

OPTIMIZED SAMPLING TIME SELECTION FOR THE SATURATION CURVE FOR MYOCARDIAL T₁ MAPPING

Mehmet Akçakaya¹, Sebastian Weingärtner¹, Sébastien Roujol¹, and Reza Nezafat¹

¹MEDICINE, BETH ISRAEL DEACONESS MEDICAL CENTER, HARVARD MEDICAL SCHOOL, BOSTON, MA, UNITED STATES

TARGET AUDIENCE: Scientists and clinicians interested in myocardial tissue characterization.

INTRODUCTION: Quantitative myocardial T₁ mapping allows assessment of diffuse myocardial fibrosis. The quantification is achieved by sampling the T₁ relaxation curve using inversion [1] or saturation recovery (SR) preparation [2] or a combination of both [3]. These images are then subsequently fit to a parametric equation pixel-wise to yield T₁ maps. In myocardial T₁ mapping, there is a degree of freedom in selecting which points on the relaxation curve are sampled. However, optimal selection of the timing of the sampling points has not been studied. In this study, we sought to develop a framework for optimal selection of timing of sampling points to achieve improved precision of SR based T₁ mapping.

THEORY: Based on the 3-point signal model for noisy observations, $a(1 - b \exp(-t_k/T_1)) + n_k$, and the least squares parameter fitting model, we derived the Fisher information matrix [4]. This was used to derive the Bayesian Cramer-Rao bound (CRB) [4] for the variance of the T₁ estimator (as a surrogate for precision) for T₁ values of interest between 950 and 1250 ms (~pre-contrast myocardium). This CRB is a function of a , b and $\{t_k\}$, which was evaluated for the SASHA sequence [2] which allows sampling of the SR curve within a heart-beat between T_{min} ($\neq 0$ due to length of saturation pulse and imaging pulses until the center of k-space) and T_{max} (due to the length of the R-R interval), plus one point at full magnetization ($t_k=\infty$). The CRB was minimized over all possible choices of sampling points $\{t_k\}$, yielding the proposed point selection. The explicit formula for the CRB (not shown here) indicates that the values of a and b only re-scale the final value of precision and do not affect the point choice.

METHODS: Phantom imaging of NiCl₂ doped agarose vials was performed to compare the proposed point selection with a uniform distribution of sampling points between T_{min} and T_{max} [3] using an SSFP sequence with body-coil (NSA=5) for 11 sampling points. In-vivo imaging was also performed on 5 healthy subjects (4 women, 23.4±3.3 years) with a 32-channel coil to verify the gains predicted by the theory. All acquisitions (proposed and uniform point selection) were repeated 5 times to average out the effects of noise. T₁ estimation was performed offline using MATLAB (v7.6, MathWorks, Natick, MA) using the 3-point model. A region-of-interest (ROI) analysis was performed on T₁ maps for both phantom and in-vivo imaging. ROIs for phantom imaging were drawn on each vial and for in-vivo imaging were drawn independently by two experienced readers in the myocardium and blood pool. The mean value and standard deviation in the ROI were recorded for each acquisition. The estimated T₁ value, T₁^{est}, is reported as an average ± standard deviation of the mean values in the ROI (over the 5 acquisitions for each sampling strategy), as a surrogate for accuracy and the inter-scan reproducibility. The precision, prec(T₁^{est}), is reported as the average ± standard deviation of the spatial standard deviation of the T₁ values in the ROI (over 5 acquisitions for each sampling strategy).

RESULTS: The point selection yielded a tri-modal distribution of points: 4 at T_{min}, 6 at T_{max}, 1 at ∞ , with a theoretical gain in precision of 24% compared to uniform selection (across the T₁ range 950 – 1250 ms). **Table 1** shows the results of phantom imaging for T₁ values > 700 ms, indicating a good match between theory and experiment. **Table 2** shows the results of in-vivo imaging for the five subjects as measured by one of the readers (due to space limitations). Over the five subjects based on the readings from both readers, there was no difference in accuracy of T₁^{est} ($P = 0.24$ and 0.88 for myocardium and blood respectively). However, there was a 17% and 24% improvement in homogeneity of the T₁ values in the myocardium and blood ($P < 0.001$ for both).

