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ABSTRACT

Extensive neuroimaging research has attempted to identify neural correlates and predictors of decision impulsivity. However, the nature and extent of decision impulsivity-brain association have varied substantially across studies, likely due to small sample sizes, limited image quality, different imaging measurement selections, and non-specific methodologies. The objective of this study was to develop a reliable predictive model of decision impulsivity-brain relationship in a large sample by applying connectome-based predictive modeling (CPM), a recently developed machine learning approach, to whole-brain functional connectivity data (“neural fingerprints”). For 809 healthy young participants from the Human Connectome Project, high-quality resting-state functional MRI data were utilized to construct brain functional connectome and delay discounting test was used to assess decision impulsivity. Then, CPM with leave-one-out cross-validation was conducted to predict individual decision impulsivity from whole-brain functional connectivity. We found that CPM successfully and reliably predicted the delay discounting scores in novel individuals. Moreover, different feature selection thresholds, parcellation strategies and cross-validation approaches did not significantly influence the prediction results. At the neural level, we observed that the decision impulsivity-associated functional networks included brain regions within default-mode, subcortical, somato-motor, dorsal attention, and visual systems, suggesting that decision impulsivity emerges from highly integrated connections involving multiple intrinsic networks. Our findings not only may expand existing knowledge regarding the neural mechanism of decision impulsivity, but also may present a workable route towards translation of brain imaging findings into real-world economic decision-making.

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1. Introduction

Impulsivity is defined as a tendency to engage in rash behaviors or as a behavior that occurs without careful deliberation (Hollander & Rosen, 2000). Accumulating evidence has suggested that substantial impulsivity is a common characteristic of psychiatric disorders such as drug abuse (Perkins & Freeman, 2018), pathological gambling (Wiehler & Peters, 2015), tobacco addiction (Green & Lawyer, 2014), and attention-deficit/hyperactivity disorder (ADHD) (Costa Dias et al., 2015). Decision impulsivity or intertemporal choice refers to a phenomenon that people on average have the tendency to favor the immediate smaller benefit rather than larger rewards in the future (Lv et al., 2019). One of the most commonly used neuropsychological measures of decision impulsivity is delay discounting task, also known as temporal discounting, which describes the undervaluing of rewards that are delayed in time (Green & Myerson, 2004), with greater delay discounting reflecting greater decision impulsivity. Therefore, the delay discounting test has provided a useful framework for investigating abnormal decision impulsivity and its neural basis in some clinical conditions, such as ADHD (Costa Dias et al., 2013, 2015), obesity (Kishinevsky et al., 2012; van der Laan, Barendse, Viergever, & Smeets, 2016), anorexia nervosa (Decker, Figner, & Steinglass, 2015; Wierenga et al., 2015), nicotine/cocaine/methamphetamine dependence (MacKillop et al., 2012; Meade, Lowen, MacLean, Key, & Lukas, 2011; Schwartz et al., 2010), and suicide attempts in late-life depression (Dombrovski et al., 2012).

Linking human behavior to brain structure and function is a central question in systems neuroscience. The unbiased assessment of brain structure and function with advanced neuroimaging techniques and novel analysis approaches has linked inter-individual variability in the brain to individualized human behavior and cognition (Kanai & Rees, 2011). As a consequence, extensive neuroimaging research has attempted to explore neural correlates of decision impulsivity in normal subjects. For examples, previous studies have found significant correlations between decision impulsivity and brain structure by using structural magnetic resonance imaging (MRI) to measure gray and white matter morphology (Bernhardt et al., 2014; Bjork, Momenan, & Hommer, 2009; Boes et al., 2009; Cho et al., 2013; Drobetz et al., 2014; Ho, Koeppel, & Barry, 2016; Mackey et al., 2017; Pehlivanova et al., 2018; Tschernegg et al., 2015; Wang et al., 2017; Yu, 2012) and using diffusion MRI to evaluate white matter integrity (Achterberg, Peper, van Duijvendoerde, Mandl, & Crone, 2016; Hampton, Alm, Venkatraman, Nugiel, & Olson, 2017; Han et al., 2018; Hanggi et al., 2016; Olson et al., 2009; Peper et al., 2013; van den Bos, Rodriguez, Schweitzer, & McClure, 2014). There are also a large number of studies identifying associations between decision impulsivity and brain function by using functional MRI (fMRI) to measure task-induced brain activation (Ballard & Knutson, 2009; Banich et al., 2013; Benningfield et al., 2014; de Water et al., 2017; Hariri et al., 2006; Ludwig et al., 2015; Luerssen, Gyurak, Ayduk, Wendelken, & Bunge, 2015; Luo, Ainslie, Pollini, Giragosian, & Monterosso, 2012; Simon et al., 2015; Wang et al., 2014; Weber & Huettel, 2008; Wittmann, Leland, &

