ARTICLE

Prediction of neurocognition in youth from resting state fMRI

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Abstract

Difficulties with higher-order cognitive functions in youth are a potentially important vulnerability factor for the emergence of problematic behaviors and a range of psychopathologies. This study examined 2013 9–10 year olds in the first data release from the Adolescent Brain Cognitive Development 21-site consortium study in order to identify resting state functional connectivity patterns that predict individual-differences in three domains of higher-order cognitive functions: General Ability, Speed/Flexibility, and Learning/Memory. For General Ability scores in particular, we observed consistent cross-site generalizability, with statistically significant predictions in 14 out of 15 held-out sites. These results survived several tests for robustness including replication in split-half analysis and in a low head motion subsample. We additionally found that connectivity patterns involving task control networks and default mode network were prominently implicated in predicting differences in General Ability across participants. These findings demonstrate that resting state connectivity can be leveraged to produce generalizable markers of neurocognitive functioning. Additionally, they highlight the importance of task control-default mode network interconnections as a major locus of individual differences in cognitive functioning in early adolescence.

Introduction

Adolescence is a time of major physical, cognitive, and psychosocial change. It is also a time of great vulnerability for the emergence of maladaptive behavioral patterns and psychopathologies [1], which can cascade into poorer mental and physical health throughout adulthood. A major task for clinical neuroscience is to identify pre-morbid

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features that place the child at elevated risk for future adverse outcomes.

One major risk factor for adolescent psychopathology is difficulty with higher-order cognitive functions, which encompass a diverse set of abilities for reasoning and problem solving, cognitive control, mental flexibility, and learning/recalling information [2–5]. Difficulties with higher-order cognitive functions have been associated with a number of disorders, including both externalizing-spectrum disorders (e.g., substance use disorders and attention-deficit/hyperactivity disorder) [6–8] as well internalizing disorders (e.g., depression and anxiety) [9–11]. The generality of these associations has led to the interesting suggestion that deficits in some kinds of higher-order cognitive functions (e.g., cognitive control) represent transdiagnostic vulnerability factors for psychopathology [12–14].

Concurrently, there is great interest in the neural underpinnings of higher-order cognitive functions [15], and in developing predictive models of these functions based on resting state connectivity [16–18]. Emerging network models focus on interrelationships between brain networks involved in active control of task processing [19, 20] and default mode network (DMN). Task control networks include frontoparietal network (FPN), cingulo-opercular

(CO) network, and dorsal attention network (DAN), involved in top-down control [21, 22], as well as salience network (SAL) and ventral attention network (VAN), important for detection of unexpected events and ongoing monitoring [23, 24]. DMN—active in task-free states and implicated in spontaneous thought, evaluation, and memory [25, 26]—works in both cooperative and antagonistic ways with task control networks [27–30]. Higher-order cognitive functions are thought to rely on a complex interplay between this set of networks, in which task control networks supply top-down regulatory signals that modulate spontaneous processing unfolding in association cortices within DMN [19, 31].

Importantly, from early childhood to young adulthood, there is extensive development of functional interconnections between task control networks and DMN [32–34], suggestive of growing informational exchange and maturing top-down regulatory relationships. These observations raise an intriguing question about whether differences in connectivity patterns among these networks during youth are predictive of differences in higher-order cognitive functioning.

The present study investigates this question leveraging the first data release from the Adolescent Brain Cognitive Development (ABCD) national consortium study, which will comprehensively characterize a cohort of over 11,000 adolescents using behavioral, psychosocial, and neuroimaging measures over the course of 10 years. To accomplish this goal, data are collected from 21 sites nationwide. The baseline assessment of the study cohort has recently been completed, and utilized a number of behavioral tasks that probe multiple aspects of higher-order cognitive functions [35]. Previous work by Thompson and colleagues on 4521 youth from the first release of baseline ABCD data distinguished three major higher-cognitive domains: General Ability, Speed/Flexibility, and Learning/Memory that explained a substantial portion of the variance in behavioral measures [36].

