Diffusion Textures: A Novel Way to Represent Brain Tissue Microstructure

Marco Reisert[1], Katharina Göbel[1], and Bibek Dhital[1]
[1]*Medical Physics, University Medical Center Freiburg, Freiburg, Germany*

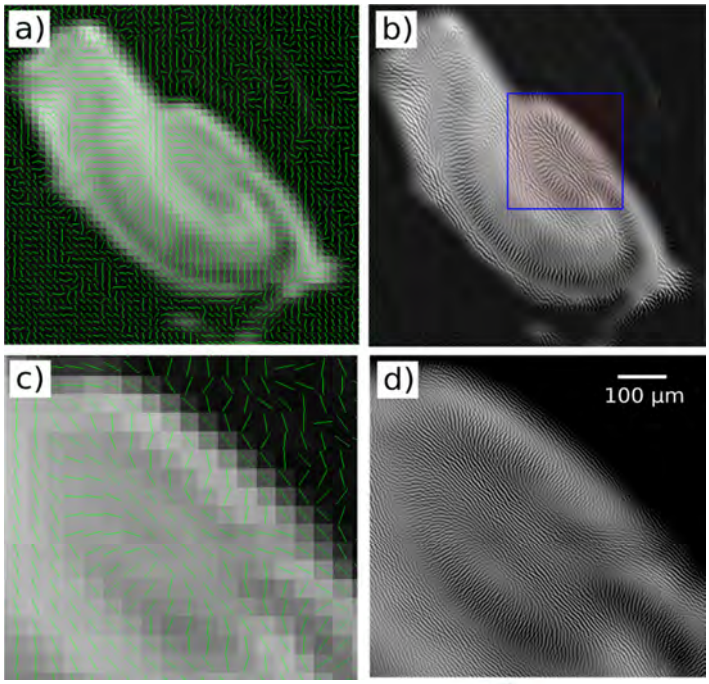
TARGET AUDIENCE: Analysis of Diffusion Weighted MRI, Microstructure Imaging

Introduction: Diffusion weighted magnetic resonance imaging (DWI) gives a unique opportunity to look inside tissue microstructure of human brain white matter. DWI analysis attempts to quantify cellular-level tissue organization in each voxel to derive diagnostic relevant parameters. Usually we try to explain the DWI-signal by identifying the different microscopic components and making assumption about their physical and statistical properties. This leads to analytical models containing the relevant parameters like diffusivities and volume fractions. Depending on parameters like diffusion time, gradient strengths and sequence design itself, different DWI measurements are more or less sensitive to different microstructural features and different models are appropriate. However, there is still a multitude of different models[1] and discussion is controversial. All these approaches are based on a reductionist point of view. In this work we want to propose an alternative, more a phenomenological description of the measurement. Instead of stating some analytical model which is statistical derived from some physical assumptions about microstructure statistics, we propose to directly reconstruct the tissue microstructure. Of course, this is not uniquely possible, we are rather interested to find one instance of the microstructure following the statistics which has generated the observed DWI signal. It is very similar to the problem of finding the shape of an object from its autocorrelation function[2].

Method: The actual equation we use to describe the signal can be understood as the squared modulus of a local Fourier transformation of some tissue function *I*:

$$S(r,q) = \left| \frac{1}{\sqrt{Dt}} \int I(r_1) e^{-\frac{(r_1-r)^2}{4Dt} + iq(r_1-r)} dr_1 \right|^2 ,$$

where the diffusivity *D* and the time *t* are fixed parameters. Our interest is to recover the tissue function *I* from the measurement *S*. We call the function *I* a *diffusion texture*. In fact, if we know all values for *r* and *q* this is uniquely possible up to a global phase factor (the function *S* can be understood as the Husimi Q-representation of the 'wave'-function *I*, and there is indeed a one-to-one mapping[3]). Similar forms for *S* can also be derived from a second-order perturbation theory of the signal for free water. So, the goal is to estimate a high resolution image *I* from local powerspectra (much higher resolution than original image resolution). Of course, in the case of DWI the q-space coordinate is sampled very sparsely, so we have to cope with incomplete information and ambiguities. To reconstruct *I* we use an alternating algorithm, similar to methods used for magnitude-only reconstructions of localized signals[4]. We applied our idea to an organotypic hippocampal slice (OHSC)[5] measured with a 2D DTI sequence on a 7T Bruker BioSpec animal scanner. (EPI, TE= 38.81 ms, resolution 39×39×100 μm, 12 gradient directions on circle, bvalue 1000, 10 repetitions, scan time = 9h 36min)



Results: In Figure a) we show principal directions of an ordinary DTI analysis, the gray values in the background correspond to the mean over all diffusion weighted images. Figure b) shows the diffusion texture *I* reconstructed with 10-fold spatial oversampling. Figure c) and d) show a close-up view of the hippocampal 'Hilus' with ordinary DTI (c) and the diffusion texture analysis (d) with 35-fold oversampling. Finally, Figure e) shows an immunohistochemical staining of 20 μm thick OHSC cryosections for comparison.

Discussion: We proposed a novel way to analyze and visualize DWI data. One may argue that we have just another way to create some fancy images, however the structure and texture of the diffusion texture is directly related to the signal itself. The original, coarse resolution 5D-diffusion signal is converted into an equivalent high resolution 3D-representation. The approach shares some similarities with tract density imaging[6] and line integral convolution methods[7], however our approach is much more direct and does not require any fiber extraction/tracking.

References: (1) Panagiotaki et al, Neuroimage, 2012, (2) P. T. Callaghan et al, Nature 351, 1991, (3) Cartwright, Physica A: Statistical Mechanics and its Applications, 1975, (4) N. Canterakis, IEEE Transactions on Acoustics, Speech and Signal Processing, 1983, (5) Göbel et al, Proc. of ISMRM 2014, 1052, (6) Clamante et al, Neuroimage, 2010, (7) McGraw et al, MICCAI 2002