Whole-Brain Neighbourhood Tractography

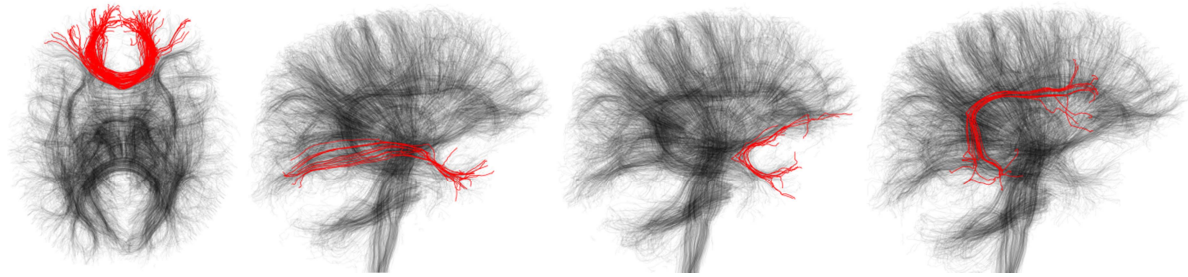
Kiran K Seunarine[1], Jonathan D Clayden[1], and Christopher A Clark[1]
[1]*Imaging and Biophysics Unit, UCL Institute of Child Health, London, United Kingdom*

Introduction: Tractography allows the segmentation of the white-matter tracts of the brain, which enables in-vivo studies of brain connectivity and tract-specific white-matter microstructure. Typically tracts are manually segmented using regions of interest (ROIs), which allows selection of the subset of streamlines that pass between the regions [1]. Well-known limitations of this approach are that it requires good anatomical knowledge and that it is time consuming. More generally, false-positive streamlines are also problematic when segmenting tracts. Neighbourhood tractography (NT) [2,3] attempts to overcome these limitations by using reference tracts to describe the paths of the major white-matter structures. The method searches for the streamlines in the test data that match these reference tracts. Later work extends the approach to include models of dispersion that allows the filtering out of anatomically unfeasible streamlines. The main benefits of this approach are that the process is highly automated, gives reproducible results and is portable between subjects. However, existing NT methods seed tractography from a single seed-voxel defined by the model and therefore tend not capture the full extent of the white-matter tracts. Here, we extend the NT algorithm further to exploit whole-brain tractography in order to increase the extent of the tract captured by the model and compare it to the single-seed NT approach.

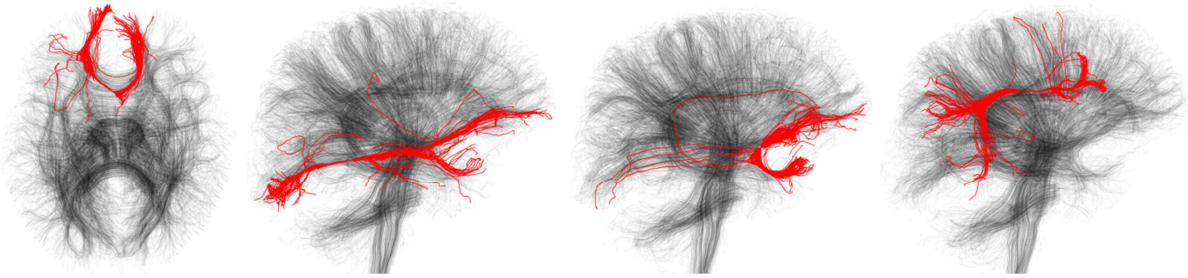
Methods: The algorithm is trained using diffusion MRI datasets from eleven subjects. First, tractography is seeded in all white-matter voxels to generate a set of streamlines across the whole brain to use as training data. The tract of interest is then manually segmented for each training dataset, which provides a set of streamlines with which to obtain a reference tract and model of dispersion between the reference and "candidate" tracts. Since streamlines are seeded across the brain, the seed point on a given "candidate" streamline is not guaranteed to be in the same relative location along the tract as the seed of the reference tract. To overcome this problem, we define an "anchor point" on the candidate tract, which determines the point on the streamline that is best matched to the seed point on the reference tract. In this work we use the training data to define a new reference tract. The median streamline of the streamlines belonging to the tract of interest is found for each subject and transformed into standard space. The median of these medians is then used as the reference tract and the dataset from which the reference tract was derived is removed from subsequent training. Finally, the remaining training streamlines are used to estimate a model of dispersion based on the approach described in [3]. Here, the model is updated to incorporate information about the displacement of the anchor points of the candidate streamlines from the seed point of the reference tract. This allows the model to disregard streamlines that are far from the tract of interest.

To test the method, we compare segmentations generated using whole-brain NT to those from the single-seed NT algorithm [3]. Both methods use the same reference tract and their models are trained using 11 of the datasets; the remaining dataset is used for testing the models. Tractography was seeded in all voxels with FA>0.4. The tracts chosen for the comparison are the left arcuate fasciculus (af), left inferior longitudinal fasciculus (ilf), left uncinate fasciculus (uf) and genu of the corpus callosum (gcc).

Data: Data were acquired for 12 healthy volunteers (5 female; mean age 28.27±3.23 years) on a Siemens Avanto 1.5T scanner. The diffusion sequence consisted of 60 gradient directions at b=1000 s mm^{-2} with 3 additional b=0 images for normalisation. Reconstructed image resolution was 2.5×2.5×2.5 mm. Total scan time was approximately 20 minutes.



Whole-brain neighbourhood tractography



Original neighbourhood tractography algorithm

Figure 1 – Examples of segmentations for the (from left to right) gcc, ilf, uf and af using (top) whole-brain NT and the (bottom) single-seed NT algorithm. For the whole-brain NT segmentations, red streamlines indicate matches to the tract of interest; other streamlines are shown in black. The segmentations from the single-seed NT algorithm are overlaid onto tract density images for clarity.

Results: Figure 1 shows segmentations of the reconstructed tracts using (top) the whole-brain NT algorithm and (bottom) the single-seed NT approach for the test dataset. The red streamlines show the segmentation of the various tracts for both algorithms. The segmentations from the single-seed algorithm are very narrow at the seed location, where the streamlines must go through the seed voxel, and contain far more false-positives than the whole-brain NT algorithm.

Discussion & Conclusions: This work shows that combining whole-brain tractography with the NT algorithm results in good coverage of tracts of interest while maintaining many of the benefits of the original single-seed NT approach. Although user input is required for the training step, after the model has been generated the process is completely automated and requires no further input from the user. In future work we aim to improve the method by implementing an unsupervised algorithm for training the model, which will completely automate the procedure.

References: [1] M. Catani et al (2008). Cortex 44:1105-1132 **[2]** J.D. Clayden, et al (2006). NeuroImage 33(2):482-492 **[3]** J.D. Clayden, et al (2007). IEEE TMI, 26(11):1555-1561

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