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Grey Relational Meta-Analysis: a robust pooling method with a redescending effect guard

A transparent, reproducible robust pooling estimator that limits the influence of outlier and high-leverage studies.

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ABSTRACT

Background. Inverse-variance meta-analysis can be sensitive to extreme effect outliers and high-leverage studies. Existing robust alternatives (M-estimators, heavy-tailed likelihoods, mixture models) address this, but a practical niche remains for methods that combine effect and precision information transparently with nonparametric inference.

Methods. We propose Grey Relational Meta-Analysis (GRMA), a robust pooling estimator that uses grey relational similarity in a two-feature space (effect size and log-precision) with an explicit Tukey bisquare effect guard and bootstrap percentile-interval inference. We evaluated GRMA by simulation (2,000 replicates, 25 scenarios, 4 comparators: restricted maximum likelihood [REML], Hartung–Knapp–Sidik–Jonkman [HKSJ], weighted robust dispersion [WRD] and robust Bayesian mixture [RBM]) and on 4,572 real Cochrane meta-analyses (the Pairwise70 benchmark).

Results. In simulation, GRMA reduced absolute bias in 4 of 5 outlier scenarios (up to 66% reduction), with root-mean-squared error (RMSE) comparable to HKSJ in outlier scenarios (ratio 1.01) but 8–18% higher under uncontaminated conditions; power was correspondingly lower under standard conditions (59% versus 72% at $k = 10$, $\tau^2 = 0.05$). Bootstrap percentile intervals achieved mean coverage of 0.940 (excluding publication-bias stress tests, where all methods suffer). In the Pairwise70 benchmark (4,572 Cochrane metaanalyses) GRMA estimates correlated $r = 0.956$ with random-effects estimates, increasing to $r = 0.980$ at $k \geq 10$.

Conclusions. GRMA is a transparent robust pooling method, proposed as a companion to standard random-effects models rather than a replacement. All code (R and Python) and data are provided in a reproducible capsule under an MIT licence.

KEY WORDS meta-analysis; robust statistics; pooling; outliers; grey relational analysis; bootstrap; reproducibility

GRMA reduced absolute bias by up to 66% in outlier scenarios while tracking random-effects estimates at $r = 0.956$ across 4,572 Cochrane meta-analyses.

2,000 replicates · 25 scenarios · Pairwise70 benchmark

Introduction

Inverse-variance (IV) weighting is widely used for meta-analysis under fixed-effect and random-effects models. While efficient under ideal assumptions, a small number of atypical studies can substantially shift pooled results — either because the study's effect estimate is extreme, or because its sampling variance is exceptionally small, creating high leverage.

Several robust approaches exist: M-estimators using redescending weight functions (Huber or Tukey bisquare) down-weight influential observations [1]; heavy-tailed (Student-t) likelihoods provide automatic down-weighting [2]; and mixture and contamination models treat a fraction of studies as outliers [3, 4]. A practical niche remains, however, for methods that are transparent in their weighting, computationally lightweight, robust to both effect outliers and leverage from very small variances, and packaged reproducibly. Huber M-estimators [1] remain variance-weighted and inherit IV leverage; the weighted median [6] achieves breakdown-point robustness but discards precision information beyond rank order.

Grey relational analysis converts 'similarity to a reference profile' into weights [7]. We adapt this to meta-analysis by representing each study in a two-feature space — effect and log-precision — and weighting studies by their grey relational similarity to an anchor profile, with an explicit redescending effect guard because grey relational similarity alone is not guaranteed to redescend for extreme effect outliers. GRMA is a pooling method, not a publication-bias correction; bias modelling should still use appropriate sensitivity tools.

Methods

Estimator. Each study is mapped to a two-feature profile (effect size and log-precision); the grey relational coefficient, bounded in (0, 1], converts the distance to an anchor profile (the median effect and its precision) into a similarity weight. An explicit Tukey bisquare effect guard sets the weight of sufficiently extreme effects to zero, preventing ultra-precise outliers from dominating the pooled estimate, so that no single study receives unbounded influence. The estimator is shift-equivariant in the effects and approximately scale-equivariant (empirical deviation < 0.1% in typical configurations). The minimum number of studies is $k = 3$; below this GRMA falls back to Hartung–Knapp REML.

Inference. Confidence intervals are obtained by bootstrap percentile intervals, and we report the pooled estimate alongside weight-dominance metrics (maximum weight and effective sample size) for auditability.