The present work examines links between neurocognitive scores for these domains and resting state brain connectivity patterns. We first produced resting state connectomes for each subject, using stringent methods to control for the effects of head motion, a potentially serious confound in resting state studies [37]. In a sample of 2013 subjects who met quality control and other inclusion criteria, we next applied a recently developed multivariate predictive modeling method, brain basis set (BBS) [38, 39]. This method takes advantage of the fact that though functional connectomes are large and complex, encompassing tens of thousands of connections, there is massive redundancy in the set of connections that differ across people. This allows a small set of components—we used 75 in the present study—to capture most meaningful inter-individual variation in connectomes [38, 39]. We coupled BBS with leave-one-site-out cross-validation to guard against identifying spurious relationships and to provide evidence of generalizability. We demonstrate that resting state connectivity patterns yield robust, generalizable predictions of scores in the General Ability neurocognitive domain, with variation in connections within and between task control networks and DMN playing an especially prominent role in individual-differences.

Results

In leave-one-site out cross-validation analysis, resting state functional connectivity patterns are associated with neurocognition

We applied BBS to separately train predictive models for each of the three neurocognitive component scores and tested these predictive models in a leave-one-site out cross-validation framework. We observed statistically significant correlations between actual versus predicted neurocognitive scores, averaging across folds of the cross-validation, for all

Table 1 Summary of analyses

Analysis	General Ability	Speed/flexibility	Learning/memory
1. Main (leave-one-site-out)	$r = 0.31; p < 0.0001^*$	$r = 0.06; p = 0.02$	$r = 0.15; p < 0.0001^*$
2. Demographic controls	$r = 0.29; p < 0.0001^*$	$r = 0.05; p = 0.11$	$r = 0.10; p = 0.01$
3. Split-half - train 1, test 2	$r = 0.30; p < 1 \times 10^{-6}$	$r = 0.05; p = 0.10$	$r = 0.12; p < 0.0001^*$
4. Split-half - train 2, test 1	$r = 0.33; p < 1 \times 10^{-6}$	$r = 0.09; p = 0.005$	$r = 0.15; p < 1 \times 10^{-6}$
5. Low motion, 75 subj. min	$r = 0.30; p < 0.0001^*$	$r = 0.04; p = 0.27$	$r = 0.01; p = 0.58$
6. Low motion, 50 subj. min	$r = 0.30; p < 0.0001^*$	$r = 0.02; p = 0.64$	$r = 0.04; p = 0.22$

Predictive models for General Ability produced highly statistically significant results in the main leave-one-site-out analysis (row 1), and these results were stable across a number of stringent robustness checks (rows 2–6). P values were calculated by permutation methods for all analyses except the split half analyses, which employ standard parametric statistics. Bold values indicate statistically significant at $p < 0.05$; *observed correlation was higher than all 10,000 correlations in the permutation distribution
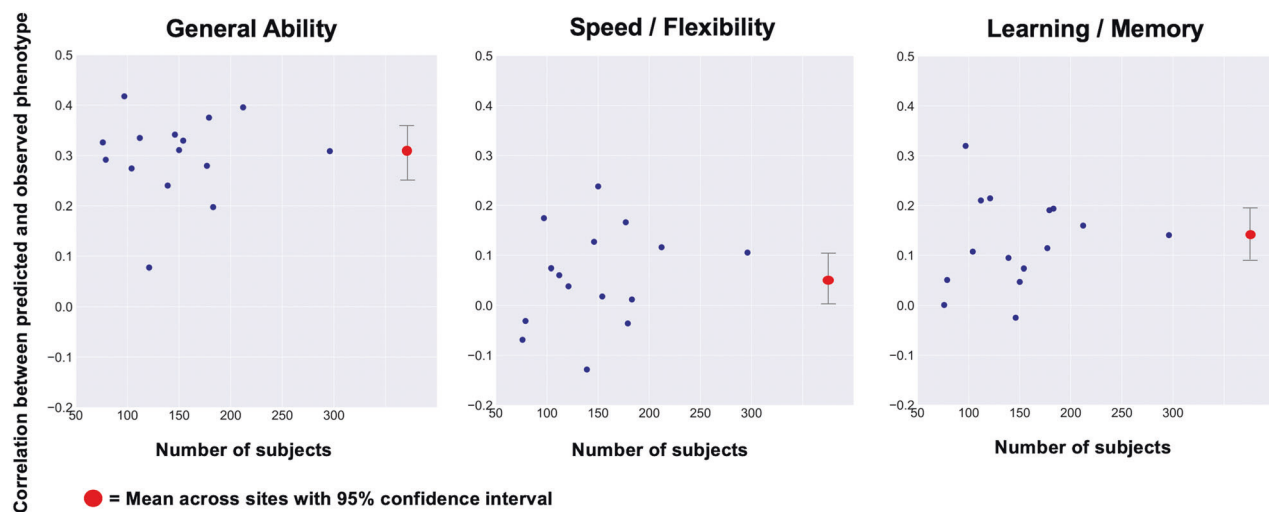
Fig. 1 Per-site results of predictive models. We built multivariate models for predicting participants' neurocognitive scores and tested these models with leave-one-site-out cross-validation across 15 sites. Predictive models for the General Ability neurocognitive domain exhibited particularly strong generalization across sites

