Deep learning for analysis of diffusion-MRI based white matter tractometry

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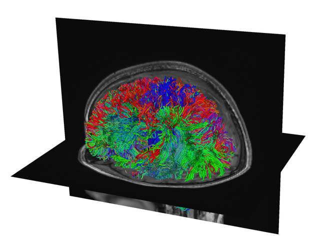
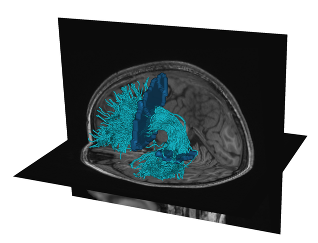
Introduction

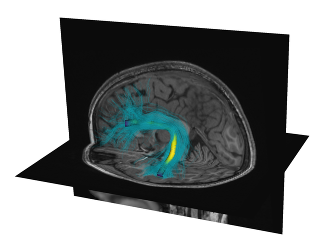
- Tractometry uses diffusion MRI (dMRI) to quantify brain tissue properties within white matter connections *in vivo* [1].
- The Healthy Brain Network Processed Open Derivatives (HBN POD2) is a large (n>2,000) pediatric dMRI dataset that has been processed and automatically QC'd[2, 3].
- The pyAFQ software was used to create tract profiles for statistical analysis [4].
- In previous work, we demonstrated that regularized regression provides accurate predictions of individual age in HBN from tractometry data (WM-based "brain age")[5].



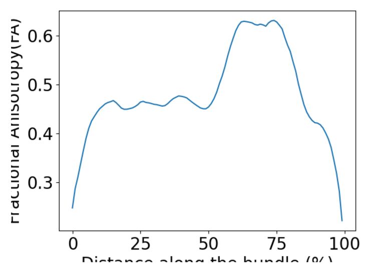
Whole brain tractography



Selecting a bundle with ROIs



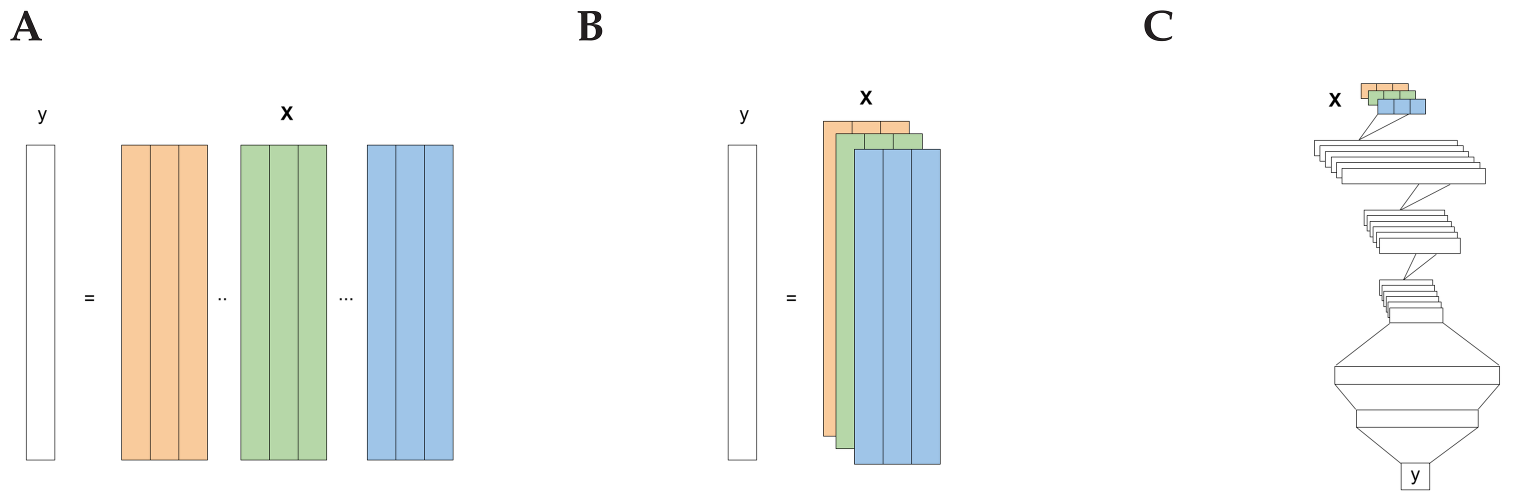
Extracting values along the length of the tract



Tract profile

Question: Would convolutional neural networks provide improvements in inferences from tractometry?

