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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees 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	MRI - either the 7T Biospec 30/70 Avance spectrometer or the 3T siemens Prisma Scanner
Data analysis	Matlab 2018, SPM12, Explorer DTI 4.8.6

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The data that support the findings of this study are available from the corresponding author upon request.

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	We aimed to collect data from as many species as possible. this is by far the largest sample size ever collected
Data exclusions	All brains that could be scanned were used in the study (with no exclusions)
Replication	when possible, we scanned multiple specimens per species and we used these replications to test the robustness of the results. All replication tests revealed the same results
Randomization	We did not use any randomization, as data was not grouped into any 'treatments' except for their phylogenetic orders.
Blinding	Data analysis and collection were not performed in a blind manner as we did not divide the data into groups.

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
☐	☒ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☐	☒ MRI-based neuroimaging

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Rattus norvegicus - wistar and Mus musculus - icr. We used both males and females of ca. 1 year old
Wild animals	we have more than 100 species - all names are provided in the manuscript
Field-collected samples	Brains were collected from dead animals. No animals were deliberately euthanized for this study. Brain collection was based on incidental death of animals in Zoos in Israel and on naturally dying animals collected abroad. All animals were collected with permission of the national park authority (approval no. 2012/38645) or its equivalent in the relevant countries. Animals' brains were extracted within 24 hours following death and placed in Formaldehyde (10%) for a fixation period of a few days to a few weeks (depending on the brain size). Twenty-four hours prior to MRI scan, the brains were placed in phosphate buffered saline (PBS) for rehydration. As we only received the brains, after animals died, there was no need for housing, maintenance, etc.
Ethics oversight	We had permission from the National park authorities to collect brains and from the TAU IACUC to use laboratory animals (permit 04-18-020).

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	13 males, 14 females, mean age 37 +/-9. Israelis
Recruitment	Through an advertisement according to the IRB approval
Ethics oversight	Sheba medical center IRB and TAU IRB

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

Magnetic resonance imaging

Experimental design

Design type	Pre-clinical 7T (Biospec 70/30, Bruker, Germany) and clinical 3T (Prisma, Siemens, Germany)
Design specifications	The MRI protocol was similar for all species and included high resolution anatomical scans (T2 or T1 weighted MRI) that were used as anatomical reference and diffusion MRI scans. The diffusion MRI included high angular resolution diffusion imaging (HARDI) acquisition. The HARDI dataset consisted of a series of diffusion weighted spin-echo echo planar imaging images covering the whole brain scanned at 60 gradient directions (in the 7T scanner) and 64 gradient directions (in the 3T scanner) with additional 3 non-diffusion weighting images (B0). The b value was 1,000 s/mm2 in all scans. In the 7T scans TR was longer than 12000ms (depending on number of slices) and TE was 20ms, Big/Small delta were 10/4.5ms. In the 3T scans TR was 3500ms, with TE of 47ms, small/big delta were 17/23ms. We kept the matrix size constant across all species (128x96) so the 2D image pixel resolution (per slice) was linearly scaled according to brain size. We ran a control analysis to make sure that this decision did not influence our results (see below). The number of slices varied due to differences in brain shape and was between 46-68. The number of scan-repetitions and the acquisition time was different for each species and depended on brain size and on signal to noise ratio (SNR). We tried to keep SNR above a value of 20 resulting in acquisition times of 48 hours for the small brains (~0.15ml) and 25 minutes for the large brains (>1000ml). SNR was defined as the mean signal strength of the brain divided by the SD of the noise (an area in the non-brain part of the image).
Behavioral performance measures	There was no behavioral study

Acquisition

Imaging type(s)	structural and diffusion MRI
Field strength	3T or 7 T
Sequence & imaging parameters	The MRI protocol was similar for all species and included high resolution anatomical scans (T2 or T1 weighted MRI) that were used as anatomical reference and diffusion MRI scans. The diffusion MRI included high angular resolution diffusion imaging (HARDI) acquisition. The HARDI dataset consisted of a series of diffusion weighted spin-echo echo planar imaging images covering the whole brain scanned at 60 gradient directions (in the 7T scanner) and 64 gradient directions (in the 3T scanner) with additional 3 non-diffusion weighting images (B0). The b value was 1,000 s/mm2 in all scans. In the 7T scans TR was longer than 12000ms (depending on number of slices) and TE was 20ms, Big/Small delta were 10/4.5ms. In the 3T scans TR was 3500ms, with TE of 47ms, small/big delta were 17/23ms. We kept the matrix size constant across all species (128x96) so the 2D image pixel resolution (per slice) was linearly scaled according to brain size. We ran a control analysis to make sure that this decision did not influence our results (see below). The number of slices varied due to differences in brain shape and was between 46-68. The number of scan-repetitions and the acquisition time was different for each species and depended on brain size and on signal to noise ratio (SNR). We tried to keep SNR above a value of 20 resulting in acquisition times of 48 hours for the small brains (~0.15ml) and 25 minutes for the large brains (>1000ml). SNR was defined as the mean signal strength of the brain divided by the SD of the noise (an area in the non-brain part of the image).
Area of acquisition	Whole brain

Diffusion MRI ☒ Used ☐ Not used

Parameters: We have used: 60 gradient directions (in the 7T scanner) and 64 gradient directions (in the 3T scanner) with additional 3 non-diffusion weighting images (B0). The b value was 1,000 s/mm2 in all scans. No cardiac gating was applied

Preprocessing

Preprocessing software	Matlab 2018 + Explore DTI 4.8.6+ SPM12
Normalization	No normalization was applied
Normalization template	No normalization template was applied
Noise and artifact removal	Motion + Eddy current correction
Volume censoring	We did not use volume censoring

Statistical modeling & inference

Model type and settings	We used regression analysis (Pearson) and GLM
Effect(s) tested	We analyzed correlations between different graph parameters

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

Statistic type for inference (See Eklund et al. 2016)	We analyzed correlations between different graph parameters
Correction	None - there were no multiple tests. We did not correct for phylogeny and refer to this in the methods

Models & analysis

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

Graph analysis	we used weighted graphs. Species were the dependent variables. We used the following network parameters: mean short past and normalized cost (edge length).