Fully automated probabilistic white-matter tractography with anatomical priors: Application to Huntington's disease

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Introduction

White-matter tractography has become an increasingly popular application of diffusion MRI. However, conventional tractography methods are often cumbersome to apply to large populations because of the need for manual intervention, *e.g.*, to place start, end, or waypoints, to define inclusion or exclusion masks, or to tune parameters such as constraints on the tract bending angle, particularly for weaker connections that are more difficult to trace. In this work we combine a Bayesian framework for diffusion tractography with prior information on the tracts of interest from a set of training subjects to perform tractography in a robust and automated manner. We apply this method to trace the corticospinal tract (CST) and the three branches of the superior longitudinal fasciculus (SLF1, SLF2, SLF3) on 33 Huntington's disease patients and 22 healthy controls and investigate population differences in fractional anisotropy (FA) along these tracts.

Methods

Fifty-five volunteers were scanned in a 3T Siemens Trio to acquire diffusion-weighted images at 2x2x2 mm resolution with 60 gradient directions. Of these volunteers, 33 were Huntington's disease patients and 22 were age-matched controls. We performed automated probabilistic tractography on these images to identify the four paths of interest (CST, SLF1, SLF2, SLF3) as follows. Let F be the unknown path that we would like to trace. We estimate the posterior probability of F given the measured diffusion-weighted (DW) images Y, $p(F|Y) \propto p(Y|F)\, p(F)$. We adopt the form of the image likelihood, $p(Y|F)$, from [1], which assumes a multi-compartment model of diffusion and Gaussian noise at every voxel. We estimate the prior probability of the path, $p(F)$, from a manual labeling of the path in a set of training subjects.

The training set used here consisted of 10 healthy volunteers who were scanned in a 3T Siemens Trio to acquire diffusion-weighted images at 2x2x2 mm resolution with 60 gradient directions. This data set was provided by the Mental Illness and Neuroscience Discovery (MIND) Institute [2]. Using each training subject's fractional anisotropy and primary eigenvector maps, an expert labeled each of the tracts of interest. We used these points to fit a spline representing the true shape of each tract in each training subject. We then computed a histogram of these splines to estimate the prior probability of a voxel being intersected by each of the tracts.

We incorporated these priors into the Bayesian framework described above to estimate the path posteriors in the 55 test subjects (Huntington's disease patients and matched controls). No manual intervention was performed on the data of the test subjects. The posteriors were estimated by a Markov-chain Monte Carlo (MCMC) approach. In addition to the path priors that we obtained from the training subjects, we also used centroids of the manually drawn points from the training subjects to initialize the MCMC algorithm for the test subjects. Finally, for each test subject we identified the path that maximized the posterior probability and we quantified white-matter integrity by computing the FA along this path.

Results

Fig. 1 shows plots of the FA along the left CST, SLF1, SLF2, and SLF3, averaged among patients and healthy controls, with standard error bars. Fig. 2 shows p-values from a two-sided unpaired T-test on the FA of two populations. The p-values have been mapped onto the manually labeled tracts of one of the training subjects.

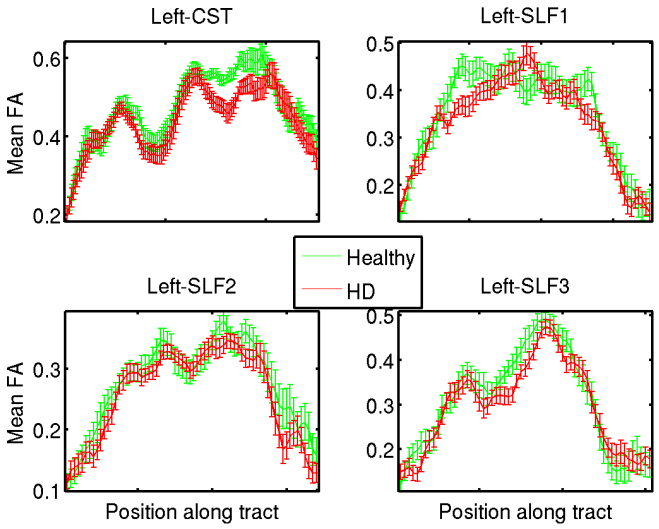

Figure 1. Average FA (with standard error bars) along the maximum a posteriori path for healthy controls and HD patients

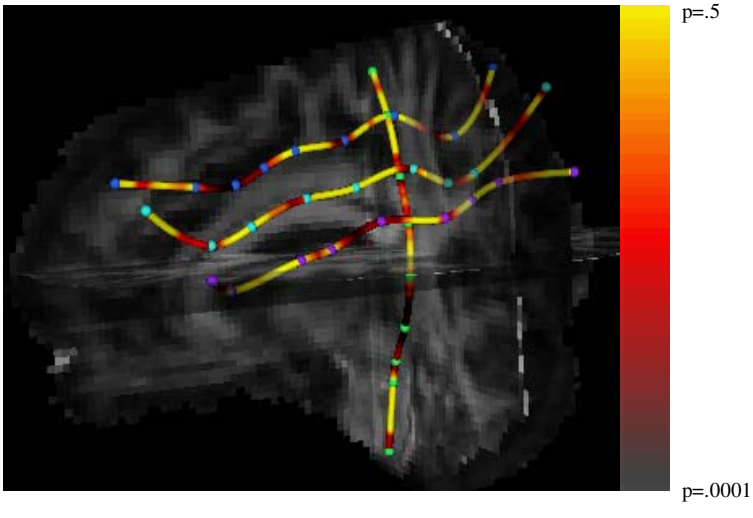

Figure 2. P-value for T-test on FA difference between healthy controls and HD patients, overlaid on manual labeling of the CST (green), SLF1 (blue), SLF2 (cyan), and SLF3 (purple) on one of the training subjects

Conclusions

This preliminary study shows significant reduction of white-matter integrity in the Huntington's disease patients compared to the healthy controls, as quantified by FA, in several parts of the CST and SLF. These results illustrate that the proposed approach to probabilistic tractography, which is robust and completely automated, can be applied to trace white-matter pathways, even weaker ones such as the SLF, in large populations. We are currently investigating the degree to which including patients in the training set affects the estimated path posteriors, as well as the inter- and intra-rater reliability of the manual path labeling for the estimation of path priors.

References

[1] Jbabdi, S., Woolrich, M.W., Andersson, J.L., Behrens, T.E.J.: A Bayesian framework for global tractography. NeuroImage 37, 116–29 (2007).
[2] Mental Illness and Neuroscience Discovery Institute. http://themindinstitute.org/.