

Hybrid tractography analysis in patients with brain lesions^{*}

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For non-invasive studies of the white matter of the brain in vivo, data from diffusion-weighted magnetic resonance imaging (MRI) are processed to reconstruct fiber pathways and extract quantitative metrics. During these processes, we encounter several challenges related to fiber crossing, partial volume effects, and inherent ambiguities as an inverse problem [1]. A novel hybrid approach based on both deterministic and probabilistic tractography has been proposed as a potential solution to improve segmentation [1]. Since this method is built on reinforcement learning and our research samples are quite large, a high-performance computational tool is essential. Thus, we utilized the HSE University HPC Cluster "cHARISMa" to reconstruct 171 bundles for each of the 267 patients at two time points: before and after surgery. Importantly, the HPC cluster facilitates parallel computations, specifically, NVIDIA CUDA through the use of Nvidia GPUs, allowing us to run multiple processes simultaneously to optimize both human and technical resources.

In the current research, we are interested in language-related tracts, including three segments of the arcuate fasciculus, the frontal aslant tract, the inferior longitudinal fasciculus, the inferior fronto-occipital fasciculus, and the uncinate fasciculus bilaterally (see Fig. 1). To quantitatively investigate the differences in fiber characteristics before and after resection and their implications for language impairments, we extract diffusion and volumetric metrics for each of the tracts, followed by subsequent statistical analysis.

To date, we have compared the selected tracts and observed a decrease in both volume and number of fibers across all bundles. The next steps include investigating associations between tractography metrics and language impairments assessed by the Russian Aphasia Test (RAT) [2]. The RAT allows us to comprehensively assess language abilities [2]. Thus, after statistical analysis, we will be able to determine the causality of specific language impairments in patients following left-hemisphere glioma or epileptogenic lesion surgery.

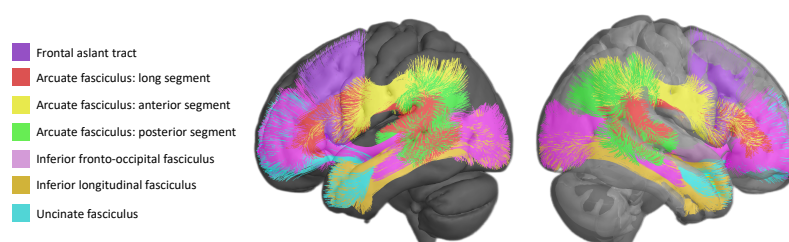


Figure 1. Associative tracts included into the analysis

References

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