Title

Connectome-based model predicts individual psychopathic traits in college students

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25 psychopathic traits; connectome-based predictive modeling; resting-state functional

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27

28 **Abstract**

29 **Background:** Psychopathic traits have been suggested to increase the risk of violations of
30 socio-moral norms. Previous studies revealed that abnormal neural signatures are associated
31 with elevated psychopathic traits; however, whether the intrinsic network architecture can
32 predict psychopathic traits at the individual level remains unclear.

33 **Methods:** The present study utilized connectome-based predictive modeling (CPM) to
34 investigate whether whole-brain resting-state functional connectivity (RSFC) can predict
35 psychopathic traits in the general population. RS functional magnetic resonance imaging data
36 were collected from 84 college students with varying psychopathic traits measured by the
37 Levenson Self-Report Psychopathy Scale (LSRP).

38 **Results:** We found that RSFC of the negative networks predicted individual differences in
39 total LSRP and secondary psychopathy scores but not primary psychopathy score. Particularly,
40 nodes with the most connections in the predictive connectome anchored in the prefrontal
41 cortex (e.g., anterior prefrontal cortex and orbitofrontal cortex) and limbic system (e.g.,
42 anterior cingulate cortex and insula). In addition, the connections between the occipital
43 network (OCCN) and cingulo-opercular network (CON) served as a significant predictive
44 connectome for total LSRP and secondary psychopathy score.

45 **Conclusion:** CPM constituted by whole-brain RSFC significantly predicted psychopathic
46 traits individually in the general population. The prefrontal cortex and limbic system at the
47 anatomic level and the CON and OCCN at the functional network level plays a special role in
48 the predictive model—reflecting atypical executive control and affective processing for
49 individuals with elevated psychopathic traits. These findings may provide some implications

50 for early detection and potential intervention of psychopathic tendency.

51 **Keywords:** psychopathic traits; connectome-based predictive modeling; resting-state

52 functional connectivity.

53 **Introduction**

54 Psychopathy is a dimensional personality construct which is characterized by a discernible
55 cluster of personality traits, including shallow affect, reduced control of impulse, high risk
56 taking, pathological lying (Douglas, Nikolova, Kelley, & Edens, 2015). Individuals with
57 elevated psychopathic traits demonstrate increased maladaptive behavior, such as violence
58 and aggression, and therefore have negative impacts on the stability and security of society (R.
59 D. Hare, 2006). Psychopathic traits are captured by two factors—primary and secondary
60 psychopathy which are linked to different behavioral features and may be related to different
61 causes (Lee & Salekin, 2010). Primary psychopathy is mainly associated with interpersonal
62 and affective features which has been widely proved to be related to emotional deficits and
63 are more likely to originate from neurobiological dysfunctions. In contrast, secondary
64 psychopathy is more associated with the lifestyle/antisocial feature which is closely related to
65 impulsivity and antisocial behavior and are more likely to root in environmental causes
66 (Skeem, Johansson, Andershed, Kerr, & Loudon, 2007; Yildirim & Derksen, 2015).

67 Despite that previous research has identified dysfunctional neurobiological signatures for
68 people with elevated psychopathic traits (Cohn et al., 2015; Korponay et al., 2017), few has
69 examined whether intrinsic network architecture can predict psychopathic traits at the
70 individual level by using resting-state functional magnetic resonance imaging (rs-fMRI).
71 Investigations on prediction about individualized psychopathic traits using rs-fMRI may
72 increase our understanding of the neurobiological substrates associated with psychopathic
73 traits and may provide some implications for early detection and potential intervention for
74 psychopathic tendency in the future.

Resting-state functional connectivity (RSFC) —defined as temporal dependency of low-frequency (0.01–0.1 Hz) BOLD fluctuations between anatomically separated brain regions at the resting state— has the potential to serve as neural fingerprints of human behavior (Friston, Frith, Liddle, & Frackowiak, 1993; Van Den Heuvel & Pol, 2010). RSFC has been validated to be a good predictor of personality traits, social behaviors, and psychiatric disorders (Finn et al., 2015; Gordon et al., 2017). Psychopathic traits are related to decreased RSFC between brain regions involved in affective processing (Motzkin, Newman, Kiehl, & Koenigs, 2011), social cognition (Glenn & Raine, 2008), and moral decision making (Pujol et al., 2012). In particular, the prefrontal cortex (PFC) is typically associated with psychopathic traits (N. E. Anderson & Kiehl, 2012; Viding & McCrory, 2018). For example, the ventromedial prefrontal cortex (vmPFC), a brain region responsible for value evaluation, emotion regulation, and moral judgment, is found to be dysfunctional in individuals with elevated psychopathic traits (R. J. R. Blair, 2007; Gangopadhyay, Chawla, Dal Monte, & Chang, 2020; T. A. Hare, Camerer, & Rangel, 2009).

