Preparation Scheme Optimization for Abdominal MRF

Tom Griesler[1,2], Jesse Hamilton[1,2], Evan Cummings[1,2], Nicole Seiberlich[1,2], Gastao Cruz[2]

[1]Department of Biomedical Engineering, University of Michigan, Ann Arbor, MI, USA
[2]Department of Radiology, University of Michigan, Ann Arbor, MI, USA

Synopsis
Motivation: Increase encoding efficiency of abdominal MRF acquisitions.
Goals: Investigate the predictive power of Cramer-Rao bound based cost functions on the performance of magnetization-prepared MRF sequences.
Approach: Randomly create sequences. Select promising candidates based on CRLB cost functions and use them in simulations and *in vivo* experiments. Evaluate precision and accuracy of the resulting relaxation time maps.
Results: The CRLB cost function values depend on the selection and placement of preparation modules and correlate with the quantification performance of the resulting sequences. Only 0.09% of randomly created sequences provide a lower CRLB for both T_1 and T_2 than established preparation schemes.

Impact
Provide a tool for the optimization of magnetization-prepared MRF sequences.

Main
Introduction
In analogy to cardiac MRF[1], abdominal MRF often employs sequences which consist of several blocks, each preceded by a magnetization preparation. The absence of ECG triggering in abdominal MRF, however, allows increased flexibility in sequence design and opens up a potential for optimization that has not been exploited so far. In this work, we investigate the suitability of the Cramer-Rao Lower Bound (CRLB) as a predictor of relaxation time quantification precision in the context of magnetization-prepared MRF.

Methods
In previous works, the CRLB has been used as a cost function in iterative algorithms to optimize flip angles and repetition times of MRF sequences[2,3]. However, since the selection of preparation modules is a discrete and thus non-differentiable problem, we decided to cover the optimization space with a brute-force approach in this case. The idea is to compute a CRLB cost function for a large number of randomly created sequences, select promising candidates and evaluate these in simulations and *in vivo*. The sequences consist of a variable number of blocks (between 8 and 16 in our case), which in turn consist of a preparation module (no preparation, 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 10s. 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 selected candidates are used for further investigation: First, the whole MRF experiment is simulated using the XCAT phantom[4], taking into account undersampling, coil sensitivity, and noise effects. For both simulation and experiment, we use a spiral k-space trajectory with 48-fold undersampling. Different reconstruction techniques are employed (zero-filling, low-rank reconstruction and low-rank reconstruction with additional locally low-rank denoising). In the resulting relaxation time maps, an ROI is drawn in the liver and the mean and standard deviation of T_1 and T_2 are 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[1]. Of the 1 million sequences examined, approximately 14% outperform this sequence in terms of $cost_1$, 1.3% in terms of $cost_2$. Only 0.09% of the analyzed sequences provide a lower $cost_3$. The cost function values of all examined sequences are visualized in Figure 1, selected sequences are shown in Figure 2. Other established preparation schemes (Gvernby[5], Jaubert[6]) lead to higher cost function values.

The quantification precision is assessed by computing the standard deviations of the relaxation times in the liver ROI obtained from simulation with different noise levels and reconstruction techniques (cf. Figure 3 & 4). Generally, relaxation time quantification precision correlates strongly with the used reconstruction method. Within one method, however, it also correlates with the corresponding cost function value. The sequence with lowest $cost_3$ performs slightly better than the reference sequence for both T_1 and T_2 quantification (6.9% resp. 7.8% reduction of the standard deviation using low-rank reconstruction). Regarding accuracy, they yield comparable results, while sequences with high cost function values lead to both high standard deviations and significant biases.

Discussion

We show in this work that the CRLB can be used as a predictor of the performance of magnetization-prepared MRF sequences. Furthermore, we find that, under otherwise identical conditions, the selection and placement of preparation modules has a high impact on the precision and accuracy of the resulting relaxation time maps. Only a small portion of randomly created sequences yield comparable or better results than the preparation scheme presented by Hamilton. Next steps could include the exploitation of additional degrees of freedom in the design of abdominal MRF sequences. The application of gradient-free optimization methods or machine learning to investigate the thus further enlarged optimization space could be advantageous.

