

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

Joanna Qiao¹, Jason Yeatman², Ariel Rokem¹, Adam Richie-Halford²

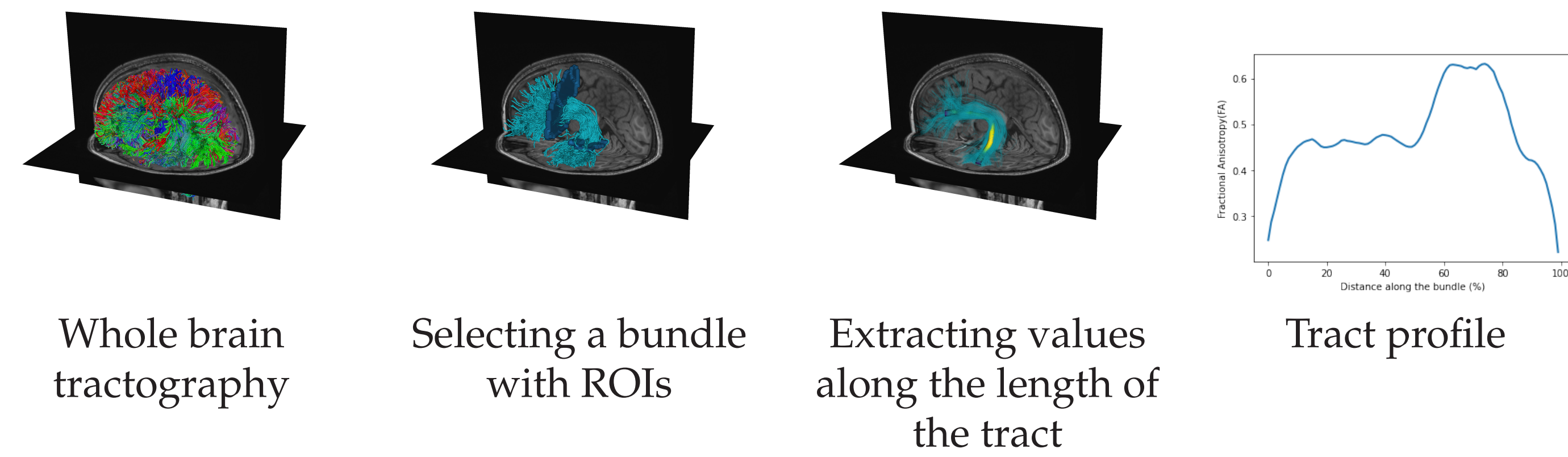
Contact: arokem@uw.edu, adamrh@stanford.edu

