

Verflux: A Browser-Based Platform for End-to-End Systematic Reviews and Meta-Analysis

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Abstract

Systematic reviews and meta-analyses are the cornerstone of evidence-based research, yet the workflow remains fragmented across literature databases, reference managers, spreadsheets, and statistical environments such as R or Stata. This fragmentation imposes a substantial technical and financial barrier, particularly for early-career researchers and investigators in resource-limited settings. This article introduces **Verflux**, a browser-based platform that integrates the complete systematic review pipeline—multi-database searching, dual-reviewer screening, structured data extraction, risk-of-bias assessment, GRADE certainty rating, meta-analysis, figure generation, and PRISMA 2020 reporting—into a single web application requiring no software installation and no programming. The statistical engine implements effect-size estimators and inverse-variance fixed-effect and random-effects models (DerSimonian–Laird and Paule–Mandel) with heterogeneity statistics, prediction intervals, and small-study-effect diagnostics, with every formula referenced to its primary methodological source. A worked verification example using a seven-study continuous-outcome dataset reproduces the expected standardised mean difference, heterogeneity statistics, and prediction interval to within rounding, demonstrating numerical agreement with established meta-analytic conventions. By consolidating the workflow and removing the programming barrier, Verflux aims to lower the cost and complexity of rigorous evidence synthesis while remaining compliant with the standards journals expect.

Keywords: systematic review; meta-analysis; PRISMA 2020; GRADE; risk of bias; forest plot; evidence synthesis; research software

1 Introduction

Systematic reviews and meta-analyses occupy the apex of the evidence hierarchy because they synthesise the totality of relevant studies under a transparent, reproducible protocol [1]. Producing one to a publishable standard, however, requires the coordinated use of several disconnected tools: bibliographic databases for searching, a reference manager for deduplication, a screening application for study selection, spreadsheets for data extraction, separate instruments for risk-of-bias and certainty assessment, and finally a statistical environment for pooling effect sizes and generating figures. Each handoff between tools introduces opportunities for transcription error, version drift, and loss of an auditable trail.

The statistical stage is the most common bottleneck. The dominant tools for meta-analysis—the `meta` and `metafor` packages in R [2, 3], or commercial environments such as Stata—assume fluency in command-line programming. For many clinicians, students, and researchers in low- and middle-income settings, this requirement is prohibitive, and licensed commercial software is frequently inaccessible on cost grounds. Screening-focused web tools reduce part of the burden but typically stop short of meta-analysis, certainty rating, and standards-compliant reporting [4], leaving the reviewer to re-enter data into yet another environment.

This article describes **Verflux**, a browser-based platform designed to remove both barriers simultaneously. Verflux unifies the eight canonical stages of a review into one continuous, project-based workflow and performs all statistical computation server-side, so that the researcher writes no code and installs no software. The design goal is methodological rigour without a technical toll: results are computed from formulas referenced to their primary sources, figures export at publication resolution, and reporting fol-

lows the PRISMA 2020 statement [1]. The remainder of this paper describes the software architecture (Section 2), the statistical methods and their references (Section 3), a worked numerical verification (Section 4), a feature comparison with existing tools (Section 5), and a discussion of intended use and limitations (Sections 6–7).

2 Software Description

2.1 Design overview

Verflux is a server-rendered web application accessed through any modern browser on any operating system. It requires no local installation, no plug-ins, and no programming language runtime on the client. Work is organised into *projects*; each project carries the full record of searches, screening decisions, extracted data, appraisals, analyses, and report artefacts, so that the complete provenance of a review is retained in one place. Projects may be shared with co-reviewers to support collaborative screening with automated conflict detection.

2.2 The eight-stage pipeline

The interface is organised as a guided pipeline in which the output of each stage becomes the input of the next; the reviewer may move forward or backward at any point without losing state.

- Search.** A federated query is issued across nine bibliographic sources, including PubMed/MEDLINE, Scopus, Europe PMC, CrossRef, OpenAlex, Google Scholar, and Web of Science. Boolean operators, year ranges, and study-type filters are supported, and cross-database duplicates are detected and merged automatically.
- Screen.** Records are screened at the title/abstract and full-text stages with bulk decisions, keyboard shortcuts, and an abstract viewer. A blinded dual-reviewer mode

records two independent decision sets and surfaces disagreements in a conflict-resolution queue; inter-rater agreement is summarised with Cohen's κ [5].

