

Import data from Cochrane review

`read.mtv()` Review Manager, version 4
`read.rm5()` Review Manager, version 5

Import your own data set

Example data sets

Binary outcome:

Cisapride, Fleiss1993bin, Olkin1995, Pagliaro1992

Continuous outcome:

Amlodipine, Fleiss1993cont, woodyplants

Incidence rates:

lungcancer

Optional step: define defaults for R session

`settings.meta()` statistical methods and printing / plotting
`cilayout()` layout of confidence and prediction intervals

Meta-Analysis

Comparison of two groups:

`metacont()` continuous outcome
`metabin()` binary outcome
`metainc()` incidence rate outcome
`metacr()` outcome from data of Cochrane review

Single group:

`metacor()` single correlations
`metamean()` single means
`metaprop()` single proportions
`metarate()` single incidence rates

Generic method:

`metagen()` any outcome

`print.meta()` concise printout of meta-analysis results *

`summary.meta()` detailed printout of meta-analysis results with individual study results *

Forest plot:

`forest.meta()` forest plot *

`labels.meta()` study labels for forest plot *

Evaluation of small-study effects:

`funnel.meta()` funnel plot *

`radial.meta()` radial plot *

`metabias.meta()` tests for funnel plot asymmetry *

`trimfill.meta()` trim-and-fill method *

Meta-regression:

`metareg()` meta-regression

`bubble.meta()` bubble plot *

Sensitivity analyses:

`metainf.meta()` Leave-one-out method *

`metacum.meta()` Cumulative meta-analysis *

Additional figures:

`baujat.meta()` Baujat plot *

`drapery()` Drapery plot

`labbe.metabin()` L'Abbé plot *

Risk of bias assessment:

`rob()` risk of bias assessment (RoB)

`barplot.rob()` RoB bar plot *

`traffic_light()` RoB traffic light plot

Additional functions:

`metamerge()` merge two meta-analyses based on the same data set

`metaadd()` add (external) meta-analysis results to existing meta-analysis

`metabind()` combine (subgroup) meta-analysis results to generate concise summary / forest plot

`estimates.meta()` extract results from meta-analysis *

`nnt.meta()` calculate numbers needed to treat (NNT) to benefit or harm *

`or2smd()` - `smd2or()` conversion from log odds ratio to standardised mean difference (and v.v.)

Presentation and additional analyses

Auxiliary functions

`update.meta()` update meta-analysis *

`weights.meta()` meta-analysis weights *

`as.data.frame.meta()` study data as data frame *

`longarm()` transform data from pairwise comparisons to long arm-based format

Transformations: `cor2z()` - `p2logit()` - `p2asin()` - `VE2logVR()`

Back transformations: `z2cor()` - `logit2p()` - `asin2p()` - `asin2ir()` - `logVR2VE()`

* This is a generic function not exported in R package **meta**. Call the function by its generic name, e.g., `forest()`.