Package 'DELocal'

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Title Identifies differentially expressed genes with respect to other local genes

Version 1.9.0

Description The goal of DELocal is to identify DE genes compared to their neighboring genes from the same chromosomal location. It has been shown that genes of related functions are generally very far from each other in the chromosome. DELocal utilzes this information to identify DE genes comparing with their neighbouring genes.

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URL `https://github.com/dasroy/DELocal`

BugReports `https://github.com/dasroy/DELocal/issues`

Encoding UTF-8

LazyData false

RoxygenNote 7.2.3

biocViews GeneExpression, DifferentialExpression, RNASeq, Transcriptomics

Imports DESeq2, dplyr, reshape2, limma, SummarizedExperiment, ggplot2, matrixStats, stats

Suggests biomaRt, knitr, rmarkdown, stringr, BiocStyle

VignetteBuilder knitr

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`DELocal` *Finds differentially expressed genes by comparing neighboring genes*

Description

Finds differentially expressed genes by comparing neighboring genes

Usage

```
DELocal(
  pSmrExpt,
  nearest_neighbours,
  pDesign,
  pValue_cut = 0.05,
  pLogFold_cut = 0
)
```

Arguments

`pSmrExpt`	SummarizedExperiment object
`nearest_neighbours`	How many nearest neighbours within 1 Mb window to evaluate?
`pDesign`	design formula
`pValue_cut`	cut off value for adjusted p-value
`pLogFold_cut`	cut off value for relative log fold change compared to neighbouring genes

Value

A data.frame with top significant genes with the following columns:

relative.logFC: relative logFC compared to neighbouring genes

P.Value: raw p-value

adj.P.Value: adjusted p-value

B: log-odds that the gene is differentially expressed

Examples

```
count_matrix <- as.matrix(read.table(file = system.file("extdata",
                                                              "tooth_RNASeq_counts.txt",
                                                                  package = "DELocal")))
colData <- data.frame(condition=gsub("\\..*",x=colnames(count_matrix),
                                     replacement = ""))
gene_location <- read.table(file = system.file("extdata", "gene_location.txt",
                                    package = "DELocal"))
smrExpt <- SummarizedExperiment::SummarizedExperiment(
                                        assays=list(counts=count_matrix),
                                        rowData = gene_location,
                                        colData=colData)
contrast= c("condition","ME13","ME14")
require(dplyr)
```

```
x_genes <- SummarizedExperiment::rowData(smrExpt) %>%
      as.data.frame() %>%
      filter(chromosome_name=="X") %>% rownames()
DELocal_result <- DELocal(pSmrExpt = smrExpt[x_genes,],
                         nearest_neighbours = 5, pDesign = ~ condition,
                         pValue_cut = 0.05, pLogFold_cut = 0)
```

`plotNeighbourhood` *Returns median expression from different conditions of genes from a neighbourhood of a gene of interest*

Description

Returns median expression from different conditions of genes from a neighbourhood of a gene of interest

Usage

```
plotNeighbourhood(
  pSmrExpt,
  pNearest_neighbours = 5,
  pDesign = ~condition,
  colorFactor = "condition",
  pGene_id
)
```

Arguments

`pSmrExpt`	SummarizedExperiment object
`pNearest_neighbours`	How many nearest neighbours within 1 Mb window to plot
`pDesign`	design formula
`colorFactor`	The coloring factor
`pGene_id`	The gene of interest

Value

a list which contains both the data from the neighbourhood and a ggplot object

Examples

```
count_matrix <- as.matrix(read.table(file = system.file("extdata",
                                                        "tooth_RNASeq_counts.txt",
                                                            package = "DELocal")))
colData <- data.frame(condition=gsub("\\..*",x=colnames(count_matrix),
                                     replacement = ""))
gene_location <- read.table(file = system.file("extdata", "gene_location.txt",
                                    package = "DELocal"))
smrExpt <- SummarizedExperiment::SummarizedExperiment(assays=list(counts=count_matrix),
                                            rowData = gene_location,
                                            colData = colData)
contrast= c("condition","ME13","ME14")
```

```
require(dplyr)
x_genes <- SummarizedExperiment::rowData(smrExpt) %>%
      as.data.frame() %>%
      filter(chromosome_name=="X") %>% rownames()
DELocal::plotNeighbourhood(pSmrExpt = smrExpt, pGene_id = "ENSMUSG00000059401")
```

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