

Filtering of spurious streamlines via streamline orientation and pathway density

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Synopsis

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Motivation: Tract extraction from whole-brain tractograms requires either an extensive knowledge of inclusion and exclusion zones or manual efforts to obtain clean tracts.

Goal: Automated filtering of spurious streamlines accelerates the tract extraction process. The algorithm should be versatile, while preserving tract shape and minimizing parameter adjustments.

Approach: We developed a filtering algorithm based on streamline orientation and density along an average trajectory. Our method was compared to four other filtering implementations.

Results: Our algorithm is applicable to a wide variety of tracts with a high and low streamline count. It offers efficient filtering and provides a conservative filtering preserving tract morphology.

Impact: We introduced an efficient filtering algorithm, removing spurious streamlines and preserving tract morphology across tracts of low and high density with default parameters. Additionally, the computed average trajectory enables the analysis of metrics in multi-fixel models along the tract pathway.

Introduction

Probabilistic tractography has uncovered more neural pathways compared to deterministic algorithms by allowing orientations with a lower diffusivity to contribute to the propagation of streamlines. While this has enabled a more complete overview of the existing pathways, it has also brought with it a higher number of false positive streamlines^{1,2}. In bundles extracted by targeting specific regions of interest, these false positives often appear as spurious streamlines, requiring the use of exclusion zones to filter them out.

We believe that the majority of spurious streamlines can be removed using algorithmic criteria, simplifying the process of exclusion zone selection and reducing the need for exhaustive trial-and-error testing for each tract. We have developed tools to efficiently compute the mean tract trajectory, which can be used to clean up tracts and study the microstructure of linear fascicles along their pathways.

Methods

Filtering

We considered two types of spurious streamlines in a tract $\mathcal{T}$: *oversteps* and *missteps* (Fig. 1).

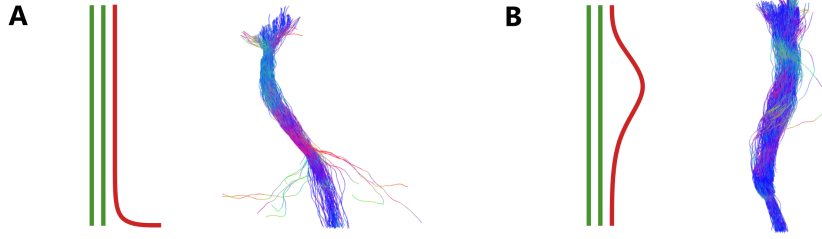


Figure 1: Schematic representation (left) and tractography example (right) of the two types of spurious streamlines on a corticospinal tract. **A** Oversteps, which present a coherent pathway but an incorrect end point and **B** Missteps, which have the correct destination but deviate along their pathway.

Oversteps depicted in Fig. 1A, refer to inaccuracies in streamline endpoints. These inaccuracies can be detected based on the overall streamline orientation. To achieve this, streamlines endpoints are first extracted and categorized as start and end points (Fig. 2A-B). The orientations of the streamlines, denoted as $\mathbf{u}_i$, are then transformed into polar coordinates $\mathbf{u}_i = (x, y, z) \rightarrow \mathbf{u}_i = (\theta, \phi)$ centered on the average orientation of the tract (Fig. 2C-D). Subsequently, the kernel density $\hat{d}_h(\mathbf{u})$ is estimated for all streamline orientations.

$$\hat{d}_h(\mathbf{u}) = \frac{1}{lh} \sum_{i=1}^l K\left(\frac{\mathbf{u} - \mathbf{u}_i}{h}\right), \quad (1)$$

where l is the number of streamlines in the tract and K is a symmetric bi-variate Gaussian kernel with a bandwidth h . Streamlines $\mathcal{L}$ with an insufficient number of neighbors are then removed from the set $\mathcal{T}$ (Fig. 2D).

$$\text{Criterion: } \mathcal{L}_i \notin \mathcal{T} \text{ if } \hat{d}_h(\mathbf{u}_i) \leq \frac{n}{2\pi \cdot h^2}, \quad (2)$$

where n is the approximate number of neighboring streamlines necessary to be classified as non-isolated.

Missteps illustrated in Fig. 1B, represent imperfections within the streamline pathways. To address these, an average bundle trajectory is calculated. The computation of the average trajectory proceeds iteratively: planes are positioned at the midpoint between two nodes, with their normal aligned to the direction of these points. A new node is then added to the average trajectory at the centroid of the points where the streamlines and plane intersect (Fig. 3A).