3. **Extract.** Data are captured at the arm level for both continuous and dichotomous outcomes, with auto-population from a DOI or PMID and an unlimited number of outcomes per study.
4. **Risk of bias.** Six validated instruments are provided: RoB 2 for randomised trials [6], ROBINS-I for non-randomised studies of interventions [7], the Newcastle–Ottawa Scale [8], QUADAS-2 for diagnostic-accuracy studies [9], and AXIS for cross-sectional studies [10]. Domain-level judgements feed an automatically generated traffic-light summary.
5. **GRADE.** Certainty of evidence is rated per outcome across the five downgrading and three upgrading domains of the GRADE framework [11], producing a summary-of-findings table.
6. **Analysis.** Fixed-effect and random-effects meta-analysis is performed, with subgroup analysis, leave-one-out sensitivity analysis, and small-study-effect testing (Section 3).
7. **Plots.** Forest plots with weight-proportional markers and prediction intervals, and funnel plots with pseudo-confidence regions, are rendered and exported as 300 DPI images.
8. **Report.** A PRISMA 2020 flow diagram is constructed from the project's own counts, a methods paragraph is generated, and data export is offered in CSV, JSON, RIS, HTML, and Word formats.

2.3 Implementation

All statistical computation is performed server-side and returned to the browser for display, so numerical results are independent of the client device. Figures are produced at print resolution (300 DPI). The reporting module builds the PRISMA 2020 flow diagram directly from the recorded screening counts, ensuring that the published figure and the underlying data cannot diverge.

3 Statistical Methods

This section states the estimators implemented by Verflux. Each is referenced to the primary methodological source against which the implementation is verified.

3.1 Effect-size estimators

For continuous outcomes, the standardised mean difference is computed as Hedges' g , applying the small-sample correction factor J to Cohen's d [12]:

$$d = \frac{\bar{x}_1 - \bar{x}_2}{s_p}, \quad g = Jd, \quad J = 1 - \frac{3}{4(n_1 + n_2 - 2) - 1}, \quad (1)$$

where s_p is the pooled standard deviation. The variance of g is

$$\text{Var}(g) = \frac{n_1 + n_2}{n_1 n_2} + \frac{g^2}{2(n_1 + n_2)}. \quad (2)$$

For dichotomous outcomes, the (log) odds ratio, risk ratio, and risk difference are supported with their standard variance expressions [13].

3.2 Pooling models

Under the inverse-variance fixed-effect model, each study i receives weight $w_i = 1/v_i$, and the pooled estimate is

$$\hat{\theta}_{\text{FE}} = \frac{\sum_i w_i \theta_i}{\sum_i w_i}, \quad \text{SE} = \sqrt{\frac{1}{\sum_i w_i}}. \quad (3)$$

The random-effects model adds the between-study variance τ^2 to each within-study variance, $w_i^* = 1/(v_i + \tau^2)$. The default τ^2 estimator is DerSimonian–Laird [14]:

$$\hat{\tau}_{\text{DL}}^2 = \max\left(0, \frac{Q - (k - 1)}{\sum_i w_i - \frac{\sum_i w_i^2}{\sum_i w_i}}\right), \quad (4)$$

with the iterative Paule–Mandel estimator offered as an alternative [15, 16].

3.3 Heterogeneity

Cochran's Q , the I^2 statistic, and H^2 are reported [17]:

$$Q = \sum_i w_i (\theta_i - \hat{\theta}_{\text{FE}})^2, \quad I^2 = \max\left(0, \frac{Q - (k - 1)}{Q}\right) \times 100\%. \quad (5)$$

For random-effects models a 95% prediction interval is computed following IntHout *et al.* [18]:

$$\hat{\theta} \pm t_{k-2, 0.975} \sqrt{\hat{\tau}^2 + \text{SE}^2(\hat{\theta})}. \quad (6)$$

3.4 Small-study effects

Funnel-plot asymmetry is assessed using Egger's regression test [19] and Begg's rank correlation test [20]; Orwin's fail-safe N is available as a sensitivity diagnostic. All estimators are verified against their primary references [13, 12, 14, 19].

4 Numerical Verification

To confirm correct implementation, a worked example is presented for a continuous outcome across seven hypothetical two-arm randomised trials (treatment versus control). Per-study standardised mean differences (Hedges' g) and their 95% confidence intervals are shown in Table 1; the pooled random-effects synthesis and heterogeneity statistics are summarised in Table 2. The values follow directly from the estimators in Section 3 and reproduce the results expected from standard meta-analytic software to within rounding, providing a transparent benchmark that any reader can recompute.

The synthesis indicates a moderate-to-large pooled effect favouring the treatment arm with substantial heterogeneity ($I^2 = 71.9\%$), and a prediction interval that crosses the null—an interpretation that the random-effects model surfaces but the fixed-effect summary alone would obscure. This worked example illustrates that the platform's reported quantities are consistent, internally coherent, and reconstructable from first principles.

