

Feasibility of myocardial T1 mapping from Cine-IR images by image warping

V. Positano¹, M. Milanesi¹, P. Masci¹, T. K. Foo², J. C. Hardy², L. Marinelli², A. Barison^{1,3}, D. De Marchi¹, M. Lombardi¹, and L. Landini⁴

¹MRI Laboratory, "G- Monasterio" Foundation and Institute of Clinical Physiology, Pisa, Italy, ²Global Research Center, General Electric, Niskayuna, New York, United States, ³Scuola Sant'Anna, Pisa, Italy, ⁴Department of Information Engineering, University of Pisa, Italy

Introduction: In vivo myocardial T_1 quantification is challenging because of severe time constraints due to cardiac and respiratory motion. The multipoint approach (Look and Locker) allows sampling the relaxation curve multiple times after an initial preparation pulse achieving the full coverage of the curve in a single breath-hold [1]. The recognized limitation of this approach is that pixel-by-pixel T_1 mapping of the heart is difficult because data acquisition is performed continuously throughout the cardiac cycle without regard for cardiac motion. Hence, T_1 values are usually evaluated only in a single region of interest (ROI), manually defined for every frame. The objective of this study is to develop an image analysis procedure able to provide T_1 mapping for multipoint sequences automatically compensating for cardiac motion.

Materials and methods: Three short-axis heart images (i.e. basal, middle, and apical views) from 10 patients scheduled for myocardial viability assessment by CMR-DE were acquired on a 1.5 T scanner (GE Excite, Wilwaukee, Waukesha, WI, USA) using a Cine-IR FastGRE pulse sequence consisted of one non-selective adiabatic inversion pulse applied right after the R-wave trigger [2]. The inversion pulse is followed by a cine acquisition, where each cardiac phase experience a different time delay from the inversion pulse and thus shows a different T_1 weighting. SA images were acquired about 5 minutes after a gadolinium bolus injection (Gadovist®; Bayer Schering Pharma; Berlin, Germany, 0.1 mmoli/Kg), just before standard delay enhancement acquisition.

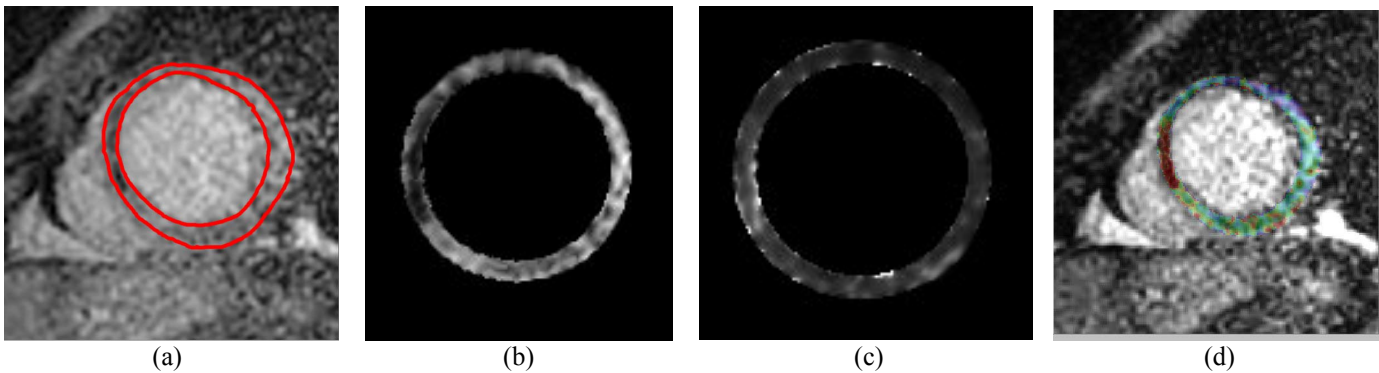


Figure 1: a: Manual segmentation of the myocardium; b: warping of myocardium signal on the reference model; c: evaluation of the T_1 map on the model; d: warping back of the T_1 map on the myocardium.

Image analysis was performed by HIPPO MIOT software [3]. Endocardial and epicardial contours were manually defined on each frame (Fig 1.a). A series of 9×9 ROIs was extracted from the center of endocardial contour for every frame, leading to the evaluation of the blood signal relaxation curve in the left ventricle. The blood relaxation curve was used to calculate the signal polarity, evaluating the fitting quality for every number of assigned negative points and tacking the best result. Signal curve was fitted to the $A+B\exp(t/T_1)$ model. For each frame, 120 chords were traced from each endocardial contour center, obtaining a collection of 240 ordered points that defined the myocardial region. The same number of points was defined on a myocardium model represented by a circular crown. Using a Delaunay triangulation and the previously defined couples of points as constraints for the warping operation the myocardial region was transformed on the model (Fig 1.b). The procedure was repeated along all frames leading to a sequence of aligned circular crown models. For each image pixel in the strictly interior of the circular crown model, the signal value was evaluated along all TE values in a 3×3 region surrounding the pixel, obtaining a pixel-by-pixel relaxation curve fitted to the previously defined model and the corresponding model T_1 map (Fig 1.c). The warping operation can be inverted mapping the T_1 model map on real myocardium in each frame (Fig 1.d).

Results: Pixel-by-pixel T_1 mapping was feasible in all subjects. Location of myocardial necrosis was visually assessed by an expert observer using a two point scale (T_1 significantly low or normal) and mapped on a 16-segments AHA model [4]. A second observer, blinded from the previous one, performed the same analysis on CMR-DE images. This analysis was taken as gold standard. Sector-to-sector correspondence was found in 154 of the all 160 segments.

Discussion: The proposed image analysis technique allows myocardial T_1 mapping from Cine-IR images by warping the myocardium signal in each frame on a standardized model, evaluation of pixel-by-pixel T_1 distribution on the model, and finally warping back the resulting T_1 map on each frame. Although a more strong validation is needed to confirm the preliminary results presented in this study, myocardial T_1 mapping seems to be feasible on Cine-IR images.

References: [1] Messroghli DR et al MRM 2004;52:141-46 [2] Gupta A et al Radiology 2004;233:921-926 [3] Positano V et al NMR Biomed 2007;20:578-90 [4] Cerqueira MD et al Circulation 2002;105:539-542