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

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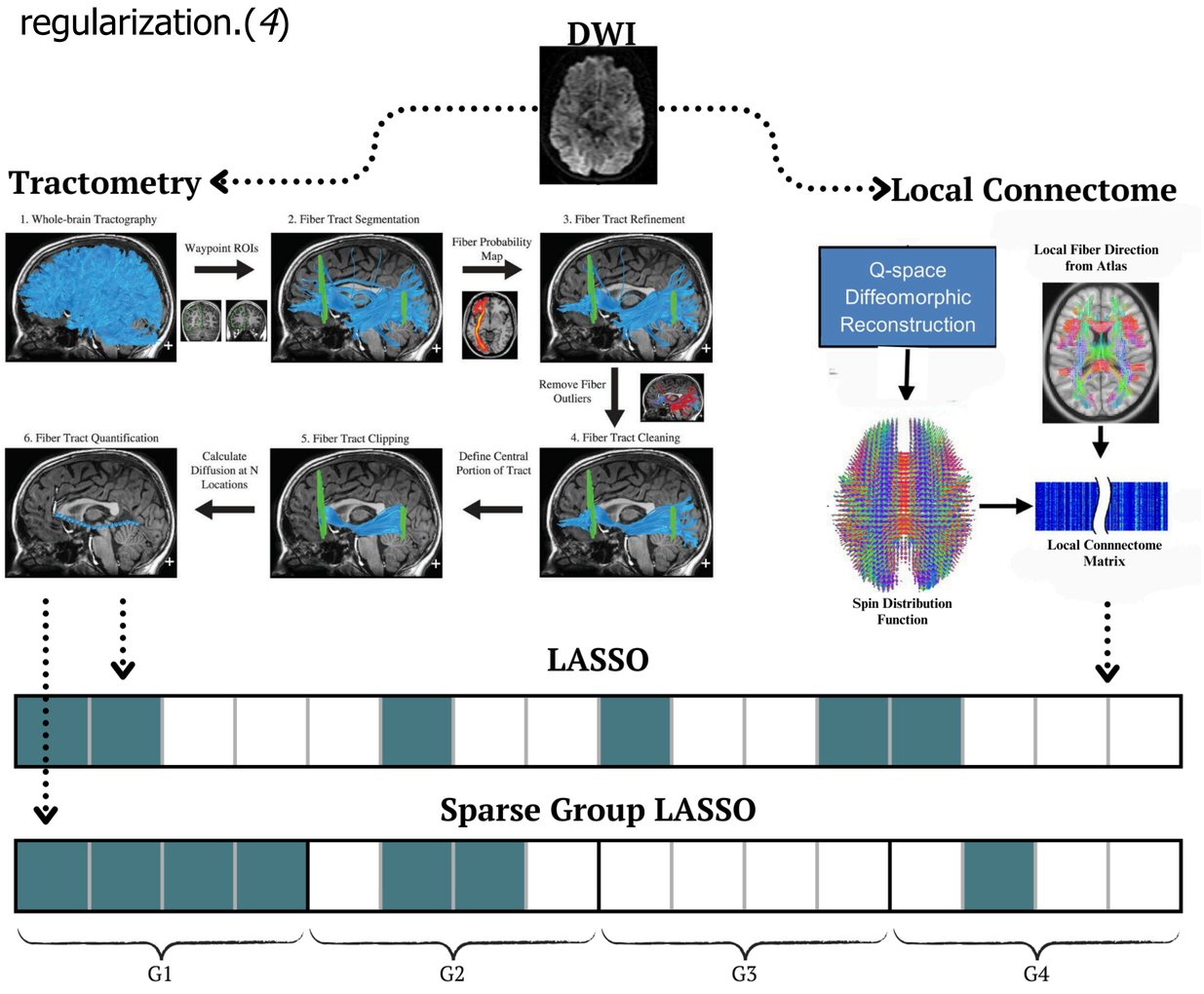
## Background

- 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.
- Researchers have several options to process dMRI data into input features for brain-behavior modeling.
- Characteristics of feature sets determine which regularization methods are suitable for modeling fitting.

