

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement
<input type="checkbox"/>	<input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
<input type="checkbox"/>	<input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of all covariates tested
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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)
<input type="checkbox"/>	<input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
<input checked="" type="checkbox"/>	<input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
<input checked="" type="checkbox"/>	<input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
<input type="checkbox"/>	<input checked="" type="checkbox"/> Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), 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	No software was used for data collection
Data analysis	Functional Magnetic Resonance Imaging of the Brain (fMRIB) Software Library (FSL) version 6.0; Network Correspondence Toolbox (NCT) https://github.com/rubykong/cbig_network_correspondence ; Factor analysis of HCP behavioral domains: https://github.com/connectomicslab/hcp-behavioral-domains ; SHapely Additive exPlanations (SHAP): https://shap.readthedocs.io/en/latest/ . Random forest machine learning regression: https://scikit-learn.org/stable/modules/generated/sklearn.ensemble.RandomForestClassifier.html

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](#)

The HCP dataset is publicly available on an open access repository (<https://db.humanconnectome.org/app/template/Login.vm>), which can be accessed after signing a data use agreement.

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	Sex was self-reported by subjects. Interactions between sex and brain network activation in relation to task performance and mental health were evaluated.
Reporting on race, ethnicity, or other socially relevant groupings	Race and ethnicity were self-reported by subjects. Race/ethnicity was not evaluated as a variable of interest.
Population characteristics	829 individuals (Female= 446) who were an average age of 28.66 years of age (± 3.65 , range 22-36)
Recruitment	HCP-YA is a publicly available dataset.
Ethics oversight	Washington University in St Louis Institutional Review Board approved the HCP-YA 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](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

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

Sample size	We selected the HCP-YA study cohort because of its large sample of subjects with fMRI data collected during the emotional face matching task, making it suitably powered for the study of individual differences in brain function. Sample size represents the maximum number of subjects collected that met inclusion/exclusion criteria described below.
Data exclusions	Briefly, individuals were excluded by the HCP if they reported a history of major psychiatric disorder, neurological disorder, or medical disorder known to influence brain function. For the present study, we additionally excluded subjects with HCP-YA quality assessment flags, subjects with excessive head motion (i.e., 1 or more frames with framewise displacement > 2 mm), and subjects without complete EFMT fMRI data.
Replication	Analyses repeated across 2 independent HCP-YA with carefully separated family structures to avoid data leakage. replications successful.
Randomization	No randomization; N/A to current study (no group differences examined)
Blinding	No blinding; N/A to current study (no group differences examined)

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	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input type="checkbox"/>	<input checked="" type="checkbox"/> MRI-based neuroimaging

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a

Magnetic resonance imaging

Experimental design

Design type	task fMRI
Design specifications	two, 2 min and 16 second runs were acquired sequentially during session two of HCP-YA, first with right-left (RL) phase encoding and then with left-right (LR) phase encoding
Behavioral performance measures	emotion interference; cognition, positive affect, negative affect, processing speed, substance use.

Acquisition

Imaging type(s)	functional
Field strength	3T
Sequence & imaging parameters	HCP-YA neuroimaging data were acquired with a standard 32-channel head coil on a Siemens 3 T Skyra modified to achieve a maximum gradient strength of 100 mT/m ^{11,66,67} . Gradient-echo EPI images were acquired with the following parameters: TR=720 ms, TE=33.1 ms, flip angle=52°, FOV=280×180 mm, Matrix=140×90, Echo spacing=0.58 ms, BW=2290 Hz/Px. Slice thickness was set to 2.0 mm, 72 slices, 2.0 mm isotropic voxels, with a multiband acceleration factor of 8.
Area of acquisition	whole-brain
Diffusion MRI	<input type="checkbox"/> Used <input checked="" type="checkbox"/> Not used

Preprocessing

Preprocessing software	The HCP fMRI minimal preprocessing pipeline is described in detail in Glasser et al. (2013). Briefly, minimal pre-processing of fMRI data corrects for spatial distortions, realigns volumes to compensate for subject motion, registers the fMRI data to the structural image, reduces the bias field, normalizes the 4D image to a global mean, and masks the data with a final FreeSurfer-generated brain mask. We additionally applied 4 mm spatial smoothing, 150 sec temporal smoothing, removal of non-steady-state frames (first 15 frames), and ICA-FIX automated denoising method, which denoises residual subject motion, physiological motions, and artifacts, to the HCP minimally preprocessed EFMT fMRI data.
Normalization	Normalization to MNI space
Normalization template	MNI
Noise and artifact removal	Independent component analysis (ICA)-FIX

Volume censoring

No volume censoring

Statistical modeling & inference

Model type and settings

tensor independent component analysis

Effect(s) tested

correlations between network activation loadings and task-based emotion interference and mental health factor scores, controlling for age, sex and education

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

Statistic type for inference

network-wise

(See [Eklund et al. 2016](#))

Correction

bonferroni

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

Pearson correlation

Multivariate modeling and predictive analysis

network activation loadings used to predict task-based emotion interference and mental health factor scores using random forest regression. model evaluated with MSE and correlation between actual and predicted values