

Intersubject similarity of personality is associated with intersubject similarity of brain connectivity patterns

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ARTICLE INFO

Keywords:

NEO-FFI
Functional connectome
Individual difference
Network similarity
Personality neuroscience

ABSTRACT

Personality is a central high-level psychological concept that defines individual human beings and has been associated with a variety of real-world outcomes (e.g., mental health and academic performance). Using 2 h, high resolution, functional magnetic resonance imaging (fMRI) resting state data of 984 (primary dataset $N = 801$, hold-out dataset $N = 183$) participants from the Human Connectome Project (HCP), we investigated the relationship between personality (five-factor model, FFM) and intrinsic whole-brain functional connectome. We found a pattern of functional brain connectivity (“global personality network”) related to personality traits. Consistent with the heritability of personality traits, the connectivity strength of this global personality network is also heritable (more similar between monozygotic twin pairs compared to the dizygotic twin pairs). Validated by both the repeated family-based 10-fold cross-validation and hold-out dataset, our intersubject network similarity analysis allowed us to identify participants' pairs with similar personality profiles. Across all the identified pairs of participants, we found a positive correlation between the network similarity and personality similarity, supporting our “similar brain, similar personality” hypothesis. Furthermore, the global personality network can be used to predict the individual subject's responses in the personality questionnaire on an item level. In sum, based on individual brain connectivity pattern, we could predict different facets of personality, and this prediction is not based on localized regions, but rather relies on the individual connectivity pattern in large-scale brain networks.

1. Introduction

Personality is a central, high-level psychological concept that defines individual human beings. Differences in personality are associated with distinct vulnerability for psychopathology (Kotov et al., 2010), and a variety of social measures such as occupational and academic performance (Poropat, 2009; Rothmann and Coetzer, 2003). Understanding the biological basis of personality is valuable to gain more insight into vulnerability and resilience, aptness for skills and areas of expertise, and even to better understand our individuality as human beings. Neuroimaging is the most promising tool to investigate the biological basis of personality. The unbiased assessment of brain activity and connectivity with novel analysis tools allows associating inter-individual variability in brain structure and function with a wide range of human behaviors and cognitive functions (Kanai and Rees, 2011).

Neuroimaging studies have linked individualized brain structure and function to different personality traits, and the brain correlates of the five-factor model (FFM) of personality have been extensively explored.

The FFM is the most accepted model of human personality. And a large number of studies have provided solid support for the conclusion that the five factors (i.e., neuroticism, extraversion, openness, agreeableness, and conscientiousness) can well capture key descriptors of different behavioral tendencies (Costa et al., 1991; Digman, 1990; McRae and John, 1992). In an attempt to identify biological underpinnings of personality, structural MRI studies, for instances, studied the correlation between local gray matter volume (e.g. amygdala, orbitofrontal cortex, parahippocampal gyrus, middle temporal gyrus, superior frontal gyrus) and extraversion (Cremers et al., 2011; DeYoung et al., 2010; Kapogiannis et al., 2013; Lu et al., 2014; Omura et al., 2005). Other studies investigated the association between functional connectivity based on resting-state fMRI data and the FFM measures of personality (Adelstein et al., 2011; Aghajani et al., 2014; Beaty et al., 2016; Sampaio et al., 2014). Most of these studies used seed-based functional connectivity analyses or independent component analyses (ICA). The factors within the FFM encompass a variety of behavioral tendencies (e.g., emotional instability and sensitivity to stress) or cognitive functions (e.g., attention,

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<https://doi.org/10.1016/j.neuroimage.2018.10.062>

Received 5 June 2018; Received in revised form 16 October 2018; Accepted 24 October 2018

Available online 30 October 2018

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social cognition, and empathy) and thus, we propose that personality can be more comprehensively captured by brain-wide, large-scale interactions between distinct regions across the entire brain instead of local characteristics of a few brain regions or smaller-scale circuits.

Recent analytical advancements and in particular large-scale data sets based on most advanced functional neuroimaging technology that focuses on the human functional connectome might provide an opportunity to understand the biological basis of personality substantially better. Human neuroimaging studies have shown that the functional connectome, like fingerprints, show highly individualized patterns, allowing identification at the single-subject level (Finn et al., 2015; Kaufmann et al., 2017; Xu et al., 2016). More importantly, distinct brain connectivity patterns are behaviorally relevant: complex relationships between individuals' brain connectivity measures and independent non-imaging measures (e.g., education, IQ, reading ability) (HCP MegaTrawl: <https://db.humanconnectome.org/megatrawl/>) or a single axis of co-variation spanning from positive to negative attributes that links diverse non-imaging measures in the HCP has been reported (Smith et al., 2015). Combined with machine learning algorithms, connectivity patterns can be used to predict individual differences in general intelligence (Finn et al., 2015), sustained attention, symptoms of attention deficit hyperactivity disorder (Rosenberg et al., 2015), and even higher-level cognitive concepts such as creativity in subjects that were not included in the initial analysis (Beatty et al., 2018). For personality research, the individual differences of the functional connectome have been used to successfully predict individual differences in particular personality traits (e.g., trait narcissism, neuroticism, extraversion, and openness) (Dubois et al., 2018; Feng et al., 2018; Hsu et al., 2018; Kong et al., 2018), revealing a potential association between brain connectivity and personality.

In this study, we hypothesized that subject pairs with highly similar brain connectivity patterns also have highly similar personality profiles ("similar brain, similar personality" hypothesis). To quantify how similar the brain connectivity/personality are, we proposed an intersubject similarity analysis grounded in representation similarity analysis (RSA), a novel, but an already widely used method in task-based fMRI data analysis (Cohen et al., 2017; Kriegeskorte and Kievit, 2013). To perform validation for the intersubject similarity analysis, we first adopted the method in a heritability estimation framework. We know from previous studies that both functional connectome and personality traits are heritable (Colclough et al., 2017; Doehnermann et al., 2014; Ge et al., 2017; Glahn et al., 2010; Jang et al., 1996; Sinclair et al., 2015; Yang et al., 2016). For replication and validation, we thus exploited one feature of the HCP: The inclusion of monozygotic [MZ] and dizygotic [DZ] twin pairs. We hypothesized that both connectome and personality are more similar within MZ than DZ pairs. Finally, we explored the power of the connectivity pattern in predicting individual item scores of FFM in initially unseen subjects. After repeating the prediction for each item, we reconstructed the unseen subject's personality based solely on his or her brain connectivity.

2. Materials and methods

2.1. Human Connectome Project (HCP) data

Resting-state fMRI data were acquired from the HCP Young Adult cohort (<http://www.humanconnectome.org>). We used the HCP "PTN" (Parcellation + Timeseries + Netmats) dataset, which consists of extensively processed 3T resting-state fMRI data. Previous publications have reported the full details regarding the sample, data acquisition, and preprocessing procedures (Barch et al., 2013; Essen et al., 2013; Glasser et al., 2013). To avoid over-fitting and evaluate the generalizability of our findings, we used the HCP S900 release as the primary dataset and subjects from the recently released HCP S1200 dataset as the hold-out dataset. Briefly, the raw HCP S900 PTN dataset included 820 subjects, but we only used 801 subjects (all aged 22–35 except for 6 subjects older

than 36, 443 females) in our study (3 subjects were excluded due to incomplete item-level personality data; 16 subjects were excluded because their framewise displacement (FD) values are larger than the group mean FD plus 3 standard deviation). Based on the same criteria, we generated the hold-out dataset from the HCP S1200 release. The hold-out dataset included 183 subjects (all aged 22–35 except for 3 subjects older than 36, 81 females). To ensure the comparability between the primary and hold-out dataset, group comparisons (e.g., sex, age, personality scores) were performed and reported in the result. The "PTN" dataset has been used successfully to relate individuals' functional connectivity data to non-imaging data (e.g., education, tobacco intake, IQ, reading ability) in a single multivariate analysis (Smith et al., 2015) or univariate-regression analysis (HCP MegaTrawl: <https://db.humanconnectome.org/megatrawl/>).

2.2. Estimation of functional connectome

We used the time series released with the HCP PTN dataset to estimate the functional connectome at the individual level. More specifically, before the extraction of time series, all rs-fMRI data underwent standard data pre-processing and group ICA parcellation (Smith et al., 2015). To get the subject level rs-fMRI time series data, for a given "parcellation" (group-ICA decomposition), one representative time series per ICA component was derived by mapping the ICA spatial maps onto each subject's rs-fMRI data. For each subject, we used the time series from 300 ICA components (we consider each ICA component as a network "node") in our network analyses (Fig. 1a). We derived the node-time series, using a method called dual-regression stage-1 (Smith et al., 2015). To estimate one time series for each ICA map, all the ICA maps were used as spatial regressors against the full time series data. This results in 300 nodes' time series and each series contain 4800 time points from four concatenated 15 minutes rs-fMRI sessions. Functional connectomes were calculated based on the node-time series for each subject, creating a 300×300 matrix (Fig. 1a). More specifically, we calculated temporal correlations between nodes' time series, thereafter these Pearson correlation scores (r) were converted into z statistics with Fisher's r -to- z transformation.

