

# Archival Report

## A Connectome-wide Functional Signature of Transdiagnostic Risk for Mental Illness

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### ABSTRACT

**BACKGROUND:** High rates of comorbidity, shared risk, and overlapping therapeutic mechanisms have led psychopathology research toward transdiagnostic dimensional investigations of clustered symptoms. One influential framework accounts for these transdiagnostic phenomena through a single general factor, sometimes referred to as the “p” factor, associated with risk for all common forms of mental illness.

**METHODS:** We build on previous research identifying unique structural neural correlates of the p factor by conducting a data-driven analysis of connectome-wide intrinsic functional connectivity ( $n = 605$ ).

**RESULTS:** We demonstrate that higher p factor scores and associated risk for common mental illness maps onto hyperconnectivity between visual association cortex and both frontoparietal and default mode networks.

**CONCLUSIONS:** These results provide initial evidence that the transdiagnostic risk for common forms of mental illness is associated with patterns of inefficient connectome-wide intrinsic connectivity between visual association cortex and networks supporting executive control and self-referential processes, networks that are often impaired across categorical disorders.

**Keywords:** Connectivity, fMRI, P factor, Psychopathology, Resting-state, Transdiagnostic

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Emerging research has identified a general factor of psychopathology that accounts for shared risk among internalizing, externalizing, and thought disorders across diverse samples (1–6). In contrast to the traditional clinical science model that compares cases of individuals meeting criteria for a categorical disorder to those not meeting these criteria (i.e., “healthy” control subjects), this general psychopathology or “p” factor reflects an individual’s latent liability for mental illness (7). For individuals with clinical disorders, higher p factor scores portend greater chronicity and symptom severity (1,7). In healthy individuals, higher p factor scores reflect relative risk for developing future clinical disorder. Moreover, the p factor provides a framework for explaining the high rates of comorbidity as well as the shared genetic variance among categorical mental disorders (8,9). As such, the p factor represents a potentially useful avenue for better understanding the shared and unique etiology of common mental illness. However, the biological mechanisms through which the p factor confers general risk for psychopathology remain unclear. Identifying such mechanisms is necessary for effectively leveraging the p factor to derive novel targets for clinical intervention and prevention.

Clinical neuroscience has begun to adopt transdiagnostic methodologies to accelerate the search for common neurobiological abnormalities across disorders (10). For example, a recent large meta-analysis of six categorical disorders reported a shared pattern of reduced gray matter volume in a distributed network supporting attention and cognitive control (11). In addition, we have recently examined the structural

neural correlates of the p factor specifically (12). In our work, higher p factor scores and thus risk for common mental illness was associated with reduced gray matter volumes in the occipital lobes and neocerebellum. Furthermore, higher p factor scores were associated with reduced fractional anisotropy in pontine pathways linking the neocerebellum with the thalamus and prefrontal cortex. This network of brain regions is thought to be a forward monitor of incoming sensory information, generating and updating internal models for motor and cognitive tasks (13). In addition, activation of the neocerebellum has been associated with cognitive control tasks (14), reflecting its contribution to the extended cognitive control network, including the dorsolateral and medial prefrontal cortex (15). Thus, our observed p factor associations along with meta-analytic results suggest that transdiagnostic risk for common forms of mental illness may be associated with structural deficits in a network of brain regions supporting cognitive control. However, the putative functional consequences of these observed structural associations have not yet been examined.

Resting-state functional connectivity is a powerful tool in clinical neuroscience because it can be readily administered across patient populations (16,17), demonstrates trait-like stability (18) as well as moderate heritability (19,20), and represents a powerful probe of the intrinsic architecture of neural networks that play a primary role in shaping task-based network activity and associated behaviors (21). In addition, altered intrinsic functional connectivity within the default mode network (DMN) and frontoparietal network (FPN), both of which

are linked to higher order cognition, have been broadly linked to psychopathology across categorical disorders (22–24). Thus, resting-state measures of intrinsic network connectivity represent one avenue for extending the structural associations of the p factor to variability in functional neural dynamics representing mechanisms through which risk may emerge.

