ImageNomer: developing an fMRI and omics visualization tool to detect racial bias in functional connectivity

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MBB Lab
ImageNomer

Introduction: challenges and goals

Challenges

- Both functional connectivity (FC) and genomic data may contain from tens of thousands to millions of features
- fMRI datasets may range in size from small (<100 subjects), to large (PNC <2,000 subjects), to huge (UKBB 50,000 subjects)

Goals

1. **Quality Control** In large datasets, a researcher may not even look at every FC matrix (or other type of data)
2. **Dataset Familiarity** How to find relationships, explore data, and get basic statistics on a dataset?
3. **Identifying Hidden Confounds** Are there confounders that go undetected because of limited familiarity with data or from confirmation bias?

Our solution

We create an interactive web-based software for visualization and exploration of connectivity-based fMRI and omics data called **ImageNomer**

ImageNomer provides the following capabilites:

- **Exploration** Visualize subjects and get statistics about a cohort
- **Correlation** Quickly find correlations between images, phenotypes, and genomics data
- **Analysis** Summarize and get distribution of weights from machine learning models

ImageNomer interface

■ Subjects Panel   ■ Groups Panel   ■ Phenotypes Panel   ■ Views (Tools) Tabs   ■ FC Explorer View

Figure 1. The FC explorer view of the ImageNomer interface.

ImageNomer architecture

System Libraries

Python Backend
Stores data
Performs computations
Creates plots

Flask Server
Handles requests
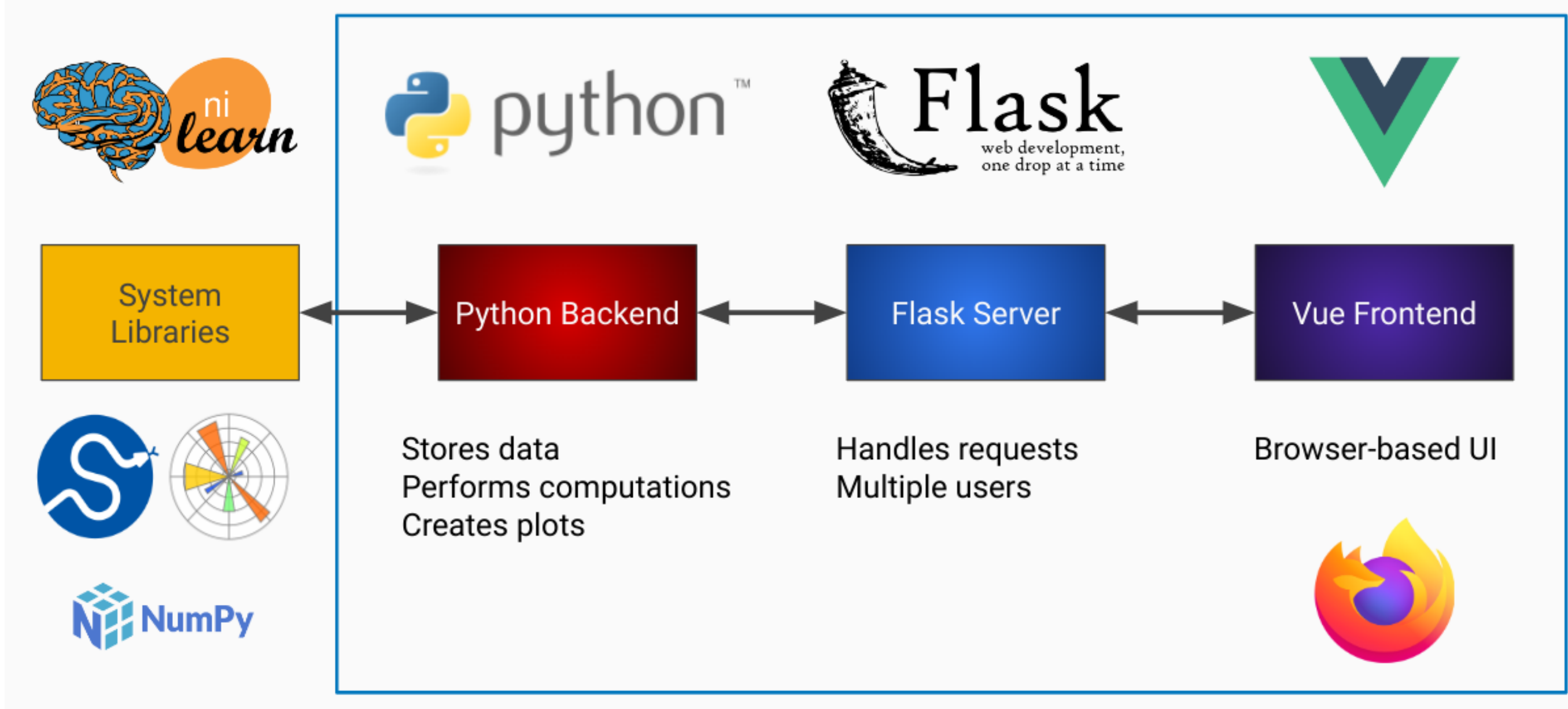Multiple users

