nature portfolio

Corresponding author(s): Leonardo L. Gollo

Last updated by author(s): Dec 30, 2024

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	All behavioral and raw MRI data used in this study were from the public dataset (https://openneuro.org/datasets/ds003871/versions/1.0.2). The timeseries of independent components used to recognize the brain functional networks and the smoothed whole brain GMV can be found in the GitHub Repository(https://github.com/xiaohajiayouo/Mapping_and_Modeling_Age-Related_Changes-in-_Intrinsic_Neural_Timescales). In addition, this folder has 200 samples of produced neuronal networks. Each one contains the network dynamics (timeseries), the branching ratio, and the corresponding computed intrinsic timescale. All data present in this manuscript has been sorted out and tidied up into Excel files.
Data analysis	Resting-state MRI scans were obtained from the available public dataset of the University of North Carolina samples at Greensboro. The functional and structural image processing and analysis has been detailed in the manuscript. The computational neuronal network was modeled as random networks of excitable spiking neurons. Aging in these neuronal networks was simulated by removing both neurons and synaptic connections. The neuronal network modeling and post-data analysis, including statistical analyses, were carried out with customized code, which is available on Github (https://github.com/xiaohajiayouo/Mapping_and_Modeling_Age-Related_Changes-in-_Intrinsic_Neural_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

All behavioral and raw MRI data used in this study were from the public dataset https://openneuro.org/datasets/ds003871/versions/1.0.2. The timeseries of independent components used to recognize the brain functional networks and the smoothed whole brain GMV can be found in Github (https://github.com/xiaohajiayouo/Mapping_and_Modeling_Age-Related_Changes-in-_Intrinsic_Neural_Timescales. In addition, this folder has 200 samples of produced neuronal networks. Each one contains the network dynamics (timeseries), the branching ratio, and the corresponding computed intrinsic timescale. All data present in this manuscript has been sorted out and tidied up into Excel files.

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	No sex or gender based analysis performed in this study. We focus on the brain dynamics of different age group.
Reporting on race, ethnicity, or other socially relevant groupings	The empirical data did not involve any specific race, ethnicity, or other socially relevant groups. Potential confounding effects include noise components from cerebral white matter and cerebrospinal areas, estimated motion parameters identified during the realignment step of preprocessing, outlier scans from outlier identification
Population characteristics	Resting-state fMRI scans used in this study were obtained from the available public dataset of the University of North Carolina samples at Greensboro. The participants included 28 healthy elderly adults (61–80 years old, mean: 69.82, SD:5.64) and 34 healthy young adults (18–32 years old, mean: 22.21, SD: 3.65).
Recruitment	The empirical data used in this study were obtained from public dataset with no copyright conflict reserved.
Ethics oversight	All aspects of this study were approved by the Monash University Human Research 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

Life sciences study design

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

Sample size	For empirical part, the MRI scans of 62 participant were used.
Data exclusions	Head motion effects were controlled by calculating the individual framewise displacements (FD). As the outlier scans have been removed from the raw data, none of the remaining participants had head motion greater than 0.5 mm. No significant difference in FD was observed between the two groups FD.
Replication	For the empirical data, we used the public data. The computational methods developed are available.
Randomization	For the empirical data, the two cohorts have been allocated according to their age. For the modeling part, some results were done by matching the sample size of the empirical data by randomly selecting a subset of networks from a larger pool sample.
Blinding	The empirical data were from public dataset. The investigators are aware of the age of the two cohorts.

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

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.

Novel plant genotypes

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.

Authentication

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, mosiacism, off-target gene editing) were examined.

Magnetic resonance imaging

Experimental design

Design type

Resting-state

Design specifications

Before completing the behavioral tasks, but after completing the neuropsychological measures, whole-brain imaging was performed on a Siemens 3.0T MRI scanner.

Behavioral performance measures

The mnemonic discrimination ability is measured by lure discrimination index (LDI) which is calculated as the probability of the difference in response to lures and foils in a visual mnemonic discrimination task.

Acquisition

Imaging type(s)

Functional and structural data

Field strength

3.0

Sequence & imaging parameters

T1 anatomical images (1 mm isotropic voxels, 192 slices with thickness of 1mm, repetition time (TR) = 2300 ms, and Time of echo (TE) = 2.26 ms), and functional MRI (32 slices with 4.0 mm thickness and no skip, TE = 30 ms; TR = 2000 ms; flip angle = 70, field of view = 220 mm, matrix size = 74 × 74 × 32 voxels). The fMRI scan lasted for 10 minutes, which resulted in 300 volumes.

Area of acquisition

Whole brain MRI scan, The functional regions were recognized by the group independent component analysis.

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software

We used CONN for fMRI processing and denosing.
The first five volumes of each scan were discarded to generate a steady BOLD activity signal to allow for magnetic stability. Similarly to previous studies, the functional data were then processed with the following steps: (1) Realignment to correct head motion for verification details; (2) slice time correction; (3) outlier identification; (4) normalization (normalize to 3 mm MNI space using a template from the SPM software package; (5) spatial smoothing with a Gaussian kernel of 8 mm full-width at half-maximum (FWHM).

Head motion effects were controlled by calculating the individual framewise displacements (FD). As the outlier scans have been removed from the raw data, none of the remaining participants had head motion greater than 0.5 mm. No significant difference in FD was observed between the two groups FD (p = 0.92).

Normalization

We normalize to 3 mm MNI space using a template from the SPM software package

Normalization template: 3 mm MNI

Noise and artifact removal: A linear regression of potential confounding effects in the BOLD signal and temporal band-pass filtering

Volume censoring: Volumes were excluded if the signal for that time point fell three standard deviations outside the mean global signal for the entire run or if the scan-to-scan head motion exceeded .5 mm in any direction.

Statistical modeling & inference

Model type and settings: N/A

Effect(s) tested: ANVOA

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

Anatomical location(s): group independent component analysis

Statistic type for inference: N/A

(See Eklund et al. 2016)

Correction: FDR corrected

Models & analysis

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