We investigate intrinsic functional connectivity correlates of the p factor in a volunteer sample of 614 university students from the Duke Neurogenetics Study (DNS). While our previous research in this sample identified discrete structural correlates of the p factor in the occipital lobes, neocerebellum, and pons, we opted for a whole-brain exploratory analysis of intrinsic connectivity to capture functional differences beyond these regions and impose minimal assumptions about the nature of p factor associations in the brain. While there are many exploratory methods for investigating resting state functional connectivity, we performed a connectome-wide association study (CWAS) (25) of the p factor using multidimensional matrix regression (MDMR) (26). In contrast to traditional seed-based approaches, MDMR allows a search across the whole brain for multivariate connectivity patterns that vary with p factor scores, while at the same time making few assumptions about the data or expected effects. Unlike clustering (27) or independent components analysis (28), MDMR does not require a priori estimates of the dimensionality of the data or choosing networks or connections of interest. In addition, MDMR does not require arbitrary decisions about thresholding matrices [as in many graph analysis techniques (29)], while retaining the advantages of interpretability and visualization of traditional seed based approaches. For these reasons, we conducted a CWAS to identify associations between p factor scores and intrinsic functional connectivity.

## METHODS AND MATERIALS

### Participants

Data for this study come from the DNS, which was designed to allow for examination of predictive links between genes, brain, behavior, and risk for mental illness among 18- to 22-year-old university students. DNS participants were recruited primarily from the Duke University student body via flyers and online postings. After successful completion of the DNS protocol, participants received financial compensation as well as a free 23andMe account. While all 1333 DNS participants completed mental health assessments and structural neuroimaging, resting-state functional magnetic resonance imaging (fMRI) was collected on only a subset because of revisions of the MRI protocol to accommodate two new task-fMRI scans, which led to removal of the resting-state scans from the protocol. Specifically, resting-state data were collected on 614 consecutive participants; therefore, this subsample is broadly representative of the entire DNS sample and does not suffer from further selection bias. All participants provided informed consent in accordance with the Duke University Medical Center Institutional Review Board guidelines before participation. All participants were in good general health and free of the following conditions, known to artifactually influence MRI data collection: 1) medical diagnoses of cancer, stroke, head injury with loss of consciousness, untreated migraine headaches, diabetes requiring insulin treatment, and chronic kidney or liver disease; 2) use of

psychotropic, glucocorticoid, or hypolipidemic medication; and 3) conditions affecting cerebral blood flow and metabolism (e.g., hypertension). One goal of the DNS was to study mental health and illness; therefore, participants were not excluded if they met criteria for substance abuse or a mental illness.

### Clinical Diagnosis

Current and lifetime DSM-IV Axis I disorder or select Axis II disorders were assessed with the electronic Mini-International Neuropsychiatric Interview (30) and Structured Clinical Interview for the DSM-IV subtests (31), respectively. Importantly, diagnosis was not an exclusion criterion, as the DNS seeks to establish broad variability in multiple behavioral phenotypes related to psychopathology. Allowing for a broad spectrum of symptoms is particularly critical for accurately deriving p factor scores. Nevertheless, no participants were taking any psychoactive medication during or at least 14 days before their participation. Of the 605 participants with data included in our analyses, 133 individuals had at least one DSM-IV diagnosis, including 76 with alcohol use disorders, 24 with nonalcohol substance use disorders, 33 with major depressive disorder, 26 with bipolar disorder, 7 with panic disorder (no agoraphobia), 9 with panic disorder including agoraphobia, 4 with social anxiety disorder, 8 with generalized anxiety disorder, 10 with obsessive-compulsive disorder, and 7 with eating disorders. While this is a university-based convenience sample that is not representative of the broader population in intelligence or parental education (due to the selective admissions criteria of Duke University), the sample is broadly representative of the general population in terms of rates of mental illness (32).

