

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

Naeem Ur Rehman^{1,*}, Khalid Saif Ullah¹, Usama Tufail¹

¹NielloSoft (PVT) LTD, Lahore, Pakistan

*Correspondence: naeemurrehman2019@gmail.com • <https://verflux.com>

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Abstract

A systematic review or meta-analysis is seldom carried out inside one program. In practice the work is divided among a literature database, a reference manager, a screening tool, a spreadsheet, one or more appraisal templates, and a statistics package such as R or Stata, and the final analytic step demands programming skill that many researchers lack and a licence that many cannot afford. Verflux closes that division. It is a browser-based platform that carries a review through its full course inside one project: protocol registration, searching across about nine databases and a trial registry, forward and backward citation chasing, screening by two independent reviewers, data extraction, risk-of-bias appraisal, GRADE certainty rating, meta-analysis, figure generation, and PRISMA 2020 reporting, with no installation and no code. The analytic engine pools effect sizes with inverse-variance fixed-effect and random-effects models (DerSimonian–Laird and Paule–Mandel), reports heterogeneity statistics and prediction intervals, screens for small-study effects, and extends to subgroup analysis, meta-regression, cumulative meta-analysis, and a frequentist network meta-analysis with treatment rankings; every estimator is tied to its original published source. Its outputs were validated both by hand and against established meta-analysis software, agreeing to within rounding. By folding the whole process into one tool and removing the coding barrier, Verflux makes rigorous evidence synthesis more accessible without relaxing the standards reviewers and journals expect.

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

1 Introduction

A well-conducted systematic review with meta-analysis is among the strongest forms of evidence: it collects the relevant studies on a question under a protocol set in advance and combines their results into a single estimate, with a measure of how far the studies disagree [1]. The method is well established; the difficulty lies in the tools. A typical review passes through a database interface, a reference manager, a screening application, a spreadsheet, separate appraisal and certainty instruments, and a statistics package for pooling and plotting. Every move between these programs is a chance to mistype a value, lose the current version of a file, or break the record of how a decision was made. None of the tools was built to hand its work to the next, so a reviewer can spend nearly as much time moving data between them as analysing it.

The analysis stage is where most reviews stall. The common tools for it, meta and metafor in R [2, 3] or commercial software such as Stata, expect the user to write code, and the commercial licences are unaffordable in many settings. Web-based screening services help with selection but usually stop before pooling, certainty rating, and reporting [4], so the data move into yet another program.

Verflux was built to remove both problems. It holds every stage of a review, from protocol to report, in one project and runs all computation on the server, so the user installs nothing and writes no code. Each result traces back to a cited method, figures export at publication resolution, and reporting follows PRISMA 2020 [5]. Because the work stays in one place, the record of how each result was produced is kept rather than scattered across separate files and machines. The whole review, from first search to final report, runs in a single browser tab.

2 Software Description

2.1 Design overview

Verflux is a server-rendered web application that opens in any current browser on any operating system, with no local install, plug-in, or language runtime required on the client. Each review is held in a *project* that stores its searches, screening decisions, extracted values, appraisals, analyses, and outputs together, so that the full history of how a result was reached stays in one place. A project can be opened to co-reviewers for independent screening with automatic conflict detection.

2.2 The review pipeline

A review in Verflux moves through the familiar stages, but they are joined into one continuous flow rather than scattered across separate programs, and a reviewer can move back and forth between them without losing earlier work. A project usually opens with a structured protocol on the PICO(S) template, which carries a field for a PROSPERO registration number and can be exported as a standalone document. Searching is then driven from a single query against about nine sources at once, among them PubMed/MEDLINE, Scopus, OpenAlex, CrossRef, Europe PMC, Web of Science, the Cochrane CENTRAL register, Embase, and the ClinicalTrials.gov registry, with Boolean operators, date ranges, and study-type filters, and with cross-database duplicates merged automatically; references can also be imported from RIS or BibTeX files, and a citation-chasing tool follows the works that cite, or are cited by, an included study through OpenCitations and CrossRef. Screening proceeds in two passes, by title and abstract and then at full text, with bulk actions, keyboard shortcuts, and a blinded dual-reviewer mode in which two reviewers decide independently; their disagreements are queued for resolution and their agreement is summarised as

Cohen's κ [6]. Data are extracted at the study-arm level for continuous and dichotomous outcomes, with auto-fill from a DOI or PMID and no limit on the number of outcomes per study.

Appraisal draws on five validated instruments (RoB 2 for randomised trials [7], ROBINS-I for non-randomised studies [8], the Newcastle–Ottawa Scale [9], QUADAS-2 for diagnostic-accuracy studies [10], and AXIS for cross-sectional studies [11]), whose domain judgements feed an automatic traffic-light summary, and the certainty of evidence is then rated for each outcome across the GRADE domains [12]. The analysis stage performs fixed-effect and random-effects meta-analysis alongside subgroup analysis, meta-regression, cumulative meta-analysis, leave-one-out diagnostics, tests for small-study effects, and a frequentist network meta-analysis for questions that involve several treatments (Section 3). Forest plots with weight-proportional markers and prediction intervals, and funnel plots with pseudo-confidence regions, render in the browser and export at 300 DPI; and the reporting stage builds a PRISMA 2020 flow diagram from the project's own screening counts, generates a draft methods paragraph and a 27-item PRISMA 2020 checklist, and exports the data as CSV, JSON, RIS, HTML, or Word.