Conclusion

The precision of relaxation times determined with abdominal MRF can be predicted using the CRLB. It strongly depends on the selection and placement of preparation modules.

References

1. Hamilton JI, Jiang Y, Chen Y, Ma D, Lo WC, Griswold M, Seiberlich N. MR fingerprinting for rapid quantification of myocardial T_1 , T_2 , and proton spin density. Magn Reson Med. 2017 Apr;77(4):1446-1458. doi: 10.1002/mrm.26216.

2. Bo Zhao, Haldar JP, Congyu Liao, Dan Ma, Yun Jiang, Griswold MA, Setsompop K, Wald LL. Optimal Experiment Design for Magnetic Resonance Fingerprinting: Cramér-Rao Bound Meets Spin Dynamics. IEEE Trans Med Imaging. 2019 Mar;38(3):844-861. doi: 10.1109/TMI.2018.2873704.
3. Lee PK, Watkins LE, Anderson TI, Buonincontri G, Hargreaves BA. Flexible and efficient optimization of quantitative sequences using automatic differentiation of Bloch simulations. Magn Reson Med. 2019 Oct;82(4):1438-1451. doi: 10.1002/mrm.27832.
4. Segars WP, Sturgeon G, Mendonca S, Grimes J, Tsui BM. 4D XCAT phantom for multimodality imaging research. Med Phys. 2010 Sep;37(9):4902-15. doi: 10.1118/1.3480985.
5. Kvernby, S., Warntjes, M.J.B., Haraldsson, H. et al. Simultaneous three-dimensional myocardial T1 and T2 mapping in one breath hold with 3D-QALAS. J Cardiovasc Magn Reson 16, 102 (2014). doi: 10.1186/s12968-014-0102-0.
6. Jaubert O, Arrieta C, Cruz G, Bustin A, Schneider T, Georgiopoulos G, Masci PG, Sing-Long C, Botnar RM, Prieto C. Multi-parametric liver tissue characterization using MR fingerprinting: Simultaneous T_1 , T_2 , T_2 *, and fat fraction mapping. Magn Reson Med. 2020 Nov;84(5):2625-2635. doi: 10.1002/mrm.28311.

