Orientation dispersion estimated from multidimensional diffusion MRI: does it match simulated realistic microstructure?

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Objectives

Biophysical models provides measures directly related to tissue microstructure [1, 2, 3] through modeling assumption that can be invalidated in pathological situations [4]. The diffusion tensor distribution (DTD) framework [5] characterizes the distribution of Gaussian diffusion compartments inside a voxel, from which we can compute the microscopic anisotropy (μ FA) or the orientation parameter (OP). Our goal is to help with the interpretation of the diffusion tensor distribution parameters by relating the orientation parameter (OP) with fiber dispersion in a white matter bundle.





Figure 1. (Top row) We set the value of the μ FA at 0.5 and the size variance at 0. The first figure shows an OP close to 0, the middle one, an OP at 0.5 and the last, an OP close to 1. (Second row) For the first two figures, we still have no variance in size, OP is set at 1. The first one shows a μ FA close to 1 whereas the second shows one close to 0. The third figure shows the impact of the size variance on a distribution with OP at 0.5 and μ FA at 0.5.

Results

• For a given substrate, OP_{*qt*} increases with the segment length.



Figure 4. Geometric OP_{gt} computed for several lengths of segments as a function of the target dispersion for our col-





Substrate generation.

• Generation of 11 numerical substrates with CACTUS [6]: side length of $200\mu m$; intracellular volume fraction at 0.72; a gamma distributed radius with $\kappa = 1$ and a mean radius of $2.5 \mu m$; dispersion which ranges from 0° to 25° with a step of 2.5° (see Figure 2)



Figure 2. Cubes of 50 μ m at the center of realistic white matter substrates generated with CACTUS [6] with angular dispersion ranging from 0° (left) to 25° (right).

• For the intracellular signal, the OP estimation from the DTD is strongly correlated to OP_{at}, with the best accuracy obtained for a segment length of $10\mu m$. The bottom figure suggests that when we have dispersion in the substrate, we can no longer model the extracellular part of the signal as a single gaussian compartment, which contradicts the assumptions made in most biophysical models of white matter [1, 2, 3].



Figure 5. Estimated OP from the signal for our collection of substrates as a function of geometric OP_{at} computed from the substrate for several lengths of segments for the intracellular signal (top) and extra-cellular signal (bottom).

• We want to compare angular dispersion and orientation parameter (OP) described in Q-space trajectory imaging (QTI) [5] (ranges from 0 to 1).



Discussion

Orientation parameter.

- Assimilation of the segment of the fibers as rank-one tensors, defining a distribution of tensors in order to compute OP_{qt} [5, 7]. This allows us to have a measure for the ground-truth of the orientation parameter OP.
- The segment length, which impacts the estimation of OP_{qt} , should be in the same order as the characteristic diffusion length, so about $15 - 18 \mu m$ ($\sqrt{2D\tau}$, τ is the effective range 60 - 80 ms).

Signal simulation and DTD estimation.

- The signal was generated for an acquisition scheme [8], including linear, spherical and planar tensor encoding (see Figure 3).
- The tensors were implemented with the framework NOW [9] to generate a gradient trajectory for a spherical b-tensor before applying proper scaling and rotation [8] to generate all 120 waveforms.
- The signal was simulated through Monte-Carlo simulation [10] (1,000,000 particles, 101 ms, 1,000 timesteps, either only intra-cellular contribution or extra-cellular contribution, diffusivity of $2\mu m^2/ms$).

- For an orientation parameter ranging from 0.5 to 1, we identified a clear link between the estimated OP and the dispersion of fibers within the substrates.
- The characteristic diffusion length was estimated around $15 18 \mu m$ and the best accuracy was obtained with segments of $10\mu m$.
- Extra-axonal diffusion is more complex than we generally assume and cannot be represented by a single diffusion tensor.

Future Work

- Extending the experiment for crossing bundles.
- Investigating the influence of the acquisition scheme.
- Adding other parameters (microscopic anisotropy for DTD; axonal radius or density for substrates) and to assess their influence on the estimation of each other.
- Adding other cell structures (glial cells, soma, etc.) to see their influence the estimation of math-
- From the simulated signal, we compute the DTDs and estimate its parameters using the QTI implementation in Dipy[7].

Figure 3. (left) Repartition of the 120 b-tensor encoded acquisitions corresponding to the Q3 scheme [8] used for the simulations; (right) template gradient trajectory to implement the spherical tensor encoding (STE) b- tensors.

ematical parameters.

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