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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☒	☐ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Data used for analyses were obtained from the Human Connectome Project (HCP) consortium, an open-access database with magnetic resonance imaging (MRI) and behavioral data. As we did not collect any of the data, we do not report any software used for data collection.
Data analysis	A number of software packages were used to process and analyze the MRI and behavioral data. Concerning analyses of MRI data please see below for a list of software used and their relevant versions: FSL==6.0.6 FreeSurfer==7.4.1 AFNI==23.1 ANTS 2.5.1 Matlab==r2019b Python==3.11.8 mrtrix3==3.0.4 connectome-workbench 2.0.1 ibm-ilog-cplex 12.10 R ==4.3.2 We provide custom code in a github repository that can be used to recreate the processing of MRI data, generation of neural features, and running of brain-behavior analyses. This github will be made public upon acceptance of our paper for publication.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Data used for analyses in the main text are publicly available and provided by the Human Connectome Project at www.humanconnectome.org

Data used for analyses in the supplemental materials are not publicly available due to restrictions stemming from the consent process. At the time of data collection, participants were not asked to provide consent for their data to be shared publicly or with other researchers.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	Our study includes a balanced dataset with respect to sex (54% female). Sex was determined by self report within the HCP dataset. Our study focused on theoretical predictions with respect to all humans. Thus, sex differences were deemed beyond the scope of this study and no specific hypotheses were made.
Reporting on race, ethnicity, or other socially relevant groupings	Our study did not use any constructs of race and/or ethnicity.
Population characteristics	The dataset consisted of healthy young adults from the Human Connectome Project aged 22 -36 years, mean age28.6 +/- 3.7, and 54% female,
Recruitment	Subject selection was based on whether all MRI data (i.e., diffusion-weighted, functional, and structural) and behavioral data were available.
Ethics oversight	The Institutional Review Board of the University of Illinois Urbana-Champaign reviewed and approved this study.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☒ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	We conducted a neuroimaging study in 831 individuals examining the relationship between brain structure and function, and general intelligence. We asssessed quantitative brain data using functional, structural, and diffusion-weighted MRI scans from the Human Connectome Project. Quantitative behavioral data were collected using a battery of cognitive performance tests. Advanced methods were used to jointly model brain structure and function to generate multi-modal representations of the brain's global topology. Neural connections making up this global topology were then used to predict individual differences in general intelligence. Follow up analyses were carried out to investigate relationships between specific topological properties and general intelligence.
Research sample	Our research sample was obtained from an existing dataset made publicly available by the Human Connectome Project (www.humanconnectome.org). The dataset consists of young adults aged 22 - 36 years of age. All behavioral and magnetic resonance imaging (MRI) data can be obtained after creating a free account on their website.
Sampling strategy	As the authors used an open access dataset, they did not collect any of the analyzed data. Details on data acquisition can be found here: https://doi.org/10.1016/j.neuroimage.2012.02.018
Data collection	Please see above reference for details on data acquisition.
Timing	Please see the above reference for details on timing.
Data exclusions	Participants were excluded if they had missing: 1) MRI data (i.e., structural, function, or diffusion-weighted); 2) cognitive measures

Data exclusions	used in the factor analysis to generate g scores; 3) a Mini-mental State Exam score lower than 27; 4) had a relative root mean squared movement of 0.20mm and above; and 5) had an excessive number of zeroes in their final multi-modal connectome. This was calcualted by summing the number of zeroes within each participant's connectome, z-scoring this sum, and removing participants with a z-score of 3.5 and above.
Non-participation	As this was an open access dataset that the authors did not collect themselves, this information is not known.
Randomization	There were no separate experimental groups in this study.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☐	☒ MRI-based neuroimaging

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A

Magnetic resonance imaging

Experimental design

Design type	Resting state.
Design specifications	Two 30 minute resting-state sequences, and diffusion-weighted data were used for our main analyses. These data can be found at www.humanconnectome.org and obtained after making a free account.
Behavioral performance measures	This study did not require the participant to perform a task in the scanner.

Acquisition

Imaging type(s)	Functional.
Field strength	3 Tesla
Sequence & imaging parameters	Resting state: [gradient echoplanar imaging; TR 720ms; TE 33.1ms; flip angle 52 degrees; 2.0x2.0x2.0mm voxel size; acceleration factor 8].
Area of acquisition	Whole brain

Diffusion MRI ☒ Used ☐ Not used

Parameters	TR 5520 ms; TE 89.5; 1.25x1.25x1.25 mm voxel size; acceleration factor 3; 90 directions/shell; b 1000, 2000, 3000 s/mm^2

Preprocessing

Preprocessing software

All data were downloaded in a minimally preprocessed format. Extensive details of this preprocessing pipeline are provided here: https://dow.org/10.1016/j.neuroimage.2013.04.127

