Package 'CEDA'

January 7, 2022

Type Package

Title CRISPR Screen and Gene Expression Differential Analysis

Version 1.0.2

Description Provides analytical methods for analyzing CRISPR screen data at different levels of gene expression. Multi-component normal mixture models and EM algorithms are used for modeling.

Depends R(>= 3.5.0), limma

Imports stats, mixtools, ggplot2

Suggests knitr, rmarkdown

License Apache License (== 2.0)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

VignetteBuilder knitr

NeedsCompilation no

Author Lianbo Yu [aut, cre],
Kevin R. Coombes [aut]

Maintainer Lianbo Yu <Lianbo.Yu@osumc.edu>

Repository CRAN

Date/Publication 2022-01-07 13:32:58 UTC

R topics documented:

`alphaBeta` *Calculating a significance score of a gene based on the corresponding sgRNAs' p-values of the gene.*

Description

Code was adapted from R package gscreend.

Usage

```
alphaBeta(pvec)
```

Arguments

`pvec`	A numeric vector of p-values.

Value

A min value of the kth smallest value based on the beta distribution B(k, n-k+1), where the n is the number of probabiliteis in the vector. This min value is the significance score of the gene.

`calculateGeneLFC` *Calculating gene-level log fold ratios*

Description

Log fold ratios of all sgRNAs of a gene are averaged to obtain the gene level log fold ratio.

Usage

```
calculateGeneLFC(lfcs, genes)
```

Arguments

`lfcs`	A numeric vector containing log fold change of sgRNAs.
`genes`	A character string containing gene names corresponding to sgRNAs.

Value

A numeric vector containing log fold ratio of genes.

`calculateGenePval` *Calculating gene level p-values using modified robust rank aggregation (alpha-RRA method) on sgRNAs' p-values*

Description

Code was adapted from R package gscreend. The alpha-RRA method is adapted from MAGeCK.

Usage

```
calculateGenePval(pvec, genes, alpha)
```

Arguments

`pvec`	A numeric vector containing p-values of sgRNAs.
`genes`	A character string containing gene names corresponding to sgRNAs.
`alpha`	A numeric number denoting the alpha cutoff (i.e. 0.05).

Value

A list with four elements: 1) a list of genes with their p-values; 2) a numeric matrix of rho null, each column corresponding to a different number of sgRNAs per gene; 3)a numeric vector of rho; 4) a numeric vector of number of sgRNAs per gene.

`EMFit` *Fitting multi-component normal mixture models by R package mixtools*

Description

The function normalmixEM in R package mixtools is employed for fitting multi-component normal mixture models.

Usage

```
EMFit(x, k0, mean_constr, sd_constr, npara, d0)
```

Arguments

`x`	A numeric vector
`k0`	Number of components in the normal mixture model
`mean_constr`	A constrain on means of components
`sd_constr`	A constrain on standard deviations of components
`npara`	Number of parameters
`d0`	Number of times for fitting mixture model using different starting values

Value

Normal mixture model fit and BIC value of the log-likelihood

`makeRhoNull` *Generating the null distribution of the significance score of a gene.*

Description

Code was adapted from R package gscreend.

Usage

```
makeRhoNull(n, p, nperm)
```

Arguments

`n`	An integer representing sgRNA number of a gene.
`p`	A numeric vector which contains the percentiles of the p-values that meet the cut-off (alpha).
`nperm`	Number of permutation runs.

Value

A numric vector which contains all the significance scores (rho) of genes generated by a permutation test where the sgRNAs are randomly assigned to genes.

`mda231` *CRISPR screen data of cell line MD231.*

Description

A dataset containing the expression data of sgRNAs in a CRISPR screen experiment of cell line MD231.

