TAKEAWAYS

- The Adolescent Brain and Cognitive Development (ABCD) Study has publicly shared a large (~12,000 subjects), high-quality dataset collected on 21 different MRI scanners.
- Scans show variance across scanners that is similar in magnitude to age/sex effects.
- Empirical Bayes methods (ComBat) do a pretty good job of eliminating scanner variance, though it is not complete.



Detecting and harmonizing scanner and site differences in the ABCD study



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-INTRODUCTION

- Our original question:
 - Is it better to collect scans at one site or at lots of sites?
- As a way to start to answer that question, we pivoted to a more easily addressable question:
 - Does the data from a study collected at many sites still contain information about scan collection site?

METHODS

- Site classification
 - Scikit-Learn multinomial logistic regression, L2 penalty, regularization strength of
 - 1, SAGA solver, 10k max iterations, 3-fold cross-validation
 - Significance assessed via permutation
- Percent Variance explained
 - Subtract R2 for nested models predicting each metric

- ABCD is a great dataset:
 - \circ Lots of subjects (11,875) and sites (21)
 - Resting state, task-based contrasts, task-based conditions
- Analysis of Release 1.0 on Bioarchive: www.biorxiv.org/content/10.1101/309260v1
- Preregistered analysis of Release 2.0

- Significance assessed via permutations
- ComBat Correction
 - Scale and location correction for each metric at each scanner with empirical Bayes to improve estimates
 - Significance of uncorrected vs ComBat assessed with bootstraps



-RESULTS-			
	SCANNER CLASSIFICATION		
	rsFMRI	tFMRI	
		Uncorrected	ComBat







Figure 5: Percent variance explained

by the participants' family. Percent variance

Exploratory analysis of percent variance explained

explained was determined by intraclass correlation.



Figure 6: Percent variance explained

Distributions of the percent variance explained by site, scanner, and age & sex combined are shown with and without combat correction. Dashed lines indicate threshold for significant percent variance explained at p = 0.005 determined from 1,000 permutations. Percent variance explained calculated as difference in R^2 in nested models.

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