 10 and 16 in our case), which in turn consist of a preparation module (no, inversion, or T_2 preparation) and a subsequent FISP readout with 40 excitations of constant flip angle and repetition time. Both the number, selection and placement of blocks are randomized. The total duration of the sequence is set to 10 s. A total of one million sequences are generated and evaluated with regard to three cost functions:

$$cost_1 = \sqrt{\frac{CRLB(T_1)}{T_1^2}}$$
$$cost_2 = \sqrt{\frac{CRLB(T_2)}{T_2^2}}$$
$$cost_3 = cost_1 + cost_2$$

As optimization target we choose liver tissue with T_1=660ms, T_2=40ms. The investigated sequences are sorted based on the cost functions and most promising candidates are selected for further investigation: First, the whole MRF experiment is simulated using the XCAT phantom, taking into account undersampling and noise effects. Different reconstruction techniques are employed. In the resulting relaxation time maps, an ROI is drawn in the liver and the average and standard deviation of T_1 and T_2 is calculated. Finally, selected sequences are used for *in vivo* experiments on ?? healthy volunteers. All measurements are performed on a clinical 1.5 T scanner (Siemens Magnetom Sola).

Results

The preparation scheme proposed by Hamilton for cardiac MRF with 16 acquisition blocks is used as a reference[2]. Of the 1 million sequences examined, approximately 16% beat this sequence in terms of $cost_1$, 1.5% in terms of $cost_2$. Only 0.11% of the analyzed sequences provide a lower cost function $cost_3$. The cost function values of all examined sequences are visualized in Figure 1, selected sequences are shown in Figure 2.

The standard deviations of the ROI relaxation times obtained from simulation with different noise levels and reconstruction techniques are shown in Figure 3. Overall, it can again be concluded that the reference sequence is hard to outperform. The is especially true when advanced reconstruction algorithms are employed. However, sequences performing poorly in terms of the cost functions also produce bad results in the simulation, confirming the predictive power of the CRLB cost function.

%% Paragraph about in vivo measurements %%

Discussion

We show in this work that the choice of the preparation scheme has a large impact on the accuracy of relaxation time quantification in abdominal MRF. The results demonstrate how hard it is to find a better preparation scheme than the one presented by Hamilton. Next steps could be to exploit additional degrees of freedom in the design of abdominal MRF sequences. To investigate the thus even further enlarged optimization space in a meaningful way, advanced methods like neural networks could be advantageous.

Conclusion

The accuracy of relaxation times determined with abdominal MRF depends on the employed preparation scheme. It can be predicted using the CRLB. Established preparation schemes are already close to optimal.

