

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

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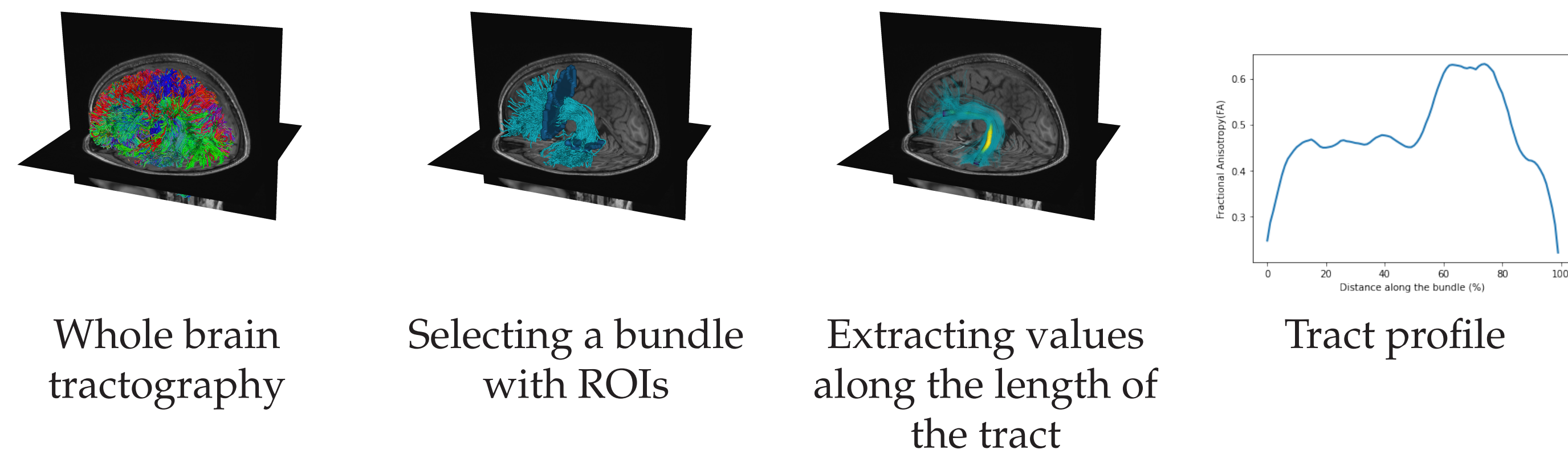
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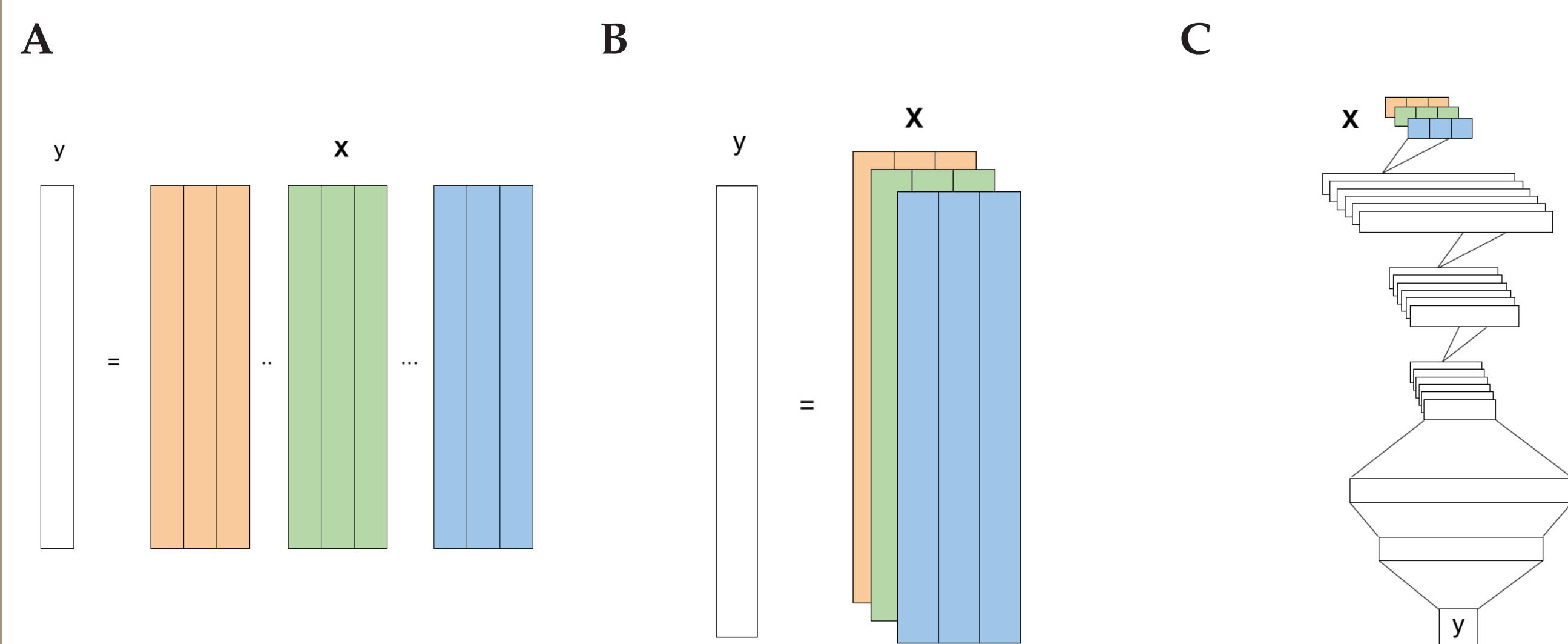
## Introduction

- 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?

