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1st Floor
24 Hills Road
Cambridge CB2 1JP, UK
P 01223 855340
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eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see EQUATOR Network), life science research (see the BioSharing Information Resource), or the ARRIVE guidelines for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Sample size was chosen to obtain a representative estimate of L2/3 auditory cortex neurons (about 4000 ~ 10% of all L2/3 AC neurons).

Replicates

- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Data were sampled from n=3 mice. No exclusion criteria were used. Details of replications of analyses are described in Results and Methods.

Statistical reporting

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

All this information is given in Results and Figure Legends.
Briefly:
Fig1B: mean +- SD shown for the norm (see caption).Fig1C: mean +- SEM over cross-validation folds (LOOCV). Significance shown when p<0.01 (two-tailed t-test, exact p-value not reported). For chance level (gray trace): mean(over cross-validation folds and over time) +- SD over time of the mean over cross-validation folds. Stimulus classification and cross-validation are explained in Methods.Fig2: Dimensionality reduction (PCA) and subspace correlation are explained in the Methods.Fig2A-C: mean +- SD (over stimuli), error bars smaller than symbol sizes.Fig3E: mean +- SD over bootstrap sub-samplings (see caption)Fig4A: p-value evaluated over multiple random shuffles of the dependent variable
(subspace correlation).Fig4B: mean +- SD over bootstrap sub-samplings (see caption)Fig4C: Trajectories are reconstructed as explained in the Methods.Fig4D: p-value evaluated with upper tail test using the mean value of R^2 over the cross-validations folds for each dataset (see caption); 500 surrogates datasets for mice 1 (for mice 2, 3 and pooled activity see supplementary figures). Reduced rank regression explained in the methods.Fig4F: The value of R^2 for individual cross-validation folds is shown, along with the mean over folds (dark bars; see caption).Fig5F: mean +- SEM across trials.Fig5G,H,I : mean +- SD over multiple subsamplings of stimuli (10-fold CV used; see caption). Single-cell and recurrent model fitting procedures are explained in the Methods.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

Group allocation

- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

N/A

Additional data files ("source data")

- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
- Where provided, these should be in the most useful format, and they can be uploaded as "Source data" files linked to a main figure or table
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are "available upon request"

Please indicate the figures or tables for which source data files have been provided:

N/A