Paulus, 2007), resting-state regional neural activity (Lv et al., 2019; Wang et al., 2017), functional connectivity (Anandakumar et al., 2018; Calluso, Tosoni, Pezzulo, Spadone, & Committeri, 2015; Han et al., 2013; Hanggi et al., 2016; Holmes et al., 2018; Li et al., 2013; van den Bos et al., 2014; van den Bos, Rodriguez, Schweitzer, & McClure, 2015; Wang et al., 2017) and functional networks (Chen, Guo, & Feng, 2017; Chen, Guo, Suo, & Feng, 2018; Chen, Hu, Chen, & Feng, 2019; Elton, Smith, Parrish, & Boettiger, 2017). However, these prior studies have yielded inconsistent findings with the exception of the prefrontal cortex and striatum. Moreover, existing literature has focused largely on establishing decision impulsivity-brain relationship in a correlative manner and placed less emphasis on decision impulsivity prediction using machine learning methods.

The integration of easily accessible brain imaging measures together with powerful machine learning approaches has provided a step toward individualized prediction of decision impulsivity (Chen, Guo, Zhang, & Feng, 2019; Li et al., 2013; Lv et al., 2019; Wang et al., 2016; Zha et al., 2019). However, the predictive ability has varied substantially across studies, which is likely due to limited statistical power from relatively small sample sizes, limited image quality, different neuroimaging measurement selections, and non-specific machine learning methodologies.

In the Human Connectome Project (HCP) dataset, delay discounting-measured decision impulsivity and high-quality resting-state fMRI data were publicly available for a large sample of healthy young adults (Van Essen et al., 2012, 2013). Among various neuroimaging measures, resting-state functional connectivity has been considered a unique “neural fingerprint” that can accurately identify specific subjects from a large group (Finn et al., 2015; Xu et al., 2016). With respect to methodology, connectome-based predictive modeling (CPM) is a recently developed machine learning approach for generating brain-behavior models from whole-brain functional connectivity profiles (Shen et al., 2017). Here, by applying CPM to the large-scale cohort HCP data, we aimed to examine whether decision impulsivity can be effectively and reliably predicted from an individual’s unique pattern of brain connectivity.

2. Materials and methods

2.1. Participants and resting-state fMRI data

812 participants were selected from the HCP “PTN” (Parcellation + Timeseries + Netmats) dataset (<http://www.humanconnectome.org>). These participants are healthy young adults within an age range of 22–37 years, which corresponds to a period after the completion of major neurodevelopment and before the onset of neurodegenerative changes (Van Essen et al., 2012). Each subject underwent four resting-state fMRI scans where subjects were instructed to keep their eyes open and move as little as possible (14.4 min per scans). Data from the 812 subjects were reconstructed using an improved version of the data reconstruction software (referred to as “recon2”). The four fMRI scans were concatenated into continuous time series consisting of 4800 time

points at a repetition time of .72 sec. The full details regarding the sample and data acquisition have been reported in prior publications (Van Essen et al., 2012, 2013). The HCP scanning protocol was approved by the Institutional Review Board of Washington University in St. Louis, MO, USA. Written informed consent was obtained from each participant.

