

Evaluating Accuracy and Reliability of Brain-Behavior Models Using Diffusion MRI

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Background

- Diffusion MRI measures tissue properties of white matter, which contains long-range connections between different brain regions.
- Raw diffusion data can be engineered into different “feature sets” for use in predictive models.
- Comparison of a variety of feature sets and models for both accuracy of predicutions and variance/bias of beta coefficients can help determine which models are more optimal for different feature sets.

Methods

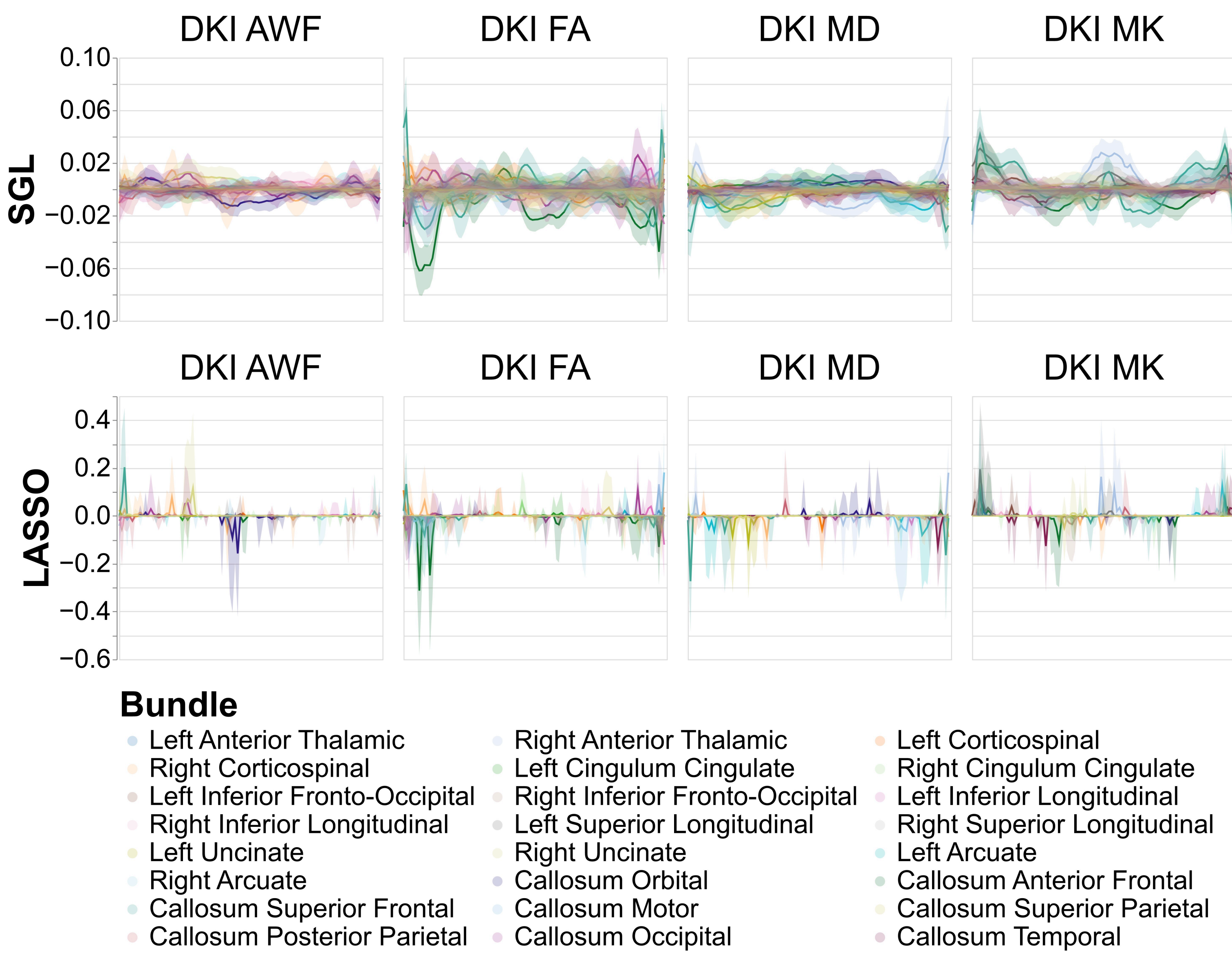
- We used diffusion data 1041 participants from the Human Connectome Project, processed into “tract profiles” using pyAFQ (cite) and “local connectome” features using DSI-Studio (cite).
- LASSO models were run on both tract profiles and local connectome to predict a variety of cognitive outcomes.
- Sparse Group LASSO (SGL) models were run on only tract profiles, to take advantage of the inherent grouping of the data.
- Models were implemented in **R** and trained using nested cross-validation and bootstrap resampling.
- Explanation of / diagram of SGL here.
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Results

- There were no significant differences in the accuracy of models using tract profiles and local connectomes as their input features (Figure 1.)
- There were significant differences in the variability of model weights for LASSO and SGL models.

	LASSO	LC	SGL
Age	3e-01	1.8e-01	3.1e-01
Crystalized Intelligence	7.2e-02	9e-02	7.6e-02
Fluid Intelligence	3.5e-02	2.7e-02	4.8e-02
Global Intelligence	6.8e-02	7.7e-02	8.9e-02
Impulsivity	7.1e-03	2.7e-02	8.2e-03
Endurance	1e-01	1e-01	1e-01
Verbal Memory	3.3e-03	1.2e-02	3.7e-03
Reading Ability	3.9e-02	8.1e-02	4.8e-02
Attention	3.3e-03	6.4e-03	4.4e-03
Spatial Orientation	7e-02	6.1e-02	7.2e-02

Table 1. Caption.



Caption for the picture.

References

Created with (Allaire et al. 2024)

Allaire, JJ, Yihui Xie, Christophe Dervieux, Jonathan McPherson, Javier Luraschi, Kevin Ushey, Aron Atkins, et al. 2024. *Rmarkdown: Dynamic Documents for r*. <https://github.com/rstudio/rmarkdown>.