

# Package ‘easyRNASeq’

March 26, 2013

**Version** 1.4.2

**Date** 2011-10-15

**Type** Package

**Title** Count summarization and normalization for RNA-Seq data.

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**Description** Calculates the coverage of high-throughput short-reads against a genome of reference and summarizes it per feature of interest (e.g. exon, gene, transcript). The data can be normalized as ‘RPKM’ or by the ‘DESeq’ or ‘edgeR’ package.

**Depends** graphics, methods, parallel, utils, genomeIntervals (>= 1.14.0), Biobase (>= 2.18.0), BiocGenerics (>= 0.4.0), biomaRt (>= 2.14.0), edgeR (>= 3.0.0), Biostrings (>= 2.26.0), BSgenome (>= 1.26.0), DESeq (>= 1.10.0), GenomicRanges (>= 1.10.0), IRanges (>= 1.16.0), Rsamtools (>= 1.10.0), ShortRead (>= 1.16.0)

**Suggests** BSgenome.Dmelanogaster.UCSC.dm3 (>= 1.3.17), GenomicFeatures (>= 1.10.0), RnaSeqTutorial (>= 0.0.10)

**License** Artistic-2.0

**LazyLoad** yes

**Enhances** edgeR, genomeIntervals, DESeq, ShortRead

**biocViews** GeneExpression, RNAseq, Genetics, Preprocessing

**Collate** ‘AllClasses.R’ ‘AllGenerics.R’ ‘DESeq-methods.R’ ‘easyRNASeq-accessors.R’ ‘easyRNASeq-counts.R’ ‘easyRNASeq-internal-annotation.R’ ‘easyRNASeq-internal-counts.R’ ‘easyRNASeq-internal-methods.R’ ‘easyRNASeq-internal-normalize.R’ ‘easyRNASeq-islands.R’ ‘easyRNASeq-methods.R’ ‘easyRNASeq-normalize.R’ ‘easyRNASeq-package.R’ ‘edgeR-methods.R’ ‘genomeIntervals-methods.R’ ‘GenomicRanges-methods.R’ ‘IRanges-methods.R’ ‘print-methods.R’ ‘ShortRead-methods.R’ ‘show-methods.R’ ‘easyRNASeq-annotation.R’ ‘parallel-methods.R’

## R topics documented:

count	2
DESeq additional methods	3
DESeq and edgeR common methods	4
easyRNASeq	5
easyRNASeq accessors	8
easyRNASeq annotation methods	9
easyRNASeq correction methods	10
easyRNASeq coverage methods	12
easyRNASeq island methods	13
easyRNASeq package	14
easyRNASeq summarization methods	16
edgeR additional methods	17
genomeIntervals additional methods	18
GenomicRanges additional methods	19
IRanges additional methods	20
parallel additional methods	21
print methods	21
RNAseq class	22
ShortRead additional methods	23
show methods	25
<b>Index</b>	<b>26</b>

---

count

*count method*

---

### Description

This function is to supersed the easyRNASeq function in order to consolidate the option parameters as well as the option output. Ideally, the only output would be a SummarizedExperiment.

### Arguments

filesDirectory	The directory where the files to be used are located.
outputFormat	By default, easyRNASeq returns a <a href="#">SummarizedExperiment</a> . If one of DESeq,edgeR,RNAseq, matrix is provided then the respective object is returned. Ideally, this option should get deprecated and only a SummarizedExperiment returned.
...	currently additional arguments to the easyRNASeq function.

### Value

Returns a [SummarizedExperiment](#). If the outputFormat option has been set, a corresponding object is returned: a count table (a matrix of m features x n samples), a [DESeq:newCountDataset](#), a [edgeR:DGEList](#) or [RNAseq](#).

### Author(s)

Nicolas Delhomme

**See Also**

[RNAseq SummarizedExperiment](#) [edgeR:DGEList](#) [DESeq:newCountDataset](#) [easyRNASeq:knownOrganisms](#)  
[ShortRead:readAligned](#)

**Examples**

```
## Not run:
library("RnaSeqTutorial")
library(BSgenome.Dmelanogaster.UCSC.dm3)

## creating a count table from 4 bam files
sumExp <- count(filesDirectory=system.file(
  "extdata",
  package="RnaSeqTutorial"),
  pattern="[A,C,T,G]{6}\\\\.bam$",
  readLength=30L,
  organism="Dmelanogaster",
  chr.sizes=seqlengths(Dmelanogaster),
  annotationMethod="rda",
  annotationFile=system.file(
    "data",
    "gAnnot.rda",
    package="RnaSeqTutorial"),
  count="exons"
)

## the counts
assays(sumExp)
## the sample info
colData(sumExp)
## the 'features' info
rowData(sumExp)

## End(Not run)
```

---

DESeq additional methods

*Extension for the DESeq package*

---

**Description**

- `multivariateConditions` is simply an accessor for the `multivariateConditions` slot of a [CountDataSet](#) object.

**Arguments**

`obj` An object of class [CountDataSet](#)

**Value**

- `multivariateConditions` returns a boolean describing whether the data to analyze is multivariate or not

**Author(s)**

Nicolas Delhomme

**See Also**

[CountDataSet](#)

**Examples**

```
## Not run:  
## these are helper function for the DESeq package  
## refer to its vignette first  
cds <- newCountDataSet(countData,conditions)  
cds <- estimateSizeFactors(cds)  
cds <- estimateDispersions(cds)  
mVar <- multivariateConditions(cds)  
  
## End(Not run)
```

---

DESeq and edgeR common methods

*DESeq and edgeR common methods*

---

**Description**

`plotDispersionEstimates(obj,...)` extends the **DESeq** and **edgeR** packages by offering the functionality to plot the dispersion estimate as described in their respective vignettes: [CountDataSet{DESeq}](#) and [edgeR](#).

