

# Package ‘DELocal’

May 15, 2024

**Title** Identifies differentially expressed genes with respect to other local genes

**Version** 1.4.0

**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 utilizes this information to identify DE genes comparing with their neighbouring genes.

**License** MIT + file LICENSE

**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

**git\_url** <https://git.bioconductor.org/packages/DELocal>

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DELocal	<i>Finds differentially expressed genes by comparing neighboring genes</i>
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### 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)

```

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plotNeighbourhood	<i>Returns median expression from different conditions of genes from a neighbourhood of a gene of interest</i>
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**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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