Selection of sampling points for saturation recovery based myocardial T1 mapping

Citation
Akcakaya, Mehmet, Sebastian Weingartner, Warren J Manning, and Reza Nezafat. 2014. “Selection of sampling points for saturation recovery based myocardial T1 mapping.” Journal of Cardiovascular Magnetic Resonance 16 (Suppl 1): W32. doi:10.1186/1532-429X-16-S1-W32. http://dx.doi.org/10.1186/1532-429X-16-S1-W32.

Published Version
doi:10.1186/1532-429X-16-S1-W32

Permanent link
http://nrs.harvard.edu/urn-3:HUL.InstRepos:12406805

Terms of Use
This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA

Share Your Story
The Harvard community has made this article openly available. Please share how this access benefits you. Submit a story.

Accessibility
Selection of sampling points for saturation recovery based myocardial T₁ mapping

Mehmet Akcakaya¹*, Sebastian Weingartner¹,², Warren J Manning¹,³, Reza Nezafat¹

From 17th Annual SCMR Scientific Sessions
New Orleans, LA, USA. 16-19 January 2014

Background
Quantitative myocardial T₁ mapping allows assessment of focal and diffuse fibrosis in the myocardium, by sampling the T₁ relaxation curve using inversion [1] or saturation recovery (SR) preparation [2] or a combination of both [3], followed by the acquisition of multiple images with different contrasts, which are subsequently fitted to a parametric equation pixel-wise to yield the T₁ maps. In myocardial T₁ mapping, there is a degree of freedom in selecting which points on the relaxation curve are sampled. However, this topic has not been studied. In this study, we sought to develop an estimation theoretic framework for optimal selection of sampling points and characterized the variance of the corresponding T₁ estimator for sampling of the SR curve.

Methods
Based on the signal model, $y_k = a (1 - b \exp(-x_k/T₁)) + n_k$, and the least squares model, we derived the Fisher information matrix [4]. This was used to derive the Bayesian Cramer-Rao bound [4] for the variance of the T₁ estimator for T₁ values of interest between 950 and 1250 ms (~pre-contrast myocardium). The bound was evaluated for the SASHA sequence [2] which allows sampling

| Vial | T₁ (ms) (uniformly distributed points) | std(T₁) (uniformly distributed points) | T₁ (proposed point selection) | std(T₁) (proposed point selection) | std wrt. uniform | theory std wrt. uniform |
|------|---------------------------------------|----------------------------------------|-------------------------------|------------------------------------|------------------|------------------------|
| 1    | 1457 ± 7.7                           | 69.5                                   | 1456 ± 7.4                    | 48.4                              | 0.69             | 0.71                   |
| 2    | 1144 ± 14.5                          | 56.1                                   | 1130 ± 7.1                    | 41.1                              | 0.73             | 0.76                   |
| 3    | 1151 ± 11.5                          | 53.3                                   | 1155 ± 8.6                    | 43.2                              | 0.81             | 0.76                   |
| 4    | 729 ± 10.3                           | 31.3                                   | 724 ± 2.1                     | 26.3                              | 0.84             | 0.86                   |
| 5    | 980 ± 11.2                           | 34.6                                   | 981 ± 10.4                    | 25.2                              | 0.73             | 0.78                   |
| 6    | 823 ± 13.3                           | 29.9                                   | 822 ± 7.7                     | 24.2                              | 0.81             | 0.83                   |
| 7    | 1148 ± 18.4                          | 53.0                                   | 1144 ± 8.3                    | 37.8                              | 0.71             | 0.76                   |
| 8    | 1130 ± 10.6                          | 56.1                                   | 1137 ± 10.4                   | 45.2                              | 0.81             | 0.76                   |
| 9    | 963 ± 13.8                           | 50.0                                   | 962 ± 6.2                     | 35.5                              | 0.71             | 0.79                   |

Figure 1. Results of the phantom imaging over vials with T₁ values > 700 ms using the proposed and uniform sampling strategies, where each acquisition was repeated 5 times. The ratio of the standard deviation of the T₁ estimator for each proposed sampling strategy and that of the uniform sampling strategy is reported as “standard deviation (std) with respect to (wrt) uniform.” There is a gain in using the proposed point selection strategy, which is significantly different than 1 (P < 0.001). The values match those predicted by theory (P = 0.23).
within a heart-beat between $T_{\text{min}}$ and $T_{\text{max}}$ with one point at full magnetization recovery ($x_k = \infty$), and minimized over the choice of sampling points $\{x_k\}$ yielding the proposed point selection. Phantom imaging of NiCl$_2$ doped agarose vials was performed to compare the proposed point selection with a uniform distribution of sampling points between $T_{\text{min}}$ and $T_{\text{max}}$ [3] using an SSFP sequence with body-coil (NSA = 5) for 11 sampling points. Standard deviation (std) of T1 values within the vials was used as a surrogate for the variance of the estimator. Imaging was also performed on 5 healthy adult subjects (4 women, 23.4 ± 3.3 years) with a 32-channel cardiac-coil to verify the gains predicted by the theory. Both proposed and uniform point selection acquisitions were repeated 5 times per subject to average out the effects of noise. ROIs were drawn in the myocardium and the blood. Both the T1 estimate (average T1 values in the ROI) and the std of the estimator (std of T1 values in the ROI) are reported as mean ± std across 5 scans.

**Results**

The point selection yielded a tri-modal distribution of points: 4 at $T_{\text{min}}$, 6 at $T_{\text{max}}$, 1 at $\infty$, with a theoretical gain in std of 24% compared to uniform selection. Figure 1 shows the results of phantom imaging for T1 values > 700 ms, indicating a good match between theory and experiment. Figure 2 depicts the measurements from the in-vivo data, averaged over five scans. Overall, there was a 23.6% and 26.8% reduction in the std of the T1 maps in the myocardium and blood respectively using the proposed approach.

**Conclusions**

The proposed framework allows for choosing the location of points on the T1 relaxation curve to achieve higher levels of precision without increasing the scan time.

**Funding**

NIH:K99HL111410-01; R01EB008743-01A2.

**Authors’ details**

1Medicine, Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, Massachusetts, USA. 2Computer Assisted Clinical Medicine, University Medical Center Mannheim, Heidelberg University, Mannheim, Germany. 3Radiology, Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, Massachusetts, USA.

Published: 16 January 2014

**References**

1. Messroghi: MRM 2004.
2. Chow: MRM 2013.
3. Weingartner: MRM 2013.
4. Gill: Bernoulli 1995.

doi:10.1186/1532-429X-16-S1-W32

**Cite this article as:** Akcakaya et al.: Selection of sampling points for saturation recovery based myocardial T1 mapping. Journal of Cardiovascular Magnetic Resonance 2014 16(Suppl 1):W32.