Import data from Cochrane review Binary outcome: Cisapride, Fleiss1993bin, read.mtv() Review Manager, version 4 data sets Example Olkin1995, Pagliaro1992 read.rm5 () Review Manager, version 5 Continuous outcome: Amlodipine, Fleiss1993cont, woodyplants Import your own data set Incidence rates: lungcancer Optional step: define defaults for R session statistical methods and printing / plotting settings.meta() cilayout() layout of confidence and prediction intervals Comparison of two groups: metacont() continuous outcome binary outcome metabin() **Meta-Analysis** metainc() incidence rate outcome outcome from data of Cochrane review metacr() Single group: single correlations metacor() metamean() single means single proportions metaprop() single incidence rates metarate() Generic method: any outcome metagen() print.meta() concise printout of meta-analysis results ' summary.meta() detailed printout of meta-analysis results with individual study results * Presentation and additional analyses Forest plot: forest.meta() forest plot * labels.meta() study labels for forest plot * Evaluation of small-study effects: funnel.meta() funnel plot * metabias.meta() tests for funnel plot asymmetry * trimfill.meta() trim-and-fill method * radial.meta() radial plot * Meta-regression: Sensitivity analyses: metainf.meta() Leave-one-out method * metareg() meta-regression bubble.meta() bubble plot * metacum.meta() Cumulative meta-analysis * Additional figures: Risk of bias assessment: baujat.meta() Baujat plot * rob () risk of bias assessment (RoB) drapery () Drapery plot barplot.rob() RoB bar plot labbe.metabin() L'Abbé 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.) update.meta() update meta-analysis * weights.meta() meta-analysis weights * Auxiliary functions as.data.frame.meta() study data as data frame longarm() transform data from pairwise comparisons to long arm-based format <u>Transformations:</u> 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().