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Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	PsychoPy Version 1.82.01 was used to present the stimuli during the experiment.
Data analysis	Analysis of Functional NeuroImages (AFNI) Version 18.1.09 was used to preprocess and analyze the MRI data. Advanced Normalization Tools (ANTs) was used to normalize subjects' structurals to a template. GraphPad Prism version 7.00 for Mac was used to conduct the Kolmogorov–Smirnov test, t-tests, and ANOVA.

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 upon request. 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

Data and analysis code from this manuscript is available by request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Behavioural & social sciences study design

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

Study description	This is a quantitative experimental study. We conducted a one-way repeated measures ANOVA in Supplementary Figure S1 comparing short, medium, and long distances from video boundaries.
Research sample	Participants were UC Irvine undergraduates and other young adults from the area. They were ages 18-29 (mean=21.42, SD=2.85). Ten were female, and 9 were male. No genotypic information was collected, and they were free of neuropsychiatric disorders.
Sampling strategy	Sampling was through a convenience sample of UC Irvine community members, recruited through local advertising on campus. Sample size was calculated a priori based on prior experience and based on power analyses which suggest that for high resolution functional MRI studies, a minimum of 16 subjects is required to achieve 80% power at an alpha of .05.
Data collection	A computer running PsychoPy Version 1.82.01 was used to present the stimuli during the experiment and to record behavioral responses. One additional MRI-certified person from the laboratory was always present to ensure MRI safety. Our hypotheses concerned brain-behavior relationships and experimental conditions were within-subject.
Timing	September 1, 2015-March 18, 2016
Data exclusions	Six participants who had >20% of trials censored due to motion were excluded from the analysis. This was a pre-established criterion.
Non-participation	One participant ended participation early due to being uncomfortable in the MRI scanner.
Randomization	We did not separate participants into groups. The order of trial presentation at test was randomized using Python's "random" function.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants

Methods

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	See above
Recruitment	Recruitment flyers were posted on campus at UC Irvine, and previous participants who indicated their interest in MRI studies were contacted. There is a potential self-selection bias for participants who are interested in/familiar with research, but it is unclear how this might impact results.

Magnetic resonance imaging

Experimental design

Design type	Task event-related design
Design specifications	Each participant completed two 9:27 test blocks containing 36 trials each. Each trial was 9 seconds long, and the inter-trial interval was 0.5 seconds long.
Behavioral performance measures	For each trial, participants used a scroll wheel to indicate when each still frame occurred during the episode. This response was recorded, as well as the time when the participant stopped moving the scroll wheel. Average error was 155.54 seconds, with a standard deviation of 163.58 seconds. Additionally, a control experiment was conducted, in which a separate group of participants completed the task without ever having seen the episode. We used a nonparametric Kolmogorov-Smirnov test and determined that the two distributions were significantly different (K-S D=0.4991, p<0.0001).

Acquisition

Imaging type(s)	Functional and structural
Field strength	3T
Sequence & imaging parameters	Gradient echo EPI, field of view was 180 x 65.8 x 180. Slice thickness was 1.8mm. Orientation was . TE=, TR=2.5, flip angle=70, matrix=(1.607,0,0,-89.196,0,1.607,0,-89.196,0,0,1.994,-31.903):112,112,33
Area of acquisition	Slices were acquired as a partial axial volume without offset or angulation and were centered on the medial temporal lobe.

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	Analysis of Functional NeuroImages (AFNI) Version 18.1.09 was used to preprocess and the MRI data. First data were brain extracted (3dSkullStrip). Using AFNI's afni_proc.py, functional data were slice timing corrected (3dTshift), motion corrected (3dvolreg), and blurred to 2mm (3dmerge). Each subject's functional data was aligned to their anatomical scan (3dallineate).
Normalization	Each subject's functional data was aligned to their anatomical scan (3dallineate). Then, we used ANTs (Advanced Normalization Techniques) software to align each subject's data to a common template (0.65mm isotropic). This method uses both linear and nonlinear normalization.
Normalization template	Normalization was to a custom in-house template based on a sample of 12 healthy participants with structural segmentations of medial temporal lobes. The atlas was created using ANTS atlas creation tool.
Noise and artifact removal	Using AFNI's afni_proc.py, motion parameters (roll, pitch, yaw) were regressed out of each run. Additionally, anaticor was used to regress out signal from locally averaged white matter.
Volume censoring	Using AFNI's afni_proc.py, TRs pairs where the Euclidian Norm of the motion derivative exceeded 0.3mm were excluded from the analysis. Six participants were excluded due to excessive motion (>20% of TRs excluded due to the Euclidian Norm of the motion derivative exceeding 0.3mm)

Statistical modeling & inference

Model type and settings	Mass univariate analysis at the voxel level. We used 3D deconvolution approach which employs multiple linear regression.
Effect(s) tested	The regressors of interest were task conditions (high, medium and low precision).

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

Anatomical location(s)	Using custom segmentations from the in-house atlas focusing on hippocampal subfields and medial temporal lobe subregions.
Statistic type for inference (See Eklund et al. 2016)	Inference was conducted based on ROI-based averages for GLM analyses, and thus was not subject to voxel or cluster selection issues expounded upon by Ecklund et al. (2016).
Correction	ROI based analyses were corrected for multiple comparisons at the second level using Holm-Bonferroni sequential rejection correction.

Models & analysis

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