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

## Methods

- Processed into "tract profiles" (see (*1*) for processing details and to access data; 9,600 features) using pyAFQ and "local connectome fingerprint" (128,894 features) using DSI-Studio (*2*) (shared by (*3*)).
- Predictive models were trained using tractometry or local connectome matrices as input features and LASSO or Sparse Group LASSO regularization.(*4*)




Tractometry and LC processing diagrams adapted from (*5*) and (*2*).

- Prediction targets were various cognitive phenotypes drawn from prior predictive modeling investigations(*3*).
- Models implemented in R and trained using nested group cross-validation and boostrap resampling by family.
- Models evaluated with and without grouped cross-validation to check for "leakage" from related inviduals.

## Acknowledgements

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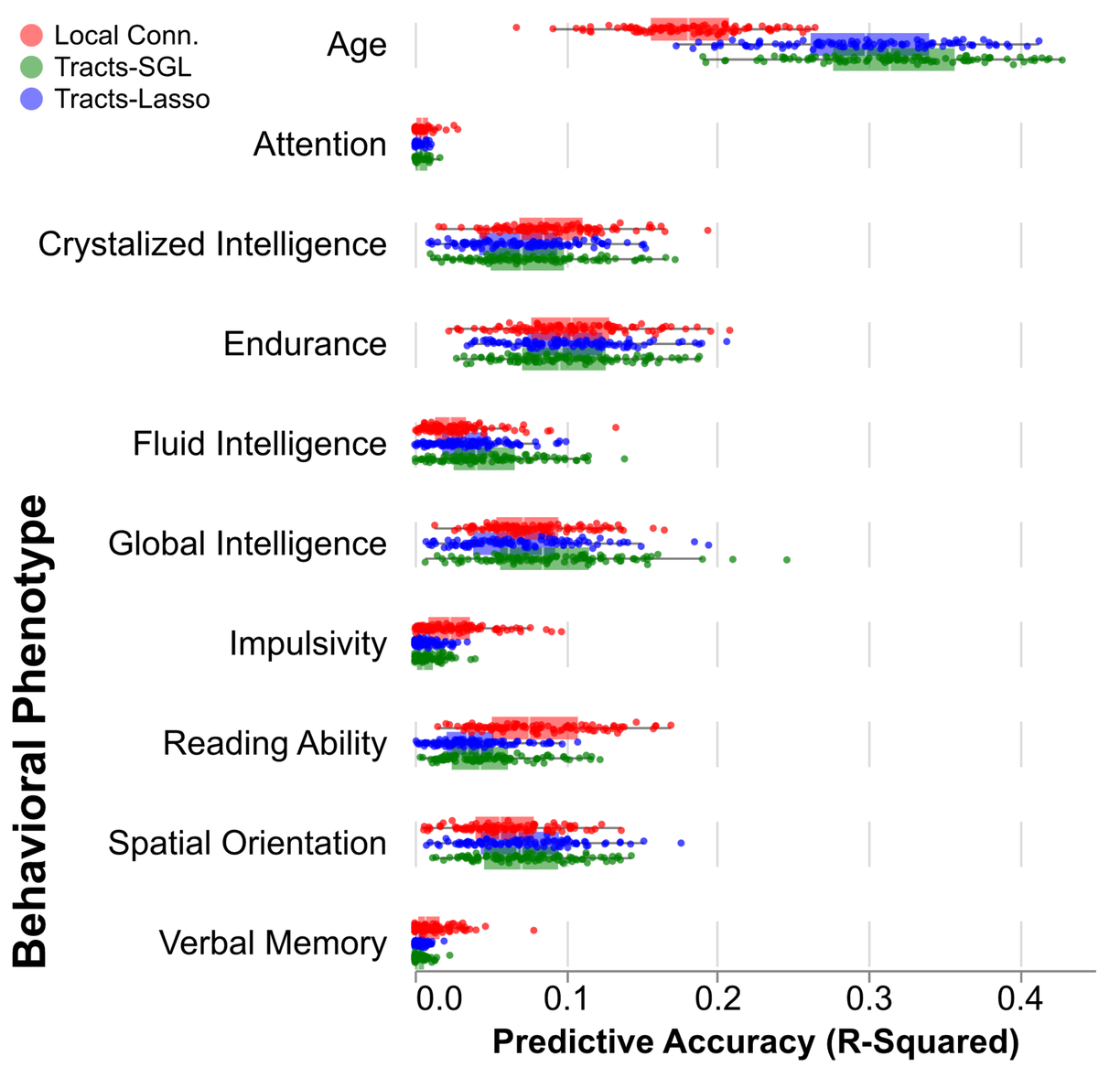
## References

