Package ‘Rmmquant’

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Type Package
Title RNA-Seq multi-mapping Reads Quantification Tool
Version 1.22.0
Date 2023-04-05
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.Mmusculus.UCSC.mm9.knownGene, org.Mm.eg.db, DESeq2, apeglm, BiocStyle
LinkingTo Rcpp
RoxygenNote 7.0.2
biocViews GeneExpression, Transcription
Suggests knitr, rmarkdown, testthat
VignetteBuilder knitr
git_url https://git.bioconductor.org/packages/Rmmquant
git_branch RELEASE_3_19
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

eexample <- RmmquantClassExample()
counts(example)
Rmmquant

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Rmmquant: RNA-Seq multi-mapping Reads Quantification Tool

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Description

Counts the number of reads per gene.

Author(s)

Matthias Zytnicki, <matthias.zytnicki@inra.fr>

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RmmquantClass-class

An S4 class for Rmmquant.

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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.
RmmquantClassExample  Example of Rmmquant constructor.

Description
Example of Rmmquant constructor.

Usage
RmmquantClassExample()

Value
An RmmquantClass.

Examples
example <- RmmquantExample()

RmmquantExample  Example of Rmmquant use

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.

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**Value**

A SummarizedExperiment.

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**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)
```

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**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

Rmmquant object validation function.

Usage

validateRmmquant(object)

Arguments

object A RmmquantClass object.

Value

TRUE, if succeed, otherwise a character.
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