

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 (<i>n</i>) 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. <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>
☒	☐ 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 <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 as the principal imaging data comes from the human connectome project database.
Data analysis	Freesurfer v7.4.0, MRtrix 3.0.3, Python 3.10.4, TractSeg, All scripts necessary to reproduce the results in the manuscript are published in this github repository. https://github.com/paul-triebkorn/reservoir_connectivity_timescales

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 imaging data used in this study are accessible from the human connectome project database. <https://db.humanconnectome.org/app/template/Login.vm>

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	Findings apply to both gender/sex. Gender and sex were not considered during study design. Sex and gender were taken from the human connectome project database. No sex/gender specific analysis was done. This work primarily focusses on understanding general neural mechanisms, which we assume to be universal across sex and gender.
Reporting on race, ethnicity, or other socially relevant groupings	No race, ethnicity or socially relevant variables were used for further grouping of the subjects.
Population characteristics	We used data from 56 female and 44 male participants in the age range of 22-35 years old.
Recruitment	The first 100 subjects, as given by their folder structure, from the human connectome project database were selected.
Ethics oversight	n.a. as data were used from the human connectome project database. The human connectome project was approved by the Washington University institutional review board

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

Life sciences study design

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

Sample size	No sample size calculation was performed. Preliminary exploration with only 50 subjects already showed the effects of interest. To increase the power of our study we increased the number of subjects to 100, as that provided a good tradeoff between increase in power and computational cost.
Data exclusions	No data was excluded.
Replication	Results are fully reproducible, as the code uses deterministic algorithms. Any stochastic component of the code uses a specific random seed such that even those parts are fully reproducible. Replicability in a different dataset was not tested.
Randomization	Not applicable, because we were interested in the overall group effect of brain architecture only. No subgroups were considered.
Blinding	No blinding because no subgroups were created.

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	No functional MRI was used. Just structural and diffusion weighted MRI.
Design specifications	n/a
Behavioral performance measures	n/a

Acquisition

Imaging type(s)	structural and diffusion
Field strength	3T
Sequence & imaging parameters	0.7 mm isotropic voxel size, 3D MPRAGE, FOV = 224 mm, matrix = 320, 256 sagittal slices in a single slab), TR = 2400 ms, TE = 2.14 ms, TI = 1000 ms, FA = 8°, Bandwidth (BW) = 210 Hz per pixel, Echo Spacing (ES) = 7.6 ms
Area of acquisition	whole brain
Diffusion MRI	☒ Used ☐ Not used
Parameters	1.25mm isotropic voxel size, FOV PE×Readout=210×180, matrix size PE×Readout = 144×168, 111 slices, 3 shells at b=1000, 2000 and 3000 s/mm ² , 270 non-colinear directions, LR/RL phase encoding

Preprocessing

Preprocessing software	MRtrix 3.0.3, FreeSurfer7.4.0, FSL, TractSeg 2.7, Python
Normalization	The Schaeffer parcellation was mapped onto the subjects cortical surfaces by surface based registration.
Normalization template	Schaeffer parcellation
Noise and artifact removal	We used minimally preprocessed data from the human connectome project. Noise and artifact removal has been performed on them already.
Volume censoring	n/a

Statistical modeling & inference

Model type and settings	n/a
Effect(s) tested	n/a
Specify type of analysis:	☒ Whole brain ☐ ROI-based ☐ Both
Statistic type for inference	n/a
(See Eklund et al. 2016)	
Correction	n/a

Models & analysis

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