

# Package ‘BioInsight’

July 21, 2025

**Title** Filter and Plot RNA Biotypes

**Version** 0.3.1

**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 ( $\geq 2$ )

**Encoding** UTF-8

**RoxygenNote** 7.1.1

**Imports** knitr, wordcloud, RColorBrewer

**Depends** R ( $\geq 2.10$ ), edgeR, limma

**Suggests** testthat ( $\geq 3.0.0$ ), biomaRt

**NeedsCompilation** no

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**Repository** CRAN

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**Config/testthat/edition** 3

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 describeRNA

*describeRNA*


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## Description

This function provide filterByExpr with two customized 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.

## Usage

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

## Arguments

counts	data.frame where you have gene counts
biotypes	data.frame where you have a gene_biotype column
groups	factor with groups and samples (see Examples)
report	if TRUE will generate a .pdf file in /tmp/ folder ('wordcloud' and 'RColorBrewer' are necessary)
verbose	if TRUE will print your result in your console ('knitr' is necessary)
filter	Your threshold (see edgeR::filterByExpr)

## Details

For filter you may want to use "1" if you want the default option from filterByExpr. If 2 "Slightly" above the default will be applied. If "3" A more restrictive option will be applied.

## Note

You can use trace(describeRNA, edit=T) to set different values as threshold for "filter" option.

## 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, row.names=1, header=TRUE)
biotypes = system.file("extdata", "Rattus_Norvegicus_biomart.tsv", package="BioInsight")
biotypes = read.table(biotypes, row.names=1, header=TRUE)

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

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

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