

pyAFQ: Automated Fiber Quantification, in Python

Presented by John Kruper¹, September 4th, 2020



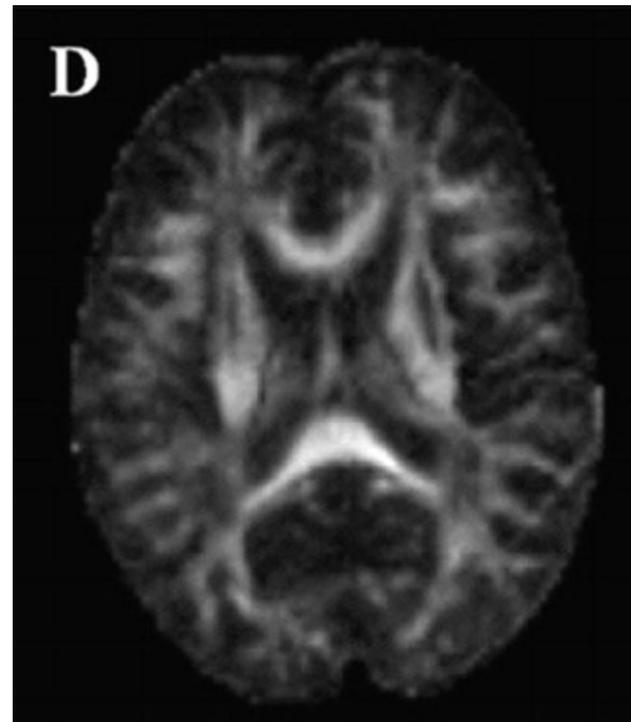
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The White Matter

- Why study the white matter?
 - Can detect, characterize, and monitor diseases [1, 2, 3]
 - Changes during experiences of [intensive learning](#) [4]
 - Could account for individual variances in cognition [5]
- How do we study the white matter?
 - Diffusion MRI (dMRI) are used to characterize brain tissue
 - For example, diffusion tensors are used to study the white matter
 - Provides non-invasive and *in vivo* measurements



Axial slice of fractional anisotropy (FA) measurements from dMRI scans [1]

How do we make inferences from an individual brain?

- One common approach is to register to common template
 - Problem: individuals 3d geometry different
- Instead we look at the bundles using waypoint ROIs

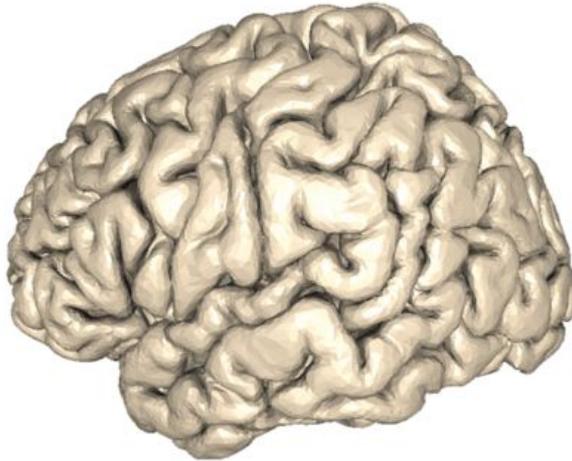
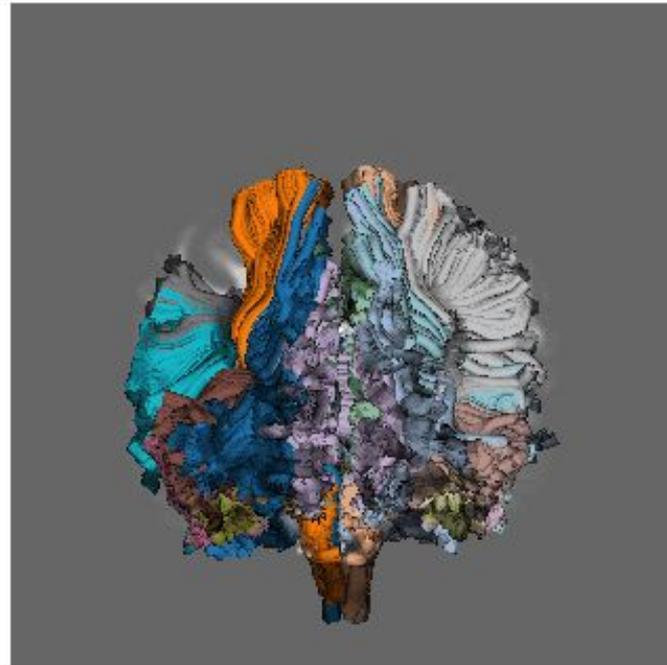


