High-resolution Isotropic Whole Brain T2 Mapping with Model-based Super-resolution Reconstruction

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Synopsis

We propose a method to reconstruct 1-mm^3 isotropic T2 maps based on multiple 2D multi-echo spin-echo (MESE) acquisitions. To compensate for the prolonged scan time due to multiple acquisitions, data were highly (10-fold) undersampled. The data was reconstructed by combining a classical super-resolution approach with an iterative model-based reconstruction. The method was tested on a phantom and four healthy volunteers. T2 values were compared against fully sampled MESE data. The proposed technique allows the assessment of T2 values in brain structures at high isotropic resolution.

Purpose

High-resolution isotropic brain T2 mapping with multi-echo spin-echo (MESE) acquisitions is difficult due to the slice thickness limitation of a 2D sequence[1]. If used as a 3D acquisition, SAR limits are easily exceeded due to the high power deposition of non-selective refocusing pulses[2]. These limitations can be addressed by using super-resolution (SR) reconstruction where multiple low-resolution (LR) images are acquired with a different FOV[1] or orientation[3,4,] and combined by solving a non-linear problem. However, the need for multiple orientations results in a substantial increase in scan duration. We propose to combine model-based[5] and SR[1] reconstruction to obtain high-resolution (1-mm^3 isotropic) T2 maps based on an undersampled MESE acquisition.

Theory

A high-resolution series of images x_n (with $n = 1, \ldots, N$, and N the number of spin-echoes) is estimated by minimizing the difference to LR k-space $y_{j,n,c}$ with S_c coil sensitivities (with $c = 1, \ldots, C$, and C the number of coils), T_j representing a rotation or translation of the FOV (with $j = 1, \ldots, J$, and J the number of LR k-spaces), $\downarrow$ downsampling operator, F Fourier transform and P undersampling. Subsequently, the image corresponding to the signal model $x_n = M_0 exp(-t_n/T2)$ is calculated by fitting a mono-exponential decay onto x_n (with echo-time t_n), intrinsically estimating $T2$ and M_0:

$$\arg\min_{T2,M_0,x_n} \sum_{i=1}^{C} \sum_{n=1}^{N} \sum_{j=1}^{J} \| PF\{S_c \downarrow T_j x_n\} - y_{j,n,c}\|^2 + \lambda_\| x_n - M_0 exp\left(-\frac{t_n}{T2}\right)\|^2$$

where the first term ensures data-consistency of the HR image with the acquired data and the second term ensures model-consistency. To balance the two terms, a regularization parameter λ is introduced. The optimization is done iteratively by alternating between minimising data- and model-consistency (see Figure 1)

Methods

Simulations were performed on a numerical phantom[6] to ascertain the trade-off between number of rotations and the acceleration factor. To this end, T2 maps were reconstructed from the simulated undersampled LR k-spaces for an increasing number of rotations and acceleration factors. The differences from the gold-standard T2 map were visually inspected and the root mean square error (RMSE) was calculated.

Data from a multipurpose phantom and four healthy subjects were acquired at 3T (MAGNETOM Skyra, Siemens Healthcare, Erlangen, Germany) with a 10-fold- accelerated GRAPPATINI[7] prototype sequence (60 sagittal slices, (1x1x4) mm^3 resolution, TR=5.4s, ΔTE=10ms, ETL=16). The acquisition was repeated four times with each scan rotated about the longitudinal axis at incremental steps of 45° (TA=18:04min). For comparison, 29 axial slices with 4mm thickness were acquired with a fully sampled MESE sequence. For the phantom, a single slice was acquired using a conventional single-echo SE sequence with three TEs (12,50,100 ms).

The proposed approach was compared to two other methods. The first approach is the "LR model-based + SR" reconstruction where the T2 maps were reconstructed on the individual LR orientations using model-based reconstruction followed by up-sampling to a HR grid. The second approach is the 'SR only' reconstruction without the model consistency term.

ROI analysis was performed on the phantom and in vivo T2 maps. T2 values from different compartments of the phantom were compared to the T2 values from fully sampled MESE and SE data. T2 values from ROIs were compared across volunteers to assess the consistency of T2 values.

Results

Numerical simulations showed that the best trade-off is 10-fold acceleration with four rotations (RMSE=7.8 ms, TA=18 mins). Five rotations and 6-fold acceleration showed the least error (RMSE=3.2 ms) but required an acquisition time of 37 minutes (Figure 2). Fourteen-fold acceleration with five rotations had an acquisition time of 14 minutes but an RMSE of 12.5 ms.

The proposed algorithm (Figure 3) showed improved resolution over LR images for both phantom and brain. Comparison between the proposed methods and the 'SR only' and 'LR model-based + SR reconstruction' showed that integrating SR and model knowledge in one cost function improves the reconstruction (Figure 4).

ROI analysis of the phantom compartments revealed that at shorter T2, the proposed method was comparable with the fully sampled MESE. However, the error increased with higher T2 values (compartments 3 and 4 showing a relative difference of 10-12%, and 15% for compartment 5). For the volunteers' data, the values found in the brain structures were consistent across subjects (8.5-13.1ms standard deviation).