### Derivation of P Factor Scores

In previous work (12), our group replicated the p factor in the DNS using confirmatory factor analysis of self-report and diagnostic interview measures of internalizing, externalizing, and thought disorder symptoms. These p factor scores were extracted using the standard regression method from those analyses and standardized to a mean of 100 (SD = 15), with higher scores indicating a greater propensity to experience all forms of psychiatric symptoms. Details on the derivation of the p factor scores can be found in the Supplement.

### Image Acquisition

Each participant was scanned using one of two identical research-dedicated 3T MR750 scanners (GE Healthcare, Little Chalfont, United Kingdom) equipped with high-power, high duty cycle 50-mT/m gradients at 200 T/m/s slew rate, and an eight-channel head coil for parallel imaging at high bandwidth up to 1 MHz at the Duke-UNC Brain Imaging and Analysis Center. A semiautomated high-order shimming program was used to ensure global field homogeneity. A series of 34 interleaved axial functional slices aligned with the anterior commissure–posterior commissure plane were acquired for full-brain coverage using an inverse-spiral pulse sequence to reduce susceptibility artifacts (repetition time = 2000 ms, echo time = 30 ms, flip angle = 60°, field of view = 240 mm, 3.75 × 3.75 × 4 mm voxels, interslice skip = 0). Four initial

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radiofrequency excitations were performed (and discarded) to achieve steady-state equilibrium. For each participant, two back-to-back 4-minute 16-second resting-state fMRI scans were acquired. Participants were instructed to remain awake, with their eyes open during each resting state scan. To allow for spatial registration of each participant's data, T1-weighted images were obtained using a three-dimensional Ax fast spoiled gradient echo BRAVO with the following parameters: repetition time = 8.148 ms, echo time = 3.22 ms, 162 axial slices, flip angle = 12°, field of view = 240 mm, matrix = 256 × 256, slice thickness = 1 mm with no gap, and total scan time = 4 minutes 13 seconds.

### Image Processing

Anatomical images for each subject were skull stripped, intensity normalized, and nonlinearly warped to a study-specific average template in the standard stereotactic space of the Montreal Neurological Institute template using the advanced normalization tools (ANTs) SyN registration algorithm (33,34). Time series images for each subject were despiked, slice time corrected, realigned to the first volume in the time series to correct for head motion using AFNI tools (35), coregistered to the anatomical image using FSL's boundary based registration (36), spatially normalized into Montreal Neurological Institute space using the nonlinear ANTs SyN warp from the anatomical image, resampled to 2-mm isotropic voxels, and smoothed to minimize noise and residual difference in gyral anatomy with a Gaussian filter set at 6-mm full width at half maximum. All transformations were concatenated so that a single interpolation was performed.

Time series images for each participant were further processed to limit the influence of motion and other artifacts. Voxelwise signal intensities were scaled to yield a time series mean of 100 for each voxel. Motion regressors were created using each subject's six motion correction parameters (3 rotation and 3 translation) and their first derivatives (37,38) yielding 12 motion regressors. White matter and cerebrospinal fluid nuisance regressors were created using CompCorr (39). Images were bandpass filtered to retain frequencies between 0.008 and 0.1 Hz, and volumes exceeding 0.25-mm framewise displacement or 1.55 standardized DVARS (40,41) were censored. Nuisance regression, bandpass filtering, and censoring for each time series was performed in a single processing step using AFNI's 3dTproject. Participants were excluded if they had fewer than 185 time points left after censoring (resulting in inadequate degrees of freedom to perform nuisance regressions), resulting in a final sample of 605 subjects.