Further, RSFC in the dorsolateral prefrontal cortex (dlPFC) and orbitofrontal cortex (OFC) is associated with psychopathic traits in a male criminal sample, suggesting poor performance in risky decision making and inhibition control for individuals high on psychopathic traits (Korponay et al., 2017). Moreover, psychopathic traits are associated with dysfunction of the limbic system, including the cingulate cortex, insula, and parahippocampal regions (Kiehl, 2006). A recent study reported decreased RSFC between the prefrontal and limbic-paralimbic regions for individuals with elevated psychopathic traits in a criminal sample, resulting in a weaker emotional and cognitive integration (Contreras-Rodríguez et al., 2015).

97 Furthermore, abnormal functional connectivity within and between functional brain
 98 networks has been reported to be associated with psychopathic traits (Espinoza et al., 2018;
 99 Thijssen & Kiehl, 2017). The functional brain networks refer to a collection of interconnected
 100 brain regions that interact to perform circumscribed functions (Bressler & Menon, 2010) and
 101 are related to a broad range of cognitive and affective functions (Raz, 2004; Sheline et al.,
 102 2009). Further, previous studies have indicated that the default mode network (DMN),
 103 executive-control /frontoparietal network (FPN), and salience/cingulo-opercular network
 104 (CON) may be particularly associated with psychopathic traits (Cohn et al., 2015; C. L.
 105 Philippi et al., 2015). For example, an neuroimaging study reported associations between
 106 psychopathic traits and power spectra (reflecting the degree of fluctuation in amplitudes of the
 107 intrinsic activity within the network) of the DMN and spatial maps (resembling the
 108 correspondence between a voxel time course and a region time course) of the FPN and CON
 109 in incarcerated adolescents, implicating deficits in self-referential processing, social cognition,
 110 and emotion regulation for adolescents with elevated psychopathic traits (Thijssen & Kiehl,
 111 2017).

112 Although a plethora of evidence has identified abnormal neural correlates of extremely
 113 high psychopathic traits by utilizing RSFC in the correctional samples which only represent a
 114 small part in the psychopathy spectrum (Johanson, Vaurio, Tiihonen, & Lhteenvuo, 2020), it
 115 remains unclear whether these findings can be generalized to the general population with
 116 elevated psychopathic traits. Moreover, quantitative prediction of psychopathic traits at the
 117 individual level has not yet been investigated. Compared to the group-level analyses,
 118 predictions at the individual level of psychopathic traits could provide better clinical

119 implications in the detection and potential intervention of psychopathic tendency (Lueken et
120 al., 2016).

121 Connectome-based predictive modeling (CPM) —a data-driven machine learning
122 approach— has been widely applied in predicting human behavior and personality traits by
123 using whole-brain RSFC data (Finn et al., 2015; Shen et al., 2017). Compared with
124 conventional correlation or regression analyses, CPM sufficiently extracts brain connectivity
125 data to build predictive models and employs cross-validation to protect against overfitting
126 (Shen et al., 2017; Yip, Scheinost, Potenza, & Carroll, 2019). This method has been
127 well-validated in generating predictive model based on neural features (Feng, Wang, Li, & Xu,
128 2019; Ren et al., 2020). For example, CPM has been used to predict temperament (Jiang et al.,
129 2018) and propensity to trust (Lu et al., 2019) based on whole-brain RSFC.

