

Package ‘metawho’

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Type Package

Title Meta-Analytical Implementation to Identify Who Benefits Most from Treatments

Version 0.1.0

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Description A tool for implementing so called 'deft' approach (see Fisher, David J., et al. (2017) <DOI:10.1136/bmj.j573>) and model visualization.

Suggests testthat, covr, knitr, rmarkdown

Depends R (>= 3.5), metafor

Imports stats, dplyr, purrr, magrittr

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

VignetteBuilder knitr

NeedsCompilation no

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deft_do	<i>Implement deft method</i>
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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 <code>c('Male', 'Female')</code> .
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 <code>method="FE"</code> . 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

Fisher, David J., et al. "Meta-analytical methods to identify who benefits most from treatments: daft, deluded, or deft approach?." *bmj* 356 (2017): j573.

Wang, Shixiang, et al. "The predictive power of tumor mutational burden in lung cancer immunotherapy response is influenced by patients' sex." *International journal of cancer* (2019).

Examples

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

deft_prepare	<i>Prepare log transformation data for effect size estimation according to confidence level and distribution</i>
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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, distribution = c("N", "t"), conf_level = 0.05,  
            df = Inf, var = FALSE)
```

Arguments

data	a data.frame contains at least columns 'trial', 'hr', 'ci.lb', 'ci.ub'.
distribution	a character specify distribution. 'N' for normal, 't' for student distribution. Default is N for normal distribution.
conf_level	a number specify confidence level, default is 0.05.
df	a number specify degree of freedom for t distribution
var	default is FALSE. If TRUE, the sampling variance will be computed.

Value

a data.frame

Author(s)

Shixiang Wang w_shixiang@163.com

References

Wang, Shixiang, et al. "The predictive power of tumor mutational burden in lung cancer immunotherapy response is influenced by patients' sex." International journal of cancer (2019).

Examples

```
### 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)  
### trials  
trial <- c("Rizvi 2015", "Rizvi 2015",
```

```
      "Rizvi 2018", "Rizvi 2018",
      "Hellmann 2018", "Hellmann 2018")
### 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,
    stringsAsFactors = FALSE
  )

deft_prepare(wang2019)
```

wang2019

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

Wang, Shixiang, et al. "The predictive power of tumor mutational burden in lung cancer immunotherapy response is influenced by patients' sex." *International journal of cancer* (2019).

Examples

```
data("wang2019")
```

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