

# Package: DGEAR (via r-universe)

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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](https://doi.org/10.1007/978-94-011-3488-0_5).

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DGEAR

*Differential Gene Expression Analysis with R*

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### Description

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

### Usage

```
DGEAR(dataframe, con1, con2, exp1, exp2, alpha, votting_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).
votting_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, votting_cutoff = 2)
```

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gene_exp_data	<i>A dataset containing gene expression data</i>
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**Description**

This dataset contains statistically simulated gene expression data for ease of exercise.

**Usage**

```
gene_exp_data
```

**Format**

A data frame with 10 rows and 20 columns, the columns represents samples, say first 10 columns 1 to 10 being control and 11 to 20 being experiment. Whereas, the rows of the dataset contains genes. First 5 out of 10 genes, gene1-gene5 are the true DEGs as the expression values for the first 10 samples are ~13 times higher than the rest.

**Examples**

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

---

perform_anova	<i>Function for ANOVA One-Way Test</i>
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---

**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**

```
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)
```

---

perform\_dunnett\_test *Function for Dunnett's Test*

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**Description**

Function for Dunnett's Test

**Usage**

```
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**

```
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                    *Function for Half's-T-Test Analysis*

---

**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                    *Function for t-Test Analysis*

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**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).

**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_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**

```
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**

```
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)
```

---

`read_and_preprocess_data`*Function to read data and perform initial pre-processing*

---

**Description**

Function to read data and perform initial pre-processing

**Usage**

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

**Arguments**

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

**Value**

A large list containing the data file and the input values

**Examples**

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

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