Automated assessment of tract similarity in group diffusion MRI data

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Introduction

Automated segmentation of neural white matter fasciculi from diffusion MRI (dMRI) data is one major aim of tractography algorithms. Whilst the accuracy of their output can be difficult to verify due to the absence of a gold standard, tractography algorithms show considerable promise as a tool for use in clinical and nonclinical studies of neural white matter. However, the output from tractography algorithms is usually strongly dependent on the location of the user-specified "seed point", and manual verification of the plausibility of the output is generally required for each "tract" generated. The process of manual seed point placement and tract plausibility checking in tractography based group studies is time consuming and potentially prone to bias and error; but there is no robust, accepted technique for performing systematic segmentation automatically across subjects. Here we describe a new method for automated quantification of tract similarity that could be used as a basis for such a technique.

Methods

Six normal volunteers (2 male, 4 female; mean age 27 ± 3.4 years) were recruited for this study. Each subject underwent a dMRI protocol with 51 noncollinear diffusion weighting gradient directions at a *b*-value of 1000 s mm^{-2}. In order to investigate the variation in similarity scores between acquisitions, 2 of the subjects were scanned twice, and 3 were scanned three times. Those subjects that went through the protocol three times were taken out of the scanner between the second and third NEX, and the slice locations were repositioned for the third NEX. The data were initially preprocessed to remove skull data and eddy current distortion effects from the images using FMRIB Software Library tools (FMRIB, Oxford, UK). The underlying tractography algorithm used in this study was the BEDPOST/ProbTrack algorithm [1].

A tract similarity score was developed by establishing measures of tract shape similarity (S_1) and length similarity (S_2), and combining the two:

$$S(r,x) \equiv \sqrt{S_1(r,x) \cdot S_2(r,x)}$$

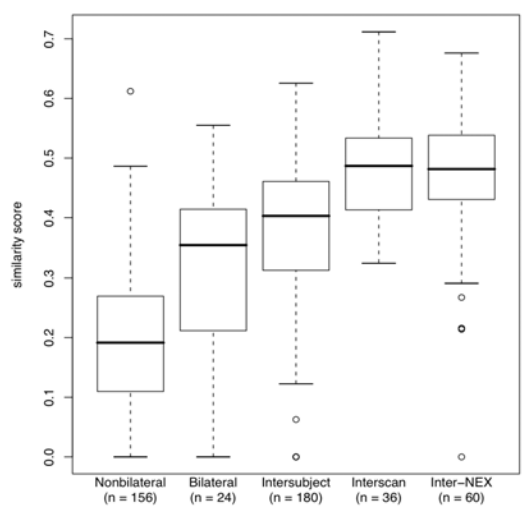
The score S is asymmetric because one of the two tracts is treated as a reference (r) and the other as a candidate (x). Its value is always between 0 and 1, where 1 denotes the best possible match. Central to the calculation of both score components, S_1 and S_2, is an algorithm based on a simplification and specialization of the work of Sebastian *et al.* on general curve alignment [2]. The algorithm compares the directionality of the main paths through the two tracts. Seed points were placed on a standard (MNI) brain in genu and splenium of corpus callosum, left and right anterior limb of internal capsule (ALIC), and left and right sagittal stratum (SS); and transferred to each scan's native space as per [3]. Note that the placement of seed points in this way is only approximately accurate, but it provides an independent source of points for testing the similarity scoring. Similarity scores were calculated for all permutations of seed points within each subject's first scan (labeled "bilateral" for left–right comparisons of ALIC and SS where appropriate, and "nonbilateral" otherwise); all permutations of subjects for each seed point ("intersubject"); and between 1st and 2nd scans ("inter-NEX") and 2nd and 3rd scans ("interscan"), where available, for each subject and seed point. We expect that similarity scores will be lowest for the nonbilateral comparisons, and highest for the interscan and inter-NEX cases where the same seed region and same subject are being compared.

Results

The figure is a box plot showing the range of similarity scores for the five different categories of comparison. The thick horizontal line across each box represents the median, the box shows the interquartile range, the whiskers show the extent of the bulk of the data, and circles show outliers more than 1.5 interquartile ranges from the box. The means (± s.d.) for each group were 0.19 (± 0.13) for nonbilateral, 0.33 (± 0.14) for bilateral, 0.38 (± 0.12) for intersubject, 0.48 (± 0.09) for interscan and 0.47 (± 0.12) for inter-NEX. Two sample, one tailed *t*-tests showed significant differences between nonbilateral and bilateral scores ($P < 0.0001$), between bilateral and intersubject scores ($P < 0.05$), and between intersubject and interscan scores ($P = 10^{-7}$). There was no significant difference between interscan and inter-NEX similarity scores.

Discussion

These results demonstrate that it is possible to meaningfully quantify tract similarity in a way that produces greater similarity scores between data from the same seed region in different brains, than between data from different seed regions in the same brain. In addition, we have found that average similarity scores for a single seed region and single subject are consistent across scans, since inter-NEX and interscan scores are indistinguishable. Data on score spread, such as standard deviations, are provided, but little interpretation can be made of them since a considerable proportion of the variation will arise from the seed point placement process. These results provide a robust foundation for reliably and automatically segmenting tracts from a group of brain volumes for comparison, a key prerequisite to objective group studies of white matter with dMRI. By using this similarity measure to choose the "best" tract from a number of candidates, when compared to a predefined reference tract checked by an expert, segmentation reproducibility could be substantially improved. This could lead to routine "selection" of named fasciculi based on a standard set of reference tracts.



References

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