Usage

```
mda231
```

Format

A data frame with a list of two elements:

sgRNA Raw Read counts of sgRNAs

negene A list of non-essential genes

medianNormalization *Median normalization of sgRNA counts*

Description

This function adjusts sgRNA counts by the median ratio method. The normalized sgRNA read counts are calculated as the raw read counts devided by a size factor. The size factor is calcuated as the median of all size factors caculated from negative control sgRNAs (eg., sgRNAs corresponding to non-targeting or non-essential genes).

Usage

```
medianNormalization(data, control)
```

Arguments

data	A numeric matrix containing raw read counts of sgRNAs with rows corresponding to sgRNAs and columns correspondings to samples.
control	A numeric matrix containing raw read counts of negative control sgRNAs with rows corresponding to sgRNAs and columns corresponding to samples. Sample ordering is the same as in data.

Value

A list with two elements: 1) size factors of all samples; 2) normalized counts of sgRNAs.

Examples

```
count <- matrix(rnbinom(5000 * 6, mu=500, size=3), ncol = 6)
colnames(count) = paste0("sample", 1:6)
rownames(count) = paste0("sgRNA", 1:5000)
control <- count[1:100,]
normalizedcount <- medianNormalization(count, control)
```

normalMM *Performing empirical Bayes modeling on limma results*

Description

This function perform an empirical Bayes modeling on log fold ratios and return the posterior log fold ratios.

Usage

```
normalMM(data, theta0)
```

Arguments

data	A numeric matrix containing limma results and log2 gene expression levels that has a column nameed 'lfc' and a column named 'exp.level.log2'
theta0	Standard deviation of log2 fold changes under permutations

Value

A numeric matrix containing limma results, RNA expression levels, posterior log2 fold ratio, log p-values, and estimates of mixture model

Examples

```
nmm.fit <- normalMM(data,theta0)
```

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permuteLimma *Modeling CRISPR data with a permutation test between conditions by R package limma*

Description

The lmFit function in R package limma is employed for group comparisons under permutations.

Usage

```
permuteLimma(data, design, contrast.matrix, nperm)
```

Arguments

data	A numeric matrix containing log2 expression level of sgRNAs with rows corresponding to sgRNAs and columns to samples.
design	A design matrix with rows corresponding to samples and columns to coefficients to be estimated.
contrast.matrix	A matrix with columns corresponding to contrasts.
nperm	Number of permutations

Value

A numeric matrix containing log2 fold changes with permutations

Examples

```
y <- matrix(rnorm(1000*6),1000,6)
condition <- gl(2,3,labels=c("Control","Baseline"))
design <- model.matrix(~ 0 + condition)
contrast.matrix <- makeContrasts("conditionControl-conditionBaseline",levels=design)
fit <- permuteLimma(y,design,contrast.matrix,20)
```

`runLimma` *Modeling CRISPR screen data by R package limma*

Description

The lmFit function in R package limma is employed for group comparisons.

Usage

```
runLimma(data, design, contrast.matrix)
```

Arguments

`data`	A numeric matrix containing log2 expression levels of sgRNAs with rows corresponding to sgRNAs and columns corresponding to samples.
`design`	A design matrix with rows corresponding to samples and columns corresponding to coefficients to be estimated.
`contrast.matrix`	A matrix with columns corresponding to contrasts.

Value

A data frame with rows corresponding to sgRNAs and columns corresponding to limma results

Examples

```
y <- matrix(rnorm(1000*6),1000,6)
condition <- gl(2,3,labels=c("Treatment","Baseline"))
design <- model.matrix(~ 0 + condition)
contrast.matrix <- makeContrasts("conditionTreatment-conditionBaseline",levels=design)
limma.fit <- runLimma(y,design,contrast.matrix)
```

`scatterPlot` *Scatter plot of log2 fold ratios against gene expression levels*

Description

This function generates a scatter plot of log2 fold ratios of sgRNAs against the corresponding gene expression levels.

Usage

```
scatterPlot(data, fdr, ...)
```

Arguments

`data`	A numeric matrix from the output of normalMM function
`fdr`	A level of false discovery rate
`...`	Other graphical parameters

Value

No return value

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