## *eLife's* transparent reporting form

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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:

The sample size (number of sessions and number of cells for each animal) is detailed in the Methods (section *Data sets*). We did not pre-determine the exact sample size. However, we aimed to collect ~500 neurons from each animal. This is typical for our study and well above the current standards in primate neurophysiology. In our experience, ~1000 cells are sufficient to reveal significant correlations with behavioral phenomena.

**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)

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In primate neurophysiology studies, a data point is given by one session or one neuron. Thus each animal provides a full data set. Replication is normally ensured by repeating experiments in two animals. In the present study, all the behavioral results held true for each of two animals, as illustrated in Fig.2 and Fig.3. In the analyses of neuronal activity, we pooled data from the two animals. All the results were replicated as a trend in each monkey, albeit with lower statistical power (i.e., in some cases, data for individual animals did not reach significance threshold). Criteria used to identify outliers and exclude data points are detailed in the Methods (section *Data sets*). In practice, exclusion criteria were only relevant for Fig.6 and Fig.S2. As noted in the figure legends, including all the data in the analysis did not substantially alter the conclusions.

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## 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:

Statistical analysis methods and exact values of N, measure, effect size and p values are listed in each figure or figure legend, throughout the manuscript.

(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:

Group allocation does not apply to our study.
In each session, trials from the two task modalities, simultaneous offers and sequential offers, were randomized.  This information can be found in the Methods (section *Animal subjects, choice tasks and neuronal recordings*).

## 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:

Source data files will be available at https://github.com/PadoaSchioppaLab/choicebias