### Connectome-wide Association Study

To make the analysis computationally tractable, time series were extracted from a parcellated atlas instead of using voxelwise data. We used the Lausanne atlas parcellated into 1015 equally sized regions through the program `easy_lausanne` ([github.com/mattcieslak/easy\\_lausanne](https://github.com/mattcieslak/easy_lausanne)). Time series data for each subject were then processed using a CWAS. Described extensively elsewhere (25), a CWAS consists of three processing steps. First, beginning with a single region of interest (ROI) time series, seed-based connectivity analysis is

conducted to generate a whole-brain functional connectivity map for each participant. Second, the average distance (1 – the Pearson correlation) between each pair of participant's functional connectivity maps is computed, resulting in a distance matrix encoding the multivariate similarity between each participant's connectivity map. Finally, MDMR is used to generate a pseudo-*F* statistic quantifying the strength of the association between the phenotype of interest, here *p* factor scores, and the distance matrix created in the second step. The advantage of MDMR is allowing covariates to be entered into the regression and using nonparametric permutation to generate *p* values for each ROI. These three steps are repeated for each of the 1015 ROIs, resulting in a whole-brain map that represents the association between *p* factor scores and whole-brain connectivity at each ROI. A CWAS was performed to identify seed regions with whole-brain patterns of connectivity are related to *p* factor scores. Participant sex was included as a covariate, and 500,000 permutations were performed to generate *p* values. To minimize false positives across the 1015 ROIs, a false discovery rate (42) correction was applied. The threshold for statistical significance was set at  $q = .05$ .

### Seed-Based Analyses

MDMR identifies a set of ROIs with patterns of whole-brain connectivity associated with *p* factor scores. However, it is still unclear how the connectivity of these ROIs relates to the scores. Previous research using a CWAS (25,43,44) has demonstrated the utility of using traditional seed-based connectivity follow-up analyses to better understand the networks and brain regions that drive the associations discovered through MDMR. Similar analyses were performed here for each ROI identified via MDMR. Seed-based connectivity maps were created and correlations were converted to *Z* statistics via the Fisher *R* to *Z* transform. Whole-brain correlations between these connectivity values and *p* factor scores were calculated, including sex as a covariate. Importantly, these follow-up analyses do not represent independent statistical tests because they were performed post hoc to the familywise error-controlled MDMR findings. Accordingly, these follow-up analyses maps are not thresholded to visualize all information that was relevant to the MDMR step.

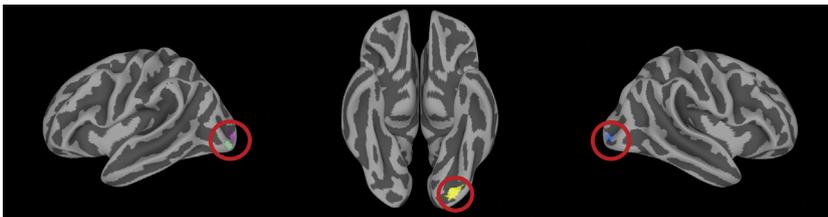
## RESULTS

### Demographics

From the 614 participants who completed two resting-state scans, 605 had data that survived quality control procedures. Of these, 336 were women, and the mean ± SD age was 20.23 ± 1.19 years. Scores for the *p* factor ranged from 76.71 to 191.96 (mean ± SD, 99.80 ± 15.39).

### Multidimensional Matrix Regression

Whole-brain maps from 1015 ROIs were compared to estimate the multivariate distance (dissimilarity) between each subject map at every ROI. MDMR was then used to statistically test the association between these distances and individual *p* factor scores. MDMR revealed that four ROIs had whole-brain connectivity patterns that were significantly associated with *p*



**Figure 1.** Data-driven multidimensional matrix regression analysis revealed four regions with whole-brain connectivity patterns significantly associated with p factor scores: two adjacent parcels of the left middle occipital gyrus (left panel), left lingual gyrus (middle panel), and right middle occipital gyrus (right panel). These four clusters are projected onto a surface volume for visualization.

