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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	Paravision (Version 6.01) software developed by Bruker Biospin to acquire rsfMRI data in awake mice.
Data analysis	The code to reproduce the main results and metadata generation is available through a public Github repository (https://github.com/danielgb87/cmodes/tree/main)

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 in theis study is publicly available in open-source repositories. Specifically, raw rsfMRI data can be found in the following repositories:
Human – HNU: http://fcon_1000.projects.nitrc.org/indi/CoRR/
Human – MSC: https://openneuro.org/datasets/ds000224/versions/1.0.3/download

Macaque – NC: http://fcon_1000.projects.nitrc.org/indi/PRIME/newcastle.html
Mouse: "awake_rsfMRI_mouse_NatComms2024", Mendeley Data, V1, doi: 10.17632/vtk54hzzfb.1
Please note mouse data have been embargoed until April 1st 2024

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	The present study used data from different public sources, as well as collected mouse data. Specifically, human rsfMRI data from the HNU cohort consisted of 30 subjects (15 females, 15 males); MSC dataset consisted of 10 subjects (5 males, 5 females). Macaque data from the Newcastle cohort consisted of 10 macaques (2 females, 8 males, from which females were removed due to excess head-motion). Mouse data was collected from 44 male mice. This study investigated large-scale brain network dynamics across three mammalian species, and sex nor age were considered as covariates within the design, so no sex or age-specific features were investigated.
Reporting on race, ethnicity, or other socially relevant groupings	No ethnicity, ravce, or social-related groupings were done in this study
Population characteristics	Human HNU dataset (15 females, 15 males, age 24+/-2.41 years old); Human MSC dataset (5 females, 5 males, 29.1+/-3.3 years old); Macaque Newcastle dataset (8 males, 2.28+/-2.33 years old, 11.76+/-3.38 kg in weight); Mouse dataset (44 males, < 12 months old).
Recruitment	no recruitment of human subjects was done, and all available subjects were used. Macaque exclusion of animals was done exclusively due to excess head motion.
Ethics oversight	In vivo experiments in mice were conducted in accordance with the Italian law (DL 26/214, EU 63/2010, Ministero della Sanita, Roma) and with the National Institute of Health recommendations for the care and use of laboratory animals. The animal research protocols for this study were reviewed and approved by the Italian Ministry of Health and the animal care committee of Istituto Italiano di Tecnologia (IIT). All surgeries were performed under anesthesia.

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	Data from 40 humans, 8 macaques, and 44 mice were included in our main analyses. In humans, replication of results was confirmed within test-retest sessions, as well as across independent datasets. In macaques, replication was done in a test-retest fashion. Sample size was enhanced or limited by the availability of open-source material, and within sizes in state-of-the art interspecies fMRI studies of similar nature. Due to the exploratory nature of the present study, it was not possible to hypothesize a priori an effect size and determine a sample size. For this reason, reproducibility analyses are performed.
Data exclusions	Two females in the macaque datasets were removed due to excess head-motion. Four other males were excluded due to no availability of a second retest session. This information has been reported in our methods section
Replication	Replication was performed within the limits of data availability. In humans, results were reproduced in two independent datasets, each with >5 test-retest sessions. In macaques, two sessions were used to test replicability of results. Mice results were compared with previous studies.
Randomization	For all species investigated, there was no subject allocation to any specific experimental group.
Blinding	No group allocation.

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	Macaque: Newcastle dataset - 10 adult rhesus macaques (Macaca Mulatta, 2 females) Mouse: 44 adult (<12 months) C57Bl6/J male mice.
Wild animals	No wild animals were used in this study
Reporting on sex	Sex was not used as a covariate in this study.
Field-collected samples	no field-collected samples
Ethics oversight	Data used in this study belongs to publicly available open-source databases. Mice data was collected in accordance with the Italian law (DL 26/214, EU 63/2010, Ministero della Sanita, Roma) and with the National Institute of Health recommendations for the care and use of laboratory animals.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Plants

Seed stocks	no plants used in this study
Novel plant genotypes	no plants used in this study
Authentication	no plants used in this study

Magnetic resonance imaging

Experimental design

Design type	Resting state fMRI
Design specifications	Human HNU dataset: 10 sessions of 10-min scans over the course of a month from n = 30 young healthy adults with no history of neurological or psychiatric disorders, head injuries, nor substance abuse. Before scanning, participants were asked to relax and remain still with their eyes opened, avoiding falling asleep. During scanning, a black crosshair was shown in the middle of a grey background. More details: http://fcon_1000.projects.nitrc.org/indi/CoRR/ Human MSC dataset: Five out of 10 randomly selected sessions were used from separate days, and included 30-min scans from n = 10 healthy young adults. Participants were asked to visually fix on a white crosshair against a black background. More details: doi:10.18112/openneuro.ds000224.v1.0.3 Macaque NC dataset: rhesus macaque monkeys (Macaca Mulatta) scanned with no contrast agents in which two independent fMRI session were perform a week apart. More details: http://fcon_1000.projects.nitrc.org/indi/indiPRIME.html Mice: For awake scanning, the mouse was secured (using the headpost) to the custom-made MRI-compatible animal cradle. The surgical, habituation, and experimental protocols were designed in a previous study. More details: https://

www.cell.com/current-biology/pdf/S0960-9822(21)01691-2.pdf
of the mouse was gently restrained by taping its back to the cradle arc

