An algorithm for fast and accurate T2* mapping based on Auto-Regression on Linear Operations (ARLO) of data

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Target Audience Researchers and clinicians interested in MR relaxometry.

PURPOSE Mono-exponential fitting of the MR signal decay to obtain transverse relaxation times (T2 or T2*) has been central to many quantitative MR methods for mapping tissue properties. For example, T2* is widely used to quantify iron deposition in the liver (1-2), brain (3), and heart (4) as well as in edema. Non-linear least squares based Levenberg-Marquardt (LM) (1) and Log-Linear (LL) (2) are the most popular methods for exponential fitting. The iterative LM algorithm is generally regarded as more accurate but computationally more expensive than the non-iterative LL algorithm which is fast but sensitive to noise. Here we propose a novel fast and accurate method for calculating T_2^* called Auto Regression on Linear Operations (ARLO) and compare it with LM and LL using simulated and in vivo data.

METHODS ARLO applies a linear operation on the exponential decay signal $m(t) = M_0\, exp(-t/T_2^*)$ and estimates T2* via a maximum-likelihood fit of the resulting autoregressive (AR) model. As an example, integrating $m(t)$ over *3* consecutive echoes yields the following integrated signal:

$$s_i = \int_{t_i}^{t_{i+2}} m(t)\, dt = T_2^*[m(t_i) - m(t_{i+2})] \equiv T_2^* \delta_i \qquad [1]$$

This integral can be computed numerically using the Simpson's rule:

$$s_i \cong \frac{\Delta TE}{3}[m(t_i) + 4m(t_{i+1}) + m(t_{i+2})] \qquad [2]$$

By equating the right-hand sides of Eqs.1&2 and solving for $m(t_{i+2})$, we obtained the following AR model of order 2 for the time series of the measured signal $m(t)$:

$$m(t_{i+2}) = -\frac{\frac{4\Delta TE}{3}}{T_2^* + \frac{\Delta TE}{3}} m(t_{i+1}) + \frac{T_2^* - \frac{\Delta TE}{3}}{T_2^* + \frac{\Delta TE}{3}} m(t_i) + n(t_{i+2}) \qquad [3]$$

The AR model coefficients (which only depend on T2*) can be obtained as a maximum-likelihood estimate by minimizing the following cost function (5):

$$T_2^* = \arg\min_{T_2^*} \frac{1}{(T_2^* + \Delta TE/3)^2} \sum_{i=1}^{N-2} (s_i - T_2^* \delta_i)^2 \qquad [4]$$

whose closed-form solution gives the value of T2*:

$$T_2^* = \frac{\sum_{i=0}^{N-2} s_i^2 + \Delta TE/3 \sum_{i=0}^{N-2} s_i \delta_i}{\Delta TE/3 \sum_{i=0}^{N-2} s_i^2 + \sum_{i=0}^{N-2} s_i \delta_i} \qquad [5]$$

To assess the speed and accuracy of ARLO (Eq.5) compared with LM and LL, computer simulations using known T_2^* values were performed at various SNR and number of receiver coils, assuming 16 equidistant echoes (1.3-23.3 ms). Next, multi-echo GRE data were acquired in the iron overloaded livers (n=15) and hearts (n=1) at 1.5T, as well as in healthy brains (n=2) at 3T. Data truncation (4) and Rician noise bias correction were applied prior to data fitting. ARLO and LL fitting did not require a T2* initial guess. All data were processed using Matlab on an Intel Core i7 2.8 GHz processor, except brain data which were processed using C++ implementations on the host computer of a GE HDxt scanner.

RESULTS **Accuracy**: Simulations (Fig.1) showed ARLO and LM delivered lower bias (higher accuracy) and smaller standard deviation (higher precision) than LL over the investigated range of SNR (20-100) and number of receivers (1 and 8), and for T_2^* between 1.5 and 10 ms. The T_2^* errors of ARLO and LM were consistently ≤ 4%. LL was more sensitive to noise (5.2-13.9% error), especially at shorter T_2^* and higher number of coils. In liver patients, both LM and ARLO provided excellent T2* maps, while LL T2* maps were grainy (Fig.2). Liver ROI analysis showed that LL had limited correlation and agreement with both LM (R^2 = 0.69) and ARLO (R^2 = 0.68), while ARLO agreed well with LM (R^2 = 0.998, slope of regression line = 0.991, -0.03 ms bias and -0.18 - 0.11 ms confidence interval) (P<0.01) (Fig.3). The three methods provided similar T2* maps in the brain (Fig.4) and the heart (Fig.5). **Speed**: The average fitting time in Matlab for 4 liver slices was 88 ± 29 s for LM and 6 ± 2 s for LL and only to 0.7 ± 0.2 s for ARLO, representing a 125 and 8 times gain in computational speed by ARLO. The whole brain fitting time using our C++ implementations was 35 sec and 9.25 min for LL and LM, respectively, while ARLO took only 2.7 sec.

