nature research

Corresponding author(s): Michael Hausser, Dimitar Kostadinov

Last updated by author(s): Feb 27, 2019

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	Virtual reality environment was created using ViRMEn in Matlab 2016a. Imaging data were acquired using Scanimage 2015 in Matlab 2016a. Electrphysiology data were acquired using SpikeGLX. Behavioral data and trail triggers were acquired using PackIO (reference 63).
Data analysis	Data analysis was performed in Matlab and Python using a combination of custom written scripts and available software. Segmentation of calcium imaging data was performed using Suite2p (reference 57), imaging event detection was performed using MLspike (reference 58), and spike sorting was performed using Kilosort2 (https://github.com/MouseLand/Kilosort2, reference 64) and curated using Phy (https://github.com/kwikteam/phy). Recording tracks were aligned to the Allen Mouse Common Coordinate Framework (CCF, references 67 and 68) using 'Allen CCF tools', a custom GUI for 3D alignment of electrode tracks to histology (reference 69).

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 and analysis code that support the findings of this study are available from the corresponding authors upon reasonable 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	No statistical methods were used to pre-determine sample sizes, but our sample sizes are similar to those reported in previous publications (see references 15, 20, and 26).
Data exclusions	No animals were excluded except in obvious cases where animals did not learn the required behavioural task or data could not be collected due to poor viral expression or occluded chronic windows. There were a few instances where cells or trials were excluded from analysis. When we analyzed responses of Purkinje cells assigned to particular microzones (i.e. Figures 3F, 6G, and 7G), we excluded neurons that were not categorically grouped in to a microzone, as described in the methods subsection 'Identification of Purkinje cell microzones'. When measuring lick latency in the naive condition in Figure 5E, we excluded trials before mice began licking to reward delivery. This is noted in the figure legend. In our analysis of fast and slow reaction wheel turns in Supplementary Figure 1, we excluded one session from our analysis because it only contained 4 trials in the slow reaction time condition.
Replication	Behavioral training and imaging experiments were done in batches rather than all at once. Data from multiple batched of mice were used in this study. Thus, the general findings of the study were replicated internally several times.
Randomization	No randomization of experimental subjects was necessary as all mice were trained and recorded under the same conditions. Behavioral events within each training session were randomized on a trial-by-trial basis within the temporal ranges and incidence rates described in the text.
Blinding	Data collection and analysis were not performed blind to the conditions of the experiment, but analysis relied on code that was standardized for all experimental conditions.

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	We used male Pcp2(L7)-Cre mice (line Jdhu – B6.Cg-Tg(Pcp2-Cre)3555Jdhu/J) aged between 3 and 6 months.
Wild animals	No wild animals were used in this study.
Field-collected samples	No field-collected samples were used.
Ethics oversight	All animal procedures were approved by the local Animal Welfare and Ethical Review Board at University College London and performed under license from the UK Home Office in accordance with the Animals (Scientific Procedures) Act 1986.

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