

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, graphics, stats, plyr

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EBSEA	<i>Exon Based Startegy for Expression Analysis of genes</i>
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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(data, group, paired = FALSE, plot = FALSE)
```

Arguments

data	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
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

Laiho, A., & Elo, L. L. (2014). A note on an exon-based strategy to identify differentially expressed genes in RNA-seq experiments. *PloS One*, 9(12), e115964.

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 mean greater than 1 or user defined mean.

Usage

```
filterCounts(x, mean)
```

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
mean	The mean value to filter the genes below the threshold

Value

A dataframe of filtered counts of exons

See Also

[EBSEA](#)

Examples

```
data(origCounts)
res <- filterCounts(origCounts)
```

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, ebsea.out)
```

Arguments

<code>gene</code>	Gene Name. The gene name should be the from the genes in count data.
<code>ebsea.out</code>	Result object 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', result)
```

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