1. University of Washington, 2. Stanford University



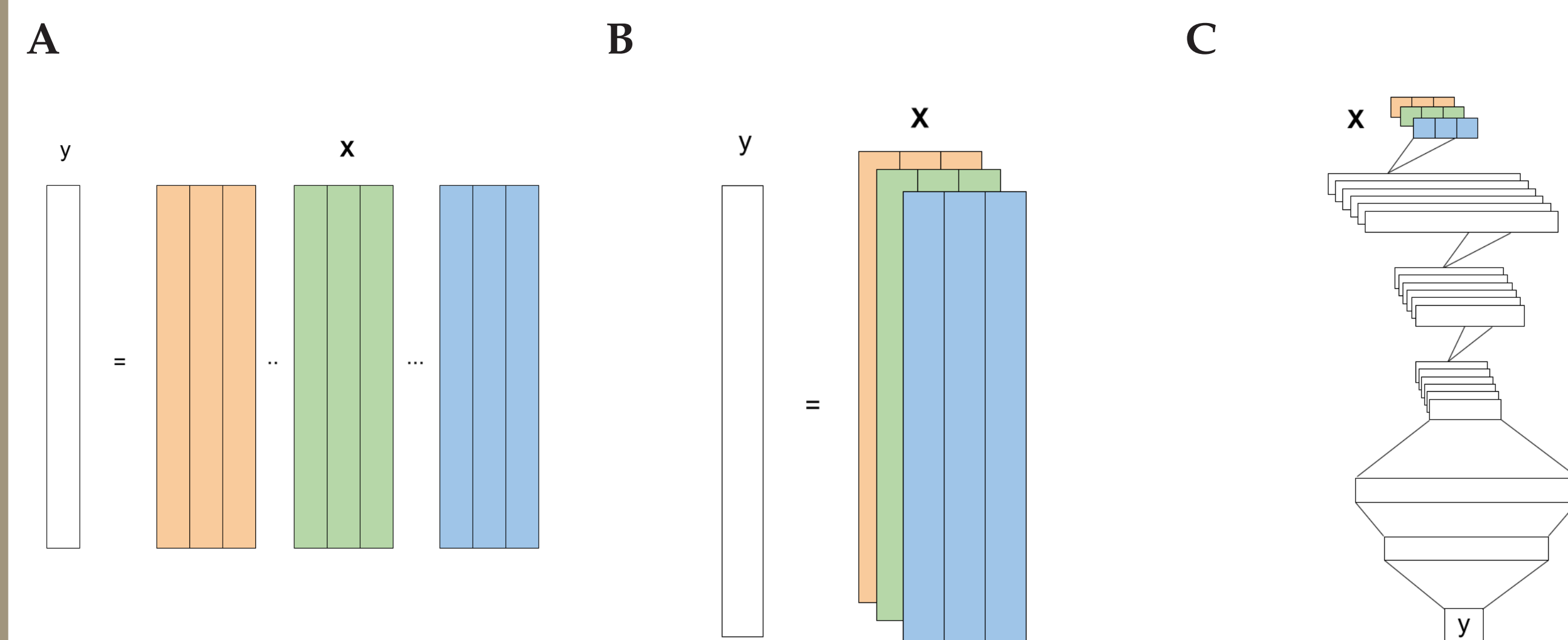
Introduction

- 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].
- These models cannot capitalize on non-linear effects and sequence features, but deep learning models are well-suited to do that.



Question: Does deep learning provide improvements in inferences from tractometry?

