

Performance on online cognitive assessments is correlated with personality and lifestyle phenotypes



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Introduction

Personality and cognitive traits can have a profound impact on individual quality of life. Together with environmental factors, a significant body of literature points to a genetic component of individual variation in human behavior. Specifically, cognitive traits such as risk-taking tendency, impulsivity, and processing speed have shown heritability of up to 67% in twin studies^{1,2}. Uncovering novel causal relationships between cognition and the combination of genetics, lifestyle, and demographics can deepen our understanding of human cognition.

In the present study, we developed and deployed two cognitive assessments to our database of 2M+ research participants, the Balloon Analog Risk Task (“BART”) and the Digit Symbol Substitution Test (“DSST”). Higher BART scores have been associated with neuropsychiatric disorders that involve risk-seeking behavior³. The DSST is a test of processing speed, attention, and cognitive efficiency and is broadly sensitive to brain dysfunction⁴. At the time of analysis in September 2017, 27,270 and 36,161 individuals completed the BART and DSST tasks, respectively.

In order to validate the implementation of these tasks and understand BART and DSST performance, we mined the 23andMe phenotype database and analyzed associations with 385 phenotypes in the categories of educational attainment, personality, and lifestyle (diet, exercise, sleep). We identified over 90 phenotypes that correlate with BART or DSST performance, thereby validating our data collection process and highlighting the power of the 23andMe research model to crowdsource discoveries in the field of human cognition.

Methods

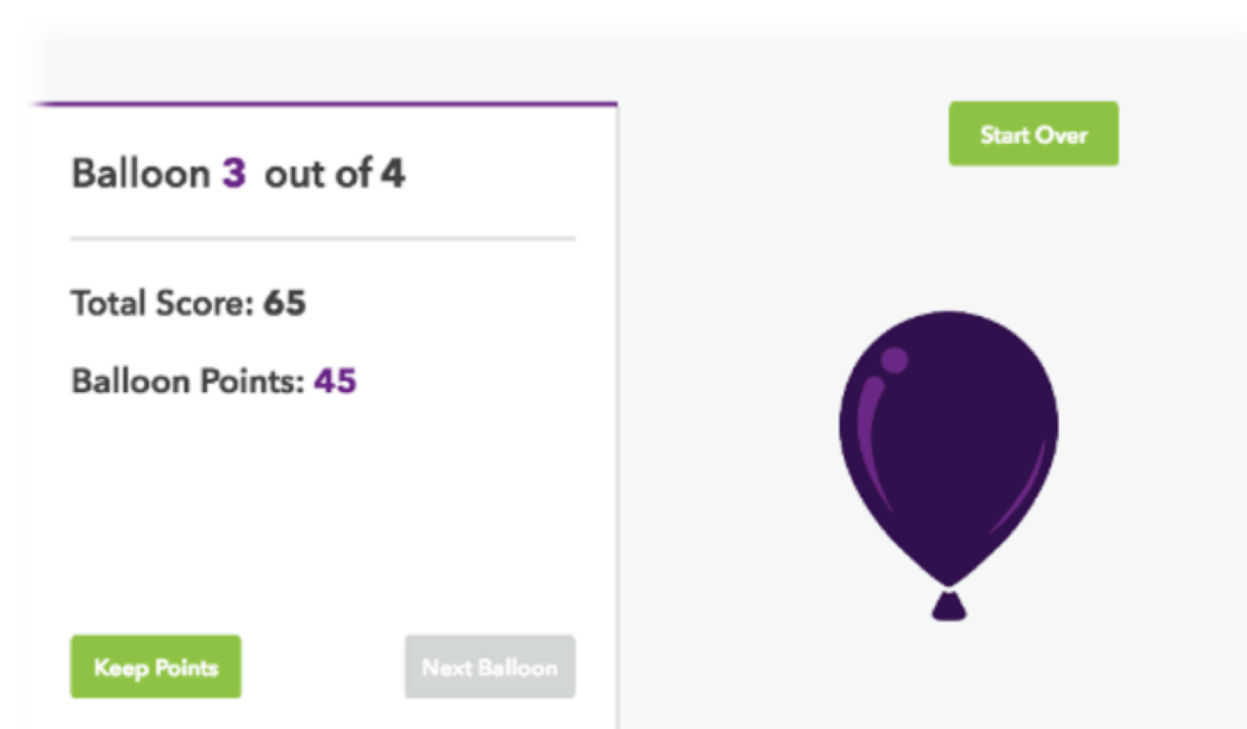


Figure 1a. Screen shot of the Balloon Analog Risk Task (BART)