2.2. fMRI data preprocessing and construction of functional connectome

All resting-state fMRI data were minimally-preprocessed with echo planar imaging gradient distortion correction, motion correction, field bias correction, spatial transformation and normalization into a common Montreal Neurological Institute space (Glasser et al., 2013), and artifact removal using independent component analysis (ICA) + FIX (Salimi-Khorshidi et al., 2014). For functional network connectivity analysis, network nodes can be defined by using existing atlases based on cytoarchitecture or anatomy. However, a potential pitfall in using such atlases is that the mean time series of a node may not represent any of the constituent time series if different functional areas are included within a single node (Shen, Tokoglu, Papademetris, & Constable, 2013). Therefore, group-level ICA was used here to define the whole-brain network nodes in a data-driven fashion, which are considered more functional homogeneous and may be better at capturing individual differences of real functional boundaries than those defined by existing atlases (Calhoun, Adali, Pearson, & Pekar, 2001). The group-level ICA parcellation was performed using FSL's MELODIC tool (Beckmann & Smith, 2004) and spatial-ICA was applied at several different dimensionalities (15, 25, 50, 100, 200, and 300). The dimensionality determines the number of ICA components; a higher number typically means that the significant areas within the spatial component maps will be smaller. Given that larger spatial components lack regional specificity, we used 100, 200 and 300 group-ICA components to define brain network nodes. That is, 200 components were used for the main analyses in light of their moderate spatial extent, and 100 and 300 components were used for the validation analyses. For each node, one representative time series was derived by mapping the corresponding ICA spatial map onto each participant's fMRI data using the standard "dual-regression stage-1" approach, in which the ICA map was used as a spatial regressor against the full time series data. This resulted in 200 nodes' time series that can be used to construct functional connectome at the individual level. Specifically, the partial temporal correlation coefficients between the time series of all possible pairs of nodes were computed, which estimates direct connection strengths better than achieved by Pearson's correlation. The resultant correlation values were converted into z statistics with Fisher's r-to-z transformation, resulting in a symmetric 200×200 connectivity matrix in which each element represents the strength of connection between two nodes (hereafter referred to as an edge).

2.3. Decision impulsivity assessment

Decision impulsivity was assessed using the delay discounting measure, the schematic representation of which is shown in Fig. 1. A detailed description of the delay discounting

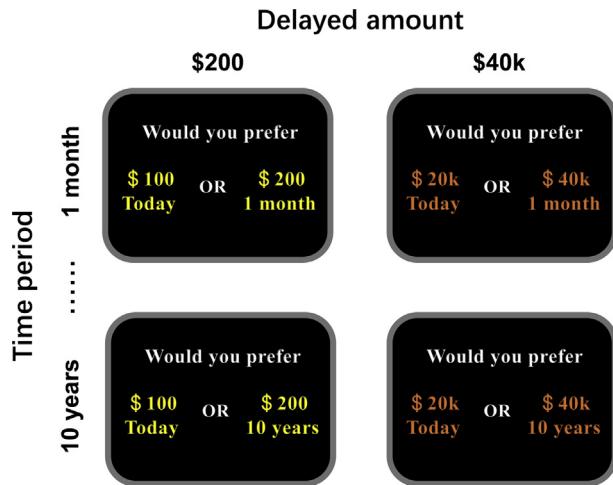


Fig. 1 – Schematic representation of the delay discounting design.

measure can be found in HCP_S500_Release_Reference_Manual.pdf on the HCP website. In brief, participants are presented with two choices on each trial, i.e., a smaller amount "today" or a larger amount at a later point in time. Participants make choices at each of 6 time periods (1 month, 6 months, 1 year, 3 years, 5 years and 10 years) and for two delayed amounts (\$200 and \$40,000). For each combination of time period and delayed amount (e.g., \$200 in 1 month or \$40,000 in 6 months), participants make 5 choices, and the value that would have been used for the immediate amount in a 6th choice is taken as the indifference point for that condition. The participants make all five choices for a particular combination of time period and delayed amount before moving on to the next combination of time period and delayed amount. Finally, area-under-the-curve (AUC) measures for the two amounts (DDisc_AUC_200 and DDisc_AUC_40k) are computed to provide valid and reliable indices of how steeply an individual discounts delayed rewards (Anandakumar et al., 2018; Chen, Hu, et al., 2019; Jimura, Chushak, & Braver, 2013; Myerson, Green, & Warusawitharana, 2001); these variables were selected due to their good psychometric properties. A smaller AUC reflects greater delay discounting, i.e., a greater decision impulsivity. We used the AUC measures to search the edges containing information relevant for the subsequent prediction analyses. Only 809 subjects (407 female) were used in this study because 3 participants were excluded due to incomplete delay discounting data.

