Article type: Rapid Communication

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Automated white matter tractography: Advances in neuroimaging analytics.

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Received: 03-Jan-2025, Manuscript No. AANN-25-169288; **Editor assigned:** 04-Jan-2025, PreQC No. AANN-25-1692885(PQ); **Reviewed:** 18-Jan-2025, QC No AANN-25-1692885; **Revised:** 21-Jan-2025, Manuscript No. AANN-25-1692885(R); **Published:** 28-Jan-2025, DOI:10.35841/aann -10.1.182

Introduction

White matter tractography, derived from diffusion MRI, has become a crucial technique for mapping the brain's structural connectivity by reconstructing the trajectories of white matter fiber bundles. Traditionally, tractography has relied on manual or semi-automated methods, requiring expert intervention to define seed regions, adjust tracking parameters, and interpret results. While these approaches have provided valuable insights into brain architecture, they are time-consuming, prone to operator bias, and difficult to scale for large datasets. Automated white matter tractography aims to address these limitations by leveraging advances in computational neuroimaging analytics, enabling consistent, reproducible, and efficient reconstruction of white matter pathways. The adoption of automated techniques facilitates population-level studies, clinical diagnostics, and integration into surgical planning workflows by producing high-quality tract reconstructions with minimal user intervention [1].

One major advancement in automated tractography is the development of robust whole-brain segmentation and parcellation frameworks that can serve as a foundation for identifying specific white matter tracts. These frameworks typically employ standardized anatomical atlases, such as the JHU ICBM-DTI-81 or HCP MMP1.0 atlas, in combination with automated registration algorithms to align individual brain data to a common space. Once parcellated, these regions of interest can be systematically used as seeds and targets for tract reconstruction without manual selection. Furthermore, advances in fiber orientation estimation—using high angular resolution diffusion imaging (HARDI) and constrained spherical deconvolution—have improved the accuracy of automated tracking by resolving crossing, kissing, and fanning fibers, which are major limitations of earlier diffusion tensor models. This enhanced modeling enables more reliable delineation of complex tracts such as the arcuate fasciculus and superior longitudinal fasciculus [2].

Automated tractography pipelines have also benefited from the integration of machine learning techniques for both tract identification and quality control. Supervised learning approaches, trained on expertly labeled tractography datasets, can automatically recognize specific tracts by learning their spatial and diffusion profile characteristics. Deep learning methods, particularly convolutional neural networks (CNNs), have been applied to streamline fiber classification and filtering, removing anatomically

Citation: Matsumoto Y. Automated white matter tractography: Advances in neuroimaging analytics. J NeuroInform Neuroimaging. 2025;10(1):182.

implausible streamlines while retaining biologically meaningful pathways. In addition, automated quality control systems can detect and flag tracking errors or incomplete reconstructions, ensuring the reliability of outputs without requiring extensive manual review. These AI-driven enhancements improve scalability, allowing researchers to process hundreds or thousands of datasets efficiently in large neuroimaging studies [3].

The clinical relevance of automated tractography has grown significantly, particularly in neurosurgical planning and the study of neurological disorders. In neurosurgery, automated mapping of eloquent white matter pathways, such as the corticospinal tract or language-related fasciculi, can help guide tumor resections and minimize postoperative deficits. Automated pipelines ensure that these critical structures are consistently identified, even in cases where pathology has distorted the surrounding anatomy. In neurodegenerative diseases such as multiple sclerosis or Alzheimer's disease, automated tractography can quantify microstructural changes in white matter tracts, providing objective biomarkers for disease progression and treatment response. Similarly, in psychiatric disorders like schizophrenia or major depressive disorder, automated approaches have enabled large-scale investigations of connectivity abnormalities that would have been impractical with manual methods [4].

Despite these advances, several challenges remain in the development and deployment of automated tractography systems. Variability in diffusion MRI acquisition parameters, scanner hardware, and preprocessing pipelines can affect tract reconstruction accuracy, necessitating harmonization strategies for multi-site studies. Automated methods, while consistent, may still propagate systematic errors if underlying modeling assumptions are violated or if data quality is suboptimal. Another limitation is the difficulty in validating tractography results against ground truth, as histological validation is rarely feasible in vivo. There is also a need for greater transparency and interpretability in machine learning-based approaches, as clinicians must be able to trust and understand the outputs used for critical decision-making. Continued research is therefore focused on improving robustness, integrating multimodal imaging data, and developing consensus standards for automated tractography validation and reporting [5].

Conclusion

Automated white matter tractography represents a significant leap forward in neuroimaging analytics, offering consistent, reproducible, and scalable mapping of the brain's structural connectivity. Advances in diffusion modeling, atlas-based parcellation, and machine learning have collectively transformed tractography from a labor-intensive, expert-driven process into a streamlined, high-throughput methodology suitable for both research and clinical applications. By enabling large-scale studies, improving neurosurgical planning, and facilitating quantitative analysis of white matter integrity in neurological and psychiatric disorders, automated tractography has expanded the impact of diffusion MRI in neuroscience. While challenges related to variability, validation, and interpretability persist, ongoing innovations are steadily addressing these issues, paving the way for broader adoption and more reliable integration into clinical workflows. As the field advances, automated tractography will continue to play a pivotal role in elucidating the structural foundations of brain function and dysfunction.

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