**Arguments**

<code>obj</code>	An object of class <a href="#">CountDataSet</a> or of class <a href="#">DGEList</a>
<code>...</code>	See details

**Details**

- [CountDataSet{DESeq}](#) A character string describing the first condition, to be provided as `cond=value`
- [edgeR](#) Unused, just for compatibility.

**Value**

none

**Author(s)**

Nicolas Delhomme

**Examples**

```

## Not run:
## edgeR
## create the object
dgeList <- DGEList(counts,group)
## calculate the sie factors
dgeList <- calcNormFactors(dgeList)
## plot them
apply(combn(rownames(dgeList$samples),2),
2,
function(co,obj){plotNormalizationFactors(obj,co[1],co[2]),dgeList)
## the dispersion estimates
plotDispersionEstimates(obj)

## DESeq
## these are helper function for the DESeq package
## refer to its vignette first
cds <- newCountDataSet(countData,conditions)
cds <- estimateSizeFactors(cds)
cds <- estimateDispersions(cds)
plotDispersionEstimates(cds,conditions[1])

## End(Not run)

```

---

easyRNASeq

*easyRNASeq method*


---

**Description**

This function is a wrapper around the more low level functionalities of the package. Is the easiest way to get a count matrix from a set of read files. It does the following:

- use [ShortRead/Rsamtools methods](#) for loading/pre-processing the data.
- fetch the [annotations](#) depending on the provided arguments
- get the reads [coverage](#) from the provided file(s)
- summarize [the reads](#) according to the selected summarization features
- optionally [apply](#) a data correction (i.e. generating RPKM).
- use [edgeR methods](#) for post-processing the data or
- use [DESeq methods](#) for post-processing the data (either of them being recommended over RPKM).

**Arguments**

annotationFile The location (full path) of the annotation file

annotationObject

A [RangedData](#) or [GRangesList](#) object containing the annotation.

annotationMethod

The method to fetch the annotation, one of "biomaRt", "env", "gff", "gtf" or "rda". All methods but "biomaRt" and "env" require the annotationFile to be set. The "env" method requires the annotationObject to be set.

chr.map	A data.frame describing the mapping of original chromosome names towards wished chromosome names. See details.
chr.sel	A vector of chromosome names to subset the final results.
chr.sizes	A vector or a list containing the chromosomes' size of the selected organism or simply the string "auto". See details.
conditions	A vector of descriptor, each sample must have a descriptor if you use outputFormat DESeq or edgeR. The size of this list must be equal to the number of sample. In addition the vector should be named with the filename of the corresponding samples.
count	The feature used to summarize the reads. One of 'exons', 'features', 'genes', 'islands' or 'transcripts'. See details.
filenames	The name, not the path, of the files to use
filesDirectory	The directory where the files to be used are located. Defaults to the current directory.
filter	The filter to be applied when loading the data using the "aln" format
format	The format of the reads, one of "aln", "bam". If not "bam", all the types supported by the <b>ShortRead</b> package are supported too. As of version 1.3.5, it defaults to bam.
gapped	Is the bam file provided containing gapped alignments?
ignoreWarnings	set to TRUE (bad idea! they have a good reason to be there) if you do not want warning messages.
min.cov	When computing read islands, the minimal coverage to take into account for calling an island
min.length	The minimal size an island should have to be kept
max.gap	When computing read islands, the maximal gap size allowed between two islands to merge them
nbCore	defines how many CPU core to use when computing the geneModels. Use the default parallel library
normalize	A boolean to convert the returned counts in RPKM. Valid when the outputFormat is left undefined (i.e. when a matrix is returned) and when it is DESeq or edgeR. Note that it is not advised to normalize the data prior DESeq or edgeR usage!
organism	A character string describing the organism
outputFormat	By default, easyRNASeq returns a matrix. If one of DESeq, edgeR, RNAseq, <a href="#">SummarizedExperiment</a> is provided then the respective object is returned.
pattern	For easyRNASeq, the pattern of file to look for, e.g. "bam\$"
plot	Whether or not to plot assessment graphs.
readLength	The read length in bp
silent	set to TRUE if you do not want messages to be printed out.
summarization	A character defining which method to use when summarizing reads by genes. So far, only "geneModels" is available.
type	The type of data when using the "aln" format. See the ShortRead library.
validity.check	Shall UCSC chromosome name convention be enforced? This is only supported for a set of organisms, see <a href="#">easyRNASeq:knownOrganisms</a> , otherwise the argument 'chr.map' can be used to complement it.
...	additional arguments. See details