1. J. Kruper *et al.*, *Frontiers in Neuroscience* (2024).
2. F.-C. Yeh *et al.*, *PLoS Comput. Biol.* (2016).
3. J. Rasero *et al.*, *PLoS Comput. Biol.* (2021).
4. A. Richie-Halford *et al.*, *PLoS Comput. Biol.* (2021).
5. J. D. Yeatman *et al.*, *PLoS One* (2012).

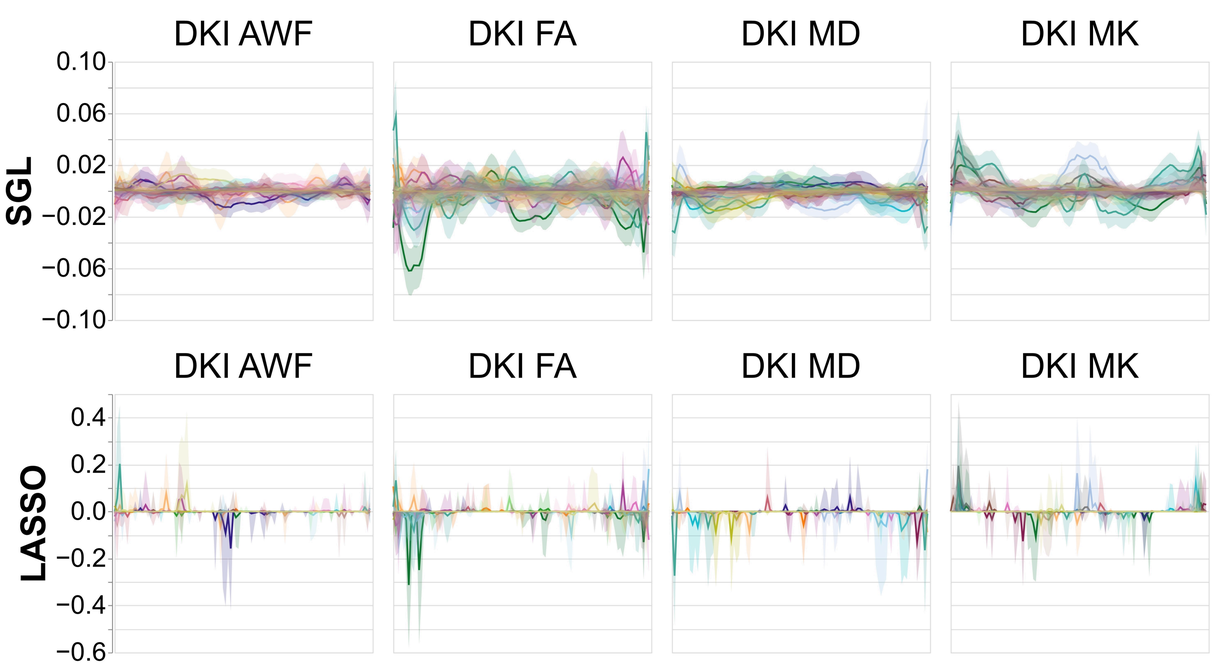
**Poster Github**

## Results




**Model accuracies for behavioral phenotypes.** All models, regardless of regularization method or feature set performed equivalently. These $R^2$ values are in line with previous literature evaluating brain-behavior predictive models.(*3*)

- Despite concerns about "leakage", there was no difference between model accuracies with and without grouping by family for cross-validation splits for all phenotypes.




**"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. The shaded areas show the 95% confidence intervals of the model weights. Note the reduced y-axis range for SGL. This pattern was consistent across phenotypes.

## Conclusions

- Tractometry contains as much predictive information as local connectome, with much fewer features.
- Utilizing a variety of regularization methods that and feature engineering to take advantage of data characteristics can maximize interpretability of models through more stable model weights.