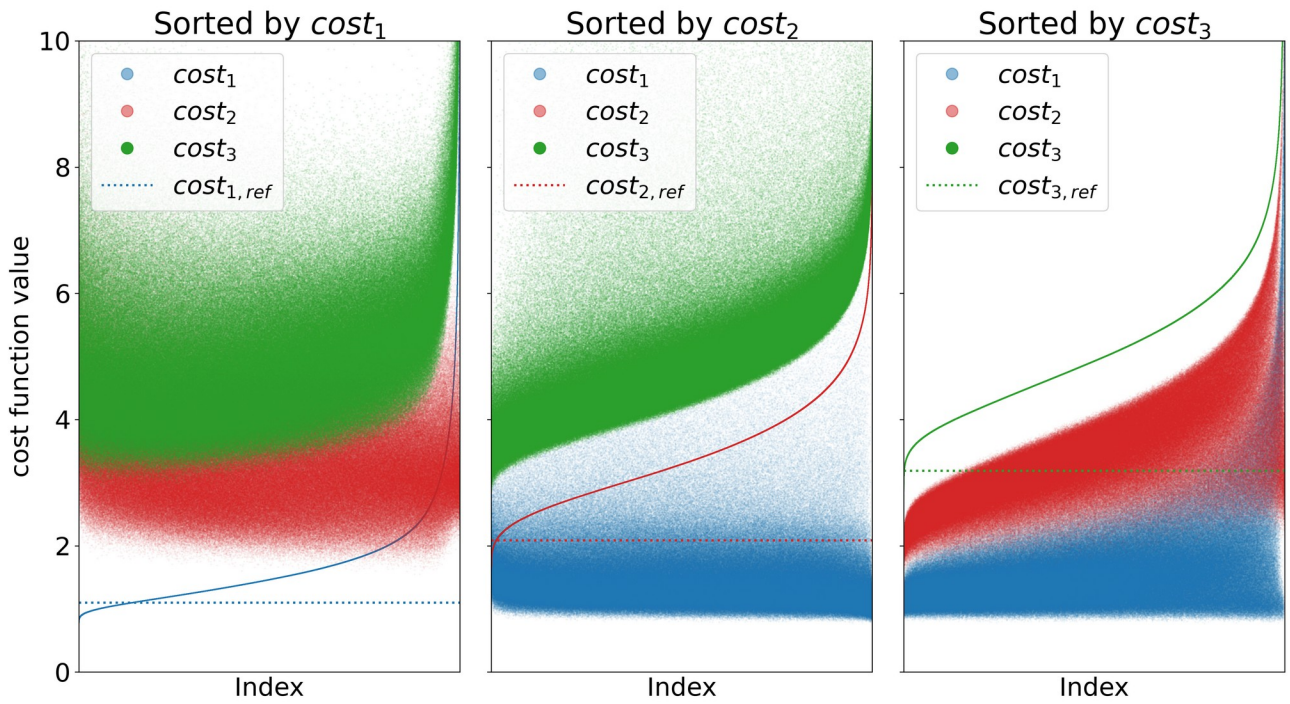

Figure 1: Cost function values of the 1 million randomly created sequences. In each subplot, they are sorted based on one of the cost functions. The corresponding cost function values of the reference sequence are shown by the dotted lines.