2.3. Personality data

We used the NEO-FFI personality data within the HCP behavioral measurements. The five-factor model is one of the most applied questionnaires to capture the major facets of human personality: a) neuroticism; b) extraversion/introversion; c) agreeableness; d) openness; and e) conscientiousness (Costa and McCrae, 2008; Goldberg, 1993). In the HCP project, the 60 item version of the Costa and McCrae Neuroticism/Extraversion/Openness Five-Factor Inventory (NEO-FFI) (McCrae and Costa, 2004) was implemented. We used both the total score on each personality factor and subjects' responses to each of the 60 individual personality items. The total score on each factor was used to search for the connections that contained information relevant for the following identification and prediction analyses. To better capture the individual differences in personality traits, we mapped the NEO Five-Factor Inventory (5 personality dimension and each dimension contains 12 items) into a 5×12 matrix (defined as the "personality profiles") for each subject considering each personality factor as a row and each item of the questionnaire subscale as a column (Fig. 1b). We observed high Cronbach's Alphas for all personality dimensions ($\alpha_{\text{Agreeableness}} = 0.766$, $\alpha_{\text{Openness}} = 0.751$, $\alpha_{\text{Conscientiousness}} = 0.819$, $\alpha_{\text{Neuroticism}} = 0.835$, $\alpha_{\text{Extraversion}} = 0.771$), replicating the sub-scale reliability measures (Egan et al., 2000). To be noted, there was an error in the HCP database in which the item 59 at that time of download (12/01/2016) was not reverse-coded. This issue was also reported by another user before on the HCP list server. We corrected this error and used the self-calculated total score of Agreeableness in our analysis.

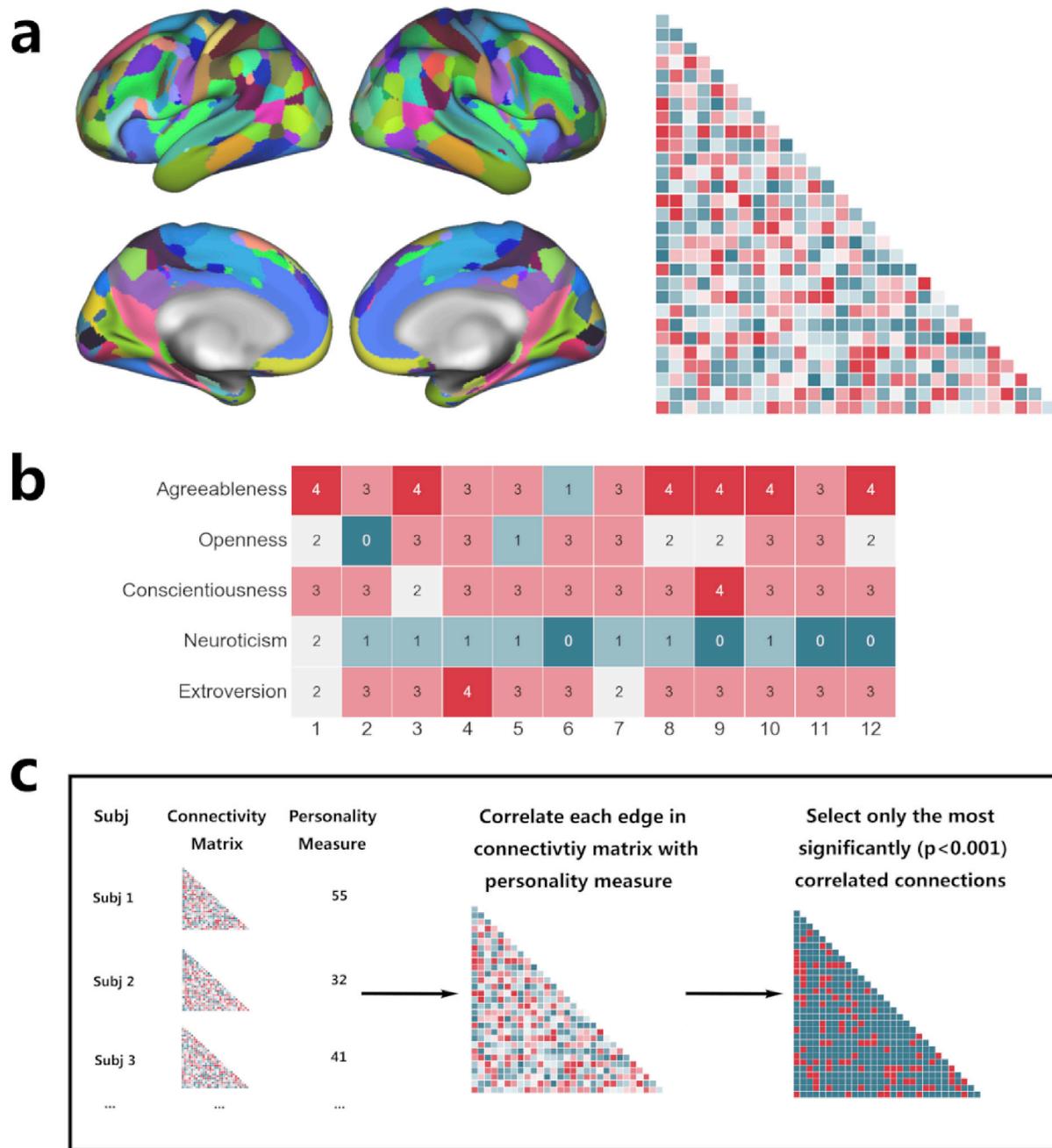


Fig. 1. (a) Whole-brain connectome estimation. 300 distinct brain regions yielded by independent component analysis based brain parcellation and correlation matrix. To be noted, the showed correlation matrix is just for the demonstration purpose and do not calculated based on the real data. (b) An example of the personality profile matrix. NEO-FFI personality data was transformed into the matrix considering each personality factor as a row and each item of the questionnaire subscale as a column. (c) For each personality dimension, each connection within the connectome is correlated with the personality measures to select connections whose correlation value is significant ($p < 0.001$). The identification procedure was repeated for each leave-one-family-out training sample.

2.4. Family structure data

The family structure of the subjects is available under the restricted data usage terms, requiring users to protect the anonymity of the subjects (Glasser et al., 2013). We grouped subjects into families or twins' pairs according to their family ID or twins' status. All of the possible same-sex monozygotic (MZ) twins and dizygotic (DZ) twin pairs were extracted from our sample. There are in total 92 MZ twin pairs and 49 same-sex DZ twin pairs. We considered only twin pairs which were confirmed by genotyping. The family structure data were used to (1) estimate the heritability of brain or personality measures and (2) to perform the family-based 10-fold cross-validation (details below).

2.5. Identification of the global personality network

To assess the relationship between functional connectivity strength and personality in an unbiased way, we performed the correlation analysis between each connection within the whole-brain functional connectome and sum scores for each personality dimensions across subjects. The resulting r values were thresholded at $p < 0.001$ (Fig. 1c). To evaluate the stability of these personality-associated connections and guarantee the independence of the subsequent analyses, the identification of personality-associated connections was only performed in a training family sample generated by leave-one-family-out cross-validation. We qualitatively evaluated the stability by calculating the percent of

connections that consistently correlated with the personality measures during the cross-validations.

We defined the dimension specific network (e.g., Agreeableness network) as the set of brain connections that passed the predefined statistical threshold during every iteration ($N = 365$) of the leave-one family-out cross-validation. In other word, connections that were only occasionally associated with personality scores during iterations were not included. We further created the global personality network which contains all the significant connections within five dimension specific networks, so each connection within this network at least correlated with one personality dimension. We use several essential indices for each dimension-specific network in the Result Section 3.2. N_{positive} : number of edges that positively correlates with personality scores; N_{negative} : number of edges that negatively correlates with personality scores; percent of total edges: percentage of significant edges relative to all possible edges in the brain; r_{positive} : the average Pearson correlation value for positively correlated edges; r_{negative} : the average Pearson correlation value for negatively correlated edges; r^2_{positive} : the average coefficient of determination for positively correlated edges; r^2_{negative} : the average coefficient of determination for negatively correlated edges. In brief, 528 edges (0.01% of total edges) were included in the Agreeableness network, 88 edges (0.001% of total edges) were included in the Openness network, 140 edges (0.003% of total edges) were included in the Conscientiousness network, 31 edges (0.0006% of total edges) were included in the Neuroticism, and 53 edges (0.001% of total edges) were included in the Extroversion network.

To better understand the connectivity patterns of the global personality network and dimension specific networks, we (1) identified the anatomical overlap (connections associated with two or more factors) between factor specific networks and calculated their percent within the global personality network; (2) calculated the percent of non-overlapped connections within the global personality network for each factor specific network. Since the brain regions involved in the global personality network are widespread across almost the entire brain, the attempt to visualize all the regions and connections involved will be uninformative. For better visualization, we located the regions with high relevance within these networks using a network measure, degree (or “degree centrality”) (Rubinov and Sporns, 2010). Firstly, within each factor specific network, we calculated the degree for each region within the network. More specifically, degree centrality was calculated by counting how many connections linked certain region. We plotted the top 5% of the regions with the highest degree. Then, the same method was applied to the global personality network, and top 10% of the regions with the highest degree were plotted.

