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.

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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")
result <- EBSEA(origCounts, group)

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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)

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)
visualizeGenes

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')
result <- EBSEA(origCounts, group)
visualizeGenes('FBgn0000017', group, origCounts, result)
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