Methods

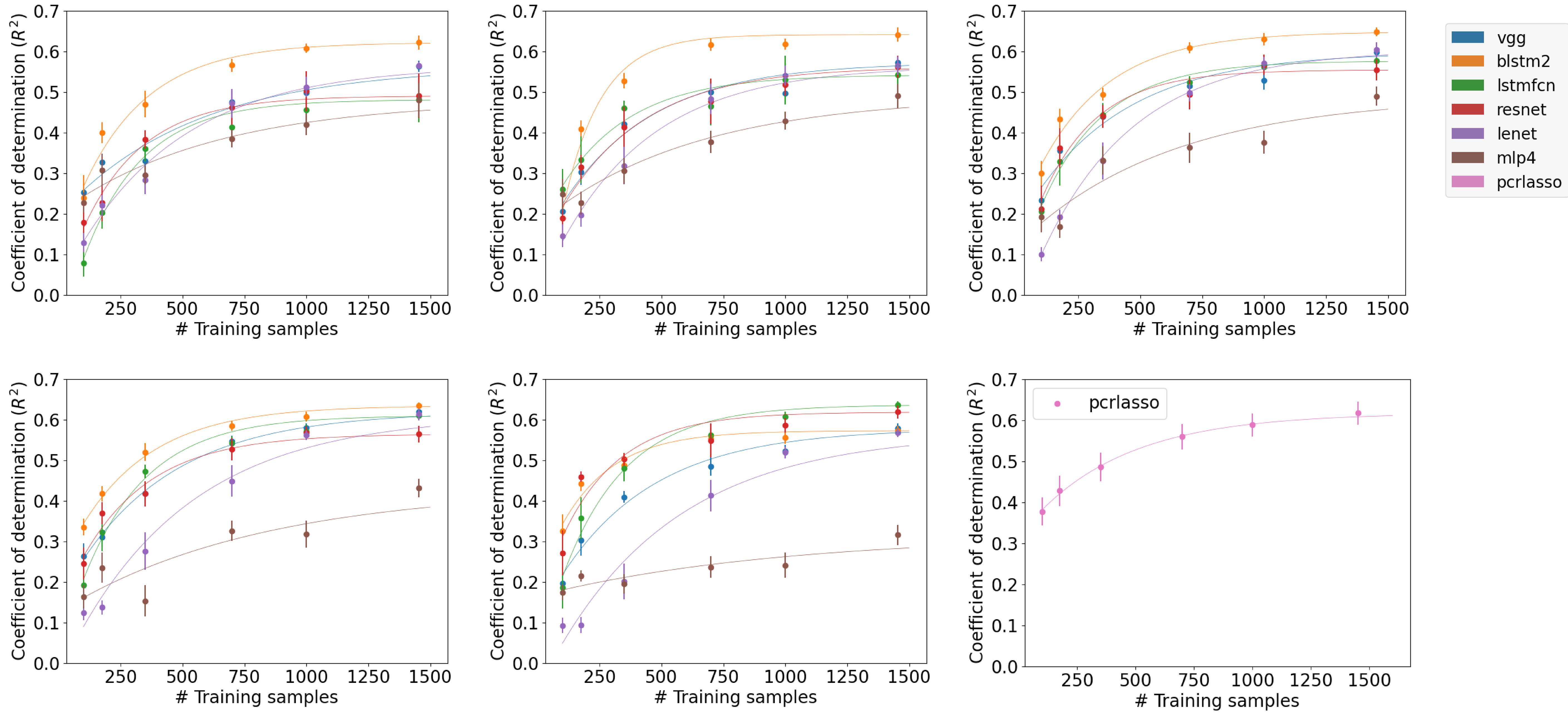


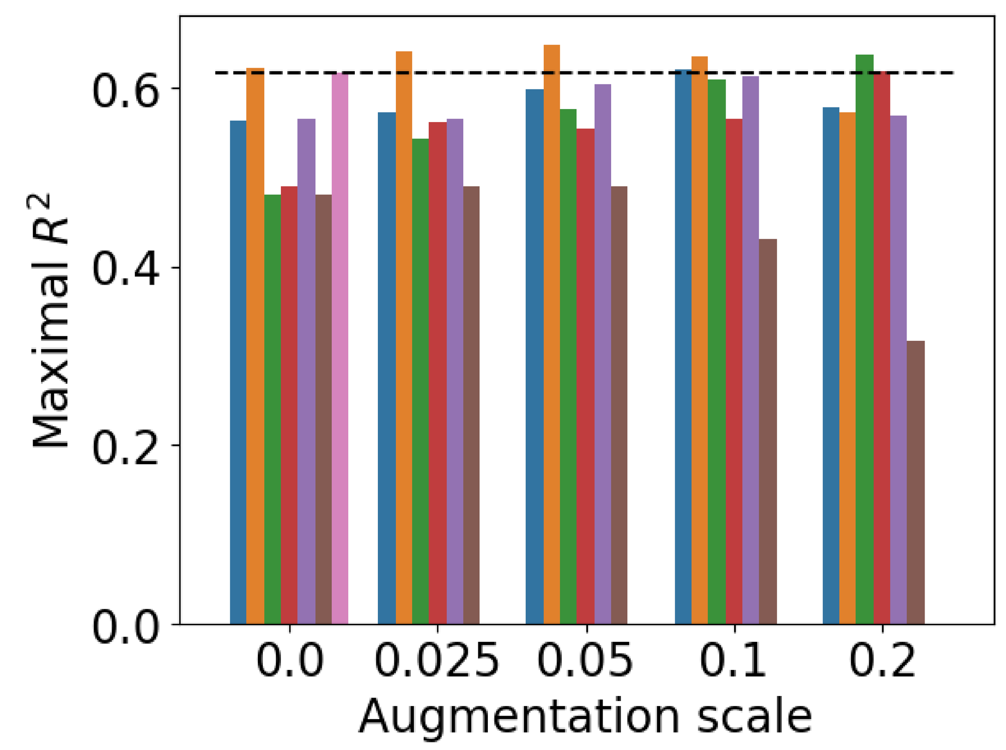
- (**A**) In a linear tractometry model, $\mathbf{y} = \beta X$. (**B**) To move towards a convolutional neural networks, we stack the data from different tracts and metrics (FA, MD, MK) as different measurement "channels" . (**C**) Training samples are then passed to a network (here as schematic)
- We used the 1817 subjects from HBN POD2 that had passing QC scores and age information.
- A variety of convolutional neural networks were implemented in `AFQ-Insight` (`https://richiehalford.org/AFQ-Insight`)
- To evaluate the models, we set aside a test set of 20% of the subjects (363 subjects)
- To compare model dependence on training set size, we trained with variable train set sizes (100, 175, 350, 700, 1000, 1453 subjects)