2.6. Validation of the intersubject similarity analysis via heritability estimation

Given that MZ twins share 100% of their genes and DZ twins share 50%, MZ twins should be more similar to each other than DZ twins if gene account for variation between individuals in terms of functional connectome and personality profiles. This step can be viewed as the benchmark to verify our functional connectome estimation and proposed similarity analysis. We transformed all of the 300×300 functional connectomes to triangles by removing all the self-correlations ($r = 1$) in the diagonal and mirrored right upper triangles, resulting in triangles with 44850 connectivity strengths. To quantitate how similar two functional connectomes/personality profiles are, we applied the intersubject similarity analysis grounded in the representation similarity analysis (RSA)(Cohen et al., 2017; Kriegeskorte and Kievit, 2013), a widely used method in task-based fMRI data analysis. The similarity index was calculated by comparing the functional connectome/personality profiles of one subject with another subject. Specifically, 2-D arrays (both connectome and personality measures) were transformed to 1-D vectors, and correlational analyses were performed between 2 vectors. This produced a similarity index for subject pairs based on the person correlation

coefficient between the pattern of brain connectivity or personality profiles. This method has been used to describe within-subject brain network reconfiguration analyses (similarity between task functional connectome and rest functional connectome for single subject)(Schultz and Cole, 2016).

To calculate the personality similarity between participants, individuals' personality questionnaire responses were represented as a personality matrix for each participant. Specifically, we mapped the NEO Five-Factor Inventory (5 personality factors and each factor contains 12 items) into a 5×12 matrix (defined as “personality profiles”) for each subject considering each personality factor as a row and each item of the questionnaire subscale as a column. Then similarity indices were calculated by comparing the functional connectivity pattern and personality profiles between two participants. This produced three similarity indices for each pair of participants: (1) one based on the correlation of the pair's pattern of whole-brain connectome; (2) the other on the correlation of the pair's personality profiles; (3) and the last one based on the correlation of the pair's global personality network.

2.7. Intersubject network similarity analysis

2.7.1. Similarity analysis validated by cross validation

We created a functional connectome database that consisted of all the functional connectome (triangles without self-correlations and repeated connectivity strengths) for all the subjects within the primary dataset. Then, family-based repeated 10-fold cross validation was adopted to divide the primary dataset into a training sample (9/10 of the all families) and testing sample (1/10 of the families). The family-based cross-validation procedure can further prevent data leakage in case the model has already seen one of the family members during the training. To be noted, the global personality network was calculated only within the training sample for independence. The similarity index of the global personality network between the “to be predicted” (TBP) subject (one of the subjects from the testing sample) and all the other subjects in the training sample was computed using the network similarity analysis used in the heritability estimation. The subject with the highest connectome similarity score was identified as the match for the TBP subject. To be noted, until now, the match was only based on the similarity at the neural level. Finally, to test our “similar brain, similar personality” hypothesis, we computed the personality similarity index between the TBP subject and the identified most similar subject (Fig. 4a). We repeated these steps for all of the subjects within the training sample, resulting in the average personality similarity index for the iteration. The 10-fold cross-validation was further repeated for 10 times, resulting in a total of 100 iterations. Therefore, the standard deviation for personality similarity can be estimated.

To investigate if our intersubject network similarity analysis generated pairs of subjects with significantly similar personality, we performed nonparametric permutation testing. In each iteration, instead of finding the subject with highest network similarity index, we randomly drew the subject as the “matched” subject and computed the personality similarity index. This procedure was repeated 5000 times. A null distribution of personality similarity was sampled by randomization, and this null distribution was used for significance testing. The statistical significance of the similarity index (mean value across the repeated 10-fold cross-validation) generated by the network-similarity based match can be accessed by comparing it with the similarity scores generated by the 5000 randomly matches. To further support our “similar brain, similar personality” prediction, we investigated the linear relationship between the personality network similarity and personality similarity. For each of the most similar pairs identified, we performed the Pearson correlation between the network similarity index and personality similarity index across subject pairs. This correlation was performed for all sets of subject pairs generated by the repeated 10-fold cross-validation, getting the slope of the best linear fit for each set. Finally, we performed a one-sample *t*-test on these estimates to test whether the potential linear relationship can be generalized across sets of subject pairs.

2.7.2. Similarity analysis validated by hold-out dataset

As the more stringent test of generalizability, we applied a network similarity method to predict personality profiles for the hold-out sample based on the global personality network identified within the primary sample. The procedure is highly similar to what we described in the cross validation analysis. The difference is that for each subject within the hold-out dataset, we searched for the most similar subject within the primary dataset and used that subject as the matched subject. The significance of the similarity index and the “similar brain, similar personality” hypothesis was evaluated in the same way.

2.8. Item-by-item predictions based on the global personality network

Unlike previous studies which predicted sum scores based on the functional connectome (Finn et al., 2015; Rosenberg et al., 2015; Xilin Shen et al., 2017), we investigated the possibility to predict subjects' response to each item of the questionnaire. The idea underlying this item-by-item prediction is similar to a recent study that used subjects' functional connectivity patterns during rest to predict individual differences in brain responses in a set of cognitive tasks (Tavor et al., 2016). In that study, to avoid fitting predictive models for each voxel (there will be more than 100000 voxels in total), Tavor and colleagues used group ICA to break down the cortex into 50 non-overlapping regions of interests. Thereafter, they used the general linear model to fit connectivity features to activation data within each of these 50 parcels. In our study, we regarded each item of the NEO-FFI as the “parcel” to be predicted. Different from the activation data, which is a continuous variable, subjects' response to the item are ranked variables (range from 0 to 4). Therefore, the standard multi-class one-vs-the-rest classification was performed using a logistic regression classifier with L1 regression regularization, as instantiated in the *scikit-learn* (http://scikit-learn.org/stable/modules/linear_model.html#logistic-regression). Specifically, for each item of the NEO-FFI, we trained the item-specific predictive model to predict the item-level rating based on the connectivity strengths within the global personality network. To check for the generalizability of the predictive models, all of the aforementioned steps were performed using two validation methods: repeated family-based 10-fold cross-validation and independent test of the hold-out dataset.

2.8.1. Prediction validated by cross-validation

For training, the predictive model was based on the relationship between the connectivity features within the personality network and subjects' responses within the training sample (9/10 of the families). The classification models were used to predict the rating of the participants from the testing sample for a specific item. This prediction was repeated for each item of the NEO-FFI (total $N = 60$) and each subject. In this way, each subject's personality profiles can be predicted based on his/her connectivity pattern.

We calculated the classification accuracy by investigating whether our models can predict the subjects' item-wise responses above chance level. Furthermore, we used a similar method adopted in the brain activation prediction literature (Tavor et al., 2016) to evaluate our overall predictive performances for the personality item. Similarly, we hypothesize that our models' prediction for subjects' personality profiles is more similar to the subject's own personality profiles than to other subjects' personality profiles. To test this hypothesis, we calculated the average similarity index between the subject's measured and his or her own predicted personality profiles for all for testing subjects (“correlation with self”). For each cross-validation iteration, each subject's predicted personality profiles will be randomly matched to another subject's (“correlation with others”) measured personality profiles for 1000 times, and the two mean similarity indices (“self” vs. “others”) were computed. The computation was repeated for each iteration (total number of iterations = 100), and we tested if the “correlation with self” is significantly higher than the “correlation with others” using the paired *t*-test.

2.8.2. Prediction validated by the hold-out dataset

Item-specific predictive models were trained within the primary dataset. Without any further model fitting, models were applied to predict the item-level response of the participants from the hold-out dataset. (Fig. 5a). We also evaluated the predictive performance using both the classification accuracy and similarity index. Since we do not have different iteration for the hold-out dataset, the significance of the similarity index was accessed by compared the similarity index (“correlation with self”) with the null distribution (permutation = 5000 times) of similarity indices (“correlation with others”).

2.9. Control analysis

In addition to our primary analyses, we performed several control analyses to assess (1) test-retest reliability, and the effect of (2) different numbers of ICA components used for parcellation, (3) different statistical thresholds used to identify significant connections, (4) shorter time courses (estimate the functional connectome using 75 (1 min), 150 (2 min), 300 (4 min), and 600 (8 min) scans), (5) removal of potential confounds (e.g. gender, age, IQ, head motion and so on). These controls are essential steps, because we had to make several arbitrary choices during the connectome construction and the following feature selection (e.g., different numbers of ICA components, threshold).

2.9.1. Test-retest reliability

Since the rs-fMRI data within the HCP was acquired over two consecutive days, it gives us a unique opportunity to evaluate test-retest reliability. According to a previous HCP study, the individual functional connectomes estimated from day1 and day2 fMRI data are highly stable and consistent (Finn et al., 2015). Therefore, we hypothesized that the identified global personality network and our primary results would be reproducible when day1 and day2 fMRI data are analyzed separately. We estimated three kinds of subject-level whole-brain functional connectome using the first 2400 time points (day1), last 2400 time points (day2), and all 4800 time points (day1-day2 combined) and included them into the same identification and prediction pipeline.

