SATA: Achieving volume saturation of streamline bundles in tractography

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Target audience: Researchers, physicians and clinicians interested in tract-based statistics and tractometry.

PURPOSE

In the field of neuroscience, tractograms are often segmented into groups of streamlines, also called bundles or tracts[1]. Then, metrics and statistics along these bundles are performed, called tractometry[2,3]. One common tractometry output is the measure of volume or spatial extent of a bundle of interest. For example, capturing the symmetry or asymmetry of the arcuate fasciculus (AF) between hemispheres of the brain based on volume of the AF[4]. **How many streamlines are needed to reliably compute volume or spatial extent of a bundle?** Here, we present a method to answer this question and reveal important biases of current tractography pipelines. We show that it must be used before tractometry to ensure that bundles are full so that their spatial extent can be compared across hemispheres and between different subjects.

METHODS

Saturation Analysis (SATA): A white matter fascicle is a physical object. If we were able to meticulously prepare a post-mortem brain and perform a perfect Klingler-style dissection and resection of a fascicle, the volume of white matter tissue collected would have a certain quantity in mm^3. Hence, in principle, the volume of a white matter fascicle should be invariant to the MR machine used or the tractography processing pipeline used. Saturation Analysis (SATA) is built on this principle. More specifically, at one point during the tractography process, the volume of a bundle will gradually cease growing while streamlines keep being added, indicating its saturation. Starting from a few streamlines, the bundle takes its basic shape and is the embryo of the future fully grown bundle. At first, adding a few streamlines to the set will make it develop quite fast. After a certain amount of streamlines, the growth rate will start decreasing as the shape of the bundle reaches maturity. New streamlines will have less and less effect on the volume since the spatial extent of the bundle has already been visited by the previous. Finally, saturation point is reached when no more volume is engendered by new streamlines. The SATA procedure follows this logic in an iterative procedure by subsampling given bundles to follow the progression. As a random and local process, tractography, whether deterministic, probabilistic or global, is not guaranteed to produce streamlines optimally distributed amongst all bundles of the brain. For example, a long and fanning structure such as the corticospinal tract (CST) and a short hook-like structure such as the uncinate fasciculus (UF) might not have the same saturation property in the tractogram. Thus, some tracts can be incompletely filled while others being saturated depending on the underlying signal, white matter structure shape and tractography parameters[5].

Datasets and experiments: Human Connectome Project (HCP) subject 100307, 152831, 210011, 734045, and 937160 were used for the experiments with a multi-shell fibre ODF reconstruction done with Dipy[6]. We used whole brain particle filter anatomically constrained tractography[7] with default parameters to initialize 50 million seeds. The seeds were uniformly and randomly located either in the grey matter / white matter interface (GMWMI) or in the whole white matter (WM) mask. Both probabilistic and deterministic tracking were done, combined with seeding strategies, resulting in four tractograms per subject. After the tracking process, Freesurfer[8] in conjunction with TractQuerier[9] were used to automatically extract the AF, CST, IFOF, and UF bundles. These four association and projection bundles are interesting because they cover a wide variation of shapes and properties. Finally, TractQuerier segmentation definitions were carefully adapted and outlier removal[10] was performed to make sure no spurious streamlines contaminate the segmented bundles.

RESULTS

The figure shows the saturation curve for all segmented bundles from the probabilistic GMWMI seeding tractogram of subject 100307. A model has been fitted on the curves to compute or predict the saturation points. The stars indicate the point where one streamline adds less than 1 mm^3 to the volume. To help visualization, bundles have been displayed with a graduation of seven filling ratios. The colour bar indicates the corresponding amounts, marked as dots on the curve, from 1/64th to the whole sampling of the tractogram. The CST and UF right saturated the earliest with just over 1/8th of the streamlines resulting from the tractography. At the opposite, both IFOF didn't reach fullness, but the model predicts saturation at 5000 and 7500 streamlines.
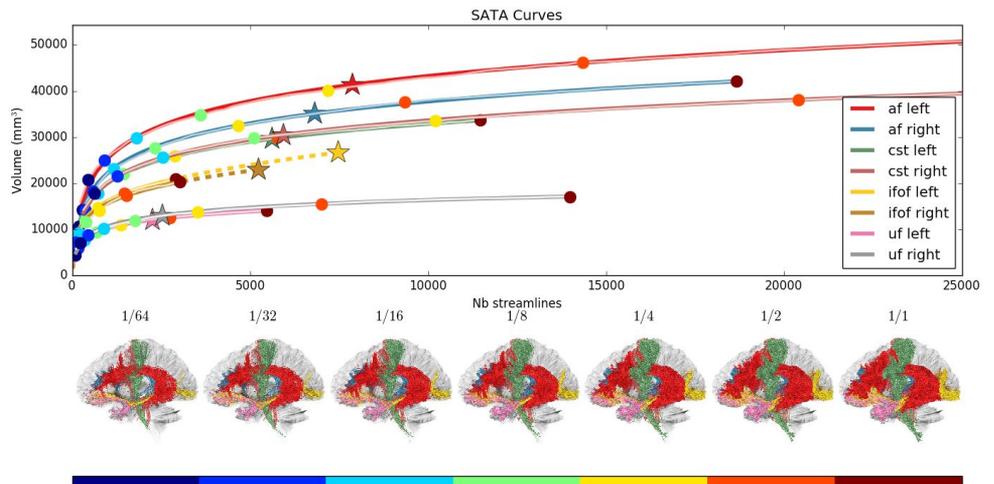
DISCUSSION

The results suggest that each tract has unique needs in terms of seeding. To be sufficiently defined by tractography, some need more streamlines than others because of geometrical properties and ease of tracking particularities. For example, tractography induces biases by overfilling bundles with greater white matter traversal (AF), and missing those passing near grey matter and nuclei (IFOF). Also, results not shown here suggest that SATA can reveal reproducibility issues in test-retest experiments and algorithm specific saturation performance.

CONCLUSION

Bundle volume saturation analysis is a novel way of assessing tractography properties. SATA gives confidence in the volume saturation of bundles, it suppresses tractography biases that could mislead studies and it helps to choose tracking strategies depending on the application. SATA is a first step to better understanding the limits and biases of tracking algorithms and data in the context of tractometry analysis. We strongly recommend using SATA to quantify bundles spatial extent to substantially reduce biases tractometry.

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