

pyAFQ: Automated Fiber Quantification, in Python

Presented by John Kruper¹, September 4th, 2020



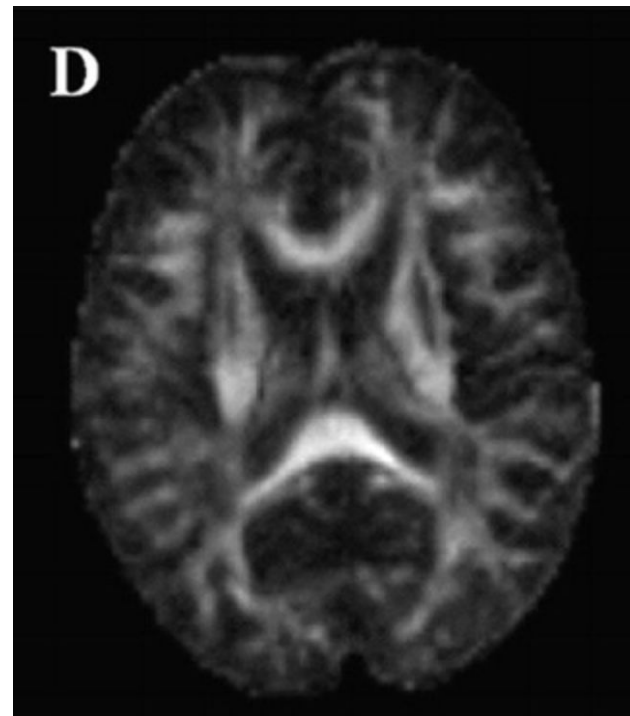
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The White Matter

- 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?

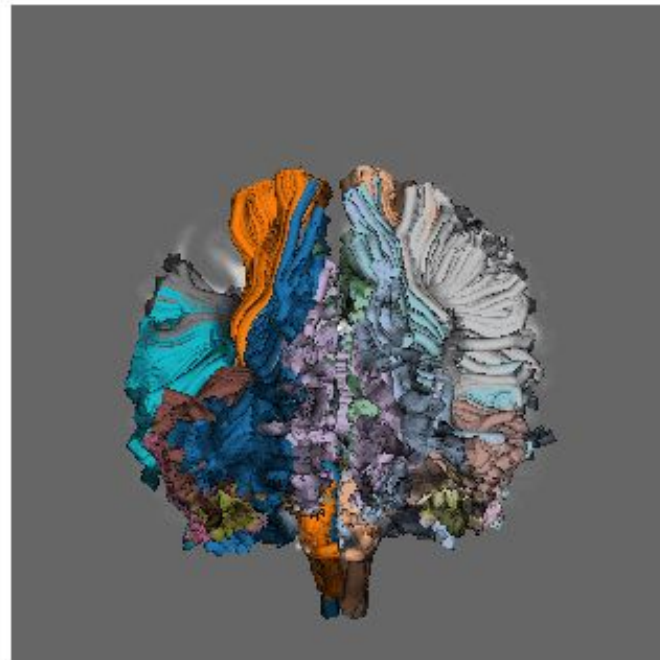
- One common approach is to register to common template
 - Problem: individuals 3d geometry different
- Instead we look at the bundles using waypoint ROIs



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

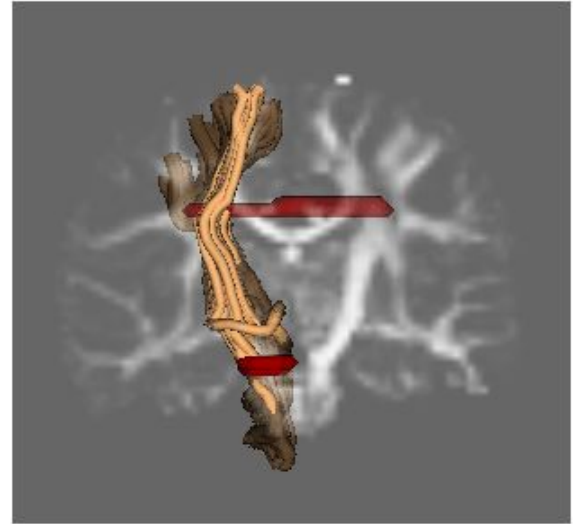
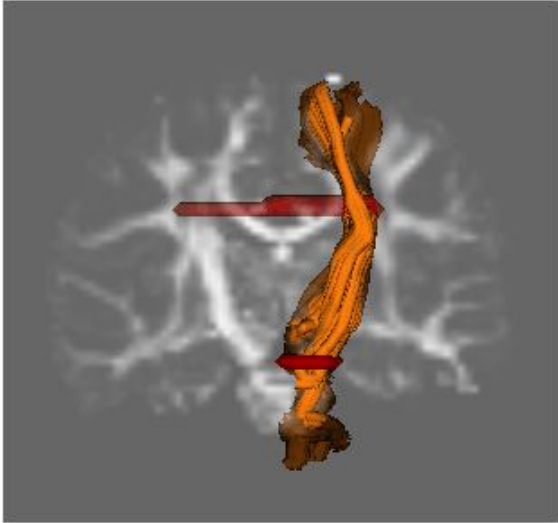
So what is pyAFQ?