2.9.2. Effect of number of ICA components

To rule out the possibility that our result is highly dependent on the 300-ICA components-based network matrix generation, we further estimated the 200 and 100 ICA components-based network matrix for each subject and inputted them into our identification and prediction pipeline. The secondary purpose of this step is that we can statistically evaluate if the identification and prediction performance will be worse if the network matrix contains fewer nodes. Because the network with more nodes will demand more computational resources, the results can provide useful information on how to choose a reasonable number of nodes to balance the algorithm's performance and computational load.

2.9.3. Different statistical thresholds to select the connections for the global personality network

Theoretically, all of the connections within the whole brain functional connectome can be used as features in the identification and prediction analysis. However, to further reduce the computational load and exclude the features that do not contain personality information, we ran a feature selection before identification and prediction. The chosen threshold (uncorrected $p = 0.001$) was arbitrary and could potentially affect the following analyses. Therefore, we used three more thresholds (uncorrected $p = 0.01$, uncorrected $p = 0.05$, FDR-corrected $p = 0.05$) to perform feature selection and investigated how the different thresholds affect the identification and prediction analyses.

2.9.4. Effect of shorter time course

One of the advantages of HCP rs-fMRI dataset is that there are a total of 4800 time points acquired for each subject, allowing the accurate

estimation of individual human connectome. However, most of the published rs-fMRI studies only used 200–400 time points and acquiring 4800 time points is a rather high burden for the participant and demanding for the scanning facility. Therefore, in order to investigate whether our proposed analysis pipeline is also useful for the conventional rs-fMRI datasets with shorter time course, we estimated four connectomes using 75 time points (1m), 150 time points (2 ms), 300 time points (4 ms), 600 time points (8 ms) separately and tried to (1) evaluate the stability of global personality networks and (2) identify pairs of subjects and predict item responses based on these “short” connectome.

2.9.5. Effect of removal of potential confounds

There are several demographic (gender, age), behavioral (IQ) and data related (head motion, multiband reconstruction algorithm) variables that could affect the connectivity-personality relationship (Dubois et al., 2018). To investigate if our methods can extract the personality information except for these potential confounds, we used a multiple linear regression to regress these variables from each of the personality score and each personality item and remove their confounding effects. The variables we regressed out are following: Gender (*Gender*), Age Group (*Age*), IQ (*PMAT24_A_CR*), brain size (*FS_BrainSeg_Vol*), head motion (we computed the mean of framewise displacement across all the rfMRI runs), multiband reconstruction algorithm (*fMRI_3T_ReconVrs*). More specifically, we performed the multiple linear regression to remove the variance shared with the listed cofounds only within the training data (in each 10-fold cross-validation), and the model was applied to the training data and left-out test subject. The underlying reasoning is to avoid that the model sees any left-out test subject before the final prediction. We repeated all of our network identification steps and primary analysis using the regressed out personality data to see if the proposed methods can still extract personality information from the connectome. It is important to note that we had to use the linear regression model instead of the multinomial logistic regression to predict the responses after the removal of potential confounds at the item level, because item responses have been transformed from rank variables to continuous variables after the removal.

2.10. Data and code availability

All the neuroimaging data used in this study (S900 extensively processed 3T rfMRI data, S1200 extensively processed 3T rfMRI data) are available to download from the Human Connectome Project website. All the behavioral data except for the restricted family structure data can be downloaded from the HCP website. Matlab and Python scripts were written to perform the analyses described; this code is available from the authors upon request and will be released via the personal GitHub as soon as possible. All the machine learning modules within the analyses (e.g. leave-one-out cross validation) were achieved via the scikit-learn library (0.18) (Pedregosa et al., 2011).

3. Results

3.1. Comparisons between the primary and hold-out dataset

Initially, we compared sex, age, total scores on each personality dimension between the primary ($N=801$) and hold-out dataset ($N=183$). The primary dataset has significantly higher number of women (55.3%) than the hold-out dataset (44.26%) ($\chi^2=9.02$, $p=0.002$). The two dataset, however, do not differ in the distribution of age group ($\chi^2=3.21$, $p=0.36$), neuroticism ($t=-1.4$, $p=0.15$), extraversion ($t=0.38$, $p=0.69$), agreeableness ($t=0.99$, $p=0.31$), openness ($t=-0.84$, $p=0.40$), or conscientiousness ($t=1.58$, $p=0.11$).

3.2. Identification of the global personality network

To identify connections related to personality dimensions, we correlated all the connectivity strength values within the whole-brain functional connectome with each of the sum scores of personality dimensions and retained the connections which showed a significant correlation ($p < 0.001$). We identified the connections that correlated with different personality dimensions during all iteration, and thus identified five personality factor specific networks (**Agreeableness Network**: $N_{\text{positive}}=254$ (0.005% of total edges), $r_{\text{positive}}=0.139$, $r^2_{\text{positive}}=0.019$; $N_{\text{negative}}=274$ (0.006% of total edges), $r_{\text{negative}}=-0.139$, $r^2_{\text{negative}}=0.019$; **Openness Network**: $N_{\text{positive}}=49$ (0.001% of total edges), $r_{\text{positive}}=0.141$, $r^2_{\text{positive}}=0.019$; $N_{\text{negative}}=39$ (0.0008% of total edges), $r_{\text{negative}}=-0.139$, $r^2_{\text{negative}}=0.019$; **Conscientiousness Network**: $N_{\text{positive}}=57$ (0.001% of total edges), $r_{\text{positive}}=0.134$, $r^2_{\text{positive}}=0.018$; $N_{\text{negative}}=83$ (0.001% of total edges), $r_{\text{negative}}=-0.135$, $r^2_{\text{negative}}=0.018$; **Neuroticism Network**: $N_{\text{positive}}=16$ (0.0003% of total edges), $r_{\text{positive}}=0.130$, $r^2_{\text{positive}}=0.016$; $N_{\text{negative}}=15$ (0.0003% of total edges), $r_{\text{negative}}=-0.131$, $r^2_{\text{negative}}=0.017$; **Extraversion Network**: $N_{\text{positive}}=36$ (0.0008% of total edges), $r_{\text{positive}}=0.136$, $r^2_{\text{positive}}=0.018$; $N_{\text{negative}}=17$ (0.003% of total edges), $r_{\text{negative}}=-0.134$, $r^2_{\text{negative}}=0.017$) (Fig. 2a–e). These networks separated from each other spatially (only 0.006% connections associated with more than 1 factor, Fig. 2b) and the number of the significant connections within each network varied substantially ($N_{\text{Agreeableness}}=528$; $N_{\text{Openness}}=88$; $N_{\text{Conscientiousness}}=140$; $N_{\text{Neuroticism}}=31$; $N_{\text{Extraversion}}=53$). To facilitate understanding of the anatomical substrates of the each network and to generate an easily interpreted visualization, we used a network measure (degree) to identify regions that are within the top five number of significant connections within each factor specific network (Fig. 2f–j).

To obtain a general description of personality-related connections based on all five personality dimensions at once, we performed the correlational analysis across all of the participants within the primary dataset. We found 1613 connections (**0.03% of total edges**) significantly associated with at least one personality dimension. The identified connections are highly stable across the 365 iterations (during each iteration, one family was left out): 79.6% of the connections were consistently correlate with personality measures during more than 95% of iterations. We combined all connections that were at least associated with one personality factor during each iterations into a global personality network which included 835 connections (**0.01% of total edges**) linking 265 brain regions (88% of the 300 regions). The global personality network will be used for the following intersubject similarity analysis and item-wise prediction analysis.

3.3. Validation of the intersubject similarity analysis via heritability estimation

We computed the similarity index and heritability of the whole-brain functional connectome, personality profiles, and global personality network, for the 92 monozygotic [MZ] and 49 dizygotic [DZ] twin pairs respectively. The similarity index for the whole-brain functional connectome was higher ($t=8.568$, $p=1.79 \times 10^{-14}$) in MZ twins (mean=0.746, SD=0.051) than in DZ twins (mean=0.656, SD=0.071) (Fig. 3a), indicating significant heritability ($h^2=0.180$). The heritability of the entire personality profile is also verified by similarity analyses (MZ=0.579(SD=0.167), DZ=0.454(SD=0.158), $p=3.67 \times 10^{-5}$, $h^2=0.249$) (Fig. 3b). We performed the heritability estimation for different personality dimensions separately and found significant heritability for Openness ($p=0.03$, $h^2=0.196$), Conscientiousness ($p=0.04$, $h^2=0.22$), Neuroticism ($p=0.06$, $h^2=0.20$), but not for Agreeableness ($p=0.24$, $h^2=0.10$), Extraversion ($p=0.51$, $h^2=0.06$) (Fig. 3c). Importantly, we found the connectivity basis of personality traits (global personality network) is significantly heritable

