

# From Pipettes to $p$ -Values: A Framework for Companion Statistical Reporting in Experimental Neuroscience

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## Abstract

Statistical inference in experimental neuroscience is routinely detached from the experimental record: analytic choices are reported in prose summaries that do not expose the code, assumptions, or decision pathways that produced the results. This detachment limits reproducibility and impairs peer review. Here, we describe the Companion Statistical Report (CSR), a structured, versioned document format designed to accompany empirical neuroscience manuscripts as peer-reviewed as a peer-reviewed resource. The CSR integrates data provenance, preprocessing decisions, exploratory analyses, model specifications, assumption diagnostics, inference with effect sizes, and sensitivity analyses into a single executable document, authored in Quarto 1.8 and supporting both R and Python workflows. We provide an open template hosted at on GitHub that implements this format with institutional branding, parameterization, and version tracking. The template was developed by the Bertrand Russell Research Excellence Group (NEC) at the School of Medicine, Rio de Janeiro State University. By making analytic choices auditable and reproducible by design, CSRs are designed to reduce the gap between what neuroscience experiments measure and what published statistics claim, offering a tractable and immediately implementable step toward greater transparency.

**Keywords:** reproducibility; statistical reporting; experimental neuroscience; open science

## 1. Introduction

The reproducibility problem in experimental neuroscience is not primarily a problem of fraud or selective reporting, though both occur. It is, in large part, a structural problem: the conventions governing how neuroscience results are reported were established before computational reproducibility was technically feasible, and they have not been revised to reflect what is now possible [1,2]. These conventions reflected the computational constraints of their time and represented reasonable practice within those constraints; the issue is not that they were poorly conceived, but that they have not evolved alongside the tools now available. A methods section stating that data was analyzed with a one-way ANOVA followed by Tukey correction provides none of the information needed to evaluate whether that model was appropriate, whether the data met its assumptions, what preprocessing preceded it, or how the analyst arrived at that choice among alternatives. The result is research in which statistical claims are systematically underspecified [3,4].



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The consequences are well documented. Underpowered designs, inflated effect sizes, and analytic flexibility, the capacity of researchers to make post hoc decisions that increase the probability of a significant result without declaring those decisions, have been identified as major contributors to non-replication across biomedical fields [1,5,6]. In neuroscience specifically, the mismatch between the biological structure of experimental data and the assumptions of the tests applied to them is pervasive: observations nested within animals, repeated measurements across time, and outcomes that are proportional or bounded are regularly analyzed with methods that assume independence, normality, and unbounded continuous distributions [7,8]. None of these mismatches is detectable from a prose methods description.

Existing initiatives have addressed parts of this problem. Preregistration constrains hypotheses before data collection [9]. Data sharing mandates make raw observations available [10]. Reporting guidelines such as ARRIVE 2.0 improve the description of experimental conditions [11]. What remains largely unaddressed is the statistical layer: the chain of decisions linking raw data to published numbers. Registries of analysis plans help when they are used, but they do not produce a reviewable, executable record of what was done. Code repositories, when provided, are rarely structured for human reading and do not integrate prose rationale with computational steps.

We propose the Companion Statistical Report (CSR) as a practical response to this gap. A CSR is a structured, executable document submitted and reviewed alongside the main manuscript. It narrates the complete statistical workflow, in code and prose, making every decision from data import to final figure available for inspection and reproduction. The CSR does not replace the manuscript; it provides the analytic substrate that the manuscript's claims rest on. Here, we describe the design of the CSR format, its technical implementation as an open Quarto template, and the rationale for each of its structural components.

## 2. Materials and Methods

### 2.1. Template Development Environment

The CSR template was developed in Quarto 1.8 [12], an open-source scientific publishing system built on Pandoc that supports literate programming in R, Python, Julia, and Observable. Quarto was selected over R Markdown because it provides a language-agnostic architecture, consistent chunk option syntax across engines, native support for cross-references, and active maintenance by Posit, PBC. The template was authored and tested in RStudio 2024.12.0 (Posit, PBC, Boston, MA, USA) using R 4.4.2 [13]. Python compatibility was verified using a Jupyter kernel via the reticulate package.

