

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

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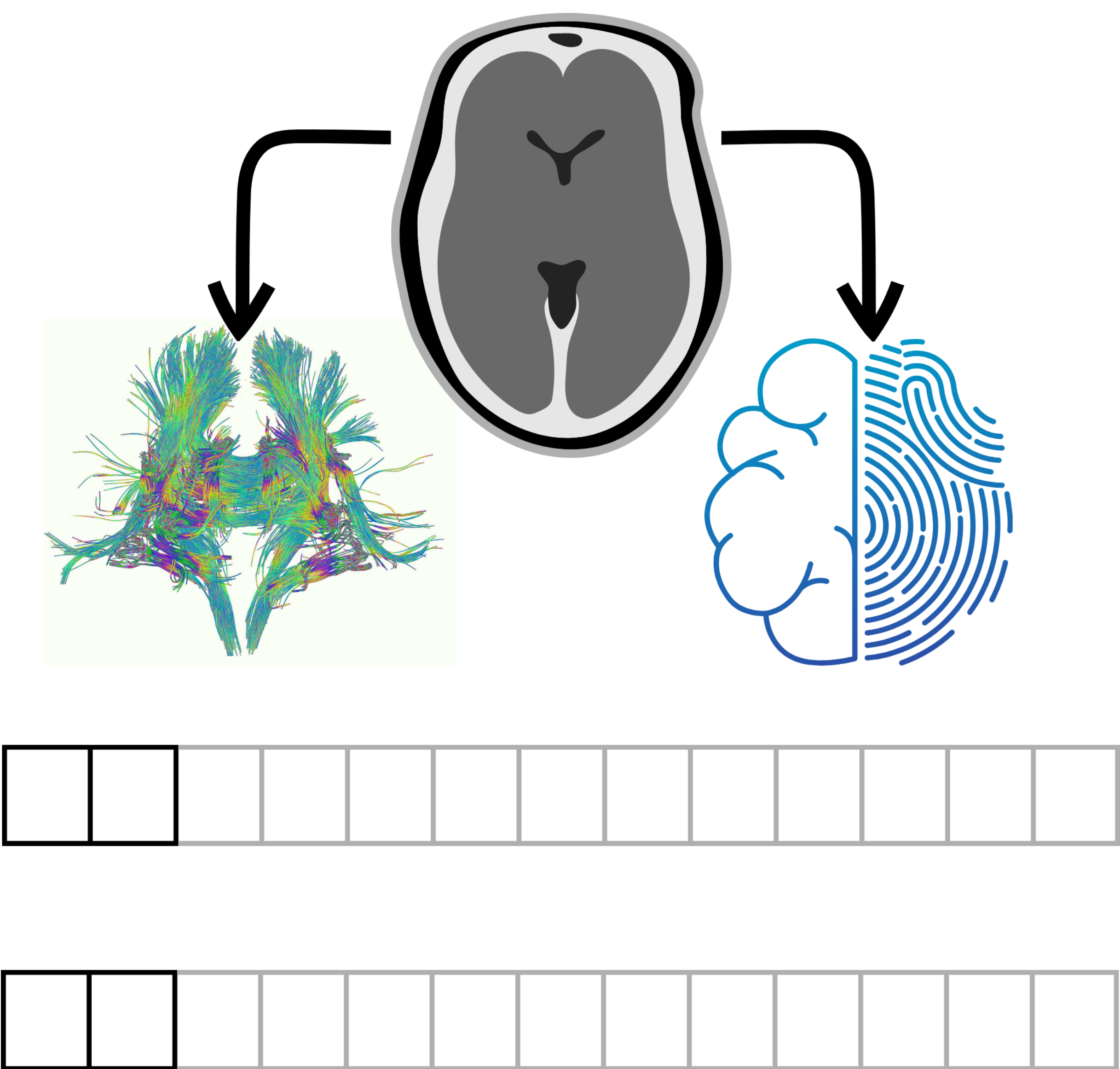
Background

- Diffusion MRI (dMRI) measures tissue properties of white matter, which contains long-range connections between different brain regions.
- Brain-behavior models can be used link neuroimaging features and phenotypes.
- dMRI can be processed into model input features in several ways.
- There are a multitude of different regularization methods for predictive models.

Question: How do sets of features derived from different dMRI processing methods compare in model accuracy and variability?

