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

Presentation and additional analyses

`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
`blup.meta()` calculate best linear unbiased predictors *
`estimates.meta()`, `estimates.blup.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.)

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
`pairwise()` calculate pairwise comparisons from wide or 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().