2.4. Connectome-based predictive modeling

CPM is a recently developed approach for identifying brain networks associated with a behavioral variable of interest from whole-brain functional connectivity, which can be then used to predict novel participants' behavior at the single-subject level (Shen et al., 2017). Here, CPM was performed using previously validated custom MATLAB scripts which are freely available online (<https://www.nitrc.org/projects/bioimagesuite/>). Overall, inputs to CPM were whole-brain functional connectivity matrices and behavioral data (i.e., DDisc_AUC_200 and DDisc_AUC_40k scores). First, the input

data were divided into a training set and a testing set. In the training set, each edge in the connectivity matrices was correlated with the behavior data using Pearson's correlation analyses with a statistical significance threshold of $p < .01$ to identify positive and negative predictive networks. For positive networks, edges were significantly positively associated with the behavioral data; for negative networks, edges were significantly negatively associated with the behavioral data. Next, a single-subject summary value was created by summing the significant edge weights in each network. Then, a predictive model was built that assumes a linear relationship between the single-subject summary value of connectivity data (independent variable) and the behavioral variable (dependent variable). In the testing set, the summary value was calculated for each subject and was then input into the predictive model. The resulting value was the predicted behavioral variable for the current test subject. Here, we employed a leave-one-out cross-validation analysis (i.e., internal validation) to test the prediction performance. Briefly, one subject was left out and all other subjects were used to build the predictive model; the left-out subject's predicted behavioral variable was generated by the predictive model; this step was repeated in an iterative manner until all subjects had a predicted behavioral variable. Model performance was assessed by the magnitude and statistical significance of the Pearson's correlation between actual and predicted behavioral values. The statistical significance of the correlation between actual and predicted behavioral values was assessed using permutation testing. To generate an empirical null distribution of the test statistic (i.e., prediction correlation values), we randomly shuffled the correspondence between connectivity matrices and behavioral variables 5,000 times and reran the CPM pipeline using the shuffled data. Based on the null distribution, the p value for the leave-one-out prediction was calculated as the proportion of sampled permutations that were greater than or equal to the true prediction correlation, i.e., p value = the number of permutations that generated correlation values greater than or equal to the true correlation values/5000. Statistical significance was set at $p < .05$.

2.5. Validation analyses

The following procedures were conducted to further evaluate the reproducibility of our findings. First, a significance threshold of $p < .01$ was used to select edges that were positively and negatively correlated with decision impulsivity scores. To determine whether our main results depended on the choice of different edge selection thresholds, we reran the CPM analyses using two other thresholds (i.e., $p < .05$ and $.001$) to identify edges significantly related to decision impulsivity scores. Second, considering that different parcellation strategies may influence the results, we constructed functional connectome using two other parcellation schemes (i.e., 100 and 300 group-ICA components) and repeated the entire analyses. Third, we also calculated delay discounting rate (k) according to the hyperbolic function (Green & Myerson, 2004). As the original k was not normally distributed, a \log_{10} transformation was applied ($\log k$) (Lv et al., 2019; van den Bos et al., 2014; Wang et al., 2014). Then, the CPM analyses were

conducted again to predict the $\log k$. Finally, 10-fold and 20-fold cross-validation analyses were used to further test the CPM prediction performance in novel subjects.

3. Results

3.1. Prediction performance of decision impulsivity scores

The average scores were .52 (SD = .28, ranging from .02 to .98) for DDisc_AUC_40k and .27 (SD = .21, ranging from .02 to .98) for DDisc_AUC_200. The CPM models, based on functional connectivity within both the positive and negative networks, reliably predicted DDisc_AUC_40k scores (positive network: $r = .248$, 95%CI .180–.313, $p = .0162$; negative network: $r = .237$, 95%CI .174–.303, $p = .0188$) (Fig. 2A and B). However, DDisc_AUC_200 scores were successfully predicted from functional connectivity within the positive network ($r = .228$, 95%CI .171–.291, $p = .0100$) (Fig. 3A), but not that within the negative network ($r = .188$, 95%CI .123–.249, $p = .3420$) (Fig. 3B).

3.2. Network anatomy

Because of the nature of cross-validation, it is likely that a slightly different set of edges will be selected as features in each iteration of the cross-validation. For illustrative purpose, we defined final decision impulsivity scores-relevant networks using data from all 809 training subjects. Overall, network anatomies for the networks associated with decision impulsivity scores were complex and included edges between nodes across the brain. For DDisc_AUC_40k scores, the positive and negative networks consisted of 475 and 364 edges, respectively (Fig. 2C and D). Highest-degree nodes (i.e., nodes with the most edges) for the positive network included nodes belonging to somato-motor network (SMN) (Fig. 2E); highest-degree nodes for the negative network included nodes belonging to default mode network (DMN), subcortical network (SN) and SMN (Fig. 2F). For DDisc_AUC_200 scores, the positive and negative networks consisted of 318 and 262 edges, respectively (Fig. 3C and D). Highest-degree nodes for the positive network included nodes belonging to visual network (VN), dorsal attention network (DAN), and SMN (Fig. 3E); highest-degree nodes for the negative network included nodes belonging to DMN, VN, and cerebellum (Fig. 3F).