Methods

- Diffusion MRI from 1041 Human Connectome Project participants.
- Processed into “tract profiles” (2400 features) using pyAFQ and “local connectome fingerprint” (100,000) using DSI-Studio (cite).
- LASSO regularized models fit to tract profiles and local connectomes separately.
- Sparse Group LASSO (SGL) models fit to tract profiles, grouped by tract.
- Prediction targets were various cognitive phenotypes.
- Models implemented in  and trained using nested cross-validation and bootstrap resampling.
- Placeholder for more details?

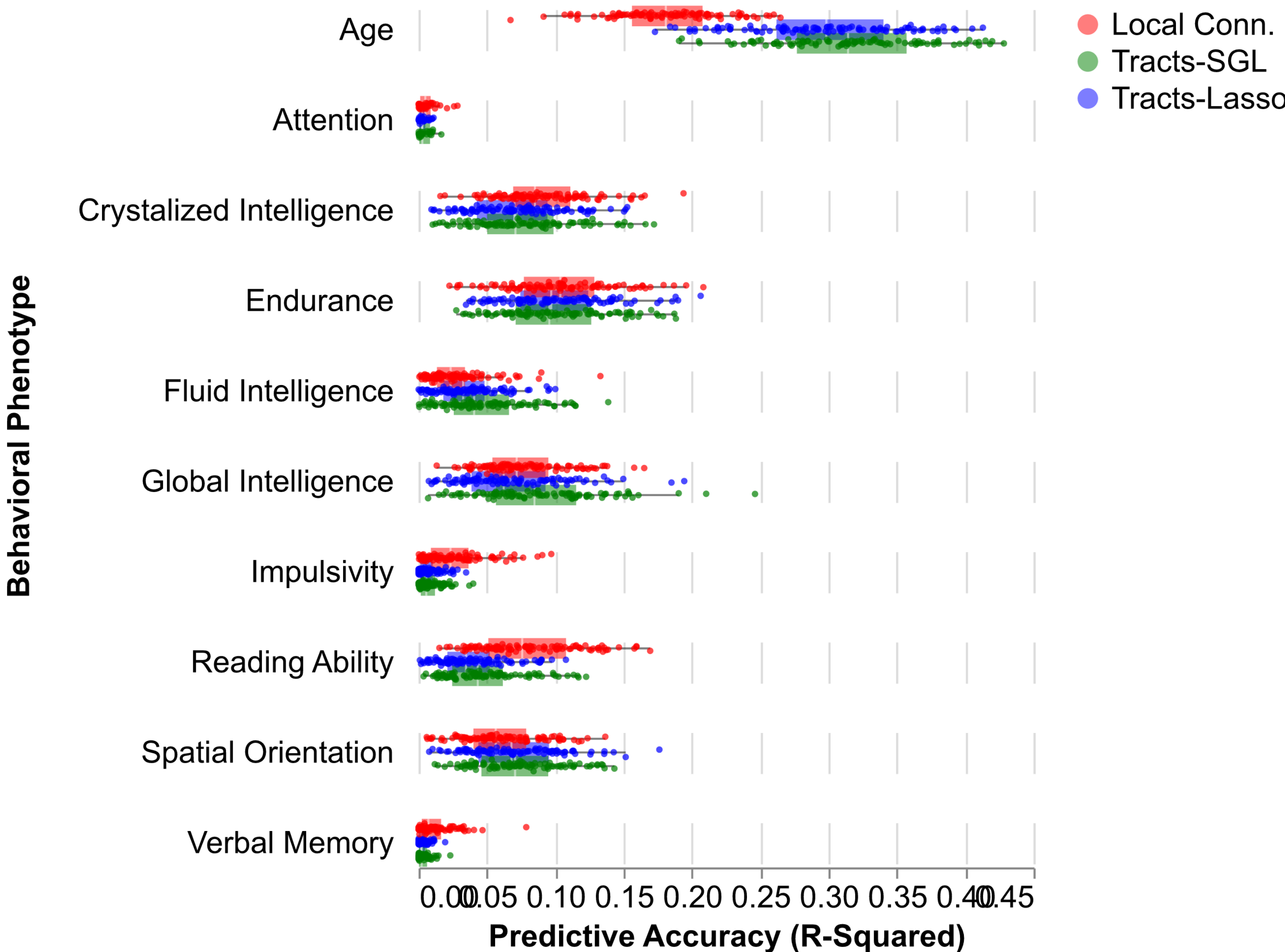


Caption for the picture.