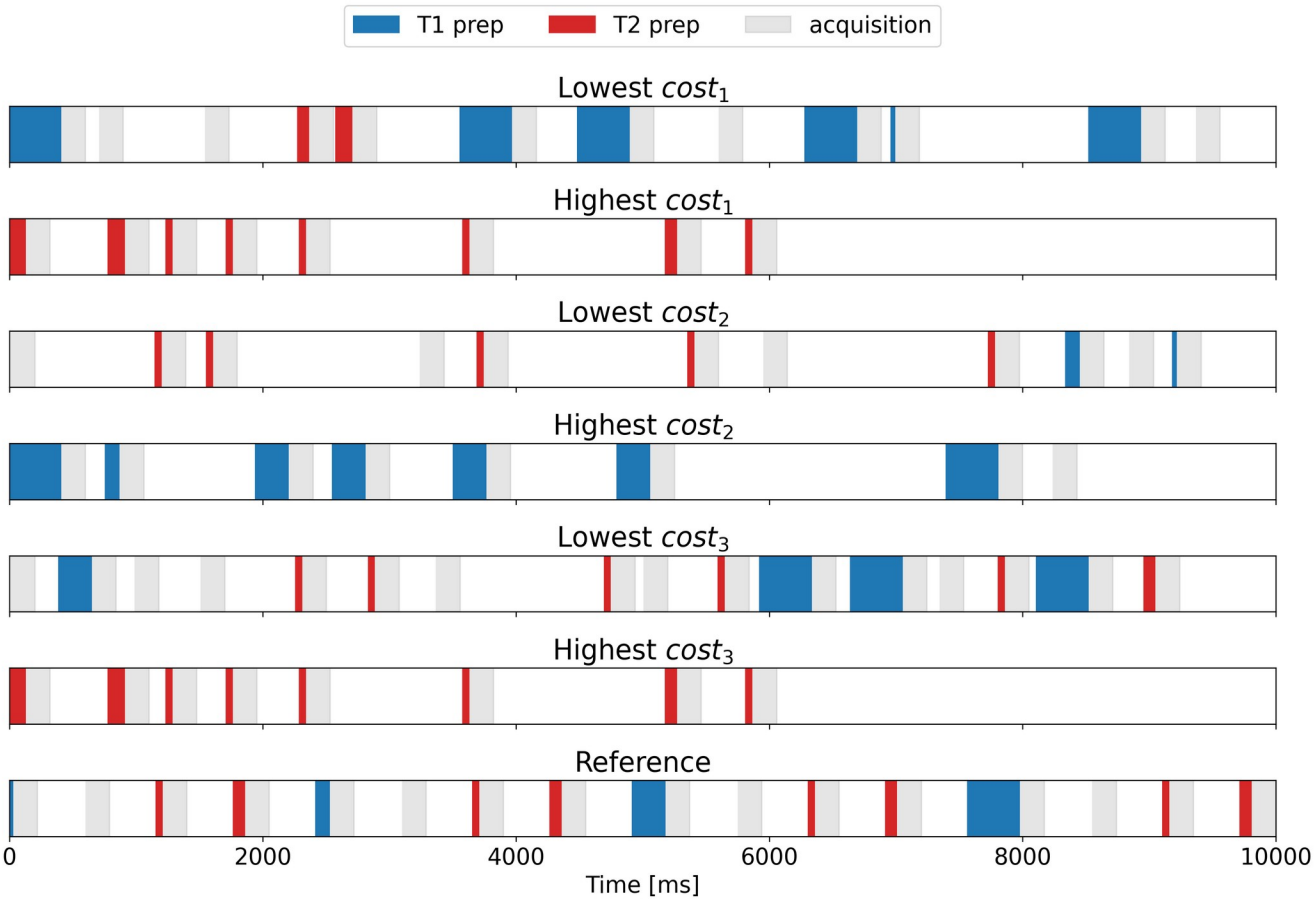

Figure 2: Sequences that result in the lowest and highest cost function values (top 6 rows) and reference sequence (bottom). Blue: T_1 preparation. Red: T_2 preparation. Gray: Acquisition block.

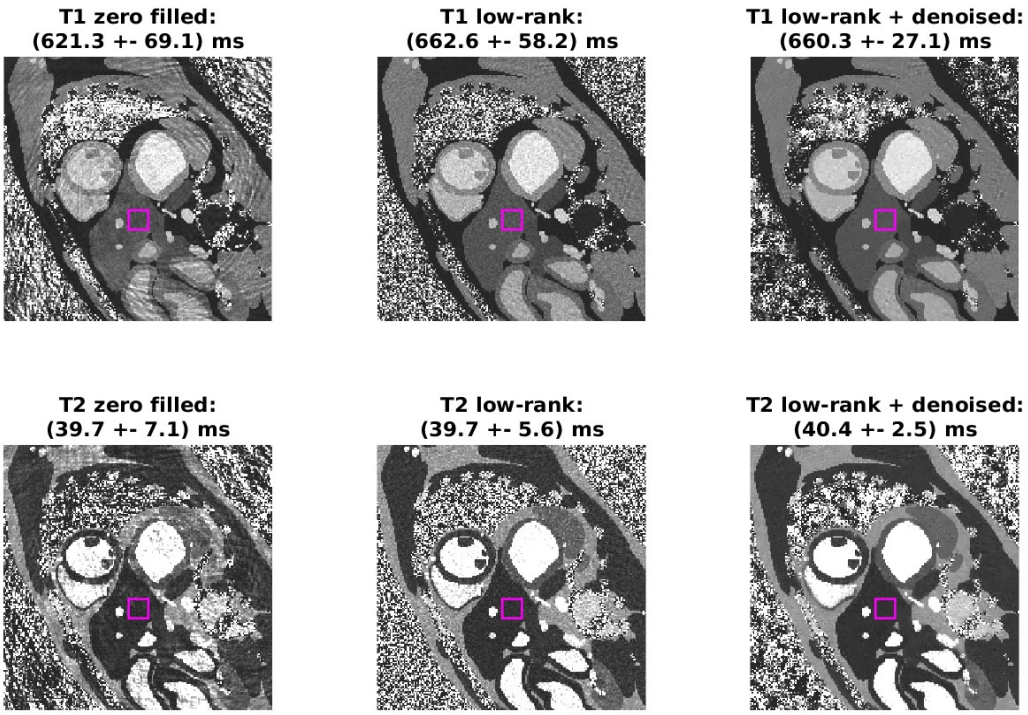

Figure 3: Exemplary relaxation time maps from different reconstructions of simulated MRF data. An ROI is drawn in the liver for further analysis (marked in magenta).

