

## 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 ( $n$ ) 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<br><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. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted<br><i>Give <math>P</math> 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 type="checkbox"/>            | <input checked="" 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 $d$ , 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 | n/a                                                                                                                                                                                                                                 |
| Data analysis   | All code for analysis can be found in the author's github, <a href="https://github.com/LindenParkesLab/nct_xr">https://github.com/LindenParkesLab/nct_xr</a> , which is listed in the Code availability statement in the manuscript |

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](#)

This study made use of multiple datasets. The primary human neuroimaging dataset, known as the Human Connectome Project (HCP), is available at [\url{https://db.humanconnectome.org/}](https://db.humanconnectome.org/). The secondary human neuroimaging dataset, known as Microstructure-Informed Connectomics (MICA-MICs), is available at [\url{https://osf.io/j532r/}](https://osf.io/j532r/). Human gene Texpression and cell-type data are available at [\url{https://portal.brain-map.org/}](https://portal.brain-map.org/) and [\url{https://cellxgene.cziscience.com/collections/d17249d2-0e6e-4500-abb8-e6c93fa1ac6f}](https://cellxgene.cziscience.com/collections/d17249d2-0e6e-4500-abb8-e6c93fa1ac6f), respectively. Finally, data from the mouse brain is also available at [\url{https://portal.brain-map.org/}](https://portal.brain-map.org/).

These data were chosen as they provided (i) a primary human dataset for discovery, (ii) a second human dataset for replication, and (iii) a non-human dataset for cross-species generalization. These replication efforts were successful.

## 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                                        | Results were obtained controlling for binary sex. This is stated in the relevant portions of the manuscript. Our goal was to uncover general principles of brain organization, and not to perform sex-specific analyses           |
| Reporting on race, ethnicity, or other socially relevant groupings | These characteristics were not controlled for in our analyses                                                                                                                                                                     |
| Population characteristics                                         | The sample comprised 960 individuals. The age and sex characteristics of this sample are described in the manuscript. Other characteristics are described in other publications from the original authors that acquired the data. |
| Recruitment                                                        | Recruitment was performed by authors not involved in the current study. Recruitment is described in the relevant papers from those groups                                                                                         |
| Ethics oversight                                                   | Ethical approval was obtained from different sources depending on the dataset. No data was acquired by the authors of this manuscript. All ethical approval was sought elsewhere by relevant groups                               |

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     | All data used in this manuscript was provided via open-access. Thus, all dataset characteristics and recruitment strategies were determined and implemented by groups of authors not involved in this study |
| Data exclusions | All data used in this manuscript was provided via open-access. Thus, all dataset characteristics and recruitment strategies were determined and implemented by groups of authors not involved in this study |
| Replication     | All data used in this manuscript was provided via open-access. Thus, all dataset characteristics and recruitment strategies were determined and implemented by groups of authors not involved in this study |
| Randomization   | All data used in this manuscript was provided via open-access. Thus, all dataset characteristics and recruitment strategies were determined and implemented by groups of authors not involved in this study |
| Blinding        | All data used in this manuscript was provided via open-access. Thus, all dataset characteristics and recruitment strategies were determined and implemented by groups of authors not involved 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 &amp; experimental systems

|                                     |                                                        |
|-------------------------------------|--------------------------------------------------------|
| n/a                                 | Involved 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                                 | Involved 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                     | Resting-state function and diffusion-weighted imaging of structure |
| Design specifications           | N/A                                                                |
| Behavioral performance measures | N/A                                                                |

## Acquisition

|                               |                                                                                 |
|-------------------------------|---------------------------------------------------------------------------------|
| Imaging type(s)               | functional, structural, diffusion                                               |
| Field strength                | 3                                                                               |
| Sequence & imaging parameters | Variable since multiple datasets were used. See original dataset-related papers |
| Area of acquisition           | Whole brain                                                                     |
| Diffusion MRI                 | <input checked="" type="checkbox"/> Used <input type="checkbox"/> Not used      |
| Parameters                    | Variable since multiple datasets were used. See original dataset-related papers |

## Preprocessing

|                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Preprocessing software | <p>\item[Diffusion-weighted magnetic resonance imaging (dMRI).] Probabilistic tractography was run on each subject's minimally preprocessed dMRI data using MRtrix \cite{tournier_mrtrix3_2019}, following recommendations in \cite{tahedi_structural_2025}. We generated <math>10^7</math> streamlines. The 400-region variant of the Schaefer parcellation \cite{schaefer_local-global_2018} was used to extract structural connectivity (SC) weights. We normalized the raw streamline counts by dividing them by the sum of the region sizes of their respective node pairs. Region sizes were estimated using subject-specific versions of the parcellation file. Then, we log-normalized the weights. These size- and log-normalized SC weights were taken as adjacency matrices, <math>A</math>, and used for NCT analysis. Note that <math>A_{ij}=0</math> for <math>i=j</math>. In cases where a group-averaged <math>A</math> matrix was used for analysis, we averaged over the entries of individuals' <math>A</math> matrices and thresholded using an edge consistency-based approach. Specifically, edges in the group-averaged <math>A</math> matrix were only retained if non-zero SC weights were present in at least 60% of participants' <math>A</math> matrices \cite{de_reus_estimating_2013}. If not, then weights were set to zero.</p> <p>\item[Functional magnetic resonance imaging (fMRI).] Minimally preprocessed fMRI data (\verb rfMRI_REST1_LR ) were parcellated using the 400-region variant of the Schaefer parcellation \cite{schaefer_local-global_2018}. Then, additional nuisance regression was performed that comprised the global signal (GS), the backward temporal derivative of the GS, as well as the square terms of both. This procedure created regional rs-fMRI time series that were used to create brain activity states for NCT analysis (see Section \ref{methods:brain_states}).</p> |
|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

\item[T1-weighted and T2-weighted magnetic resonance imaging (T1w, T2w).] Following prior work \cite{glasser\_mapping\_2011}, we used the ratio of T1w to T2w MRI data as an \textit{in vivo} proxy of intracortical myelin content. Vertex-level myelin maps were downloaded from the HCP-YA database for each subject (\verb|/MNINonLinear/fsaverage\_LR32k/[subj\_id].MyelinMap\_BC\_MSMA11.32k\_fs\_LR.dscalar.nii|). As above, these maps were parcellated using the 400-region variant of the Schaefer parcellation \cite{schaefer\_local-global\_2018}.

Normalization

Diffusion data were processed in native space and extracted to a connectome where they became comparable across subjects

Normalization template

N/A

Noise and artifact removal

A variety of methods were used depending on the data type (e.g., function, structure)

Volume censoring

N/A

## Statistical modeling & inference

Model type and settings

Many diverse analyses were performed. All details are outlined in the relevant sections of the manuscript

Effect(s) tested

Mean differences, correlations

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 | Involved in the study

☒ ☐ Functional and/or effective connectivity

☐ ☒ Graph analysis

☐ ☒ Multivariate modeling or predictive analysis

Graph analysis

Weighted graph using streamline counts extracted from diffusion-weighted imaging data

Multivariate modeling and predictive analysis

control energy, PCA, explained variance, root mean squared error, correlation