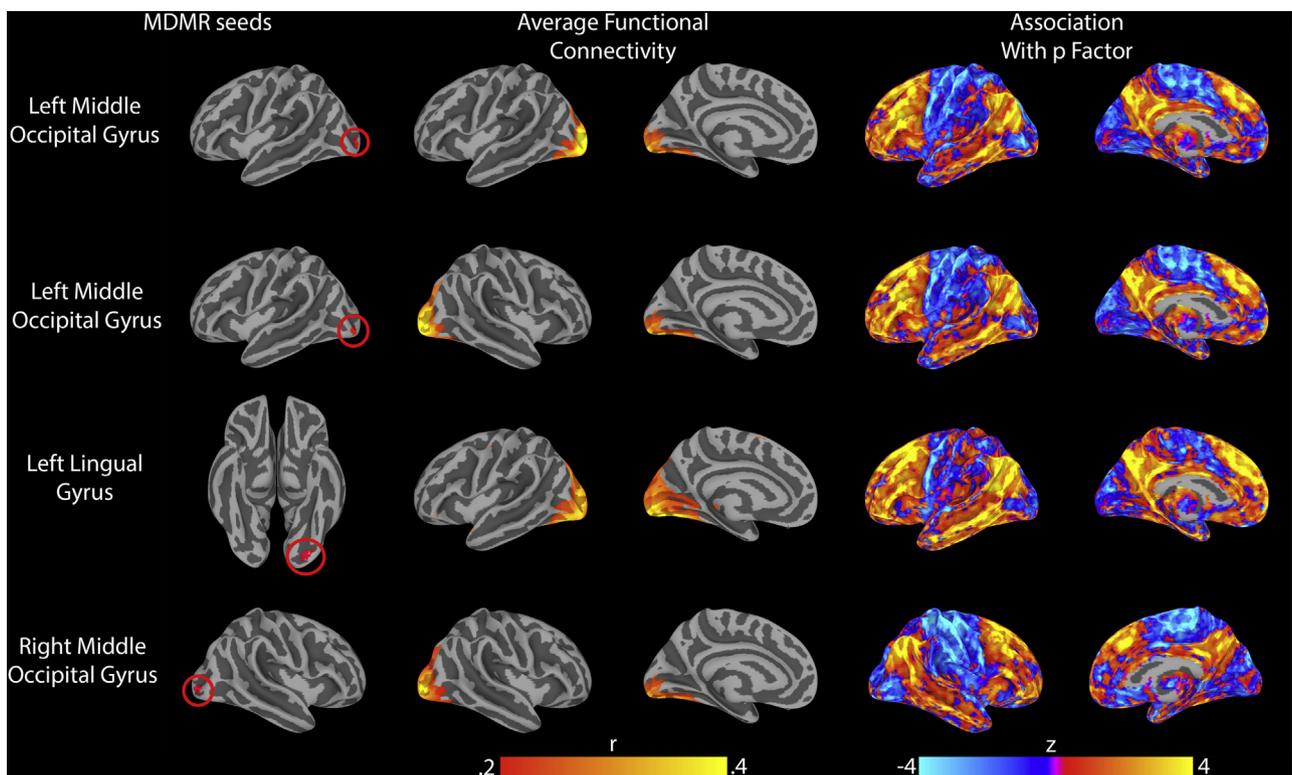
factor scores. This included the left lingual gyrus ( $x = 28, y = 85, z = -18$ , corrected  $p = .9680$ ), right middle occipital gyrus ( $x = -31, y = 94, z = 0$ , corrected  $p = .9743$ ), and two adjacent parcels of the left middle occipital gyrus ( $x = 32, y = 93, z = -5$ , corrected  $p = .9949$ ) and ( $x = 30, y = 96, z = 0$ , corrected  $p = .9949$ ) (Figure 1).