5 Comparison with Existing Tools

Table 3 situates Verflux against four widely used tools: RevMan, the R *meta/metafor* ecosystem, Rayyan, and

Table 1. Per-study standardised mean difference (Hedges' g) for the seven-study verification dataset.

Study	g	95% CI	Weight (RE)
Adeel 2021	-0.857	[-1.309, -0.405]	13.7%
Bukhari 2022	-0.341	[-0.722, 0.041]	15.1%
Chaudhry 2022	-0.413	[-0.920, 0.094]	12.7%
Daud 2023	-1.154	[-1.514, -0.793]	15.5%
Ehsan 2024	-0.241	[-0.696, 0.213]	13.6%
Farooq 2024	-0.903	[-1.282, -0.524]	15.1%
Gohar 2025	-0.176	[-0.593, 0.240]	14.4%

Table 2. Pooled random-effects synthesis (DerSimonian–Laird) for the verification dataset, $k = 7$.

Quantity	Value
Pooled SMD (random effects)	-0.594
95% confidence interval	[-0.891, -0.297]
Test of overall effect	$z = -3.92, p < 0.001$
Fixed-effect SMD	-0.623
Cochran's Q (df = 6)	21.35, $p = 0.002$
I^2	71.9%
τ^2	0.115
H^2	3.56
95% prediction interval	[-1.549, 0.361]

Table 3. Feature comparison of Verflux with representative systematic review and meta-analysis tools. ✓ = supported; – = not supported.

Capability	Verflux	RevMan	R (meta)	Rayyan	Stata
No software installation required	✓	–	–	✓	–
No R / Python / coding required	✓	✓	–	✓	–
Multi-database search built in	✓	–	–	–	–
Screening + extraction + RoB	✓	✓	–	Partial	–
GRADE certainty assessment	✓	✓	–	–	–
Forest and funnel plots	✓	✓	✓	–	✓
PRISMA 2020 flow diagram	✓	–	–	–	–
Real-time collaboration	✓	–	–	✓	–
Egger's / Begg's tests	✓	–	✓	–	✓
Runs on any operating system	✓	Partial	✓	✓	Partial

Stata. The distinguishing characteristics of Verflux are the integration of all stages—search through reporting—in one environment, the absence of any programming or installation requirement, and a built-in PRISMA 2020 flow-diagram generator.

6 Discussion

Verflux is positioned for researchers who require methodological rigour but lack the time, training, or licensing budget to operate a programming-based statistical pipeline. By keeping search, screening, extraction, appraisal, synthesis, and reporting inside one project record, the platform removes the inter-tool transcription steps that are a common source of error and of lost auditability. Performing computation server-side means that results do not depend on the client device or on a correctly configured local software stack, which is a recurring obstacle when reviews are produced collaboratively or in teaching settings.

The accessibility orientation is deliberate. A browser-only tool with regionally appropriate payment options lowers the entry barrier for students and for investigators in settings where commercial statistical licences are impractical. In educational contexts, the guided eight-stage structure mirrors the canonical methodology, making the platform suitable for training in evidence synthesis as well as for production reviews. None of these conveniences alters the underlying statistics: every estimator is the same one used by established packages and is referenced to its primary source.

7 Limitations

Verflux is intended for the standard pairwise and aggregate-data workflow and does not currently implement network

(multiple-treatments) meta-analysis, individual-participant-data synthesis, or fully Bayesian estimation. Coverage of bibliographic sources, while broad, depends on the access policies and rate limits of the underlying database providers, and federated searching does not replace a librarian-mediated strategy where one is required. As with any synthesis tool, the validity of the output depends on the quality of the included studies and the appropriateness of the chosen model; the software supports, but does not substitute for, methodological judgement. Verified numerical agreement with reference software, as illustrated in Section 4, should be confirmed by users against their own benchmark analyses before relying on the platform for a definitive review.

8 Conclusion

Verflux consolidates the full systematic review and meta-analysis workflow into a single browser-based platform that requires neither installation nor programming, while remaining faithful to established statistical methods and to PRISMA 2020 reporting standards. By lowering the technical and financial barriers to rigorous evidence synthesis, it broadens access to a methodology that has historically demanded specialised software skills. The platform is available at <https://verflux.com>.

Availability and Requirements

Project name: Verflux.

Project home page: <https://verflux.com>.

Operating system: Platform-independent (web browser).

Programming requirement for the user: None.

License / access: One-time licence; free trial available.

Version described: 1.0.

How to Cite

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Conflict of Interest

N. U. Rehman is the developer and owner of the Verflux platform described in this article. The remaining authors declare no competing interests.

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