Package 'meaca'

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Type Package

Title Mixed-effects Enrichment Analysis with Correlation Adjusted

Version 0.2.1

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Description This package produces all results needed in the paper
    Use four spaces when indenting paragraphs within the Description.

Depends R (>= 3.2.1)

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imports dplyr,
    ggplot2

LazyData true

Encoding UTF-8

RoxygenNote 5.0.1

R topics documented:

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btw_gene_corr   *Estimate sample correlation.*

Description

    Average correlations for genes

Usage

```
btw_gene_corr(expression_data, trt, geneset, standardize = T,
  minSetSize = 5)
```

Arguments

`expression_data`
          the expressoin matrix.

`trt`	treatment labels
`geneset`	an object from `read_gene_set`
`standardize`	'TRUE' or 'FALSE', whether the data should be standaridzed
`minSetSize`	the minimum number of genes contained for a gene set to be considered.

Value

a list

`set_name`	The name of the gene set
`testSetCor`	Average correlation for genes in the test set
`interCor`	Average correlation between genes in the test set and those not in the test set
`backSetCor`	Average correlations for genes not in the test set.

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estimate_sigma	*Estimate sample covariance.*

Description

Estimate sample covariance and calculate the gene-level statistics

Usage

```
estimate_sigma(expression_data, trt)
```

Arguments

`expression_data`
          the expression matrix.

`trt`	sample labels. 0 for control and 1 for treatment

Value

a list

`sigma`	a covariance matrix
`t_val`	a vector of gene level test statistics

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meaca_multiple *meaca-multiple.*

Description

meaca for testing multiple gene sets.

Usage

```
meaca_multiple(expression_data, trt, geneset, standardize = T,
  minSetSize = 5, fdr_method = "BH")
```

Arguments

expression_data

the expressoin matrix.

trt   treatment labels.

geneset   gene sets to be tested, an object from `read_gene_set`.

standardize   whether the data should be standaridzed.

minSetSize   the minimum number of genes contained for a gene set to be considered.

fdr_method   which method is ued to adjust the p values. see arguments in function `p.adjust`.

Value

a data frame

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meaca_single *meaca-single.*

Description

meaca for single gene set test.

Usage

```
meaca_single(expression_data, trt, go_term, standardize = F)
```

Arguments

expression_data

the expressoin matrix.

trt   treatment labels.

go_term   an indicator vector. 1 for genes in the test, 0 otherwise.

standardize   whether the data should be standaridzed.

Value

a list

stat	the test statistic
p1	chi-square test p value
status	"up" or "down", the direction of differential expression
p2	two-sided test p-value using normal distribution

Examples

```
t1 <- simulate_expression_data(size = 50, n_gene = 500, n_test = 100,
                               prop = c(0.1, 0.1), de_mu = 2, de_sd = 1,
                               rho1 = 0.1, rho2 = 0.05, rho3 = -0.05,
                               data_gen_method = "chol", seed = 123)
meaca_single(t1$data, trt = t1$trt, go_term = t1$go_term)
```

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standardize_expression_data
                      standardize expression data, with method described in the paper.

Description

Standardize the expression data.

Usage

```
standardize_expression_data(expression_data, trt)
```

Arguments

expression_data
                the expression matrix.

trt   sample labels. 0 for control and 1 for treatment

Value

a matrix of the same dimension as input data.

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