### Follow-up Intrinsic Connectivity Analyses

The follow-up connectivity analyses of each seed identified through MDMR revealed the primary network associations for each seed as well as their pattern of whole-brain connectivity associated with p factor scores. These analyses showed striking convergence across MDMR-selected ROIs, wherein the mean whole-brain pattern of connectivity for each seed showed subtle variation but largely outlined the canonical resting-state visual processing network (45). The connectivity

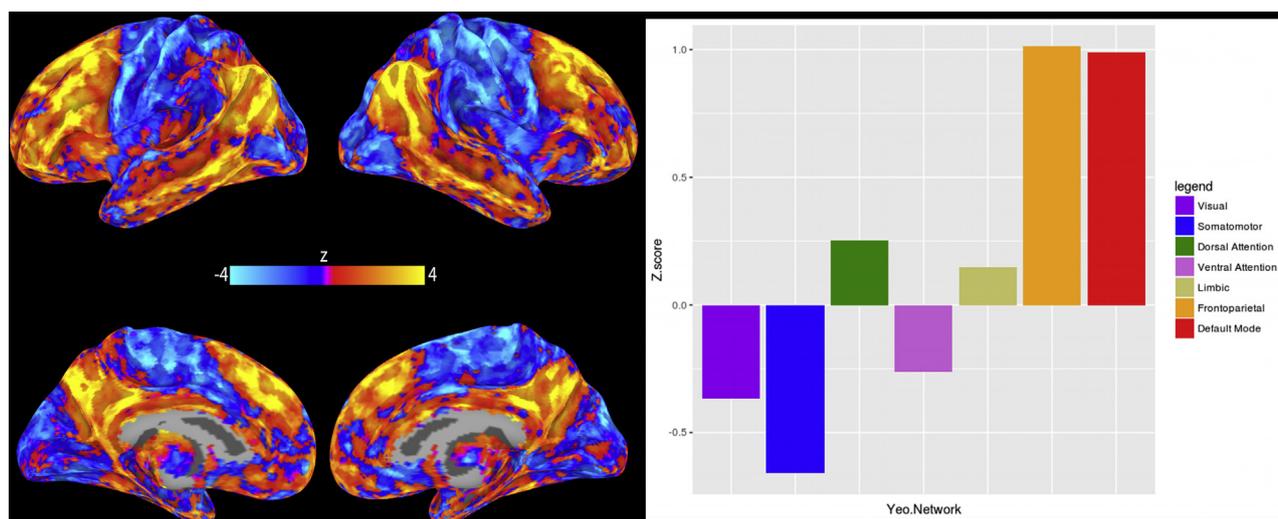
of each ROI with visual and somatosensory regions decreased with increasing p factor scores, while the connectivity between each ROI and transmodal association regions (46) increased with increasing p scores (Figure 2).

Additional analyses were conducted to better characterize the above consistent patterns of p factor associations with the intrinsic connectivity of all seeds by averaging the independent whole-brain connectivity maps. The resulting average z scores were summarized for each of the seven Yeo networks (47) to quantify their respective contribution to the associations with p factor scores (Figure 3). These analyses revealed the DMN and FPN as the major networks for which intrinsic functional connectivity was positively correlated with p factor scores. In contrast, a more modest but notable negative correlation was observed between p factor scores and the intrinsic functional connectivity



**Figure 2.** Follow-up connectivity analyses of the four seeds identified through multidimensional matrix regression (MDMR) revealed a highly conserved pattern of altered connectivity between visual association cortex and both frontoparietal and default mode networks as a function of p factor scores. All results were projected from the volume onto a surface to aid visualization. (Left panel) MDMR-derived seed regions. (Middle panel) Average intrinsic connectivity for each seed. (Right panel) Connectome-wide intrinsic connectivity patterns for each seed as a function of p factor scores.

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**Figure 3.** (Left panel) Mean pattern of intrinsic connectivity as a function of p factor scores across the networks associated with each of the four multi-dimensional matrix regression-derived seeds in the visual association cortex. (Right panel) The relative contributions of seven canonical intrinsic cerebral networks [as determined by Yeo *et al.* (47)] to this mean pattern of connectivity.

between the visual association cortex and somatomotor network.

