Towards online reconstruction of quantitative magnetization-transfer imaging

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Introduction

Quantitative magnetization-transfer imaging (qMT) offers a unique contrast yielding detailed information to characterize tissue properties (2,4). It is especially sensitive to pathological disorders affecting myelinisation, such as multiple sclerosis (2). In contrast to magnetization-transfer ratio imaging qMT has been proven to offer reproducible datasets (6).

A challenging aspect of qMT is the complex model describing a solid and a semi-solid pool exchanging magnetization, which leads to long scanning times and difficult post processing (1,2,4). On the imaging end, recent efforts include attempts towards whole-brain imaging (2) and optimized acquisition schemes (5). Post-processing is a protracted endeavor because either differential equations must be solved numerically or demanding equations are needed to estimate qMT maps (1). We present a fast fitting algorithm which greatly reduces post-processing time.

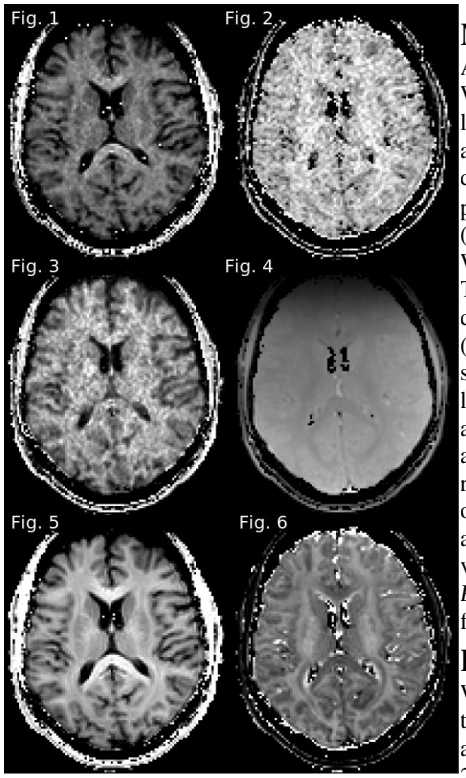

Fig. 1-4: Reconstruction using 10 datapoints. Fig. 1: $f/R_a(1\text{-}f)$, Fig. 2: T_{2b}, Fig. 3: $1/R_aT_{2a}$ and Fig. 4: gM_0. Fig. 5 shows the $f/R_a(1\text{-}f)$ map using the full dataset. Fig. 6 shows the error introduced by fixing RM_0. The error remains below 0.5%.

Methods

All measurements were performed at 3T (Siemens MAGNETOM Trio) using an 8-channel head coil. We used a spoiled gradient-echo sequence with Gaussian off-resonance saturation pulses (13 logarithmically distributed off-resonance frequencies between 1 kHz and 30 kHz; 5 saturation-pulse amplitudes between 163 rad/s and 815 rad/s). Offset frequencies below 1 kHz were not used to avoid direct saturation of the free water pool biasing the results (6). 5 sec of dummy cycles and 9 repetitions per saturation scheme resulted in a scanning time of 61 min for a voxel size of $1.6\times1.6\times4.0\,\text{mm}^3$. T_1 ($T_{a\text{obs}}$) mapping was achieved using a Look-Locker sequence with a GRAPPA acceleration factor of 3. With additional B_0 and B_1 mapping, the overall scanning time was 75 min.

The datasets were fitted using Ramani's model based on the work of Henkelman et al. (1,3). The full dataset was fitted as well as a subset with 10 saturation schemes similar to those used by Ramani et al. (1) which would correspond to a scanning time of 2.5 min per slice. To speed up post processing, several strategies were implemented in the algorithm: As T_{2b} (T_2 of bound fraction) is known to vary little in the human brain, a combination of a brute-force algorithm and a Levenberg-Marquardt algorithm (least square) was used. In a first step, the T_{2b} was fixed in 4 logarithmic steps between 3 µs and 27 µs estimating, $f/R_a(1\text{-}f)$, $1/R_aT_{2a}$ and gM_0 using the Levenberg-Marquardt algorithm. f is the ratio of the bound protons M_{0b} to the overall pool size $M_{0b} + M_{0a}$. R_a is the longitudinal relaxation rate of the free water pool and g a scaling factor. Starting parameters were 0 for both $f/R_a(1\text{-}f)$ and $1/R_aT_{2a}$ and the maximum signal intensity from all saturation schemes for gM_0. In a second step, the estimated values with the lowest deviations were used as start parameters for a fit with T_{2b} as a free parameter. R_b was fixed to 1 Hz as suggested in Ref. (1) and RM_0 was set to 3000 Hz reducing the number of fitted parameters to four.

Results

With our new fitting procedure, the post-processing time was reduced to less then 45 sec per slice for the full dataset. Fig. 5 shows the $f/R_a(1\text{-}f)$ values for the full dataset. Using only the offset frequencies and amplitudes as suggested in Ref. (1), the fitting times were reduced to 8 sec per slice (1 core of a 2.3 GHz Intel Xeon E5345 quadcore CPU). Figs. 1-4 show the estimated parameter maps. In contrast to Fig. 5, Fig 1 is biased. This should be taken into consideration, when estimating $f/R_a(1\text{-}f)$ maps with fewer data points. Using 4 CPU cores, a computer setup typical for modern scanners, the fitting time was only 2 sec per slice. Fitting RM_0 always resulted in values of roughly 3000 Hz; hence, fixing this parameter seemed appropriate, inasmuch as it does not seem to provide diagnostic potential (2) Fig. 6 shows the deviation map for values of RM_0 between 500 Hz and 10 MHz.

Discussion

The presented algorithm was found promising for potential online reconstruction on modern scanners, which might be useful in future clinical application of qMT. An improved algorithm recognizing divergence in anatomically irrelevant voxels during the fitting procedure might further improve the post processing. Finally, with the next generation of computers, post processing of qMT should not present a problem.

References

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