Resolving Diffusion Compartments Using Single-Shell Data via Estimation with Enhanced Sparsity

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Target Audience: Diffusion MRI researchers who are interested in teasing apart signal contributions from white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF) compartments using single-shell data for more accurate estimation of the fiber orientation distribution function (FODF).

Purpose: Constrained spherical deconvolution (CSD) [1] has been recently extended to include deconvolution kernels not only for the WM, but also for GM and CSF [2]. This approach takes advantage of the decay information given by multi-shell data as well as the tissue segmentation information provided by the anatomical T1 scan. We show in this abstract that with the enhanced sparsity given by L0-"norm" regularization, resolving the diffusion compartments can be achieved by using single-shell data in addition to the baseline scans with no diffusion weighting. In contrast to [2], our method does not require tissue segmentation based on T1 images, obviating the need for registration of the anatomical scans to the diffusion scans.

Methods: *Data* - Diffusion-weighted images of the brain of an adult subject were acquired using a Siemens 3 T TIM Trio MR scanner with an EPI sequence. Diffusion gradients were applied in 120 non-collinear directions with diffusion weighting b = 2000 s/mm^2. The imaging matrix was 128 × 128 with a field of view (FOV) of 256 × 256 mm^2. The slice thickness was 2 mm. Six non-diffusion-sensitized images (b = 0 s/mm^2) were acquired. A T_1-weighted structural image with 1 mm isotropic resolution was also acquired as anatomical reference. *Tissue Segmentation* – In contrast to [2], we segment the image into WM, GM, CSF directly based on the diffusion data. Our approach is based on the observation the fractional anisotropy (FA) image can be used to separate WM and non-WM voxels and the mean diffusivity (MD) image can be used to separate GM and CSF voxels. We first scale the FA and MD images to have a value range of [0, 1]. An FA/MD value of less than 0.2/0.5 is considered as low and otherwise as high. A voxel is regarded as containing WM if FA is high and MD is low, GM if FA is low and MD is low, and CSF if FA is low and MD is high. *Parameters of Response Functions* – Once the tissue segmentation results have been obtained, we determine the parameters of the WM, GM, and CSF response functions. The WM response functions are uniformly distributed axial-symmetric diffusion tensors with axial and radial diffusivities determined based on WM voxels with FA greater than 0.7. The GM/CSF response function is an isotropic tensor with diffusivity determined based on GM/CSF voxels with FA less than 0.2. *FODF Estimation* – These response functions are sampled in directions and at the *b*-value determined by the DW data. Note that, in order to capture the decay information, we treat b=0 s/mm^2 as an additional shell and sample the response functions accordingly. These response functions are then included as column vectors in a matrix A. The FODF for each voxel is then estimated by solving a non-convex, non-smooth, and discontinuous L0-norm penalized least-squares problem [3]: $\min_f \|Af - s\|_2^2 + \lambda\|f\|_0$, where s is the signal vector (including the baseline signal), f is a vector representing the volume fractions associated with the response functions, and λ is the tuning parameter. The FODF is given by the WM volume fractions.

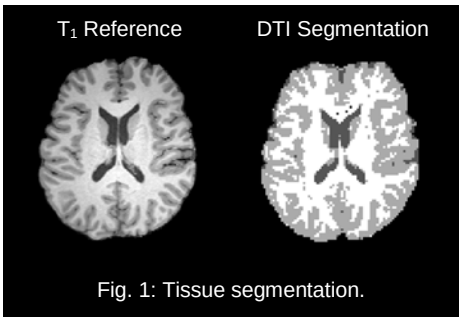

Fig. 1: Tissue segmentation.

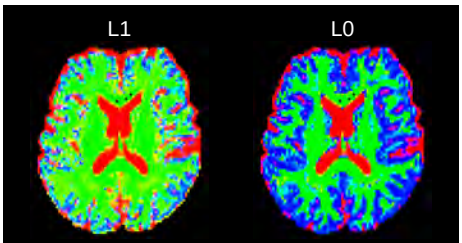

Fig. 2: Volume fraction maps.

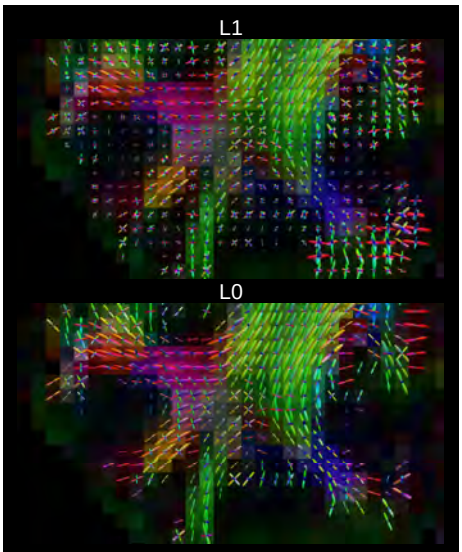

Fig. 3: WM FODFs at WM-GM interface.

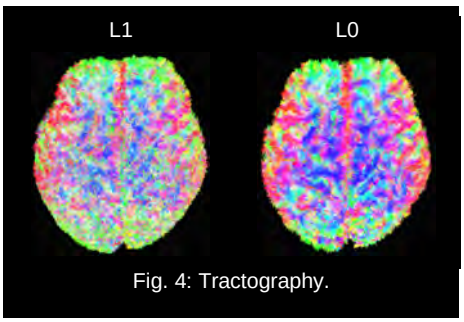

Fig. 4: Tractography.

Results: We compared the proposed method with a state-of-the-art method [4] based on reweighted L1 minimization (approximates L0 minimization). Note that we solve an L1-norm *penalized* problem instead of a *constrained* problem as in [6] to avoid having to explicitly select the sparsity to limit the number of active compartments. The compartment volume fraction maps (Fig. 2) indicate that the proposed method yields cleaner compartment estimates especially for cortical gray matter, gives better WM FODF estimates with lesser false-positive peaks in the WM-GM interface (Fig. 3), and provides tractography outcome with cleaner cortical connections (Fig. 4).

Discussion: The results have demonstrated that brain tissue types can be resolved using single-shell DW data in addition to the baseline scan. This implies that even with the currently vastly available single-shell data, FODF estimation can be improved by proper signal compartmentalization.

References: [1] Tournier et al., NeuroImage 35(4), 1459-1472, 2007. [2] Jeurissen et al., NeuroImage 103(14), 411–426, 2014. [3] Z. Lu, Mathematical Programming 147, 125-154, 2014. [4] Daducci et al., Medical Image Analysis, 18, 820–833, 2014.