Image from [Yeatman, Richie-Halford, Smith, Keshavan, Rokem \(2018\)](#)

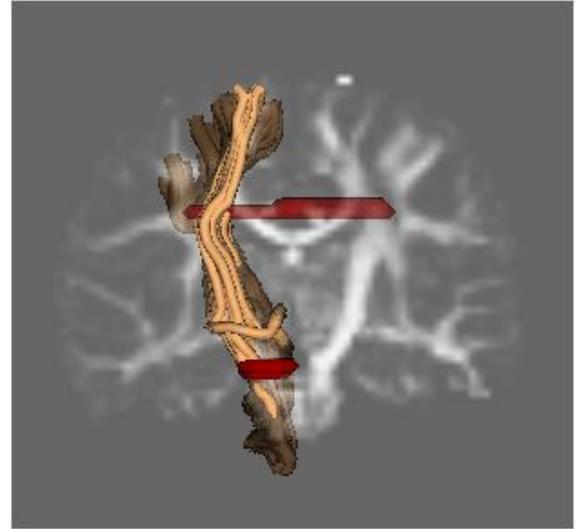
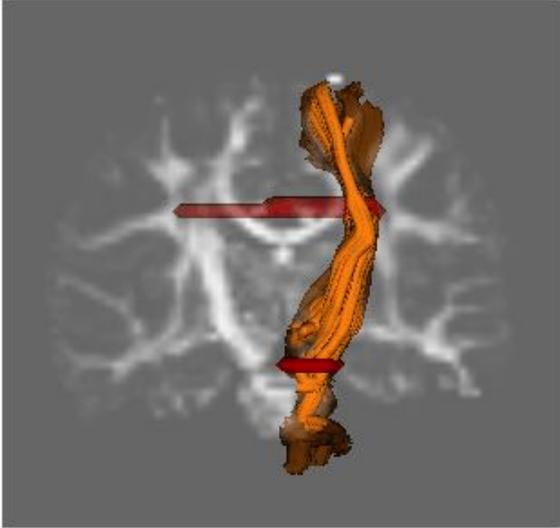
So what is pyAFQ?

- pyAFQ performs tractometry automatically, in python
- Why python?
 - Open source scripting language
 - Wide ecosystem of software tools in python
 - Lingua franca for reproducible open source scientific computing
- pyAFQ makes analysis faster and standardizes computational techniques
- There is a version of an existing software called [AFQ](#) written in Matlab
 - pyAFQ results closely match results from mAFQ



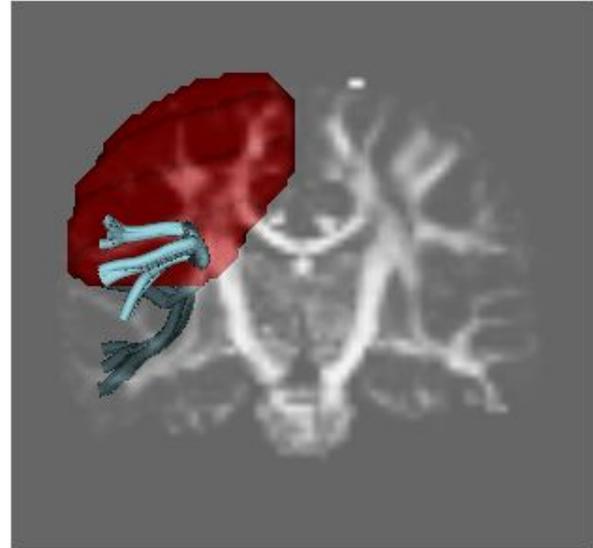
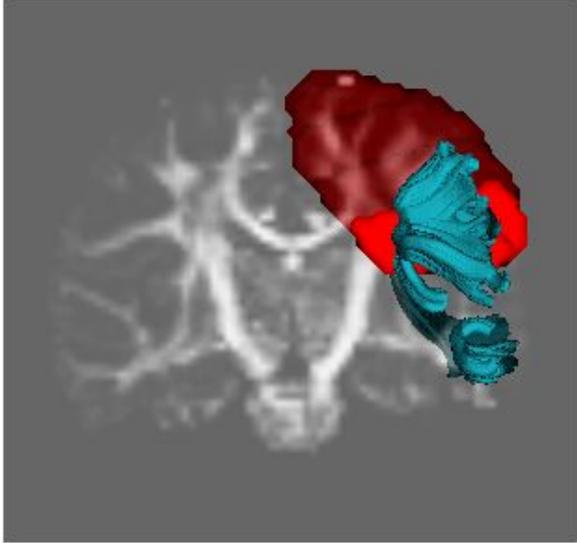
Data: [Human Connectome Project](#)