## Details

- ... Additional arguments for different functions:
  - For the **biomaRt** `getBM` function
  - For the `readGffGtf` internal function that takes an optional arguments: `annotation.type` that default to "exon" (used to select the proper rows of the gff or gtf file)
  - For the `DESeq` `estimateDispersions` method
  - For the `list.files` function used to locate the read files.
- the `annotationObject` When the `annotationMethods` is set to `env` or `rda`, a properly formatted `RangedData` or `GRangesList` object need to be provided. Check the paragraph `RangedData` in the vignette or the examples at the bottom of this page for examples. The data.frame-like structure of these objects is where `easyRNASeq` will look for the exon, feature, transcript, or gene identifier. Depending on the count method selected, it is essential that the `akin` column name is present in the `annotationObject`. E.g. when counting "features", the `annotationObject` has to contain a "feature" field.
- the `chr.map` The `chr.map` argument for the `easyRNASeq` function only works for an "organism-Name" of value 'custom' with the "validity.check" parameter set to 'TRUE'. This data.frame should contain two columns named 'from' and 'to'. The row should represent the chromosome name in your original data and the wished name in the output of the function.
- `count` The count can be summarized by exons, features, genes, islands or transcripts. While exons, genes and transcripts are obvious, "features" describes any features provided by the user, e.g. enhancer loci. These are processed as the exons are. For "islands", it is for an under development function that identifies de-novo expression loci and count the number of reads overlapping them.
- `chr.sizes` If set to "auto", then the format has to be "bam", in which case the chromosome names and size are extracted from the BAM header

## Value

Returns a count table (a matrix of m features x n samples). If the `outputFormat` option has been set, a corresponding object is returned: a `SummarizedExperiment`, a `DESeq::newCountDataset`, a `edgeR::DGEList` or `RNAseq`.

## Author(s)

Nicolas Delhomme

## See Also

[RNAseq](#) [SummarizedExperiment](#) [edgeR::DGEList](#) [DESeq::newCountDataset](#) [easyRNASeq::knownOrganisms](#) [ShortRead::readAligned](#)

## Examples

```
## Not run:
library("RnaSeqTutorial")
library(BSgenome.Dmelanogaster.UCSC.dm3)

## creating a count table from 4 bam files
count.table <- easyRNASeq(filesDirectory=
  system.file(
    "extdata",
    package="RnaSeqTutorial"),
```

```

pattern="[A,C,T,G]{6}\.bam$",
format="bam",
readLength=36L,
organism="Dmelanogaster",
chr.sizes=as.list(seqlengths(Dmelanogaster)),
annotationMethod="rda",
annotationFile=system.file(
  "data",
  "gAnnot.rda",
  package="RnaSeqTutorial"),
count="exons")

## an example of a chr.map
chr.map <- data.frame(from=c("2L","2R","MT"),to=c("chr2L","chr2R","chrMT"))

## an example of a RangedData annotation
gAnnot <- RangedData(
  IRanges(
    start=c(10,30,100),
    end=c(21,53,123),
    space=c("chr01","chr01","chr02"),
    strand=c("+","+","-"),
    transcript=c("trA1","trA2","trB"),
    gene=c("gA","gA","gB"),
    exon=c("e1","e2","e3"),
    universe = "Hs19"
  )

## an example of a GRangesList annotation
grngs <- as(gAnnot,"GRanges")
grngsList<-split(grngs,seqnames(grngs))

## End(Not run)

```

---

easyRNASeq accessors    *Accessors for RNAseq class*

---

## Description

These functions and generics define ‘accessors’ (to get and set values) for objects in the **easyRNASeq** package.

## Arguments

obj	An object derived from class RNAseq.
count	The type of count you want to access, ‘genes’, ‘features’, ‘exons’, ‘transcripts’ or ‘islands’
summarization	If count is set to genes, precise the type of summarization, ‘bestExons’ or ‘geneModels’
unique	For the ‘exons’ count only. Should the counts returned be unique for their identifier (i.e. the matrix row names)?
value	The replacement value.

**Value**

Usually, the value of the corresponding slot, or other simple content described on the help page of easyRNASeq.

**Author(s)**

Nicolas Delhomme

**Examples**

```
rnaSeq<-new("RNAseq")
##set organisme name of an RNAseq object
organismName(rnaSeq) <- "Dmelanogaster"
##get organisme name of an RNAseq object
orgName<-organismName(rnaSeq)
```

---

easyRNASeq annotation methods

*Fetch genic annotation from a gff/gtf file or using biomaRt*

---

**Description**

The annotation can be retrieved in two ways

- `biomaRtUse` `biomaRt` and `Ensembl` to get organism specific annotation.
- `gff/gtfUse` a `gff` or `gtf` local annotation file.

When using **biomaRt**, it is important that the `organismName` slot of the `RNAseq` object is set the prefix of one of the value available using the `biomaRt listDatasets` function, e.g. "Dmelanogaster". When reading from a `gff/gtf` file, a version 3 formatted `gff` (`gtf` are modified `gff3` from `Ensembl`) is expected. The function `genomeIntervals readGff3` is used to read the data in. Another annotation caveat is the reference names, *i.e.* the chromosome/scaffold names used in the alignment files and those fetched when retrieving the genic annotation might differ. **easyRNASeq** tries to be clever in this case and guess the correspondance. However, it is not always obvious. Organisms were this has been checked can be listed with the `knownOrganisms` function.

**Arguments**

<code>obj</code>	An object of class <code>RNAseq</code>
<code>method</code>	one of <code>biomaRt</code> , <code>gff</code> , <code>gtf</code>
<code>filename</code>	If the method is <code>gff</code> or <code>gtf</code> , the actual <code>gtf</code> , <code>gff</code> filename
<code>ignoreWarnings</code>	set to <code>TRUE</code> (bad idea! they have a good reason to be there) if you do not want warning messages.
<code>...</code>	See details

**Details**

... are for additional arguments, passed to the `biomaRt getBM` function or to the `readGffGtf` internal function that takes an optional arguments: `annotation.type` that default to "exon". This is used to select the proper rows of the `gff` or `gtf` file.