References

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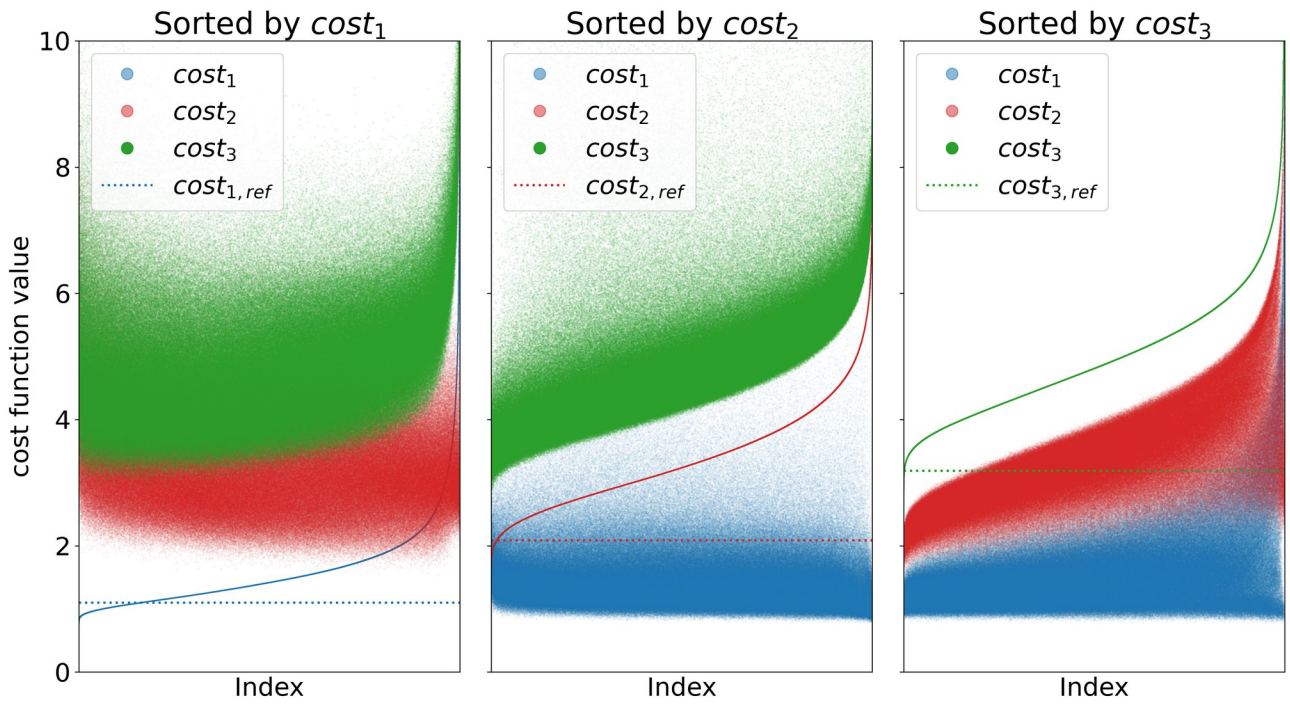

Figure 1: Cost function values of the 1 million randomly created sequences. In each subplot, they are sorted based on one of the cost functions. The corresponding cost function values of the reference sequence are shown by the dotted lines.

