# Model-based streamline rejection for probabilistic tractography

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## Introduction

False positive connections are an inevitable part of *in vivo* probabilistic tractography. Due to the probabilistic sampling process, some streamlines generated by tractography algorithms are typically extraneous, and do not accurately reflect the topology of the underlying white matter fasciculus. When tractography is used as a segmentation tool, such as in group contrast studies involving white matter tracts, these extraneous streamlines are problematic because the region of the brain visited by the streamline set will include areas outside the tract of interest. The commonest solution is to apply a voxelwise threshold to visitation maps derived from the streamline set, but this method is insensitive to the meaning of the voxel values, and the choice of threshold level varies widely from study to study. In this work we adopt a different approach, using intuitively-encoded prior information to reject streamlines which do not match the expected trajectory of the tract. This approach has the added advantage of obviating the usual fall-off in "connection likelihood" with increasing distance from the seed point; and unlike region-of-interest methods, the rejection criterion is based on the topology of the tract in each individual subject.

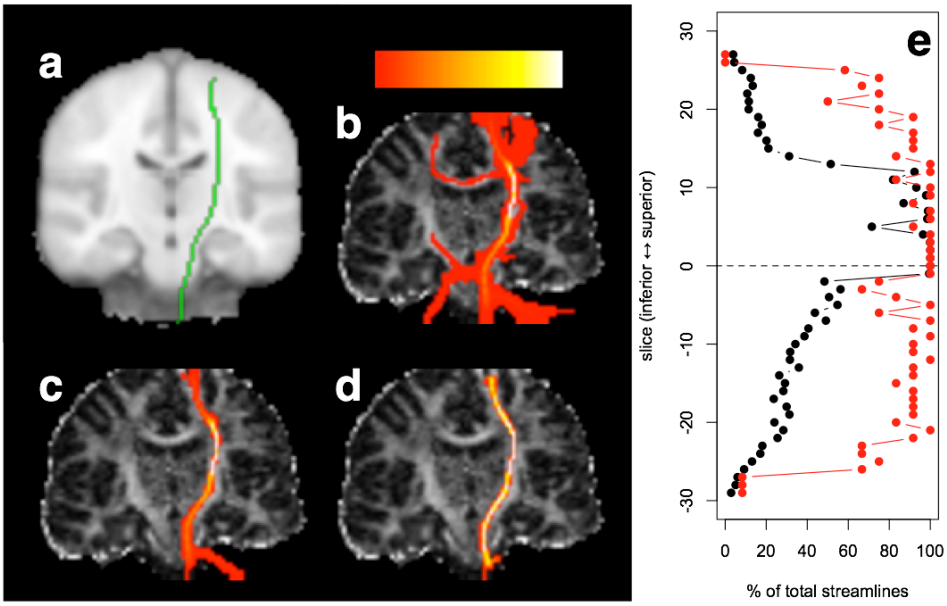


***Fig. 1***: *Effect of streamline rejection on segmentation of the left pyramidal tract, shown by visitation maps in maximum intensity coronal projections. The reference tract, in MNI space (a), is used to choose a matching tract in diffusion space, which includes some extraneous pathways (b). The tract is shown after thresholding at 1% (c) and after applying streamline rejection (d, no threshold). The graph (e) shows the largest voxel value in each slice of the maps before (black) and after (red) rejection. Dashed line indicates the seed slice.*

## Methods

Data were acquired from eight healthy young volunteers (4 male, mean age 31.9 ± 5.3 yr). Each subject was scanned on three separate occasions on a GE Signa LX 1.5 T clinical system. Echo-planar diffusion-weighted images were acquired along 64 noncollinear directions at a *b*-value of 1000 s mm$^{-2}$, along with 7 *b*=0 images. Reconstructed image resolution was 2 x 2 x 2 mm. Scan time was approximately 20 min.

The prior information about tract shapes and lengths is encoded in reference tracts, which are based on a human white matter atlas [1]. The probabilistic neighbourhood tractography (PNT) method [2,3] was used to fit a model of tract shape variability across the data set, and to simultaneously find best matching tracts in each brain volume. The tractography algorithm used to generate all tracts was FSL ProbTrack [4].

The single seed point associated with each best matching tract is used to generate a set of 5000 probabilistic streamlines. The PNT algorithm uses the median of this set to evaluate the similarity of the tract to the reference tract, but any extraneous streamlines will not be well represented by this median. However, we can use the model to prune the set. We retain a streamline, *s*, with probability min{1, $l_s/l_m$}, where $l_s$ is the likelihood of the streamline and $l_m$ the likelihood of the median (which are both well-defined probability values). In other words, all streamlines more likely than the median to match the reference are retained, while others will be selected in proportion to their difference from the median. All streamlines accepted in this way are then truncated to the length of the reference tract, in recognition of the fact that beyond the end of the reference, no *a priori* information about shape is available.

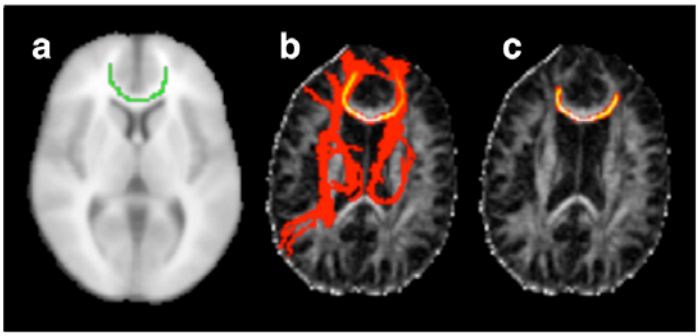


***Fig. 2***: *Streamline rejection and truncation in the genu. The reference tract (a) is shortened in this case, so that the selected tract (b) does not project into the cortex after truncation (c). Each image is a maximum intensity axial projection.*

## Results

The effect of the streamline rejection process we have developed is shown for a typical case in Fig.1. While the median trajectory of the tract selected by PNT (Fig. 1b) is a good match to the reference tract in this subject, various false positive connections remain. Thresholding the tract at the 1% level removes most of these, but a significant transpontine branch is left over. By contrast, the tract after streamline rejection shows just the pathway of interest, without the need to apply any threshold. Fig. 1e shows that the usual sharp fall-off in visitation count with distance from the seed point does not occur in the pruned tract.

Fig. 2 shows another example, this time in the corpus callosum genu. The reference tract has been truncated in this case, and so the final segmentation both rejects extraneous pathways and ends short of the cortex. This could be helpful in minimising the contribution of grey matter regions to the segmentation.

## Discussion

We have developed here a method of probabilistic streamline rejection, based on a tract shape model, as an alternative to voxelwise thresholding for the removal of false positives in tractography. Unlike thresholding, our rejection method is sensitive to the meaning of the data and based on explicit principles, namely: (1) that streamlines poorly represented by the median should be ignored, and (2) that beyond the end of the reference tract no information is available, so streamlines should be truncated. There is no threshold level or other parameter that has to be set by the user. Moreover, the usual decline in visitation with distance from the seed point is not seen, since streamlines which terminate near to the seed point will have much lower likelihood than those which continue.

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**References: [1]** Hua, K. et al., *NeuroImage* **39**:336 (2008); **[2]** Clayden, J.D. et al., *IEEE Trans Med Imag* **26**:1555 (2007); **[3]** Clayden, J.D. et al., in revision at *NeuroImage*; **[4]** Behrens, T.E. et al., *Magn Reson Med* **50**:1077 (2003).