**Value**

A [RangedData](#) containing the fetched annotations.

A vector containing the known organisms

**Author(s)**

Nicolas Delhomme

Nicolas Delhomme

**Examples**

```
## Not run:
library("RnaSeqTutorial")
obj <- new('RNAseq',
  organismName="Dmelanogaster",
  readLength=36L,
  chrSize=as.list(seqlengths(Dmelanogaster))
)

obj <- fetchAnnotation(obj,
  method="gff",
  filename=system.file(
    "extdata",
    "annot.gff",
    package="RnaSeqTutorial"))

## End(Not run)
knownOrganisms()
```

---

easyRNASeq correction methods

*easyRNASeq count table correction to RPKM*

---

**Description**

Convert a count table obtained from the easyRNASeq function into an RPKM corrected count table.

**Arguments**

feature.size	Precise the feature (e.g. exons, genes) sizes. It should be a named numeric list, named after the feature names.
from	Determine the kind of coverage to use, choice limited to: exons, features, transcripts, bestExons, geneModels or islands.
lib.size	Precise the library size. It should be a named numeric list, i.e. named after the sample names.
obj	An object of class <a href="#">RNAseq</a> or a matrix, see details
simplify	If set to TRUE, whenever a feature (exon, feature, ...) is duplicated in the count table, it is only returned once.
...	additional arguments. See details

**Details**

RPKM accepts two sets of arguments:

- `RNAseq`, character the ... are additional arguments to be passed to the `readCounts` method.
- `matrix`, named vector normalize a count matrix by providing the feature sizes (e.g. gene sizes) as a named vector where the names match the row names of the count matrix and the lib sizes as a named vector where the names match the column names of the count matrix.

**Value**

A matrix containing RPKM corrected read counts.

**Author(s)**

Nicolas Delhomme

**See Also**

[readCounts](#)

**Examples**

```
## Not run:
## get an RNAseq object
rnaSeq <- easyRNASeq(filesDirectory=
  system.file(
    "extdata",
    package="RnaSeqTutorial"),
  pattern="[A,C,T,G]{6}\\..bam$",
  format="bam",
  readLength=36L,
  organism="Dmelanogaster",
  chr.sizes=as.list(seqlengths(Dmelanogaster)),
  annotationMethod="rda",
  annotationFile=system.file(
    "data",
    "gAnnot.rda",
    package="RnaSeqTutorial"),
  count="exons",
  outputFormat="RNAseq")

## get the RPKM
rpkm <- RPKM(rnaSeq,from="exons")

## the same from a count table
count.table <- readCounts(rnaSeq,count="exons")

## get the RPKM
## verify that the feature are sorted as the count.table
all(.getName(rnaSeq,"exon") == rownames(count.table))
feature.size <- unlist(width(ranges(rnaSeq)))

## verify that the samples are ordered in the same way
all(names(librarySize(rnaSeq)) == colnames(count.table))

## get the RPKM
```

```
rpkm <- RPKM(count.table,
feature.size=feature.size,
lib.size=librarySize(rnaSeq))

## End(Not run)
```

---

easyRNASeq coverage methods

*Compute the coverage from a Short Read Alignment file*

---

## Description

Computes the genomic reads' coverage from a read file in bam format or any format supported by **ShortRead**.

## Arguments

obj	An <a href="#">RNAseq</a> object
chr.map	A data.frame describing the mapping of original chromosome names towards wished chromosome names. See details.
chr.sel	A vector of chromosome names to subset the final results.
filename	The full path of the file to use
filter	The filter to be applied when loading the data using the "aln" format
format	The format of the reads, one of "aln", "bam". If not "bam", all the types supported by the ShortRead package are supported too.
gapped	Is the bam file provided containing gapped alignments?
ignoreWarnings	set to TRUE (bad idea! they have a good reason to be there) if you do not want warning messages.
isUnmappedQuery	additional argument for scanBamFlag <b>Rsamtools</b>
type	The type of data when using the "aln" format. See the <b>ShortRead</b> package.
validity.check	Shall UCSC chromosome name convention be enforced
what	additional argument for ScanBamParam <b>Rsamtools</b>
...	additional arguments. See details

## Details

... for fetchCoverage: Can be used for readAligned method from package **ShortRead** or for scanBamFlag method from package **Rsamtools**.

## Value

An [RNAseq](#) object. The slot readCoverage contains a SimpleRleList object representing a list of coverage vectors, one per chromosome.

## Author(s)

Nicolas Delhomme

**See Also**

[Rle ShortRead:readAligned](#)

**Examples**

```
## Not run:
library("RnaSeqTutorial")
library(BSgenome.Dmelanogaster.UCSC.dm3)

obj <- new('RNAseq',
  organismName="Dmelanogaster",
  readLength=36L,
  chrSize=as.list(seqlengths(Dmelanogaster))
)

obj <- fetchCoverage(
  obj,
  format="bam",
  filename=system.file(
    "extdata",
    "ACACTG.bam",
    package="RnaSeqTutorial")
)

## End(Not run)
```

---

easyRNASeq island methods

*Identify expressed regions de-novo*

---

**Description**

Process the coverage to locate regions with a minimum coverage (min.cov). If regions are separated by a gap shorter than a maximum length (max.gap), they are unified. Only islands longer than min.length are returned. These functions are now outdated and would need to be actualized.

