Package ‘corrmeta’

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Title Correlated Meta-Analysis

Version 1.0.1

Maintainer Woo Seok Jung <`jungw@wustl.edu`>

Description Performs Correlated Meta-Analysis ('corrmeta') across multiple OMIC scans, accounting for hidden non-independencies between elements of the scans due to overlapping samples, related samples, or other information. For more information about the method, refer to the paper Province MA. (2013) <doi:10.1142/9789814447973_0023>.

biocViews Genetics, GenomeWideAssociation, SNP, StatisticalMethod, Software

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Encoding UTF-8

RoxygenNote 7.3.3

VignetteBuilder knitr

LazyData true

Suggests testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown, qpdf

Config/testthat/edition 3

Imports dplyr, polycor, stats, tidyr, magrittr

NeedsCompilation no

Author Woo Seok Jung [aut, cre],
Michael Province [aut, cph]

Depends R (>= 3.5.0)

Repository CRAN

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Contents

`fishp` *Calculate Fisher's method p-value and meta-analysis statistics*

Description

Calculate Fisher's method p-value and meta-analysis statistics

Usage

```
fishp(df, vars, df_sigma, sum_sigma)
```

Arguments

`df`	data frame with "markname" and study names as column names.
`vars`	character vector of study names to include in the meta-analysis.
`df_sigma`	data frame of tetrachoric correlations.
`sum_sigma`	sum of tetrachoric correlations.

Value

A data frame with columns 'markname', 'sum_chisq', 'sum_z', 'sum_sigma_var', 'pvalue', 'meta_z', 'meta_p', 'meta_nlog10p'

Examples

```
data(snp_example)
head(snp_example)
varlist <- c("trt1","trt2","trt3")
tc <- tetracorr(snp_example, varlist)
fishp(snp_example, varlist, tc$sigma, tc$sum_sigma)
```

`generate_random_p_values`

Generates a list of random p-values with mixed significant and insignificant values

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Description

Generates a list of random p-values with mixed significant and insignificant values

Usage

```
generate_random_p_values(n, ratio_significant)
```

Arguments

`n`	number of samples
`ratio_significant`	fraction of p-values to be significant

Value

list of n randomly generated significant and insignificant p-values

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`polycorr` *Calculate Polychoric Correlations*

Description

This function calculates the polychoric correlations between pairs of variables in a given data frame. It returns a data frame with the row and column names of the variables, the polychoric correlation coefficient, and its standard error.

Usage

```
polycorr(data, varlist)
```

Arguments

`data`	data frame with "markname" and study names as column names.
`varlist`	character vector of study names to include in the meta-analysis.

Value

data frame with polychoric correlation coefficients and standard errors

Author(s)

Woo Jung

See Also

`polychor`

Examples

```
data(snp_example)
varlist <- c("trt1","trt2","trt3")
polycorr(snp_example, varlist)
```

`pvalues_to_zscores` *Convert P-values to Z-scores*

Description

This function takes a data frame of p-values and converts them to Z-scores using the quantile function for the standard normal distribution.

Usage

```
pvalues_to_zscores(df_pvalues)
```

Arguments

`df_pvalues`	data frame containing p-values

Value

data frame containing Z-scores

Author(s)

Woo Jung

See Also

`qnorm`

Examples

```
data(snp_example)
head(snp_example)
pvalues_to_zscores(snp_example)
```

`snp_example` *Example SNP summary dataset*

Description

This data set provides 3 simulated 19-sample SNP-trait association p-values

Usage

```
snp_example
```

Format

A dataframe containing 19 observations across 3 SNP scans

`snp_example_missing` *Example SNP summary dataset with missing values*

Description

This data set provides 3 simulated 19-sample SNP-trait association p-values where some samples are removed to reflect missing values.

Usage

```
snp_example_missing
```

Format

A dataframe containing 19 observations across 3 SNP scans

`tetracorr` *Calculate Tetrachoric Correlations*

Description

This function calculates the tetrachoric correlations between pairs of variables in a given data frame. It returns a list containing a data frame with the tetrachoric correlation coefficients, and the sum of the tetrachoric correlations if the input variable was in p-value form.

Usage

```
tetracorr(data, varlist)
```

Arguments

`data`	data frame with "markname" and study names as column names.
`varlist`	character vector of study names to include in the meta-analysis.

Value

list containing a data frame with tetrachoric correlation coefficients, and the sum of the tetrachoric correlations if the input variable was in p-value form.

Author(s)

Woo Jung

See Also

`polychor`

Examples

```
data(snp_example)
head(snp_example)
varlist <- c("trt1","trt2","trt3")
tetracorr(snp_example, varlist)
```

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