Vue Frontend
Browser-based UI

Figure 2. ImageNomer is made up of three loosely coupled parts: the web-based frontend, the Flask server, and the Python backend which is integrated with system libraries.

Live Demo

- Live demo available at `https://aorliche.github.io/ImageNomer/live/`
- Follow documentation link to find a tutorial using a Fibromyalgia dataset

Summary of findings

We find that **fMRI predicts race, not intelligence**

- FC explains 10% of variance in intelligence, as measured by cognitive battery
- Race prediction accuracy is 85%
- Controlling for race removes any ability to predict intelligence

On the other hand, **fMRI legitimately predicts age and sex**

- FC explains 35% of variance in age, and only 10 features can explain up to 15%
- Sex prediction accuracy is 78%

Background on fMRI and functional connectivity

- fMRI is an endophenotype that has been used to predict age, sex, intelligence, and disease status, such as pre-clinical Alzheimer's disease
- The most common way to use fMRI for prediction is through functional connectivity (FC)
- FC is the Pearson correlation between the BOLD signal of different brain regions (Equation 1)

$$\rho_{xy} = \frac{\sigma_{xy}^2}{\sqrt{\sigma_{xx}^2 \sigma_{yy}^2}} \tag{1}$$

Validation study on intelligence prediction

Previous studies have identified a small ability to predict subject intelligence based on FC

- Other studies have found that dynamic connectivity predicts which social group subjects identify with (Schmalzle et al. 2017 10.1073/pnas.1616130114)
- No attempt was made to control for ethnicity

Can we use ImageNomer to either validate the small effect of FC on intelligence or find a confound?

Dataset and methods

Philadelphia Neurodevelopmental Cohort

- Used fMRI scans from 1,445 out of 1,529 healthy adolescents
- SNP data for 9,267 subjects
- 8-23 years old
- Dataset enriched for European (EA) and African (AA) ancestry
- Intelligence measured by WRAT = Wide Range Achievement Test (effect of age regressed out)
- Prediction made with regularized linear models; features chosen by correlation, model weights, LASSO, and greedy selection.
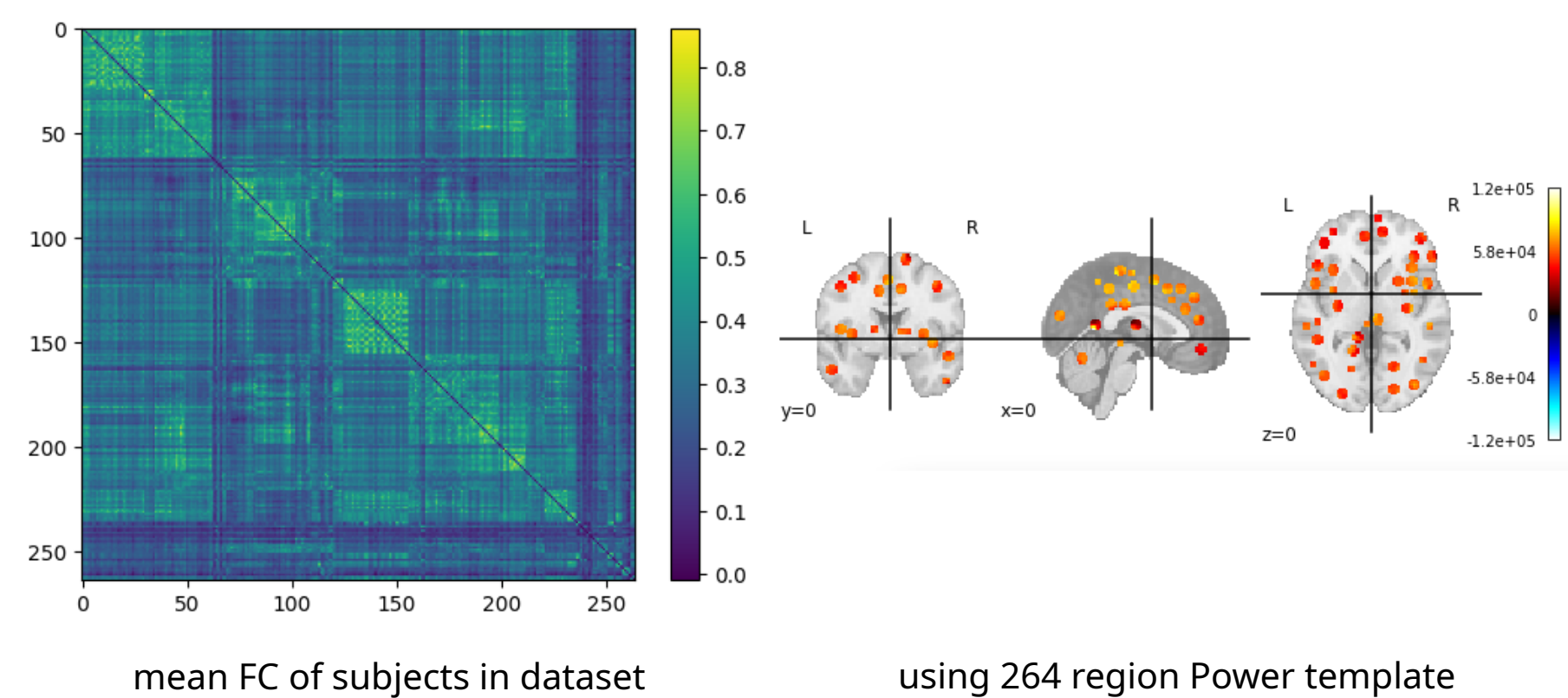