three neurocognitive scores, with the strongest results observed for General Ability (Table 1, row 1).

Predictive models for General Ability scores specifically demonstrate strong cross-site generalizability and are robust to potential confounds

Figure 1 shows the results of BBS-based predictive models for each neurocognitive domain on a per site basis. For General Ability, results were consistent across sites, with statistically significant correlations between predicted and actual scores achieved in 14 out of 15 held-out sites (all p values < 0.05). For the other two neurocognitive scores, results were more inconsistent, with statistically significant results observed in 2 of 15 held out sites for speed/flexibility and 7 out of 15 sites for learning/memory.

We next performed a number of additional analyses to assess the robustness of the predictive models for the three neurocognitive domains. First, we included a number of covariates in the BBS models, including age, gender, race/ ethnicity, highest parental education, household marital status, and household income. In leave-one-site-out analysis, correlations between actual versus predicted neurocognitive scores remained statistically significant for General Ability and Learning/Memory, but not Speed/Flexibility (Table 1, row 2).

Second, we performed a split-half analysis using the exact splits used by Thompson and colleagues [36] in their original validation of the three neurocognitive domains. In their analysis, Bayesian PCA was trained on each of the splits and the learned factor structure was used to derive neurocognitive scores for the other split. By using their

splits, we were able to assess prediction of neurocognitive scores when these scores are learned in an entirely independent sample. We found that the split-half analysis yielded predictions of neurocognitive scores that at were highly similar to our main leave-one-site-out results (Table 1, rows 3 and 4).

Third, we examined the robustness of our results with respect to head motion. We first identified a subset of subjects with ultra-low head motion (mean FD < 0.2). From this subset, we excluded subjects from sites with less than 75 subjects, leaving 547 subjects in 5 sites. In this subsample, motion had virtually no remaining relationship with neurocognitive scores (correlations between motion and the three neurocognitive scores were, respectively, 0.006, 0.009, −0.001; all p's > 0.84). In leave-one-site-out analysis, General Ability results remained similar in size and highly statistically significant, but Speed/Flexibility and Learning/Memory were no longer statistically significant (Table 1, row 5). We then re-ran the analysis with the site size threshold lowered to 50 subjects. This analysis involved 906 subjects across 11 sites (correlations between motion and the three neurocognitive scores were, respectively, −0.05, −0.03, −0.01; all p's > 0.15). Leave-one-site-out analysis again revealed similarly strong results for General Ability, but Speed/Flexibility and Learning/Memory remained statistically insignificant (Table 1, row 6).

