A simple iterative reduction method for optimization of quantitative magnetization transfer imaging

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Introduction: Quantitative magnetization transfer imaging (QMTI) [1] yields the parameters – F, k_f, R_{1f}, T_{2f}, and T_{2r} – of the two-pool model for magnetization transfer (MT). Data are usually acquired using spoiled gradient-echo sequences with shaped off-resonance saturation pulses. The amplitude (or flip angle, α) and central frequency (Δ) of these saturation pulses are set according to the needs of the experiment, traditionally to cover the Z-spectrum uniformly [1,2]. Naturally, QMTI can benefit from optimized selection of the MT weightings. A previous study [3] used global Cramer-Rao Lower-Bound (CRLB) optimization of α-Δ pairs to yield sets of 10 and 15 MT weightings for brain white matter (WM) imaging, for the constant-wave-power-equivalent model of QMTI. We present a simple method for the selection of optimal MT weightings, by iterative reduction of the MT sampling from a discrete space. The optimal number of MT weightings is also investigated.

Methods: The "reduction" method begins with a broad N-point sampling, $\mathbf{X}^{(N)}$, of the Z-spectrum, and iteratively reduces the sampling by one point at a time, using an A-optimality criterion, to produce an optimized sampling. At each iteration, all sub-samplings $\mathbf{X}_j^{(n-1)}$ ($j = 1 \ldots n$), with n-1 points, of the current n-point sampling $\mathbf{X}^{(n)}$ are considered: the total estimate variance $\sigma_{n-1,j}^2$ is computed for all $\mathbf{X}_j^{(n-1)}$, using numerical propagation of error through the signal equation [4]. The $\mathbf{X}_j^{(n-1)}$ that results in the smallest increase in $\sigma_{n-1,j}^2$ relative to σ_n^2 (from $\mathbf{X}^{(n)}$) is retained, thereby eliminating the α-Δ pair which provides the least information. The computation is repeated until the desired number of MT weightings is reached. In this study, the optimized sampling was derived based on typical MT model parameters for WM at 1.5 T [1] ($F = 0.16$, $k_f = 4\ s^{-1}$, $R_{1f} = 1.7\ s^{-1}$, $T_{2f} = 35$ ms and $T_{2r} = 12$ µs), from $N = 320$ MT weightings (2 TRs × 5 α × 32 Δ), for the rectangular-pulse model [1]. QMTI data were acquired on a 1.5 T scanner (Siemens, Erlangen, Germany) in a single female subject, using uniform and optimized 10-point samplings. The impact of sampling on reproducibility was retrospectively evaluated in 5 healthy adults (3M/2F, age 26-38) scanned four times each, with subsets of uniform 60-point data.

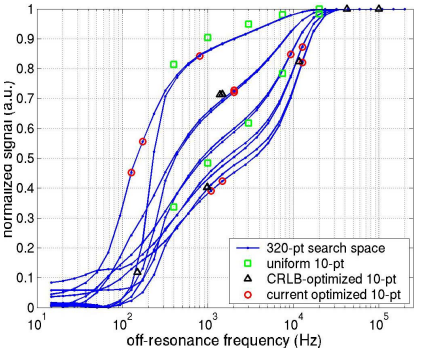

Figure 1. Visual comparison of sampling schemes: uniform 10-point [1] (squares), 10-point optimized using CRLB [3] (triangles), and current method (circles). Blue lines indicate the initial 320-point search space. Note the similar clustering of α-Δ pairs in the optimized methods.

Results: The 10-point optimized scheme derived for WM is illustrated in Fig. 1, with the optimized scheme of [3], and the uniform scheme of [2]. Optimizations performed for a grey matter model, and simultaneously for models of white and grey matter, resulted in optimization schemes with at most two slightly different MT weightings. Example maps acquired using the optimized and uniform 10-point protocols are shown in Fig. 2, showing a clear difference in map quality. Differences between the respective k_f maps and T_{2f} indicate that the sampling of the Z-spectrum might introduce systematic parameter biases. The variance-efficiency (= [variance × scan time]$^{-1/2}$) of our optimized sampling method is plotted against the number of MT-weightings, in Fig. 3. The peak at $N = 7$ suggests this as the optimal number of MT weightings in this case. The longitudinal variability of QMTI parameters from the optimized sub-sampling was comparable to that of the 60-point scheme, as plotted in Fig. 4, while variability increased substantially for uniform sub-sampling, demonstrating the utility of optimized sampling.