- 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



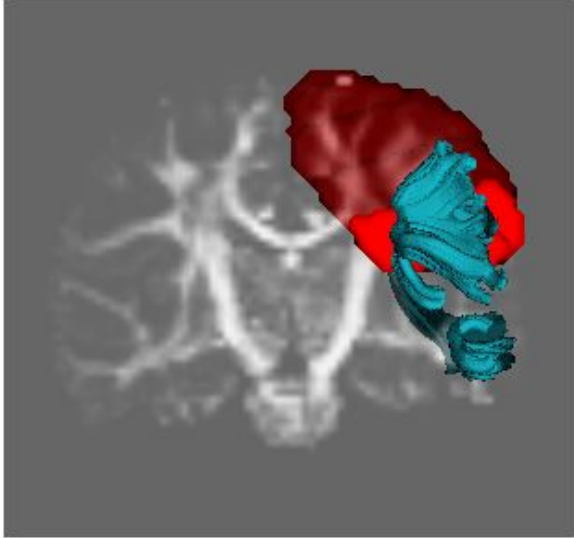
Data: [Human Connectome Project](#)

Visualizations generated by pyAFQ



Corticospinal tract
Data: Jason Yeatman, Stanford

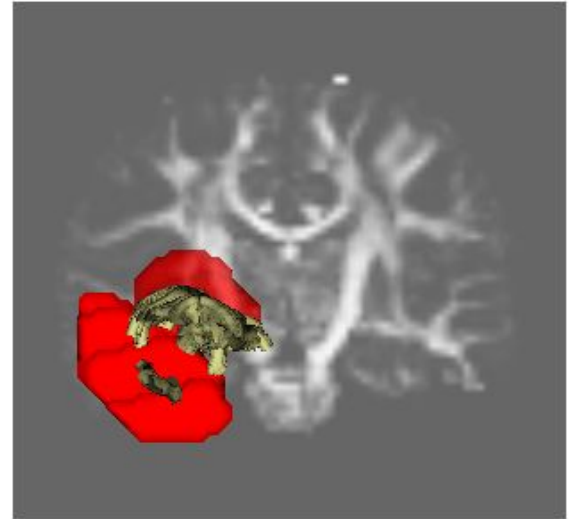
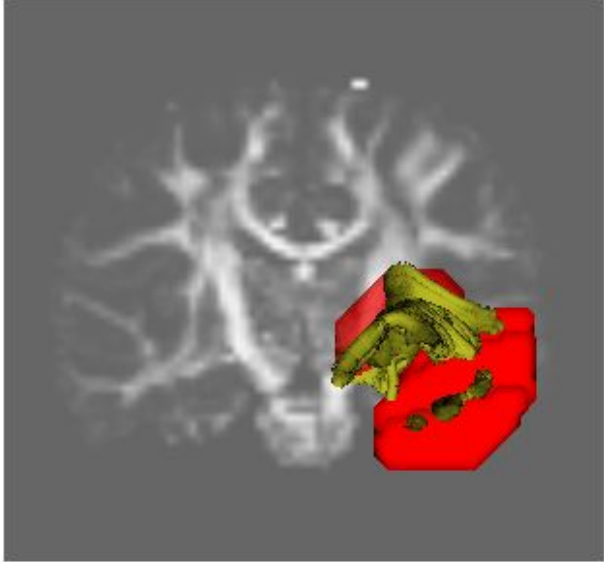
Gifs generated by pyAFQ