The preceding analyses demonstrate that results for General Ability are generalizable across sites and robust to a number of potential confounds including demographic covariates and head motion. In contrast, correlations for Speed/Flexibility and Learning/Memory were smaller in the main analysis and did not survive one or more subsequent robustness checks.
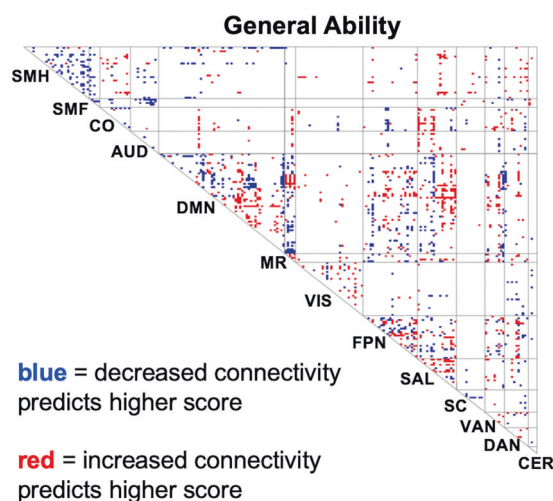
Fig. 2 Consensus maps of connections that are predictive of general ability scores. Our predictive model for General Ability neurocognitive scores yielded reliable predictions across held out sites. Visualization of the predictive model reveals that connections in task control networks and DMN are especially well represented. SMH somatomotor-hand, SMF somatomotor-faces, CO cingulo-opercular, AUD auditory, DMN default mode network, MR memory retrieval, VIS visual, FPN fronto-parietal, SAL salience, SC subcortical, VAN ventral attention, DAN dorsalattention, CER cerebellum

Connections within and between task control networks and DMN play a prominent role in prediction of General Ability scores

Figure 2 displays a consensus map that highlights connections that were weighted more heavily in predictive models for General Ability. Connections within and between task control networks and DMN are notably prominent in this map. More precisely, we use the term "task control-DMN intersection" to refer to: (i) connections within a task control network; (ii) connections within DMN, and (iii) connections that link a task control network node with a DMN node. Such connections represent roughly 20% of the total number of connections (6754 out of 34716 total) in the connectome. They represent, however, 43% of the suprathreshold connections in the consensus map for General Ability (Fig. 2, where a $z = 2$ threshold is used).

To further assess the importance of connections in the task control-DMN intersection, we dropped all connections outside this intersection and redid our BBS-based predictive modeling. The correlation between actual versus predicted neurocognitive scores, averaging across folds of the cross-validation, were: General Ability $r = 0.26$ (permutation p value < 0.0001, i.e., observed correlation was higher than all 10,000 correlations in the permutation distribution).

We in addition assessed whether predictions for General Ability were better than could be achieved using 1000 randomly selected sets of six networks that excluded DMN and the five task control networks. Results showed that our
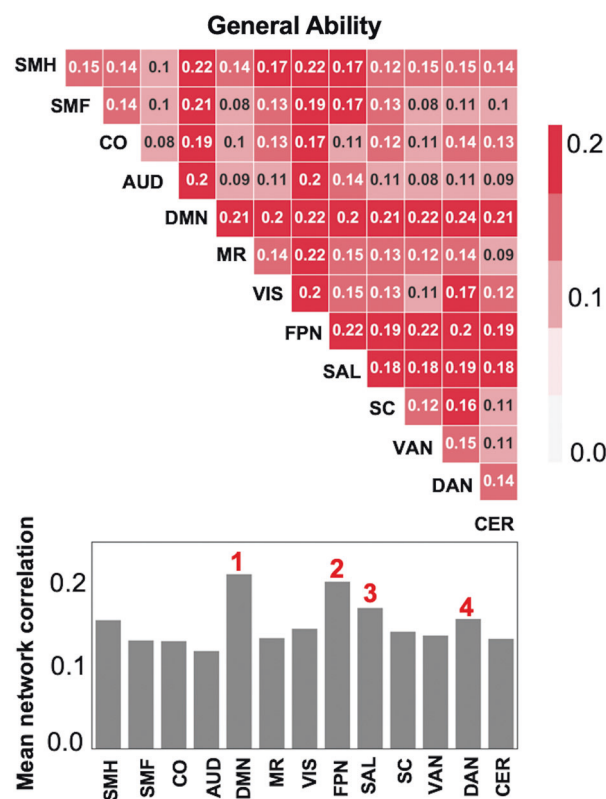
Fig. 3 Prediction of general ability neurocognitive scores with two networks. To assess the importance of specific networks for the success of the BBS predictive models for General Ability, we trained new BBS models with just two networks (top row). We also calculated the mean performance for each network (bar graphs in bottom row). Values indicate correlations between actual and predicted scores, averaged across folds of the cross-validation analysis. These analyses revealed prominent roles for DMN as well as three task control networks: FPN, SN, and DAN. SMH somatomotor-hand, SMF somatomotor-faces, CO cingulo-opercular, AUD Auditory, DMN default mode network, MR memory retrieval, VIS visual, FPN fronto-parietal, SAL salience, SC subcortical, VAN ventral attention, DAN dorsal attention, CER cerebellum

