A Novel Algorithm for Improved Pixel-by-Pixel T2* Mapping

Yanqiu Feng[1], Peter D Gatehouse[2,3], David N Firmin[2,3], Dudley J Pennell[2,3], Wufan Chen[1], and Taigang He[2,3]
[1]*School of Biomedical Engineering, Southern Medical University, Guangzhou, China,* [2]*Cardiovascular Biomedical Research Unit, Royal Brompton Hospital, London, United Kingdom,* [3]*National Heart and Lung Institute, Imperial College, London, United Kingdom*

Target audience: Clinicians and engineers who are interested in the liver T2* relaxometry

Introduction

MRI relaxometry mapping (pixel-by-pixel) is sensitive to the noise especially when high-resolution or rapid scans are required. Averaging repeated scans can improve the signal-to-noise (SNR) but with increased imaging time. It is well known that SNR of an image can be improved by averaging pixels in spatial domain. The traditional local means (LM) method through averaging spatially adjacent signals can suppress noise but at the cost of blurring clinically-revellent spatial varying details. Non local means [1] can reduce noise and preserve well the edges by only averaging pixels with similar local patterns; however, if directly applied to filter multiple relaxometry images, NLM will cause distortion to the decaying signal because it can't ensure the weights, in the mean calculation, between two certain pixels are same for the images of different TEs.

Considering decay signals as the objects to be averaged, we aimed at improving the precision of T2* mapping through selectively Averaging the Decay signals with Similar Underlying Relaxation rates (ADSUR) before curve fitting. This novel algorithm was tested on simulation data and an *ex vivo* heart with iron overload.

Methods

The ADSUR algorithm is formulated as:

$$\overline{\boldsymbol{s}(x_i)} = \sum_{x_j \in V_i} w(x_i, x_j)\boldsymbol{s}(x_j),$$

where $\boldsymbol{s}(x_j)$ denotes the decay signal, a vector containing the intensities at pixel x_i of images at all TEs, $\overline{\boldsymbol{s}(x_i)}$ is the output at x_i, V_i is the neighbourhood of x_i and $w(x_i, x_j)$ is the weight indicating the similarity between two decay signals:

$$w(x_i, x_j) = \exp\left(\left\|LM(\boldsymbol{s}(x_i)) - LM(\boldsymbol{s}(x_j))\right\|^2 / \mathrm{h}\right)/z_i\,, \forall x_j \neq x_i,$$

where *LM* denotes the LM filtering, introduced to smooth the influence of noise on the weights calculation. $\|\ \|$ denotes the Euclidean distance, h controls the decay rates of weights as a function of Euclidean distance and z_i is a normalizing factor. The weight $w(x_i, x_j)$ will be large if the underlying relaxation rates of the signals at x_i and x_j are similar. Therefore, signals of T2* similar to that of the current signal contribure more to the output signal.

For the simulation, data were synthesized at TEs = [0.93, 2.27, 3.61, 4.95, 6.29, 7.63, 8.97, 10.40, 11.80, 13.20, 14.60, 16.00 ms] with true T2* = [0.67, 0.8, 1.0, 1.25, 1.67, 2.0, 2.5, 3.33, 5, 6.67, 10, 20 ms] under different SNRs (15, 30, 60). For the *ex vivo* heart, MRI images were acquired on a 1.5T MRI scanner, at 12 TEs from 3.1ms to 29.5 ms with equal TE spacing 2.4ms.The number of excitation (NEX) was set to 1 and 32 for a comparison, representing low and high SNR images with the later as the reference. Four curve-fitting models are utilized: the truncation [2], offset [3], SQEXP, and NCEXP [4]. T2* maps from the original, LM-filtered and ADSUR-filtered data were presented. Root mean square errors (RMSE) were calculated for T2* maps from simulated data to quantitatively evaluate the precision of T2* mapping.