Details concerning further processing of minimally preprocessed data are provided in our github repository. In summary, resting-state images were smoothed with a 4mm kernal at 75% brightness threshold using FSL's susan. They were then high-pass filtered at 0.01 Hz and linearly detrended using AFNI's 3dTproject. Finally, they underwent independent component analysis using FSL's melodic-ica to extract spatial co-activation patterns. Further processing and tractography was carried out on diffusion-weighted data according to the mrtrix3 software pipeline (https://doi.org/10.1016/j.neuroimage.2019.116137) to obtain structural connectomes. For tractography, we used multi-tissue multi-shell constrained spherical deconvolution (https://doi.org/10.1016/j.neuroimage.2014.07.061). Here, images were bias corrected using the dwibiascorrect function. Then multi-tissue response functions were calculated using the dwi2response function with the dhollander algorithm. Response functions were averaged across all participants. These group-averaged response functions were used to estimate fiber orientation distribution functions (fODFs), which were then normalized using the mtnormalise function. Tractography was run with the iFOD2 algorithm, 50 million streamlines, a fODF amplitude cutoff of 0.06, a minimum tract length of 5 millimeters, a maximum tract length of 275 millimeters, a step size of 1.25 millimeters, and an angle cutoff of 45 degrees. The code for the joint structure-function model was provided by the original authors (https://doi.org/10.1038/s41598-018-23051-9). An optimized version of this code can be found in our github repository.

Normalization

Resting-state images were registered to MNI space in one shot that included motion correction, distortion correction, T1w registration (linear), and registration from T1w space to MNI space (nonlinear).

Normalization template

MNI152

Noise and artifact removal

Resting-state images underwent independent component analysis using FSL's melodic-ica to decompose the data into independent sources of signal and noise. The resulting components were then classified based on several parameters. First, the frequency content of spatial components was calculated from the Fourier-transformed mixture matrix supplied by the melodic-ica output. Components with a large amount of high frequency content were discarded. Second, spatial components were robustly correlated with resting-state motion parameters. Components with a moderate correlation with in-scanner motion were discarded. Third, a Pearson's skewness index was calculated from the distribution of activation values for each component. Noise components are assumed to exhibit a zero-mean Gaussian distribution. Thus, components with a Pearson's skewness index close to 0 were discarded. Finally, spatial components whose voxels were not substantially within grey matter were discarded.

Volume censoring

We did not implement volume censoring.

Statistical modeling & inference

Model type and settings

Task-based fMRI was not performed

Effect(s) tested

Task-based fMRI was not performed

Specify type of analysis: ☒ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference

Task-based fMRI was not performed

(See Eklund et al. 2016)

Correction

Task-based fMRI was not performed

Models & analysis

n/a	Involved in the study
☐	☒ Functional and/or effective connectivity
☐	☒ Graph analysis
☐	☒ Multivariate modeling or predictive analysis

Functional and/or effective connectivity	We adopted a network generation method that jointly models structural connectomes with functional co-activation patterns derived from resting-state independent component analysis. The resulting connections represent the capacity of a structural connection to transmit functional information between regions exhibiting some co-activation pattern. The method is dependent on several constraints: 1) the link capacity constraint that defines an upper bound on the amount of information that can be carried by a given structural connection. This is informed by the number of streamlines a connection exhibits; 2) the node demand constraint that ensures that the information flow gathered at a given node for each functional co-activation pattern is sufficient to support the brain activity at that node. This ensures that the resulting joint structure-function connections are strong enough to support the observed functional co-activation patterns across regions; and 3) the feasibility constraint that ensures the information flow of a given connection does not exceed the maximal functional activation of the two nodes it connects.
Graph analysis	We generated global small worldness, clustering coefficient, and average shortest path length metrics at the subject level. The Telesford et al. (2012) method was used in conjunction with joint structure-function connectomes. The resulting metrics were then correlated with general intelligence scores.
Multivariate modeling and predictive analysis	We implemented a connectome-based predictive model in a l5-fold cross-validation framework to predict out-of-sample g scores from joint structure-function connections. Univariate feature selection was used that correlated each connection with the behavioral outcome. Connections that were significantly related to the behavioral outcome were retained. Retained connections were used to fit an elastic net model that was used to predict general intelligence scores. We evaluated the performance of this model by generating a Pearson correlation, coefficient of determination (i.e., explained variance), and normalized root mean square deviation between observed and predicted general intelligence scores. The significance of these metrics was evaluated using a permutation test. This consisted of keeping the whole cross-validation procedure the same, except for randomly shuffling the behavioral outcomes between subjects. This was done 1000 times to build an empirical null distribution. p-values were calculated as the number of times this 'null' model performed better in comparison to the predictive model, divided by the number of permutations used (1000).