

## 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 analysis

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](#)

All data used for this manuscript are third-party data, which are available at the respective databases. The MEG UK Partnership data is held by the MEG UK Partnership, for which access can be requested at <https://meguk.ac.uk/database/>. The Cam-CAN dataset is available upon request to <https://camcan-archive.mrc-cbu.cam.ac.uk/dataaccess/datarequest.php>. The HCP dataset is freely available at <https://db.humanconnectome.org/app/template/Login.vm> but will require an application for sensitive data (see [https://www.humanconnectome.org/storage/app/media/documentation/LS2.0/LS\\_Release\\_2.0\\_Access\\_Instructions\\_June2022.pdf](https://www.humanconnectome.org/storage/app/media/documentation/LS2.0/LS_Release_2.0_Access_Instructions_June2022.pdf)). The Replay dataset will be freely available upon request (subject to participant consent) to [yunzhe.liu.16@ucl.ac.uk](mailto:yunzhe.liu.16@ucl.ac.uk). The Wakeman-Henson dataset is publicly available at OpenNeuro (<https://openneuro.org/datasets/ds000117/versions/1.0.5>).

## 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	Only reporting on sex, as gender was not collected
Reporting on race, ethnicity, or other socially relevant groupings	Data not available
Population characteristics	MEG UK (N=55): mean age 37.8 (range 19-62), 26 male/29 female Cam-CAN: mean age 54.6 (range 18-88), 310 male/302 female HCP: mean age 39 (range 22-35), 42 male/37 female, 13 mono- and 11-dizygotic twin pairs Replay dataset1: mean age 24.9 (range 19-34), 11 male/14 female Replay dataset2: mean age 25.5 (range 19-34), 10 male/16 female Wakeman-Henson: age range 23-37, 11 male/8 female
Recruitment	See original data publications
Ethics oversight	No ethical approval was required for the analysis of the public data. The ethical approvals for each of the datasets were acquired by the respective study teams, as outlined below: MEG UK: ethical approval was granted by the University of Nottingham Medical School Research Ethics Committee. Cam-CAN: ethical approval was granted by the Cambridgeshire Research Ethics Committee HCP: ethical approval was granted by the local ethics committee. Replay dataset1: ethical approval for the experiment was obtained from the Research Ethics Committee at University College London under ethics number 9929/002 Replay dataset2: ethical approval for the experiment was obtained from the Research Ethics Committee at University College London under ethics number 9929/002 Wakeman-Henson: ethical approval was obtained from the Cambridge University Psychological Ethics Committee

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://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	Sample sizes were limited by the availability of public datasets, and were not predetermined based on power calculations.  Dataset 1 (MEG UK), N=55 Dataset 2 (Cam-CAN), N=612 Dataset 3 (HCP), N=79 Dataset 4 (Replay), N=43 Dataset 5 (Wakeman-Henson), N=19
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Data exclusions	MEG UK: 22 subjects were excluded from the original dataset (N=77) because of excessive head movements or artifacts in the data. Cam-CAN: 41 subjects were excluded from the original dataset (N=653) because of incompleteness of the data HCP: 21 subjects were excluded from the original dataset (N=100) because of excessive noise. Replay dataset1: 4 subjects were excluded from the original dataset (N=25) because of large motion artifacts or missing trigger information Replay dataset2: 4 subjects were excluded from the original dataset (N=26) because of large motion artifacts or failure to complete the task.
Replication	Core results were replicated in five independent dataset, all of which were successful.
Randomization	Subjects were not allocated to a specific group - existing allocations were used based on the original study designs.
Blinding	Blinding was not relevant to this study because of the absence of a priori hypotheses regarding participant demographics. Furthermore, the availability of public datasets limited blinding.

## 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

### Methods

n/a	Involved in the study	n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies	<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines	<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology	<input type="checkbox"/>	<input checked="" type="checkbox"/> MRI-based neuroimaging
<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		

## Plants

Seed stocks	<i>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.</i>
Novel plant genotypes	<i>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.</i>
Authentication	<i>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.</i>

## Magnetic resonance imaging

### Experimental design

Design type	<i>Indicate task or resting state; event-related or block design.</i>
Design specifications	<i>Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.</i>
Behavioral performance measures	<i>State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).</i>

## Acquisition

Imaging type(s)

Field strength

Sequence & imaging parameters

Area of acquisition

Diffusion MRI  Used  Not used

## Preprocessing

Preprocessing software

Normalization

Normalization template

Noise and artifact removal

Volume censoring

## Statistical modeling & inference

Model type and settings

Effect(s) tested

Specify type of analysis:  Whole brain  ROI-based  Both

Statistic type for inference

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

Correction

## Models & analysis

n/a | Involved in the study

Functional and/or effective connectivity

Graph analysis

Multivariate modeling or predictive analysis

Multivariate modeling and predictive analysis