

### 3D visualisation of connectomes using streamtubes

Kerstin Pannek<sup>1</sup>, Roslyn Boyd<sup>1</sup>, and Stephen Rose<sup>2</sup>

<sup>1</sup>The University of Queensland, Brisbane, Queensland, Australia, <sup>2</sup>The Australian E-Health Research Centre, CSIRO, Brisbane, Australia

**Target audience:** Researchers interested in the structural connectome

**Purpose:** Connectomes are typically represented in matrix form. Often, streamline number or mean diffusion metrics (e.g. FA) are encoded as matrix values. Matrix representation does not, however, allow the easy assessment of the anatomical plausibility of connections, or encoding of diffusion metrics along different locations of the tract. To improve visual assessment of the connectome, we suggest the use of streamtube representation of connections.

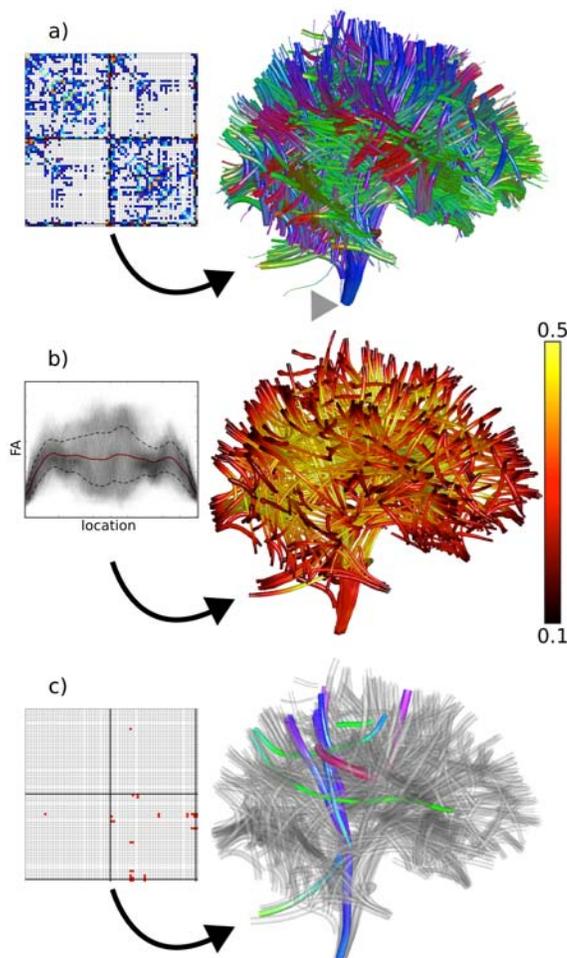


Figure 1: a) Encoding streamline number as tube thickness; b) encoding local FA mean and relative standard deviation as tube colour and thickness; c) presenting sub-networks

streamtubes allows visualization of confidence in the existence of a connection (Figure 1a) and local attributes of the connections (Figure 1b). Tube thickness, colour and opacity can be fine-tuned for optimized visualization of cortical or deep structures. The opacity and colour of individual streamtubes can be adjusted to highlight subsets of connections, such as connections of altered connectivity (Figure 1c).

**Conclusion:** The presented techniques can be used to visualize connectomes of individuals and populations, to visually explore tract attributes (such as FA) along a connection, and to facilitate anatomical interpretation of sub-networks.

**References:** 1. Colby JB, Soderberg L, Lebel C, Dinov ID, Thompson PM, and Sowell ER. Along-tract statistics allow for enhanced tractography analysis. *Neuroimage*. 2012;59(4):3227-42. 2. Zalesky A, Fornito A, and Bullmore ET. Network-based statistic: identifying differences in brain networks. *Neuroimage*. 2010;53(4):1197-207.

**Methods:** MRI data were acquired at 3T. **Preprocessing.** Whole brain tractograms were generated from HARDI data ( $b = 3000 \text{ s/mm}^2$ ). Target regions were obtained using FreeSurfer parcellation of high-resolution structural data (MPRAGE, 0.9 mm isotropic). Connections between each pair of regions were extracted. **Streamline number.** For each pair of regions, the mean tract was calculated after b-spline interpolation as described previously<sup>1</sup>. The number of streamlines for each connection recorded. Mean tracts were plotted as streamtubes in Matlab. Streamtube colour indicates the local tangent (red: left-right; blue: inferior-superior; green: anterior-posterior). Streamtube thickness indicates streamline number (here:  $\log_{10}(\text{streamline number})$ ). Note that thickness and opacity can easily be scaled to allow visualization of tracts located deeper within the brain). **Along-tract statistics.** FA was sampled for every interpolated streamline<sup>1</sup>. Along-tract FA means and standard deviations were calculated for every connection. Mean tracts were plotted as streamtubes, with colour indicating the average FA value at each location, and thickness indicating the relative standard deviation of the FA value at each location. Note that population mean and variability can be encoded in a similar fashion, and calculation of along-tract metrics is not restricted to FA. **Sub-networks.** As an example, pathways of altered connectivity in children with unilateral cerebral palsy compared to typically developing children were identified using the network based statistic<sup>2</sup>. Connections that were not identified as significantly different were plotted as transparent gray streamtubes, while connections with altered connectivity were plotted as opaque, directionally colour-coded streamtubes. Streamtube thickness was determined by the number of streamlines contained in each connection, as described above. Note that tube colour and thickness could also indicate other variables, such as mean and variability of FA across a population, or local p-values obtained from along-tract statistical analysis.

**Results:** Example connectomes are shown in Figure 1. Streamline number was encoded as tube thickness in Figure 1a. A large number of thick tubes with high streamline count are seen. Confidence in the existence of these connections is high, compared to thinner tubes with low streamline number (e.g. gray arrowhead). The overall shape of the brain can be seen. Local FA mean and standard deviations were encoded as colour and thickness of the tubes in Figure 1b. As expected, FA values were overall higher in deep white matter structures, and were lower when approaching the cortex. Local FA standard deviations were homogeneous within the connections. Connections of altered connectivity in unilateral cerebral palsy are shown in Figure 1c. Transparent gray streamtubes outline the shape of the brain, putting the coloured, significantly altered connections into anatomical context.

**Discussion:** Representation of connections contained in the connectome using streamtubes allows visualization of confidence in the existence of a connection (Figure 1a) and local attributes of the connections (Figure 1b). Tube thickness, colour and opacity can be fine-tuned for optimized visualization of cortical or deep structures. The opacity and colour of individual streamtubes can be adjusted to highlight subsets of connections, such as connections of altered connectivity (Figure 1c).