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

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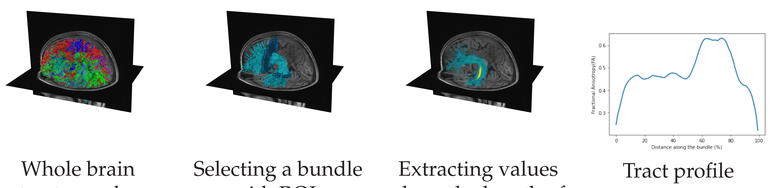
## Introduction

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

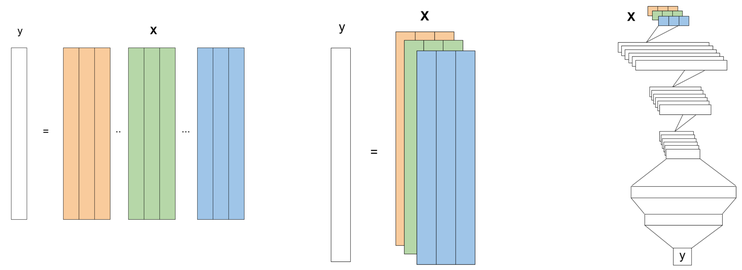


Whole brain tractography | Selecting a bundle with ROIs | Extracting values along the length of the tract | Tract profile

- 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?**

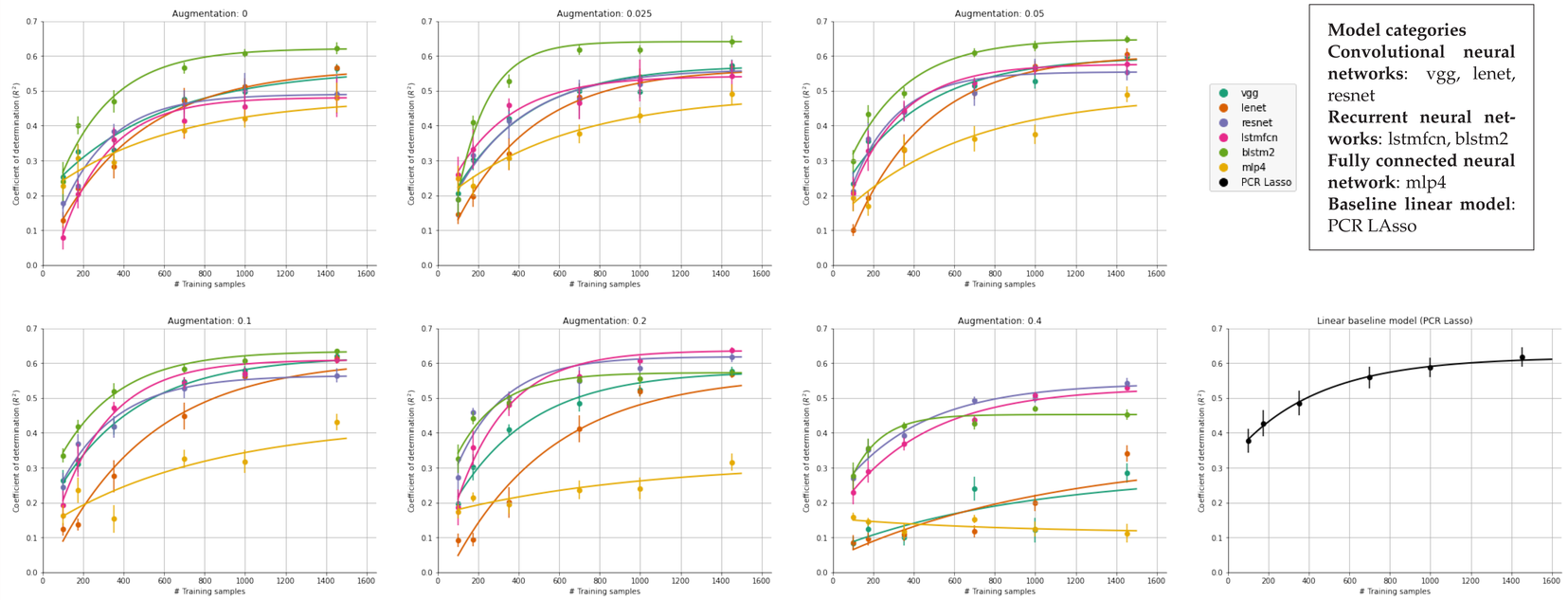
## Methods




- (**A**) In a linear tractometry model, $\mathbf{y} = \beta X$. (**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`)
- 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 $\alpha$.

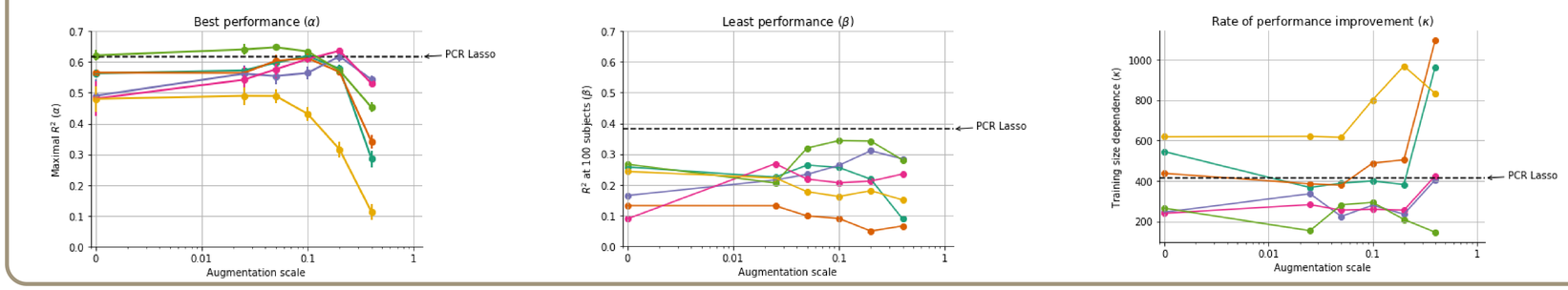
## Results

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




**Model categories**
**Convolutional neural networks**: vgg, lenet, resnet
**Recurrent neural networks**: lstmfcn, blstm2
**Fully connected neural network**: mlp4
**Baseline linear model**: PCR LAsso

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

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[4] John Kruper et al. Evaluating the reliability of human brain white matter tractometry. *Aperture*, 1:10.52294/e6198273–b8e3–4b63–babb–6e6b0da10669, 2021.

[5] 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

NIH National Institute of Mental Health
amazon web services
Azure
eScience Institute
ADVANCING DATA-INTENSIVE DISCOVERY IN ALL FIELDS