A probabilistic model for matching white matter tracts reconstructed from group diffusion MRI data

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Introduction

Over the course of barely more than a decade, diffusion magnetic resonance imaging (dMRI) has already proven to be an extremely productive way of gathering information about the brain's white matter *in vivo*. This medical imaging technique, combined with associated developments in computational modelling, has made it possible to reconstruct and visualise the pathways along which information is transferred between brain regions. Fibre tracking (or "tractography") algorithms are capable of automatically segmenting irregularly shaped structures that would be difficult and error-prone for a human observer to isolate by hand, thus facilitating clinical studies with an interest in certain pathways in particular. However, most of the algorithms that have been developed begin tract reconstruction from a seed point, which is typically placed by a human observer. The final segmentation can be very sensitive to the placement of this point, so a strong element of subjectivity remains in the results.

We have recently demonstrated proof of concept for an approach to automated seed point placement in which a set of points are each used to generate a "candidate" tract, and the single seed point is chosen whose corresponding tract matches best to a predefined reference tract [1]. In that case, each candidate seed point is treated as a hypothesis, and the hypothesis with the best evidence to support it—in terms of tract similarity—is chosen. In the present work we take this approach further, developing a formal probabilistic model for the shape and length relationships between tracts, which resolves many of the shortcomings of the previous method.

Methods

Volunteer data previously acquired on a GE Signa LX 1.5 T scanner, with 51 diffusion weighting directions and a b-value of 1000 s mm^{-2}, were used for this study (cf. [1]). The dMRI data were preprocessed to remove skull data and eddy current distortions from the images, using FMRIB Software Library tools (FMRIB, Oxford, UK).

For each seed point, the BEDPOST/ProbTrack tractography algorithm [2] generates a set of 5000 "probabilistic streamlines", each describing a path in two directions from the seed point. Rather than work with this full distribution of streamlines, we instead calculate a median line, which is assumed to have shape and length properties that are representative of the set. This median line is then parameterised as a uniform B-spline curve such that one of the knot points falls on the seed point. Fig. 1 shows the original set of streamlines (black), the median line (red), and the internal knot points of the B-spline (blue), in axial projection. The knot point spacing is chosen to reduce the residual standard error of the fit below a threshold in the reference tract, which here represents the corpus callosum splenium, and is then fixed for all other tracts.

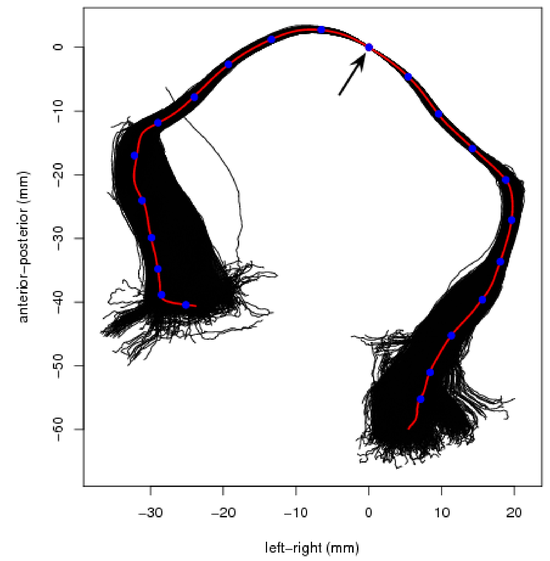

***Fig. 1**: The reference splenium tract, in axial projection. The origin of coordinates is the seed point (indicated by the arrow).*

We then generatively model the likelihood of the B-spline parameterisation for the ith tract, $P(\mathbf{d}^i)$, in terms of the angles between interknot vectors in the candidate tract and the equivalent vectors in the reference tract; and use a latent variable, z^i to indicate whether tract i matches the reference tract ($z^i = 1$) or not ($z^i = 0$). The principle is that we expect the general direction of these interknot vectors to be well predicted by the reference tract, but with broad enough distributions to allow for differences in individual brain morphology. We fit the model parameters with maximum likelihood estimation and then calculate the posterior matching probabilities according to

$$P(z^i = 1 \mid \mathbf{d}) = \frac{P(\mathbf{d}^i \mid z^i = 1)P(z^i = 1)}{\sum_j P(\mathbf{d}^j \mid z^j = 1)P(z^j = 1)},$$

where $\mathbf{d} = (\mathbf{d}^i)$, the combined parameterisations of all tracts. The prior distributions, $P(z^i)$, are uniform over tracts.

Using well established image registration techniques, the seed point that was used to generate the reference tract was transferred to the brain volume of another subject. The tractography algorithm was then seeded at every point in a 7×7×7 image voxel neighbourhood around this location, providing a group of candidate tracts.

Results

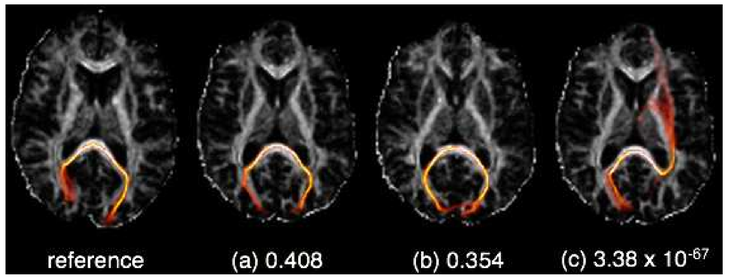

***Fig. 2**: Maximum intensity projections of three candidate tracts, with associated posterior probabilities given.*

Fig. 2 shows the results of applying our tract matching model in a sample case. The reference tract in this figure corresponds to Fig. 1, while (a) and (b) show the two candidate tracts with posterior probabilities above 0.1. The tract generated from the seed point chosen using registration is shown in (c). Its posterior probability can be seen to be many orders of magnitude smaller.

Discussion

We have described a probabilistic model of the relationship between tract shapes, and applied it to the clinically pertinent problem of finding a specific tract from a dMRI data set. Given a set of candidate tracts, the model gives a quantitative indication of how well matched each is to a predefined reference tract, thus allowing for selection of the best match as that tract which has the highest posterior probability. By applying this matching process to each subject in a study group, a set of comparable tracts could be segmented automatically for subsequent analysis.

References

[1] Clayden et al. (2006). *NeuroImage* **33**(2):482–492.

[2] Behrens et al. (2003). *Magn Reson Med* **50**(5):1077–1088.

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