Parametric Spherical Deconvolution: Inferring Multiple Fiber Bundles using Diffusion MR Imaging

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Introduction. Diffusion MR imaging has made it possible to reveal the microgeometry of nervous tissue *in vivo*. The axonal membranes of the nerve fibers, which are coherently oriented in the white matter of the brain and spinal cord, seem to form the major determinant of anisotropic water diffusion [1]. The well-known diffusion tensor model [2] however proved inadequate for describing crossings and branchings of fiber tracts within a voxel. We focus on explicit forward models, which map the microscopic tissue structure onto the water diffusion process and further onto the observable MR signals, to expose these complex fiber populations.

Theory. The general approach used in this work rests on the spherical convolution of the fiber orientation density $p(\omega)$ with the signal response of a single fiber [3-5]. Since the nerve fibers have an approximately cylindrical geometry, the water diffusion in a fiber with the orientation ω may be described by the rotationally symmetric tensor $D(\omega) = (\lambda_1 - \lambda_2)\omega\omega^t + \lambda_2 I_3$. Let b be the diffusion weighting factor and g the normalized diffusion encoding gradient direction. Then the forward model

$$\frac{E_b(g)}{E_0} = P_0 \exp(-b\lambda_0) + (1 - P_0)\int_{S^2} \exp(-bg^t D(\omega) g)\, p(\omega) d\omega$$

yields the measurable MR signals, where the first term on the right hand side represents the isotropic diffusion in the glial cells and the extra-axonal compartment. The water diffusivities $\{\lambda_0, \lambda_1, \lambda_2\}$ are supposed to be invariant throughout the white matter. We differentiate between three levels of description: a single fiber, a fiber subpopulation (also called a fiber bundle), and the entire fiber population. The key idea is to discretize the fiber population into a finite number of subpopulations, which is *a priori* unknown. We propose to completely parameterize the fiber orientation density by a finite mixture of Bingham densities [6]

$$p(\omega) = \sum_{i=1}^{N} P_i' f_B(\omega \mid B_i)$$

with the volume fractions P_i' for the fiber bundles i = 1, ..., N. The eigenstructure of B_i describes the (asymmetric) spreading of the fibers within the ith bundle. The characteristic properties of a density function, namely non-negativity and normalization, are inherently fulfilled. The Bingham distribution can be regarded as a trivariate Gaussian distribution that is conditioned upon the two-dimensional unit-sphere S^2. The resulting parametric spherical convolution model can be formulated in a closed analytic form. The inverse problem of estimating the orientations and volume fractions of the fiber bundles is solved by Bayesian statistics. We employ the Bayes factor framework to select the forward model (i.e. the number of fiber bundles) that best explains the noisy MR measurements without adding unnecessary complexity.

Results. We demonstrate the proposed approach with diffusion-weighted data sets featuring high angular resolution (60 diffusion encoding gradients with a b-value of 1000 s/mm², TE = 100 ms, 1.72×1.72×1.7 mm³ voxel resolution, three repetitions) acquired by a whole-body 3 T Magnetom Trio scanner (Siemens, Erlangen). The water diffusivity of the isotropic compartment is set to λ_0 = 0.0012 mm²/s, and the apparent diffusion coefficients of a single nerve fiber are estimated at λ_1 = 0.0018 and λ_2 = 0.0002 mm²/s. Figure 1 shows the expected orientation of the fiber bundles in a part of the MR volume. The underlying map depicts the fractional anisotropy. The coronal slice exposes the crossing of the callosal fibers (cf) and the corona radiata (cr). The Bayes factor decides how many fiber bundles are located in each voxel. Furthermore, we can observe a narrow band (marked with (*) in Figure 1) which causes difficulties in discretizing the fiber population into distinct subpopulations. The diffusion-weighted MR signal appears to be almost isotropic in these voxels which therefore have small fractional anisotropy values. We hypothesize that these voxels are composed of three fiber bundles, namely the callosal fibers, the corona radiata, and the superior longitudinal fasciculus.

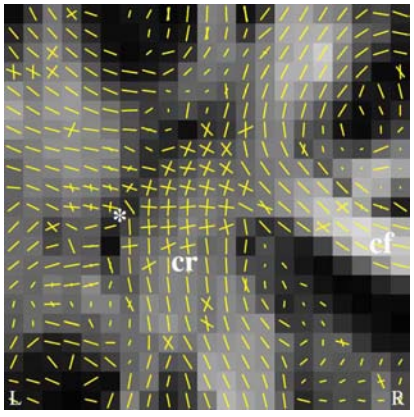

Fig. 1. Mean fiber bundle orientations.

Discussion. Complex fiber populations are a common feature in the human brain and should not be ignored when exploring the connectional architecture of white matter. The proposed approach allowed for the disentanglement of multiple fiber bundles within a voxel. We assumed that the unknown diffusivity parameters are fixed throughout the white matter, which is clearly a simplification. On the other hand, since the nerve fibers form the smallest components, this invariant seems to be more natural than other choices (e.g., the constant diffusivity assumption in multiple tensor models). The rigorous estimation of these parameters by experiment or blind deconvolution is future work.

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