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Reporting Summary

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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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ | 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
<i>Give P values as exact values whenever suitable.</i> |
| ☐ | ☒ | 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 The code used in this study, along with usage instructions, is publicly available at: https://github.com/Kyrrego/MovieFC_Behav_Mapping

Data analysis The code used in this study, along with usage instructions, is publicly available at: https://github.com/Kyrrego/MovieFC_Behav_Mapping

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 Human Connectome Project(HCP) 7T Dataset used in this study is publicly available at <https://db.humanconnectome.org/>. Preprocessed shen268 atlas movie-watching BOLD time series data can be found at: https://github.com/esfynn/movie_cpm.

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	In the Human Connectome Project(HCP) 7T release data used in this study, there are 106 female and 70 male participants. In this study, we developed a model to predict the subjects' biological sex from their functional connectivity data.
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable in this study.
Population characteristics	See below in the behavioral & social sciences section.
Recruitment	The recruitment protocols of the Human Connectome Project(HCP) dataset used in this study can be found at https://www.cpccontacts.humanconnectome.org/study/hcp-young-adult/project-protocol/recruitment .
Ethics oversight	The Human Connectome Project(HCP) dataset used in this study is an open access dataset, which was approved by the Institutional Review Board (IRB) at Washington University in St. Louis.

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)

Behavioural & social sciences study design

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

Study description	This study uses quantitative analysis.
Research sample	This study uses the Human Connectome Project(HCP) 7T dataset, which is publicly available at https://db.humanconnectome.org/ .
Sampling strategy	In this study, we used data from 176 participants who completed both the 7T imaging sessions and behavioral assessments.
Data collection	The fMRI data is collected by a Siemens Magnetom 7T scanner. The behavioral data is collected with the methods of NIH Toolbox for Assessment of Neurological and Behavioral function.
Timing	The resting state fMRI and movie-watching fMRI acquisitions were collected over 2 days. On each day, participants first completed a 15-minute resting-state scan, followed by two movie-watching runs of about 15 minutes each.
Data exclusions	In this study, we only used the resting-state and movie-watching fMRI data, cognition scores, sex and age data in the HCP 7T dataset.
Non-participation	Not applicable.
Randomization	Not applicable.

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	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.

Magnetic resonance imaging

Experimental design

Design type	Resting-state and movie-watching
Design specifications	The resting state fMRI and movie-watching fMRI acquisitions were collected over 2 days. On each day, participants first completed a 15-minute resting-state scan, followed by two movie-watching runs of about 15 minutes each.
Behavioral performance measures	The behavioral data is collected with the methods of NIH Toolbox for Assessment of Neurological and Behavioral function.

Acquisition

Imaging type(s)	Functional
Field strength	7 Tesla
Sequence & imaging parameters	Sequence: Gradient-echo EPI TR: 1000 ms TE: 22.2 ms Flip angle: 45 deg FOV: 208 x 208 mm (RO x PE) Matrix: 130 x 130 (RO x PE) Slice thickness: 1.6 mm; 85 slices; 1.6 mm isotropic voxels
Area of acquisition	Whole brain
Diffusion MRI	☐ Used ☒ Not used

Preprocessing

Preprocessing software	This is described in the preprocessing pipeline for the HCP 7T release, which can be found at https://doi.org/10.1016/j.neuroimage.2013.04.127 .
Normalization	This is described in the preprocessing pipeline for the HCP 7T release, which can be found at https://doi.org/10.1016/j.neuroimage.2013.04.127 .
Normalization template	This is described in the preprocessing pipeline for the HCP 7T release, which can be found at https://doi.org/10.1016/j.neuroimage.2013.04.127 .
Noise and artifact removal	Standard preprocessing of fMRI data, including motion correction, distortion correction, high-pass filtering, and nonlinear

Noise and artifact removal	alignment to MNI template space was used in the FIX-denoised volume-space data from the HCP 7T release. We also applied global signal regression (GSR) by removing the global mean time series signal from each voxel's BOLD time series.
Volume censoring	Not applicable.

Statistical modeling & inference

Model type and settings	In this study, we developed a deep neural network model to predict cognition scores and sex from functional connectivity.
Effect(s) tested	We conducted sensitivity analysis to assess the predictive importance of brain connections.
Specify type of analysis:	☐ Whole brain ☐ ROI-based ☒ Both
Anatomical location(s)	In this study, we use the shen268 atlas for brain parcellation.
Statistic type for inference	We report both ROI-level (shen268 atlas) and connection-level analyses.
(See Eklund et al. 2016)	
Correction	In parts of this study, permutation tests were used to estimate p-values.

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	Functional connectivity was computed using the Shen 268-region atlas. For each region, we averaged voxel-wise preprocessed signals to obtain mean BOLD time series, then calculated pairwise Pearson correlations between all regions, producing a 268×268 matrix for each movie clip or rest run. The upper triangular (excluding the diagonal) was vectorized into a 35,778-dimensional feature vector.
Multivariate modeling and predictive analysis	In this study, we developed a deep neural network model to predict cognition scores and sex from functional connectivity. Prediction accuracy for cognitive scores was assessed using the Spearman correlation between observed and predicted values, while prediction accuracy for sex was evaluated using the area under the curve (AUC).