

## 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](#).

### 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

Behavioral task was presented using TEMPO Experiment Control System (Reflective Computing). Neurophysiology data was recorded by Plexon MAP system (Plexon)

Data analysis

MATLAB versions R2016a and R2017a (MathWorks)

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

The data relevant to this study are available upon request from the corresponding author.

## 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

For a reference copy of the document with all sections, see [nature.com/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

## Life sciences

### Study design

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

|                 |  |
|-----------------|--|
| Sample size     | The properties of some neurons in SEF are sufficiently well understood that a power analysis can guide data sampling. The variance of neural discharge rates scale with the mean, so with $\alpha = 0.05$ and $\beta = 0.2$ , the nature of the modulation patterns that must be measured for the various studies require from 26 (Cohen $d = 0.8$ ) to 64 neurons (Cohen $d = 0.5$ ). However, many signals in SEF are less well characterized and exhibit more diversity and complexity. While a power analysis cannot be done without knowledge of population characteristics (Dell et al. 2002), we implement less formal algorithms to specify when to terminate data collection for a particular study. Based on the experience of our laboratory, neuron sampling within a region of interest for a particular study stops when two criteria are satisfied: (1) new discoveries demonstrate reliability as assessed by statistical analysis of neural modulation in relation to particular events ( $\alpha = 0.05$ , $\beta = 0.2$ , from 26 (Cohen $d = 0.8$ ) to 64 neurons (Cohen $d = 0.5$ )) and (2) mean values of derived neural measures do not change with further sampling over 2-3 experimental sessions. The time and number of samples needed to reach this termination criterion depends on how commonly sampled are the neurons of interest. The rarest response property that we can study effectively is exhibited by $\sim 10\%$ of a population. Our statistically specified goal, therefore, is to obtain a meaningful sample of this 10% in more than one monkey. Typically, the maximum number of such rare neurons that can be sampled within a given region of interest is between 20 and 30 (out of 200-300 neurons total). A sample of 40-60 such neurons would require 2 monkeys. In all cases, common results must be obtained from at least 2 monkeys to justify a rigorous, reproducible publication (Roelfsema & Treue 2014). |
| Data exclusions | The exclusion criteria are described in the Methods section of the paper. Neurons modulated in irrelevant task intervals or not at all were not analyzed for this report. Also, for the analysis of various functional signals, trials in which two or more distinct events coincided in time were removed unless the confounding factors could be appropriately accounted for (e.g., Supplementary Dig 2).  |
| Replication     | Replications consisted of repeated measures of different cortical sites in the same animal as well as repeating the same experiment in a second animal. Repeated samples obtained from a given location resulted in indistinguishable patterns.  |
| Randomization   | The experimental task involved pseudo-randomization of task conditions to ensure appropriate performance.  |
| Blinding        | Data collection and analysis were not performed blind to the experimental conditions. Neurophysiology experiments on animal subjects do not suffer from biases that arise due to lack of such blinding.  |

## Materials & experimental systems

Policy information about [availability of materials](#)

|                                     |  |
|-------------------------------------|--|
| n/a                                 | Involvement in the study                             |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Unique materials            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies                  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines       |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Research animals |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |

### Research animals

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

|                                  |   |
|----------------------------------|---|
| Animals/animal-derived materials | Data from two macaque monkeys: one male ( <i>M. radiata</i> 8.8 kg, $\sim 6$ years old) and one female ( <i>M. mulatta</i> 6 kg, $\sim 8$ years old) macaque. |
|----------------------------------|---|

## Method-specific reporting

- n/a | Involved in the study
- ChIP-seq
- Flow cytometry
- Magnetic resonance imaging

## Magnetic resonance imaging

### Experimental design

- Design type
- Design specifications
- Behavioral performance measures

### Acquisition

- Imaging type(s)
- Field strength
- Sequence & imaging parameters
- Area of acquisition
- Diffusion MRI  Used  Not used

### Preprocessing

- Preprocessing software
- Normalization
- Normalization template
- Noise and artifact removal
- Volume censoring

### Statistical modeling & inference

- Model type and settings
- Effect(s) tested
- Specify type of analysis:  Whole brain  ROI-based  Both
- Statistic type for inference   
(See [Eklund et al. 2016](#))
- Correction

### Models & analysis

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