Visualizations generated by pyAFQ



Corticospinal tract
Data: Jason Yeatman, Stanford

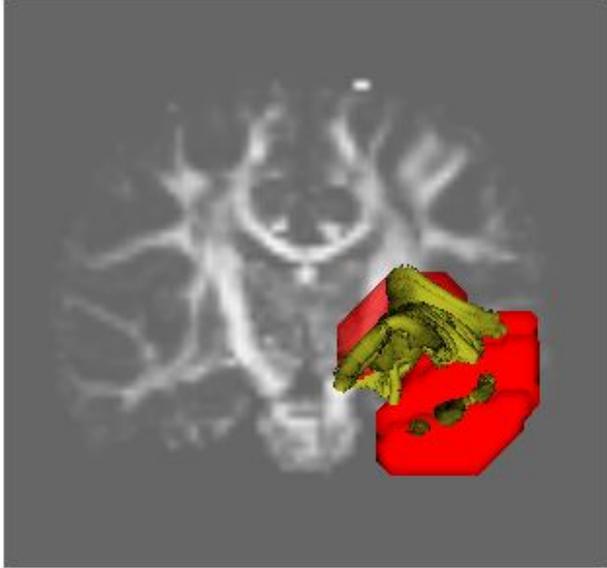
Gifs generated by pyAFQ



Arcuate

Data: Jason Yeatman, Stanford

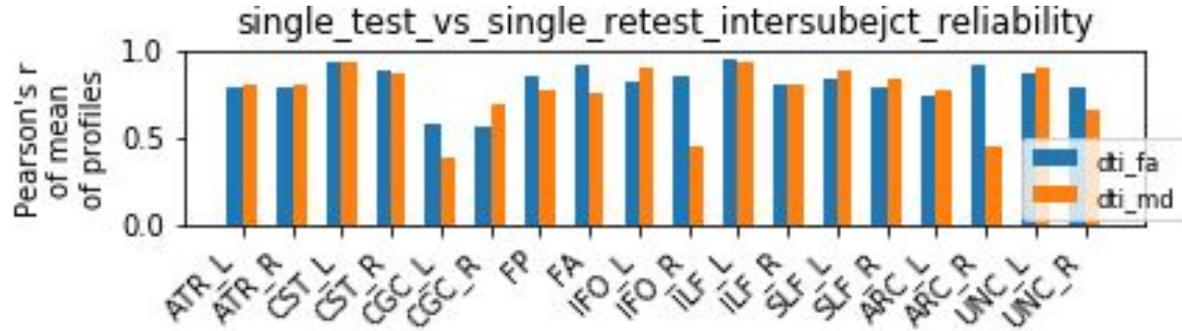
Gifs generated by pyAFQ



Uncinate

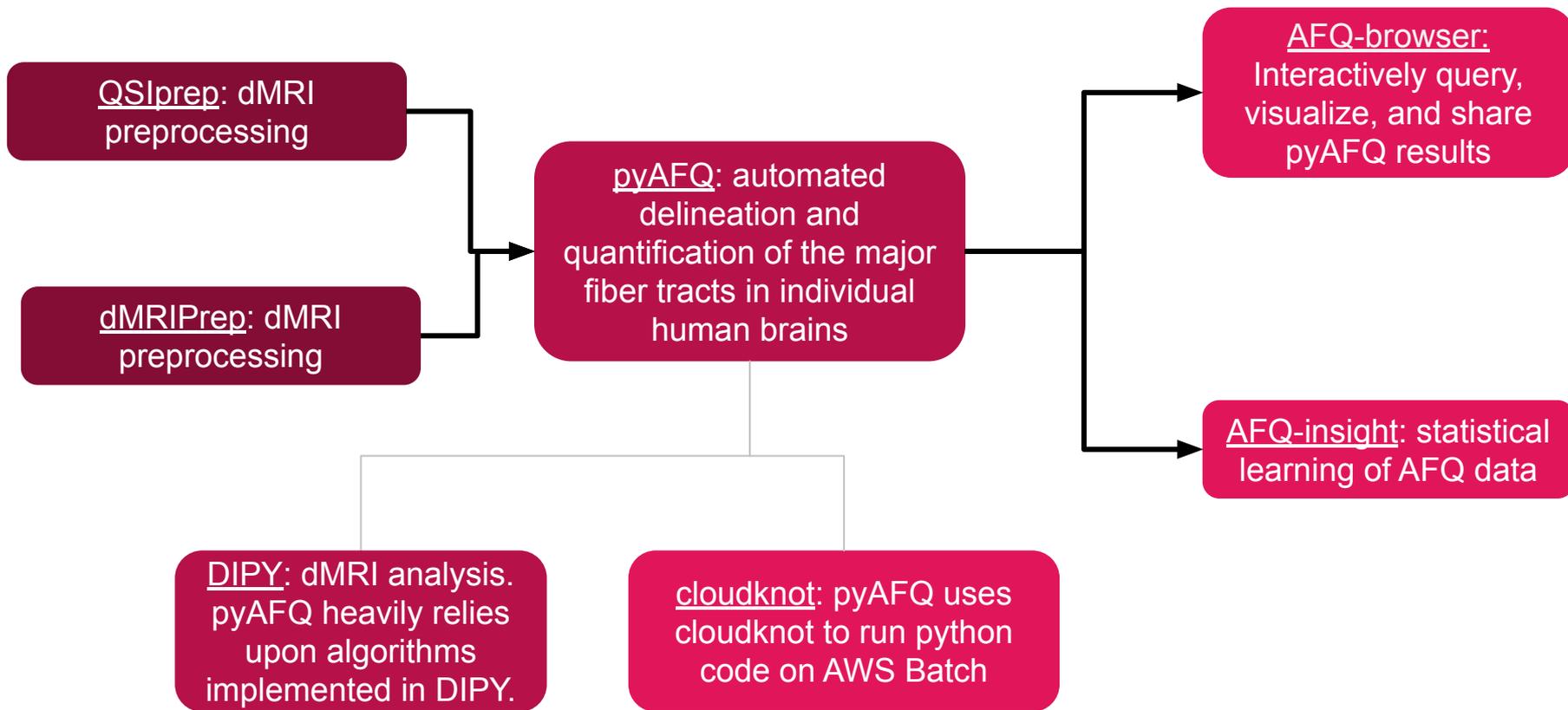
Data: Jason Yeatman, Stanford

Intersubject reliability plot generated by pyAFQ



Data: [Human Connectome Project](#)

Integration with the ecosystem



Version 0.4 recently released

- Includes several new registration templates and techniques
- Can use [plotly](#) to generate HTML-based visualizations of bundles
- Added Integration with [pyBIDS](#)
- Bug fixes / other improvements

Next steps (Version 0.5):

- Integrate Particle Filtering Tractography from dipy
- Integrate Multi-Shell Multi-Tissue CSD from dipy
- Make it easier to use custom-made ROIs in the API

Acknowledgements

- The development of AFQ projects is supported through grant 1RF1MH121868-01 (PI: Rokem) from the National Institutes for Mental Health/The BRAIN Initiative.
- Additional support is provided through NIBIB grant 5R01EB027585-02 (PI: Eleftherios Garyfallidis, Indiana University).
- We are also grateful for support from the Gordon and Betty Moore Foundation and the Alfred P. Sloan Foundation to the University of Washington eScience Institute Data Science Environment, as well as support from the Washington Research Foundation to eScience and to the University of Washington Institute for Neuroengineering.
- pyAFQ heavily draws from the free, open source python package: [dipy](#)

References

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- [2] Horsfield, M.A. and Jones, D.K. (2002), Applications of diffusion-weighted and diffusion tensor MRI to white matter diseases – a review. *NMR Biomed.*, 15: 570-577. doi:10.1002/nbm.787
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