

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

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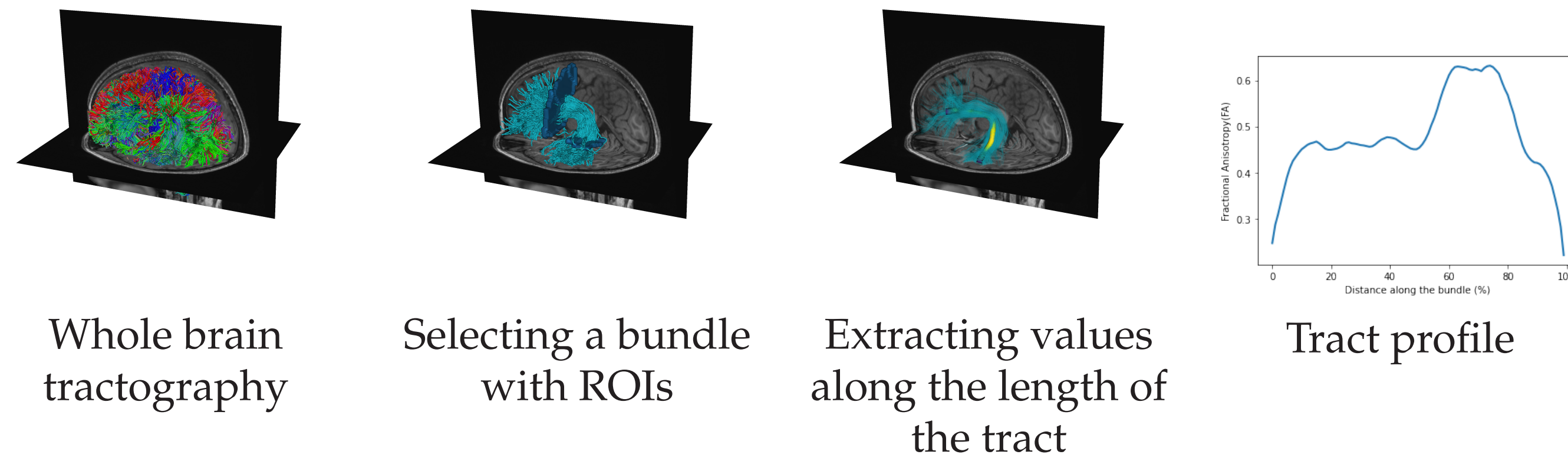
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## Introduction

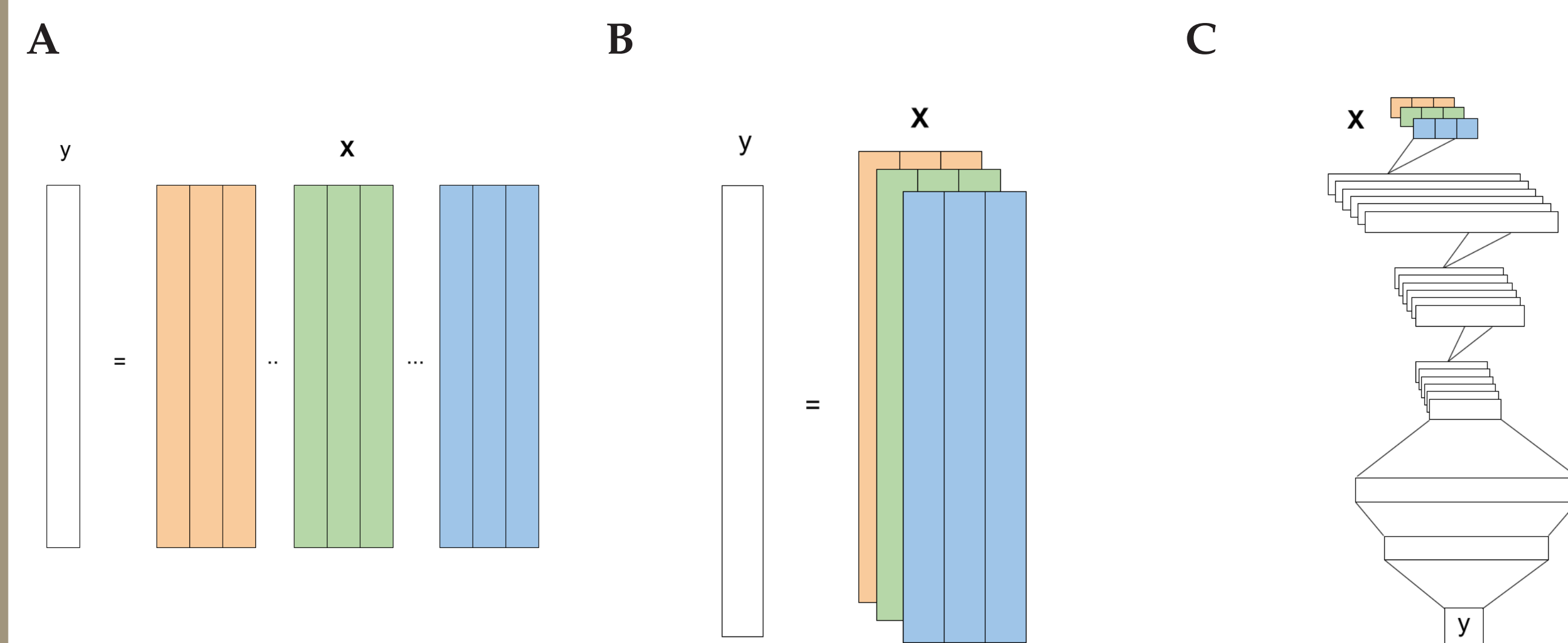
- Tractometry uses diffusion MRI (dMRI) to quantify brain tissue properties within white matter connections *in vivo* [1].