observed prediction success using the task control-DMN intersection exceeded all 1000 values when these networks were excluded. Finally, we examined prediction of General Ability scores retaining just two networks, and we computed summary statistics that quantify the importance of each network (Fig. 3). We found that DMN and fronto-parietal network emerged as the top two most important networks, with other task control networks (e.g., salience network and dorsal attention network) also showing high importance.

Discussion

This study examines behavioral and imaging data from 9 to 10 year old participants in the ABCD Consortium study whose data were included in the first data release [35, 40].

Using a multivariate predictive modeling approach, we sought to identify resting state connectivity patterns that are predictive of three major domains of higher-order cognitive functions: General Ability, Speed/Flexibility, and Learning/Memory. Our first main finding is that resting state connectivity patterns yield predictions for scores in the General Ability neurocognitive domain that are generalizable across sites and robust to potential confounds. Our second main finding is that connections within and between task control networks and DMN are particularly important for individual-differences in the General Ability domain. There is a critical window in mid-adolescence when youth start experimenting with substances and a number of serious mental illnesses have their onset [1]. Our findings elucidate a neural basis for higher-order cognitive functions in youth prior to entering this window, and could potentially inform efforts at earlier detection and more tailored interventions for vulnerable youth.

Resting state fMRI has emerged as a leading method for mapping the brain's intrinsic network architecture [41–43] and predicting individual differences in phenotypes [44, 45]. An important open question has been whether predictive models based on resting state connectivity patterns trained in one dataset can effectively generalize to unseen data, in particular when the unseen data is collected at a different sites using different MRI scanners. Results observed with General Ability scores—statistically significant predictions in 14 out of 15 held-out sites—demonstrate that successful generalization using imaging data from unseen sites and scanners can indeed be achieved. Moreover, the size of the effect (roughly 10% of the variance in General Ability scores, a potentially clinically meaningful amount) and the robustness of the effect (correlations are nearly unchanged after extensive demographic controls and restriction to an ultra-low motion subsample) suggest that resting state connectomes hold promise as objective measures of at least some components of neurocognition.

In contrast, for the other two neurocognitive domains, Speed/Flexibility and Learning/Memory, effect sizes were much smaller, results were not generalizable across sites, and results did not survive robustness checks involving demographic covariates and head motion. In explaining this result, it is possible that these two neurocognitive domains do not have sizable signatures in resting state connectomes, or that the BBS classifiers used for the present analysis are not sensitive to their signatures, or a combination of both. For example, if resting state signatures of these neurocogntive domains are mainly localized in small, spatially discrete structures (e.g., the caudate nucleus or the hippocampus), classifiers that rely on distributed whole-connectome information, including the BBS method used in the present report, will be unlikely to recover them. In future studies, alternative classifiers (e.g., supervised methods), modalities (e.g., task-based methods), or search strategies (e.g., regions of interest approaches) could be utilized.

