A Bayesian Algorithm Using Spatial Priors for Multi-Exponential T2 Relaxometry from Multi-Echo Spin Echo MRI

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Introduction: T2 relaxometry has proven its potential to decode the underlying tissue structure changes due to various diseases such as multiple sclerosis [1]. However, because of the extent of the ill-posedness of the problem, the returned T2 distributions and subsequently the myelin water fraction (MWF) maps are very sensitive to noise and high SNR of 500-1000 is needed for robust data fitting [2]. Conventional L2-norm regularization imposing the temporal smoothness of the T2 distribution can improve the stability of the solution [3]. However, that may not be adequate particularly at low SNR. Here, we propose a new spatial regularization method to improve on the noise robustness of the reconstruction algorithm and compare its performance to conventional regularization.

Theory: Assuming the underlying T2 distribution consists of discrete T2 points logarithmically chosen over a range of relevant T2 values, the signal at any echo time TE_k for a single voxel is given by: $\mathbf{y} = \mathbf{Ax} + \boldsymbol{\varepsilon}$, with $\mathbf{A}_{ki} = \exp(-TE_k/T_2(i))$ and $\mathbf{y}$ is echo data in column form and $\mathbf{x}$ is a column vector consisting of all volume fractions α_i with respective T2 values of T2(i), and $\boldsymbol{\varepsilon}$ denotes the noise vector (white Gaussian). For spatial regularization, a corresponding forward equation for multiple voxels can be formed: $\bar{\mathbf{y}} = \mathbf{A}_{ex}\bar{\mathbf{x}} + \bar{\varepsilon}; \bar{\mathbf{x}} \geq 0$ where the single-voxel quantities $\mathbf{x}$, $\mathbf{y}$, $\boldsymbol{\varepsilon}$ are collected into multi-voxel column vectors $\bar{\mathbf{x}}, \bar{\mathbf{y}}, \bar{\varepsilon}$ and the diagonal blocks of the block diagonal matrix $\mathbf{A}_{ex}$ is the matrix $\mathbf{A}$. In a typical multi-echo spin echo (MESE) analysis, contributions of 50-80 T2 points are calculated using 32-48 image echoes.

To improve the noise robustness of reconstruction, the prior expectations regarding the spatial smoothness of tissue organizations is being introduced using a Bayesian spatial approach which minimizes $\hat{\mathbf{x}} = \arg\min_{\bar{\mathbf{x}}} \left\|\mathbf{A}_{ex}\bar{\mathbf{x}} - \bar{\mathbf{y}}\right\|^2 + \mu_T \left\|\bar{\mathbf{x}}\right\|^2 + \mu_S \left\|\mathbf{W}\mathbf{D}_S\bar{\mathbf{x}}\right\|^2; \mathbf{x} \geq 0 \quad (1)$ where μ_T and μ_S are regularization parameters. The first term is the data fidelity term, while the second term is the conventional temporal regularization term which penalizes large values in inferred T2 distributions. The third term imposes spatial constraints. Matrix $\mathbf{D}_S$ is a first difference operator whose norm $\|\mathbf{D}_S\bar{\mathbf{x}}\|$ penalizes non-smooth solutions. Matrix $\mathbf{W}$ is a diagonal matrix, whose elements are given by a half-sigmoid function over T2 points with inversion point around T2 = 50 ms, which ensures that the lower T_2 range does not get over-regularized in comparison to the higher T2 range.

Data and Methods: First, a numerical phantom consisting of lesions with varying sizes (single pool with T2 of 100 ms) surrounded by matrix (two pools with geometric means T2 of 20 ms and 100 ms) was used to evaluate the developed algorithm. Next, 3D MESE T2 relaxometry data from seven healthy volunteers were acquired at 1.5T (GE HDxt 15.0, GE Healthcare) and consisted of 32 image echoes with TE varying from 5 ms to 300 ms [4].

