CMR-FOOTPRINTING: QUANTIFYING TISSUE PARAMETERS WITH CLINICAL PULSE SEQUENCE SIMULATIONS IMPROVES MEASUREMENT ACCURACY - AN EXAMPLE WITH MOLLI T1 MAPPING

Christos G. Xanthis[1,2], Sebastian L. Bidhult[1], Georgios Kantasis[1,2], Mikael Kanski[1], Einar Heiberg[1,3], Håkan Arheden[1], and Anthony H. Aletras[1,2]

[1]Cardiac MR group Lund, Dept. of Clinical Physiology, Lund University, Lund, Skåne, Sweden, [2]Department of Computer Science and Biomedical Informatics, University of Thessaly, Lamia, Lamia, Greece, [3]Department of Biomedical Engineering, Faculty of Engineering, Lund University, Lund, Skåne, Sweden

Purpose: MR simulations have been used in a limited scope, with the exception of MR-fingerprinting [1]. The purpose of this study is to propose CMR-footprinting, a method for extracting quantitative tissue CMR data from clinical pulse sequences with the aid of comprehensive, massively parallel MRI simulations on a large population of spins aiming to compute all possible outcomes of a pulse sequence for a range of physiologically relevant tissue relaxation times. A MOLLI example was used.

Methods: Phantoms with unknown T1 and T2 values were scanned with a MOLLI pulse sequence at 1.5T (figure 1). The identical MOLLI pulse sequence was then simulated for all physiological combinations of T1 and T2 with a comprehensive, massively parallel, GPU-based MRI simulator [2,3] thus resulting in a database of all possible physiological signal intensities (one for each TI for every T1, T2 pair). The unknown relaxation values could then be directly determined by searching the database in order to find the simulated signal intensities that best matched (least squared difference) the true signal intensities. A total of approx. 400,000 simulations of the entire imaging pulse sequence were performed with a step of 1msec for T1 of 200 to 1700msec and T2 of 20 to 300msec.

The phantoms used had T1s and T2s of native myocardium, native blood and post-Gd myocardium. The T1 and T2 reference standard values were measured with Saturation Recovery (Tsat = 0.01-15sec) and Spin-Echo (TE = 0.01-1.8sec) respectively (TR>10sec). Two MOLLI sequences with schemes A) 5-3s-3 and B) 5-0s-3 were tested. The T1 values obtained with CMR-footprinting were compared against conventional post-processing (figure 1).

			Blood (pre-Gd)	Normal Myocardium (pre-Gd)	Normal Myocardium (post-Gd)
		Reference values (T1/T2)	1569/198	1044/49	350/51
A	MOLLI 5(3s)3 SENSE off, no partial echo, TR/TE: 2.6/1.29, rBW=100kHz, ACQ matrix 80x79, ACQ dur. = 205msec, slice thickness 6mm, FOV 200mm x 200mm	**CMR-footprinting (T1)**	**1545±2.6**	**1009±0.8**	**343±0.6**
		conventional MOLLI (T1)	1501±3	959±1.7	313±0.8
B	MOLLI 5(0s)3 SENSE off, no partial echo, TR/TE: 2.6/1.29, rBW=100kHz, ACQ matrix 80x79, ACQ dur. = 205msec, slice thickness 6mm, FOV 200mm x 200mm	**CMR-footprinting (T1)**	**1518±3.3**	**997±1.8**	**352±0.6**
		conventional MOLLI (T1)	1401±3.9	893.9±1.6	312±0.8

Figure 1. Relaxation times (in msec) for the three-phantom setup. Conventional MOLLI T1 maps were obtained from the scanner. T1 maps were obtained with CMR-footprinting from these MOLLI experiments. These showed overall improved accuracy and good performance even with the 5-0s-3 scheme (MOLLI B) on phantoms with long T1s.

Results and Discussion: CMR-footprinting improved T1 accuracy compared to the conventional MOLLI T1 maps. Both MOLLI schemes (A and B), with CMR-footprinting, demonstrated better accuracy compared to conventional post-processing, even for long T1s with a zero seconds pause (B). Figure 2 shows results from a healthy volunteer.

Conclusions: In this study, we demonstrated CMR-footprinting, a new method showing how quantitative CMR with clinical pulse sequences can be improved by comparing the signals acquired from the MRI scanner to the entire pool of possible outcomes that are produced by simulations of the identical pulse sequence for different tissue types. This represents a paradigm shift in quantitative CMR with existing clinical pulse sequences. MR-footprinting is different from MR-fingerprinting where specialized pulse sequences are needed. The MOLLI-based example demonstrated this approach by improving overall T1 accuracy and performing well even with the 5-0s-3 scheme and long T1s.

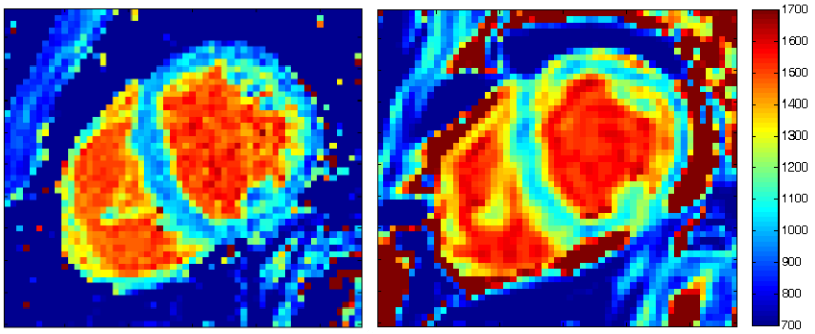

Figure 2 T1 maps of a healthy volunteer. Left image: Conventional MOLLI map derived from a clinical pulse sequence (scheme 5-3s-3, SENSE = 2, partial echo factor = 0.85, TR/TE: 3/1.42, rBW=134 kHz, ACQ matrix 124x110, ACQ duration = 175msec). Right image: T1 map obtained from MOLLI-based tissue signal intensities using the CMR-footprinting (scheme 5-3s-3, SENSE off, no partial echo, TR/TE: 2.6/1.32, rBW=100 kHz, ACQ matrix 64x65, ACQ duration = 172msec). Left image: Myocardium T1 = 992±6msec, Blood T1 = 1492±10msec. Right image: Myocardium T1 = 1070±4msec, Blood T1 = 1540±7msec.

References: [1] Ma D, Gulani V, Seiberlich N, et al. Magnetic resonance fingerprinting. Nature 2013;495: 187-192. [2] C.G. Xanthis, I.E. Venetis, A.V. Chalkias, et al. MRISIMUL: A GPU-Based Parallel Approach to MRI Simulations. IEEE Trans. Med. Imag. 2014;33(3):607-617. [3] C.G. Xanthis, I.E. Venetis, A.H. Aletras. High performance MRI simulations of motion on multi-GPU systems. J. Cardiovasc. Magn. Reson. 2014;16(48).