The outlier streamlines are then identified and removed based on their positional density $\hat{d}_h(\mathbf{x}_{p,i})$ at each plane p (Fig. 3B).

$$\hat{d}_h(\mathbf{x}_p) = \frac{1}{lh} \sum_{i=1}^l K\left(\frac{\mathbf{x}_p - \mathbf{x}_{p,i}}{h}\right), \quad (3)$$

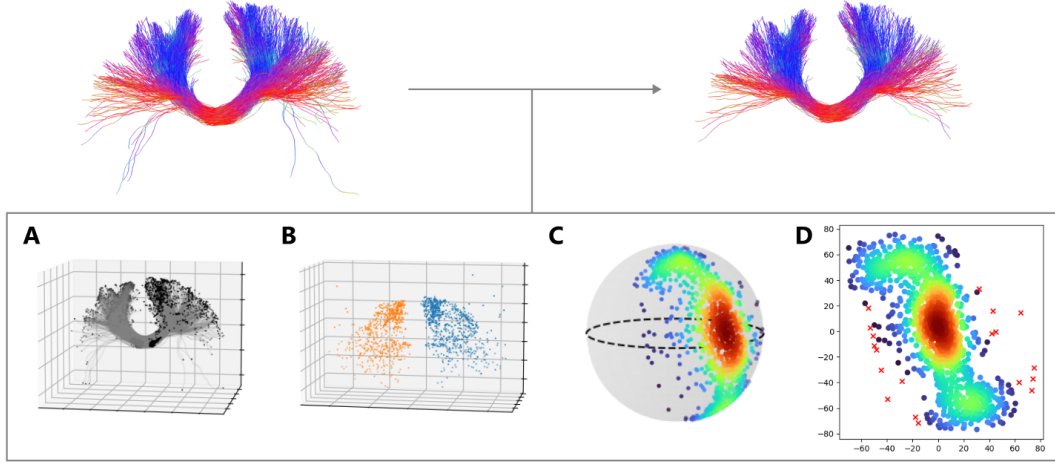


Figure 2: Filtering process to remove streamlines with isolated endpoints. **A** Extraction of streamline endpoints. **B** Classification of starts and ends based on mean streamline orientation. **C** Representation of the orientation density of the streamlines. **D** Kernel density estimate and removal of streamline with low orientation density (red crosses).

with $\mathbf{x}_{p,i}$ the coordinate vector of streamline i at plane p . Similarly to the previous criterion, isolated streamlines are then removed from the set $\mathcal{T}$.

$$\text{Criterion: } \mathcal{L}_i \notin \mathcal{T} \text{ if } \hat{d}_h(\mathbf{x}_{p,i}) \leq \frac{n}{2\pi \cdot h^2}. \quad (4)$$

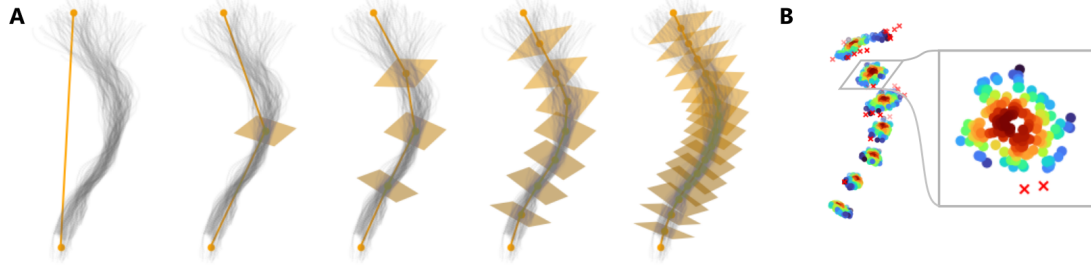


Figure 3: Visualization of the filtering process for pathway deviations. **A** An average bundle trajectory is iteratively computed. **B** At each step, outlier streamlines (red crosses) are identified based on their position density on the plane perpendicular to the trajectory.

The implemented code is open-source and available³. The streamline filter generated with our method was compared with filtering techniques employing density thresholding, RFBC⁴, CCI⁵ and Bundle-Cleaner⁶. The local modeling was estimated with msmt-CSD⁷ and the probabilistic tractography was performed with iFOD2⁸.

Along-tract analysis

The mean trajectory and perpendicular planes previously computed for the streamline filtering can be leveraged to segment the tract ROI into subsections (Fig. 4A) to provide along-tract analyses of

microstructural metrics (Fig. 4B).

To illustrate, the fractional anisotropy (FA) of a bundle of the corpus callosum was estimated with a single-fixel (DTI⁹) and multi-fixel model (DIAMOND¹⁰) with UNRAVEL¹¹ to visualize the impact of crossing fibers on metric estimation.

