nature portfolio

Corresponding author(s): DAPR COMMSBIO-26-3332

Last updated by author(s): Apr 15, 2026

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	E-Prime 2.0 (stimulus presentation and response logging); Siemens 3T MRI scanner (Siemens, Germany)
Data analysis	fMRI preprocessing: Gretna toolbox (MATLAB-based); standard SPM pipeline including slice-timing correction, head motion correction, spatial normalization (MNI space), spatial smoothing (6mm FWHM Gaussian), nuisance regression (CSF, WM, 24-parameter motion model) HMM analysis: HMM-MAR toolbox (MATLAB); variational-Bayes optimization; dual estimation for subject-level parameters. Available at: https://github.com/OHBA-analysis/HMM-MAR Statistical analysis R (statistical computing environment); ARTool package for ART ANOVA; lme4/lmerTest for LMMs; ggplot2 for visualization Atlas Shen268 atlas (268 ROIs grouped into 10 functional networks) Code availability Custom analysis code will be made available upon reasonable request to the corresponding author.

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

- Data are not available as the larger database from which these data are sourced is currently being established and research is ongoing. Data may become available upon reasonable request to the corresponding author upon completion of the parent study.
- No publicly available external datasets were used. All data were collected in-house at the Brain Imaging Center of Southwest University, Chongqing, China.
- Data sharing is currently restricted due to ongoing data collection of the larger parent database. Additionally, participant privacy and IRB protocols require data anonymization procedures before any future sharing.

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	Sex/gender was recorded as a binary variable (male/female) based on self-report at the time of enrollment. Gender was included as a covariate in all statistical models. Young adults: 18 females, 23 males (n=41). Older adults: 45 females, 18 males (n=63). Gender distribution differed across age groups ($\chi^2(1)=12.35$, $p<0.001$), which is why it was controlled as a covariate.
Reporting on race, ethnicity, or other socially relevant groupings	All participants were recruited in Chongqing, China; the sample is predominantly Han Chinese. Race/ethnicity information was not systematically collected, as the study was conducted in a single culturally homogeneous site. This is acknowledged as a limitation for generalizability.
Population characteristics	Healthy community-dwelling adults recruited in Chongqing, China. Young adults (n=41): mean age 25.2±3.6 years, all right-handed, normal or corrected-to-normal vision, no color blindness, ≥middle-school education, no history of neurological or psychiatric disorders. Older adults (n=63): mean age 68.8±4.4 years, additionally screened with MMSE (minimum score 27) to exclude mild cognitive impairment or dementia.
Recruitment	Participants were recruited via community advertisement and university networks. Inclusion criteria: (1) no history of neurological or psychiatric disorders or substance abuse; (2) no severe head injury; (3) right-handedness; (4) normal or corrected-to-normal vision; (5) no color blindness; (6) minimum middle-school education. Exclusion post-acquisition: excessive head motion (>3mm translation or >3° rotation) or failure to meet Stroop accuracy thresholds (<60% accuracy or RT>1500ms).
Ethics oversight	The study was approved by the Institutional Review Board (IRB) at the Brain Imaging Center of Southwest University. All participants provided written informed consent before participation.

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

Behavioural & social sciences study design

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

Study description	Cross-sectional fMRI study investigating age-related differences in rest-to-task brain network reconfiguration using a color-word Stroop task. The study combined behavioral performance measures with whole-brain Hidden Markov Model (HMM) analysis to characterize dynamic brain state transitions from resting state to task in young and older adults.
Research sample	Final sample: 41 healthy young adults (18F/23M; mean age 25.2±3.6 years) and 63 healthy older adults (45F/18M; mean age 68.8 ±4.4 years), recruited from the community in Chongqing, China. All participants were right-handed with normal or corrected-to-normal vision. Older adults were screened for cognitive health (MMSE ≥27). Years of education did not differ significantly between groups (Welch's $t=-1.56$, $p=0.12$).
Sampling strategy	Convenience sampling via community advertisement and university networks. No probabilistic sampling was used. The sample was not designed to be nationally representative. Inclusion and exclusion criteria were pre-specified (see Recruitment above). Post-

	acquisition exclusions were pre-defined: excessive head motion (>3mm translation or >3° rotation) and Stroop performance failure (accuracy <60% or RT >1500ms).
Data collection	Data collected at the Brain Imaging Center of Southwest University, Chongqing, China. fMRI data acquired on a 3.0T Siemens scanner. Behavioral responses collected via a four-button response box during scanning. Stimulus presentation controlled by E-Prime 2.0. All participants completed resting-state fMRI (two 7.5-min conditions: eyes-open and eyes-closed) followed by task-based fMRI (block-design Stroop task, ~9 min). A practice session (≥80% accuracy required) preceded formal scanning.
Timing	Data collection period: ongoing as part of a larger database study. All data used in this paper were collected prior to submission. Each participant completed a single session comprising resting-state fMRI (~15 min) followed by task fMRI (~9 min).
Data exclusions	Pre-specified exclusion criteria: (1) excessive in-scanner head motion: maximum absolute translation >3mm or maximum absolute rotation >3° in any direction (5 young, 18 older adults excluded from initial sample of 47 young and 85 older adults); (2) Stroop performance failure: accuracy <60% or RT >1500ms (1 young, 3 older adults excluded). All criteria were defined prior to data analysis.
Non-participation	All recruited participants who met inclusion criteria completed the study. Exclusions were based on data quality criteria (head motion, performance thresholds) applied post-acquisition, not participant withdrawal.
Randomization	Participants were not randomly assigned to age groups, as group membership is an inherent characteristic. Within the task, Stroop blocks were presented in a fixed counterbalanced order. Resting-state scans were always acquired before the Stroop task to avoid carry-over effects from task performance.