CONCLUSIONS: The proposed framework allows for choosing the sampling times on the T₁ relaxation curve to improve precision without any penalty of accuracy.

ACKNOWLEDGEMENTS: Grant support from NIH K99HL111410-01, NIH R01EB008743-01A2.

REFERENCES: [1] Messroghli, MRM, 2004 [2] Chow, MRM, 2013 [3] Weingärtner, MRM, 2013 [4] Gill, Bernoulli, 1995.

Vial	uniformly distributed points		proposed point selection			theory prec wrt. uniform
	T ₁ ^{est} (ms)	prec(T ₁ ^{est}) (ms)	T ₁ ^{est} (ms)	prec(T ₁ ^{est}) (ms)	prec wrt. uniform	
1	1457 ± 7.7	69.2 ± 6.3	1456 ± 7.4	48.1 ± 5.2	0.70	0.71
2	1144 ± 14.5	55.7 ± 6.7	1130 ± 7.1	41.0 ± 2.5	0.74	0.76
3	1151 ± 11.5	53.2 ± 3.8	1155 ± 8.6	43.1 ± 1.4	0.81	0.76
4	729 ± 10.3	31.3 ± 1.2	724 ± 2.1	26.1 ± 3.3	0.83	0.86
5	980 ± 11.2	34.6 ± 1.2	981 ± 10.4	25.2 ± 0.6	0.73	0.78
6	823 ± 13.3	29.8 ± 2.1	822 ± 7.7	24.2 ± 2.0	0.81	0.83
7	1148 ± 18.4	52.6 ± 6.4	1144 ± 8.3	37.8 ± 1.5	0.72	0.76
8	1130 ± 10.6	55.8 ± 5.6	1137 ± 10.5	45.0 ± 3.9	0.81	0.76
9	963 ± 13.8	49.8 ± 3.4	962 ± 6.2	35.4 ± 2.2	0.71	0.79

Table 1: Results of phantom imaging for vials with T₁ > 700 ms using the proposed and uniform sampling strategies with 11 sample points (each acquisition was repeated 5 times). The ratio of prec(T₁^{est}) for each proposed sampling strategy and that of the uniform sampling strategy is reported as “precision (prec) 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 ($P = 0.23$).

subject	anatomy	uniform point selection		proposed point selection		prec wrt. uniform
		T ₁ ^{est} (ms)	prec(T ₁ ^{est}) (ms)	T ₁ ^{est} (ms)	prec(T ₁ ^{est}) (ms)	
1	myocardium	1188 ± 15.6	115.7 ± 16.2	1194 ± 15.3	91.7 ± 11.0	0.79
	blood	1925 ± 25.1	166.7 ± 16.5	1903 ± 19.2	111.8 ± 7.7	0.67
2	myocardium	1314 ± 25.4	174.4 ± 28.6	1307 ± 21.5	150.1 ± 21.2	0.86
	blood	1772 ± 24.1	205.0 ± 32.3	1755 ± 20.8	148.2 ± 7.2	0.72
3	myocardium	1204 ± 70.2	117.0 ± 16.7	1218 ± 37.8	83.0 ± 13.5	0.71
	blood	1787 ± 37.3	179.7 ± 26.5	1809 ± 35.4	138.1 ± 14.9	0.77
4	myocardium	1213 ± 49.5	107.3 ± 16.7	1207 ± 31.7	85.0 ± 5.3	0.79
	blood	1755 ± 34.7	161.4 ± 16.7	1780 ± 19.2	131.4 ± 12.8	0.81
5	myocardium	1168 ± 54.3	95.3 ± 6.8	1187 ± 14.8	76.6 ± 5.0	0.80
	blood	1772 ± 47.8	164.7 ± 18.9	1761 ± 20.8	114.2 ± 10.4	0.69

Table 2: The results of in-vivo imaging on five healthy subjects using the proposed and uniform sampling strategies, where each acquisition was repeated 5 times as measured by one of the readers. There is an improvement in prec(T₁^{est}) in all cases.