Discussion and Conclusion

Model-based super-resolution T2 mapping enables reconstruction of HR relaxation maps with a ten times faster acquisition in comparison to a fully sampled acquisition. However, total acquisition time is still not acceptable in clinical routine. Future work should explore further acceleration with different sampling patterns or simultaneous multi-slice[8]. In addition, motion correction and slice profiles were not considered for this work. Including those in future work will considerably improve the performance of the algorithm.

Acknowledgements

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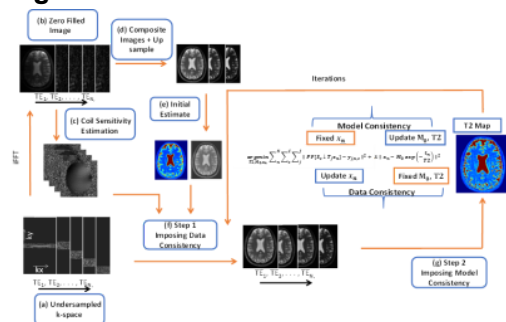
Figures

Figure 1: The schematic flowchart for model-based SR reconstruction: a) k-space data with block undersampling; b) Zero-filled image using inverse FFT in the phase-encoding direction; c) Sensitivity maps estimation; d) Composite images are formed and up-sampled to HR grid; e) Initial x_n is estimated from composite images f) Data consistency is imposed as a first step of alternating minimization; g) T2 maps estimated by imposing model consistency in the second step. With the new estimate of T2, step 1 and step 2 are repeated iteratively.
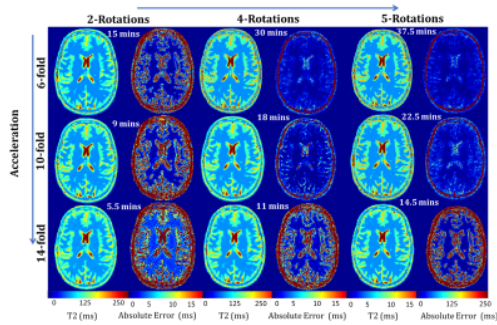
Figure 2: The gain in the quality of SR-T2 reconstruction as a function of number of rotations and acquisition time in a numerical phantom. The corresponding acquisition times are mentioned with the T2 maps. Adding more rotations results in reduced error around the edges for all acceleration factors (from left to right). At the same time, the acceleration factor effects the quality of the reconstruction (top to bottom), especially for high T2 values in the cerebral spinal fluid. Considering the increase in acquisition time with the number of rotations, the dataset that is considered optimum is 10-fold with four rotations.
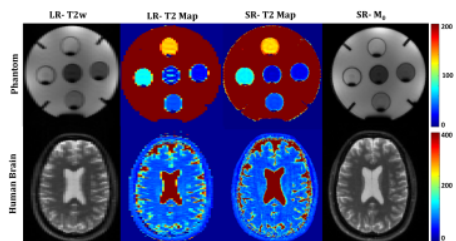

Figure 3: (a) Low-resolution T2-weighted images from the phantom and brain; (b) Respective LR T2 maps; (c) T2 maps; and (d) proton density (M0) reconstructed using proposed approach demonstrates better resolution within the compartments of phantom and in brain structures.
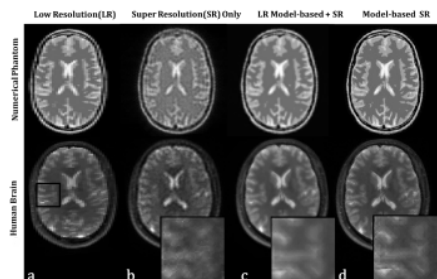

Figure 4: Reconstructed Images from numerical phantom and in vivo data. The images are shown from (a) low-resolution, (b) super resolution only, (c) LR model-based reconstruction followed by super resolution, and (d) proposed SR model-based reconstruction. The SR only reconstruction showed visible artifacts due to the undersampling as no prior information from the model was incorporated. The LR model-based + SR reconstruction showed improvement in the reconstruction; however, blurring around the edges is evident in both numerical phantom and in vivo data.
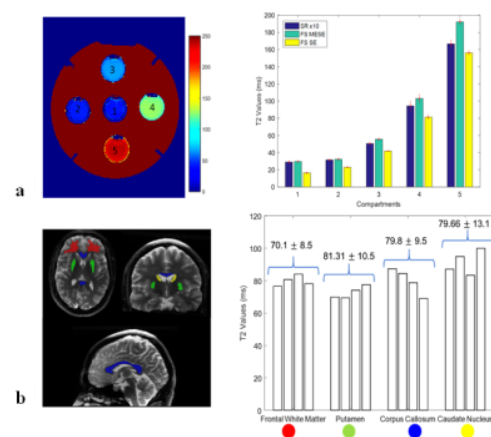

Figure 5: a) The bar chart represents the mean of the T2 values of the ROI and the error represents the standard deviation for the 10-fold accelerated, fully sampled MESE and SE acquisitions. The values measured with a MESE sequence were overestimated as compared to SE. This overestimation is caused by stimulated echoes originating from incomplete spin refocusing. T2 values from the 4th and 5th compartments are biased the most compared to the other compartments. b) ROIs drawn in different structures of brain with the bar chart representing the mean T2 values across all the volunteers.