An algorithm for fast and accurate T2* mapping based on Auto-Regression on Linear Operations (ARLO) of data
Mengchoa Pei1,2, Thanh D. Nguyen1, Nanda D. Thimmappa2, Carlo Salustri3, Fang Dong1, Mitchell A. Cooper2, Jianqi Li1, Martin Prince4, and Yi Wang1
1East China Normal University, Shanghai, Shanghai, China, 2Yifu Inc, Jiaxing, Zhejiang, China, 3Radiology, Weill Cornell Medical College, New York, NY, United States, 4Cornell University, Ithaca, NY, United States, 5East China Normal University, Shanghai, China

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 T2* 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) = M0 exp(-t/T2*) 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:

\[ s_i = \int_0^{t_2} m(t) \, dt = T_2^* \sum_0^3 (m(t_i) - m(t_{i+2})) \equiv T_2^* \delta_i \]  \hspace{1cm} [1]

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

\[ s_i \equiv \frac{4\Delta T E}{3} \sum (m(t_i) + 4m(t_{i+1}) + m(t_{i+2})) \]  \hspace{1cm} [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):

\[ m(t_{i+2}) = \frac{4\Delta T E}{3} m(t_i) + \frac{\Delta T E}{T_2^*} m(t_{i+1}) + n(t_{i+2}) \]  \hspace{1cm} [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):

\[ T_2^* = \arg \min_{T_2^*} \frac{1}{2} \sum_{i=1}^{N-2} (s_i - T_2^* \delta_i)^2 \]  \hspace{1cm} [4]

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

\[ T_2^* = \frac{\sum_{i=0}^{N-2} s_i^2 + \Delta T E / (3 \sum_{i=0}^{N-2} s_i \delta_i)}{\Delta T E / (3 \sum_{i=0}^{N-2} s_i^2 + 3 \sum_{i=0}^{N-2} s_i \delta_i)} \]  \hspace{1cm} [5]

To assess the speed and accuracy of ARLO (Eq.5) compared with LM and LL, computer simulations using known T2* 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 (2) and Rician bias noise 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 HDx 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 T2* between 1.5 and 10 ms. The T2* errors of ARLO and LM were consistently ≤ 4%. LL was more sensitive to noise (5.2-13.9% error), especially at shorter T2* 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 (R2 = 0.69) and ARLO (R2 = 0.68), while ARLO agreed well with LM (R2 = 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 LL and 6 ± 2 s for LL and only to 0.7 ± 0.2 s for ARLO, representing a 125 and 8 times gain (P<0.01) (Fig.3). The three methods provided similar T2* maps in the brain (Fig.4) and the heart (Fig.5).

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