OPTIMIZATION OF QUANTITATIVE MAGNETIZATION TRANSFER IMAGING USING A SELECTIVE INVERSION RECOVERY PULSE

K. Li[1,2], Z. Zu[1,2], J. Xu[1,2], J. C. Gore[1,2], H. M. Whitney[1,3], and D. F. Gochberg[1,2]

[1]Vanderbilt University Institute of Imaging Science, Nashville, TN, United States, [2]Department of Radiology and Radiological Sciences, Vanderbilt University, Nashville, TN, United States, [3]Department of Physics and Astronomy, Vanderbilt University, Nashville, TN, United States

Introduction: Quantitative magnetization transfer (qMT) imaging maps properties of the tissues that are usually interpreted in terms of two pools of protons, corresponding to free and immobilized fractions. The selective-inversion-recovery fast-spin-echo (SIR-FSE) qMT technique developed recently (1) includes an inversion time (t_i) which is varied between 3.5 ms and 10 s, while the delay before the next sequence repetition (t_d) is held constant. qMT parameters are determined by fitting the resulting recovery to a bi-exponential function of t_i using an approximate solution. In the current study, we employ a new protocol that varies both t_i and t_d and fits the data with minimal approximations. Cramer-Rao lower bounds (CRLB) are calculated to select the variations in both t_i and t_d that will maximize the precision-per-unit-time. Monte Carlo simulations support this approach by showing a large reduction in the resulting qMT parameter uncertainties. The optimization results are also confirmed by measurements on a series of BSA phantoms with different percent weights.

Techniques: The essential insight of the selective-inversion-recovery fast-spin-echo (SIR-FSE) sequence (Fig. 1) is that at the end of each repetition, both the macromolecular and free water pools have zero z-magnetization, due to the 90° pulse on the free water pool, followed by a series of evenly spaced 180° pulses and the MT between the two pools (1). The magnetizations of both pools in the decay and inversion recovery process are described by a bi-exponential equation. We have developed a description of the signal, from which we are able to fit the qMT parameters directly and reduce the number of approximations as taken in (1).

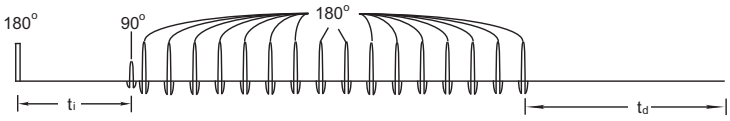

Fig. 1. SIR-FSE sequence

The goal of the optimization is to find a set of sample points, $x_1, \ldots, x_N$ that minimize the variance of the fitted parameters, where x is a combination of t_i and t_d. The objective function consists of two components. One is the CRLB, which minimizes uncertainties of the fitted qMT parameters. The other is the time cost of the acquisition scheme, to account for the expected sqrt(time) dependence of the SNR. A simulated annealing algorithm is used to search for the optimal solution. To reduce the possibility of local minima biasing our results, we repeat the optimization process from different random starting points and select the configuration with the minimum objective function. The upper limit of t_i or t_d is set to 6 s. The macromolecular direct saturation (S_m) and longitudinal recovery (R_{1m}) are assumed to be 0.83 and 0.5, respectively. The qMT parameters chosen are R_{1f}=0.5, p_m/p_f=0.10, k_{mf}=30, S_f=-0.95, and $M_f(\infty)$=1. Optimal scheme for qMT parameters in ranges are also calculated.

SIR-FSE measurements employing both acquisition schemes have been performed on 10, 15, 20, and 30% by weight bovine serum albumin (BSA). All samples were cross-linked using glutaraldehyde. Data were taken on a 7T Varian magnet with a birdcage coil.

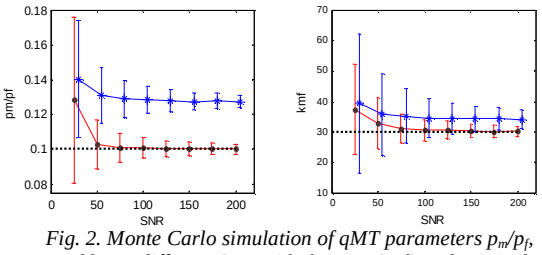

Fig. 2. Monte Carlo simulation of qMT parameters p_m/p_f, and k_{mf} at different SNR with the new (red) and original (blue) schemes. The dot line indicates the true value.

Results: Fig. 2 shows a comparison of numerical simulations employing the original acquisition scheme in (1) (which only varies t_i and makes Taylor series approximations) and the new method described in this abstract (which makes optimized variations in t_i and t_d, makes minimal approximations). Fig. 3 maps the measured qMT parameters R_{1f}, p_m/p_f, and k_{mf} acquired with the new scheme, and Fig. 4 plots R_{1f}, p_m/p_f, and k_{mf} as a function of the BSA to water weight ratio with both schemes for a central pixel in each phantom.

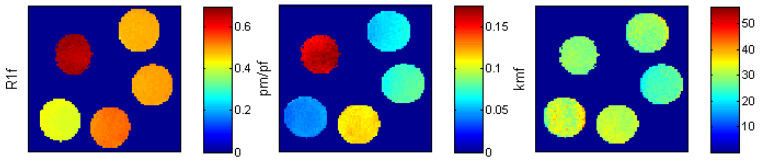

Fig. 3. R_{1f}, p_m/p_f, and k_{mf} of (starting from top left in clockwise direction) 30%BSA, 15%BSA + $MnCl_2$, 15% BSA, 20% BSA, and 10% BSA.

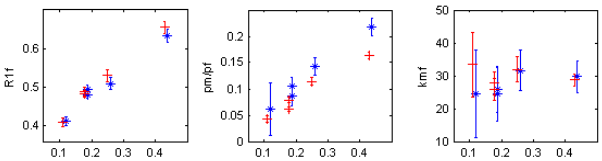

Fig. 4. Measured R_{1f}, p_m/p_f, and k_{mf} as a function of BSA to water weight ratio from the new (red) and original (blue) schemes.

Discussion: Fig. 2 illustrates that the new method is both more accurate and more precise than the original technique. Fig. 3 and Fig. 4 indicate that the pool size ratio p_m/p_f values increase linearly with the BSA to water weight ratio, as well as R_{1f}, which is in agreement with (2). The pool size ratio and k_{mf} are similar for 15% BSA and 15% BSA with $MnCl_2$, which is consistent with this being a measure of MT and not just a function of the relaxation rates. In total, this new optimized qMT method provides a superior means for determining MT parameter values.

References: (1) Gochberg DF et al [2007], MRM 57:437-441. (2) Gochberg DF et al [2003], MRM 49:501-505.

Acknowledgements: This research is supported by NIH RO1EB001452.