130 In this study, we employed CPM to predict individual differences of psychopathic traits
131 measured by the Levenson Self-Report Psychopathy Scale (LSRP) based on whole-brain
132 RSFC in a college student sample. Based on previous findings, we hypothesized that the
133 connectome consisting of decreased RSFC involving the prefrontal cortex and limbic system
134 is able to predict psychopathic traits at the individual level (N. E. Anderson & Kiehl, 2012;
135 Thijssen & Kiehl, 2017). Further, given distinctions between primary and secondary
136 psychopathy in behavioral and psychological features, we expected that the connectome in
137 predicting primary psychopathy might be constituted by RSFC mainly involving regions (e.g.,
138 amygdala, insula and PCC) related to emotional function. However, the connectome in
139 predicting secondary psychopathy might be constituted by RSFC mainly involving regions
140 (e.g., OFC, dlPFC, and ACC) related to executive control. In addition, based on limited

141 evidence on the association between psychopathic traits and large-scale networks, we

142 expected RSFC within and between the three large-scale networks—FPN, DMN and CON to

143 be able to predict individual psychopathic traits.

144

145 **Method**

146 **Participants**

147 Eighty-four healthy right-handed college students (mean age: 22.6 ± 2.59 years, 34 males and
148 50 females) were recruited from Hangzhou Normal University in China. All participants had
149 no history of neurological or psychiatric disorders. This study was conducted in accordance
150 with the Helsinki Declaration. Written informed consent was obtained from each participant
151 for this study, which was approved by the Ethics Committee of Hangzhou Normal University.

152 **Measures**

153 Psychopathic traits were assessed using the LSRP (Levenson, Kiehl, & Fitzpatrick, 1995).
154 The LSRP is a 26-item rating scale with two subscales assessing primary and secondary
155 psychopathy, and each of the items can be rated on a 4-point Likert agree/disagree scale (1
156 [strongly disagree] to 4 [strongly agree]). The total LSRP score represents the overall level of
157 psychopathic traits (i.e., total psychopathic trait score, T-PTS). The primary psychopathy
158 subscale assesses the *affective traits of psychopathy* such as lack of empathy and shallow
159 affect (i.e., primary psychopathic trait score, P-PTS). The secondary psychopathy subscale
160 assesses the *antisocial traits of psychopathy*, such as impulsiveness and antisocial behavior
161 (i.e., secondary psychiatric trait score, S-PTS) (Miller, Gaughan, & Pryor, 2008). The LSRP
162 has been validated in Chinese university student samples (Wang et al., 2018). The Cronbach's
163 Alphas were 0.80 (T-PTS), 0.79 (P-PTS), and 0.59 (S-PTS) in the present sample.

164 **Image data acquisition**

165 Imaging data were collected at the Center for Cognition and Brain Disorders of Hangzhou
166 Normal University using a 3T MRI scanner (GE Discovery 750 MRI, General Electric,

Milwaukee, WI, USA). Participants were instructed to keep their eyes closed and stay awake without performing any cognitive exercises during the 8-minute RS scan. The imaging parameters of the EPI sequence including 240 images were as follows: repetition time (TR) = 2000 ms; interleaved 43 slices; echo time (TE) = 30 ms; thickness = 3.2 mm; flip angle = 90°; field of view (FOV) = 220 × 220 mm²; and matrix size = 64 × 64. A high-resolution 3D T1-weighted anatomical image was also acquired through magnetization-prepared rapid acquisition with gradient-echo (MPRAGE) sequence with following parameters: 176 sagittal slices; TR = 8100 ms; slice thickness = 1 mm; TE = 3.1 ms; flip angle = 8°; FOV = 250 × 250 mm. This session lasted for about 5 minutes.

Preprocessing

The fMRI data preprocessing was performed with DPABI v3.0 (Data processing & Analysis for Brain Imaging, <http://rfmri.org/dpabi>) (Fig.1a) (Yan, Wang, Zuo, & Zang, 2016). The first 10 volumes were discarded for signal equilibrium and participants' adaptation to the scanning environment. The remaining 230 images were subsequently realigned for head movement correction and spatially normalized into the standard Montreal Neurological Institute space (MNI template, resampling voxel size was 3 × 3 × 3 mm³). Next, the linear trends of time courses were removed, and a band-pass temporal filtering (0.01–0.1 Hz) was applied to the time series to reduce the effect of low-frequency drifts and high-frequency physiological noise. Finally, the images were smoothed using a Gaussian filter with a kernel of full width at half maximum of 4 mm, and three common nuisance variables (i.e., white matter signal, cerebrospinal fluid signal, and 24 movement regressors including 6 standard head motion parameters, the derivative of the standard motion parameters, and the 12

189 corresponding squared items) were regressed out.

190 **RSFC**

191 Whole-brain RSFC was computed by employing the Dosenbach atlas with 142 nodes
192 excluding the cerebellum (**Supplementary Table 1 & Fig. 1b**) (Dosenbach et al., 2010).