3.3. Validation analysis

First, the prediction results derived from different edge selection thresholds are shown in Table S1. At the threshold of $p < .05$, we found that the prediction performances of decision impulsivity scores were similar to those at the threshold of $p < .01$, i.e., CPM produced good prediction for both DDisc_AUC_40k and DDisc_AUC_200 scores. At the threshold of $p < .001$, however, the predictive ability became marginally significant for DDisc_AUC_40k scores and even non-significant for DDisc_AUC_200 scores. Second, we found that our main results were largely reproduced after considering the effects of different parcellation strategies, although there was a non-significant trend for DDisc_AUC_200 prediction

DDisc_AUC_40k

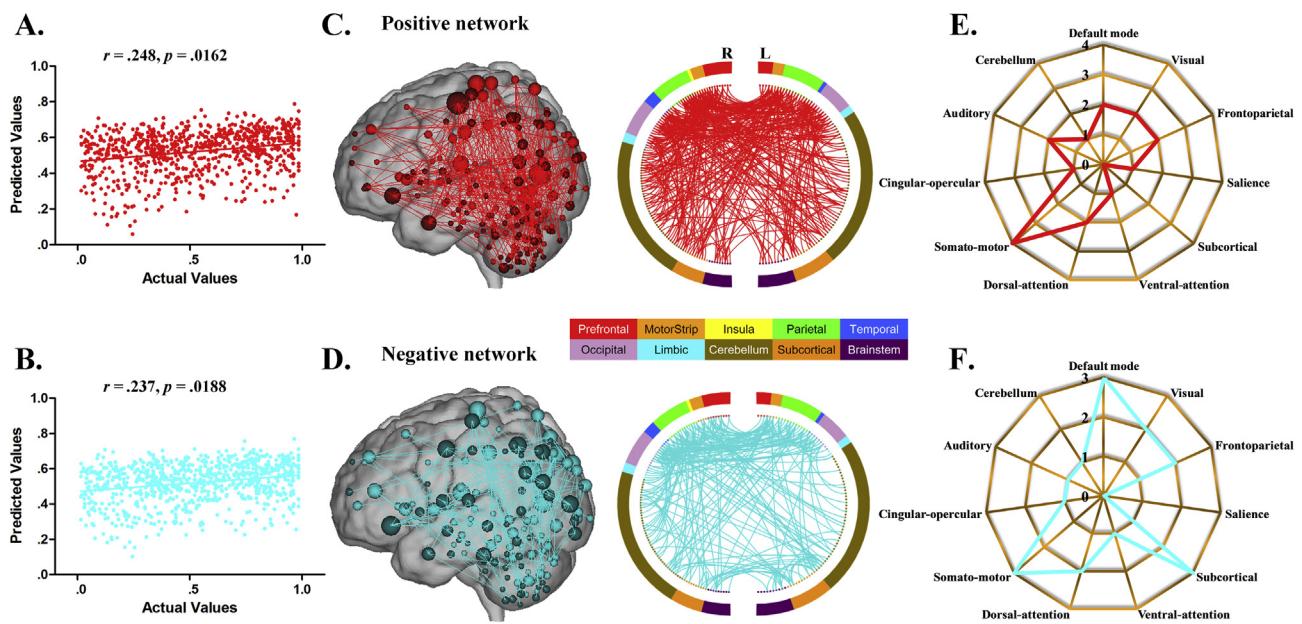


Fig. 2 – Connectome-based predictive modeling (CPM) of DDisc_AUC_40k scores. (A) and (B) Scatter plots showing the correspondence between actual (x-axis) and predicted (y-axis) DDisc_AUC_40k scores generated using CPM based on the positive and negative networks. (C) and (D) High-degree nodes (degree ≥ 6 , larger spheres indicate nodes with higher degree) and their connections in the positive and negative networks. (E) and (F) Polar plots illustrating the most relevant nodes (the top 20 high-degree nodes in the positive and negative networks) summarized by overlap with canonical neural networks.