The template targets PDF output via XeLaTeX, chosen for its Unicode support and compatibility with non-ASCII characters common in author names and institutional affiliations from non-Anglophone research environments. The YAML front matter is structured to accept parameterized inputs, including manuscript title, investigator names, version code, logo path, and a confidentiality statement, without requiring the analyst to edit LaTeX directly.

### 2.2. Version Tracking System

Each rendered CSR is identified by a structured version code of the form NEC-SXXVXXDXXXX, where S denotes the service number, V denotes the version within that service, and D denotes the document iteration. This code is validated at compile time by a regular expression check in R; documents with malformed codes do not render, preventing the circulation of unversioned reports. The version code is injected into the PDF title page, header macros, and a dedicated metadata section, creating an auditable link between each analytical iteration and the corresponding manuscript version.

### 2.3. Repository and Licensing

The template is freely available at <https://github.com/dhrhf/CSReport> (created on 28 February 2026) (Supplementary Material) under a Creative Commons license. The repository contains the .qmd source file, the institutional logo, a README describing parameterization and rendering instructions, and example output. All files required to reproduce the compiled PDF from source are included. The template is designed to be used as a GitHub repository template, allowing laboratories to fork and customize it while retaining version history.

### 2.4. Structural Design Rationale

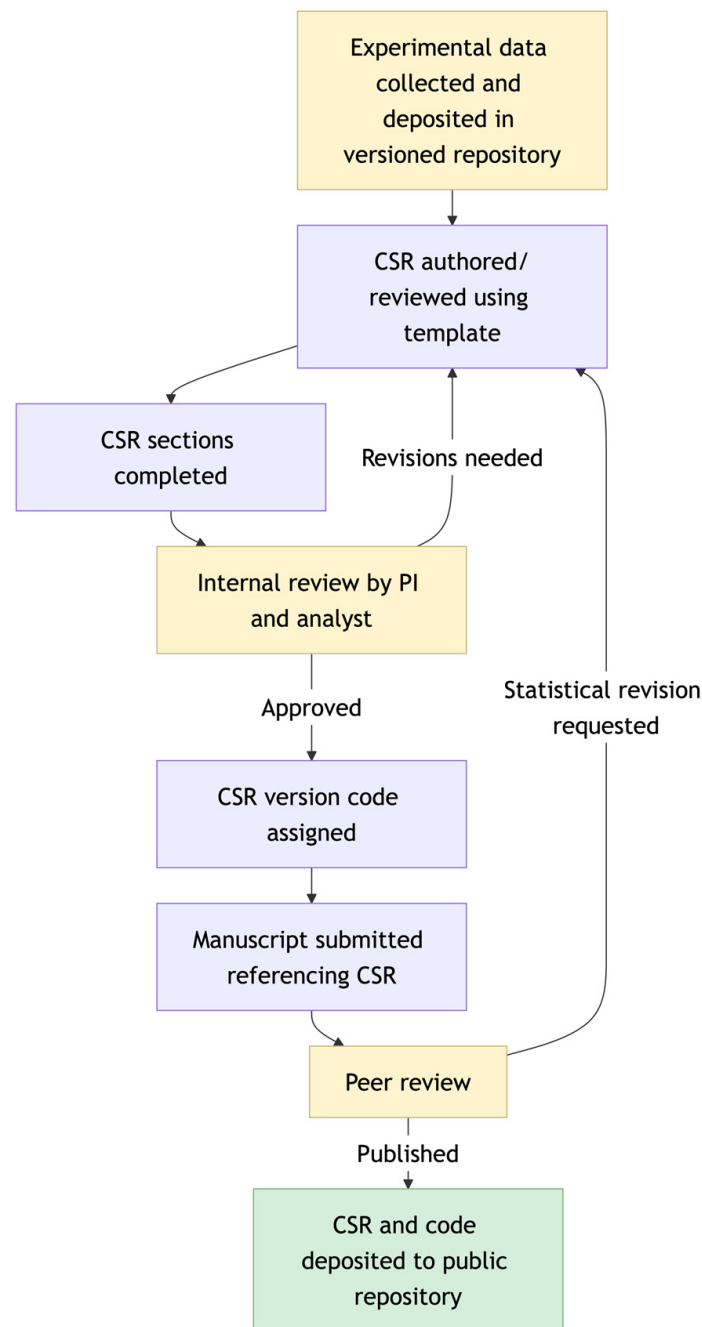
The section architecture of the CSR was derived from three sources: the statistical workflow described in established guidelines for reproducible computational research [10,11], common analytical failure modes documented in the neuroscience reproducibility literature [3], and iterative use of the template in ongoing research at NEC, including a recent transcriptomic study in which a reproducible analytical script was provided as Supplementary Material [14]. Each section was designed to enforce a specific checkpoint in the analytic workflow, as described in the Results.