193 Every node defined in the atlas was a 5 mm-radius spherical region can be assigned into five
194 pre-defined networks: default-mode (DMN), frontoparietal (FPN), cingulo-opercular (CON),
195 sensorimotor (SMN), and occipital (OCCN) network. We extracted the time courses of all
196 nodes by averaging the time course for all the voxels within a node. Pearson's correlation
197 coefficient between the time courses of each pair of nodes was calculated and subsequently
198 was transformed using Fisher's z-transformation. A symmetric 142×142 connectivity matrix
199 was constructed for each subject in which each element represents RSFC strength between
200 two nodes.

201 **CPM**

202 All the analyses listed below used the CPM framework to construct predictive models
203 predicting the targets (S-PTS, S-PTSS, S-PTS) based on whole brain RSFC using MATLAB
204 (<http://www.mathworks.com>) scripts taken from Shen's paper published in 2017
205 (<https://www.nitrc.org/projects/bioimagesuite>). First, Pearson's correlation coefficients
206 between each edge and targets were calculated across the participants (**Fig. 1c**). Edges in
207 which the p-values of the correlation were less than the threshold ($p < 0.01$) were defined as
208 important edges for the subsequent processing (**Fig. 1d**). The positive (negative) networks
209 were composed of edges that were positively (negatively) associated with psychopathic traits
210 (**Fig. 1e**). Next, the edge weights (connectivity strength) were summed up in positive and

negative networks respectively for each participant, ultimately forming single-subject positive and negative network strengths (**Fig. 1f**). Then, linear regression predictive models were constructed to predict psychopathic traits by including positive and negative network strengths as regressors. Finally, the resultant linear equation including slope and intercept was applied in new participants to obtain predictive values (**Fig. 1g**).

--- **Insert Figure 1 about here** ---

Cross-validation

A leave-one-subject-out cross-validation (LOOCV) approach was utilized to test the generalizability of the prediction. N-1 participants were set as the training set (N equals to the number of the participants) while the left-out participants were set as the testing set. The predictive model was built using the training data and then was applied to predict the testing participants' behavior. The training and testing procedures were implemented in an iteration manner until all the participants have a predictive value.

Moreover, model performance was evaluated with Pearson's correlation coefficient (r) and standard mean square error ($SMSE$) between the predictive value and actual value while controlling for confounding variables such as age, gender, and head motion. The significance of r and $SMSE$ was assessed with a permutation test of 5,000 permutations. Null distributions were generated by randomly shuffling the actual target value 5,000 times and repeating the CPM analyses with the shuffled data. The number of permutations with better performance (i.e., higher r and lower $SMSE$) than the model built with the true actual value were calculated and used to divide the total number of permutations for obtaining the p -value.

Node and network analyses

233 After the cross-validation, consensus functional connectivity that retained in every
234 iteration was obtained, and the degree centrality (i.e., the number of connections involving a
235 certain node) of nodes involved in consensus functional connectivity was calculated. The first
236 eight nodes with the largest degree centrality were defined as the most connected nodes in the
237 predictive connectivity. Also, the connections between and within five large-scale brain
238 networks (i.e., CON, DMN, FPN, OCCN, and SMN) were computed to characterize the
239 predictive connectome at the network level, and the inter- or intra-network connections with
240 the largest number regarded as connections that most contribute to the predictive connectome.

241 **Validation analyses**

242 To avoid the overfitting of the predictive model, k-fold cross-validations —2-, 5-, and 10-fold
243 cross-validations— were further applied to validate the results (Poldrack, Huckins, &
244 Varoquaux, 2020). Like LOOCV, k-fold cross-validation divides the subjects randomly and
245 equally into k subsets in which one subset was used as the testing set, and other remaining
246 subsets were used as the training set. The predictive model was trained by the training set and
247 was then used to make predictions for the testing set. The procedure repeated k times to
248 ensure each subset was used as the testing set once. Pearson correlation coefficients between
249 the predictive and actual value were calculated to evaluate the model performance. Given that
250 all the subjects were randomly divided into k subsets and model performance is largely
251 affected by the data division, the k-fold cross-validation was repeated 50 times to increase
252 reliability. The correlation coefficients were averaged to obtain a final prediction performance,
253 and a permutation test was utilized 5,000 times to test the significance of the model
254 performance.