DDisc_AUC_200

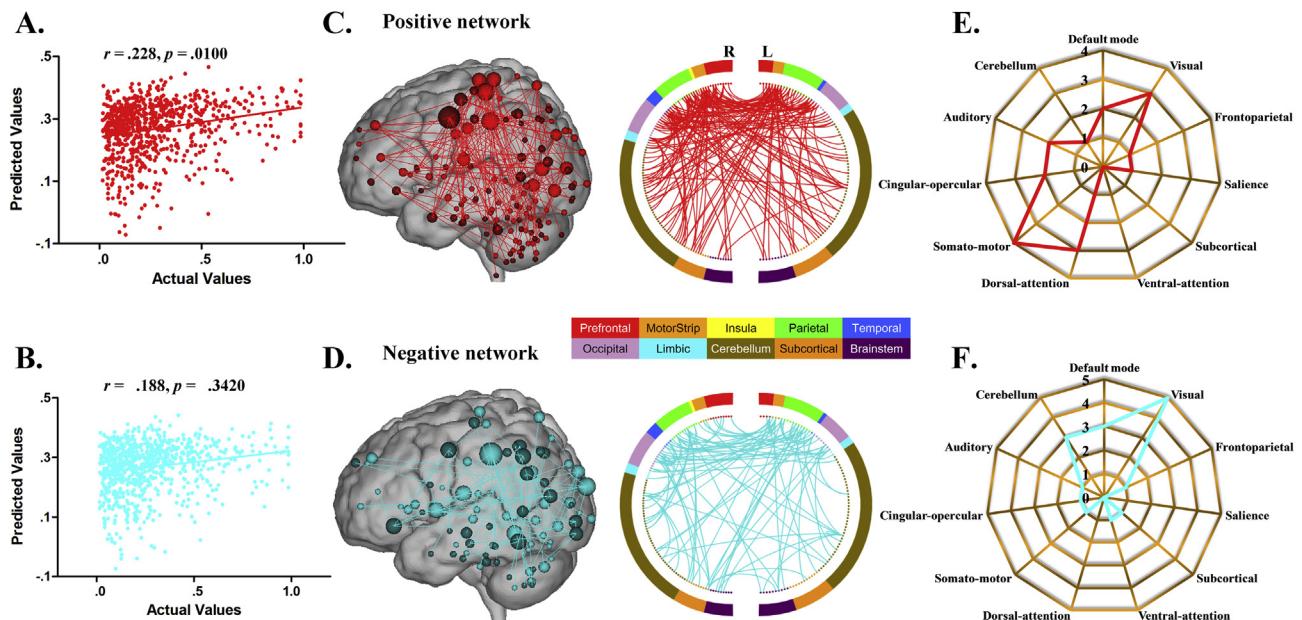


Fig. 3 – Connectome-based predictive modeling (CPM) of DDisc_AUC_200 scores. (A) and (B) Scatter plots showing the correspondence between actual (x-axis) and predicted (y-axis) DDisc_AUC_200 scores generated using CPM based on the positive and negative networks. (C) and (D) High-degree nodes (degree ≥ 6 , larger spheres indicate nodes with higher degree) and their connections in the positive and negative networks. (E) and (F) Polar plots illustrating the most relevant nodes (the top 20 high-degree nodes in the positive and negative networks) summarized by overlap with canonical neural networks.

using 300 group-ICA components (Table S2). Third, the CPM models yielded a reliable prediction of the $\log k$ that was identical to that of the AUC measures (Fig. S1). Finally, when using 10-fold and 20-fold cross-validation analyses, the prediction results of decision impulsivity scores remained unchanged (Table S3).

4. Discussion

By applying a recently developed CPM approach to a large sample of high-quality resting-state fMRI data from the HCP, our study demonstrated that decision impulsivity measured by delay discounting could be successfully and reliably predicted from an individual's unique whole-brain functional connectivity profile. Additionally, we found that the functional connectivity underpinnings of decision impulsivity involved multiple brain systems including DMN, SN, SMN, DAN, and VN, supporting the notion that impulse control emerges from complex information communication across multiple resting-state networks.

