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# Computational examples of software for white matter tractometry

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## Summary

Tractometry uses diffusion-weighted magnetic resonance imaging (dMRI) to assess the physical properties of long-range brain connections (Yeatman et al., 2012). We present an integrative ecosystem of software that performs all steps of tractometry: post-processing of dMRI data, delineation of major white matter pathways, and modeling of the tissue properties within them. This ecosystem also provides tools that extract insights from these measurements, including novel implementations of machine learning and statistical analysis methods that consider the unique structure of tractometry data (Muncy et al., 2022; Richie-Halford et al., 2021), as well as tools for visualization and interpretation of the results (Kruper et al., 2024; Yeatman et al., 2018). Taken together, these open-source software tools provide a comprehensive environment for the analysis of dMRI data.

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## References

Kruper, J., Hagen, M. P., Rheault, F., Crane, I., Gilmore, A., Narayan, M., Motwani, K., Lila, E., Rorden, C., Yeatman, J. D., & Rokem, A. (2024). Tractometry of the human connectome project: Resources and insights. *Front. Neurosci.*, *18*, 1389680. https://doi.org/10.3389/fnins.2024.1389680

Muncy, N. M., Kimbler, A., Hedges-Muncy, A. M., McMakin, D. L., & Mattfeld, A. T. (2022). General additive models address statistical issues in diffusion MRI: An example with clinically anxious adolescents. *Neuroimage Clin*, *33*, 102937. https://doi.org/10.1016/j.nicl.2022.102937

Richie-Halford, A., Yeatman, J. D., Simon, N., & Rokem, A. (2021). Multidimensional analysis and detection of informative features in human brain white matter. *PLoS Comput. Biol.*, 17(6), e1009136. https://doi.org/10.1371/journal.pcbi.1009136



- Yeatman, J. D., Dougherty, R. F., Myall, N. J., Wandell, B. A., & Feldman, H. M. (2012). Tract profiles of white matter properties: Automating fiber-tract quantification. *PLoS One*, 7(11), e49790. https://doi.org/10.1371/journal.pone.0049790
- Yeatman, J. D., Richie-Halford, A., Smith, J. K., Keshavan, A., & Rokem, A. (2018). A browser-based tool for visualization and analysis of diffusion MRI data. *Nat. Commun.*, 9(1), 940. https://doi.org/10.1038/s41467-018-03297-7