255

256

257

258 **Results**

259 Psychopathic traits (i.e., T-PTS, P-PTS, S-PTS) were not significantly correlated with age
 260 (T-PTS : $r = -0.033$, $p = 0.764$; P-PTS: $r = 0.027$, $p = 0.807$; S-PTS : $r = -0.116$, $p = 0.295$)
 261 and no significant gender differences were found (T-PTS: $t = 0.633$, $df = 82$, $p = 0.529$; P-PTS:
 262 $t = -0.153$, $df = 82$, $p = 0.879$; S-PTS: $t = 1.657$, $df = 82$, $p = 0.101$) (**Tab. 1**).

263 **--- Insert Table 1 about here ---**

264 The CPM results revealed that the negative network strength significantly predicted
 265 T-PTS ($r = 0.295$, $p(r) = 0.011$, $SMSE = 1.485$, $p(SMSE) = 0.022$, **Fig. 2a**) and S-PTS ($r =$
 266 0.309 , $p = 0.008$, $SMSE = 0.773$, $p(SMSE) = 0.014$, **Fig. 2c**) but not P-PTS ($r = 0.062$, $p =$
 267 0.309 , $SMSE = 1.234$, $p(SMSE) = 0.370$, **Fig. 2b**) after controlling for the potential
 268 confounding effect of gender, age and head motion. In contrast, the positive network strength
 269 could not reliably predict any of the targets (T-PTS : $r = 0.073$, $p(r) = 0.308$, $SMSE = 1.771$,
 270 $p(SMSE) = 0.353$; S-PTS : $r = 0.129$, $p = 0.199$, $SMSE = 0.903$, $p(SMSE) = 0.233$; P-PTS: $r =$
 271 0.008 , $p = 0.468$, $SMSE = 1.214$, $p(SMSE) = 0.425$). Across all folds of cross-validation, 78
 272 edges (4 positive and 74 negative), 34 edges (3 positive and 31 negative), and 98 edges (3
 273 positive and 95 negative) retained as consensus functional connectivity for predicting T-PTS,
 274 P-PTS, and S-PTS, respectively. Because only a few edges in the positive tail retained in all
 275 the folds of cross-validation and could not provide reliable predictions for any of the targets,
 276 the following analyses were only performed only for the negative networks.

277 --- Insert Figure 2 about here ---

278 Figure 3 summarizes the negative networks predicting T-PTS and S-PTS. For T-PTS, the most
 279 highly connected nodes included the superior temporal sulcus (STS), middle occipital gyrus
 280 (MOG), anterior prefrontal cortex (aPFC), inferior orbitofrontal cortex (IOFC), vmPFC,
 281 insula, and supramarginal gyrus (SMG) (**Tab. 2**). For S-PTS, the most highly connected nodes
 282 included the aPFC, superior frontal gyrus (SFG), MOG, OFC, calcarine, and anterior
 283 cingulate cortex (ACC) (**Tab. 3**). In terms of large-scale functional networks, the connections
 284 of the CON with OCCN predicted T-PTS and S-PTS (**Fig. 4**).

285 --- Insert Table 2 and Table 3 about here ---

286 --- Insert Figure 3 and Figure 4 about here ---

287

288 The predictive model performance was further validated and remained significant using
 289 the k-fold cross-validations (i.e., 2-, 5-, and 10-fold cross-validations) (**Tab. 4**).

290 --- Insert Table 4 about here ---

291

292 Discussion

293 In the present study, we applied CPM to predict individual variations in psychopathic traits
 294 (i.e., T-PTS, P-PTS, S-PTS). We demonstrated that whole-brain RSFC connectome predicted
 295 T-PTS and S-PTS but not P-PTS at the individual level. Inter-individual variations in
 296 psychopathic traits were predicted by RSFC connectome. Particularly, the most connected
 297 nodes located in the PFC (i.e., aPFC, OFC, and vmPFC) and limbic system (e.g., insula and
 298 ACC). In addition, predictive connectomes were primarily constituted by connections
 299 between OCCN and CON at the level of large-scale functional networks.