## 3. Results

### 3.1. A Framework for CSR-Mediated Manuscript Publication

The CSR template is designed not as a standalone document but as a node within a structured publication workflow (Figure 1). In this framework, data deposition precedes analysis: raw experimental data are committed to a versioned repository before the CSR is opened, establishing provenance independently of the analytical record. The analyst then works through the CSR sections sequentially, with each section functioning as a checkpoint that must be completed and narratively justified before the next stage of analysis proceeds. This sequencing prevents the common practice of returning to preprocessing or model selection after examining the inferential results, a form of analytic flexibility that inflates false-positive rates without leaving a detectable trace in the published record.

Internal review by the principal investigator and analyst before manuscript drafting serves a function distinct from peer review. At this stage, researchers can evaluate whether the statistical choices are appropriate for the biology, whether the effect sizes are plausible given the assay's known variability, and whether the conclusions drawn from the models are consistent with the data displayed in the figures. Revisions at this stage are captured as new CSR versions under the same version tracking system, preserving a complete record of how the analysis evolved before external scrutiny. Only after this internal approval is the version code assigned and the manuscript drafted, creating a structural dependency between the analytic record and the scientific narrative. When peer review requests statistical revisions, those revisions return to the CSR authoring stage rather than being absorbed into an edited methods paragraph, so that the published document always reflects a complete and executable analytical record rather than an accumulation of undocumented post hoc adjustments.



**Figure 1.** Proposed framework for companion statistical report-mediated publication of experimental neuroscience research. Experimental data are deposited in a versioned repository before analysis begins. The statistical analyst authors the CSR using the Quarto template, completing each structured section sequentially. The completed document undergoes internal review by the principal investigator and analyst; if revisions are required, the CSR is updated and re-reviewed within the same versioned workflow. Once approved, a version code is assigned, and the manuscript is drafted referencing the CSR directly. Both documents are submitted together for peer review. Requests for statistical revision during peer review return to the CSR authoring stage, ensuring that all analytical changes are captured in an updated, versioned document rather than in untracked edits to the manuscript methods. Upon acceptance, the final CSR and all associated code are deposited to a public repository. Arrows indicate the direction of workflow progression; feedback arrows indicate iterative revision cycles.

### 3.2. Template Architecture

The CSR template comprises eight structured sections that map onto the sequential stages of a reproducible statistical workflow (Table 1). It additionally includes three closing

sections, namely 9. Conclusions and next steps, 10. References, and 11. Session information, which serve as documentary and administrative components of the report. Each section is implemented as a Quarto division with narrative guidance embedded as commented text, allowing analysts unfamiliar with formal reporting standards to understand what is required at each stage without external instruction.

