

Package ‘Rmmquant’

January 20, 2026

Type Package

Title RNA-Seq multi-mapping Reads Quantification Tool

Version 1.28.0

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_22

git_last_commit 60d48d5

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-01-19

Author Zytnicki Matthias [aut, cre]

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

Contents

counts	2
Rmmquant	3
RmmquantClass-class	3
RmmquantClassExample	4
RmmquantExample	4
RmmquantRun	5
show,RmmquantClass-method	6
validateRmmquant	7

Index	8
--------------	---

counts	<i>Get the counts table of an RmmquantClass object.</i>
--------	---

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)
```

Description

Counts the number of reads per gene.

Author(s)

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

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	<i>Main Rmmquant function.</i>
-------------	--------------------------------

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 SummarizedExperiment.

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)
```

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.

Index

counts, 2
counts, RmmquantClass-method (counts), 2

Rmmquant, 3
RmmquantClass-class, 3
RmmquantClassExample, 4
RmmquantExample, 4
RmmquantRun, 5

show, RmmquantClass-method, 6

validateRmmquant, 7