300 Psychopathic traits have been recognized to increase the risk of violence and aggression
 301 (Porter, Woodworth, & Black, 2018). Individuals with elevated psychopathic traits exhibit
 302 deficient cognitive, affective, and social functions which may be related to their abnormal
 303 neurobiological correlates (Deming & Koenigs, 2020). Here, we demonstrated that CPM
 304 based on the whole-brain RSFC successfully predicted T-PTS and S-PTS at the individual
 305 level. However, only the negative networks in the predictive models made significant
 306 predictions whereas the positive networks failed to successfully predict psychopathic traits
 307 due to the limited number of edges. Our findings added to previous evidence that decreased
 308 RSFC involving brain regions related to emotional, social, and cognitive function
 309 (Contreras-Rodríguez et al., 2015; Espinoza et al., 2019), indicating that higher psychopathic
 310 traits may be primarily accompanied by the decline of the intrinsic whole-brain RSFC which
 311 might contribute to functional segregation of brain regions.

312 However, the whole-brain RSFC failed to predict P-PTS which has been typically
 313 associated with regions supporting emotional function such as amygdala and vmPFC. For

314 example, attenuation of amygdala reactivity during emotion recognition and evocation were
315 observed in psychopaths (Gordon, Baird, & End, 2004; Marsh & Cardinale, 2014). A rs-fMRI
316 study found decrease in FC between the amygdala and the vmPFC in individuals with
317 psychopathy (Motzkin et al., 2011). In particular, weakened amygdala-vmPFC FC contributes
318 to psychopathic symptoms in low-income males (Waller et al., 2019). Here, the whole-brain
319 RSFC was not able to predict primary, which is likely due to that the college student sample
320 with elevated psychopathic traits in this study may not have emotional deficits as severe as
321 clinical psychopaths.

322 On the one hand, we found that the high-degree nodes in the T-PTS predictive model
323 were primarily anchored in the aPFC, OFC, vmPFC which have been consistently associated
324 with psychopathic traits. The aPFC is frequently engaged in cognitive processing including
325 goal-oriented planning (Koechlin, Basso, Pietrini, Panzer, & Grafman, 1999), reallocation of
326 attention (Ramnani & Owen, 2004), and impulse control (Ramnani & Owen, 2004). The OFC
327 is responsible for inhibitory control, learning and value encoding (Rudebeck & Rich, 2018)
328 and plays an important role in regulating emotional responses such as fear and anxiety since it
329 strongly connects with amygdala and insula (Rudebeck, Saunders, Prescott, Chau, & Murray,
330 2013). The vmPFC is involved in the reinforcement-based decision making which is crucial
331 for norm compliance (R. J. R. Blair, 2007). Dysfunction of the vmPFC contributes to immoral
332 behavior that is commonly seen in psychopathic individuals (R. Blair, 2011; Koenigs,
333 Kruepke, Zeier, & Newman, 2012). In general, abnormal interactions of the regions in the
334 prefrontal cortex may contribute to poor self-control, impulsivity and aggressivity associated
335 with psychopathic traits (Hoppenbrouwers et al., 2013).

336 On the other hand, we demonstrated that high-degree nodes in the negative networks
337 involved regions supporting emotional and social processing, such as the insula, the STS and
338 SMG. The insula has been widely recognized to be involved in emotional processing (Menon
339 & Uddin, 2010). Activations of the insula during an emotional facial expression task are
340 negatively correlated with psychopathic traits (Seara-Cardoso, Sebastian, Viding, & Roiser,
341 2016). Our results indicate that altered intrinsic network architecture involving the insula may
342 be related to atypical emotional functions for individuals with higher psychopathic traits. The
343 STS and SMG is engaged in social cognition (Zilbovicius et al., 2006) and especially plays an
344 important role in overcoming emotional egocentricity (Isik, Koldewyn, Beeler, & Kanwisher,
345 2017; Silani, Lamm, Ruff, & Singer, 2013). Dysfunction of the connection involving these
346 two regions may underlie the abnormal social processing of individuals with elevated
347 psychopathic traits.

348 Secondary psychopathy has been suggested to be associated with impulsivity and
349 antisocial behavior (Dean et al., 2013). Similar to the T-PTS predictive model, nodes located
350 in the prefrontal cortex (i.e., aPFC) also had a relatively high degree in the S-PTS predictive
351 model. Additionally, the ACC served as another high-degree node in the model that
352 significantly predicted secondary psychopathy. The ACC is implicated in the emotional
353 regulation (Hornak et al., 2003), reward assessment (Knutson, Westdorp, Kaiser, & Hommer,
354 2000), and risky decision-making (Fishbein et al., 2005). Accumulating evidence indicated
355 that the ACC is robustly related to impulse control which is involved in multiple processes
356 including response inhibition and affective decision making (Castellanos-Ryan & Séguin,
357 2016; Hoerst et al., 2010; Strafella, 2019). Thus, dysfunction of the ACC may underlie

358 insufficient decision-making and poor impulsive control in individuals with high secondary
359 psychopathy score ([Koenigs, 2012](#)).

