Package 'Rmmquant'

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Type Package

Title RNA-Seq multi-mapping Reads Quantification Tool

Version 1.8.1

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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 unabiased 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, BiocStyle

LinkingTo Rcpp

RoxygenNote 6.1.1

biocViews GeneExpression, Transcription

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

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R topics documented:

`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)

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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).
`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 SummarizedExperiement.

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

```
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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show,RmmquantClass-method

Show the content of an RmmquantClass *object.*

Description

Show the content of an RmmquantClass object.

Usage

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

Arguments

object	An RmmquantClass object.

Value

A description of the object.

Examples

```
example <- RmmquantClassExample()
example
```

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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