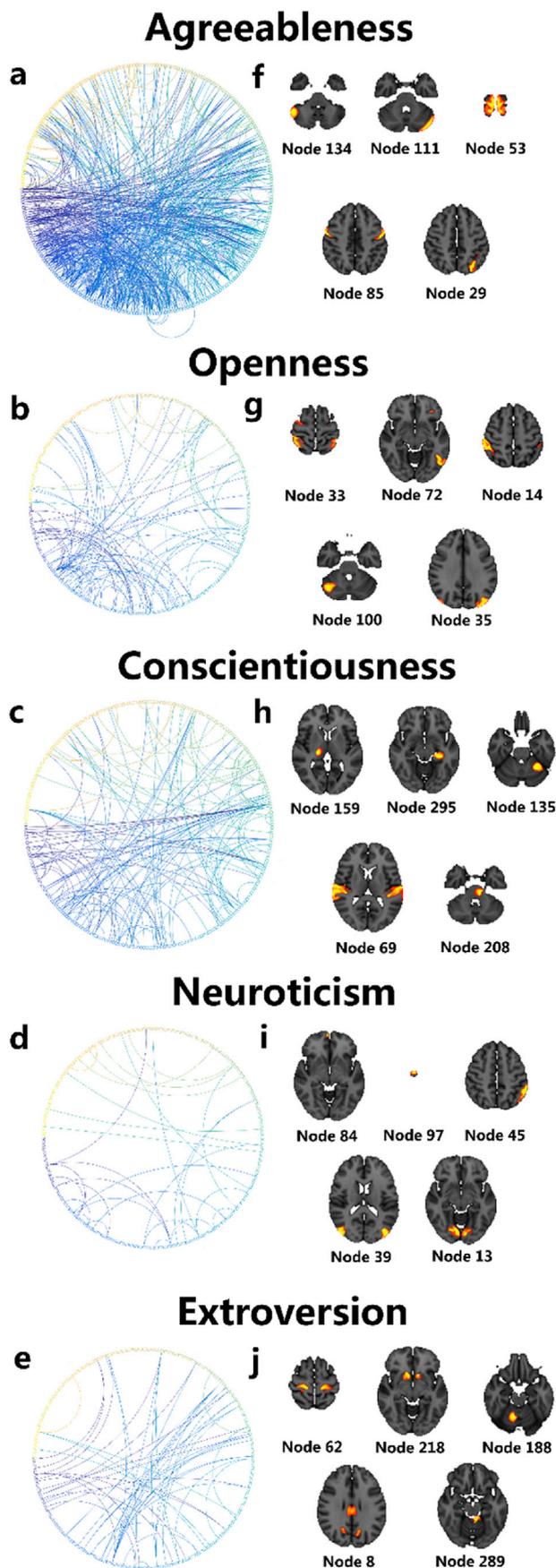


Fig. 2. (a)–(e) Pattern of brain connections associated with five different personality factors. (f)–(j) Network hubs with the top 5 significant personality-associated connections were identified within each factor specific network.

(MZ = 0.717 (SD = 0.113), DZ = 0.599 (SD = 0.167), $p = 2.16 \times 10^{-6}$, $h^2 = 0.236$) (Fig. 3d).

3.4. Intersubject network similarity analysis identified subjects who are similar in personality

Based on our “similar brain, similar personality” hypothesis, we reasoned that subject pairs with similar global personality networks should also have similar personality profiles. We used the intersubject similarity analysis to identify the subject pairs with similar functional connectivity pattern. Here, we report results from two complementary validation methods.

3.4.1. Results from cross-validation

Using the family-based repeated 10-fold cross-validation, we found that personality similarity index between the “to-be-predicted” and matched participant are significantly higher than randomly matched participant pairs (on average $r = 0.375$, $SD = 0.02$ for 100 iterations, $p = 0.0192$, 5000 permutation tests). The average person r value between the connectome similarity and personality similarity for all the iterations is significantly higher than zero ($t = 10.62$, $p = 4.08 \times 10^{-18}$).

3.4.2. Results from hold-out dataset

We identified the global personality network within the primary dataset and applied the same intersubject network similarity analysis in the hold-out dataset (Fig. 4a). On average, we found that personality similarity index between participants from the hold-out dataset and matched participant from the primary dataset are significantly higher than the randomly matched participant pairs ($r = 0.373$, $p = 0.03$, 5000 permutation tests) (Fig. 4b). Similarly, there is a statistical trend towards positive correlation between the connectome similarity and personality similarity that just failed to reach the significant threshold set ($r = 0.141$, $p = 0.055$, $N = 183$) (Fig. 4c).

3.5. Global personality network predicts participants’ personality item-by-item

We aimed at exploring whether individually specific functional connectivity patterns of the personality network can be used to predict individual answers on the FFM personality questionnaire in yet unseen participants.

3.5.1. Results from cross-validation

We evaluated the overall performance of the classification models across the 60 items. During the repeated ($N = 10$) family-based 10-fold cross-validation, the classifiers performed above chance in predicting single participant’s item-level responses in the FFM inventory (mean classifier accuracy = 39.5%; chance level = 20%, $p < 0.001$). Second, we evaluated the performance of the classification models by comparing the measured personality profiles and predicted personality profiles. The “correlation with self” index (mean $r = 0.471$, $SD = 0.016$ for 100 iterations) was significantly higher than the “correlation with others” index (paired t -test, $t = 9.83$, $p = 2.4 \times 10^{-16}$). It indicates that the predicted personality profile is more similar to the subject’s own measured personality than to other subjects’ measured personality.

3.5.2. Results from hold-out dataset

To further investigate of the generalizability, we derived the predictive models from the primary dataset and directly applied them to the hold-out dataset (Fig. 5a). On average, these classifiers performed above chance level in predicting of item-wise responses (classifier accuracy = 42.35%; chance level = 20%, $p < 0.001$) (Fig. 5b). Across all the 183 hold-out participants, on average, the classifiers predicted the personality profile was more similar to the participant’s own measured personality profile than to other participants’ personality profiles (mean $r = 0.487$, $p < 0.001$, 5000 permutation tests) (Fig. 5c).

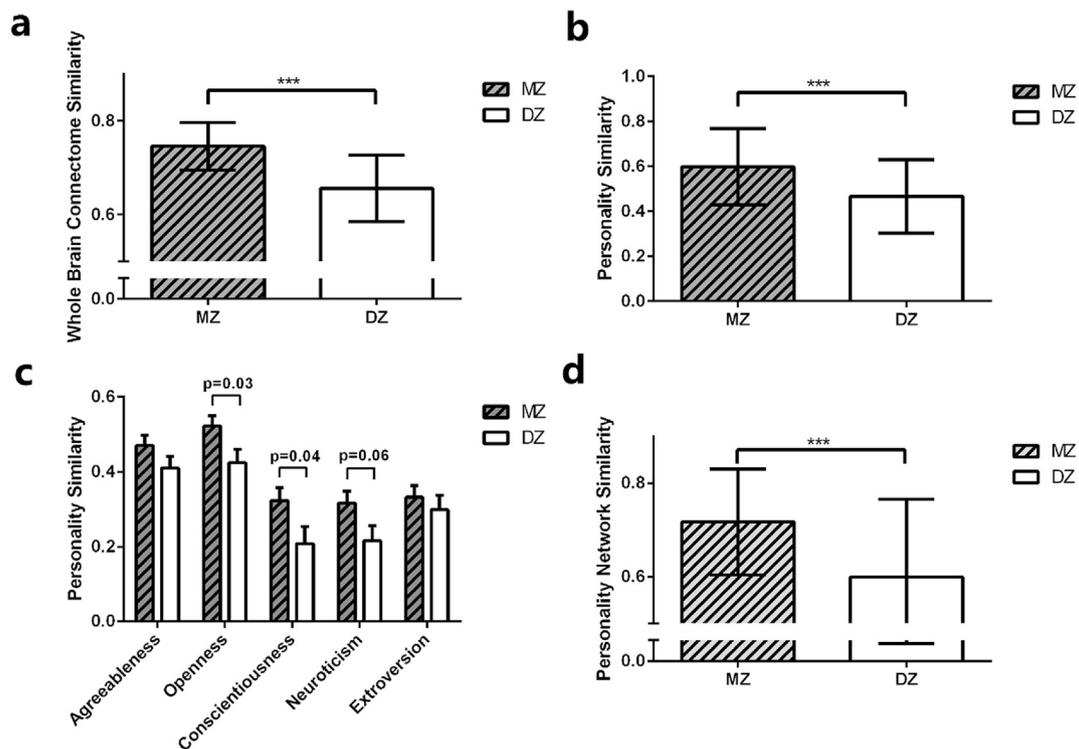


Fig. 3. Heritability estimation of the brain and personality measures. (a) Similarity index for the whole brain functional connectome was significantly higher in MZ twins than in DZ twins. (b) Similarity index for the personality profiles was significantly higher in MZ twins than in DZ twins. (c) Similarity index for the Openness, Conscientiousness, and Neuroticism, but not Agreeableness or Extraversion was significantly higher in MZ twins than in DZ twins (d) Similarity index for the global personality network was significantly higher in MZ twins than in DZ twins. MZ = Monozygotic; DZ = Dizygotic.