For the General Ability neurocognitive domain, we found that connections involving task control networks and DMN played a disproportionate role in explaining the success of BBS predictive models. This finding can potentially be interpreted in terms of recent theories of adaptive task control [19, 46]. These accounts propose that task control networks modulate activity in distributed brain regions to facilitate cognitive control during complex tasks. In addition, a number of lines of evidence point to the DMN as an important target of these top-down adaptive control signals. Modulation of the DMN is required in cases where task control networks must cooperate with DMN for coordinated processing, such as during complex problem-solving and prospective decision-making [27–29]. It is also required to avoid interference by DMN [30] during externally focused, cognitively demanding tasks, with inadequate regulation of the DMN by task control networks sometimes leading to impaired task performance [47, 48].

It is notable that previous cross-sectional studies provide evidence that connections involving task control networks and DMN exhibit substantial maturation during youth [32–34, 49, 50]. The DMN initially takes shape as early as the fetal period [51], and, in addition, there is apronounced increase in intra-DMN connectivity from early childhood to the mid-20's [34, 49]. During this time, DMN also segregates from certain task control networks, especially DAN and VAN, though there is substantial fine-grained variation across nodes in the respective networks in terms of where segregation is observed [33, 34]. Given these observations of substantial maturational changes in task control-DMN interconnections, a major strength of the ABCD study is that it will let us examine these same children through adolescence over the next 10 years, allowing us to address a number of critical open questions.

For example, we do not currently know the natural history of the connectomic differences we observed in task control networks and DMN that are associated with reduced higher-order cognitive functions in early adolescence. That is, are these connectivity differences ones that tend to "catch-up", ones that stay consistently behind, or ones that increasingly deviate from normative trajectories (i.e., get worse) across age [52, 53]? Longitudinal data will also support stronger inferences about causality. For example, it will be possible to assess whether changes in connectivity patterns within a child over time predict changes in higher-order cognitive functions and associated mental health outcomes in that individual.

In sum, results from this study establish that resting state connectivity patterns are associated with higher-order
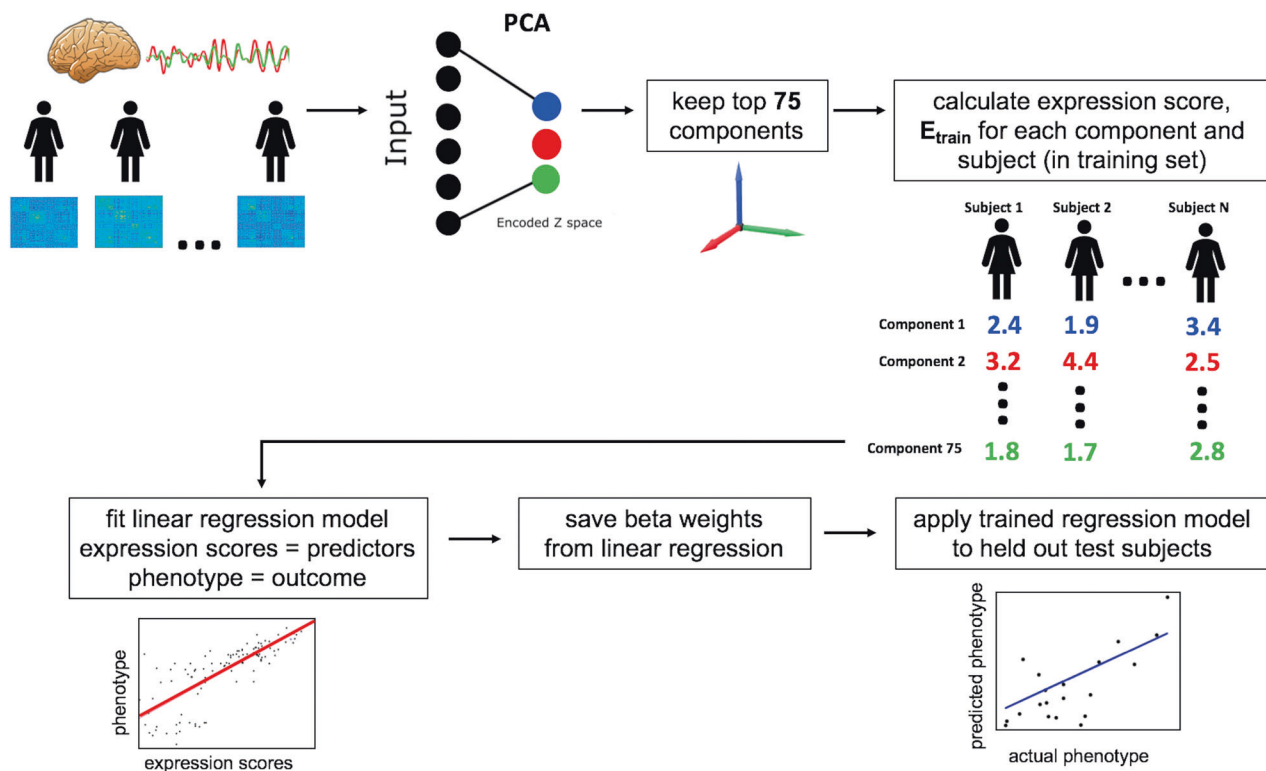
Fig. 4 Main steps of brain basis set (BBS) modeling. BBS is a multivariate predictive modeling method. It utilizes dimensionality reduction with principal components analysis (PCA) to construct a basis set for predicting phenotypes of interest

