Package 'BioInsight'

August 17, 2020

Title Filter and Plot RNA Biotypes

Version 0.1.0

Description Analyze and plot the abundance of different RNA biotypes present in a count matrix, this evaluation can be useful if you want to test different strategies of normalization or analyze a particular biotype in a differential gene expression analysis.

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Imports knitr, wordcloud, RColorBrewer

Depends edgeR, limma

Suggests testthat, biomaRt

NeedsCompilation no

Author Luiz Antonio de Jesus Rocha [aut, cre, cph]

Maintainer Luiz Antonio de Jesus Rocha <luiz.rocha@unifesp.br>

Repository CRAN

Date/Publication 2020-08-17 14:22:12 UTC

R topics documented:

describeRNA *Biotype Summary*

Description

This function provide filterByExpr with three custom options. See 'Arguments'. Different strategies can be useful either if you are trying to compare different approaches of normalization or if you want to analyze a particular biotype where a different variation of expression is expected under certain conditions. A BioInsight data frame will return with your new count matrix where you can proceed with your Differential Expression Analysis or revealRNA() to produce new plots and tables after the filter.

Usage

```
describeRNA(counts, biotypes, groups, report=FALSE, verbose=FALSE, filter=1)
```

Arguments

counts	Data.frame of counts matrix
biotypes	The count matrix with a gene_biotype column. See 'Examples'
groups	Groups as factor
report	If TRUE, a .pdf file formated in a proportion of 2:2 with a Multidimensional Scalling,barplot, dendrogram and wordcloud will be generated in a tempdir
verbose	if TRUE, a count table will be printed in the console with the numbers of biotypes
filter	Numeric from 1 to 3. See 'Details'

Details

1 "DEFAULT" from edgeR: Min.count=10, min.total.count=15; 2 "Slightly" above the DEFAULT: Min.count=15, min.total.count=25; 3 "Restricted" than DEFAULT: Min.count=25, min.total.count=40;

Note

See trace(describeRNA, edit=T) to modify the values of filterByExpr and/or the biotypes of interest.

References

Robinson MD, McCarthy DJ, Smyth GK. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. Bioinformatics. 2010;26(1):139-140. doi:10.1093/bioinformatics/btp616

Examples

```
counts = system.file("extdata", "count_matrix.tsv", package = "BioInsight")
counts = read.table(counts[1], header=TRUE, row.names=1)
biotypes = system.file("extdata", "Rattus_Norvegicus_biomart.tsv", package = "BioInsight")
biotypes = read.table(biotypes[1], header=TRUE, row.names=1)

groups = rep(as.factor(c("1","2")), each=5)

describeRNA(counts=counts,
            biotypes=biotypes,
            groups=groups,
            filter=2)

#Annotation - see biomaRt
#mart <- useMart(biomart = "ensembl", dataset = "rnorvegicus_gene_ensembl")
#genes = getBM(attributes=c("ensembl_gene_id","external_gene_name",
#                           "gene_biotype", "start_position",
#                           "end_position", "source"),
#              values = row.names(data),
#              mart = mart)
```

`revealRNA` *Explore Your BioInsight Results*

Description

Consider your count matrix filtered by describeRNA. Here i provide a function to generate the same plots with the new data for a comparison

Usage

```
revealRNA(counts, biotypes, report = FALSE, verbose = FALSE)
```

Arguments

`counts`	New count matrix generated by describeRNA function
`biotypes`	A column called gene_biotype
`report`	If TRUE, a new set of plot in a proportion of 2:2 will be generated in a temporary directory
`verbose`	If TRUE, your new table will be printed in the console

Examples

```
#describeRNA
counts = system.file("extdata", "count_matrix.tsv", package = "BioInsight")
counts = read.table(counts[1], header=TRUE, row.names=1)
biotypes = system.file("extdata", "Rattus_Norvegicus_biomart.tsv", package = "BioInsight")
biotypes = read.table(biotypes[1], header=TRUE, row.names=1)
```

```
groups = rep(as.factor(c("1","2")), each=5)

describeRNA(counts=counts,
            biotypes=biotypes,
            groups=groups,
            filter=2)

#This example consider that your new count matrix is annotated. If not, you can try to merge:
data = merge(BioInsight, biotypes, by="row.names")
x = data.frame(data$gene_biotype)
revealRNA(counts=data,
          biotypes=x,
          verbose=FALSE,
          report=FALSE)
```

Index