There have been several neuroimaging studies using machine learning approaches to predict individual decision impulsivity in healthy subjects. In a recent resting-state fMRI study on college students, multivariate pattern analyses revealed that regional homogeneity (ReHo) patterns in the dorsal medial prefrontal cortex was a predictor of decision impulsivity measured by delay discounting rate, with higher ReHo predicting lower decision impulsivity (Lv et al., 2019). By employing a combination of resting-state and task-based fMRI data, Li et al. reported that resting-state functional connectivity between brain regions activated during a delay discounting task was able to predict individuals' behavioral impulsivity (Li et al., 2013). Another task-based fMRI study showed that the whole-brain neural activity patterns during a monetary intertemporal choice task could robustly predict participants' intertemporal decision-making with high accuracy (Chen, Guo, et al., 2019). Likewise, in the study by Zha et al., local activity patterns in the ventromedial prefrontal cortex and dorsolateral prefrontal cortex during a delay discounting task were found to accurately predict intertemporal choices in healthy participants (Zha et al., 2019). Using multivariate pattern analysis and 10-fold cross-validation, Wang and colleagues found that gray matter volume in the frontal pole and middle frontal gyrus as well as resting-state functional connectivity between the frontal pole and ventromedial prefrontal cortex was predictive of the discounting rate in a delay discounting task (Wang et al., 2016). Compared to these prior studies, the present study has several potential advantages. First, the sample size represents the biggest cohort to be used to predict decision impulsivity, which increases the reliability of the results. Second, the high-quality HCP fMRI data analyzed in this study have much better spatial and temporal resolution. Third, we utilized a data-driven approach to construct each subject's whole-brain functional network, which constitutes a unique "neural fingerprint" allowing identification of individuals among a pool of people (Finn et al., 2015; Xu et al., 2016). Moreover, group ICA was used to define the whole-brain network nodes, which are considered functional homogeneous and may be

better at capturing individual differences of real functional boundaries than those defined by anatomical brain atlases (Calhoun et al., 2001). Finally, compared with the machine learning methods that were previously adopted to study brain-decision impulsivity association, CPM is optimized for whole-brain functional connectivity data and requires no a priori selection of networks. The predictive power of CPM has been demonstrated in studies of fluid intelligence (Finn et al., 2015), attention (Rosenberg et al., 2016; Yoo et al., 2018) and creativity (Beatty et al., 2018). Notably, the current observation that DDisc_AUC_40k yielded higher predictability than DDisc_AUC_200 may be due to the fact that DDisc_AUC_40k scores were more uniformly distributed from 0 to 1 than DDisc_AUC_200 scores, suggesting that a higher delayed amount may have superior sensitivity in detecting inter-individual decision impulsivity variation and its related neural correlates.

We found that functional connectivity of DMN, SN and SMN was correlated with delay discounting scores, suggesting their crucial roles in decision impulsivity. DMN is preferentially active when individuals are engaged in internally directed cognition, such as mind-wandering, autobiographical memory retrieval, envisioning the future, mental simulation, theory of mind reasoning, and creative cognition (Buckner, Andrews-Hanna, & Schacter, 2008; Buckner & DiNicola, 2019). DMN is thought to play a vital role in the organization and expression of preplanned, reflexive behaviors that are critical to our existence in a complex world but become impulsive when unconstrained by the social and physical constraints of the environment (Raichle, 2015). Medial prefrontal cortex is a core hub of DMN and its function and structure are closely linked to decision impulsivity, which has been consistently demonstrated by neuroimaging studies focusing on analyses of task-induced brain activation, resting-state regional neural activity, functional connectivity, cortical thickness, gray matter volume, and white matter connectivity (Bernhardt et al., 2014; Boes et al., 2009; Cho et al., 2013; Hampton et al., 2017; Han et al., 2013; Jimura et al., 2013; Liu & Feng, 2012; Ludwig et al., 2015; Lv et al., 2019; Pehlivanova et al., 2018; Wang et al., 2016; Zha et al., 2019). By applying ICA and large-scale brain network analysis to resting-state fMRI data, investigators revealed that delay discounting rates were correlated with both neural activity within DMN (Chen et al., 2017) and functional network connectivity between DMN and cingulo-opercular network (Chen et al., 2018). It is well established that the antagonistic connectivity between cognitive task-based networks and DMN has been identified as "anti-phase network oscillations", which could influence one's cognitive control performance in decision-making without the need for top-down inhibition (Fornito, Harrison, Zalesky, & Simons, 2012; Kelly, Uddin, Biswal, Castellanos, & Milham, 2008; Marsteller, Burianova, & Reutens, 2016). With regard to SN, converging evidence from structural, functional and diffusion MRI studies has pointed towards strong associations between decision impulsivity and striatum morphology, activation patterns, functional and anatomical connectivity (Achterberg et al., 2016; Benningfield et al., 2014; Chen, Guo, et al., 2019; Cho et al., 2013; de Water et al., 2017; Drobetz et al., 2014; Elton et al., 2017; Hampton et al., 2017; Han et al., 2018; Hanggi et al., 2016; Hariri et al.,