Results/Discussion

Figure 1 shows that, for all curve fitting models, pixel-wise fitting original images produces T2* maps with high variances. The LM algorithm produces smoother T2* maps but leads to blurring of edges and interfaces. By contrast, the ADSUR algorithm reduces the impact of noise while preserving the edges and details of rapid-changing T2*s. Quantitatively, the ADSUR algorithm produces T2* maps with improved precisions using all curve fitting models under different SNRs (Table 1).

Similar to the simulation study, in the *ex vivo* heart (Figure 2), the ADSUR algorithm applied to low SNR images produces T2* maps close to that from the high SNR images.

Conclusion

The T2* mapping can be improved by filtering the serial images with the proposed ADSUR algorithm, independent of curve-fitting models used.

Table 1:RMSEs of T2 mapping

SNR	Method	Truncation	Offset	SQEXP	NCEXP
5	ORG	3.38	1.59	1.04	0.96
	LM	0.90	0.96	0.86	0.86
	ADSUR	0.32	0.57	0.28	0.25
30	ORG	0.47	0.62	0.48	0.41
	LM	0.81	0.92	0.83	0.81
	ADSUR	0.12	0.35	0.13	0.11
60	ORG	0.22	0.40	0.25	0.21
	LM	0.80	0.91	0.82	0.80
	ADSUR	0.06	0.26	0.07	0.06

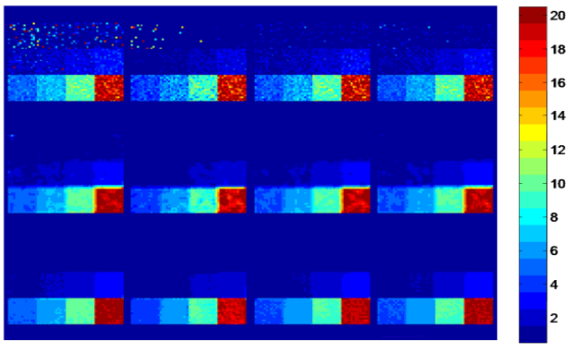

Figure 1. T2* maps estimated from original (first row), LM-filtered (second row) and ADSUR-filtered (third row) data in simulation(SNR = 15) using different fitting models. Left to right: T2* maps fitted by the truncation, offset, SQEXP and NCEXP models respectively.

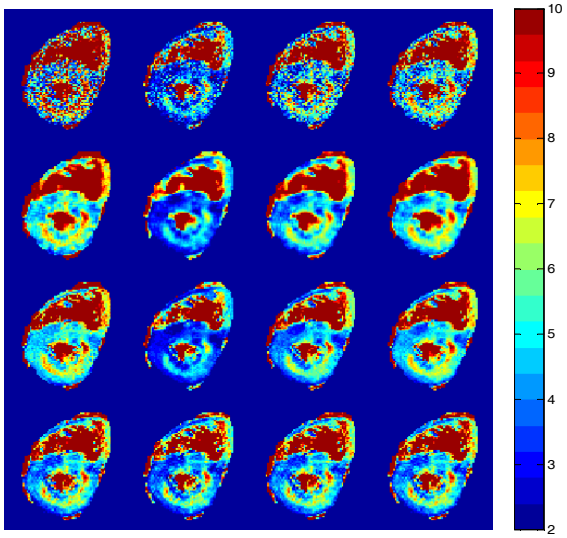

Figure 2. T2* maps of the *ex vivo* heart (NEX=1) estimated from original (first row), LM-filtered (second row) and ADSUR-filtered (third row) data using different fitting models (left to right): the truncation, offset, SQEXP and NCEXP models. The fourth row are the reference T2* maps from original images with NEX = 32.

References:

[1] Buades, et al., Multi Model & Simu, 4(2):490-530,2005; [2] He, et al., Magn Reson Med, 60(2): 350-6, 2008; [3] Ghugre, et al., J Magn Reson Imaging, 23(1): 9-16, 2006; [4] Raya, et al., Magn Reson Med, 63(1): 181-93, 2010