DISCUSSION The proposed ARLO algorithm can provide fast and accurate T2* maps, which makes it well-suited for whole-organ T2* mapping in iron overload diseases, and can prove effective in other MRI studies. ARLO can replace the LL algorithm for accurate online T2* mapping, and replace the LM algorithm for accurate fast analysis of exponential signal behaviors. The ARLO approach may be modified to handle a constant offset and may also be generalized to handle multi-exponential or multi-spectral T2/T2* decay data such as in addressing the confounding effect of fat on liver T2* quantification.

REFERENCES 1.Hankins et al. Blood 2009;113:4853. 2. Henninger et al. Eur Radiol 2012;22:2478. 3. Langkammer et al. Radiology 2010;257:455. 4. He et al. MRM 2008;60:1082. 5. Hamilton. Time series analysis. Princeton University Press, 1994.

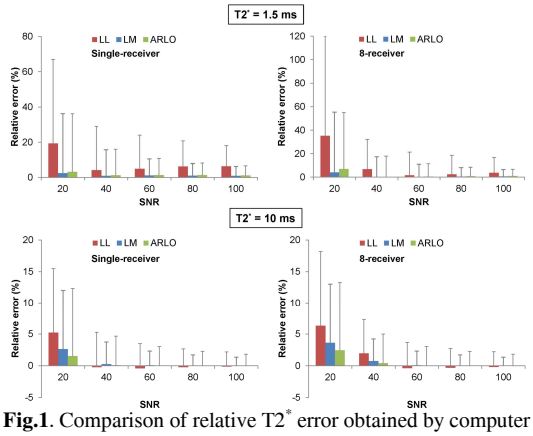

Fig.1. Comparison of relative T2* error obtained by computer simulations for conventional LL and LM and proposed ARLO algorithms.

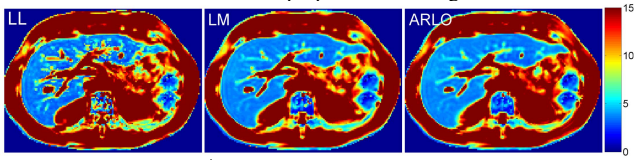

Fig.2.Comparison of T2* maps obtained from a patient with liver iron overload, demonstrating improved precision with LM and ARLO.

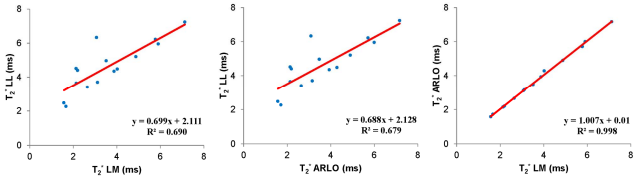

Fig.3. Linear regression plots of diseased liver T2* obtained by ROI analysis using LL, LM and the proposed ARLO algorithms (n=15).

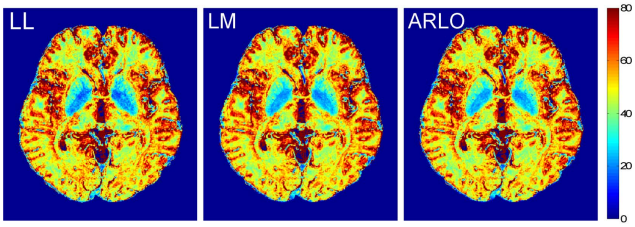

Fig.4. Example of brain T2* maps with similar quality obtained from a healthy volunteer at 3 T using LL, LM and ARLO algorithms. The total C++ fitting time for whole brain was 41 sec and 606 sec for LL and LM, respectively, while ARLO took only 3.4 sec.

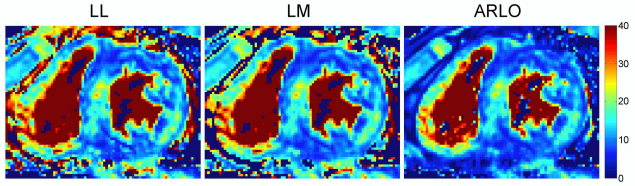

Fig.5. T2* maps obtained from a patient with myocardial iron overload.