An Overview of Functions read.table() • read in data from ASCII file given the required data (e.g., means, SDs, and read.csv() • see also 'foreign' package for in the metafor Package group sizes; counts for 2x2 tables; correlations read.delim() reading in other data formats and sample sizes), calculate the desired effect (not all functions documented) size or outcome measure for the meta-analysis (e.g., raw or standardized mean differences, log odds or risk ratios, risk differences, r-to-z transformed correlations) • rma.uni() = fixed- and random/mixed-effects models rma.uni() ("inverse-variance" method; normal-normal models) • rma.mh() = Mantel-Haenszel method (fixed-effects model) rma.mh() escalc() • rma.peto() = Peto's method (fixed-effects model) rna.peto() • vi = observed outcomes or • rma.glmm() = fixed- and random/mixed-effects models rma.glmm() effect size estimates (binomial-normal and Poisson-normal models) rma.mv() • vi = corresponding sampling • rma.mv() = fixed- and random/mixed-effects variances multivariate/multilevel models (normal-normal models) note: rma.uni() takes either 'yi' and 'vi' as input or one can supply the print() required data to calculate the desired summary() effect size or outcome measure for unnel plot asymmetry (publication bias) the meta-analysis directly; rma.mh(), rma.peto(), and rma.glmm() require that the raw counts are supplied; rma.mv() takes 'yi' and 'V' as input fitted() confint() logLik() residuals() forest() print() ranktest() predict() rstandard() anova() funnel() deviance() summary() regtest() ()auld rstudent() pemutest() labbe() fitstats() trimfill() hatvalues() radial() AIC(), BIC() hc() weights() qqnorm() coef() influence() baujat() vcov() leave1out() plot() note: blup() only for note: most functions note: regtest() not for note: anova() and note: forest() can also note: coef() also for permutest() only for 'rma.uni' objects only implemented for 'rma.glmm' or 'rma.mv' take 'vi' and 'vi' directly 'permutest.rma.uni' and 'rma.uni' objects objects; trimfill() and hc() 'rma.uni' objects; 'summary.rma' objects as input; ggnorm(), only for 'rma.uni' objects confint() not for baujat(), and plot() not 'rma.glmm' objects for 'rma.glmm' or 'rma.mv' objects

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