

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 DESeq2, graphics, stats, EmpiricalBrownsMethod

RoxygenNote 7.1.1

Encoding UTF-8

Suggests knitr, rmarkdown

VignetteBuilder knitr

Depends R (>= 4.0.0)

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EBSEA

*Exon Based Strategy for Expression Analysis of genes***Description**

EBSEA takes the filtered raw exon-level read counts as input, normalizes and performs a two-group statistical comparison with DESeq2. The exon-level results are aggregated to the gene-level using empirical Brown's method. The samples in the two groups can be paired.

Usage

```
EBSEA(data, columnData, design, test = "Wald", contrasts = NULL, plot = FALSE)
```

Arguments

| | |
|-------------------------|--|
| <code>data</code> | A dataframe of raw exon-counts |
| <code>columnData</code> | A dataframe indicated the groups of the samples. |
| <code>design</code> | Design matrix (see more information od design matrixes in DESeq2 reference manual) |
| <code>test</code> | The statistical test to be carried out. It can be either Wald or Likelihood Ratio Test. For further details about the methods you can look into DESeq2 refernce manual. Default: Wald |
| <code>contrasts</code> | a character vector with exactly three elements: the name of a factor in the design formula, the name of the numerator level for the fold change, and the name of the denominator level for the fold change Default: NULL |
| <code>plot</code> | A logical value indicating a volcano plot is produced. Default: FALSE |

Value

The function returns a list containing containing exon and gene-level results. ExonTable is a data frame containing an average expression, log2 fold-change, p-value and adjusted p-value. GeneTable is a data frame containing the gene-level p-value, and adjusted-value. Other returned elements include the raw and normalised exon-level read counts, group information and design matrix used.

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.

Examples

```
# The exon-based analysis for unpaired samples can be performed as follows:
data(exonCounts)
group <- data.frame('group' = as.factor(c('G1', 'G1', 'G1', 'G2', 'G2', 'G2', 'G2')))
row.names(group) <- colnames(exonCounts)
design <- ~group
```

```
ebsea.out <- EBSEA(exonCounts, group, design)
# The exon-based analysis for paired samples with contrast provided can be performed as follows:
data(exonCounts)
group <- data.frame('group' = as.factor(c('G1', 'G1', 'G1', 'G2', 'G2', 'G2', 'G2')),
  'paired' = as.factor(c(1,2,3,1,2,3,3)))
row.names(group) <- colnames(exonCounts)
design <- ~group
contrastInfo <- c('group', 'G2', 'G1')
ebsea.out <- EBSEA(exonCounts, group, design, contrasts = contrastInfo)
```

| | |
|------------|----------------------------------|
| exonCounts | <i>Subset of Pasilla Dataset</i> |
|------------|----------------------------------|

Description

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

Usage

```
data("exonCounts")
```

Format

A data frame with 1000 rows and 7 variables

Source

Exoncounts from Pasilla package <https://bioconductor.org/packages/release/data/experiment/html/pasilla.html>

References

Huber W, Reyes A (2020). pasilla: Data package with per-exon and per-gene read counts of RNA-seq samples of Pasilla knock-down by Brooks et al., Genome Research 2011

| | |
|--------------|--------------------------|
| filterCounts | <i>Filter Count Data</i> |
|--------------|--------------------------|

Description

Filtering of exons based on their expression levels

Usage

```
filterCounts(x, mean = 1, exonCount = 1)
```

Arguments

| | |
|-----------|--|
| x | A numeric dataframe of exon counts across the samples. Exon number in format GeneName:Exonnumber should be indicated in the row name and sample names as column names. |
| mean | Exons with average count value across the dataset less than mean are filtered out. Default: 1 |
| exonCount | After filtering the individual exons, only genes with at least the given number of exons remaining will be retained. Default: 1 |

Value

A dataframe of filtered counts of exons

Examples

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

visualizeGenes

Visualize gene

Description

Produces a visualization summarizing the normalized read count in each sample group and expression difference across the expressed exons. Top panel contains the log₂ fold-change for each expressed exon. Asterisk denotes the significance level (*: < 0.05, **: < 0.01). Bottom panel shows the averaged normalized read count for each sample group. The title of the figure shows the gene name and the adjusted gene-level p-value (fdr)

Usage

```
visualizeGenes(gene, ebsea.out)
```

Arguments

| | |
|-----------|---|
| gene | Gene name matching the input data. |
| ebsea.out | Plots the mean count and fold-change the exons of the specified gene. |

Value

Plots the mean count and fold-change across the exons of the specified gene.

Examples

```
data(exonCounts)
group <- data.frame('group' = as.factor(c('G1', 'G1', 'G1', 'G2', 'G2', 'G2', 'G2')))
row.names(group) <- colnames(exonCounts)
design <- ~group
ebsea.out <- EBSEA(exonCounts, group, design)
visualizeGenes('FBgn000017', ebsea.out)
```

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