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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	The data is provided by the Natural Scenes Dataset (NSD). Therefore, no code for data collection is used.
Data analysis	All analyses were performed using custom codes written in Python and R. The mixed-effects logistic models were fitted using R package lme4, and post-hoc tests were performed using R package emmeans.

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

The paper analyzed existing, publicly available data. The NSD dataset is freely available at http://naturalscenesdataset.org.

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	Both males and females were included in this study (2M, 6F). Biological sex/gender was self-reported by participants. Sex and gender were not included as covariates in the analyses because we did not have any a priori hypotheses or research questions about this. Neither sex nor gender is likely to influence our findings.
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity, or other socially relevant variables were not considered in the study, as they are not relevant to the research question. Those factors are not likely to influence our findings.
Population characteristics	Human participants included 2 males and 6 females. Subjects were healthy young adults between 19–32 years old at the time of participation. All participants had normal or corrected-to-normal visual acuity, normal color vision, and no MRI contraindications.
Recruitment	Participants were recruited through advertisements to the local community and were screened based on their ability to participate in this long-term neuroimaging study. In addition, NSD researchers selected participants based on data quality from an initial 7T fMRI session. This selection does induce a bias towards individuals with low head motion, high cognitive performance, and strong BOLD responses. The goal of the selection is to optimize the quality of the dataset, and does not represent an unbiased sampling of the human population. The self-selection is unlikely to influence our findings.
Ethics oversight	University of Minnesota Institutional Review Board

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	This study collects massive amounts of data on individual subjects. Analyses demonstrated in this paper are conducted at both group-level and within-subject level, demonstrating the precision and robustness of the data collected. For group-level analyses, the number of subjects used for NSD (n = 8) is sufficiently large to provide some power for statistical inference. The sample size (n = 8) was chosen based on consideration of guarding against incidental findings that occur only in a few individuals and based on consideration of subject burden (if all images had been presented to a single subject, data collection would have extended for 8 years).
Data exclusions	The NSD researchers implemented a subject-selection procedure in which the best 8 subjects out of 14 recruited subjects were selected for full NSD data collection. The criteria included factors such as head motion and BOLD signal quality in the pilot session. We used the final NSD data release in our analyses.
Replication	The published NSD data (Allen et al., 2022) has been thoroughly checked for data quality. In the study, we included extensive control analyses to ensure the robustness of our findings. A replication experiment was not performed in this study.
Randomization	All subjects performed the same set of experiments. However, the sets of stimuli chosen for each subject were largely non-overlapping. All the stimuli images were selected from the Microsoft COCO database. Each subject was assigned 10,000 images in total. One thousand out of the 10,000 images were shared across subjects, the remaining were randomly selected. Given the large number of stimuli each subject saw, we expect that the effects of interest should be homogeneous across subjects.
Blinding	Blinding is not relevant to this study given that there is little that the investigators could have done to bias the nature of the recorded data and given that the participants do not belong to any discrete groupings.

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 — The NSD used a continuous recognition task and had an event-related design.

Design specifications — In the NSD recognition task, images were presented for 3 seconds, followed by a 1-second inter-trial interval. There were 9,000 to 10,000 images presented for each participant over the course of several months (30-40 scan sessions). Each image was presented 3 times at most over the experiment.

Behavioral performance measures — Button presses and associated reaction times for each trial in the continuous recognition experiment were recorded. We quantified recognition performance using signal detection theory.

Acquisition

Imaging type(s) — Functional and structural

Field strength — 7T and 3T

Sequence & imaging parameters — The primary fMRI sequence involved gradient-echo EPI, FOV 216 mm x 216 mm, matrix size 120 x 120, slice thickness 1.8 mm, orientation axial, TR 1.6 s, TE 22.0 ms, and flip angle 62°. The detailed parameters were reported in the NSD data paper (Allen et al., 2022).

Area of acquisition — Whole-brain scans

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software — A combination of custom MATLAB and Python code, FreeSurfer 6, and selected tools from SPM, FSL, ANTs, and MRTrix3. See details in (Allen et al., 2022).

Normalization — Data used in this study was prepared by the NSD authors in the fsaverage space (surface) and subject-native spaces (volume).

Normalization template — Surface data was normalized to fsaverage template space.

Noise and artifact removal — We used single-trial beta estimation version 2 provided by the NSD in this study. The GLM preparation included voxel-wise HRF fitting and motion artifacts removal. See details in (Allen et al., 2022).

Volume censoring — No volume censor was perform.

Statistical modeling & inference

Model type and settings	Mixed-effects logistic models were used to examine the relationship between trial-level neural responses and memory decisions.
Effect(s) tested	We built a series of mixed-effects logistic models to examine the relationship between the neural global pattern similarity (nGPS) of an image probe and its recognition memory decision (new vs. old). The nGPS was defined as the averaged neural pattern similarity between the probe and all prior trials within a given temporal window. In the models, we considered nGPS from three temporal windows (Immediate, Recent, Distant), image exposures (1st, 2nd, 3rd), and their interactions as effects of interest. The model was built for each ROI separately. Likelihood ratio tests were used to determine the significance of fixed effects. For post-hoc tests of fixed effects and interactions, the Wald test with asymptotic distribution was used.

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

Anatomical location(s)	ROIs were defined in fsaverage space (cortical regions) and the subjects' native 1mm functional space (hippocampus). For all cortical ROIs, we used the multi-modal parcellation (MMP1). We focused our main subdivided the lateral parietal cortex into the angular gyrus (AnG), lateral intraparietal sulcus (LatIPS) and posterior intraparietal sulcus (pIPS) regions. We combined MMP1 label PGs and PGi regions to create AnG. For LatIPS and pIPS, we combined regions to match the definition used in Favila et al. (2018) as closely as possible. Namely, the LatIPS consisted of MMP1 label IP1, IP2 and LIPd. The pIPS consisted of MMP1 labels IP0, IPS1, MIP, VIP and LIPv. In addition, we also included ventral occipitotemporal cortex (VOTC) and hippocampus (HPC). The VOTC consisted of MMP1 labels FFC, VVC, PHA1, PHA2, PHA3, PIT, V8, VMV1, VMV2 and VMV3. The HPC used a manually traced segmentation in subject's native space that combined subregions CA1, CA2, CA3, dentate gyrus and hippocampus tail. The early visual cortex (EVC, MMP1 label: V1) and premotor cortex (M1, MMP1 label: Area4) were also included as control ROIs. All ROIs were combined across the left and right hemispheres.
Statistic type for inference (See Eklund et al. 2016)	ROI-based statistical models with correction of multiply comparisons.
Correction	For both mixed-effects logistic models and representational dissimilarity analyses, we applied Holm–Bonferroni corrections for multiple comparisons across ROIs used in the analyses.

Models & analysis

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