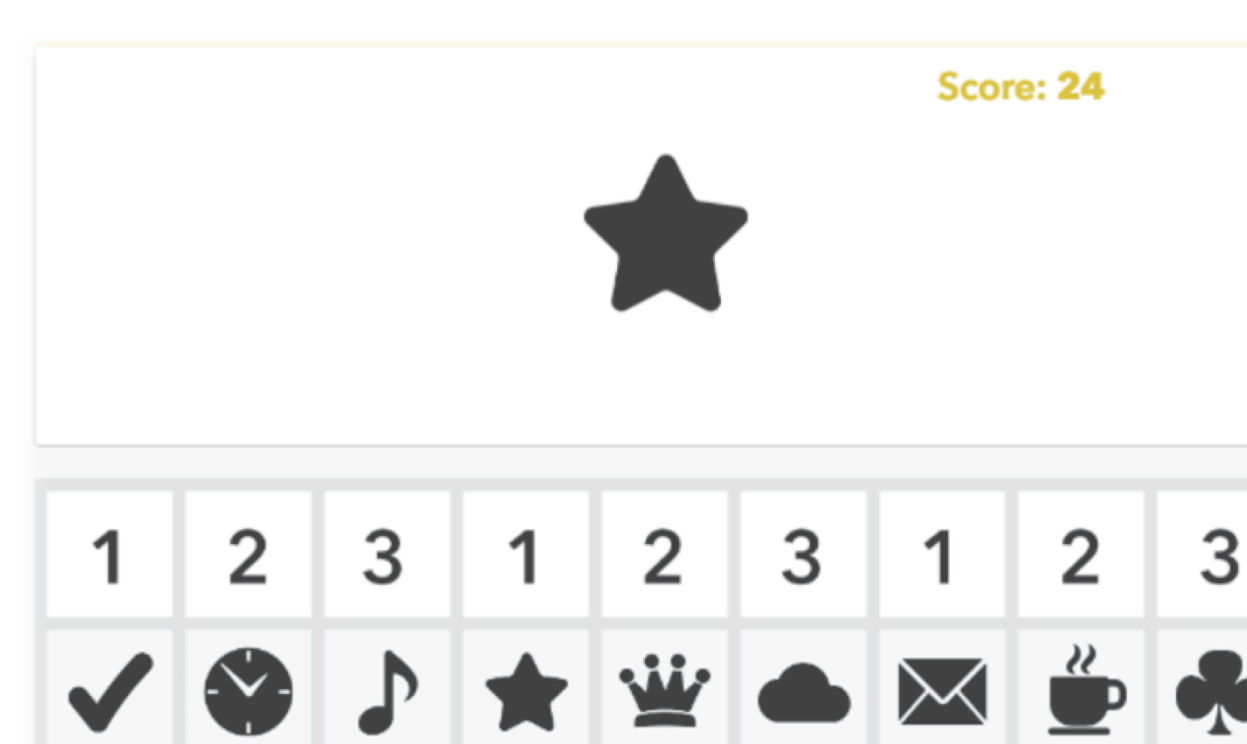


Figure 1b. Screen shot of the Digit Symbol Substitution Task (DSST).

Data collection: Participants provided informed consent and participated in the research online, under a protocol approved by the external AAHRPP-accredited IRB, Ethical & Independent Review Services. Tasks were completed independently from the participants’ desktop or laptop computer. The BART task challenged participants to earn points by inflating balloons as much as possible with a series of pumps. Popped balloons earned zero points, incentivizing a risk/reward balancing strategy. The mean number of pumps for unpopped balloons aka “adjusted pump average”⁵ served as the metric of interest, with higher scores indicating greater tendency to take risks.

The DSST task was presented as a 90 second trial to make as many matches as possible between a series of symbols and the numbers they corresponded to on a provided legend. The total number of correct trials is a well-studied indicator of processing speed² and was the metric of interest in our study.

Phenotype transformation: Raw BART and DSST phenotypes were transformed prior to testing. For each phenotype we omitted scores of zero since these were not likely to be true attempts. We transformed the BART phenotype from a continuous to an ordinal trait, binning scores by quartile. For DSST, outliers (in the 1st or 99th percentile) were Winsorized to the 2nd and 98th percentile values, respectively.

Phenotype association testing: We performed a series of logistic and linear regressions to test whether performance on BART and DSST was associated with a given binary or continuous self-reported phenotype. We restricted our analyses to individuals of European descent. We assumed an additive model for the predictor and covariates, e.g.:

$$\text{Phenotype}_i \sim \text{age} + \text{sex} + \text{pc.0} + \text{pc.1} + \text{pc.2} + \text{pc.3} + \text{pc.4} + \text{BART_pump_average}$$

where pc.0-p.4 represent genetic population covariates.

