Package ‘EBSEA’

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Type Package
Title Exon Based Strategy for Expression Analysis of genes
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Description Calculates differential expression of genes based on exon counts of genes obtained from RNA-seq sequencing data.
License GPL-2
biocViews Software, DifferentialExpression, GeneExpression, Sequencing
Imports edgeR, limma, gtools, graphics, stats
NeedsCompilation no

R topics documented:

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EBSEA Exon Based Startegy for Expression Analysis of genes

Description

EBSEA takes as input unnormalized counts of exons, normalizes them and then performs a two group comparison of the samples to detect differentially expressed between the groups. Both paired or unpaired comparison are supported. It calculates fold changes, p-values and false discovery rate of the genes between the groups.

Usage

EBSEA(countData, group, paired = FALSE, effects = NULL, plot = FALSE)
Arguments

- countData: A dataframe of exon count data
- group: A vector indicating the sample groups in the experiment
- paired: A logical indicating whether the samples are paired or unpaired. Default: FALSE
- effects: A vector indicating the paired samples.
- plot: A logical indicating whether a volcano plot is visualized. Default: FALSE

Value

EBSEA returns a list of two dataframes. ExonTable is a dataframe that contains exon statistics including log fold change, p-values, adjusted p-values, average expression and fold change. GeneTable is a dataframe that contains the corresponding fold change, log fold change, p-values and false discovery rate.

References


See Also

visualizeGenes

Examples

data(origCounts)
group <- c('Group1', 'Group1', 'Group1', 'Group2', 'Group2', 'Group2', 'Group2')
result <- EBSEA(origCounts, group)

filterCounts

Filter Count Data

Description

The exons are filtered based on their expression levels so that each exon has a cpm (count per million) of more than 1 in user defined percent of the samples.

Usage

filterCounts(x, noOfSamples)

Arguments

- x: A numeric dataframe of counts in the sample with gene and exon number as the row names and samples as the column names
- noOfSamples: Percentage of the number of samples that should have cpm greater than 1.

Value

A dataframe of filtered counts of exons
filterGenes

See Also

EBSEA

Examples

data(origCounts)
res <- filterCounts(origCounts, 20)

filterGenes

Filter Gene List

Description

The differentially expressed genes are filtered based on the FC and FDR provided by the user. The default thresholds are FC => 1.25 and fdr <= 0.01

Usage

filterGenes(x, fc = 1.25, fdr = 0.01)

Arguments

x A dataframe containing the gene statistics returned by EBSEA.
fc A fold change threshold for the genes to be filtered. Default: 1.25.
fdr A FDR threshold for the genes to be filtered. Default: 0.01.

Value

A list containing upregulated and downregulated genes.

See Also

EBSEA

Examples

data(origCounts)
group <- c('Group1', 'Group1', 'Group1', 'Group2', 'Group2', 'Group2', 'Group2')
result <- EBSEA(origCounts, group)
filteredGenes <- filterGenes(result$GeneTable)
**origCounts**  
*Subset of Pasilla Dataset*

**Description**

origCounts consists of a subset of the exon counts from the pasilla dataset.

**Usage**

data("origCounts")

**Format**

A data frame with 1000 observations on the following 7 variables.

- `treated1fb` a numeric vector
- `treated2fb` a numeric vector
- `treated3fb` a numeric vector
- `untreated1fb` a numeric vector
- `untreated2fb` a numeric vector
- `untreated3fb` a numeric vector
- `untreated4fb` a numeric vector

**Value**

Dataset

**See Also**

EBSEA

**Examples**

data(origCounts)

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**visualizeGenes**  
*Visualize Gene*

**Description**

Plots for each exon of the gene entered by the user, the mean of the counts and the fold changes.

**Usage**

`visualizeGenes(gene, group, countData, result)`
Arguments

gene Gene Name. The gene name should be the from the genes in count data.
group A vector indicating the sample group in the experiment.
countData A dataframe of the original exon count data.
result Results returned by EBSEA.

Value
A plot of mean counts and fold changes of exons of a gene.

See Also
EBSEA

Examples

data(origCounts)
group <- c('Group1', 'Group1', 'Group1', 'Group2', 'Group2', 'Group2', 'Group2')
result <- EBSEA(origCounts, group)
visualizeGenes('FBgn0000017', group, origCounts, result)
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