Two capabilities run across the whole workflow rather than belonging to any single stage. A project can be shared with role-assigned co-reviewers who screen independently, with a collaboration board and a real-time chat kept beside the data; and it can synchronise both ways with a Zotero library, while records from Mendeley or EndNote arrive through RIS.

2.3 Implementation

Because computation runs on the server and only the display is returned to the browser, results do not depend on the user's hardware or on a correctly configured local stack. Figures render at 300 DPI. The reporting module draws the PRISMA 2020 diagram straight from the stored screening counts, so the published figure and the data behind it cannot drift apart. A demonstration dataset can be loaded into a new account to trial the whole workflow before any real data are entered.

3 Statistical Methods

Verflux implements standard meta-analytic estimators, each tied to the published source against which it was checked; the full formulae are given in the extended version of this article. Continuous outcomes are summarised by the mean difference and by the standardised mean difference, the latter as Hedges' g with the small-sample correction to Cohen's d [13], and dichotomous outcomes by the (log) odds ratio, risk ratio, and risk difference [14]. Effects are combined under inverse-variance fixed-effect and random-effects models; the between-study variance is estimated by DerSimonian–Laird [16] by default, with the iterative Paule–Mandel estimator as an alternative [15, 18]. Heterogeneity is reported through Cochran's Q , the I^2 statistic, and H^2 [17], and random-effects models are accompanied by a 95% prediction interval [14].

Small-study effects and publication bias are examined with Egger's regression [19] and Begg's rank-correlation

[20] tests, the trim-and-fill procedure, and Orwin's and Rosenthal's fail-safe N . Beyond a single pooled estimate, the platform supports subgroup analysis with a between-group Q test, meta-regression on study-level moderators (publication year, mean age, percentage female, sample size, and follow-up duration), cumulative meta-analysis, and leave-one-out influence analysis. For comparisons involving several treatments it provides a frequentist network meta-analysis that ranks options by P-scores, reports a league table of all pairwise contrasts, and separates direct from indirect evidence. Every reported quantity is computed server-side and is reproducible from the cited methods.

4 Numerical Validation

Correctness was checked in two independent ways. Every quantity the platform reports was first recomputed by hand from the published formulae of the methods in Section 3, and the same analyses were then run in established meta-analysis software. Across all of the datasets used for testing, the effect sizes, pooled estimates, heterogeneity statistics, and prediction intervals returned by Verflux matched both the manual calculations and the reference programs to within rounding, confirming that the implemented formulae behave as intended.

5 Discussion

The platform is meant for people who need a defensible method but cannot spend the time, training, or money a code-driven pipeline demands. Because searching, screening, extraction, appraisal, synthesis, and reporting all sit in one project, the manual transfer of data between programs never has to happen, which removes a frequent source of error and of lost audit trails. And because the calculations run on the server, the results no longer depend on whatever software a given machine happens to have, a problem that recurs in teams and in teaching.

The focus on access was a deliberate choice. A browser-only tool priced for local conditions is within reach of students and of investigators for whom a commercial statistics licence is impractical, and its ordered stages track the recognised method closely enough to double as a teaching aid as much as a production tool. None of this alters the statistics themselves: the estimators remain those of the established packages, each tied to its original source.

6 Limitations

The platform targets the aggregate-data setting that accounts for the great majority of reviews. It does not synthesise individual-participant data, and its estimation is frequentist rather than Bayesian, so anyone who specifically needs a Bayesian treatment will still turn to dedicated software. The network meta-analysis covers connected networks of two or more treatments and returns rankings and a league table; richer variants such as component or dose-response models are slated for future releases. How much of the literature a search reaches depends ultimately on the access rules and rate limits of each provider, so automated searching should be read as an aid to, not a substitute for, a strategy worked out with an information specialist. And as with any synthesis tool, a review is only as sound as the

studies it includes and the model chosen to combine them; Verflux informs those judgements without making them, and users should check that it reproduces an analysis they already trust before relying on it for a definitive review.

7 Conclusion

Verflux draws the entire systematic review and meta-analysis process into one browser-based platform that asks for neither installation nor code. It spans protocol registration, searching with citation chasing, screening, appraisal, a wide range of meta-analytic methods including network meta-analysis, and PRISMA 2020 reporting, with every estimate anchored to its primary source. By cutting the technical and financial cost of careful evidence synthesis, the platform opens a methodology that once demanded specialist software skills to a far wider group of researchers. It 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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Competing Interests

N. U. Rehman and K. Saif Ullah are the developers and owners of the Verflux platform described in this article. The remaining author declares no competing interests.

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