# Package 'DELocal'

November 28, 2024

Title Identifies differentially expressed genes with respect to other

local genes

Version 1.6.0

<b>Description</b> 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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**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**

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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**

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

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