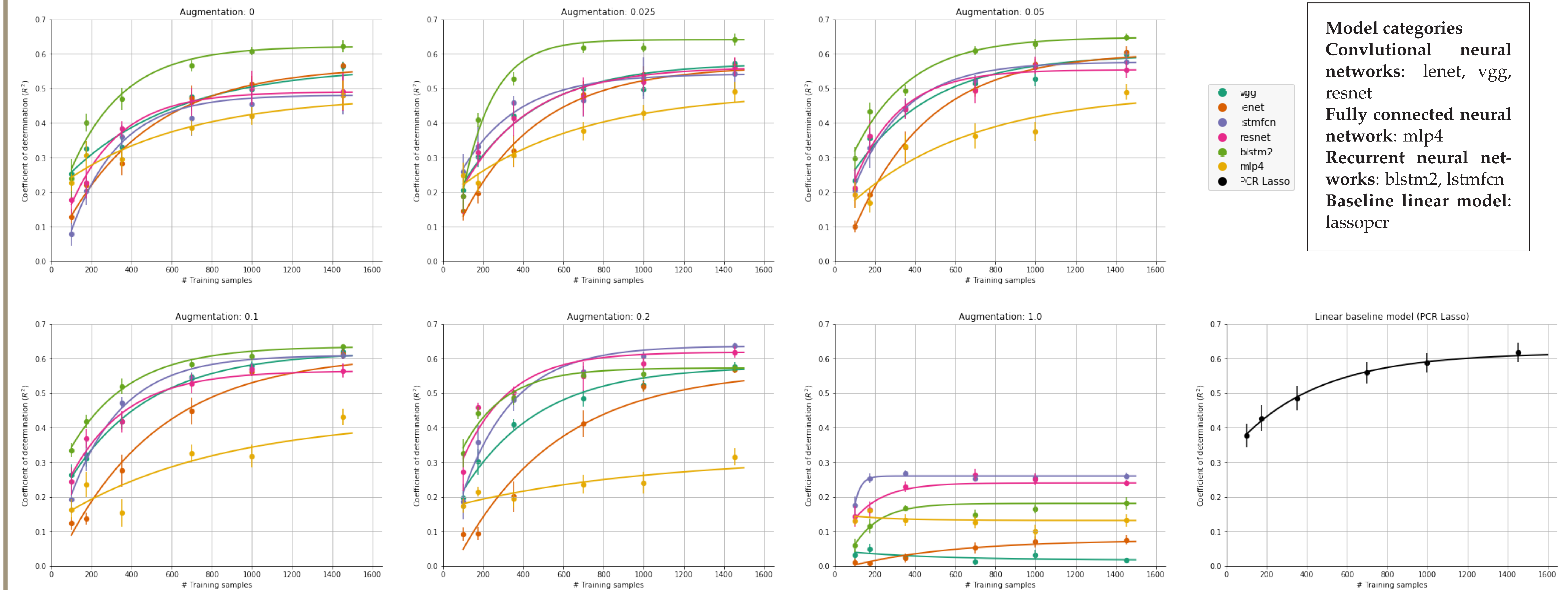
## Methods



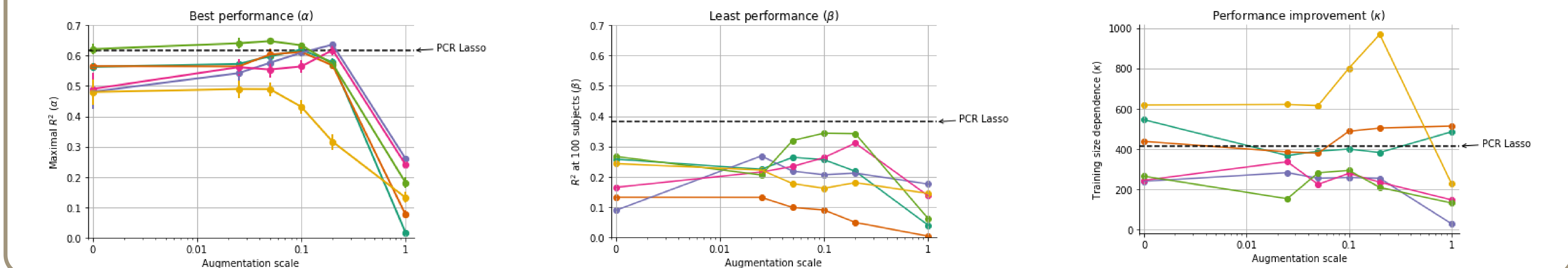
- (A) In a linear tractometry model,  $y = \beta X$ . (B) To move towards a convolutional neural networks, we stack the data from different tracts and metrics (FA, MD, MK) as different measurement “channels”. (C) Training samples are then passed to a network (here as schematic).
- We used the 1817 subjects 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
- Tuning and training these models is complicated and time-consuming
- Differences can be much more important in some cases (see poster # 387.05 on Monday afternoon)

## References

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## Acknowledgments

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