nature neuroscience

| Corresponding Author: | Bijan Pesaran | # Main Figures: | 8 |
|-----------------------|---------------|--------------------------|----|
| Manuscript Number: | NN-A47908 | # Supplementary Figures: | 10 |
| Manuscript Type: | Article | # Supplementary Tables: | 0 |
| | | # Supplementary Videos: | 0 |

Reporting Checklist for Nature Neuroscience

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read Reporting Life Sciences Research.

Please note that in the event of publication, it is mandatory that authors include all relevant methodological and statistical information in the manuscript.

▶ Statistics reporting, by figure

- · Please specify the following information for each panel reporting quantitative data, and where each item is reported.
- Each figure legend should ideally contain an exact sample size (n) for each experimental group/condition, where n is an exact number and not a range, a clear definition of how n is defined (for example x cells from x slices from x animals from x litters, collected over x days), a description of the statistical test used, the results of the tests, any descriptive statistics and clearly defined error bars if applicable.
- · For any experiments using custom statistics, please indicate the test used and stats obtained for each experiment.
- Each figure legend should include a statement of how many times the experiment shown was replicated in the lab; the details of sample collection should be sufficiently clear so that the replicability of the experiment is obvious to the reader.
- For experiments reported in the text but not in the figures, please use the page number instead of the figure number.

Note: Mean and standard deviation are not appropriate on small samples, and plotting independent data points is usually more informative. When technical replicates are reported, error and significance measures reflect the experimental variability and not the variability of the biological process; it is misleading not to state this clearly.

| | | TEST USED | | | n | | DESCRIPTIVE ST (AVERAGE, VARIA | - 1 | P VALUE | | DEGREES OF FREEDOM 8 F/t/z/R/ETC VA | k |
|---------|------------------|--|-------------|----------------|---------------------------------------|-------------|---|-------------|-------------|-------------|---|------|
| | FIGURE NUMBER | WHICH TEST? | PAGE | EXACT VALUE | DEFINED? | PAGE | REPORTED? | PAGE | EXACT VALUE | PAGE | VALUE | PAGE |
| example | 1a | one-way ANOVA | 4 | 9, 9, 10, 15 | mice from at least 3 litters/group | 4 | error bars are mean +/- SEM | 4 | p = 0.044 | 4 | F(3, 36) = 2.97 | 4 |
| example | results, pg 6 | unpaired t-test | 6 | 15 | slices from 10 mice | 6 | error bars are mean +/- SEM | 6 | p = 0.0006 | 6 | t(28) = 2.808 | 6 |
| + | 2b,c,d, e | Cluster corrected, permutation test | met hods | 30,23,6,13 | coherent neuron groupings, | figur e | mean 95% confidence interval | met hods | p = 0.05 | met hods | N/A | |
| + | 3a,b | Wilcoxon ranksum test | resu Its | 30,23,13 | coherent neuron groupings | resu Its | mean - first point statistical test falls below 0.05 for three consecutive bins | figur e | p = 0.05 | resu Its | N/A | |