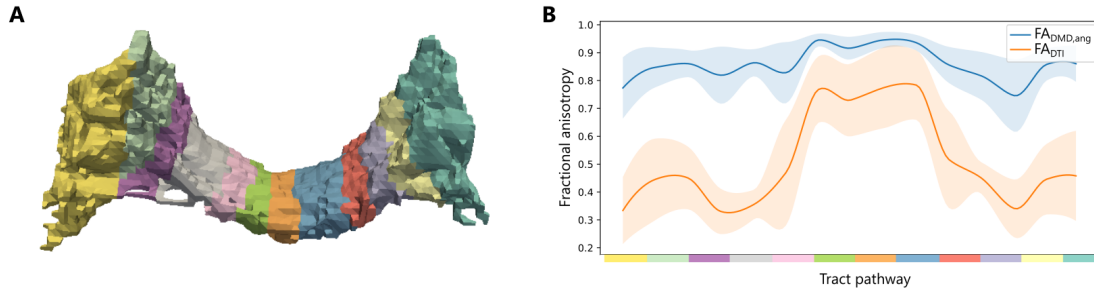


Figure 4: **A** 3D volume of the streamlines passing through the anterior midbody of the corpus callosum divided into twelve subregions along its pathway. **B** Evolution of the FA along the pathway estimated with DTI (orange) and DIAMOND with UNRAVEL (blue).

Results & Discussion

The arcuate fasciculus (AF) shown in Fig. 5A had a high number of streamlines and presented a complex shape with multiple end regions. The computation time of RFBC and BundleCleaner greatly increased with the number of streamlines. Furthermore, RFBC resulted in the loss of most of the AF's shape. Our proposed method removed spurious streamlines while preserving more of the shape of the AF compared to other techniques.

The uncinate fasciculus (UF) displayed in Fig. 5B had a low number of streamlines and presented spurious streamlines at the top, which all methods successfully eliminated. However, density thresholding and CCI removed many coherent streamlines due to the low density of the tract.

Regarding the results for the corpus callosum bundle shown in Fig. 5C, all methods yielded similar outcomes, with varying degrees of streamline removal.

The along-tract analysis on Fig. 4 highlighted the benefit of multi-fixel analysis in comparison to single-fixel models, such as DTI. With FA_{DTI} , a decrease in values was observed at the beginning and end of the tract, due to the presence of crossing fibers in the left and right hemispheres. Conversely, in the middle of the tract where a single fiber population exists, the results aligned more closely with the values obtained through $FA_{DMD,ang}$.

Conclusion

The proposed method demonstrated a conservative filtering with a low computation time, making it well-suited for tracts with a high number of streamlines and tracts of low density. Certain areas require further improvement, such as refining the removal of spurious streamlines within non-linear fascicles. Nonetheless, the algorithm should prove to be valuable for individuals seeking to filter spurious streamlines while preserving the tract morphology and to perform along-tract analyses with multi-fixel models.