**Table 1.** Sections of the Companion Statistical Report template and their primary function.

| Section                                    | Primary Function                                                                                                                                   |
|--------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|
| About this document                        | Contextualizes the CSR relative to the associated manuscript and declares its scope                                                                |
| Analysis request and scope                 | States the research questions, outcomes, and version-specific changes                                                                              |
| Data provenance and preprocessing          | Documents data origin, collection conditions, and all preprocessing decisions with justifications                                                  |
| Exploratory data analysis                  | Characterizes distributions, sample sizes, and data quality before any inferential model                                                           |
| Statistical models                         | Specifies the model family, assumptions, and rationale for model choice                                                                            |
| Inference and effect sizes                 | Reports estimates, confidence intervals, and effect sizes for all primary outcomes, alongside <i>p</i> -values                                     |
| Sensitivity analyses                       | Documents robustness of conclusions to alternative analytic choices                                                                                |
| Figures and tables for the main manuscript | Contains final, publication-ready versions of all figures and tables referenced in the manuscript, with fully self-contained and reproducible code |

The template is rendered with `echo: TRUE` by default, a deliberate departure from the convention of suppressing code in scientific documents. In a CSR, code visibility is designed to ensure that the analyst's decisions are documented in the output. This parameter, however, can be easily altered to allow for a simpler representation of the workflow.

### 3.3. Parameterization and Title Page Injection

A persistent challenge in Quarto PDF documents is injecting dynamic R values into raw LaTeX environments such as title pages. Quarto's inline R syntax is evaluated only within Markdown prose; within LaTeX blocks, it passes through unprocessed. The template resolves this with a two-layer command pattern. Static `\newcommand` definitions in header includes declare placeholder values for all title-page fields. A validation chunk then writes a sidecar file, `nec_params.tex`, containing `\renewcommand` overrides populated from the YAML params block. This file is injected at the top of the LaTeX document body via the `include-before-body` option, before the table of contents and before any other body content, ensuring that all commands are defined when first referenced. A `latex_safe()` helper function escapes special LaTeX characters in parameter strings, making the template robust to titles and names containing ampersands, underscores, or percent signs.

### 3.4. Bilingual Execution Support

The template includes parallel R and Python code blocks throughout, with Python blocks set to `eval: false` by default. Analysts working in Python activate the relevant blocks and set the Quarto execution engine to Jupyter. The session information section captures both R (`sessionInfo()`) and Python (`importlib.metadata`) environment details, producing a complete computational provenance record regardless of the language used for analysis.

### 3.5. Proof of Concept

The CSR format formalizes practices already demonstrated to be feasible in published neuroscience research. A recent weighted gene co-expression network analysis of human transcriptomic data examining brain SLC13A5 expression across the lifespan provided a fully reproducible analytical script as Supplementary Material, including data import, network construction, module identification, and figure generation in a single documented workflow [14]. The CSR template extends this approach by adding structure, narrative guidance, institutional metadata, and version tracking. A compiled example CSR, illustrating all eight template sections applied to transcriptomic data, is available at the project repository (<https://github.com/dhrhf/CSRReport>) (created on 28 February 2026), providing a concrete reference for laboratories considering adoption.

## 4. Discussion

The CSR addresses a specific and tractable problem: the absence of a standard format for making statistical workflows in experimental neuroscience both auditable and reproducible. Existing solutions are partial. Code repositories without narrative context document what was computed but not why. Preregistered analysis plans constrain decisions before data collection but do not capture the deviations, revisions, and judgment calls that occur during analysis. Supplementary methods sections in journals have no standard structure and are not executed documents. The CSR combines narrative, code, and output in a format that can be read, run, and reviewed as a single artifact. It is important to clarify that the CSR is a record of analytical decisions, not a constraint on them; different analysts may legitimately reach different conclusions from the same data, and the CSR ensures that those analytical pathways remain visible and comparable rather than being obscured in prose summaries.

The choice of Quarto as the implementation platform reflects both technical and strategic considerations. Technically, Quarto's support for multiple computational languages, its separation of document structure from rendering engine, and its active development make it the most forward-compatible option currently available for scientific literate programming [12]. Strategically, Quarto's growing adoption in data science and biostatistics communities means that the skill set required to author a CSR overlaps substantially with skills that researchers are already acquiring, reducing the marginal cost of adoption. Adoption by laboratories without prior experience in literate programming is supported by the commented guidance embedded within each section of the template and may be further facilitated through pairing with existing Quarto tutorials, short-course training in R or Python for biomedical researchers, or collaborative authorship models in which a statistical analyst co-authors the CSR.