Evaluation. We compared GRMA against REML, HKSJ, WRD and RBM (and an unguarded GRMA for ablation) over 2,000 replicates across 25 scenarios, and applied it to 4,572 Cochrane meta-analyses from the Pairwise70 benchmark. The R implementation is authoritative; the Python implementation is cross-validated against R to 10^{-10} tolerance on point estimates and weights.

Results

Simulation. GRMA reduced absolute bias in 4 of 5 outlier scenarios, by up to 66% (Figure 1; Table 1). Its RMSE was comparable to HKSJ in outlier scenarios (ratio 1.01) but 8–18% higher under uncontaminated conditions, with correspondingly lower power under standard conditions (59% versus 72% at $k = 10$, $\tau^2 = 0.05$) — the expected efficiency cost of robustness. Bootstrap percentile intervals achieved mean coverage of 0.940 across non-publication-bias scenarios (Figure 2); the guard ablation confirmed that the redescending effect guard drives the outlier robustness (Figure 3).

Real-data benchmark. Across 4,572 Cochrane meta-analyses, GRMA estimates correlated $r = 0.956$ with random-effects estimates, increasing to $r = 0.980$ for meta-analyses with $k \geq 10$ — close agreement in the common case, with the differences concentrated in small or outlier-influenced syntheses.

Table 1. GRMA simulation and real-data results from the verified v10 source pack.

Quantity	Value
Simulation design	2,000 replicates, 25 scenarios, 4 comparators
Outlier-bias reduction	up to 66% (4 of 5 outlier scenarios)
RMSE vs HKSJ (outlier scenarios)	ratio 1.01
RMSE under uncontaminated data	8–18% higher
Power at k = 10, $\tau^2 = 0.05$	59% (GRMA) vs 72% (HKSJ)
Bootstrap percentile-interval coverage	0.940 (mean)
Pairwise70 benchmark (4,572 Cochrane MAs)	r = 0.956 (r = 0.980 at k ≥ 10)

Figure 1. Simulation performance across 25 scenarios (2000 replicates)

