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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R topics documented:

`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(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

`gene`	Gene Name. The gene name should be the from the genes in count data.
`ebsea.out`	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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