## DISCUSSION

We provide a novel extension of previous structural neural correlates of the p factor to the intrinsic architecture of the whole-brain functional connectome. Our unconstrained connectome-wide MDMR analysis revealed a circumscribed relationship between p factor scores and the whole-brain intrinsic connectivity of four nodes in the visual association cortex. These findings are generally consistent with our earlier work finding a negative correlation between p factor scores and gray matter volume in the occipital cortex (12). Additional investigation of the patterns of intrinsic connectivity driving this relationship primarily implicated hyperconnectivity between the visual association cortex and the heteromodal FPN and DMN. While differences in the intrinsic functional connectivity of visual areas is not commonly thought of as a core feature of psychopathology, our findings are not unique in pointing to dysfunction in visual association cortex and are consistent with a growing body of literature implicating sensory processing in transdiagnostic research.

The selection and suppression of incoming sensory information is an important component of goal-directed behavior. Functional connectivity between visual and heteromodal association cortices (including the FPN and DMN) has been shown to be critical for selecting task-relevant information (48,49). We found that individual differences in the functional connectivity of visual association cortex with the FPN and DMN are associated with the p factor. Although speculative, our findings may indicate the more effortful or less efficient integration of bottom-up sensory information with attentional demands and executive control processes in those at higher risk for mental illness. The specificity of this pattern to visual and not other sensory association cortices may reflect the dominance of the visual modality in guiding human perception

of the external world and, possibly equally, the construction of internal models necessary for higher cognitive processes including executive control (50,51).

Supporting evidence can be found in studies of schizophrenia and bipolar disorder, where visual network connectivity has been implicated in deficits involving the binding of visual objects (52) and in processing of visual stimuli (53). Functional connectivity between frontal association and visual cortex has also been associated with disrupted working memory in depression (54,55) and in neurocognitive deficits in schizophrenia (56). While the visual cortices are not often thought of as primary to dysfunction in psychopathology, these studies suggest that visual cortical dysfunction may play a role in neurocognitive deficits present in many forms of psychopathology (57–59). In addition, when assumptions are relaxed and whole-brain, resting-state connectivity analyses are performed, connections between the visual cortex and frontal association cortex have been shown to be predictive of psychopathology in depression (60) and schizophrenia (61). It is possible that the relative sparsity of links between visual cortex dysfunction and psychopathology partially reflects a bias in resting-state analyses toward strong assumptions about where in the brain findings are expected, which could result in missing associations with visual networks. Now that many large imaging datasets that include psychiatric data have been publicly released, our findings encourage further unbiased, data-driven whole-brain analyses in search of transdiagnostic neural correlates of psychopathology.

While our findings implicate visual association cortex in the general liability for mental illness, they do so primarily through its connectivity with the FPN and DMN. These networks consist of heteromodal association cortices that process information from multiple sensory domains, and consist of brain regions most implicated in higher-order thought and executive control of other networks (46). The unique role of the FPN and DMN in complex cognition (21,62–65) place them centrally in many etiologic theories of psychopathology (22,23,66–68),

making their primary role in driving the association between visual cortex connectivity and p factor scores particularly relevant.

The FPN in particular has been linked to the core cognitive faculty of executive control (21,62,67), which contributes to mental health and general well-being by shaping successful goal-directed behavior (69). Fittingly, disrupted FPN activity has been linked to psychopathology across categorical disorders including schizophrenia (70), depression (71), and bipolar disorder (72). Building off of this body of research, an emerging theory suggests that the relative integrity of the FPN and associated executive control mechanisms are fundamental for the capacity to self-regulate, manage symptoms, and succeed in treatment (22). Our current findings are consistent with this framework by demonstrating that higher p factor scores regardless of diagnosis are associated with relative hyperconnectivity of the FPN with the visual association cortex, suggesting one way through which FPN dysfunction may be manifest as psychopathology.