**Arguments**

obj	An object of class RNAseq
max.gap	Maximum gap between two peaks to build an island
min.cov	Minimum coverage for an island to be returned
min.length	Minimum size of an island to be returned
plot	If TRUE, draw plots of coverage distribution. Help the user to select an appropriate value for the minimum coverage.
...	See details

**Details**

... are for providing additional options to the [hist](#) plot function.

**Value**

An RNAseq object with the readIsland slot set with a RangedData containing the selected islands and the readCount slot actualized with a list containing the count table per island.

**Author(s)**

Nicolas Delhomme

**Examples**

```
## Not run:
## NOTE that this function might need to be actualized
obj <- new('RNAseq',
  organismName="Dmelanogaster",
  readLength=36L,
  chrSize=as.list(seqlengths(Dmelanogaster))
)

obj <- fetchCoverage(
  obj,
  format="bam",
  filename=system.file(
    "extdata",
    "ACACTG.bam",
    package="RnaSeqTutorial")
)

obj <- findIslands(
  obj,
  max.gap=10L,
  min.cov=10L,
  min.length=200L)

## End(Not run)
```

---

easyRNASeq package      *Count summarization and normalization pipeline for Next Generation Sequencing data.*

---

**Description**

Offers functionalities to summarize read counts per feature of interest, e.g. exons, transcripts, genes, etc. Offers functionalities to normalize the summarized counts using 3rd party packages like [DESeq](#) or [edgeR](#).

**Details**

Package:    easyRNASeq  
 Type:        Package  
 Version:    1.4.2  
 Date:        2012-10-15  
 License:    Artistic-2.0

LazyLoad: yes  
 Depends: methods, parallel, biomaRt, edgeR, DESeq, genomeIntervals, Rsamtools, ShortRead, RnaSeqTutorial  
 Suggests: BSgenome.Dmelanogaster.UCSC.dm3

## Methods

The main function `easyRNASeq` will summarize the counts per feature of interest, for as many samples as provided and will return a count matrix (N\*M) where N are the features and M the samples. This data can be corrected to **RPKM** in which case a matrix of corrected value is returned instead, with the same dimensions. Alternatively a `SummarizedExperiment` can be returned and this is expected to be the default in the upcoming version of `easyRNASeq` (as of 1.5.x). If the necessary sample information are provided, the data can be normalized using either `DESeq` or `edgeR` and the corresponding package object returned. For more insider details, and step by step functions, see:

[ShortRead methods](#) for pre-processing the data. [easyRNASeq annotation methods](#) for getting the annotation. [easyRNASeq](#)

## Author(s)

Nicolas Delhomme

## See Also

The class RNAseq specification: [RNAseq](#)

The default output class specification: [SummarizedExperiment](#)

The imported packages: [biomaRt](#) [edgeR](#) [genomeIntervals](#) [Biostrings](#) [BSgenome](#) [DESeq](#) [GenomicRanges](#) [IRanges](#) [Rsamtools](#) [ShortRead](#)

The suggested packages: [parallel](#) [GenomicFeatures](#)

## Examples

```
## Not run:
library("RnaSeqTutorial")
library(BSgenome.Dmelanogaster.UCSC.dm3)

## creating a count table from 4 bam files
count.table <- easyRNASeq(filesDirectory=
  system.file(
    "extdata",
    package="RnaSeqTutorial"),
  pattern="[A,C,T,G]{6}\\.bam$",
  format="bam",
  readLength=36L,
  organism="Dmelanogaster",
  chr.sizes=as.list(seqlengths(Dmelanogaster)),
  annotationMethod="rda",
  annotationFile=system.file(
    "data",
    "gAnnot.rda",
    package="RnaSeqTutorial"),
  count="exons")
```

```
## End(Not run)
```

---

easyRNASeq summarization methods

*Count methods for RNAseq object*

---

## Description

Summarize the read counts per exon, feature, gene, transcript or island.

- `exonCounts`: for that summarization, reads are summarized per exons. An "exon" field is necessary in the annotation object for this to work. See [easyRNASeq annotation methods](#) for more details on the annotation object.
- `featureCounts` is similar to the 'exons' one. This is just a wrapper to summarize count for genomic features that are not exon related. I.e. one could use it to measure eRNAs. Again, a "feature" field is necessary in the annotation object for this to work.
- `geneCounts` sums the counts per either `bestExons` or `geneModels`. In either case, the annotation object needs to contain both an "exon" and a "gene" field.
- `islandCounts` sums the counts per computed islands.
- `transcriptCounts` sums the counts obtained by exons into their respective transcripts. Note that this often result in counting some reads several times. For this function to work you need both an "exon" and a "transcript" field in your annotation object. To avoid this, one could create transcript specific synthetic exons, i.e. features that would be unique to a transcript. To offer this possibility, transcripts count can be summarized from "features", in which case the annotation object need to have both the "feature" and "transcript" fields defined.

## Arguments

<code>obj</code>	An object derived from class <a href="#">RNAseq</a> , can be a matrix for RPKM, see details
<code>force</code>	For <code>islandCount</code> , force RNAseq to redo <code>findIsland</code>
<code>from</code>	either "exons" or "features" can be used to summarize per transcript
<code>summarization</code>	Method use for summarize genes
<code>...</code>	See details

## Details

...for

- `geneCounts`: additional options for the [.geneModelSummarization](#)
- `islandCounts`: additional options for [findIslands](#)

## Value

A numeric vector containing count per exon, feature, gene or transcript.

