Whole Brain White Matter Tract Segmentation Of Single Subject Diffusion Tensor Tractography Data

T. R. Barrick[1], N. Lawes[1], and C. A. Clark[2]

[1]Clinical Neuroscience, Saint George's, University of London, London, United Kingdom, [2]Institute of Child Health, University College London, London, United Kingdom

Introduction: Automatic or semi-automatic segmentation techniques are desirable in tractography studies as they can potentially avoid reproducibility issues associated with extracting pathways of interest by manually drawing regions of interest aswell as limiting the time required for user interaction. Previous clustering algorithms have attempted to extract large pathways from diffusion tensor tractography (DTT) data (e.g. 1,2). Here we present an algorithm for clustering of tracts throughout the white matter of the entire brain which requires the user to simply identify the constituent parts of the tract of interest. We show that this is robust when applied to DTI datasets of individual subjects. This allows rapid tract extraction to be performed without the need for group mapping or averaging of datasets, therefore maintaining characteristic features of individual subjects.

Methods: *MRI data acquisition:* 5 young healthy subjects were scanned on a 1.5T GE Signa MRI system (max. field gradient strength 22mTm^{-1}). DTI was achieved using a single shot echo planar sequence with 12 diffusion sensitised directions as described previously (3). Two interleaved acquisitions comprising 25 slices each provided whole brain coverage (resolution: in plane 2.5mm; through plane 2.8mm).

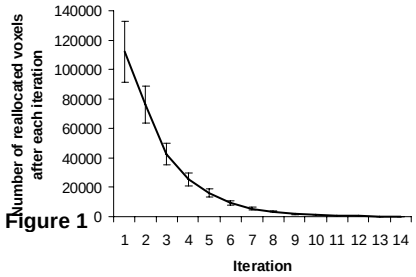

Figure 1

Tractography: Subvoxel streamline DTT was performed as described previously (3). Streamlines (vector step length 1.0mm, termination criteria FA < 0.1) were initiated from every voxel centre in the acquired space of each DTI. Streamline termination coordinates (x, y, and z in mm) and lengths (l, in mm) were computed. Voxels generating lengths less than 25mm were excluded.

Prior clustering: Prior to k-means clustering each streamline was assigned to a cluster based on its 7 parameters (x_1 y_1 z_1 x_2, y_2, z_2, l). To achieve this each parameter was divided by its maximum value (defined separately in each subject) and allocated to 1 of 10 bins (determined as equal steps from minimum to maximum for each parameter) giving a possible total number of initial clusters, $N = 10^7$. However, for all subjects not all of these were filled (N = 28335±2535) consequently leading to a manageable computational problem.

K-means clustering: Mean parameters were computed for each cluster and k-means (4) was performed. The minimum distance of a streamline to a cluster, d, was computed by,

$$d = \min_{j=1}^{j=N} \sqrt{\sum_{i=1}^{i=2} \left((x_i - \bar{x}_j)^2 + (y_i - \bar{y}_j)^2 + (z_i - \bar{z}_j)^2 \right) + (l - \bar{l}_j)^2} \ ,$$

and streamlines were allocated to appropriate clusters accordingly. Total numbers of analysed voxels across the dataset were (389525±6933) and convergence of the algorithm occurred rapidly (Figure 1). After 15 iterations the k-means algorithm was halted and clusters were automatically grouped together to generate larger clusters. This was achieved by amalgamating all clusters that had $d \leq 0.1$ according to one another's means, and reduced the number of clusters to N=9911±932. A fractional anisotropy map and an amalgamated cluster map in standard space are shown for a single subject in Figures 2i & 2ii. Adjacent to this is a colour visualisation map (Figure 2iii) of streamline tract terminations (5). Different coloured regions in the visualisation image are associated with different cluster numbers.

Final segmentation: The three segments of the left arcuate fasciculus (3,6) were then extracted from the 5 subjects. This was achieved using a semi-automated technique. For each segment a single cluster was identified that pertained to the pathway. The distance, d, between this cluster and each remaining cluster in the whole brain was calculated and the distances were ranked from lowest to highest. The tracks generated by the first 50 clusters were then visualised and only those pertaining to the segment of interest were retained.

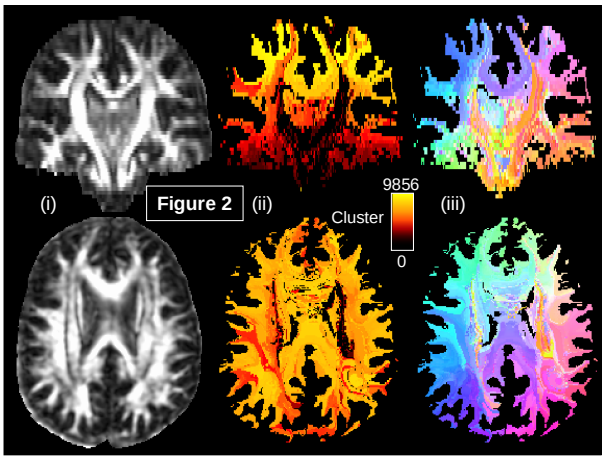

Figure 2

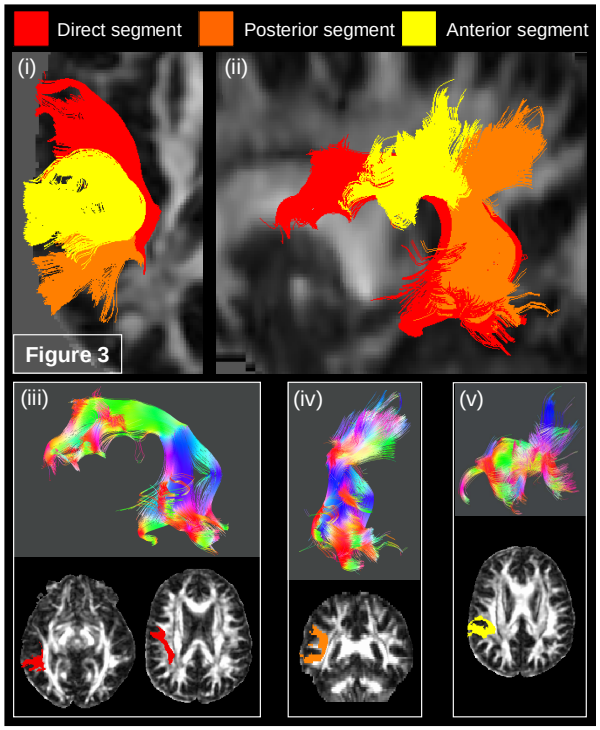

Figure 3

Results: Arcuate fasciculus segments are shown for a representative subject in Figure 3 viewed axially (Figure 3i) and sagittally (Figure 3ii). These reconstructions are similar to previously published results (3,6) and are shown coloured by the direction encoded colour scheme and overlain on image slices in standard space (Figure 3iii-v). Furthermore, the arcuate fasciculus segments of the 5 subjects analysed in the study were found to contain 14±5, 13±5 and 18±5 amalgamated clusters for the direct, anterior and posterior segments, respectively. This means that the final segmentation step, although user dependent, is very rapid.

Discussion: We have presented a novel technique for segmenting streamline DTT. The technique involves automatic clustering followed by a user-dependent final pathway extraction. The segmentation technique is advantageous over parcellation techniques based on atlases (7) because linear and non-linear transformations of single subject DTI or DTT are not necessary prior to clustering. The technique requires the user to simply identify the constituent clusters of the tract of interest and this process is straightforward and rapid.

References

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