

BAYESIAN ESTIMATION OF THE AXONAL DIFFUSION COEFFICIENTS IN BRAIN WHITE MATTER

Enrico Kaden¹, Frithjof Kruggel², and Daniel C. Alexander¹

¹Centre for Medical Image Computing, University College London, London, United Kingdom, ²Department of Biomedical Engineering, University of California, Irvine, Irvine, CA, United States

Target audience. Researchers interested in diffusion MR imaging, especially model development and statistical data analysis.

Purpose. Diffusion-weighted imaging has enabled us to study the geometry of white matter in the individual human brain noninvasively. This MR technique measures the Brownian motion of water molecules, which is impeded by the underlying tissue structure, e.g., the (myelinated) axonal membranes. The present work aims to quantify the voxel-averaged diffusion coefficients parallel to an axon and perpendicular to it without any prior knowledge about how the axons are oriented within a voxel because the fiber orientation distribution is typically not known in advance. This effort is motivated by two major problems. First, to recover the directional structure of white matter from MR measurements, we need to know the diffusion signal of a single fiber. Second, the axonal water diffusivity reflects the fiber microanatomy such as the axon diameter, the myelination, and the interaxonal space.

Methods. The general approach we adopt here rests on the spherical convolution¹⁻³ of the fiber orientation distribution $p(\omega)$ with the impulse response $h_b(g, \omega)$ of a single axon. $\omega \in S^2$ denotes the orientation defined on the unit sphere; b is the diffusion weighting factor and $g \in S^2$ the normalized gradient direction. As the microscopic environment of an axon resembles a cylindrical tube, the diffusion signal of a fiber segment including its typical surrounding volume (that is always present, even if the axons abut) may be approximated by a rotationally symmetric tensor model⁴ up to the second order. The diffusion signal of a fiber population with a complex directional architecture then takes the form

$$E_b(g)/E_0 = \int_{S^2} h_b(g, \omega) p(\omega) d\omega \quad \text{with} \quad h_b(g, \omega) = \exp(-b[(\lambda_{\parallel} - \lambda_{\perp})(g, \omega)^2 + \lambda_{\perp}]).$$

λ_{\parallel} and λ_{\perp} are the axial and radial diffusion coefficients, respectively, with the constraint $0 \leq \lambda_{\perp} \leq \lambda_{\parallel} \leq \lambda_{\text{free}}$, where λ_{free} denotes the bulk diffusivity. E_0 stands for the MR signal without diffusion weighting. Next we aim to solve the blind deconvolution problem, that is, to infer the orientation-independent parameters λ_{\parallel} and λ_{\perp} voxel by voxel over the entire brain (not only in the corpus callosum) from a diffusion experiment featuring multiple b -values and gradient directions, having no information about the fiber orientation distribution $p(\omega)$. For this purpose $p(\omega)$ is represented by a Dirichlet process model⁵, which ensures the defining properties of $p(\omega)$, i.e., antipodal symmetry, nonnegativity, and normalization, and can approximate any fiber orientation distribution as closely as desired. Nonparametric Bayesian statistics then estimates λ_{\parallel} and λ_{\perp} , regardless of the directional fiber geometry within a voxel, under a Rician noise model. We choose weakly-informative priors for the model parameters to make as few assumptions as possible. The computational issues due to the infinite-dimensional character of the Dirichlet process are addressed by an Ewens measure representation⁵. We sample from the posterior using a reversible jump Metropolis–Hastings algorithm with finite adaptation scheme.

Results. The diffusion dataset (Human Connectome Project, WU-Minn Consortium⁶, www.humanconnectome.org) was acquired by a 3 T Siemens Skyra scanner with a customized gradient insert. The spin-echo EPI sequence (TE = 89.5 ms, TR = 5520 ms, 1.25 mm isotropic voxel resolution) measured 90 gradient directions for each b -value of 1000, 2000, and 3000 s/mm². The MR images were corrected for subject motion, gradient field nonlinearities, and spatial distortions due to eddy currents and susceptibility variations. Figure 1 depicts maps of the axonal diffusion process estimated in the cerebral white matter of a healthy volunteer. The upper row shows the posterior mean of the axial and radial water diffusivities λ_{\parallel} and λ_{\perp} . In the bottom row we compare the fractional anisotropy (FA) of a single axon, which has factored out the effects due to the fiber orientation distribution, with the standard FA for the entire fiber population derived from the diffusion tensor model⁴.

Discussion. The classical tensor approach encodes the diffusion process of the axons as well as their tangential distribution. Consequently, it is difficult to draw conclusions on the fiber microanatomy from those orientation-dependent quantities. If we aim to recover the intrinsic properties of the axons, our data analysis should not depend on the directional fiber architecture. This work has proposed a new method to disentangle the axonal diffusion process from the intra-voxel fiber orientation distribution and demonstrated it in a live human subject.

Acknowledgments. The UK EPSRC funded this work with grant EP/E007748. Data were provided by the Human Connectome Project, WU-Minn Consortium (Principal Investigators: David Van Essen and Kamil Ugurbil; 1U54MH091657) funded by the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research, and by the McDonnell Center for Systems Neuroscience at Washington University.

References. [1] von dem Hagen and Henkelman. *Magnetic Resonance in Medicine*, 48:454–459, 2002. [2] Tournier et al. *NeuroImage*, 23:1176–1185, 2004. [3] Anderson. *Magnetic Resonance in Medicine*, 54:1194–1206, 2005. [4] Basser et al. *Journal of Magnetic Resonance, Series B*, 103:247–254, 1994. [5] Kaden and Kruggel. *Medical Image Analysis*, 16:876–888, 2012. [6] Van Essen et al. *NeuroImage*, 62:2222–2231, 2012.

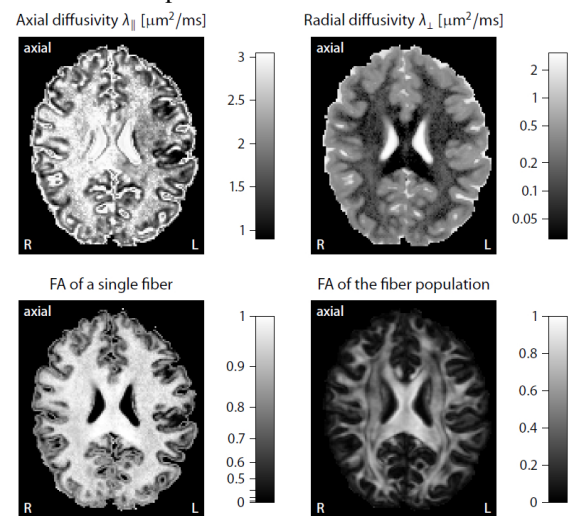


Figure 1: Bayesian estimation of the axonal diffusion process.