The version tracking system addresses a problem specific to iterative peer review. When reviewers request additional analyses or model revisions, those changes alter the statistical record. Without versioning, it is unclear which version of the analysis corresponds to which version of the manuscript. The structured version code in the CSR template creates a one-to-one mapping between analytical iterations and manuscript revisions, making the review history auditable and the final published analysis traceable to its provenance.

Existing approaches to the reproducibility problem in neuroscience have addressed different layers of the research cycle without fully closing the gap between the analytical record and the published scientific claim. Reporting guidelines such as ARRIVE, CONSORT, and SAMPL specify what should be reported but provide no mechanism to enforce compliance or verify that reported procedures match what was actually executed; survey data from neurology and neuroscience journals show that the majority of journals do not require disclosure of assumption-checking methods, provide no guidance on *p*-value interpretation,

and rely on endorsement of reporting guidelines that themselves contain only a handful of statistical items [15]. Preregistration reduces selective reporting and separates confirmatory from exploratory analyses, but many preregistrations do not include data cleaning and analysis plans, meaning that the most consequential analytical decisions, including preprocessing pipelines, model selection, and outlier handling, remain undocumented [16].

Code sharing is similarly insufficient on its own: a large-scale audit of deposited research code found that 74% of R scripts failed to execute without error, and even after environmental corrections, 56% still failed [17], demonstrating that re-executable code does not guarantee computational reproducibility. These failures arose primarily from environmental dependencies, hard-coded absolute file paths, and undeclared package versions, precisely the conditions that the CSR's mandatory session information section documents, ensuring that computational environment details are co-published with the analysis. The CSR template addresses this residual gap by situating the analytical record inside a structured, versioned, executable document that is written before the manuscript, reviewed independently, and submitted alongside it as a peer-reviewed supplementary artefact. Rather than prescribing what to report after the fact, it enforces a sequential workflow in which each analytical decision is documented at the moment it is made, creating an auditable chain from raw data deposition through to the inferential claims that appear in the published paper.

Transparency and correctness are related but distinct properties, and the CSR addresses the former while supporting, but not guaranteeing, the latter. Several mechanisms within the framework contribute to verification. First, because the CSR is rendered by executing the code it contains, a successfully compiled document is itself evidence that the analysis pipeline runs without error under the documented computational environment, a minimal but non-trivial standard, given documented failure rates of shared code [17]. Second, the mandatory session information section co-publishes software versions with results, enabling independent re-execution. Third, the 'Statistical models' and 'Sensitivity analyses' sections require diagnostic outputs, residual plots, assumption tests, and alternative model comparisons to be embedded in the document, making the basis for model acceptance or rejection inspectable. Fourth, the internal review step in the proposed publication workflow (Figure 1) serves as a structured opportunity for independent expert scrutiny of the analytical choices before external submission. None of these mechanisms guarantees that the underlying statistical choices are optimal; that judgement remains with the analyst and, ultimately, with peer reviewers who can inspect the complete record.

An important practical consideration concerns studies involving sensitive data, including human participants, clinical records, or proprietary datasets subject to data use agreements. In such cases, the CSR does not require that raw data be publicly deposited. The analytical code and the compiled CSR document, including all outputs, figures, and session information, can be shared without exposing the underlying data by separating the data access step from the analysis pipeline. Researchers may further use anonymized or de-identified datasets for demonstration within the CSR, generate synthetic datasets that preserve the distributional properties of the original data for illustrative purposes, or deposit the CSR under controlled-access arrangements through repositories such as the UK Data Archive or the Inter-university Consortium for Political and Social Research (ICPSR). The version tracking and GitHub-based workflow described here is fully compatible with private or restricted repositories for laboratories operating under data governance constraints.