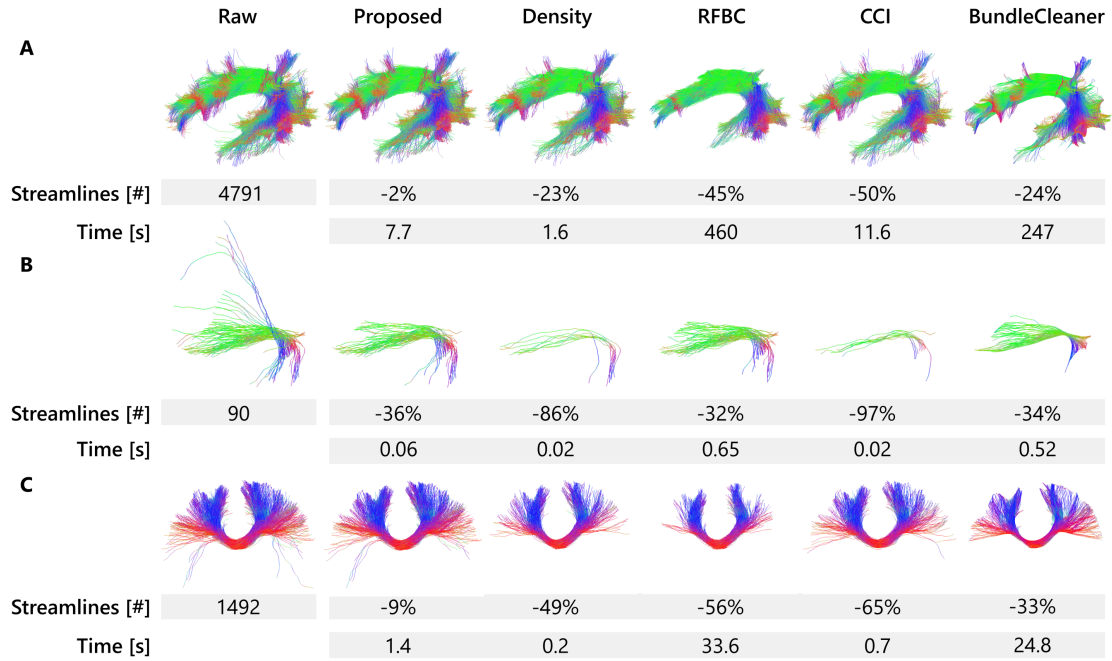


Figure 5: Filtering of tracts of the **A** arcuate fasciculus, **B** uncinate fasciculus and **C** the middle posterior bundle of the corpus callosum using five filtering methods: the proposed method, density thresholding, RFBC, CCI and BundleCleaner. All results were obtained with the default parameters, except for the corpus callosum with BundleCleaner which provided no results. The execution time and number of filtered streamlines are reported below each filtered tract.

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References

- ¹ Klaus H. Maier-Hein et al. The challenge of mapping the human connectome based on diffusion tractography. *Nature Communications*, 8(1):1349, November 2017.
- ² Kurt G. Schilling, Chantal M. W. Tax, Francois Rheault, Bennett A. Landman, Adam W. Anderson, Maxime Descoteaux, and Laurent Petit. Prevalence of white matter pathways coming into a single white matter voxel orientation: The bottleneck issue in tractography. *Human Brain Mapping*, 43(4):1196–1213, March 2022.
- ³ Nicolas Delinte. DelinteNicolas/UNRAVEL: v1.4.0, September 2023. 10.5281/ZENODO.7753501.
- ⁴ Stephan Meesters, G Sanguinetti, Eleftherios Garyfallidis, J Portegies, P Ossenblok, and R Duits. Cleaning output of tractography via fiber to bundle coherence, a new open source implementation. Human Brain Mapping Conference 2016, 2016.

- ⁵ Kesshi M. Jordan, Bagrat Amirbekian, Anisha Keshavan, and Roland G. Henry. Cluster Confidence Index: A Streamline-Wise Pathway Reproducibility Metric for Diffusion-Weighted MRI Tractography. *Journal of Neuroimaging*, 28(1):64–69, January 2018.
- ⁶ Yixue Feng, Bramsh Q. Chandio, Julio E. Villalón-Reina, Sophia I. Thomopoulos, Himanshu Joshi, Gauthami Nair, Anand A. Joshi, Ganesan Venkatasubramanian, John P. John, and Paul M. Thompson. *BundleCleaner* : Unsupervised Denoising and Subsampling of Diffusion MRI-Derived Tractography Data. preprint, Neuroscience, August 2023.
- ⁷ Ben Jeurissen, Jacques-Donald Tournier, Thijs Dhollander, Alan Connelly, and Jan Sijbers. Multi-tissue constrained spherical deconvolution for improved analysis of multi-shell diffusion MRI data. *NeuroImage*, 103:411–426, December 2014.
- ⁸ Jacques-Donald Tournier, F. Calamante, and Alan Connelly. Improved probabilistic streamlines tractography by 2nd order integration over fibre orientation distributions. *Proc. Intl. Soc. Mag. Reson. Med. (ISMRM)*, 18, January 2010.
- ⁹ P.J. Basser, J. Mattiello, and D. Lebihan. Estimation of the Effective Self-Diffusion Tensor from the NMR Spin Echo. *Journal of Magnetic Resonance, Series B*, 103(3):247–254, March 1994.
- ¹⁰ Benoit Scherrer, Armin Schwartzman, Maxime Taquet, Mustafa Sahin, Sanjay P. Prabhu, and Simon K. Warfield. Characterizing brain tissue by assessment of the distribution of anisotropic microstructural environments in diffusion-compartment imaging (DIAMOND): Characterizing Brain Tissue with DIAMOND. *Magnetic Resonance in Medicine*, 76(3):963–977, September 2016.
- ¹¹ Nicolas Delinte, Laurence Dricot, Benoit Macq, Claire Gosse, Marie Van Reybroeck, and Gaetan Renonnet. Unraveling multi-fixel microstructure with tractography and angular weighting. *Frontiers in Neuroscience*, 17:1199568, June 2023. 10.3389/fnins.2023.1199568.

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