Package ‘DGEAR’

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Type  Package
Title  Differential Gene Expression Analysis with R
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Description  Analyses gene expression data derived from experiments to detect differentially expressed genes by employing the concept of majority voting with five different statistical models. It includes functions for differential expression analysis, significance testing, etc. It simplifies the process of uncovering meaningful patterns and trends within gene expression data, aiding researchers in downstream analysis. Boyer, R.S., Moore, J.S. (1991) <doi:10.1007/978-94-011-3488-0_5>.
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R topics documented:

   DGEAR .......................................................... 2
gene_exp_data .................................................. 3
perform_anova .................................................. 3
DGEAR

Description

Main function which incorporates results from five statistical models and detects DEGs through majority voting

Usage

DGEAR(dataframe, con1, con2, exp1, exp2, alpha, voting_cutoff)

Arguments

dataframe A matrix containing the gene expression data
con1 Starting column of the control of the expression data
con2 Ending column of the control of the expression data
exp1 Starting column of the experiment of the expression data
exp2 Ending column of the experiment of the expression data
alpha Value of significance level ranging from 0 to 1 (0.05 states 5% significance) (Default = 0.05).
voting_cutoff A numeric value serves as Majority voting (Default = 2)

Details

To use this tool the necessary parameters are con1 = Control start column, con2 = Control end column, exp1 = Experiment start column, exp2 = Experiment end column, alpha = Value of significance level, voting_cutoff = Majority voting value (not more than 5, since there are 5 statistical methods which take part in the majority voting)

Value

A matrix containing Differentially Expressed Genes( DEGs) detected

Examples

library(DGEAR)
data("gene_exp_data")
DGEAR(dataframe = gene_exp_data, con1 = 1, con2 = 10,
exp1 = 11, exp2 = 20, alpha = 0.05, voting_cutoff = 2)
gene_exp_data

| gene_exp_data | A dataset containing gene expression data |

Description

This dataset contains simulated gene expression data for analysis.

Usage

gene_exp_data

Format

A data frame with 20 rows and 20 columns, where columns 1 to 10 being control and 11 to 20 being experiment.

Examples

# Data will be loaded with lazy loading and can be accessible when needed.
data("gene_exp_data")
head(gene_exp_data)

perform_anova  Function for ANOVA One-Way Test

Description

Function for ANOVA One-Way Test

Usage

perform_anova(datafile, con, exp, alpha = 0.05)

Arguments

datafile  A matrix containing the gene expression data
con  A data frame or matrix containing the expression values for the control.
exp  A data frame or matrix containing the expression values for the experiment.
alpha  Value of significance level ranging from 0 to 1 (default = 0.05 states 5 % significance).

Value

A data frame containing values for statistic score, p-values etc for each gene being tested.
Examples

```r
library(DGEAR)
data("gene_exp_data")
data = read_and_preprocess_data(datafile = gene_exp_data, con1=1, con2=10, exp1=11, exp2=20)
perform_anova(datafile = data$datafile, con= data$con, exp= data$exp)
```

---

**Description**

Function for Dunnett’s Test

**Usage**

```r
perform_dunnett_test(datafile, con, exp, alpha = 0.05)
```

**Arguments**

- `datafile`: A matrix containing the gene expression data
- `con`: A data frame or matrix containing the expression values for the control.
- `exp`: A data frame or matrix containing the expression values for the experiment.
- `alpha`: Value of significance level ranging from 0 to 1 (default = 0.05 states 5% significance).

**Value**

A data frame containing values for statistic score, p-values etc for each gene being tested.

**Examples**

```r
library(DGEAR)
data("gene_exp_data")
data = read_and_preprocess_data(datafile = gene_exp_data, con1=1, con2=10, exp1=11, exp2=20)
perform_dunnett_test(datafile = data$datafile, con= data$con, exp= data$exp)
```
perform_h_test

Description
Function for Half’s-T-Test Analysis

Usage
perform_h_test(con, exp, alpha = 0.05, FC)

Arguments
- **con**: A data frame or matrix containing the expression values for the control.
- **exp**: A data frame or matrix containing the expression values for the experiment.
- **alpha**: Value of significance level ranging from 0 to 1 (default = 0.05 states 5% significance).
- **FC**: An array or list containing fold change values for each gene, calculated by

Value
A data frame containing values for statistic score, p-values etc for each gene being tested.

Examples
library(DGEAR)
data("gene_exp_data")
data = read_and_preprocess_data(datafile = gene_exp_data, con1=1,con2=10,exp1=11,exp2=20)
perform_h_test(con= data$con, exp= data$exp, FC = data$FC)

perform_t_test

Description
Function for t-Test Analysis

Usage
perform_t_test(con, exp, alpha = 0.05)

Arguments
- **con**: A data frame or matrix containing the expression values for the control.
- **exp**: A data frame or matrix containing the expression values for the experiment.
- **alpha**: Value of significance level ranging from 0 to 1 (default = 0.05 states 5% significance).
perform_wilcox_test

Value

A data frame containing values for statistic score, p-values etc for each gene being tested.

Examples

```r
library(DGEAR)
data("gene_exp_data")
data = read_and_preprocess_data(datafile = gene_exp_data, con1=1,con2=10,exp1=11,exp2=20)
perform_t_test(con= data$con, exp= data$exp)
```

perform_wilcox_test  Function for Wilcoxon-Mann-Whitney U-Test

Description

Function for Wilcoxon-Mann-Whitney U-Test

Usage

```r
perform_wilcox_test(con, exp, alpha = 0.05)
```

Arguments

- `con`: A data frame or matrix containing the expression values for the control.
- `exp`: A data frame or matrix containing the expression values for the experiment.
- `alpha`: Value of significance level ranging from 0 to 1 (default = 0.05 states 5% significance).

Value

A data frame containing values for statistic score, p-values etc for each gene being tested.

Examples

```r
library(DGEAR)
data("gene_exp_data")
data = read_and_preprocess_data(datafile = gene_exp_data, con1=1,con2=10,exp1=11,exp2=20)
perform_wilcox_test(con= data$con, exp= data$exp)
```
Function to read data and perform initial pre-processing

**Description**
Function to read data and perform initial pre-processing

**Usage**

```r
read_and_preprocess_data(
  datafile, 
  con1, 
  con2, 
  exp1, 
  exp2, 
  alpha = 0.05, 
  votting_cutoff = 2
)
```

**Arguments**
- `datafile` A matrix or data frame containing gene expression data
- `con1` Starting column of the control of the expression data
- `con2` Ending column of the control of the expression data
- `exp1` Starting column of the experiment of the expression data
- `exp2` Ending column of the experiment of the expression data
- `alpha` Value of significance level ranging from 0 to 1 (0.05 states 5% significance) (Default = 0.05).
- `votting_cutoff` A numeric value serves as Majority voting (Default = 2)

**Value**
A large list containing the data file and the input values

**Examples**
```r
data("gene_exp_data")
read_and_preprocess_data(datafile = gene_exp_data, con1=1, con2=10, exp1=11, exp2=20)
```
Index

* datasets
  gene_exp_data, 3

DGAR, 2

gene_exp_data, 3

perform_anova, 3
perform_dunnett_test, 4
perform_h_test, 5
perform_t_test, 5
perform_wilcox_test, 6

read_and_preprocess_data, 7