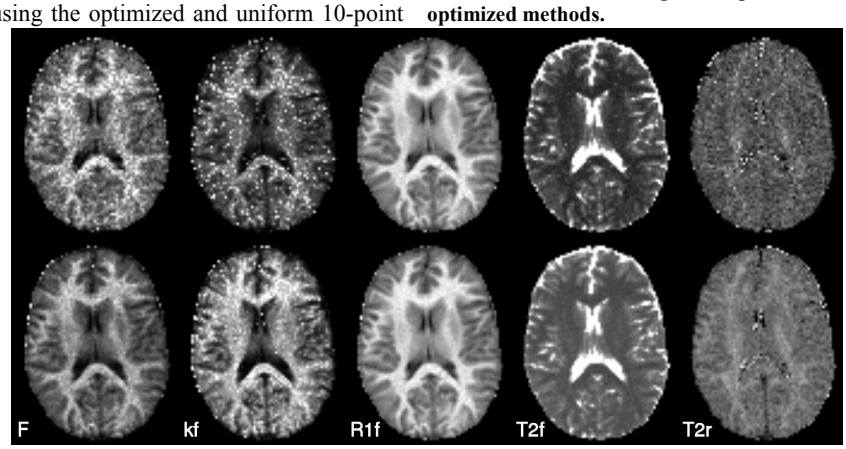

Figure 2. Example QMTI maps from uniform (top row), and optimized (bottom row), 10-point samplings, acquired in different subjects but on the same scanner, with identical SNR and windowing. Note the higher SNR in the optimized maps.

Discussion: The reduction method presented here is simple and straightforward to implement, and produces samplings that agree with a prior report [3]. We observe that optimization for multiple sets of tissue MT parameters makes little difference in the sampling scheme and yields only small gains in parameter precision. The reduction method avoids repeated points and clusters of nearby points, a feature of more general optimal designs that tends to be uninformative for model validation. Our technique is constrained by the initial search space, which needs to defined to include all of the measurements that are potentially of interest. In closing, optimization of QMTI data sampling reduces the acquisition time while maintaining parameter map quality and reproducibility.

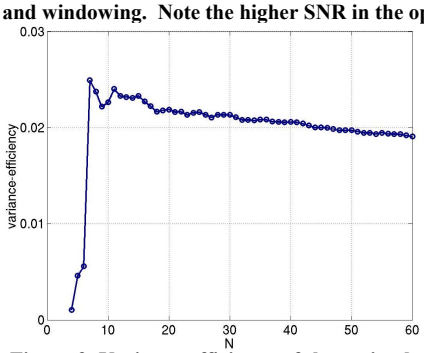

Figure 3. Variance-efficiency of the optimal MT sampling scheme derived from 320-points, for a WM model at 1.5 T, as a function of the number of MT weightings.

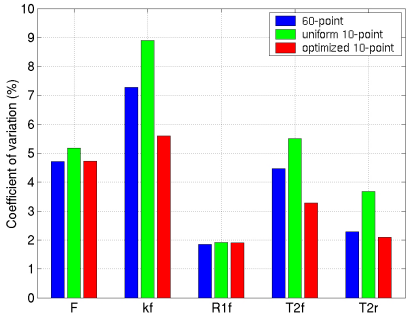

Figure 4. Longitudinal variability of QMTI, in 5 subjects, from sampling schemes with 60 uniform (blue), 10 uniform (green) and 10 optimized (red) MT samplings.

References: [1] Sled & Pike (2001) MRM 46:923, [2] Cercignani *et al*. (2005) NeuroImage 27:436, [3] Cercignani & Alexander (2006) MRM 56:803, [4] Bevington & Robinson (1963) "Data Reduction and Error Analysis for the Physical Sciences", McGraw-Hill, 336 pp.