## Author(s)

Nicolas Delhomme

**See Also**

[easyRNASeq](#) [annotation methods](#) [geneModelSummarization](#) [findIslands](#)

**Examples**

```
## Not run:
## create an RNAseq object
## summarizing 4 bam files by exons
rnaSeq <- easyRNASeq(system.file(
  "extdata",
  package="RnaSeqTutorial"),
  organism="Dmelanogaster",
  chr.sizes=as.list(seqlengths(Dmelanogaster)),
  readLength=36L,
  annotationMethod="rda",
  annotationFile=system.file(
    "data",
    "gAnnot.rda",
    package="RnaSeqTutorial"),
  format="bam",
  count="exons",
  pattern="[A,C,T,G]{6}\\bam$",
  outputFormat="RNAseq")
## summing up the exons by transcript
rnaSeq <- transcriptCounts(rnaSeq)

## End(Not run)
```

---

edgeR additional methods

*Extension for the edgeR package*

---

**Description**

This method extends the edgeR package by offering the functionality to plot the effect of the normalization factor.

**Arguments**

obj	An object of class <a href="#">DGEList</a>
cond1	A character string describing the first condition
cond2	A character string describing the second condition

**Value**

none

**Author(s)**

Nicolas Delhomme

**Examples**

```
## Not run:
## create the object
dgeList <- DGEList(counts,group)
## calculate the sie factors
dgeList <- calcNormFactors(dgeList)
## plot them
apply(combn(rownames(dgeList$samples),2),
2,
function(co,obj){plotNormalizationFactors(obj,co[1],co[2])},dgeList)

## End(Not run)
```

---

genomeIntervals additional methods

*Extension for the genomeIntervals package*

---

**Description**

**coerce** This method extends the genomeIntervals package by offering the functionality to coerce a [genomeIntervals](#) object into a [RangedData](#) object or [GRangesList](#) object.

**type** Another way to access the content of the gff type column.

**Arguments**

**from** An object of class [Genome\\_intervals](#)  
**x** An object of class [Genome\\_intervals](#)

**Value**

**coerce** A [RangedData](#) or [GRangesList](#) containing the result of the coercion.

**type** The content of the type column, usually a factor or a character vector

**Author(s)**

Nicolas Delhomme

**See Also**

[genomeIntervals](#) [object](#) [readGff3](#) [function](#)

**Examples**

```
## Not run:
annot<-readGff3(system.file("extdata","annot.gff",package="RnaSeqTutorial"))
gAnnot<-as(annot,"RangedData") type(annot)
## End(Not run)
```

---

GenomicRanges additional methods

*Extension of the GenomicRanges package*

---

## Description

Return the column name of a [GRanges](#) or [GRangesList](#) object.

## Arguments

obj                    An object of the [GRanges](#) or [GRangesList](#) class

## Details

It returns the actual column names of the elementMetadata slot of the [GRanges](#) or [GRangesList](#) object. The elementMetadata contains a [DataFrame](#) object used to store additional information provided by the user, such as exon ID in our case.

## Value

A vector of column names.

## Author(s)

Nicolas Delhomme

## See Also

[DataFrame](#) [GRanges](#) [GRangesList](#)

## Examples

```
## Not run:
## an example of a RangedData annotation
gAnnot <- RangedData(
  IRanges(
    start=c(10,30,100),
    end=c(21,53,123)),
  space=c("chr01","chr01","chr02"),
  strand=c("+","+","-"),
  transcript=c("trA1","trA2","trB"),
  gene=c("gA","gA","gB"),
  exon=c("e1","e2","e3"),
  universe = "Hs19"
)

## an example of a GRangesList annotation
grngs <- as(gAnnot,"GRanges")

## accessing the colnames
colnames(grngs)

## creating a GRangesList
```

```
grngsList<-split(grngs,seqnames(grngs))

## accessing the colnames
colnames(grngsList)

## End(Not run)
```

---

IRanges additional methods

*Extension of the IRanges package*

---

## Description

Return the ranges of the genomic annotation.

## Arguments

obj                    An object of the [RNAseq](#) class

## Details

It retrieves the object stored in the genomicAnnotation slot of the RNAseq object and apply the ranges function on it. The object retrieved can be of the [RangedData](#) or [GRangesList](#) class.

## Value

An [IRanges](#) object.

## Author(s)

Nicolas Delhomme

## Examples

```
## Not run:
library("RnaSeqTutorial")
obj <- new('RNAseq',
  organismName="Dmelanogaster",
  readLength=36L,
  chrSize=as.list(seqlengths(Dmelanogaster))
)

obj <- fetchAnnotation(obj,
  method="gff",
  filename=system.file(
    "extdata",
    "annot.gff",
    package="RnaSeqTutorial"))
ranges(obj)

## End(Not run)
```

---

parallel additional methods  
*parallel additional methods*

---

**Description**

Functions defined in the easyRNASeq package that enhance the parallel package.

**Arguments**

fun	the function to be applied in parallel
nnodes	the number of nodes to use
obj	the object which processing has to be parallelizes
...	additional arguments passed to the function fun

**Details**

The parallelize function ease the use of the parallel package. If the number of nodes provided by the user is 1, then a simple 'lapply' is used, otherwise a cluster object is created and the object dispatched for parallelization.

**Value**

the result of the [clusterApply](#) function.