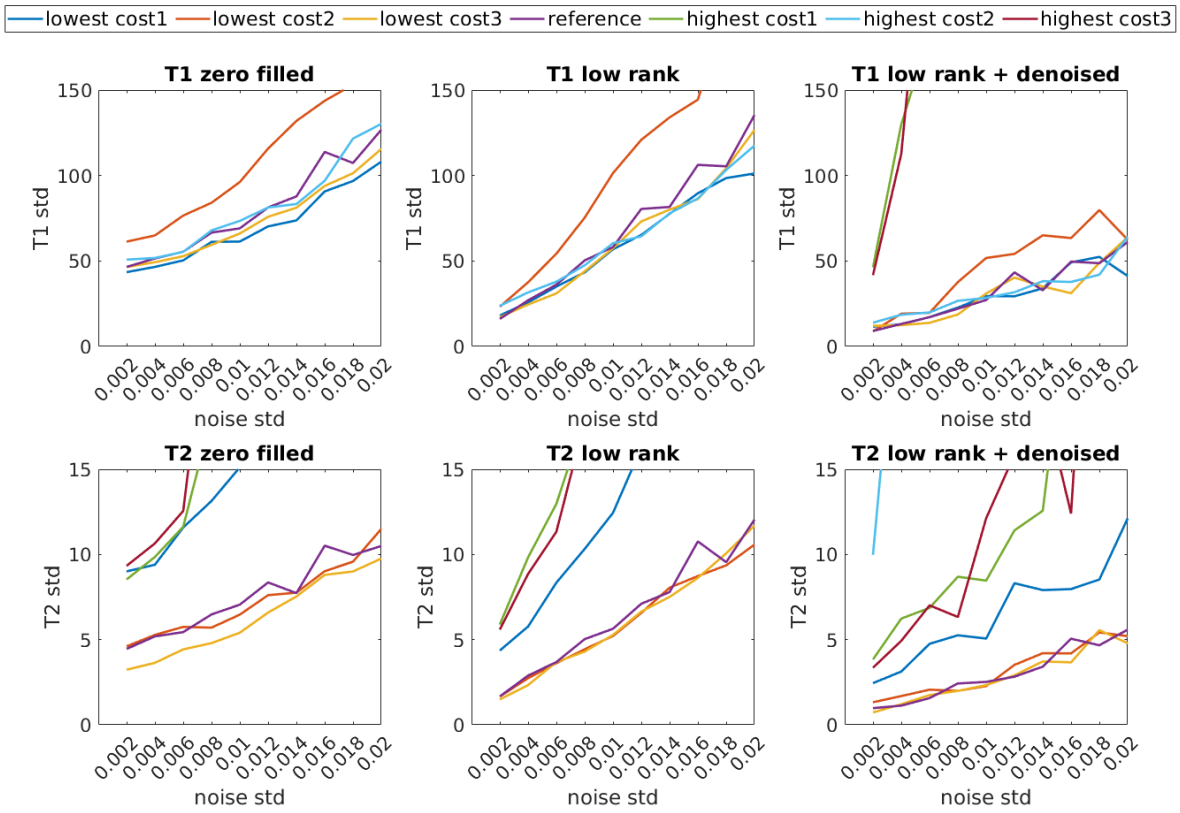

Figure 4: Standard deviations of relaxation times in the liver ROI as determined with the XCAT simulation, depending on the used sequence and reconstruction technique. The quantification precision strongly depends on the used reconstruction method. When comparing the results obtained with the same method, minor improvements can be achieved compared to the reference. As expected, sequences optimized for quantification of only one relaxation time underperform for quantification of the other.