A limitation of the current template is that it does not enforce any specific statistical framework. An analyst could complete a CSR using inappropriate models documented in reproducible code, producing a transparent but flawed analysis. The CSR is a reporting standard, not a statistical curriculum. Critically, the Statistical Models section of the template

requires the analyst to explicitly justify their choice of model and document assumption diagnostics, providing a checkpoint against the adoption of inappropriate methods without narrative justification. The template is intentionally agnostic with respect to inferential framework; Bayesian analyses, likelihood-based approaches, and non-parametric methods can be documented within the existing section structure without modification. Its value is conditional on the analyst's quantitative competence, which is why we have argued elsewhere that CSR authorship should be credited and attributed, creating accountability for the statistical choices made. Future versions of the template may incorporate structured fields for model comparison criteria and pre-specified analysis plans, moving toward a tighter integration with open science workflows. Prospective evaluation of whether mandatory CSR submission improves downstream reproducibility outcomes remains an important direction for future work. The CSR's required reporting of confidence intervals and effect sizes alongside  $p$ -values reflects the growing consensus that binary significance thresholds are insufficient and that quantitative summaries of uncertainty are essential for scientific inference.

Several practical challenges to adoption merit acknowledgement. First, laboratories without prior experience in R, Python, or Quarto face a non-trivial learning curve, though the template's embedded guidance, the availability of comprehensive Quarto documentation, and the possibility of collaborative authorship with a dedicated analyst help mitigate this barrier. Second, the CSR is designed to complement rather than replace existing reporting guidelines such as ARRIVE 2.0, CONSORT, and STROBE; it operates at the statistical layer and does not duplicate the experimental design and procedural content those guidelines address. Integration with existing workflows is therefore additive rather than substitutive. Third, mandatory CSR submission as part of peer review would impose additional workload on authors, reviewers, and editorial offices. We anticipate that this burden would be concentrated in initial adoption and would decrease as the format becomes familiar; analogous burdens were raised during the introduction of data sharing mandates and statistical analysis plan registration, both of which are now widely accepted. Journals wishing to pilot the CSR as a supplementary submission requirement could do so without modifying their core review infrastructure using the existing Supplementary Materials pathway.

The template was designed for experimental neuroscience, but its architecture is unrestricted. The section structure maps onto the analytic workflow of any field that uses regression models, mixed-effects models, or non-parametric comparisons on structured biological data. Adaptation for other domains would require only revisions to the narrative guidance within each section.

## 5. Conclusions

We have described and implemented the Companion Statistical Report, a structured document format for transparent statistical reporting in experimental neuroscience, and provided an open Quarto template that makes this format immediately usable. The template enforces a sequential analytic workflow, documents all preprocessing decisions, requires model assumptions to be stated and checked, and produces a fully executable record that can be submitted alongside a manuscript and reviewed independently of it. By lowering the technical and organizational barriers to reproducible statistical reporting, the CSR template offers a concrete path toward literature in which the gap between what was measured and what was claimed is, at minimum, visible.

**Supplementary Materials:** The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/standards6020013/s1> and <https://github.com/dhrhf/CSReport> (created on 28 February 2026).

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## Abbreviations

The following abbreviations are used in this manuscript:

|       |                                            |
|-------|--------------------------------------------|
| CSR   | Companion Statistical Report               |
| NEC   | Bertrand Russell Research Excellence Group |
| ANOVA | Analysis of Variance                       |