In addition to the FPN, our analyses implicate hyperconnectivity between the visual association cortex and DMN as a function of higher p factor scores. The DMN has been generally linked to introspection, autobiographical memory, and future-oriented thought (68). Interestingly, DMN activity is suppressed in attention demanding tasks (68,73), and altered DMN activity has been broadly observed across categorical psychiatric disorders (23,66). Connectivity between the DMN and visual association cortex is important in the suppression of internally generated distracting information (49). Taken together, transdiagnostic risk for mental illness as indexed by p factor scores may lead to more effortful or less efficient processing when internally generated thought and externally generated sensory information compete for attention.

While providing initial evidence that broad risk for all forms of common mental illness is manifest as alterations in the intrinsic connectivity of functional neural networks, our analyses were exploratory by design and replication in independent samples is needed. Given previous research implicating the FPN and DMN across categorical disorders, we focused our above discussion on the potential relevance of intrinsic connectivity between visual association cortex and these networks in the emergence of transdiagnostic risk for mental illness. While the intrinsic connectivity of these networks also exhibited an outsized influence on the association with p factor scores, variation between visual association cortex and other resting-state networks contributed as well, albeit more modestly (Figure 3). MDMR uses information from all whole-brain connections in selecting seeds, and the inferential significance comes from the aggregate of connections rather than any one connection in particular. Thus, formally testing the relative contributions of different networks is not typically conducted. While we think future studies of the p factor will benefit from using our observations of intrinsic connectivity between visual association cortex and both DMN and FPN as a priori starting points, the potential relevance of other networks should not be ignored until the patterns reported herein are replicated.

Additional limitations that can be addressed in future research include the relatively limited range of psychopathology, especially severe forms including psychosis, represented in our volunteer sample of young adults. Future research

should extend our analyses to more diverse populations including individuals with severe mental illness. While the DNS is broadly representative of population base rates of common forms of mental illness (32), it is not representative of the general population in terms of socioeconomics or intelligence. Thus, extension of these findings to population representative samples is needed. In addition, our results need to be replicated in well-powered independent samples to establish the reliability of these associations and provide unbiased estimates of the true effect sizes (74). In fact, we adopted a rigorous data-driven, unbiased approach in the current discovery analyses to minimize false positives and effect size inflation (i.e., “winner’s curse”) and bolster future attempts at replication. Our current analyses were also limited to the intrinsic connectivity of nodes within the cerebrum because our resting-state fMRI acquisition protocol did not afford full coverage of the cerebellum, including the neocerebellar sub-region identified in our earlier structural analyses. Thus, we are unable to determine the relationship between p factor scores and the intrinsic functional connectivity of the cerebellum. We anticipate that current state-of-the-art multiband image acquisition protocols will routinely allow for full coverage of the cerebellum and, subsequently, direct analyses of how its intrinsic connectivity may scale as a function of p factor scores. The observational nature of our study represents another limitation given that we cannot establish causal links between p factor scores and intrinsic connectivity. Longitudinal designs may better address causality and temporal order of these phenomena. Future research using transcranial magnetic stimulation, closed-loop fMRI, and intervention designs can further map causal relationships.

These limitations notwithstanding, our current work provides initial evidence for unique connectome-wide functional signatures of the p factor. Consistent with emerging transdiagnostic and dimensional research into the neural basis of psychopathology (11,12,44), our analyses reveal that increased broad risk for all common forms of mental illness is associated with higher intrinsic connectivity between visual association cortex and both FPNs and DMNs. Such hyperconnectivity suggests that increased risk for psychopathology may be manifest as greater effortful or less efficient executive control as well as poor regulation of self-referential information processing. These patterns place alterations of the functional connectome squarely in the middle of converging theories of network dysfunction in psychopathology, further suggesting the p factor as a promising tool in clinical neuroscience.

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## ARTICLE INFORMATION

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