

Materials Design Analysis Reporting (MDAR) Checklist for Authors

The [MDAR framework](#) establishes a minimum set of requirements in transparent reporting mainly applicable to studies in the life sciences.

eLife asks authors to **provide detailed information within their article** to facilitate the interpretation and replication of their work. Authors can also upload supporting materials to comply with relevant reporting guidelines for health-related research (see [EQUATOR Network](#)), life science research (see the [BioSharing Information Resource](#)), or animal research (see the [ARRIVE Guidelines](#) and the [STRANGE Framework](#); for details, see *eLife's* [Journal Policies](#)). Where applicable, authors should refer to any relevant reporting standards materials in this form.

For all that apply, please note **where in the article** the information is provided. Please note that we also collect information about data availability and ethics in the submission form.

Materials:

Newly created materials	Indicate where provided: section/ figure legend	N/A
The manuscript includes a dedicated "materials availability statement" providing transparent disclosure about availability of newly created materials including details on how materials can be accessed and describing any restrictions on access.		X

Antibodies	Indicate where provided: section/ figure legend	N/A
For commercial reagents, provide supplier name, catalogue number and RRID , if available.		X

DNA and RNA sequences	Indicate where provided: section/ figure legend	N/A
Short novel DNA or RNA including primers, probes: Sequences should be included or deposited in a public repository.		X

Cell materials	Indicate where provided: section/ figure legend	N/A
Cell lines: Provide species information, strain. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.		X
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		X

Experimental animals	Indicate where provided: section/ figure legend	N/A
Laboratory animals or Model organisms: Provide species, strain, sex, age, genetic modification status. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.		X
Animal observed in or captured from the field: Provide species, sex, and age where possible.		X

Plants and microbes	Indicate where provided: section/ figure legend	N/A
Plants: provide species and strain, ecotype and cultivar where relevant, unique accession number if available, and source (including location for collected wild specimens).		X
Microbes: provide species and strain, unique accession number if available, and source.		X

Human research participants	Indicate where provided: section/ figure legend) or state if these demographics were not collected	N/A
If collected and within the bounds of privacy constraints report on age, sex, gender and ethnicity for all study participants.	Demographic details (age, sex, gender, ethnicity) were not collected/reported in this study. This is a computational reanalysis of previously published human behavioral datasets; participant counts per dataset are given in Methods ("Food-choice task") and Appendix1–Table 5. Demographic information, where available, is reported in the original publications (Krajbich et al., 2010; Smith and Krajbich, 2018; Chen and Krajbich, 2016; Gwinn and Krajbich, 2016; Folke et al., 2016; Sepulveda et al., 2020).	

Design:

Study protocol	Indicate where provided: section/ figure legend	N/A
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If the study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number OR cite DOI.		X
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Laboratory protocol	Indicate where provided: section/ figure legend	N/A
Provide DOI OR other citation details if detailed step-by-step protocols are available.		X

Experimental study design (statistics details) *		
For in vivo studies: State whether and how the following have been done	Indicate where provided: section/ figure legend. If it could have been done, but was not, write "not done"	N/A
Sample size determination	Not applicable to this reanalysis: sample sizes are those of the previously published datasets being reanalyzed (no new data collection). Numbers of participants per dataset are listed in Appendix1–Table 5 and Methods ("Food-choice task"); no formal power analysis was performed for the present	
Randomisation	Not applicable: no new participants or trials were generated for this study; trial order/randomization was determined by the original studies (see cited references, Methods, Appendix1–Table 5).	
Blinding	Not applicable: this is a computational/statistical reanalysis of existing data; no new data collection or group allocation was performed, so blinding does not apply.	

Inclusion/exclusion criteria	Trial-level exclusion criteria for specific analyses are stated where used: trials in which the two items received equal ratings were excluded from consistency-dependent analyses because they cannot be classified as consistent/inconsistent (Fig. 2 legend; Results “The difference in dwell time is independent of choice consistency”). Some datasets (Folke et al., 2016; Sepulveda et al., 2020) were excluded from the last-fixation/MELFB analysis in Fig. 3 because last-dwell information was unavailable in the public data (Results; Fig. 3 legend). Dataset-level inclusion constraints (e.g., maximum permitted value difference) are listed in Appendix1–Table 5.	
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Sample definition and in-laboratory replication	Indicate where provided: section/figure legend	N/A
State number of times the experiment was replicated in the laboratory.	Not applicable in the traditional sense of laboratory replication: this study reanalyzes six previously published, independently collected datasets (Krajbich et al., 2010; Smith and Krajbich, 2018; Chen and Krajbich, 2016; Gwinn and Krajbich, 2016; Folke et al., 2016; Sepulveda et al., 2020), each run once per participant in the original studies (Methods “Food-choice task”; Appendix1–Table 5).	
Define whether data describe technical or biological replicates.	Biological replicates correspond to individual human participants (N = 28–44 per dataset; Table S5, and N = 39 for the Krajbich et al. 2010 dataset used for the main model fits, e.g. Fig. 6 legend). There are no technical replicates; each participant completed one session of choice trials per original study.	