## References

1. Button, K.S.; Ioannidis, J.P.A.; Mokrysz, C.; Nosek, B.A.; Flint, J.; Robinson, E.S.J.; Munafò, M.R. Power Failure: Why Small Sample Size Undermines the Reliability of Neuroscience. *Nat. Rev. Neurosci.* **2013**, *14*, 365–376. [[CrossRef](#)] [[PubMed](#)]
2. Begley, C.G.; Ioannidis, J.P.A. Reproducibility in Science: Improving the Standard for Basic and Preclinical Research. *Circ. Res.* **2015**, *116*, 116–126. [[CrossRef](#)] [[PubMed](#)]
3. Makin, T.R.; Orban de Xivry, J.-J. Ten Common Statistical Mistakes to Watch out for When Writing or Reviewing a Manuscript. *eLife* **2019**, *8*, e48175. [[CrossRef](#)] [[PubMed](#)]
4. Simmons, J.P.; Nelson, L.D.; Simonsohn, U. False-Positive Psychology: Undisclosed Flexibility in Data Collection and Analysis Allows Presenting Anything as Significant. *Psychol. Sci.* **2011**, *22*, 1359–1366. [[CrossRef](#)]
5. Ioannidis, J.P.A. Why Most Published Research Findings Are False. *PLoS Med.* **2005**, *2*, e124. [[CrossRef](#)] [[PubMed](#)]
6. Munafò, M.R.; Nosek, B.A.; Bishop, D.V.M.; Button, K.S.; Chambers, C.D.; du Sert, N.P.; Simonsohn, U.; Wagenmakers, E.-J.; Ware, J.J.; Ioannidis, J.P.A. A Manifesto for Reproducible Science. *Nat. Hum. Behav.* **2017**, *1*, 0021. [[CrossRef](#)]
7. Kass, R.E.; Caffo, B.S.; Davidian, M.; Meng, X.-L.; Yu, B.; Reid, N. Ten Simple Rules for Effective Statistical Practice. *PLoS Comput. Biol.* **2016**, *12*, e1004961. [[CrossRef](#)]
8. Ziemann, M.; Poulain, P.; Bora, A. The Five Pillars of Computational Reproducibility: Bioinformatics and Beyond. *Brief. Bioinform.* **2023**, *24*, bbad375. [[CrossRef](#)] [[PubMed](#)]
9. Open Science Collaboration. PSYCHOLOGY. Estimating the Reproducibility of Psychological Science. *Science* **2015**, *349*, aac4716. [[CrossRef](#)] [[PubMed](#)]
10. Wilson, G.; Bryan, J.; Cranston, K.; Kitzes, J.; Nederbragt, L.; Teal, T.K. Good Enough Practices in Scientific Computing. *PLoS Comput. Biol.* **2017**, *13*, e1005510. [[CrossRef](#)] [[PubMed](#)]
11. Sandve, G.K.; Nekrutenko, A.; Taylor, J.; Hovig, E. Ten Simple Rules for Reproducible Computational Research. *PLoS Comput. Biol.* **2013**, *9*, e1003285. [[CrossRef](#)] [[PubMed](#)]
12. Allaire, J.J.; Teague, C.; Scheidegger, C.; Xie, Y.; Dervieux, C.; Woodhull, G. Quarto 2025. Available online: <https://github.com/quarto-dev/quarto-cli> (accessed on 1 March 2026).

13. R Core Team. *R: A Language and Environment for Statistical Computing*; R Foundation for Statistical Computing: Vienna, Austria, 2024.
14. Ferreira, B.K.; Schuck, P.F.; Ferreira, G.C.; Freitas, H.R. Potential Biological Processes Related to Brain SLC13A5 Across the Lifespan: Weighted Gene Co-Expression Network Analysis from Large Human Transcriptomic Data. *Brain Sci.* **2026**, *16*, 163. [[CrossRef](#)] [[PubMed](#)]
15. Tumma, S.; Sonneborn, C.; Padate, A.; Hogue, O. Statistical Guidance Provided to Authors by Clinical Neurology and Neuroscience Journals. *Eur. J. Neurol.* **2023**, *30*, 3675–3681. [[CrossRef](#)] [[PubMed](#)]
16. Troller-Renfree, S.V.; Morales, S.; Buzzell, G.A.; Sandre, A. Heterogeneity in Pediatric Resting EEG Data Processing and Analysis: A State of the Field. *Psychophysiology* **2025**, *62*, e14733. [[CrossRef](#)] [[PubMed](#)]
17. Nab, L.; Schaffer, A.L.; Hulme, W.; DeVito, N.J.; Dillingham, I.; Wiedemann, M.; Andrews, C.D.; Curtis, H.; Fisher, L.; Green, A.; et al. OpenSAFELY: A Platform for Analysing Electronic Health Records Designed for Reproducible Research. *Pharmacoepidemiol. Drug Saf.* **2024**, *33*, e5815. [[CrossRef](#)] [[PubMed](#)]

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