- 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].
- 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?

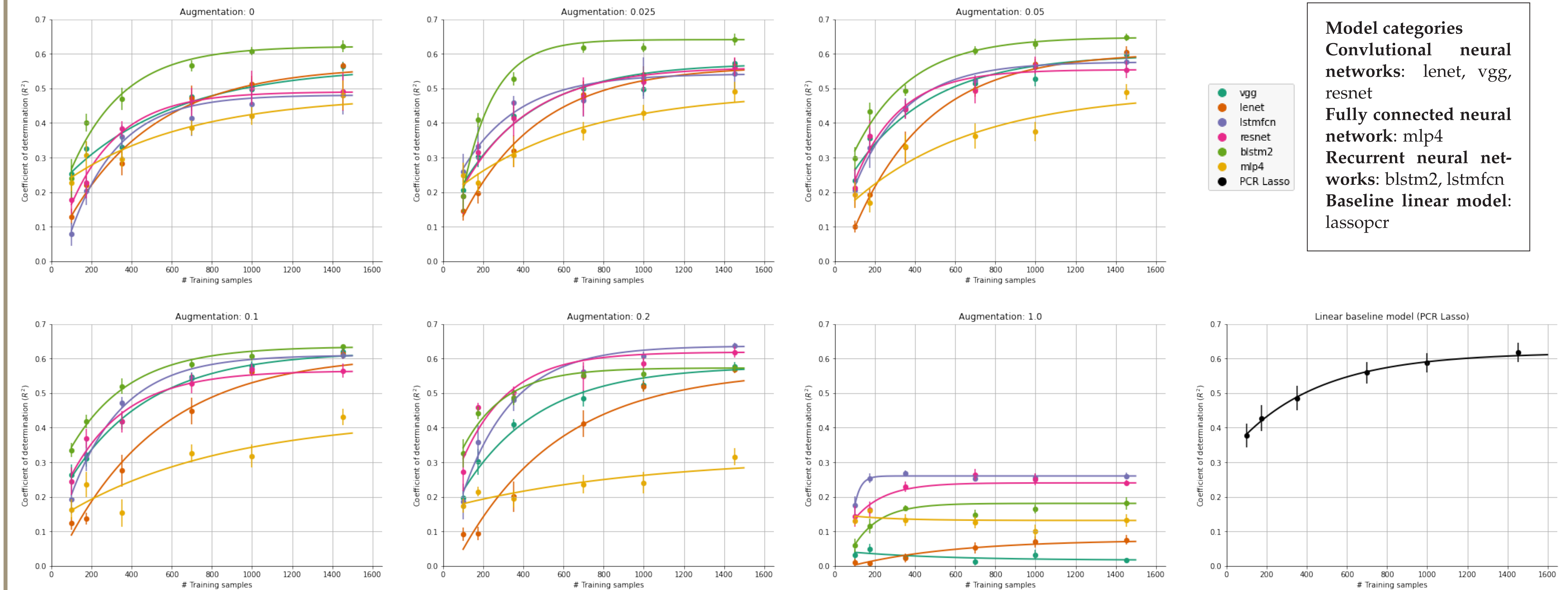
## Methods



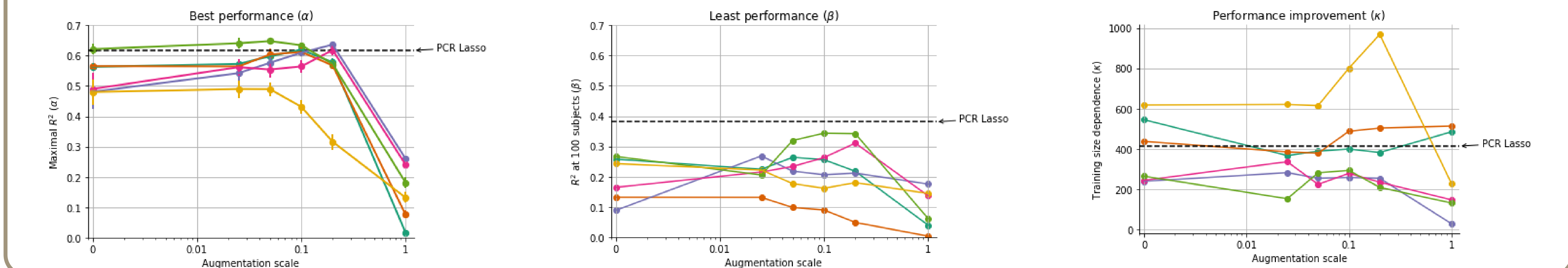
- (A) In a linear tractometry model,  $y = \beta X$ . (B) To move towards a convolutional neural networks, we stack the data from different tracts and metrics (FA, MD, MK) as different measurement “channels”. (C) Training samples are then passed to a network (here as schematic)
- We used the 1817 subjects 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,  $\alpha$  is  $R^2$  at the maximal number of training samples,  $\beta$  is  $R^2$  at the smallest number of training samples ( $x_{min}$ ) and  $\kappa$  is a free parameter that denotes that number of training samples required to achieve  $R^2$  that is 67% of the difference between  $\beta$  and  $\alpha$ .

## 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 ( $\alpha$ ) and minimal ( $\beta$ ) performance levels, and the convergence of performance with training set size ( $\kappa$ ):



## 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

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