**Author(s)**

Nicolas Delhomme

**See Also**

[clusterApply](#) [makePSOCKcluster](#) [stopCluster](#)

**Examples**

```
parallelize(list(a<-c(1,2),b<-c(2,1)),sum,nnodes=1)
```

---

print methods                      *Method to print a RNAseq object*

---

**Description**

Print information about a [RNAseq](#) object.

**Arguments**

rnaSeq	An object derived from class <a href="#">RNAseq</a>
verbose	A logical to have a verbose or not output. Default to FALSE
...	Additional arguments, currently unused.

**Value**

Print information about a [RNAseq](#) object.

**Author(s)**

Nicolas Delhomme

---

RNAseq class

*Class "RNAseq"*

---

**Description**

A class holding all the necessary information and annotation to summarize counts (number of reads) per features (i.e. exons or transcripts or genes) for RNA-Seq experiments.

**Objects from the Class**

Objects can be created by calls of the form `new("RNAseq", ...)`.

**Author(s)**

Nicolas Delhomme

**See Also**

- [RangedData](#)
- [RleList](#)
- [easyRNASeq](#) function
- [RNAseq](#) accessors
- [easyRNASeq](#) annotation methods
- [easyRNASeq](#) correction methods
- [easyRNASeq](#) coverage methods
- [easyRNASeq](#) summarization methods
- [print](#)

**Examples**

```
showClass("RNAseq")
```

---

 ShortRead additional methods

*Methods extending the ShortRead package functionalities*


---

## Description

These are functions extending the ShortRead packages capabilities:

## Arguments

.name	An internal string describing the filter
obj	An object derived from class <a href="#">AlignedRead</a>
barcodes	A character vector describing the multiplex (i.e. barcode) sequences used in the experiment.
barcodes.qty	An integer describing the number of barcodes
barcode.length	An integer describing the barcode length in bp
edition.dist	The maximal edition distance (i.e. the number of changes to apply), to accept an incorrectly sequenced barcode.
index.only	simply return the index and not the barcode themselves.
show.barcode	An integer specifying how many barcodes should be displayed in the final output.
type	The type of barcode used. independent represents barcodes generated by the illumina protocol; i.e. a separate additional sequencing step performed once the first mate has been sequenced. within represents barcodes that are part of the sequenced reads as established by Lefrancois P et al., BMC Genomics, 2009
...	additional graphic parameters

## Details

- `barcodePlot` Creates a plot showing the barcode distribution of a multiplexed sequencing library.
- `chastityFilter` Creates a [SRFilter](#) instance that filters SolexaExport read according to the chastity filtering value.
- `demultiplex` Split a single [AlignedRead](#) object into a list of [AlignedRead](#) objects according to the barcodes provided by the user.
- `naPositionFilter` Creates a [SRFilter](#) instance that filters SolexaExport read having an NA position.

When demultiplexing, the function if provided with just the [AlignedRead](#) will try to find out how many barcodes were used and what they are. This is unwise to do as many barcodes will get wrongly sequenced and not always the most frequent ones are the one you used! It's therefore strongly advised to specify the barcodes' sequences that were used.

## Value

- `barcodePlot` returns invisibly the barcode frequencies.
- `chastityFilter` returns a [SRFilter](#) instance.
- `demultiplex` returns a list of [AlignedRead](#) objects.
- `naPositionFilter` returns a [SRFilter](#) instance.

**Author(s)**

Nicolas Delhomme

**See Also**[SRFilter](#) [AlignedRead](#)**Examples**

```
## Not run:
## the barcode
barcodes=c("ACACTG","ACTAGC","ATGGCT","TTGCCA")

## the multiplexed data
alns <- readAligned(
  system.file(
    "extdata",
    package="RnaSeqTutorial"),
  pattern="multiplex_export",
  filter=compose(
    chastityFilter(),
    nFilter(2),
    chromosomeFilter(regex="chr")),
  type="SolexaExport",
  withAll=TRUE)

## barcode plot
barcodePlot(alns,
  barcodes=barcodes,
  type="within",
  barcode.length=6,
  show.barcode=20,
  main="All samples",
  xlim=c(0,0.5))

## demultiplexing
dem.alns <- demultiplex(alns,
  barcodes=barcodes,
  edition.dist=2,
  barcodes.qty=4,
  type="within")

## plotting again
par(mfrow=c(2,2))
barcode.frequencies <- lapply(
  names(dem.alns$barcodes),
  function(barcode,alns){
    barcodePlot(
      alns$barcodes[[barcode]],
      barcodes=barcode,
      type="within",barcode.length=6,
      show.barcode=20,
      main=paste(
        "Expected barcode:",
        barcode))
  },dem.alns)
```

```
## End(Not run)
```

---

show methods	<i>Display the content of a RNAseq object</i>
--------------	---

---

**Description**

Display the content of a [RNAseq](#) object.