2006; Holmes et al., 2018; Jimura et al., 2013; Luerssen et al., 2015; Peper et al., 2013; Simon et al., 2015; Tschernegg et al., 2015; van den Bos et al., 2014; Weber & Huetzel, 2008; Wittmann et al., 2007), which are in line with our findings. In addition, supplementary motor area is an important component of SMN and its functional and structural connectivity has been shown to respectively associate with delay discounting measure (Anandakumar et al., 2018) and motor impulsivity (Hampton et al., 2017), emphasizing the importance of SMN in the neural processes underlying impulsivity.

DAN is mainly composed of bilateral intraparietal sulcus and frontal eye field and is principally involved in preparing and applying goal-directed (top-down) selection for stimuli and responses (Corbetta & Shulman, 2002; Fox, Corbetta, Snyder, Vincent, & Raichle, 2006). VN is centered on medial occipital cortex (lingual gyrus, cuneus and calcarine sulcus), lateral occipital cortex, and fusiform gyrus, which are known to be implicated in visual perception and processing, visual or visuo-spatial attention and perception of emotion in facial stimuli (Golarai et al., 2007; Grill-Spector & Malach, 2004). Nonetheless, there is a paucity of previous literature demonstrating a relationship between decision impulsivity and these brain regions. The current findings of associations between delay discounting and functional connectivity of DAN and VN extend our perspective on the neural mechanism of decision impulsivity, in support of the concept that a complex human behavior usually emerges from information communication across multiple resting-state networks rather than within or between pairs of specific networks (Liegeois et al., 2019) as individual functional connectivity fingerprinting is distributed throughout the brain (Finn et al., 2015).

Our study has several limiting factors that should be mentioned. First, the lack of data from an independent sample hampers the possibility to perform an external validation analysis. Second, the HCP sample included healthy young adults with a relatively narrow age range from 22 to 37 years, which might restrict generalizability to other age ranges. Future investigations are encouraged to further improve our understanding of the inter-individual decision impulsivity differences from the lifespan perspective by enrolling a cohort of subjects with a broader age range. Finally, hypothetical instead of real money rewards were used in the delay discounting test, which may influence our interpretation to some extent. However, prior studies have demonstrated that hypothetical and real rewards yield similar results in both behavioral (Johnson & Bickel, 2002) and functional neuroimaging paradigms (Bickel, Pitcock, Yi, & Anguaco, 2009).

In conclusion, our large sample study demonstrates that resting-state functional connectivity patterns of whole-brain large-scale networks can effectively and reliably predict delay discounting. Our results also show that individual differences in functional connectivity of default-mode, subcortical, somato-motor, dorsal attention, and visual networks contribute the most to inter-individual variability in delay discounting. These findings not only may expand existing knowledge regarding the neural mechanism of decision impulsivity, but also may present a workable route towards

translation of brain imaging findings into real-world economic decision-making. Moreover, our findings have significant implications for the study of clinical conditions with impulsive symptoms (e.g., ADHD, addiction, obesity, pathological gambling, and suicide attempts), which might facilitate a deeper understanding of the etiology and development of impulsivity-related brain disorders as well as provide potential neural targets for their diagnosis and treatment.

Open practices

The study in this article earned an Open Data – Protected Access badge for transparent practices. Materials and data for the study are available at <https://www.nitrc.org/projects/bioimagesuite/>.

The dataset that supports the findings of this study is available by Human Connectome Project at <http://www.humanconnectome.org>.

MATLAB analysis code has been made publicly accessible here: <https://www.nitrc.org/projects/bioimagesuite/>.

We report how we determined our sample size, all data exclusions, all inclusion/exclusion criteria, whether inclusion/exclusion criteria were established prior to data analysis, all manipulations, and all measures in the study.

Declaration of Competing Interest

There are no conflicts of interest to declare.

CRediT authorship contribution statement

Huanhuan Cai: Methodology, Data curation, Software, Writing - original draft. Jingyao Chen: Visualization, Investigation. Siyu Liu: Visualization, Investigation. Jiajia Zhu: Conceptualization, Methodology, Software, Formal analysis, Writing - review & editing. Yongqiang Yu: Conceptualization, Supervision, Writing - review & editing.

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Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.cortex.2020.01.022>.

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