

# Package ‘Rmmquant’

November 21, 2024

**Type** Package

**Title** RNA-Seq multi-mapping Reads Quantification Tool

**Version** 1.25.0

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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.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

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

sorted 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 SummarizedExperiemnt.

**Examples**

```
example <- RmmquantExample()
```

---

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

## Description

Main Rmmquant function.

## Usage

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

---

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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