Package ‘Rmmquant’

May 7, 2024

Type Package

Title RNA-Seq multi-mapping Reads Quantification Tool

Version 1.22.0

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Description RNA-Seq is currently used routinely, and it provides accurate information on gene transcription. However, the method cannot accurately estimate duplicated genes expression. Several strategies have been previously used, but all of them provide biased results.

With Rmmquant, if a read maps at different positions, the tool detects that the corresponding genes are duplicated; it merges the genes and creates a merged gene. The counts of ambiguous reads is then based on the input genes and the merged genes.

Rmmquant is a drop-in replacement of the widely used tools findOverlaps and featureCounts that handles multi-mapping reads in an unbiased way.

License GPL-3

Encoding UTF-8

LazyData true

SystemRequirements C++11

Depends R (>= 3.6)

Imports Rcpp (>= 0.12.8), methods, S4Vectors, GenomicRanges, SummarizedExperiment, devtools, TBX20BamSubset, TxDb.Mmuseles.uscSC.mm9.knownGene, org.Mm.eg.db, DESeq2, apeglm, BiocStyle

LinkingTo Rcpp

RoxygenNote 7.0.2

biocViews GeneExpression, Transcription

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

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counts  Get the counts table of an RmmquantClass object.

Description

Get the counts table of an RmmquantClass object.

Usage

counts(object)

## S4 method for signature 'RmmquantClass'
counts(object)

Arguments

object  An RmmquantClass object.

Value

The count matrix, in a SummarizedExperiment

Examples

example <- RmmquantClassExample()
counts(example)
Rmmquant

Rmmquant: RNA-Seq multi-mapping Reads Quantification Tool

Description
Counts the number of reads per gene.

Author(s)
Matthias Zytnicki, <matthias.zytnicki@inra.fr>

RmmquantClass-class
An S4 class for Rmmquant.

Description
An S4 class for Rmmquant.

Slots
annotationFile The annotation file
readsFiles The reads files
genomicRanges The annotation, in a GenomicRanges format.
genomicRangesList The annotation, in a GenomicRangesList format.
sampleNames The name of the samples
overlap The minimum number of overlapping base pairs to declare a match.
strands Whether annotation of the same strand should be considered.
sorts Whether the files are sorted.
countThreshold The reads files
mergeThreshold The reads files
printGeneName Whether the (vernacular) gene name is reported.
quiet Shut Rmmquant up.
progress Print the progress of the tool.
nThreads The number of threads.
formats The format of the reads files (SAM or BAM).
nOverlapDiff Difference of overlap between a primary map and a secondary map.
pcOverlapDiff Ratio of overlap between a primary map and a secondary map.
counts A SummarizedExperiment storing the counts.
Description

Example of Rmmquant constructor.

Usage

RmmquantClassExample()

Value

An RmmquantClass.

Examples

example <- RmmquantExample()

Description

Example of Rmmquant use

Usage

RmmquantExample()

Value

An SummarizedExperiment.

Examples

example <- RmmquantExample()
RmmquantRun

Main Rmmquant function.

Description

Main Rmmquant function.

Usage

RmmquantRun(
  annotationFile = "",
  readsFiles = character(0),
  genomicRanges = GRanges(),
  genomicRangesList = GRangesList(),
  sampleNames = character(0),
  overlap = NA_integer_,
  strands = character(0),
  sorts = logical(0),
  countThreshold = NA_integer_,
  mergeThreshold = NA_real_,
  printGeneName = FALSE,
  quiet = TRUE,
  progress = FALSE,
  nThreads = 1,
  formats = character(0),
  nOverlapDiff = NA_integer_,
  pcOverlapDiff = NA_real_,
  lazyload = FALSE
)

Arguments

  annotationFile    The annotation file
  readsFiles        The reads files
  genomicRanges     The annotation, in a GenomicRanges format.
  genomicRangesList The annotation, in a GenomicRangesList format.
  sampleNames       The name of the samples
  overlap           The minimum number of overlapping base pairs to declare a match.
  strands           Whether annotation of the same strand should be considered.
  sorts             Whether the files are sorted.
  countThreshold    The reads files
  mergeThreshold    The reads files
  printGeneName     Whether the (vernacular) gene name is reported.
quiet Shut Rmmquant up.
progress Print the progress of the tool.
nThreads The number of threads.
formats The format of the reads files (SAM or BAM).
nOverlapDiff Difference of overlap between a primary map and a secondary map.
pcOverlapDiff Ratio of overlap between a primary map and a secondary map.
lazyload Usual for S4 functions.

Value
A SummerizedExperiment.

Examples

```r
dir <- system.file("extdata", package="Rmmquant", mustWork = TRUE)
gtfFile <- file.path(dir, "test.gtf")
samFile <- file.path(dir, "test.sam")
table <- RmmquantRun(gtfFile, samFile)
```

show,RmmquantClass-method

Show the content of an RmmquantClass object.

Description
Show the content of an RmmquantClass object.

Usage

```r
## S4 method for signature 'RmmquantClass'
show(object)
```

Arguments

object An RmmquantClass object.

Value
A description of the object.

Examples

```r
example <- RmmquantClassExample()
example
```
validateRmmquant

validateRmmquant  
*Rmmquant object validation function.*

---

**Description**

Rmmquant object validation function.

**Usage**

`validateRmmquant(object)`

**Arguments**

- `object`  
  A `RmmquantClass` object.

**Value**

TRUE, if succeed, otherwise a character.
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