360 Additionally, it is worth noting that connections between the OCCN and CON
361 constituted the predictive models of T-PTS and S-PTS in terms of the large-scale functional
362 networks. The OCCN is typically involved in visual functions such as visual perception and
363 discrimination ([Likova & Tyler, 2008](#)), and the CON is mostly engaged in saliency detection
364 and emotional processing ([Coste & Kleinschmidt, 2016](#); [Sadaghiani & D'Esposito, 2015](#)). The
365 amygdala, a key node in the CON has extensive connections with visual regions and the
366 functional connections between OCCN and CON may reflect the emotion-related modulation
367 of visual processing stream ([Morris, Buchel, & Dolan, 2001](#)). It has been previously
368 suggested that psychopathy scores were associated with abnormal connectivity within and
369 between the FPN, DMN and CON ([Carissa L Philippi et al., 2015](#); [Thijssen & Kiehl, 2017](#)).

370 Here, we provided novel evidence that decreased OCCN-CON intrinsic functional
371 connectivity was associated with higher psychopathic traits, reflecting atypical visual
372 attentional processing to emotionally salient stimuli in the environment for individuals with
373 elevated psychopathic traits. Consistent with this assumption, psychopathic traits have been
374 shown to be associated with reduced augmentation effect of emotion content on the brain
375 activity in visual processing regions in a task which requires attention to emotional features of
376 visual stimuli, suggesting abnormal interaction between visual attention and emotional
377 processing for individuals with elevated psychopathic traits ([Nathaniel E Anderson et al.,](#)
378 [2017](#)).

Several limitations in the current study should be addressed in future studies. First, the sample of the present study was college students with a relatively modest sample size ($n=84$). The college student sample is different from the community sample especially in age, social status, and intelligence level. Therefore, future work using a large community sample is warranted. Second, although the present study significantly predicted the T-PTS and S-PTS based on RSFC, the reliability of the results needs further validation. Future studies could use external samples to test the generalizability and validate the predictive models. Third, while we found that decreased OCCN-CON connections predicted psychopathic traits at the large-scale network level, it needs more evidence to verify the results as the OCCN has not been typically found to be associated with psychopathic traits. Despite these limitations, our study sheds new light on neural signatures of psychopathic traits in college students.

Conclusion

The current study demonstrated that the connectome consisting of whole-brain RSFC successfully predicted T-PTS and S-PTS at the individual level in a college student sample. Notably, high-degree nodes in the predictive models mainly included brain regions located in the prefrontal cortex and limbic system. In addition, the OCCN-CON connections also constituted the predictive connectomes. The CPM approach provides a novel tool to characterize the neural underpinnings of psychopathic traits. Moreover, our findings may advance our understanding of psychopathic traits in the non-clinical sample and may have potential applications in the early diagnosis and intervention of psychopathy.

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Figure legends

Figure 1. The workflow of connectome-based predictive modeling (CPM).

Preprocessed resting-state fMRI data (a) were used to calculate whole-brain functional connectivity based on the Dosenbach atlas (b). Correlation analyses were then performed between connectivity matrix and questionnaire measurements (e.g., total LSRP score) (c). The important edges were selected by setting a threshold of $p < 0.01$ (d). The edges were separated into the positive network (edges positively correlated with the questionnaire measurements) and negative network (edges negatively correlated with behavioral measurements) (e). For each participant, the sum of selected edges for the two networks were calculated (f). Linear predictive models were built to predict psychopathic traits. The CPM made out-of-sample predictions by applying a cross-validated approach (g). A permutation test was utilized to examine the performance of predictive models (h).

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Figure 2. Performance of the prediction models for total LSRP, primary psychopathy, and secondary psychopathy score based on the negative network. Correlation between actual and predicted values, and permutation distribution of the correlation coefficient and SMSE for the prediction of the total psychopathic traits score (a), primary psychopathic traits score (b), and secondary psychopathic traits score (c). The values obtained using the real scores are indicated by the black dash line. T-PTS: total psychopathic trait score; P-PTS: primary psychopathic trait score; S-PTS: secondary psychopathic trait score; SMSE: standard mean square error; N.S.: not significant; * $p < 0.05$.

