Package ‘Rmmquant’

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Type Package
Title RNA-Seq multi-mapping Reads Quantification Tool
Version 1.20.0
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.MmuScus.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_18
Get the counts table of an `RmmquantClass` object.

### Description

Get the counts table of an `RmmquantClass` object.

### Usage

```r
counts(object)
```

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

### Arguments

- **object**
  - An `RmmquantClass` object.

### Value

The count matrix, in a `SummarizedExperiment`

### Examples

```r
example <- RmmquantClassExample()
counts(example)
```
Rmmquant

Rmmquant: RNA-Seq multi-mapping Reads Quantification Tool

Description
Counts the number of reads per gene.

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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).
n0OverlapDiff 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()
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.
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
eexample <- RmmquantClassExample()
eexample
```
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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