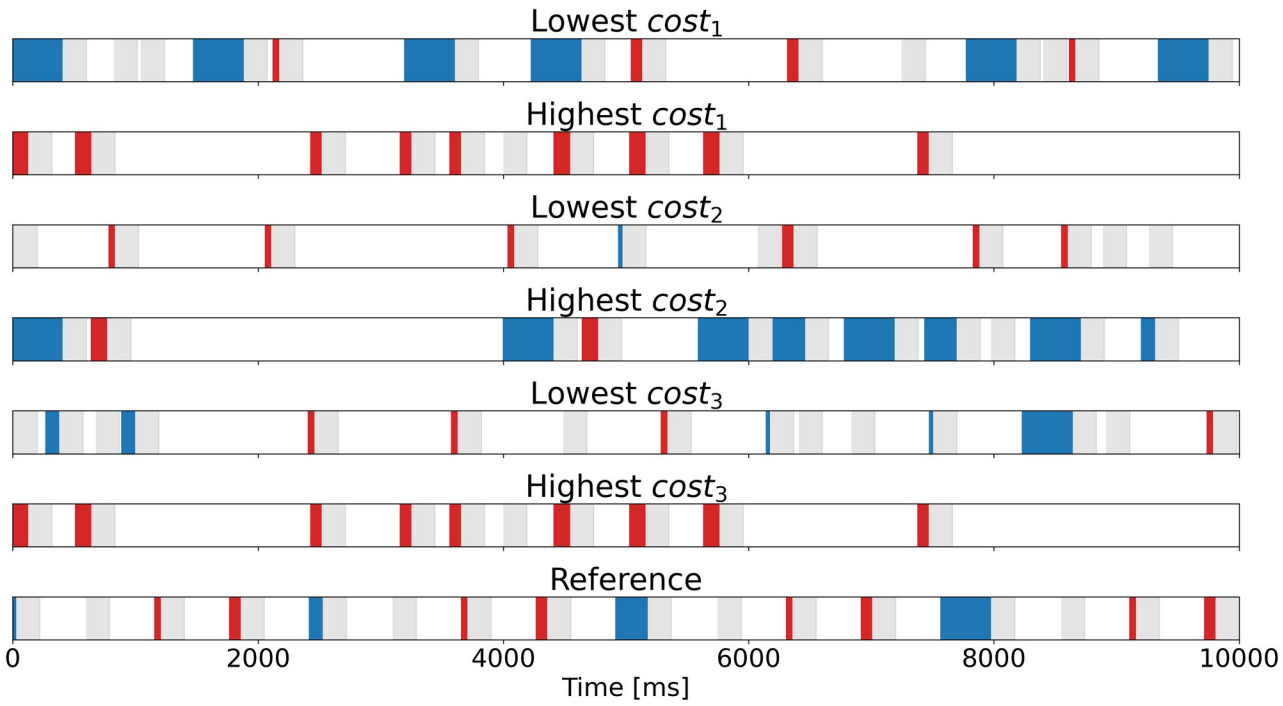

Figure 2: Sequences that result in the lowest and highest cost function values (top 6 rows) and reference sequence (bottom). Blue: T_1 preparation. Red: T_2 preparation. Gray: Acquisition block.

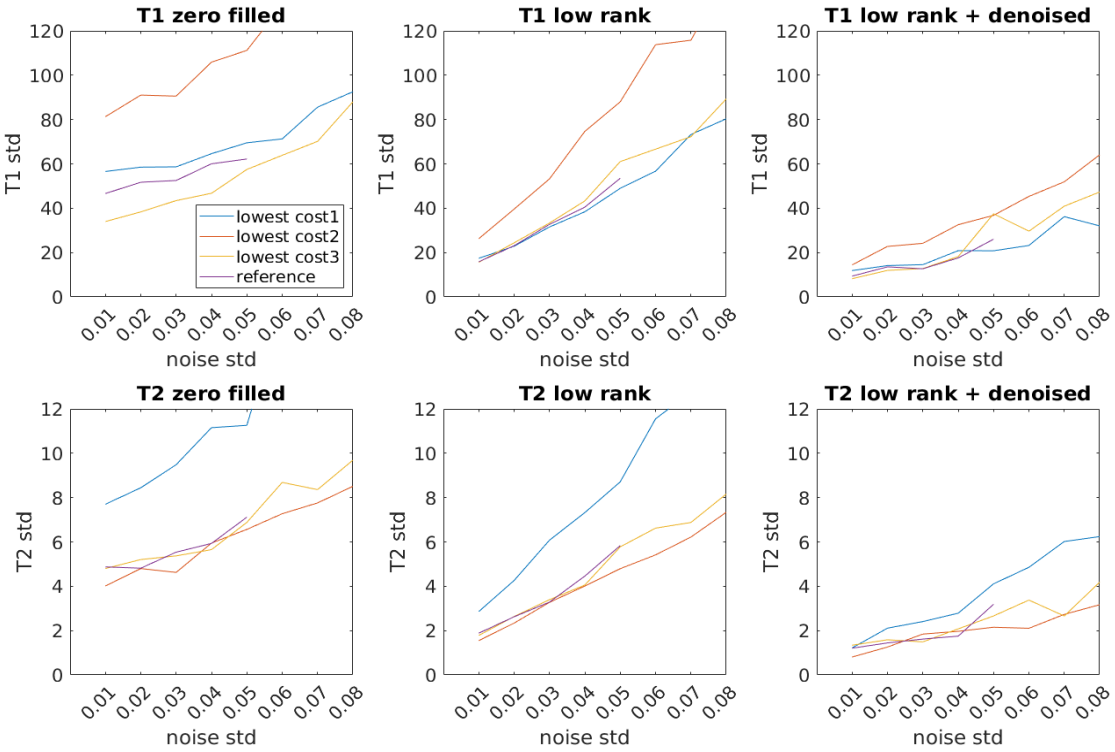

Figure 3: Standard deviations of relaxation times in the liver ROI as determined with the XCAT simulation, depending on the used sequence and reconstruction technique. As a general trend, it can be stated that the reference sequence can hardly be outperformed. Furthermore, the influence of the sequence design is reduced by the use of advanced reconstruction techniques. As expected, sequences optimized for quantification of only one relaxation time underperform for quantification of the other.