Anatomical Priors to improve Global Tractography

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TARGET AUDIENCE – Diffusion MRI researchers interested in connectivity analyses

PURPOSE

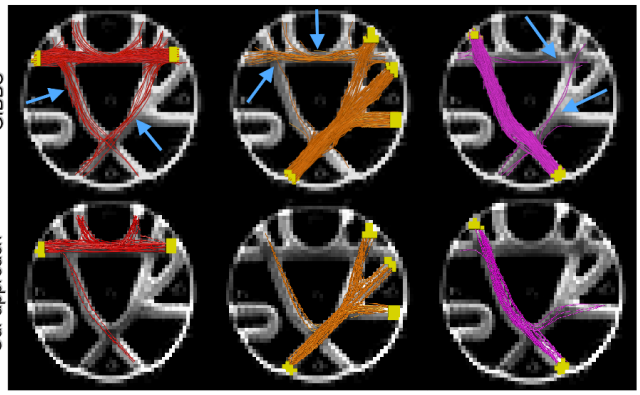
The main assumption of fiber-tracking algorithms is that fiber trajectories are represented by paths of highest diffusion, which is usually accomplished by following the principal diffusion directions in every voxel. The state-of-the-art approaches known as "global tractography" reconstruct all the fiber tracts of the whole brain simultaneously by solving global energy minimization inverse problems. Fibers obtained with these algorithms outperform all previous techniques [1] but, unfortunately, the price to pay is an increased computational cost which is not suitable in many practical settings, both in terms of time and memory requirements. Furthermore, all current global tractography approaches suffer from an important shortcoming that is crucial in the context of brain connectivity analyses [2]. As no anatomical priors are used during the optimization, the reconstructed trajectories are not guaranteed to connect cortical regions and, as a matter of fact, most of them stop prematurely in the white matter [3]. This not only affects the estimation of the connectivity and potentially biases the results, but also unnecessarily slows down the estimation procedure. In this work we have reformulated global tractography to explicitly enforce anatomical priors in the optimization with the aim of (i) improving the quality of reconstructions and (ii) reducing the computation time.

METHODS

Our method represents an extension of [3] and our contributions can be summarized as follows. First, instead of generating random segments and then requiring them to join and form chains during the optimization, we directly estimate an *initial solution of plausible trajectories* by merging the results obtained with classical fiber-tracking techniques, i.e. deterministic streamline as well as a shortest-path based algorithm [5]. Only the fiber tracts starting and ending in the gray matter (GM) are kept and the non-connecting ones are discarded because they are anatomical impossible. Then, the remaining trajectories are converted to *Catmull-Rom splines* with k control points as in [6] and a weight is assigned to each as in [4]. We chose this parametric representation for 5 main reasons. (i) Significantly less parameters are needed to store and control each fiber tract. (ii) A trajectory can be easily constrained to originate in the GM as well as to develop in the white matter (WM). (iii) Efficient algorithms exist to evaluate the spline along the path and thus compute the signal contribution in each voxel of the image. (iv) The chain-like structure as well as the smoothness of the trajectories are implicit in the formulation and do not need to be explicitly enforced. (v) The contribution of each fiber is easily controlled by the weight of the corresponding spline and no additional segments must be added to properly fit the signal. Finally, we seek for the optimal configuration of parameters (position of control points and fiber weights) with a MCMC optimization procedure as in [3] by fitting the simulated diffusion signal to the measured data. We evaluated the performance of our approach on the FiberCup phantom [1], with known ground-truth. We used the dataset with 64 directions at b = 1500 s/mm^2 and 3 mm spatial resolution. We compared our results to the state-of-the-art global tractography algorithm (a.k.a. GIBBS), as it was ranked first in a recent study [1] comparing several tractography methods on the same dataset.

RESULTS AND DISCUSSION

The figure to the right reports three representative fiber bundles recovered by GIBBS and our approach. We can clearly distinguish how our approach suppresses many false positives fibers that are not in the ground-truth as compared to GIBBS. It is as well worth to mention that the incorrect fibers shown in our approach have a considerably low weight compared to the correct fibers. Since the anatomical priors have been included from the beginning, that is, the fibers should always start and end in the GM and develop in the WM, we obtain considerably less spurious fibers that normally would prematurely end in the white matter. It is worth noting that the computation time for our approach is lower in comparison to GIBBS. It took us 20 min to obtain these tractograms, whereas GIBBS on the other hand required about 44 min using a setting with optimal parameters. This is mainly due to the fact that with the splines we reduce the parameter space and the optimization procedure converges faster and, in addition, thanks to the anatomical prior embedded in the optimization process we focus the search only on anatomical plausible fibers, without wasting time for aberrant trajectories that later on will be discarded from the analysis because they do not connect any brain region. The simplicity of our method makes it easier to include further information in the optimization, as for instance additional prior knowledge or more advanced tissue compartments.



CONCLUSION

With this work we have shown that it is possible to reduce the computation time of global tractography using the spline model. Apart from this, a more robust tractogram is achieved by included anatomical priors of fiber endpoints. In addition, its flexible nature allows further diffusion priors to be incorporated i.e additional diffusion compartments . However, this are so far only preliminary results further speed up of the method is in progress and in addition, testing on human data.

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