3.6. Results from control analyses

We performed several control analyses to assess (1) test-retest reliability, the effect of (2) different numbers of ICA components used for parcellation, (3) different statistical thresholds used to identify significant connections, (4) shorter time courses of fMRI data acquisition (estimate the functional connectome based on 75 (1 min), 150 (2 min), 300 (4 min), and 600 (8 min) number of scans separately), (5) removal of potential confounds (e.g. sex, age, IQ, head motion and so on). Control analyses showed that the identification of the global personality network were stable and reproducible. Our identification/prediction results do not depend on choices we made in the analysis pipeline as well as when controlling for confounding variables such as age, sex, IQ and head motion.

3.6.1. Test-retest reliability

To estimate the test-retest reliability of the identified global personality network, we identified the network using only the day1 or day2 connectome and overlapped them with the network identified by the primary analysis. Most of the personality-related connections (day1: 341/443 (76.9%); day2: 413/582 (70.9%)) were reported both in the primary analysis and the test-retest analysis.

For the similarity-based identification analysis, day1 and day2 connectome yielded results similar to our primary analysis (day1 $r = 0.379$, day2 $r = 0.377$, combined $r = 0.373$) (Fig. 6a). For the item prediction analysis, when we analyzed the functional connectome estimated from the day 1 and day 2 data separately, the predictive performance did not differ from our primary results (day1 $r = 0.510$, day2 $r = 0.507$, combined $r = 0.513$) (Fig. 6b).

3.6.2. Effect of number of ICA components

Using different parcellation solutions to estimate the functional

connectome also had no significant effect on the similarity calculated from the similarity-based identification analysis ($K = 100$, $r = 0.372$; $K = 200$, $r = 0.376$, $K = 300$, $r = 0.373$) (Fig. 6c). The predictive performance also did not depend on the different parcellation solutions used to construct the connectome ($K = 100$, $r = 0.477$; $K = 200$, $r = 0.474$, $K = 300$, $r = 0.471$) (Fig. 6d).

3.6.3. Different statistical thresholds to select the connections for the global personality network

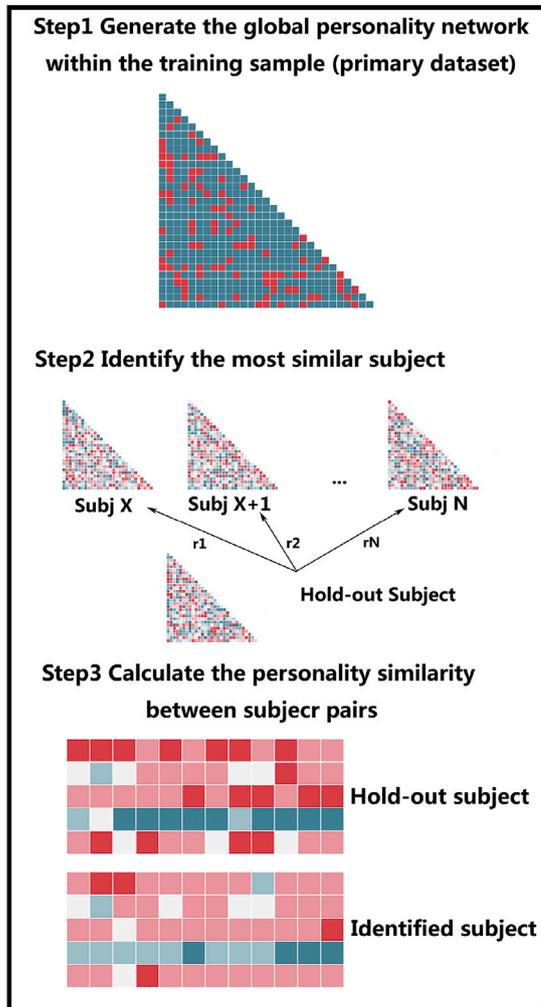
Four different statistical thresholds were used to select the connections that identified pairs of subjects with more similar personality than the randomly matched pairs (u.c. $p = 0.05$: $r = 0.375$, u.c. $p = 0.01$: $r = 0.375$, u.c. $p = 0.001$: $r = 0.373$, FDR $p = 0.05$: $r = 0.367$) (Fig. 6e). However, compared to the uncorrected global personality network ($p = 0.001$), the FDR-thresholded global personality network is less accurate in identifying the pairs of subjects with similar personality ($t = -2.12$, $p = 0.035$). We did not find a significant effect of threshold on predictive performance: (uncorr $p = 0.05$: $r = 0.471$, uncorr $p = 0.01$: $r = 0.472$, uncorr $p = 0.001$: $r = 0.471$, FDR $q = 0.05$: $r = 0.473$) (Fig. 6f).

3.6.4. Effect of shorter time course

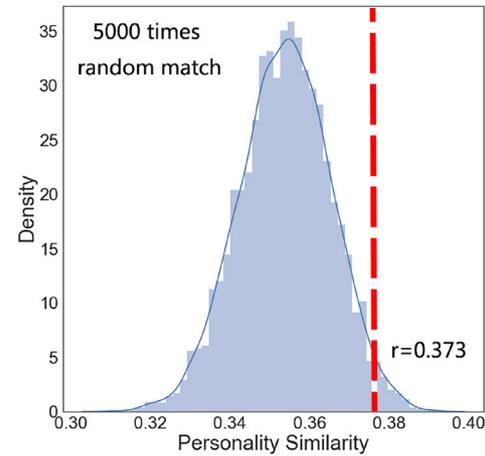
First, we investigated the effect of a shorter time course on our ability to identify the global personality network. We found that longer time series improve the ability to identify the personality-related connections that overlapped with the network reported in the primary analysis (1 min: 20/98 (20.4% overlap with primary result using complete 2 h data set); 2 min: 35/156 (22.4%); 4 min: 106/298 (35.5%); 8 min: 93/210 (44.2%); 60 min: 341/443 (76.9%))

As expected, longer time series also improved the ability to identify more similar subjects in terms of personality (1 min, $r = 0.356$; 2 min, $r = 0.366$, 4 min, $r = 0.369$, 8 min, $r = 0.370$; 60 min, $r = 0.379$; 120 min = 4800, $r = 0.373$) (Fig. 6g). Already rs-fMRI time series with

a. Intersubject network similarity analysis



b. Significant Testing



c. Correlational Analysis

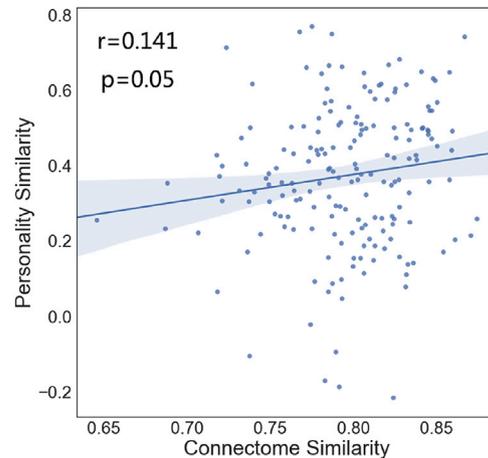


Fig. 4. Schematic of the intersubject network similarity analysis and results. (a) Given the global personality network generated from the training sample (primary dataset), we computed the correlations between the hold-out subject's connectivity matrix and all the connectivity matrices in the primary dataset. The identified subject is the one with the highest correlation value. Finally, we computed the personality similarity between the hold-out subject and the identified subject. (b) Distribution of the similarity index calculated by the 5000 times random match. The intersubject network similarity-based match generated the subject pairs ($r = 0.373$) with significant more similar personality than the random match. (c) Relationship between the network similarity and personality similarity. Intersubject connectome similarity positively correlated with personality similarity across the identified subject pairs.

300 time points (around 4 min of scanning), but not 75 time points were long enough to construct the functional connectome with significant personality information. Similar to the identification analysis, longer rs-fMRI scanning time brings benefits to predictive modelling (1 min, $r = 0.444$; 2 min, $r = 0.441$; 4 min, $r = 0.445$; 8 min, $r = 0.450$; 60 min, $r = 0.462$; 120 min, $r = 0.471$) (Fig. 6h).

3.6.5. Effect of removal of potential confounds

We directly compared the identified global personality network with and without removal of potential confounds. After removal, a large proportion of significant connections (246/266 (92.4%)) was identical within the primary analysis.

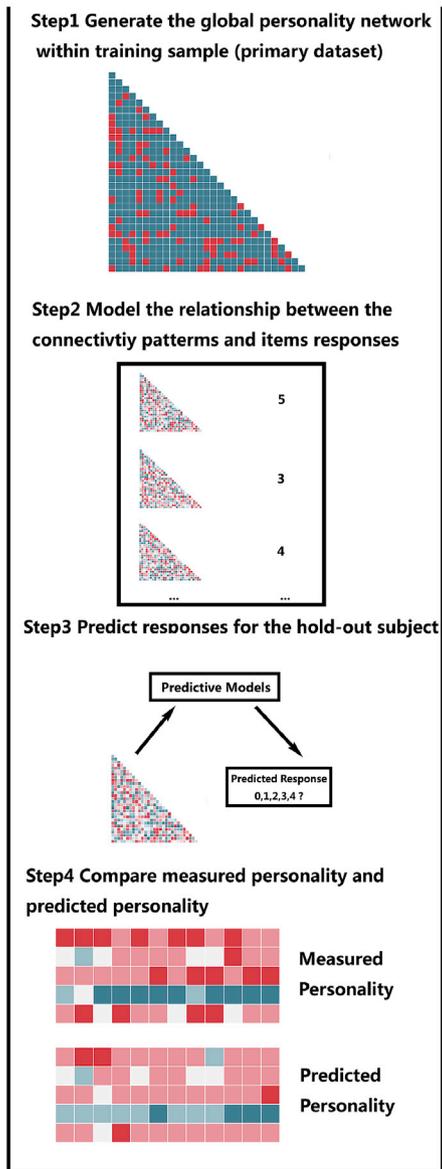
After regressing out potential confounds (sex, age, IQ, brain size, head motion, reconstruction method), compared to the random match, identification analysis does identify the subjects with higher personality similarity ($r = 0.019$, $p = 0.008$, 5000 permutation tests). Also, the predictive models can still generate predicted personality that was more similar to the subject's own measured personality than to other subjects' personality ($r = 0.038$, $p < 0.001$, 5000 permutation tests).