mean FC of subjects in dataset   using 264 region Power template

Figure 3. Mean FC of subjects in the cohort, alongside the 264-region Power template used to parcellate normalized subject brain volumes.

Results

Prediction	Modality	Metric	Null Model	Best Full Model
Age	FC	RMSE, months	38.4	26
Intelligence	FC	RMSE	15.1	13.6
Intelligence	SNPs	RMSE	15.1	14
Intelligence (AA)	FC	RMSE	13.9	13.8
Intelligence (AA)	SNPs	RMSE	13.9	13.4
Intelligence (EA)	FC	RMSE	14	14.1
Intelligence (EA)	SNPs	RMSE	14	13.6
Race	FC	Accuracy	58%	85%
Sex	FC	Accuracy	51%	78%
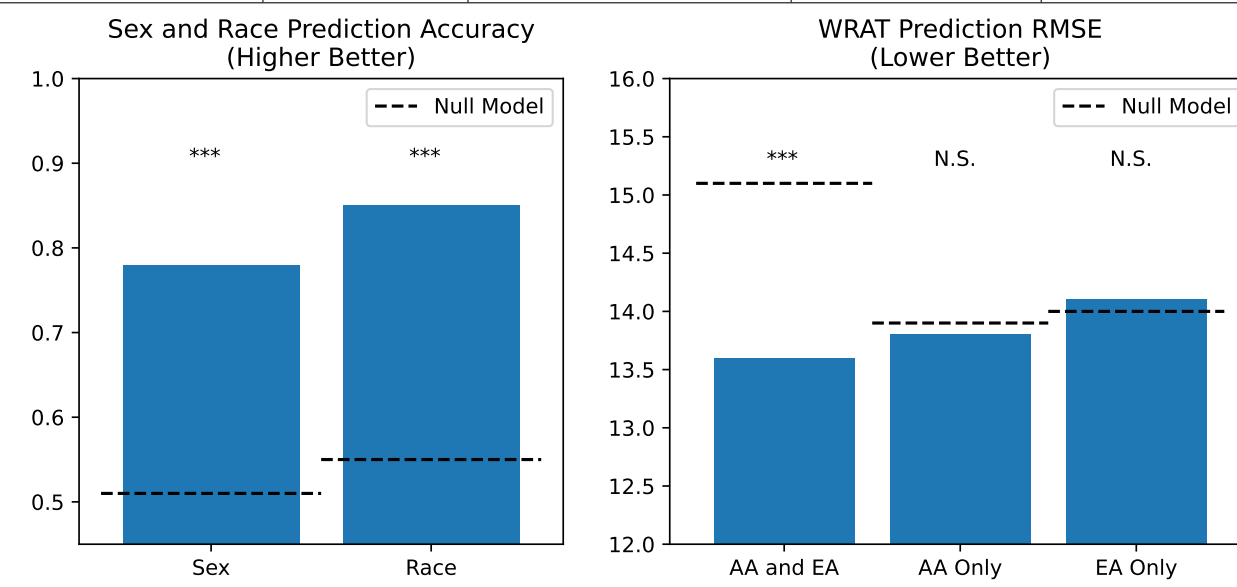
Small ability to predict intelligence disappears when controlling for race. Significant results in blue.
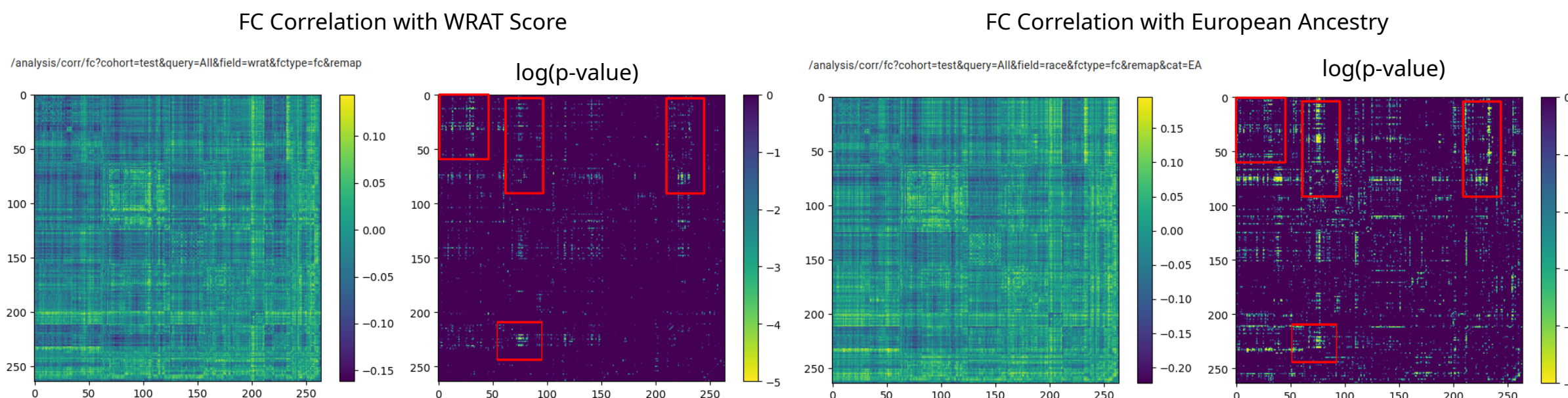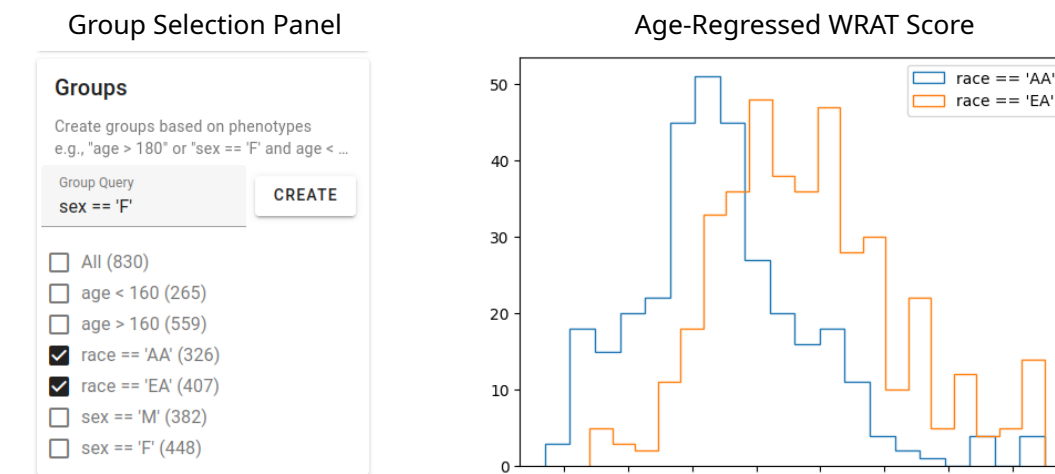
Discussion: bias is quickly identified

Figure 4. ImageNomer both identifies bias and finds that FC correlation with intelligence is actually a surrogate for correlation with race. Note that we reject a causal link between race and achievement as measured by WRAT score and only point out the importance of data exploration and identification of possible confounds.