

Automatic Tissue Decomposition using Nonnegative Matrix Factorization for Noisy MR Magnitude Images

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Introduction Due to partial volume effects, an individual MRI voxel frequently contains signal contributions from a mixture of multiple distinct tissue components (e.g., gray matter (GM), white matter (WM), cerebrospinal fluid (CSF), abnormal/injured tissue). The main goal of this work is to find spatial maps corresponding to the main constituent tissue types that are present within the FOV. These maps can provide valuable information about the organization and status of the tissue. In previous work, mapping different tissue components has often been done using explicit physical modeling of the MR contrast variations exhibited by each tissue type under different experimental conditions. However, these methods can be confounded if a simple parametric contrast model is inadequate to describe the real biological signal variations, or if the contrast behavior is unknown. In this work, we obtain maps of different tissue components using simple nonparametric methods that can be applied to any multi-contrast dataset, without requiring a contrast model.

Theory We assume that multi-contrast MRI images of the same anatomy are acquired under M different experimental conditions (i.e., different echo times in MRI relaxometry, different diffusion weightings in diffusion MRI, etc). We also assume that the image can be modeled as a partial volume mixture of K different tissue components that always have the same phase. Specifically, we model the noiseless magnitude image at spatial location \mathbf{x} and under experimental condition θ_m as: $y(\mathbf{x}, \theta_m) \approx \sum_{k=1}^K a_k(\theta_m) \rho_k(\mathbf{x})$, where $\rho_k(\mathbf{x})$ is the spatial map of the k th tissue component and $a_k(\theta_m)$ is the contrast variation for the k th tissue in the m th experiment. We propose to use regularized nonnegative matrix factorization (NMF) [1] to automatically estimate $a_k(\theta_m)$ and $\rho_k(\mathbf{x})$ under the assumptions that $a_k(\theta_m) \geq 0$ and $\rho_k(\mathbf{x}) \geq 0$, and that $\rho_k(\mathbf{x})$ is sparse (enforced using the standard ℓ_1 -norm). The sparsity constraint imposes the prior knowledge that only a small number of different tissue components are present in any given voxel. The mixture model can also be interpreted as a low-rank matrix model $Y \approx AX$, where $Y \in \mathbb{R}^{M \times Q}$ is a matrix of the $y(\mathbf{x}, \theta_m)$ values, and $A \in \mathbb{R}^{M \times K}$ and $X \in \mathbb{R}^{K \times Q}$ are nonnegative matrices corresponding to $a_k(\theta_m)$ and $\rho_k(\mathbf{x})$.

NMF is known to be effective for mixture modeling of high-SNR data [1]. However, multi-contrast MRI datasets frequently have low-SNR, leading to images that follow the noncentral Chi (NCC) statistical distribution [2]. To account for this, we make use of a recent quadratic majorize minimize framework that allows the NCC noise model to be optimized by iteratively solving the standard NMF model [3]. Our implementation uses a block principal pivoting algorithm [4] to solve the resulting optimization problem.

Methods

Multi-shell diffusion MRI images: We applied our algorithm to decompose a set of multi-shell diffusion MRI images acquired with 6 different b-values ($b = 0, 1000, 2000, 3000, 4000, \text{ and } 5000 \text{ s/mm}^2$) and 30 diffusion encoding per nonzero b-value. For each b-value, a single magnitude image was generated by combining all complex images (30 directions and 32 channels) using root sum-of-squares.

Diffusion-Relaxation MR images: We also applied the algorithm to simultaneously decompose six different *ex vivo* rat spinal cord data sets (three sham controls and three with traumatic spinal cord injury). Data was acquired with the following parameters: 7 b-values ($b = 0, 500, 1000, 2000, 3000, 4000 \text{ and } 5000 \text{ s/mm}^2$) for each of 2 echo times ($TE = 40 \text{ and } 160 \text{ ms}$), and two diffusion encoding orientations.

Results Fig.1 shows the decomposition results from multi-shell diffusion data. The proposed NCC method (bottom) provides a clear separation of WM-like, GM-like, and CSF-like tissue components. On the other hand, the conventional method without NCC modeling (top) is more ambiguous and difficult to interpret. Fig. 2 displays the decomposition results for the rat data. Interestingly, the severely injured tissues (yellow) are automatically separated into a component that is completely absent in the control cords. This injury could be difficult to detect with standard diffusion processing, particularly at the GM/WM junction. Note that no physical contrast models were used.

Discussion and Conclusion We have proposed a new NMF approach to automatically separating macroscopic tissue components from multi-contrast MRI data, and have demonstrated its potential in both healthy and injured tissues. We expect this approach to be particularly useful in cases where a tissue mixture model is desired, but contrast models are unknown or inaccurate.

References [1] H. S. Seung, *Nature* 401, 1999 [2] O. Dietrich, *MRM* 26, 2008 [3] D. Varadarajan, *IEEE ISBI*, 2013 [4] J. Kim, *IEEE ICDM*, 2008.

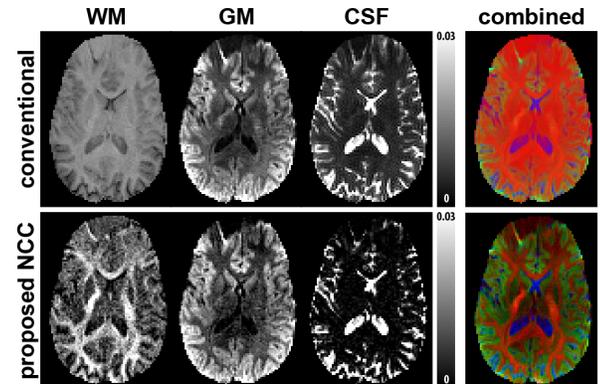


Fig. 1. Decomposed component images. (left) Individual tissue component maps. (right) A fusion of the three components into the same coordinates (red: WM; green: GM; blue: CSF).

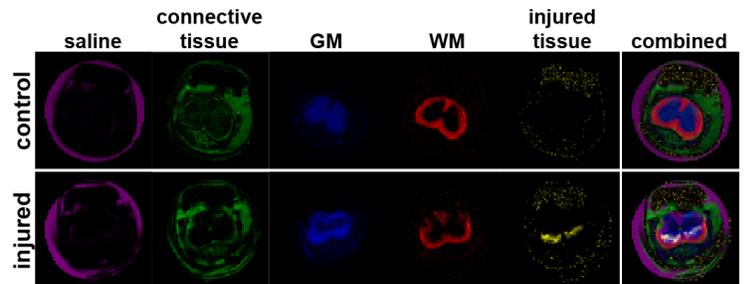


Fig. 2. Decomposed component images from rat cervical spinal cord data. (top) Control animal. (bottom) Injured animal.