4. Discussion

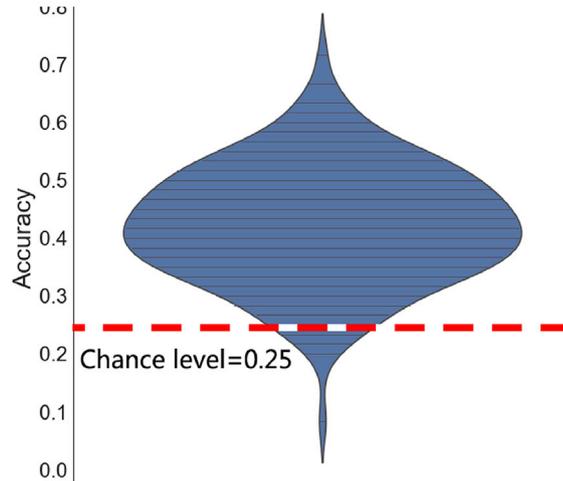
In this study, we identified a network of brain areas whose activity is temporally correlated and that is associated with personality (global personality network). This heritable global personality network involved connections between a large number of brain regions. The intersubject network similarity analysis identified subject pairs with more similar personality profiles than a random match from all subjects. Moreover, the personality network enabled us to predict responses to individual items within the personality inventory in unseen subjects. Instead of using the classical method of correlating local characteristics of brain regions/circuits with behavioral measures, we adopted recently developed connectome analyses to map the relationship between individually specific, functional connectivity patterns and individual differences in behaviors (Beaty et al., 2018; Finn et al., 2015; Rosenberg et al., 2015). Taken together, our findings suggest that personality is represented in distributed brain networks and people with similar brain connectivity patterns have similar personality profiles.

Studies used a variety of neuroimaging methods to associate

a. Itemwise prediction analysis



b. Distribution of accuracies



c. Distribution of similarities

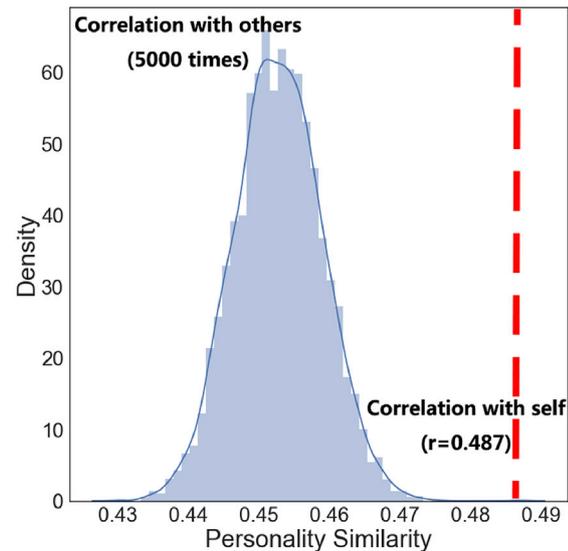


Fig. 5. Schematic of item-wise prediction analysis and results. (a) After computed the global personality network within the training sample (primary dataset), we modeled the relationship between the brain connectivity patterns and item responses for each item within the FFM personality measure. Then the hold-out subject's responses to each item were predicted by the models. Finally, we evaluated the predictive performance by comparing the measured personality and the predicted personality profiles. (b) The mean accuracy of itemwise prediction is significantly higher than the chance level (0.25). (c) Permutation test indicates that the predicted personality profile is more similar to the subject's own measured personality than to other subjects' measured personality. FFM=Five-Factor Model.

personality with local structural (e.g. volume or thickness) or functional (e.g. brain activation during tasks) brain characteristics (Canli et al., 2002; Cremers et al., 2011; DeYoung et al., 2010; Gou et al., 2014; Kapogiannis et al., 2013; Riccelli et al., 2017; Schultz and Cole, 2016; Servaas et al., 2014). However, personality, unlike some aspects of cognition that have been more or less localized to specific brain regions, is thought to be the result of an interaction that engages the entire brain. Results from the current study provide further support of this idea. The identified global personality network contains only a small fraction of all possible connections between parcellated brain regions (835 connections, 0.018% of the total 44850 connections), but these connections are spatially widespread across almost the entire brain (265 brain regions, 88.3% of the total 300 regions). Compared to studies using the same method to identify cognition-related networks (e.g., attention, reasoning, and creativity) (Beatty et al., 2016; Finn et al., 2015; Rosenberg et al.,

2015), the global personality network is more widespread and anatomically less restricted to one or more of the canonical functional networks (e.g. default mode network).

Since personality psychology has already suggested that the different factors within the five-factor model (FFM) of personality are independent of each other (Costa et al., 1991; Digman, 1990; McRae and John, 1992), the reasonable hypothesis would be that brain correlates of different personality factors would be anatomically separable. Here, almost all of the brain connections are solely associated with one personality factor, and only about 0.006% of the significant connections are associated with more than one personality factor. This result may suggest that different personality factors, as distinct psychological concepts, are represented by non-overlapping functional brain networks. Another noteworthy finding concerning the factor specific networks is that the number of connections within each network varied substantially (from $N_{\text{Neuroticism}} = 31$ to N

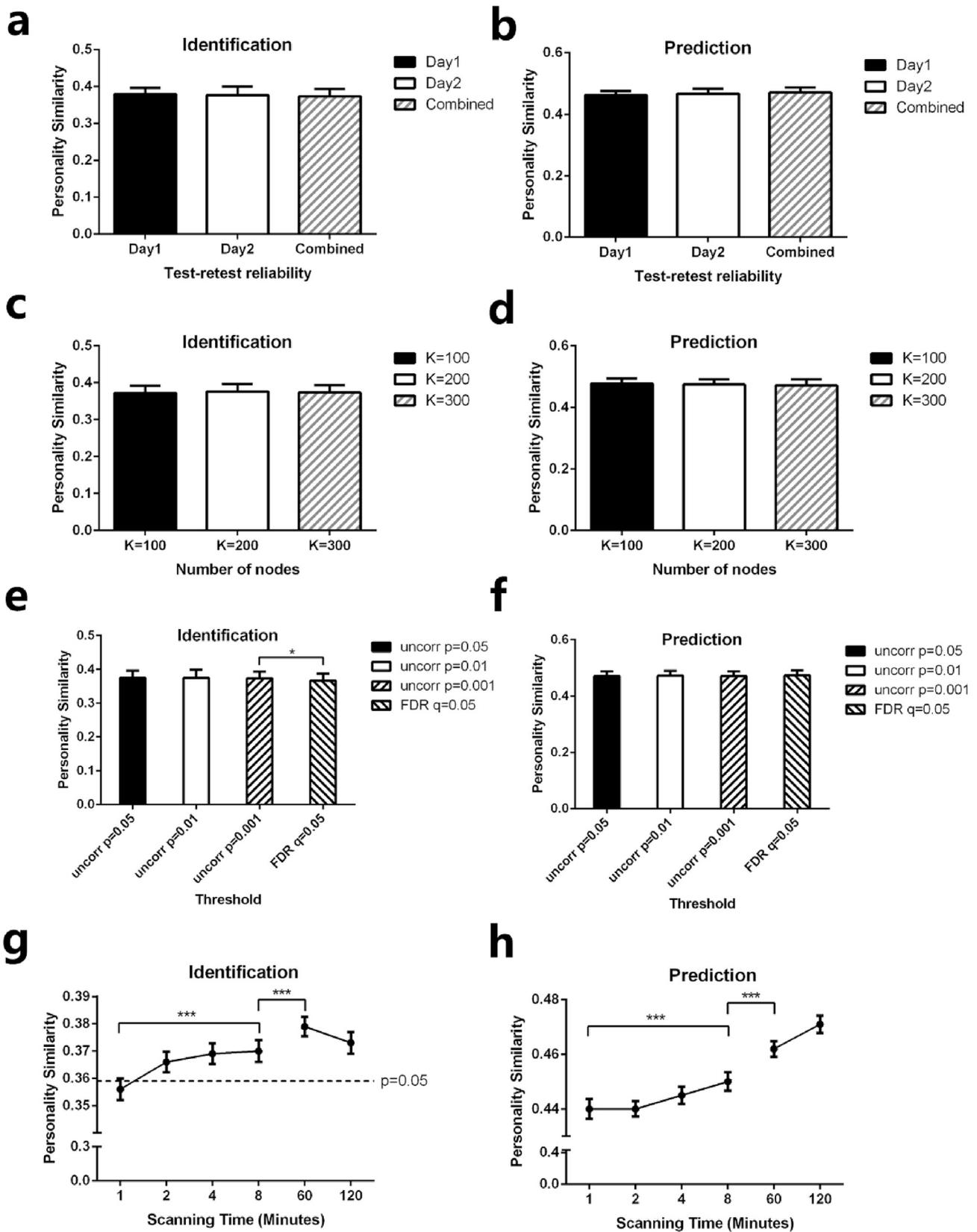


Fig. 6. Control analyses on the factors that potentially affect our primary results. (a) AND (b) The test-retest reliability of the analyses. Our results can be replicated by using the day1 and day2 rs-fMRI data separately. (c) AND (d) The effect of number of brain regions within the parcellation. The number of brain regions have no effect on our identification and predictive analysis. (e) AND (f) The effect of threshold to select significant links. The statistical threshold has no effect on the prediction analysis, but identification analysis using strict threshold (FDR correction) lower the similarity. (g) AND (h) The effect of the scanning length. The functional connectome estimated from the longer time series can be used to better identify personality similar subject pairs and predict item responses.

