Robust Myelin Quantitative Imaging Using Edge Preserving Spatial Priors

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1. Introduction: Demyelinating diseases such as multiple sclerosis cause changes in the brain white matter microstructure. Multi-exponential T2 relaxometry is a powerful technology for detecting these changes. However, issues such as higher signal-to-noise ratio requirement compared to other MR modalities and ill-posedness of the underlying inverse problem cause the myelin water fraction (MWF) obtained with conventional approaches to be noisy and spatially inconsistent (1). To overcome these problems, voxel-wise Tikhonov regularization (2) was proposed in conventional T2 relaxometry (3) by adding a stabilizing constraint on the solution, but this approach can be easily impacted by small amounts of measurement noise and image artifacts. We proposed a novel multi-voxel algorithm which solves these problems by introducing "edge-preserving" prior to impose spatial consistency and smoothness constraints. We first reduce the problem by modeling the desired T2 distribution into a set of 2 Gaussian peaks and a long-T2 peak. Then we apply a new Quadratic Pseudo-Binary Optimization (QPBO) algorithm, which resulted in spatially smooth and boundary sharpness-preserved MWF maps. Three-dimensional multi-echo MRI data were collected from three patients and three healthy volunteers, and MWF maps were obtained using the conventional and the proposed algorithm.

2. Method:

1. Theory: We first model the T2 distribution as a sum of two Gaussian distributions (one for the fast relaxing myelin water (WM) pool (T2~20 ms) and the other for the slower intra/extracellular water pool (T2~80 ms)), whose parameters (mean location, height and variance) are unknown and to be determined. We also add a very long relaxing cerebrospinal fluid (CSF) pool with unknown T2 and strength. Thus in the i-th voxel v_i we have the following set of unknown parameters to be determined: $\theta(v_i) = \{\alpha_1(i), \mu_1(i), \sigma_1(i), \alpha_2(i), \mu_2(i), \sigma_2(i), h_{CSF}(i), \mu_{CSF}(i)\}$. So the T2 distribution at that voxel as a sum of two Gaussians and a single long-T2 signal: $\boldsymbol{x}_i(\tau) = \boldsymbol{\mathcal{G}}(\theta(v_i), \tau) = \alpha_1(i)\mathcal{N}(\tau|\,\mu_1(i), \sigma_1(i)) + \alpha_2(i)\mathcal{N}(\tau|\,\mu_2(i), \sigma_2(i)) + h_{CSF}(i)\,\delta(\tau - \mu_{CSF}(i))$ [1] where each Gaussian is denoted as $\mathcal{N}(\cdot)$, δ denotes the delta function, and the T2 distribution is over the variable τ (a set of T2 sample points). By keeping τ fixed for all voxels, we have $\boldsymbol{x}_i = \boldsymbol{\mathcal{G}}(\theta(v_i))$. Secondly, we collect multi-voxel parameters into a vector $\overline{\boldsymbol{\theta}} = \{\theta(v_i), i = 1, \ldots, N_v\}$, and map the Gaussian parameters to the resulting vectors of T2 distributions for all voxels by $\overline{\mathbf{x}} = \boldsymbol{\mathcal{G}}(\overline{\boldsymbol{\theta}})$. Single voxel quantity $\mathbf{y}$ is also collected into a multi-voxel vector $\overline{\mathbf{y}}$. The expanded matrix is similarly defined as A_{exp}. We then use the nonlinear data fitting technique to minimize the non-convex function: $\widehat{\boldsymbol{\theta}} = \arg\min_{\overline{\boldsymbol{\theta}}} \left\|\overline{\mathbf{y}} - A_{exp}\boldsymbol{\mathcal{G}}(\overline{\boldsymbol{\theta}})\right\|^2 + \mu_N \left\|D_N \overline{\boldsymbol{\theta}}\right\|^2$ [2] where D_N is a diagonal matrix whose diagonal elements are the normalization factors corresponding to each element in $\theta(v_i)$, and μ_N is the regularization scalar. Thirdly, based on $\widehat{\boldsymbol{\theta}}$ as prior, we use QPBO algorithm to impose both coherent brain region smoothness and region boundary sharpness for each dimension d of $\widehat{\boldsymbol{\theta}}$: $E = \arg\min_{\widehat{\boldsymbol{\theta}}_{id}, \widehat{\boldsymbol{\theta}}_{jd}} \sum_{i=1}^{N} B_1(\widehat{\boldsymbol{\theta}}_{id}) + \mu_S \sum_{(i,j)\in Neighbor} B_2(\widehat{\boldsymbol{\theta}}_{id}, \widehat{\boldsymbol{\theta}}_{jd})$ [3] where B_1 is a unary function whose output is proportional to $\widehat{\boldsymbol{\theta}}_{id}$. B_2 is a binary function whose output is the difference between neighbor voxels $\widehat{\boldsymbol{\theta}}_{id}$ and $\widehat{\boldsymbol{\theta}}_{jd}$. μ_N and μ_S are regularization parameters which we iteratively choose among domain $[10^{-1}, \ldots, 10^{-5}]$ (4) to achieve best regularization results.