Arcuate

Data: Jason Yeatman, Stanford

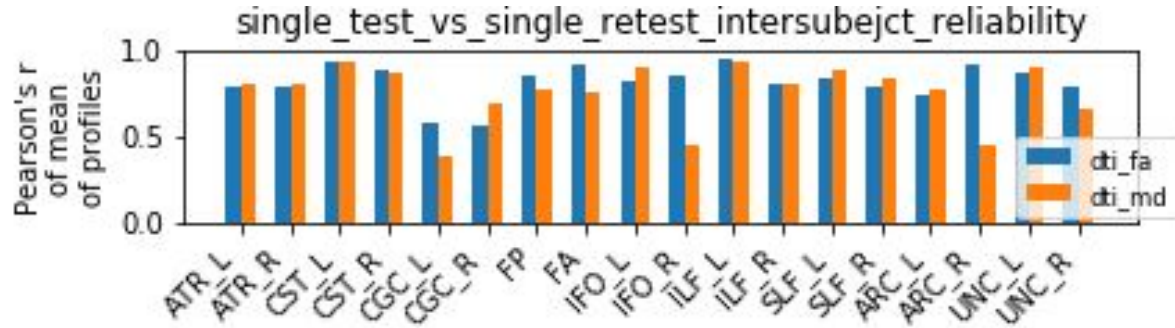
Gifs generated by pyAFQ



Uncinate

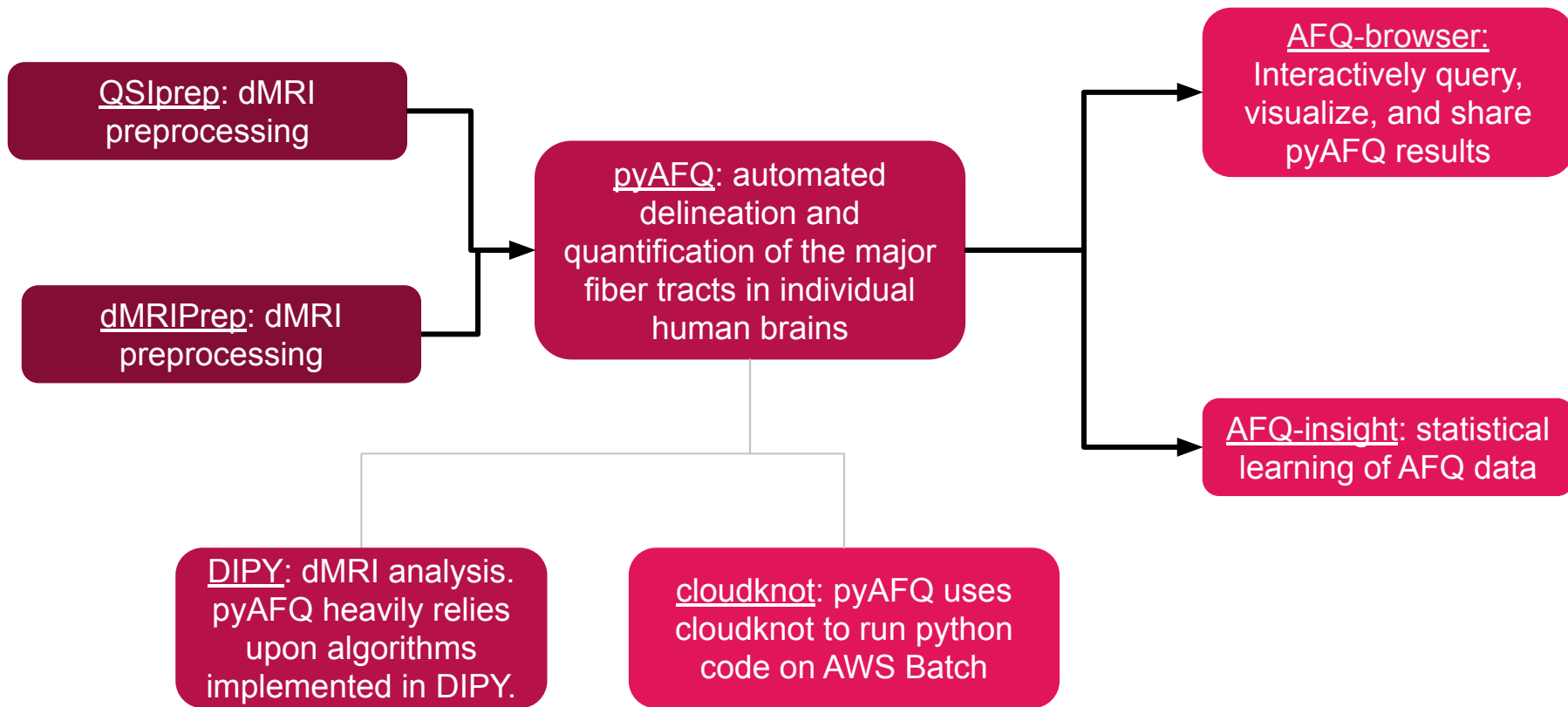
Data: Jason Yeatman, Stanford

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

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- pyAFQ heavily draws from the free, open source python package: [dipy](#)

References

- [1] Rovaris, M., Gass, A., Bammer, R., Hickman, S., Ciccarelli, O., Miller, D., & Filippi, M. (2005). Diffusion MRI in multiple sclerosis. *Neurology*, 65(10), 1526–1532.
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[4] Huber, E., Donnelly, P.M., Rokem, A. Yeatman, J.D. Rapid and widespread white matter plasticity during an intensive reading intervention. *Nat Commun* 9, 2260 (2018). <https://doi.org/10.1038/s41467-018-04627-5>

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