| | | TEST USED | | TEST USED n | | DESCRIPTIVE STATS (AVERAGE, VARIANCE) | | P VALUE | | DEGREES OF FREEDOM & F/t/z/R/ETC VALUE | | |
|---|------------------|---|----------------------------|----------------|--|--|---|-------------|---|--|---|------|
| | FIGURE NUMBER | WHICH TEST? | PAGE | EXACT VALUE | DEFINED? | PAGE | REPORTED? | PAGE | EXACT VALUE | PAGE | VALUE | PAGE |
| + | 3с | FDR corrected Wilcoxon ranksum test | resu Its | 30,23,13 | 40 permutations of coherent neuron groupings, | resu Its | error bars are mean +/- 95%Cl | figur e | p = 0.05 | figur e | z = -1.96, N/A | |
| + | 3d | Wilcoxon ranksum test | resu Its | 30,23,13 | 40 permutations of coherent neuron groupings | resu Its | mean - first point statistical test falls below 0.05 for three consecutive bins | figur e | p = 0.05 | figur e | Z = -1.96, N/A | |
| + | 4c,d | Wilcoxon ranksum test | resu Its | 30,23,13 | 40 permutations of coherent neuron groupings, | resu Its | error bars are mean +/- SEM | resu Its | p =9.6e-10, p=1.3e-10 p = 0.14 | resu Its | z=-6.423,z = -6.12,z =1.47, N/A | |
| + | 5a,b | Wilcoxon ranksum test | resu Its | 25 | 40 permutations of coherent neuron groupings | met hods | error bars are mean +/- SEM | figur e | p = 0.03, p = 0.351 | resu Its | z = -2.97, z = -0.9, N/A | |
| + | 5c,d | Wilcoxon ranksum test | resu Its | 28 | 40 permutations of coherent neuron groupings | met hods | error bars are mean +/- SEM | figur e | p = 0.0087, p = 7.1e-6 | resu Its | z = -2.6, z = -4.49, N/A | |
| + | 6a,b | Wilcoxon ranksum test | resu Its | 24 | 40 permutations of fastest grouping of neurons | met hods | error bars are mean +/- SEM | figur e | p = 2.9e-7 | resu Its | z = -5.54, N/A | |
| + | 7a,b | Wilcoxon ranksum test | resu Its | 30,23 | defined by rank ordering neurons by local coherence values | met hods | error bars are mean +/- SEM | figur e | p = 1.2e-6 | resu Its | z = -5.3, N/A | |
| + | 7c | Wilcoxon ranksum test | resu Its | 30,23 | defined by rank ordering neurons by local coherence values | met hods | error bars are mean +/- SEM | figur e | p= 0.0076 | resu Its | z = -2.66,N/A | |
| + | S1a,b | FDR corrected Wilcoxon ranksum test | figur e | 30,23,13,6 | 40 permutations of coherent neuron groupings | resu Its | error bars are mean +/- 95%Cl | figur e | p = 0.05 | figur e | z = -1.96, N/A | |
| + | S1c | FDR corrected Wilcoxon ranksum test | resu Its | 30,23,13 | 40 permutations of coherent neuron groupings | resu Its | error bars are mean +/- SEM | figur e | p = 9.6e-10, 1.3e-10, p = 0.14 | resu Its | z = -5.99, z=-5.99,z = -1.45,N/A | |
| + | S1d | FDR corrected Wilcoxon ranksum test | resu Its/ figur e | 17,13 | 40 permutations of coherent neuron groupings for each monkey | resu Its | error bars are mean +/- SEM | figur e | p=5.5e-10, p=7.5e-10, p=3.7e-10, p=3.7e-10 | figur e | z=-4.0,z=-5.99,z=- 5.99,z=-5.99,N/A | |
| + | S2a,b,c ,d | Wilcoxon ranksum test | resu Its | 117 | 40 permutations of LIP and PRR groupings | resu Its | error bars are mean +/- SEM | figur e | p = 0.47 | resu Its | r = -0.51, N/A | |
| + | S5a,b | Wilcoxon ranksum test | resu Its | 30,24,24 | defined by rank ordering neurons by baseline or delay firing rate | met hods | error bars are mean +/- SEM | figur e | p =9.7e-6 | resu Its | z = 2-4.89, N/A | |
| + | S7 | Wilcoxon ranksum test | figur e | 30,23,13,6 | Coherent neuron groupings | resu Its | error bars are mean +/- SEM | figur e | p=0.54, p=0.82 p=0.21, p=0.99, p=0.39, p=0.51 | figur e | z=-0.61,z=-0.2,z=- 1.25,z=-0.025,z=-0 .86,z=-0.67,N/A | |
| + | S8a,b | FDR corrected Wilcoxon ranksum test | figur e | 30,23,13,6 | Coherent neuron groupings | resu Its | error bars are mean +/- SEM | figur e | p = 0.05 | figur e | z = -1.96, N/A | |
| + | S8c,d | FDR corrected Wilcoxon ranksum test | figur e | 30,23,13,6 | 40 permutations of coherent neuron groupings | resu Its | error bars are mean +/- 95%Cl | figur e | p = 0.05 | figur e | z = -1.96, N/A | |
| + | S8e | Wilcoxon ranksum test | resu Its | 30,23,13 | 40 permutations of coherent neuron groupings | resu Its | error bars are mean +/- SEM | figur e | p = 3.42-6 | resu Its | z = -4.64,N/A | |
| + | S8f | Wilcoxon ranksum test | resu Its | 30,23,13 | 40 permutations of coherent neuron groupings | resu Its | error bars are mean +/- SEM | figur e | p = 1.5e-7 p = 5.8e-7 | resu Its | z=-5.25,z=-5.42,N/ A | |

| + | S9 | Wilcoxon ranksum test | figur e | 27,45 | which electrode was used | figur e | mean+/- 95% CI | figur e | p = 0.47 | figur e | z = 0.10, N/A | |
|-------------|-------|--------------------------|-------------|-------|-------------------------------|------------|--|------------|----------|-------------|----------------|--|
| + - S | 10a,b | Hartigan's Dip Test | resu Its | 72 | All coherent neuron groupings | figur e | actual value counts - all data shown | figur e | p=0.015 | resu Its | r = 0.0664,N/A | |

▶ Representative figures

1. Are any representative images shown (including Western blots and immunohistochemistry/staining) in the paper?

If so, what figure(s)?