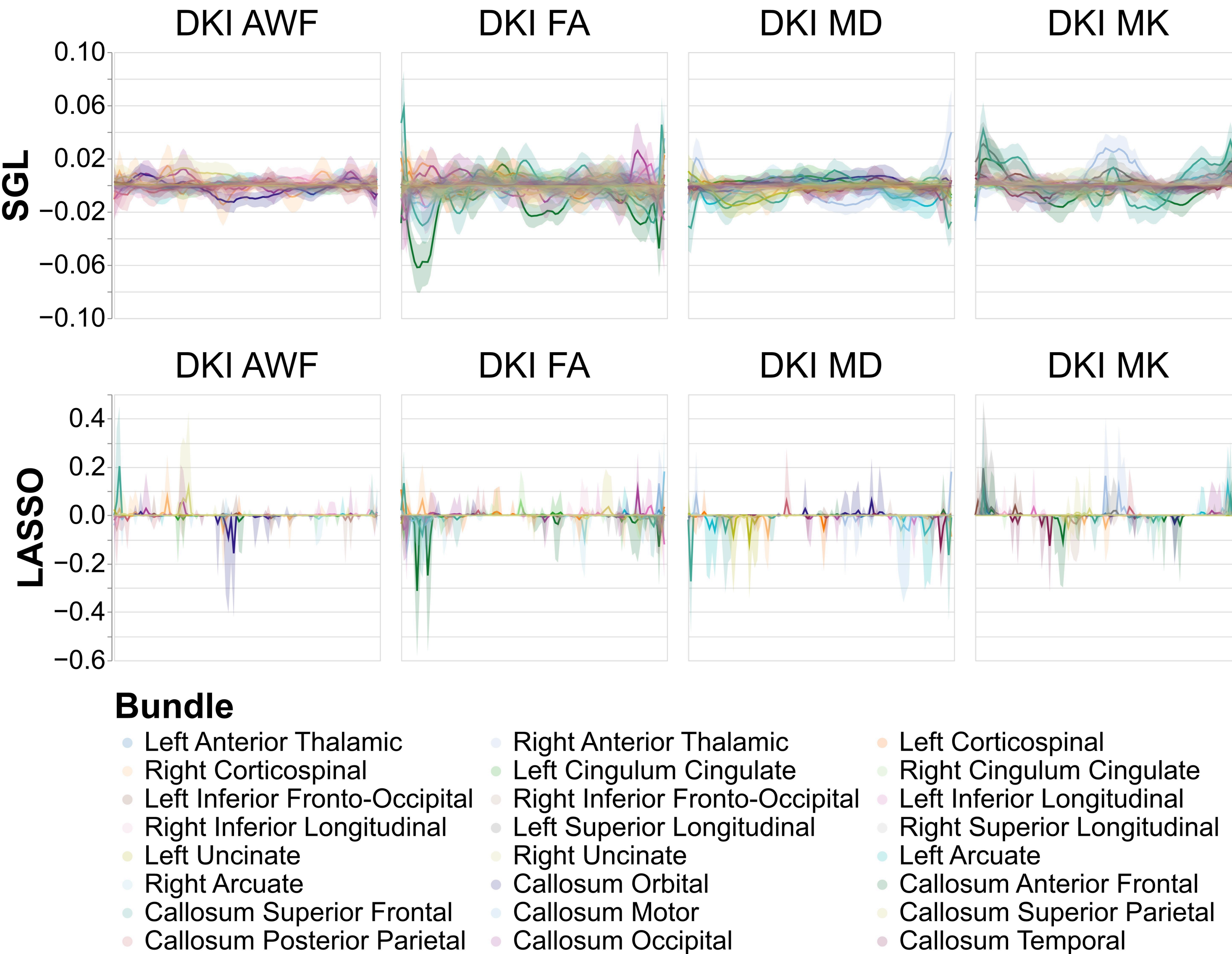
Conclusions

- Tractometry contains equivalent predictive information as compared to local connectome, with much fewer features.
- Utilizing a variety of regularization methods and feature engineering can maximize interpretability of models.
- this is more conclusions
- testing page limits
- This will be replaced with an insightful comment about the results
- Lots of space for conclusions
- Placeholder
- I just want the results to wrap to the other side
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Results



Model accuracies for behavioral phenotypes. All models, regardless of regularization method or feature set performed statistically equivalently.



“Age” prediction model weights across tracts for SGL and LASSO. Solid lines show the mean model weight across bootstraps for every tract, across every node, and the shaded areas show the 95% confidence intervals of the model weights. Note the reduced y-axis range for SGL.

Acknowledgements

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- Krell logo (DE-SC0023112) , NIH logo, NSF logo

References

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