training dataset for principal components analysis using the pca function in MATLAB, yielding n-1 components ordered by descending eigenvalues (note that that $p > n$). We select the top 75 components for our basis set based on our previous work showing that somewhere between 50 to 100 components yields optimal prediction of a broad array of behavioral phenotypes [38, 39], with inclusion of additional components typically reducing performance due to overfitting.

Next, in the training dataset, we calculate the expression scores for each of the 75 components for each subject by projecting each subject's connectivity matrix onto each principal component. We then fit a linear regression model with these expression scores as predictors and the phenotype of interest as the outcome, saving B, the 75×1 vector of fitted coefficients, for later use. In a test dataset, we again calculate the expression scores for each of the 75 components for each subject. Our predicted phenotype for each test subject is the dot product of B learned from the training dataset with the vector of component expression scores for that subject.

Leave-one-site-out cross validation

To assess of the performance of BBS-based prediction models, we used leave-one-site-out cross-validation, which

was performed separately for each of the three neurocognitive component scores. In each fold of the cross-validation, data from one of the 15 sites served as the held-out test dataset and data from the other 14 sites served as the training dataset. Additionally, at each fold of the cross-validation, we did the following: (1) PCA was performed on the training dataset yielding a 75-component basis set; (2) a BBS model was trained to predict the relevant neurocognitive factor as the outcome variable. These BBS models included covariates for head motion (mean FD and mean FD squared), and in applying these trained BBS models to the held-out test dataset, the level of these covariates was set at zero. In a secondary analysis, we used a more extensive set of covariates in these BBS predictive models, including age, gender, race/ethnicity, highest parental education, household marital status, and household income. We assessed the significance of all cross-validation-based correlations with non-parametric permutation tests [60] in which we randomly permuted the 2013 subjects' neurocognitive scores 10,000 times, as described in detail in the Supplement.

Consensus component maps for visualization

We used BBS with 75 whole-connectome components to make predictions about neurocognitive component scores.

To help convey overall patterns across the entire BBS predictive model, we constructed "consensus" component maps. We first fit a BBS model to the entire dataset consisting of all participants across the 15 included sites. We then multiplied each component map with its associated beta from this fitted BBS model. Next, we summed across all 75 components yielding a single map, and thresholded the entries at $z = 2$. The resulting map indicates the extent to which each connection is positively (red) or negatively (blue) related to the outcome variable of interest.

Compliance with ethical standards

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