Behavioral performance measures: No behavioral metrics were used in this study

Acquisition

Imaging type(s): Functional MRI

Field strength:
Human HNU: GE MR750 3T scanner (GE Medical Systems, Waukesha, WI, USA)
Human MSC: Siemens TRIO 3T MRI scanned (Erlangen, Germany)
Macaque NC: Vertical Bruker 4.7T primate dedicated scanner
Mouse: Bruker 7T scanner (Bruker Biospin, Ettlingen)

Sequence & imaging parameters:
Human HNU: Functional scans were acquired with an echo-planar imaging sequence - EPI: TR = 2 s, TE = 30 ms, flip angle = 90°, FOV = 220 × 220 mm, matrix = 64 × 64, voxel-size = 3.4 mm isotropic, 43 slices.

Human MSC: Functional scans were acquired using a gradient-echo EPI sequence: TR = 2.2 s, TE = 27 ms, flip angle = 90°, voxel-size = 4 mm isotropic, 36 slices.

Macaque NC: head-fixed animals for two separate sessions with TR = 2 s; TE = 16 ms, voxel-size = 1.2 mm isotropic.

Mouse: BGA-9 gradient set, 72 mm birdcage transmit coil, and a four-channel solenoid receiver coil: TR = 1 s, TE = 15 ms, flip angle = 60°, matrix = 100 × 100, FOV = 2.3 × 2.3 cm, 18 coronal slices 0.6 mm thick, 12 minutes total acquisition time.

Area of acquisition: whole-brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software: Preprocessing included most steps suggested by the guidelines of the Human Connectome Project using a combination of fMRI dedicated software AFNI, FSL, FreeSurfer, and SPM12 (http://fil.ion.ucl.ac.uk/spm/). Matlab version R2019b.

Normalization: Linear spatial Normalization to species-specific brain atlases was performed using FSL's FLIRT

Normalization template:
Human: MNI 2mm isotropic
Macaque: F99 Yerques template
Mouse: In-house EPI mouse brain template available at https://github.com/functional-neuroimaging/rsfMRI-templates

Noise and artifact removal: After motion correction realignment, skull-stripping and normalization (registration), all functional images for all species were corrected for nuissance signals which included average white matter, average cerebrospinal fluid, and 24 parameter motion regressors. Signals were then band-pass filtered (0.01-0.1 Hz) and spatially smoothed (FWHM of 6mm, 3mm, and 0.5mm for humans, macaques, and mice respectively).

Volume censoring: Frame (volume) censoring was performed previous to clustering of images based on Framewise Displacement (FD > 0.3mm, 0.3mm, and 0.075mm for humans, macaques, and mice respectively). Censored frames were then recovered and assigned a CAP ID based on their spatial similarity.

Statistical modeling & inference

Model type and settings: Clustering map reproducibility (voxel-wise mass-univeriate T-score normalized means, within and between dataset comparisons) was performed through non-parametric testing. Statistical significance of the mean within subject repeatability of each CAP was assessed by recomputing the spatial correlations between subject-level CAP maps after randomly shuffling (1000 permutations) the CAP-identity of fMRI frames, preserving occurrence rates. This process was repeated 1000 times, and repeatability values for each subject beneath the highest permutation value were flagged as non-repeatable. Within and between dataset reproducibility of cluster occurrence rates was done with Wilcoxon signed rank and Kruskal-Wallis tests, corrected for 8 comparisons in humans, and macaques respectively.
Significance of deviations from circular uniformity for GS-phase analyses was performed using a Rayleigh tst, FDR corrected for 8, 8, and 6 comparisons for humans, macaques, and mice respectively.
Statistical significance of transition and persistence probabilities; differences in directional transition probabilities; and Entropy of Markov Trajectories were assessed by comparing eresults to those obtained against matrices built after randomly permuting the non-repeating sequences 1000 times. Sums of HMT matrix columns were compared using One-way ANOVE and followed by Tukey Tests for multiple comparisons.

Effect(s) tested: no task based experiments were performed.

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

Anatomical location(s): for humans, data was reduced to the coarse 950-roi Craddock Parcellation exclusively for clustering purposes. Thereafter, voxel-resolution images were used.

Statistic type for inference (See Eklund et al. 2016)

Cluster averaging of concatenated fMRI frames for CAP and subsequent C-mode formation was done at the voxel level

Correction

FRD and cluster-corrections

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

z-scored concatenated timeseries were used to compute voxel-wise Pearson Correlations

Multivariate modeling and predictive analysis

C-mode occurrence rates, Gradient Variance Explained