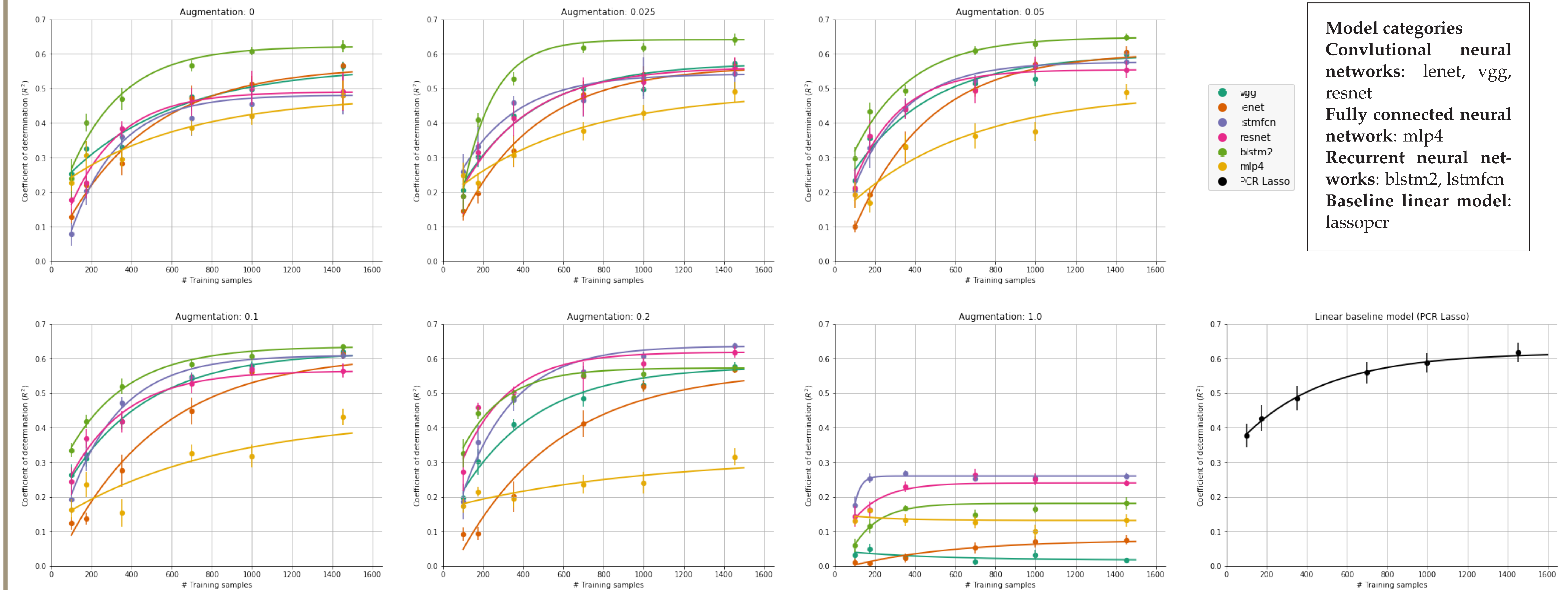
Methods



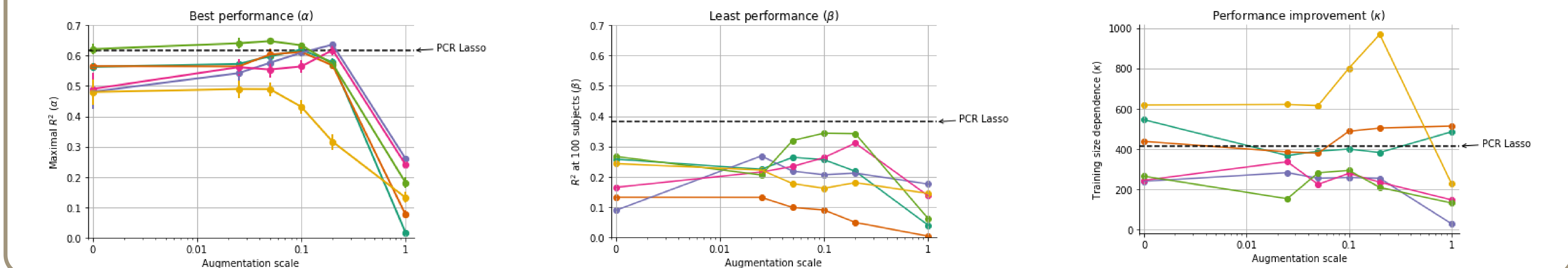
- (A) In a linear tractometry model, $y = \beta X$. (B) To move towards a convolutional neural networks, we stack the data from different tracts and metrics (FA, MD, MK) as different measurement “channels”. (C) Training samples are then passed to a network (here as schematic).
- We used the 1817 subjects 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>)
- We trained the models in “brain age” prediction. 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) and different augmentation levels
- We compared to a state-of-the-art linear model: PCR Lasso [5]
- Model performance was quantified as the coefficient of determination, R^2 , in predicting the age of the test set subjects.
- 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 .

Results

At each augmentation level, performance improves with training set size:



The models’ performance at each augmentation level is summarized through three parameters that quantify the maximal (α) and minimal (β) performance levels, and the convergence of performance with training set size (κ):



Conclusion and future work

- Neural network models (NNs) improve accuracy of tractometry analysis
- NNs are very data hungry
- Recurrent neural networks seem to perform most accurately, with moderate augmentation levels required.
- Tuning and training these models is complicated and time-consuming
- Differences between linear models and NN models can be *qualitative*, where NN models find differences not detected by linear models (see poster # 387.05 on Monday afternoon)

References

- Jason D Yeatman, Robert F Dougherty, Nathaniel J Myall, Brian A Wandell, and Heidi M Feldman. Tract profiles of white matter properties: automating fiber-tract quantification. *PLoS One*, 7(11):e49790, November 2012.
- Adam Richie-Halford et al. An analysis-ready and quality controlled resource for pediatric brain white-matter research. *Scientific Data*, 9(1):1–27, October 2022.
- Alexander et al. An open resource for transdiagnostic research in pediatric mental health and learning disorders. *Scientific Data*, 4:170181, December 2017.
- John Kruper et al. Evaluating the reliability of human brain white matter tractometry. *Aperture*, 1:10.52294/e6198273-b8e3-4b63-babb-6e6b0da10669, 2021.
- Adam Richie-Halford, Jason D. Yeatman, Noah Simon, and Ariel bf Rokem. 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

Grant 1RF1MH121868