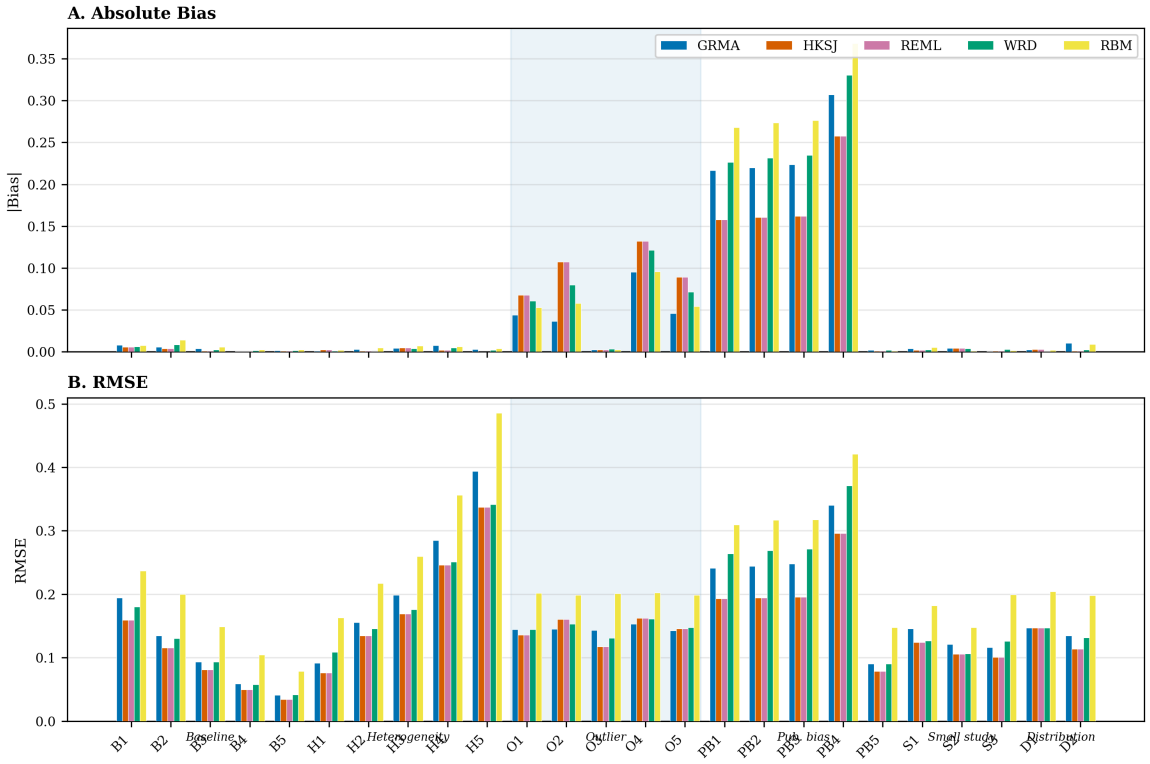

Figure 1. Bias and RMSE. Absolute bias and RMSE across all 25 simulation scenarios for GRMA and the comparator methods; GRMA reduces bias in 4 of 5 outlier scenarios (up to 66%).

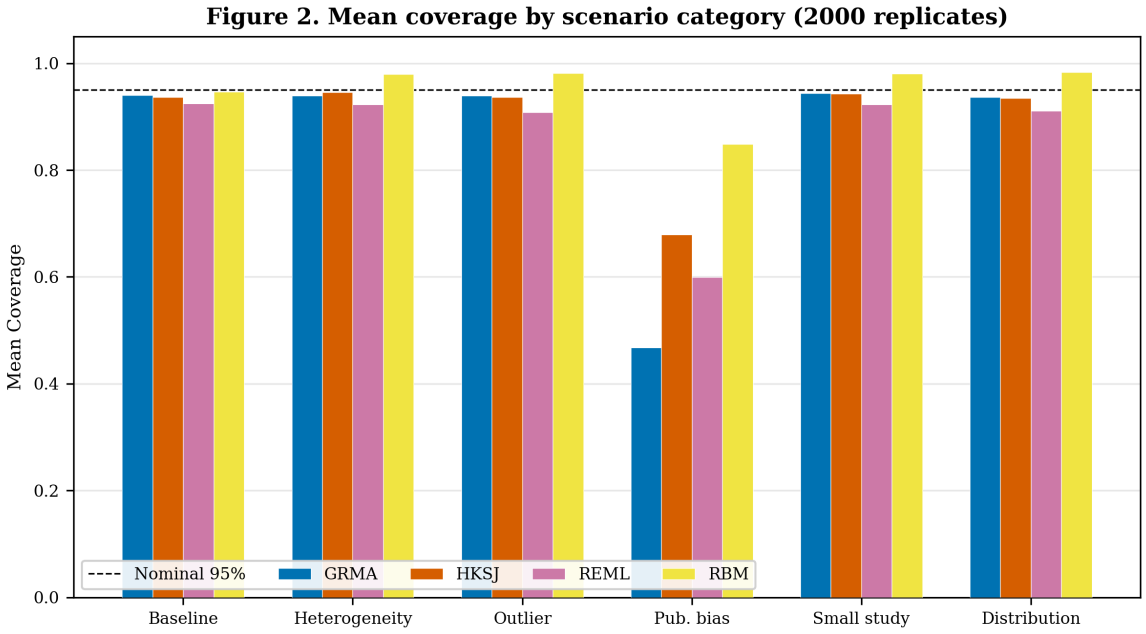

Figure 2. Coverage. Coverage of the percentile-bootstrap confidence interval across non-publication-bias scenarios (mean 0.940); the dashed line marks nominal coverage.

