

Package ‘CaMeA’

May 7, 2026

Type Package

Title Causal Meta-Analysis for Aggregated Data

Version 0.1.2

Maintainer Clement Berenfeld <clement.berenfeld@inria.fr>

Description A tool for causal meta-analysis. This package implements the aggregation formulas and inference methods proposed in Berenfeld et al. (2025) <[doi:10.48550/arXiv.2505.20168](https://doi.org/10.48550/arXiv.2505.20168)>. Users can input aggregated data across multiple studies and compute causally meaningful aggregated effects of their choice (risk difference, risk ratio, odds ratio, etc) under user-specified population weighting. The built-in function `camea()` allows to obtain precise variance estimates for these effects and to compare the latter to a classical meta-analysis aggregate, the random effect model, as implemented in the 'metafor' package <<https://CRAN.R-project.org/package=metafor>>.

License AGPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.2

Imports purrr, metafor, tibble, dplyr

Suggests knitr, rmarkdown, kableExtra

VignetteBuilder knitr

NeedsCompilation no

Author Clement Berenfeld [aut, cre],
Ahmed Boughdiri [ctb],
Charif El Gataa [aut],
Julie Josse [ctb]

Repository CRAN

Date/Publication 2026-03-10 17:20:02 UTC

Contents

camea	2
Index	5

Description

Function to perform causal meta-analysis on aggregated data of trials with binary treatment and binary outcome.

Usage

```
camea(
  measure,
  ai,
  bi,
  ci,
  di,
  n1i,
  n2i,
  slab,
  data = NULL,
  weights = NULL,
  plot = FALSE,
  log.scale = FALSE,
  random.effects = TRUE
)
```

Arguments

measure	a character string to specify which effect size or outcome measure should be calculated
ai	vector with the 2x2 table frequencies (upper left cell)
bi	vector with the 2x2 table frequencies (upper right cell)
ci	vector with the 2x2 table frequencies (lower left cell)
di	vector with the 2x2 table frequencies (lower right cell)
n1i	vector with the group sizes or row totals (first group/row)
n2i	vector with the group sizes or row totals (second group/row)
slab	optional vector with labels for the studies
data	optional data of type data frame, matrix, or dgCMatrix. If NULL, vectors must be provided directly
weights	optional vector of study weights, a value of NULL (the default) corresponds to study size / total size
plot	set to TRUE to print forestplot, default is FALSE
log.scale	set to TRUE to have log scale of the measure (only for RR, OR and SR), default is FALSE

`random.effects` set to TRUE to have random effects meta-analysis estimate (along with causal meta-analysis estimate) both in the output and in the plot, default is TRUE (possible with all measures except SR)

Details

The function can be used by either inputting "ai,bi,ci,di" or "ai,ci,n1i,n2i". Accepted measures are: "RD" = Risk Difference, "RR" = Risk Ratio, "OR" = Odds Ratio, "SR" = Survival Ratio

Value

A list with the following elements:

study_results list of effect sizes or outcome measures for each study and associated standard errors

final_result aggregated effect size or outcome measure and associated standard error

random_effects_model random-effect model estimate and standard error, if "random.effects = TRUE"

Author(s)

Clement Berenfeld, Ahmed Boughdiri, Julie Josse, Charif El Gataa.

Maintainer: Clement Berenfeld <clement.berenfeld@inria.fr>

References

Berenfeld, C., Boughdiri, A., Colnet, B., van Amsterdam, W. A. C., Bellet, A., Khellaf, R., Scornet, E., & Josse, J. (2025). Causal Meta-Analysis: Rethinking the Foundations of Evidence-Based Medicine. arXiv:2505.20168. <https://arxiv.org/abs/2505.20168>

Examples

```
## Example 1: With data frame
data <- data.frame(
  study = paste("Study", 1:5),
  treated_events = c(10, 15, 8, 12, 20),
  treated_total = c(100, 120, 80, 110, 150),
  control_events = c(15, 20, 12, 18, 25),
  control_total = c(100, 115, 85, 105, 145)
)

# Risk difference
result <- camea(measure = "RD", ai = treated_events, n1i = treated_total,
               ci = control_events, n2i = control_total,
               data = data, slab = study)

## Example 2: With vectors
treated_positives <- c(13, 5, 14, 18, 9)
treated_negatives <- c(80, 63, 72, 130, 100)
control_positives <- c(25, 18, 34, 23, 16)
control_negatives <- c(125, 98, 165, 117, 85)
```

```
# Risk ratio
result <- camea(measure = "RR", ai = treated_positives, bi = treated_negatives,
               ci = control_positives, di = control_negatives)
```

Index

camea, [2](#)