Figure 3. Negative networks for predicting total LSRP and secondary psychopathy score.
Negative networks in predicting total psychopathic trait score (a) and secondary psychopathic trait score (b). T-PTS: total psychopathic trait score; S-PTS: secondary psychopathic trait score.

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Figure 4. Within- and between-network connectivity for the negative networks.

Cells represent the total number of edges connecting nodes within (and between) each network, with darker colors indicating a greater number of edges. T-PTS: total psychopathic trait score; S-PTS: secondary psychopathic trait score.

Table legends

Table 1. Participants demographics and LSRP scores.

	Male (N=34)		Female (N=50)		<i>p</i> -value
	Mean	SD	Mean	SD	
Age (years)	23.29	3.13	22.10	2.05	0.056
T-PTS	53.15	8.02	54.22	7.35	0.529
P-PTS	33.27	5.93	33.08	5.07	0.879
S-PTS	19.88	3.21	21.14	3.55	0.101

SD: standard deviation; T-PTS: total psychopathic trait score; P-PTS: primary psychopathic trait score; S-PTS: secondary psychopathic trait score.

Table.2 Eight nodes (5%) with the most connections in the negative networks in predicting total psychopathic trait score.

Node series ^a	Anatomic regions	MNI coordinates			Network	Degree centrality	Hemi
		x	y	z			
89	STS ^b	58	-41	20	CON	9	R
135	MOG ^b	39	-71	13	OCCN	9	R
8	aPFC	27	49	26	CON	7	R
15	IOFC	39	42	16	FPN	7	R
10	aPFC	-43	47	2	FPN	6	L
13	vmPFC	8	42	-5	DMN	5	R
76	Insula	-30	-28	9	CON	5	L
97	SMG ^b	-55	-44	30	CON	5	L

MNI: Montreal Neurological Institute; aPFC: anterior prefrontal cortex; MOG: middle occipital gyrus; STS: superior temporal sulcus; SMG: supramarginal gyrus. IOFC: inferior orbitofrontal cortex; MFG : middle frontal gyrus; vmPFC: ventromedial prefrontal cortex.

a: The serial numbers are taken from Dosenbach atlas.

b: The anatomical regions were defined based on Automated Anatomical Labeling (AAL) atlas.

665 **Table.3 Eight nodes with the most connections in the negative networks in predicting**
666 **secondary psychopathic trait score.**

Node series ^a	Anatomic regions	MNI coordinates			Network	Degree centrality	Hemi
		x	y	z			
8	aPFC	27	49	26	CON	12	R
10	aPFC	-43	47	2	FPN	12	L
50	SFG ^b	-26	-8	54	SMN	10	L
135	MOG ^b	39	-71	13	OCCN	8	R
9	OFC ^b	42	48	-3	FPN	8	R
152	Calcarine ^b	-5	-80	9	OCCN	7	L
21	ACC	-1	28	40	FPN	7	L
19	ACC	-2	30	27	CON	6	L

667 MNI: Montreal Neurological Institute; aPFC: anterior prefrontal cortex; SFG: superior frontal
668 gyrus; MOG: middle occipital gyrus; OFC: orbitofrontal cortex; ACC: anterior cingulate cortex.

669 a: The serial numbers are taken from Dosenbach's atlas.

670 b: The anatomical regions were defined based on Automated Anatomical Labeling (AAL) atlas.

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672 **Table 4. Results of validation analyses.**

	T-PTS		P-PTS		S-PTS	
	<i>r</i>	<i>SMSE</i>	<i>r</i>	<i>SMSE</i>	<i>r</i>	<i>SMSE</i>
2-fold	0.203 [*]	2.687 [*]	0.058	1.471	0.223 [*]	0.967 [*]
5-fold	0.249 [*]	2.206 [*]	0.091	1.732	0.262 [*]	1.099 [*]
10-fold	0.232 [*]	1.902 [*]	0.098	2.156	0.278 [*]	1.279 [*]

673 T-PTS: total psychopathic trait score; P-PTS: primary psychopathic trait score; S-PTS: secondary
674 psychopathic trait score. *SMSE*: standard mean square error; ^{*}: $p < 0.05$