2. Data: We first simulate brain as two water pools: fast relaxing myelin water pool (where myelin portion is 14.5%) and slower intra/extracellular water pool (where myelin portion accounts for 4.5%). Then we add Gaussian noise to the simulated true brain image to produce images different SNRs, and we run our algorithm on them accordingly. Secondly, we run our algorithm on three-dimensional T2 spiral multi-echo MRI data collected from three patients and three healthy volunteers.

3. Results:

Figure 1 compares mean square error (MSE) of MWF maps with the true simulated brain at various signal-to-noise ratio (SNR). This demonstrates the improved accuracy obtained with the proposed method compared to the other two particularly at low SNR. Also note the proposed method provides better noise reduction.

Figure 2 provides the comparisons on the patient MRI data. According to FLAIR image, we can easily see that the proposed method generates better depiction of brain micro-structure especially on distinguishing lesion and healthy WM.

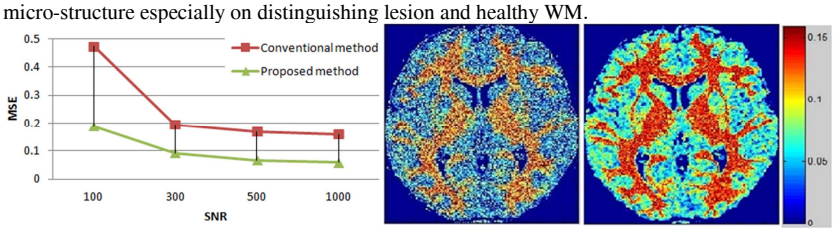

Figure 1. Brain simulation results: the curve chart in the left compares the MSEs at various SNRs. The snapshots in the right provide the MWF maps at SNR = 100 (left: conventional method, right: proposed method).

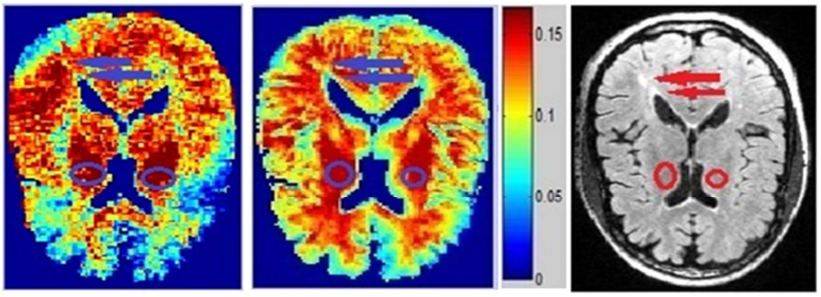

Figure 2. MWF maps selected from patient MRI. The left one is from the conventional method and the right one is from the proposed method. The right most one is the corresponding FLAIR image slice. Arrows indicate the lesions. Circles indicate the healthy WM regions.

4. Conclusion

This study demonstrated the proposed method outperformed the conventional single-voxel method. Both simulated and real data experiments show visually and numerically improved MWF measurements, and smoothly varying myelin maps. Visually there is less noise, greater spatial consistency and better resolution of small WM features in the MWF maps obtained with the proposed algorithm compared to the conventional method.

5. Reference

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