Ethics	Indicate where provided: section/ submission form	N/A
Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	This study reanalyzes previously collected, de-identified behavioral data; no new human data were collected. Ethical approval for the original data collection was obtained by the original investigators under their respective institutional review boards (see Methods “Food-choice task” and cited original publications: Krajbich et al., 2010; Smith and Krajbich, 2018; Chen and Krajbich, 2016; Gwinn and Krajbich, 2016; Folke et al., 2016; Sepulveda et al., 2020).	
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		X
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		X

Dual Use Research of Concern (DURC)	Indicate where provided: section/ submission form	N/A
If study is subject to dual use research of concern regulations, state the authority granting approval and reference number for the regulatory approval.		X

Analysis:

Attrition	Indicate where provided: section/ figure legend	N/A
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Describe whether exclusion criteria were pre-established. Report if sample or data points were omitted from analysis. If yes, report if this was due to attrition or intentional exclusion and provide justification.	Exclusion criteria are pre-established and stated in the text where applied. Trials with equal ratings for the two items were excluded from Δ Dwell/consistency analyses, as they cannot be classified as consistent or inconsistent (Fig. 2 legend). Two datasets were excluded from the last-fixation/MELFB analysis (Fig. 3) because last-dwell information was not available in the public data (Results). No other data points were omitted; these are pre-specified analytic exclusions, not attrition.	
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Statistics	Indicate where provided: section/figure legend	N/A
Describe statistical tests used and justify choice of tests.	Statistical methods are described in Methods (“Model fitting” and “Data analysis”) and throughout Results. These include mixed-effects logistic and linear regression (Eqs. 3, 12, 13, 14), one- and two-tailed t-tests on regression coefficients, Wilcoxon signed-rank tests (Fig. 7), likelihood-ratio tests (Fig. 9), and maximum-likelihood model fitting via numerical solution of the Fokker-Planck equation (Chang-Cooper method) combined with Bayesian Adaptive Direct Search (BADs) optimization (Eqs. 9, 11).	

Data availability	Indicate where provided: section/submission form	N/A
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For newly created and reused datasets, the manuscript includes a data availability statement that provides details for access (or notes restrictions on access).	See Data Availability statement: “Code and data required to reproduce the model fitting, simulations, and figures presented in this paper are available at https://github.com/arielzylberberg/PostDecisionalAttention_eLife2026 .” The behavioral data reanalyzed originate from previously published studies (cited in Methods) and were obtained from public sources or shared directly by the original authors (Acknowledgments).	
When newly created datasets are publicly available, provide accession number in repository OR DOI and licensing details where available.	Not applicable: no new experimental datasets were generated. Derived/processed data and simulation outputs used to produce the figures are provided at https://github.com/arielzylberberg/PostDecisionalAttention_eLife2026 (Data Availability).	
If reused data is publicly available provide accession number in repository OR DOI, OR URL, OR citation.	Reused behavioral datasets are cited by reference throughout Methods (“Food-choice task”): Krajbich et al. (2010), Smith and Krajbich (2018), Chen and Krajbich (2016), Gwinn and Krajbich (2016), Folke et al. (2016), Sepulveda et al. (2020). Simulations of the optimal-attention model of Callaway et al. (2021) were obtained from https://github.com/fredcallaway/optimal-fixations-simple-choice (Methods “Optimal decision models”).	

Code availability	Indicate where provided: section/ figure legend	N/A
For any computer code/software/mathematical algorithms essential for replicating the main findings of the study, whether newly generated or re-used, the manuscript includes a data availability statement that provides details for access or notes restrictions.	See Data Availability statement: all code required to reproduce the model fitting, simulations, and figures is available at https://github.com/arielzylberberg/PostDecisionalAttention_eLife2026 .	

Where newly generated code is publicly available, provide accession number in repository, OR DOI OR URL and licensing details where available. State any restrictions on code availability or accessibility.	https://github.com/arielzylberberg/PostDecisionalAttention_eLife2026 (Data Availability). No access restrictions; licensing details are provided in the repository.	
If reused code is publicly available provide accession number in repository OR DOI OR URL, OR citation.	Simulation code/output for the optimal-attention model of Callaway et al. (2021), obtained from https://github.com/fredcallaway/optimal-fixations-simple-choice (Methods “Optimal decision models”).	

Reporting:

The MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives.

Adherence to community standards	Indicate where provided: section/figure legend	N/A
State if relevant guidelines (e.g., ICMJE, MIBBI, ARRIVE, STRANGE) have been followed, and whether a checklist (e.g., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.	Not applicable: this is a computational/behavioral reanalysis and modeling study, not a clinical trial or animal study, so field-specific checklists such as CONSORT or ARRIVE do not apply. No additional community reporting checklist is provided beyond the present MDAR form.	

* We provide the following guidance regarding transparent reporting and statistics; we also refer authors to [Ten common statistical mistakes to watch out for when writing or reviewing a manuscript](#).

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

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)

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.

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