Agreeableness = 528). Thus, some personality factors appear more locally represented (e.g., Neuroticism), whereas others are supported by a more widespread connectivity pattern between a larger set of brain regions (e.g., Agreeableness). These results are not surprising since previous literature adopting conventional localization methods reported significant brain associations of Neuroticism, but not Agreeableness (Kunisato et al., 2011; Liu et al., 2013; Wei et al., 2014).

Due to the nature of our analysis, we used a network measure (degree) to identify the most-connected regions (network hubs) to achieve better visualization. Some network hubs correspond to brain areas that were previously reported to be associated with the five-factor model of personality. For example, previous literature on the brain correlates of these traits usually reported the association with sub-regions of the prefrontal cortex including the orbitofrontal cortex, lateral prefrontal cortex, and middle frontal gyrus (Cremers et al., 2011, 2010; DeYoung et al., 2010; Kunisato et al., 2011; Lu et al., 2014; Suslow et al., 2010). Additionally, because we adopted a data-driven method to identify personality related connections, it revealed several brain regions potentially related to personality (e.g., visual cortex and cerebellum), for which little evidence has been found on how they are associated with personality.

Before we used the intersubject similarity analysis to perform the identification, we validated our analysis pipelines by demonstrating that both brain connectivity patterns and personality profiles were more similar between MZ pairs compared to the DZ pairs. We further demonstrated that not only large-scale brain network and personality are heritable, but also the network connections that associate with personality appear genetically determined. The heritability of human personality traits is well established (Balestri et al., 2014; Dochtermann et al., 2014; Jang et al., 1996; Tellegen et al., 1988). We replicated this finding using the intersubject similarity analysis to compute the personality similarity index based on subjects' item-level responses. Interestingly, we estimated the heritability of each personality trait separately using the same intersubject similarity analysis and found that neuroticism is more genetically-driven than factors like Agreeableness and Extraversion. These results are similar to recent heritability estimates of the Big Five personality traits based on common genetic variants (Power and Pluess, 2015). Different heritability may explain why specific personality dimensions have a more localized effect on the brain. The personality dimensions with higher heritability (e.g., Neuroticism) may have a stronger biological basis (brain connections in the current study), and thus a smaller set of connections with significant personality information, which can be more readily identified. In contrast, other dimensions (e.g., Agreeableness) that are more environmentally or socially determined are the consequence of complex human behaviors that are associated with a larger and potentially more variable set of brain circuits.

There are several kinds of frameworks that are capable of predicting individual differences in traits and behavior using brain measures derived from human neuroimaging data: multivariate-prediction method used by the HCP Netmats MegaTrawl, support vector regression (SVR) (Harris et al., 1996) and connectome-based predictive modelling (CPM) (Shen et al., 2017). Our intersubject network similarity approach provided an intuitive alternative to predict behaviors from brain connectivity patterns. By identifying the participant(s) with the connectivity pattern most similar to the participant to be predicted, we can make quick inference about the participant to be predicted based on the behavioral profile(s) of participant(s) identified from the database. A similar method can be easily applied to the connectome constructed from other neuroimaging modalities (e.g. diffusion tensor imaging or structural imaging), and even pure behavioral/clinical data. Another finding is that the brain network similarity positively associated with personality similarity across identified participants' pairs. It suggests that the ability to make accurate behavioral predictions partly depends on our ability to identify participant(s) with highly similar brain connectivity pattern(s). So the method can largely benefit from the sample size of accessible datasets.

A variety of individual differences in cognition, behavior, and

personality have been predicted by machine learning techniques based on brain measures (Beatty et al., 2018; Cui et al., 2017; Dubois et al., 2018; Feng et al., 2018; Finn et al., 2015; Hsu et al., 2018; Rosenberg et al., 2015). Individual differences in most of these traits at issue can be represented by a single score, usually the average performance across all the trials during the related cognitive task. However, each item within the personality dimension can better represent subtle differences in behavioral tendencies and cognition than the total score (Chapman, 2007; Watson et al., 2007). The multi-sub-factor nature of the personality measure is one potential obstacle for the individual prediction. Participants with the same sum score may still have differences in their questionnaire responses and thus, connectivity patterns. Therefore, our approach moved beyond the prediction of sum scores to the prediction of responses to individual items. The idea behind is similar to the parcellation-by-parcellation prediction for task-related activity from resting-state connectivity data (Tavor et al., 2016). We treated each item of the personality questionnaire similar to a single parcel and predicted each response using item-wise predictive models. Our overall prediction accuracy was significantly higher than chance and the predicted personality profiles significantly correlated with the subject's measured personality profiles. This finding suggests that the subject-level individual connectivity pattern contains information on human personality and can more generally be used to perform detailed predictions of different human behaviors.

Our study has two limiting factors that should be mentioned. Firstly, we only used the inter-region (HCP ICA-based parcellation) functional connectivity strengths to predict personality and did not consider the individual difference in network topography. Interestingly, Kong and colleagues (Kong et al., 2018) demonstrated that individually-specific network topography predicts behavior (including personality) with an accuracy that is comparable to other studies using inter-node functional connectivity strength for behavioral prediction. Consequently, it is possible that our current prediction pipeline that did not consider individual-specific network topography is sub-optimal, and a combination of connectivity strength and network topography could further improve the accuracy of behavioral prediction. Second, in our study, the heritability of the functional connectivity was estimated by conventional heritability analyses. However, a recently established method (Ge et al., 2017), explicitly controls for within-subject fluctuations (e.g., measurement noise, different biological states) to make more accurate heritability estimations. Future studies aiming at accurate heritability estimation of brain connectivity may consider to adopt the repeated-design introduced by Ge and colleagues and improve the data quality further.

In total, we found two factors that quantitatively affected the performance of our identification or predictive algorithms. The first one was as expected the length of rs-fMRI data acquisition: the more data acquired the better the identification, and prediction. The most logical interpretation is that more time points can better capture individual characteristics of the connectome (Finn et al., 2015) and thus, they can be advantageous for extracting personality information. However, even though we found the significant increase in identification and prediction performance when we compared connectome constructed by 8 min and 60 min rs-fMRI data, future studies may carefully evaluate if the increase is worthwhile considering the additional investment and burden of long acquisition times needed. Furthermore, for the intersubject network similarity-based identification analysis, around 4 min (300 time points) scanning are enough to construct the connectome with the significant personality information. This finding suggests that our approach can be applied to the typical rs-fMRI dataset based on 8–10 min scanning, even considering the advanced scanner and data acquisition used by the HCP. Second, the statistical threshold used to select features can influence the intersubject similarity analysis but not the item-level predictive analysis. FDR-thresholded global personality network identified the pairs of subjects with similar personality significantly but less accurately.

In summary, we investigated the association between the functional connectome and the five-factor model (FFM) of personality in a large

sample of healthy individuals and validated the association in a subsample of hold-out participants. We have revealed that personality is correlated to widely distributed connectivity patterns at rest and each personality factor is associated with a spatially unique functional network in a stable way across individuals. Thus, people with similar brain connectivity patterns during rest have similar personality profiles. Moreover, the connectivity pattern can be used to predict an unseen subjects' detailed personality profile. Thus, in addition to pursuing classic questions related to the neural underpinnings of personality, a promising direction for future research will be to focus on how different functional brain systems work together to enable the individualization of personality or other complex social, cognitive, or affective constructs.

Acknowledgements

The authors would like to thank Dr. Koen V Haak and Dr. Zaixu Cui for helpful discussion. WL is funded by the PhD scholarship (201606990020) of the Chinese Scholarship Council.

Functional MRI and personality data were provided by the Human Connectome Project, WU-Minn Consortium (Principal Investigators: David Van Essen and Kamil Ugurbil; 1U54MH091657) funded by the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research; and by the McDonnell Center for Systems Neuroscience at Washington University.

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