Results

We identified 25 and 66 phenotypes that showed statistically significant correlation (Bonferroni corrected) with performance on the BART and DSST, respectively (Figure 2). The BART is positively correlated with educational attainment, experiencing car accidents, and various personality traits indicating a higher tolerance for risk or disorder. BART scores are negatively correlated with being a morning person, exercise, and personality traits that indicate a preference for order and routine. The DSST is positively correlated with educational and professional attainment, and negatively correlated with alcohol and tobacco use, as well as sleep disorders.

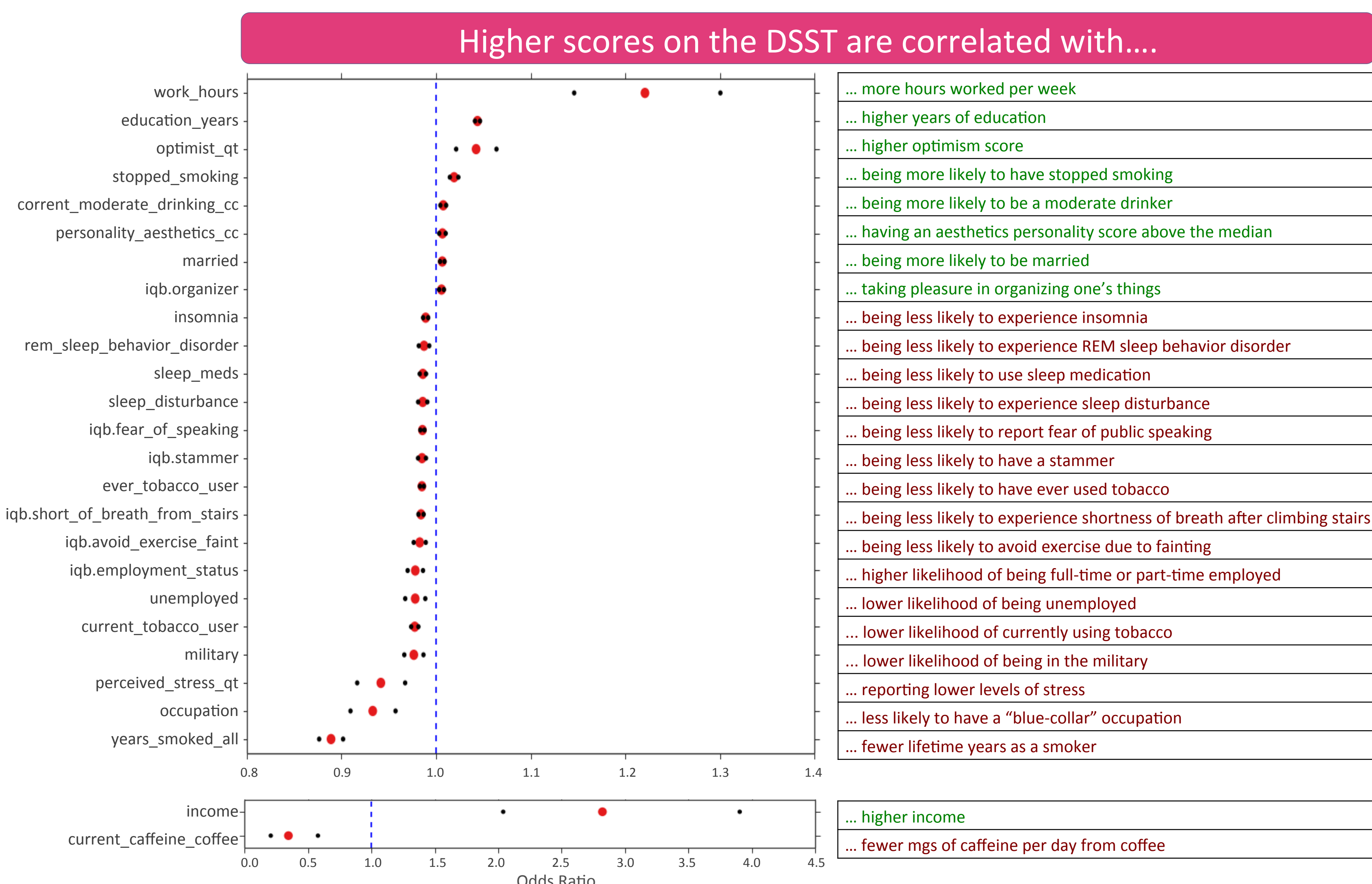
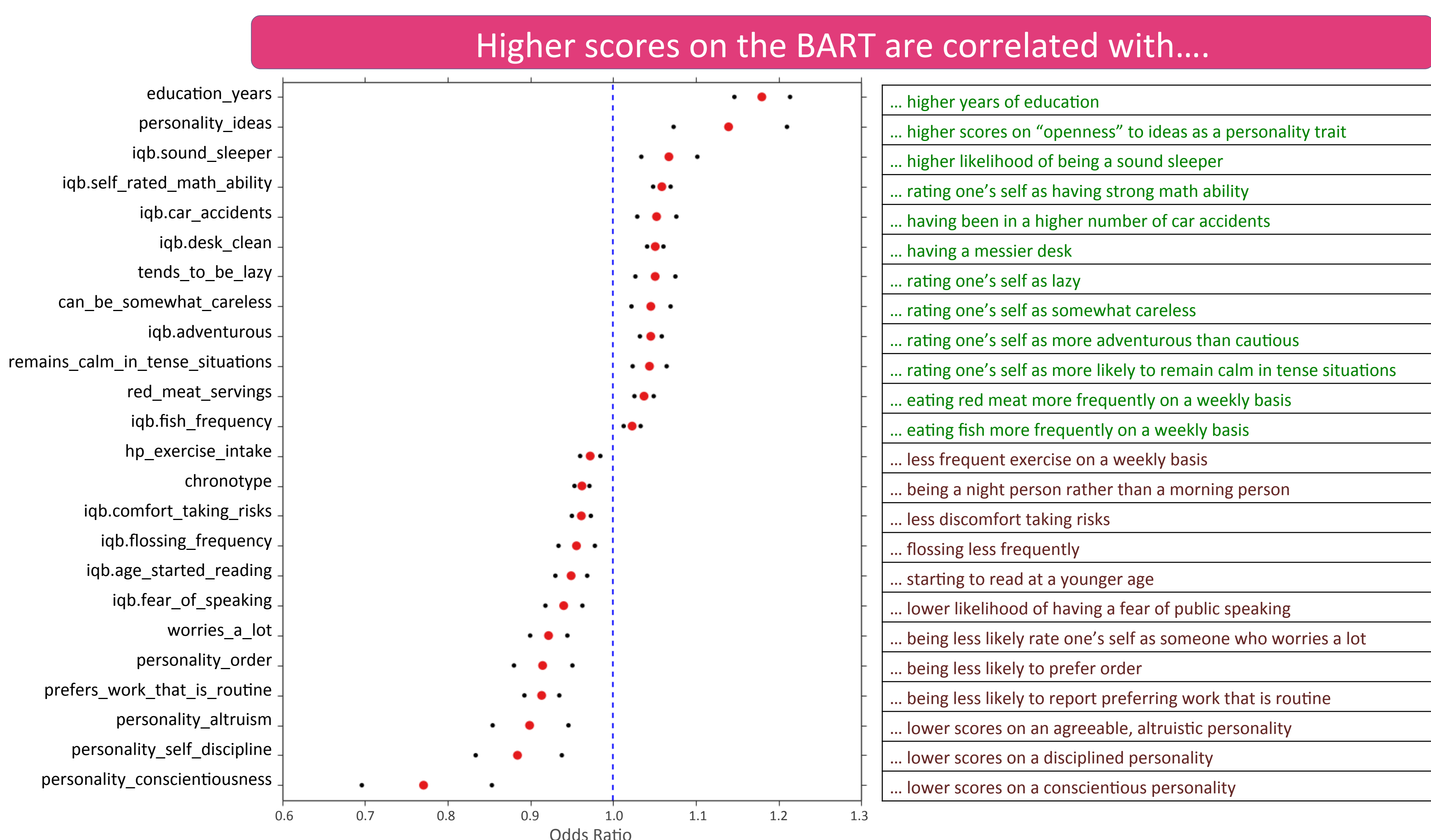


