

Package ‘corrmeta’

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Title Correlated Meta-Analysis

Version 1.0.0

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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](https://doi.org/10.1142/9789814447973_0023)>.

biocViews Genetics, GenomeWideAssociation, SNP, StatisticalMethod, Software

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Encoding UTF-8

RoxygenNote 7.3.1

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

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Depends R (>= 3.5.0)

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 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

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

`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	<i>Example SNP summary dataset</i>
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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	<i>Example SNP summary dataset with missing values</i>
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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	<i>Calculate Tetrachoric Correlations</i>
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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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