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Import data from Cochrane review
                                                                     Binary outcome:
                                                                     Cisapride, Fleiss1993bin,
        read.mtv() Review Manager, version 4
                                                               sets
                                                            Example
                                                                     Olkin1995, Pagliaro1992
        read.rm5() Review Manager, version 5
                                                                     Continuous outcome:
                                                               data
                                                                     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()
                                              layout of confidence and prediction intervals
                cilayout()
                           Comparison of two groups:
                                          continuous outcome
                           metacont()
                                          binary outcome
                           metabin()
                Meta-Analysis
                           metainc()
                                          incidence rate outcome
                           metacr()
                                          outcome from data of Cochrane review
                           Single group:
                                          single correlations
                           metacor()
                                          single means
                           metamean()
                           metaprop()
                                          single proportions
                                          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.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 *
          radial.meta() radial plot *
                                                        trimfill.meta() trim-and-fill method *
          Meta-regression:
                                                        Sensitivity analyses:
          metareg() meta-regression
                                                        metainf.meta() Leave-one-out method '
          bubble.meta() bubble plot *
                                                        metacum.meta() Cumulative meta-analysis *
          Additional figures: baujat.meta() Baujat plot *
                                                        Risk of bias assessment:
                                                        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
          pairwise () calculate pairwise comparisons from wide or long arm-based format
          Transformations: cor2z() - p2logit() - p2asin() - VE2logVR()
          Back transformations: z2cor() - logit2p() - asin2p() - asin2ir() - logVR2VE()
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^{*} This is a generic function not exported in R package **meta**. Call the function by its generic name, e.g., forest().