Figure 2. Phenotypes associated with BART and DSST performance in the 23andMe database. All associations exhibit p-values < 0.00013 and Odds Ratios greater than 1.02 or less than 0.98. Positive correlations are colored in green and negative correlations in red. Black markers indicate 95% confidence intervals. For DSST, associations with income and intake of caffeine are plotted separately to display odds ratios at optimal scale.

Discussion

We demonstrated the potential of at-home online data collection for cognitive phenotypes for over 25,000 individuals. These advanced survey tools are expected to be complementary to the more traditional questionnaires. We assessed the characteristics of two tools, the BART and DSST tasks, in a deeply phenotyped cohort (23andMe). We showed that simple metrics extracted from these tasks (“adjusted pump average” and “total number of correct trials”) are correlated as expected to education, behavioral, and personality traits. In the case of BART, we confirmed well-established associations with between risk taking and sociability, sensation seeking, and sleep^{6,7}. Consistent with findings that smoking status and alcohol consumption hasten cognitive decline^{8,9}, we found negative associations between DSST performance and smoking and alcohol consumption. In the present study, DSST performance was also associated with certain professional factors such as working more and having a white-collar occupation. Our next goal is to explore alternative metrics that can be derived from these tasks and their correlation to established phenotypes. We will then analyze the genetics of these metrics by running GWAS analysis.

Acknowledgements and References

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