# Package: CaMeA (via r-universe)

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**Type** Package

**Title** Causal Meta-Analysis for Aggregated Data

**Version** 0.1.2

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**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>. 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

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**Repository** https://ramhworkshop.r-universe.dev

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**RemoteUrl** https://github.com/cran/CaMeA

**RemoteRef** HEAD

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# Contents

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## `camea` *Causal Meta Analysis for Aggregated Data*

### 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)
```

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