Fast Whole Brain T2 Relaxometry Using Spatial Constraints

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Introduction: Multi-exponential T2 relaxometry [1] has proven its utility as a powerful research tool for detecting brain structural changes due to demyelinating diseases such as multiple sclerosis (MS) [2]. However, because of ill-posedness of the underlying inverse problem, the T2 distributions obtained with conventional approaches are sensitive to noise and high SNR data (500-1000) is needed for accurate quantification [3]. Recently, 3D T2prep spiral acquisition has been developed to provide whole brain coverage in 10-24 min [4]. The purpose of this study is to evaluate the performance of a novel multi-voxel T2 fitting algorithm with Bayesian spatial regularization on T2prep spiral data acquired in healthy volunteers.

Theory: We are looking for solutions at $n\sim40$ -60 discrete points , $T_2(1)\dots T_2(n)$, logarithmically chosen over relevant T2 values. For single voxel, the signal at any echo time TE_k can be given by: $\mathbf{y} = \mathbf{A}\mathbf{x} + \mathbf{\epsilon}$, with $\mathbf{A}_{ki} = \exp(-TE_k/T_2(i))$ where k = 21 or 24 (1.5 T data: k = 24; 3T data k = 24) and \mathbf{y} is echo data in column form and \mathbf{x} is a column vector consisting of all volume fractions α_i , and $\mathbf{\epsilon}$ denotes the noise vector. The corresponding forward eqn for multiple voxel becomes: $\overline{\mathbf{y}} = \mathbf{A}_{ex} \overline{\mathbf{x}} + \overline{\mathbf{\epsilon}}$; $\overline{\mathbf{x}} \ge 0$; where the single-voxel quantities \mathbf{x} , \mathbf{y} are collected into multi-voxel column vectors $\overline{\mathbf{x}}$, $\overline{\mathbf{y}}$ and diagonal blocks of block diagonal matrix \mathbf{A}_{ex} is the matrix " \mathbf{A} ".

A Bayesian spatial approach has been used which exploits prior expectations that the volume fractions of individual T2 sub-components should vary smoothly over coherent brain regions. This spatial approach minimizes $\hat{\mathbf{x}} = \arg\min_{\bar{\mathbf{x}}} \|\mathbf{A}_{ex}\bar{\mathbf{x}} - \bar{\mathbf{y}}\|^2 + \mu_T \|\mathbf{W}_T\bar{\mathbf{x}}\|^2 + \mu_S \|\mathbf{W}\mathbf{D}_S\bar{\mathbf{x}}\|^2$; $\mathbf{x} \ge 0$ (1) where μ_T and μ_S are unknown a priori. Here, the first term corresponds to data fidelity term while the second term is the conventional regularization term which penalizes large values in inferred T2 distributions. The third term was introduced in order to impose spatial constraints. Matrix \mathbf{D}_S is a first difference operator whose norm $\|\mathbf{D}_S\bar{\mathbf{x}}\|$ penalizes non-smooth solutions. The exponential weight \mathbf{W}_T over T2 points is used to penalize any T2-distribution in 5-15 ms T2-range and beyond this weight asymptotically approaches to unit weight. 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:

Data: Eight healthy volunteers were scanned with 3D T2prep spiral sequence at 1.5T (GE HDxt 15.0, GE Healthcare) and 3 MS patients were scanned at 3T (GE HDxt 15.0). 24 and 20 echoes between 5 and 300 ms were collected for 1.5T and 3T, respectively. For comparison, various algorithms including the conventional regularized NNLS algorithm, the spatial averaging filter, and the algorithm by Hwangs & Du [6] were implemented.

MWF.map: proposed

T2.WImage.

Method:

To achieve the minimization as formulated in (1), first voxelwise conventional regularization is performed for 100 logarithmically spaced $\mu_T \in [10^{-5},.........,10^{-1}]$. By setting μ_S = 0 and $\boldsymbol{A}_{ex} \equiv \boldsymbol{A}$ in eqn (1), the conventionally regularized formulation for single voxel can be recovered. Our preferred method to choose the regularization constant μ_T is the L-curve approach [5], which is better grounded in Bayesian approaches. The spatial regularization parameter μ_S is assumed to be spatially invariant: $\mu_S^{opt} = \mu_T^{opt} \alpha; \alpha \in \left[1,10,100,200,500,....,1000\right];$ and μ_T^{opt} is the median of all voxel-wise μ_T . A supervised trial and error strategy is used whereby we repeatedly reconstruct the MWF of a selected portion of the image (a periventricular region from a central slice). We

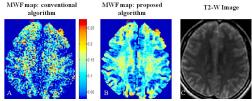


Fig 1: MWF maps of a healthy volunteer obtained with A) conventional algorithm and B) proposed multi-voxel approach algorithm. A T2-weighted anatomical image (C) is shown for reference.

assess the spatial quality of the MWF map as well as the numerical residual of multi-exponential fit to choose the optimum value of α .

Results: The average SNR was 160 \pm 9 at 1.5T and 88 \pm 4 at 3T. MWF maps shown in Fig 1 correspond to T2 relaxometry data from a healthy volunteer collected at 1.5T. The proposed algorithm provides smoother MWF maps as depicted by lower value of coefficient of variance (COV) in table 1 resulting in improved detection of WM tissues and the contrast matches quite well with T2W anatomical image. Figure 2 depicts the comparison of various regularization methods vs. the proposed method for 2 adjacent slices of an MS patients scanned at 3T GE scanner, demonstrating that the proposed method has better lesions detection ability compared to other methods.

WM structure	Coefficient of Variance (COV)	
	Conventional	Spatial
	Regularization	Regularization
Internal Capsule	0.54	0.20
Genu of CC	0.55	0.20
Splenium of CC	0.50	0.18

Table 1: Comparison of COV of MWF maps within various WM structures averaged over all volunteers scanned at 1.5 T.

Conclusions: Our results demonstrate that it's possible to extract consistent MWF map with entire brain coverage by using the spatial constraints for T2prep spiral data

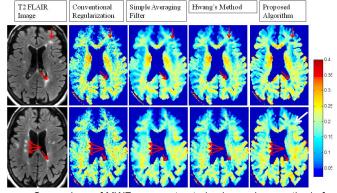


Fig 2: Comparison of MWF maps extracted using various methods for 2 adjacent slices of an MS patients scanned at 3T. Well-established lesions are indicated by red arrows, while a possible lesion location is marked by a white arrow.

with lower SNR. The developed algorithm represents an important initial step towards whole brain MWF quantification in the clinical practice.

References:

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