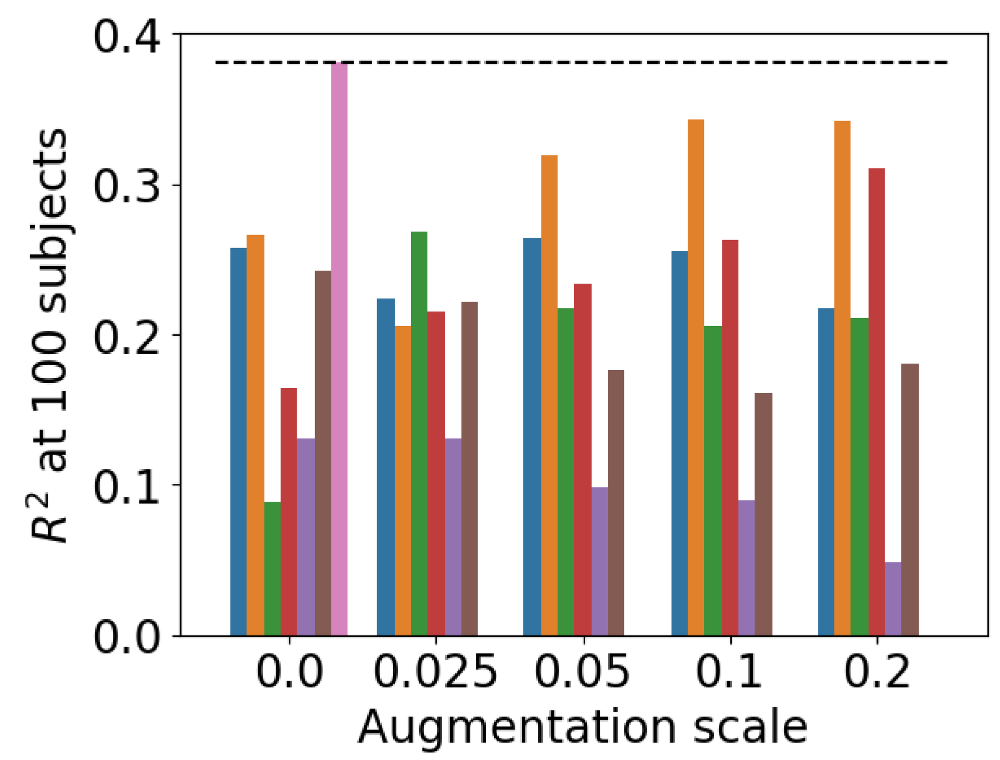
Results

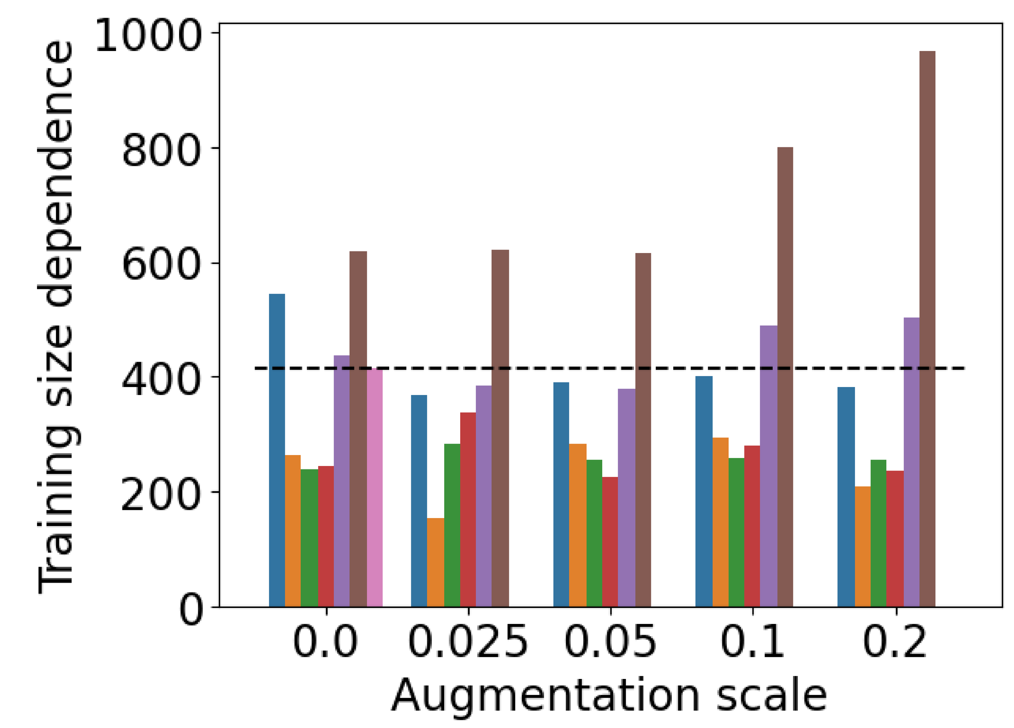
Model performance was quantified as the coefficient of determination, R^2

R^2 was modeled as: $\alpha - (\alpha - \beta)e^{-\frac{x - x_{min}}{\kappa}}$, where x is the number of training samples, α is R^2 at the maximal number of training samples, β is R^2 at the smallest number of training samples (x_min) and κ is a free parameter that denotes that number of training samples required to achieve R^2 that is 67% of the difference between β and α.









Conclusion and future work

- Neural network models (NNs) improve accuracy of tractometry analysis
- NNs are very data hungry
- Tuning and training these models is complicated and time-consuming
- Differences can be much more important in some cases (see poster # XXX)

References

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[5] Adam Richie-Halford, Jason D. Yeatman, Noah Simon, and **Rokem, A.** Multidimensional analysis and detection of informative features in human brain white matter. *PLoS Computational Biology*, in press(6):1–24, 06 2021. PMC5838108[pmc.

Acknowledgments

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