2. For each representative image, is there a clear statement of how many time s this experiment was successfully repeated and a discussion of any limitations in repeatability?

If so, on what page(s) is this reported?

Yes, Figure 1 c and d

Yes the n is stated in the results section

▶ Statistics and general methods

1. Is there a justification of the sample size?

If so, how was it justified?

On what page(s)?

Even if no sample size calculation was performed, authors should report why the sample size is adequate to measure their effect size.

however the sample sizes in this work are similar to those reported in previous publications. Online methods

Statistical methods were not used to predetermine sample sizes

2. Are statistical tests justified as appropriate for every figure?

On what page(s)?

Yes, non parametric tests such as permutation tests and RankSum tests were used to ensure the most conservative estimates as well as to ensure no assumptions about the distribution of the data.

a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined? Statistical methods are outlines in the section Neuronal Methods and Analysis and each test and p value is restated with the numbers provided in the results section.

b. Do the data meet the assumptions of the specific statistical test you chose (e.g. normality for a parametric test)?

Where is this described?

Non-parametric tests (Ranksum and permutation tests) have been used.

c. Is there any estimate of variance within each group of $\,$ data?

Is the variance similar between groups that are being statistically compared?

Where is this described?

The variance within each population of neurons is stated in each section in which comparisons are made. Variance was similar between groups being tested.

d. Are tests specified as one- or two-sided?

Yes, online methods

e. Are there adjustments for multiple comparisons?

Yes, Figure 2, b,c,d e are cluster corrected. Figure 3 c is FDR corrected.

| 3. 4. | Are criteria for excluding data points reported? Was this criterion established prior to data collection? On what page(s) is this described? Define the method of randomization used to assign subjects (or | Neurons that did not respond to the task or too few trials recorded were excluded from further analysis. This criteria was established prior to data collection. Described in the online methods. No randomization was done |
|------------------------------------|--|--|
| | samples) to the experimental groups and to collect and process data. If no randomization was used, state so. | |
| | On what page(s) does this appear? | |
| 5. | Is a statement of the extent to which investigator knew the group allocation during the experiment and in assessing outcome included? | No blinding was done as this was not critical to the experimental results |
| | If no blinding was done, state so. | |
| | On what page(s)? | |
| 6. | For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? | Yes - online methods |
| | On what page(s)? | |
| 7. | Is the species of the animals used reported? | Yes - Macaca mulatta, online methods |
| | On what page(s)? | |
| 8. | Is the strain of the animals (including background strains of KO/transgenic animals used) reported? | N/A |
| | On what page(s)? | |
| 9. | Is the sex of the animals/subjects used reported? | Yes, both males, online methods |
| | On what page(s)? | |
| 10. | Is the age of the animals/subjects reported? | No |
| | On what page(s)? | |
| 11. | For animals housed in a vivarium, is the light/dark cycle reported? On what page(s)? | Yes, 7am/7pm, online methods |
| | on what page(a). | |
| 12. | For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? | Yes, one cage mate, online methods |
| | On what page(s)? | |
| 13. | For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? | Yes, experiments were always conducted during the light cycle, online methods) |
| | On what page(s)? | |

| 14. | . Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported? | This was the first study that the animals were used for. |
|-----|--|--|
| | On what page(s)? | |
| | a. If multiple behavioral tests were conducted in the same group of animals, is this reported? On what page(s)? | N/A |
| 15. | . If any animals/subjects were excluded from analysis, is this reported? On what page(s)? | No animals were excluded |
| | a. How were the criteria for exclusion defined? Where is this described? | N/A |
| | b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study. Where is this described? | N/A |
| | Reagents Have antibodies been validated for use in the system under study (assay and species)? | No antibodies were used |
| | a. Is antibody catalog number given?On what page(s) does this appear? | N/A |
| | b. Where were the validation data reported (citation, supplementary information, Antibodypedia)?On what page(s) does this appear? | N/A |
| 2. | If cell lines were used to reflect the properties of a particular tissue or disease state, is their source identified? | No cell lines were used |
| | On what page(s)? | |
| | a. Were they recently authenticated?On what page(s) is this information reported? | N/A |

▶ Data deposition

Data deposition in a public repository is mandatory for:

- a. Protein, DNA and RNA sequences
- b. Macromolecular structures
- c. Crystallographic data for small molecules
- d. Microarray data

Deposition is strongly recommended for many other datasets for which structured public repositories exist; more details on our data policy are available here. We encourage the provision of other source data in supplementary information or in unstructured repositories such as Figshare and Dryad.

| 1. | Are accession | codes for | deposit | dates | provided | ? |
|----|---------------|-----------|---------|-------|----------|---|
| | | | | | | |

No

On what page(s)?