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	Cross-sectional 2 (Age Group: young, older) × 4 (Condition: rest–eyes open, rest–eyes closed, Stroop control, Stroop conflict) mixed design. Age Group is a between-subjects factor; Condition is a within-subjects factor. Resting-state fMRI (two conditions: eyes-open fixation and eyes-closed) and task-based fMRI (block design Stroop task with control and conflict blocks). Both resting-state and task-state data acquired in the same session.
Design specifications	Resting-state: Two 7.5-min runs (450 time points each; TR=2s). Task: Block design Stroop task (~9 min, 275 time points; TR=2s). Four task blocks of 40 trials each (total=160 trials), ~2 min per block, separated by 20s inter-block rest.
Behavioral performance measures	Reaction time (RT, ms; correct trials only), Accuracy (% correct), and Inverse Efficiency Score (IES = RT/Accuracy). Conflict effect computed as Conflict – Control difference scores.

Acquisition

Imaging type(s)	Functional MRI (EPI sequence) and T1-weighted structural MRI.
Field strength	3.0 Tesla (Siemens scanner with standard 12-channel head coil)
Sequence & imaging parameters	Echo Planar Imaging (EPI); TR=2s; TE=30ms; flip angle=90°; FOV=224×224mm²; 62 slices; voxel size=2×2×2mm³; 450 time points (rest) / 275 time points (task).
Area of acquisition	Whole brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	Gretna toolbox (MATLAB-based). Steps: (1) removal of first 10 time points; (2) slice-timing correction; (3) head motion correction (spatial realignment); (4) spatial normalization to MNI space (EPI template for rest; individual T1 co-registration then MNI normalization for task); (5) spatial smoothing (6mm FWHM Gaussian); (6) nuisance regression (CSF signal, WM signal, 24-parameter motion model).
Normalization	Standard MNI space (Montreal Neurological Institute). Resting-state: direct normalization to EPI template. Task-state: functional images co-registered to individual T1, which was then normalized to MNI space.
Normalization template	MNI152 standard brain template
Noise and artifact removal	Head motion correction via spatial realignment; nuisance regression of CSF signal, white matter signal, and 24 head motion parameters (6 motion parameters, their first derivatives, and their squares). Participants with excessive motion (>3mm translation or >3° rotation) were excluded.
Volume censoring	Not applied. Motion exclusion was handled at the participant level (global exclusion of participants exceeding motion thresholds), not at the volume/frame level.

Statistical modeling & inference

Model type and settings	Hidden Markov Model (HMM) with multivariate Gaussian observation model (mean activation vector μ and covariance matrix Σ per state). Group-level HMM fitted on concatenated data (all participants × all conditions). Subject-level parameters obtained via dual estimation. State number K=4 selected by lowest free energy across K=1–20, repeated 10 times (median K used).
Effect(s) tested	Primary: Age Group (young vs. older) × Condition (eyes-open rest vs. Stroop conflict) interaction on brain state in-degree (ART ANOVA). Secondary: Brain state in-degree × Accuracy × Age Group interaction on RT Difference (linear regression). All effects controlled for gender and years of education as covariates.

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

Statistic type for inference (See Eklund et al. 2016)	Non-parametric ART ANOVA (for state temporal metrics); linear mixed-effects models (for behavioral data); linear regression with BCa bootstrapping (for brain-behavior associations). All tests two-sided.
Correction	BH (Benjamini-Hochberg) FDR correction applied across 4 ART ANOVA tests (one per brain state). No voxel-wise multiple comparisons correction required (ROI-based network analysis). BCa bootstrap CIs (5000 resamples) used to verify robustness of key interaction terms.

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	Functional connectivity details: State-specific covariance matrices (Σ) from the HMM Gaussian observation model were used to characterize functional connectivity patterns for each brain state. Network-level connectivity (10 functional networks from Shen268 atlas) was visualized and compared across rest-specific and task-specific states. No graph-theoretic metrics were computed.
Graph analysis	*Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*
Multivariate modeling and predictive analysis	Multivariate modeling details: Linear regression models with multiple predictors (brain state in-degree × accuracy × age group interactions) were used to test brain-behavior associations. HMM itself is a multivariate

model capturing joint dynamics across 268 brain regions simultaneously.