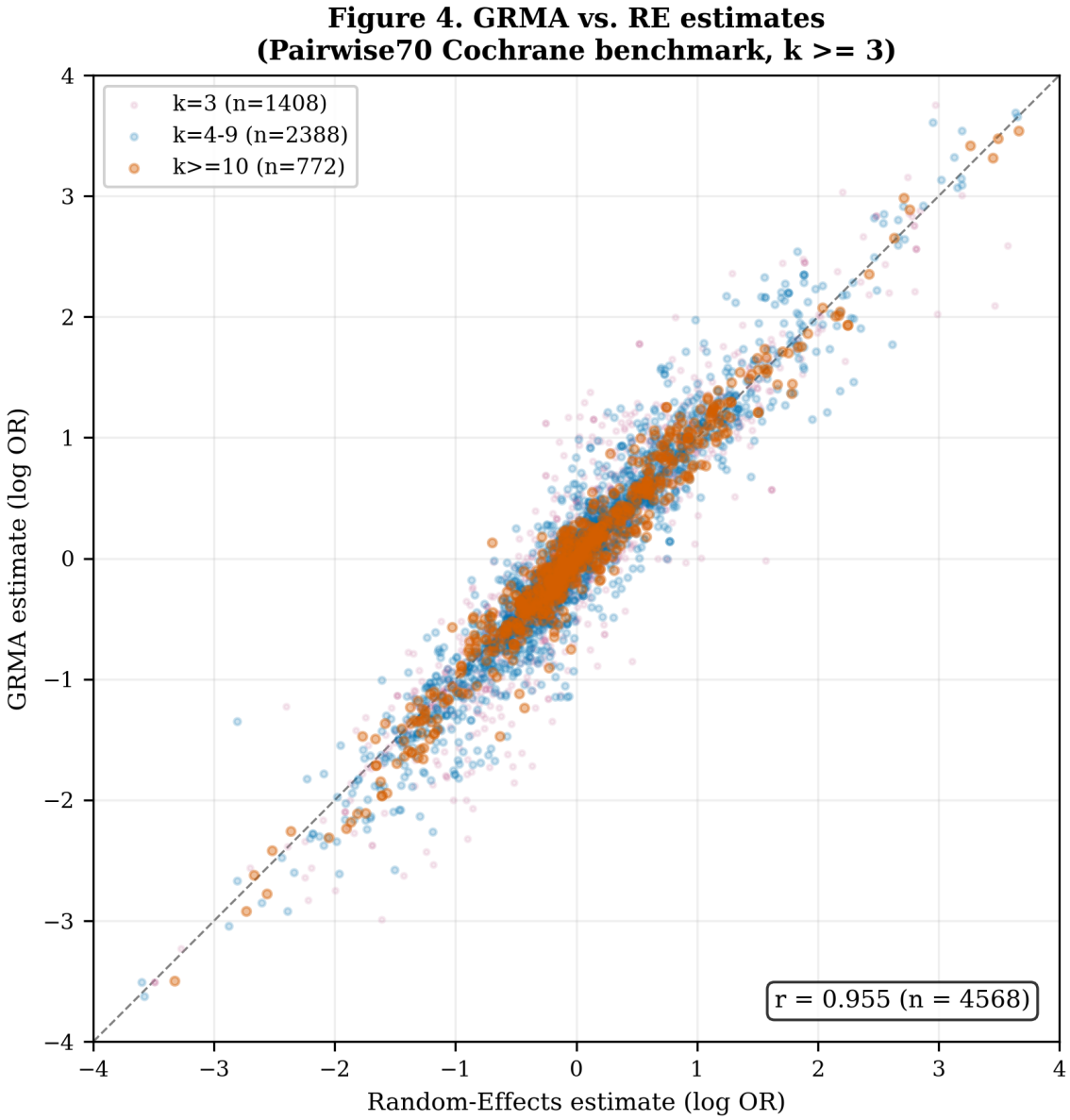

Figure 3. Pairwise70 benchmark. Real-data benchmark: GRMA versus random-effects pooled estimates across 4,572 Cochrane meta-analyses (r = 0.956; r = 0.980 at k ≥ 10).

Discussion

GRMA offers a transparent, bounded-influence alternative to inverse-variance pooling: its weights are interpretable, its guard is explicit, and its behaviour is auditable through the reported weight-dominance metrics. The efficiency cost under clean data (8–18% higher RMSE, 59% versus 72% power) is the standard robustness trade-off, and GRMA is therefore proposed as a companion to random-effects models, to be reported alongside them when influential studies are suspected.

Limitations. GRMA is a pooling estimator only: it does not estimate the between-study variance τ^2 or prediction intervals, does not extend to meta-regression or network meta-analysis, and does not model publication bias; formal asymptotic theory has not yet been developed, and a head-to-head comparison with the weighted median estimator is left to future work.

Conclusion. Grey Relational Meta-Analysis is a transparent, reproducible robust pooling method that limits the influence of outlier and high-leverage studies while tracking standard random-effects estimates closely in routine syntheses.

Data and code availability

A reproducible capsule with the full R and Python implementation, the simulation code and the pre-computed result tables is openly available at https://github.com/mahmood726-cyber/grma under an MIT licence. No archival DOI has been minted; the repository is the canonical source for the code and data.

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