To achieve the minimization as formulated in (1), 50-80 T2 points are logarithmically chosen over a range of 5-600 ms. By setting $\mu_S = 0$ and $\mathbf{A}_{ex} \equiv \mathbf{A}$ in Eq (1) , the conventionally regularized formulation for single voxel can be recovered which is then minimized for 100 logarithmically spaced $\mu_T \in [10^{-5},.....,10^{-1}]$. The regularization constant μ_T is chosen by L-curve method [5] as it is better grounded in Bayesian approaches. The suitable μ_T is allowed to vary voxelwise. The spatial regularization parameter μ_S is chosen to be spatially invariant constant for a particular data: $\mu_S^{opt} = \mu_T^{opt}\alpha; \alpha \in [1,10,100,200,500,....,1000]$; and μ_T^{opt} is the median of all voxel-wise μ_T. A sparse version of the nonnegative least square method [5] has been used which exploits the sparseness of system matrix corresponding to Eq (1). A supervised trial and error strategy was used whereby the MWF of a periventricular region from a central slice was reconstructed repeatedly. The spatial uniformity of the MWF map as well as the residual of the multi-exponential fit were used to select the optimum value of α. For calculation of MWF, contributions of T2 points between 5 ms- 50 ms are assumed to be due to myelin.

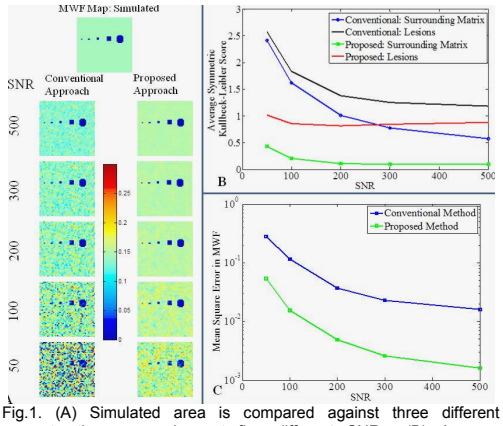

Fig.1. (A) Simulated area is compared against three different reconstruction approaches at five different SNRs. (B) Average symmetric Kullbeck-Leibler (SKL) score as a function of SNRs for three different approaches. Separate averages have been calculated for lesions and surrounding matrix. (C) Relative mean square of reconstructed MWF maps as a function of SNRs.

Results:

Simulation: Fig.1 shows the simulated and reconstructed MWF maps at various SNR. The proposed method is visually superior to the conventional approach with reduced coefficient of variance (COV). The simulated distributions were also compared with the extracted distributions using averaged symmetric Kullbeck-Leibler (SKL) score (lower score implies better agreement between distributions). The proposed method was found to perform better based on both averaged SKL score (Fig 1B) and mean square error (Fig 1C).

Human experiment: Average SNR measured from the splenium of corpus callosum was 316 ± 31 (n=7). MWF maps from a central slice of one subject are shown in Fig 2. The spatial variations of MWF map within major WM structures, as measured by COV, are significantly reduced for proposed algorithm (table 1) and are also visually more consistent with corresponding anatomical T2 FLAIR images. Further, WM and GM masks were obtained using SPM5 software [6] and numbers of voxels with multiple detected pools were counted. The proposed algorithm was able to resolve two water pools in 20-30% more WM voxels, demonstrating improved detection of the myelin water compartment within myelin-rich WM tissues. A similar improvement was observed in GM tissues. Over 7 subjects, the average MWF were 16.7 ± 1.8% (genu of CC), 14.6 ± 3.1% (splenium of CC), and 14.2 ± 1.5% (internal capsule) which were comparable with previously reported values.

Brain structures	Convention-al algorithm	Proposed algorithm	P-value
Genu of CC	0.38 ± 0.08	0.20 ± 0.05	0.02
Splenium of CC	0.34 ± 0.11	0.18 ± 0.03	0.02
Internal capsule	0.31 ± 0.06	0.18 ± 0.04	<.001

Table 1: Comparison of COV of MWF maps within various WM structures averaged over all volunteers.

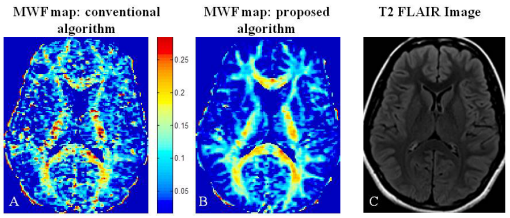

Fig.2. Comparison of MWF maps obtained with the conventional (A) and proposed (B) algorithms. T2-Flair anatomical images are shown in (C) for reference. Note the improved detection of myelin water compartment and reduced spatial variability of the proposed algorithm.

Conclusions: Our preliminary results demonstrate that the use of weak spatial constraints improves the robustness of multi-exponential T2 data fitting. The developed algorithm may allow better MWF reproducibility for longitudinal or multi-site patient studies and warrants further evaluation.

References:

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