

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:

A sample size of 17 was used in the experiment. This sample size was chosen to be comparable with other studies of working memory and decision-making psychophysics and to be slightly larger than average to examine individual differences in participant strategy.

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:

Our experiment was not replicated within subjects. Each subject performed 50-100 trials per condition (block, set size, delay). We excluded trials which had a response error outside of the 95% error distribution to focus analysis on trials which were to the correct response, as described in the Methods. Subjects whose data was not well fit by our models were reported but not included in group analysis of subjects well fit by the models.

**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:

Our data are analyzed and shown for the subject pool of 17 and in some cases individually in the supplemental figures. Analysis included a test of whether the mean response error was significantly different from zero across several set sizes, delays, and blocks, which was performed through a Bonferroni corrected student's *t*-test (Fig. 3, 7, S3-S6). We also performed an ANOVA to determine the effects of delay and set size on error variance in various conditions (Fig. 3, 7). To assess the model fits we used a form of parametric bootstrapping for cross-validation as described in the Methods and shown in Figs. 4, 8. Additionally, we tested whether subjects were significantly more likely to be fit by either of our models at a given set size and block using Wilcoxon Sign Rank test (Fig 6, 10) and whether subject strategy use was predictive using a Fisher's exact test due to the relatively small number of subjects.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, *N*s, 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:

Our data analysis was performed on a single subject basis and thus there are no group allocations.

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"



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

All MATLAB code used to analyze the data and generate the figures is available on our public GitHub code repository. Data will be made available via open Dryad when appropriate.