Package ‘metawho’

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Type Package
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Version 0.2.0
Description A tool for implementing so called 'deft' approach (see Fisher, David J., et al. (2017) <DOI:10.1136/bmj.j573>) and model visualization.
License GPL-3
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BugReports https://github.com/ShixiangWang/metawho/issues
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deft_do

Implement deft method

Description

deft' method is a meta-analytical approach to pool conclusion from multiple studies. More details please see references.

Usage

deft_do(prepare, group_level, method = "FE")

Arguments

prepare a result data.frame from deft_prepare function or a data.frame contains at least 'trial', 'subgroup', 'yi' and 'sei' these four columns.
group_level level of subgroup, should be a character vector with length 2 and the reference should put in the first. For example, if you have 'Male' and 'Female' groups and want compare 'Female' with 'Male', then should set c('Male', 'Female').
method character string specifying whether a fixed- or a random/mixed-effects model should be fitted. A fixed-effects model (with or without moderators) is fitted when using method="FE". Random/mixed-effects models are fitted by setting method equal to one of the following: "DL", "HE", "SJ", "ML", "REML", "EB", "HS" or "GENQ". Default is "REML". See 'Details'.

Details

About model fit, please see metafor::rma().

Value

a list which class is 'deft'.

Author(s)

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References


Examples

data("wang2019")
deft_do(wang2019, group_level = c("Male", "Female"))
deft_prepare

Prepare log transformation data for effect size estimation according to confidence level and distribution

Description

A variety of different outcome measures which used in meta-analysis as input are in the form of log, such as hazard ratio (HR). This function is used to do log transformation to calculate effect size and standard error. Then the result can be easier used for model fit.

Usage

deft_prepare(data, conf_level = 0.05)

Arguments

data a data.frame contains at least columns 'trial', 'hr', 'ci.lb', 'ci.ub' and 'ni'.
conf_level a number specify confidence level, default is 0.05.

Value

a data.frame

Author(s)

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References


Examples

```r
### specify hazard ratios (hr)
hr <- c(0.30, 0.11, 1.25, 0.63, 0.90, 0.28)
### specify lower bound for hr confidence intervals
ci.lb <- c(0.09, 0.02, 0.82, 0.42, 0.41, 0.12)
### specify upper bound for hr confidence intervals
ci.ub <- c(1.00, 0.56, 1.90, 0.95, 1.99, 0.67)
### specify sample number
ni <- c(16L, 18L, 118L, 122L, 37L, 38L)
### trials
### subgroups
```
subgroup <- rep(c("Male", "Female"), 3)

entry <- paste(trial, subgroup, sep = "-")
### combine as data.frame

wang2019 <-
data.frame(  
  entry = entry,  
  trial = trial,  
  subgroup = subgroup,  
  hr = hr,  
  ci.lb = ci.lb,  
  ci.ub = ci.ub,  
  ni = ni,  
  stringsAsFactors = FALSE
)

deft_prepare(wang2019)

deft_show

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**deft_show**

Show deft result

**Description**

Show deft result

**Usage**

deft_show(
  deft,  
  element,  
  study_labels = NULL,  
  headings = list(study = ifelse(element == "all", "Study-subgroup", "Study"), n = "N",  
                  measure = NULL, ci = "HR (95% CI)"),  
  trans = base::exp,  
  show_model = ifelse(element == "all", FALSE, TRUE),  
  show_stats = list(`I^2` = rlang::quo(sprintf("%0.1f\%", I2)), p =  
                   rlang::quo(format.pval(QEp, digits = 2))),  
  ...  
)

**Arguments**

deft result from deft_do.

element 'all' or 'subgroup'.

study_labels labels for studies.

headings a list for controlling plot headings.
trans an optional transform function used on the numeric data for plotting the axes
show_model a logical value, if TRUE, show model result, otherwise only show forest plots for studies
show_stats a list of stats to show at the bottom of the forest plot for e.g. heterogeneity
... other arguments except 'panels', 'trans', 'study_labels', and 'show_stats' passed to forestmodel::forest_rma().

Value
a ggplot object

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Examples
data("wang2019")
res <- deft_do(wang2019, group_level = c("Male", "Female"))
p1 <- deft_show(res, "all")
p1
p2 <- deft_show(res, "subgroup")
p2

Hazard ratio (HR) for disease progression analysis comparing TMB-high with TMB-low in three NSCLC datasets

Description
Hazard ratio (HR) for disease progression analysis comparing TMB-high with TMB-low in three NSCLC datasets

Format
a data.frame

Source

Examples
data("wang2019")
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