▶ Computer code/software

Any custom algorithm/software that is central to the methods must be supplied by the authors in a usable and readable form for readers at the time of publication. However, referees may ask for this information at any time during the review process.

1. Identify all custom software or scripts that were required to conduct the study and where in the procedures each was used.

No custom software or scripts were used

2. Is computer source code/software provided with the paper or deposited in a public repository? Indicate in what form this is provided or how it can be obtained.

No however all scripts can be provided on request

▶ Human subjects

1. Which IRB approved the protocol?

Where is this stated?

No humans were used

2. Is demographic information on all subjects provided?

On what page(s)?

N/A

3. Is the number of human subjects, their age and sex clearly defined?

On what page(s)?

N/A

4. Are the inclusion and exclusion criteria (if any) clearly specified?

On what page(s)?

N/A

5. How well were the groups matched?

Where is this information described?

N/A

| 6. | Is a statement confirming that informed consent was obtained from all subjects included? | N/A |
|----------|---|---|
| | On what page(s)? | |
| 7. | For publication of patient photos, is a statement confirming that consent to publish was obtained included? On what page(s)? | N/A |
|) | fMRI studies | |
| | r papers reporting functional imaging (fMRI) results please ensure that thormation is clearly provided in the methods: | nese minimal reporting guidelines are met and that all this |
| 1. | Were any subjects scanned but then rejected for the analysis after the data was collected? | fMRI was not used |
| | If yes, is the number rejected and reasons for rejection described? | N/A |
| | On what page(s)? | |
| 2. | Is the number of blocks, trials or experimental units per session and/ or subjects specified? | N/A |
| | On what page(s)? | |
| 3. | Is the length of each trial and interval between trials specified? | N/A |
| 4. | Is a blocked, event-related, or mixed design being used? If applicable, please specify the block length or how the event-related or mixed design was optimized. | N/A |
| 5. | Is the task design clearly described? Where? | N/A |
| 6. | How was behavioral performance measured? | N/A |
| 7. | Is an ANOVA or factorial design being used? | N/A |
| 8. | For data acquisition, is a whole brain scan used? | N/A |
| | If not, state area of acquisition. | |
| | a. How was this region determined? | N/A |

| 9. | s the field strength (in Tesla) of the MRI system stated? | N/A |
|-----|--|-----|
| | a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated? | N/A |
| | b. Are the field-of-view, matrix size, slice thickness, and TE/TR/ flip angle clearly stated? | N/A |
| 10. | Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated? | N/A |
| 11. | Is the coordinate space for the anatomical/functional imaging data clearly defined as subject/native space or standardized stereotaxic space, e.g., original Talairach, MNI305, ICBM152, etc? On what page(s)? | N/A |
| 12. | If there was data normalization/standardization to a specific space template, are the type of transformation (linear vs. nonlinear) used and image types being transformed clearly described? On what page(s)? | N/A |
| 13. | How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.? | N/A |
| 14. | Were any additional regressors (behavioral covariates, motion etc) used? | N/A |
| 15. | Is the contrast construction clearly defined? | N/A |
| 16. | Is a mixed/random effects or fixed inference used? | N/A |
| | a. If fixed effects inference used, is this justified? | N/A |
| 17. | Were repeated measures used (multiple measurements per subject)? | N/A |
| | a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated? | N/A |
| 18. | If the threshold used for inference and visualization in figures varies, is this clearly stated? | N/A |
| 19. | Are statistical inferences corrected for multiple comparisons? | N/A |
| | a. If not, is this labeled as uncorrected? | N/A |

| 20. Are the results based on an ROI (region of interest) analysis? | N/A | | | | |
|--|-----|--|--|--|--|
| a. If so, is the rationale clearly described? | N/A | | | | |
| a. If 30, 13 the rationale elearly described: | | | | | |
| b. How were the ROI's defined (functional vs anatomical localization)? | N/A | | | | |
| | | | | | |
| 21. Is there correction for multiple comparisons within each voxel? | N/A | | | | |
| 22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined? | N/A | | | | |
| • Additional comments | | | | | |
| Additional Comments | | | | | |
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