**Methods**

**list("signature(object = \"RNAseq\")**) Display the values of the different slots of the [RNAseq](#) object.

# Index

- \*Topic **classes**
  - RNAseq class, [22](#)
- \*Topic **connection**
  - easyRNASeq annotation methods, [9](#)
  - easyRNASeq island methods, [13](#)
- \*Topic **data**
  - easyRNASeq annotation methods, [9](#)
  - easyRNASeq island methods, [13](#)
- \*Topic **manip**
  - easyRNASeq accessors, [8](#)
- \*Topic **methods**
  - count, [2](#)
  - DESeq additional methods, [3](#)
  - DESeq and edgeR common methods, [4](#)
  - easyRNASeq, [5](#)
  - easyRNASeq annotation methods, [9](#)
  - easyRNASeq correction methods, [10](#)
  - easyRNASeq coverage methods, [12](#)
  - easyRNASeq island methods, [13](#)
  - easyRNASeq summarization methods, [16](#)
  - edgeR additional methods, [17](#)
  - GenomicRanges additional methods, [19](#)
  - IRanges additional methods, [20](#)
  - parallel additional methods, [21](#)
  - print methods, [21](#)
  - ShortRead additional methods, [23](#)
  - show methods, [25](#)
- \*Topic **package**
  - easyRNASeq package, [14](#)
  - .geneModelSummarization, [16](#), [17](#)
- accessors (easyRNASeq accessors), [8](#)
- AlignedRead, [23](#), [24](#)
- barcodePlot (ShortRead additional methods), [23](#)
- barcodePlot,AlignedRead-method (ShortRead additional methods), [23](#)
- barcodePlot,DNAStringSet-method (ShortRead additional methods), [23](#)
- barcodePlot,ShortReadQ-method (ShortRead additional methods), [23](#)
- biomaRt, [15](#)
- Biostrings, [15](#)
- BSgenome, [15](#)
- chastityFilter (ShortRead additional methods), [23](#)
- chastityFilter,SRFilter-method (ShortRead additional methods), [23](#)
- chrSize (easyRNASeq accessors), [8](#)
- chrSize,RNAseq-method (easyRNASeq accessors), [8](#)
- chrSize<- (easyRNASeq accessors), [8](#)
- chrSize<-,RNAseq,integer-method (easyRNASeq accessors), [8](#)
- chrSize<-,RNAseq,list-method (easyRNASeq accessors), [8](#)
- clusterApply, [21](#)
- coerce,Genome\_intervals,GRangesList-method (genomeIntervals additional methods), [18](#)
- coerce,Genome\_intervals,RangedData-method (genomeIntervals additional methods), [18](#)
- colnames (GenomicRanges additional methods), [19](#)
- colnames,GenomicRanges-method (GenomicRanges additional methods), [19](#)
- colnames,GRangesList-method (GenomicRanges additional methods), [19](#)
- count, [2](#)
- count,character-method (count), [2](#)
- CountDataSet, [3](#), [4](#)
- DataFrame, [19](#)
- demultiplex (ShortRead additional methods), [23](#)
- demultiplex,AlignedRead-method (ShortRead additional methods), [23](#)

- demultiplex,DNAStringSet-method  
(ShortRead additional methods),  
23
- demultiplex,ShortReadQ-method  
(ShortRead additional methods),  
23
- DESeq, 14, 15
- DESeq additional methods, 3
- DESeq and edgeR common methods, 4
- DESeq methods, 15
- DESeq:newCountDataset, 2, 3, 7
- DGEList, 4, 17
- easyRNASeq, 5, 15
- easyRNASeq accessors, 8
- easyRNASeq annotation methods, 9, 15
- easyRNASeq correction methods, 10, 15
- easyRNASeq coverage methods, 12, 15
- easyRNASeq island methods, 13
- easyRNASeq package, 14
- easyRNASeq package-package  
(easyRNASeq package), 14
- easyRNASeq summarization methods, 15,  
16
- easyRNASeq,character-method  
(easyRNASeq), 5
- easyRNASeq,RNAseq-method (RNAseq  
class), 22
- easyRNASeq-package (easyRNASeq  
package), 14
- easyRNASeq:knownOrganisms, 3, 6, 7
- edgeR, 4, 14, 15
- edgeR additional methods, 17
- edgeR methods, 15
- edgeR:DGEList, 2, 3, 7
- exonCounts (easyRNASeq summarization  
methods), 16
- exonCounts,RNAseq-method (RNAseq  
class), 22
- featureCounts (easyRNASeq  
summarization methods), 16
- featureCounts,RNAseq-method (RNAseq  
class), 22
- fetchAnnotation (easyRNASeq annotation  
methods), 9
- fetchAnnotation,RNAseq-method (RNAseq  
class), 22
- fetchCoverage (easyRNASeq coverage  
methods), 12
- fetchCoverage,RNAseq-method (RNAseq  
class), 22
- fileName (easyRNASeq accessors), 8
- fileName,RNAseq-method (RNAseq class),  
22
- fileName<- (easyRNASeq accessors), 8
- fileName<-,RNAseq-method (RNAseq  
class), 22
- findIslands, 16, 17
- findIslands (easyRNASeq island methods),  
13
- findIslands,RNAseq-method (RNAseq  
class), 22
- geneCounts (easyRNASeq summarization  
methods), 16
- geneCounts,RNAseq-method (RNAseq  
class), 22
- geneModel (easyRNASeq accessors), 8
- geneModel,RNAseq-method (RNAseq  
class), 22
- geneModel<- (easyRNASeq accessors), 8
- geneModel<- ,RNAseq-method (RNAseq  
class), 22
- Genome\_intervals, 18
- genomeIntervals, 15
- genomeIntervals additional methods, 18
- genomicAnnotation (easyRNASeq  
accessors), 8
- genomicAnnotation,RNAseq-method  
(RNAseq class), 22
- genomicAnnotation<- (easyRNASeq  
accessors), 8
- genomicAnnotation<- ,RNAseq-method  
(RNAseq class), 22
- GenomicFeatures, 15
- GenomicRanges, 15
- GenomicRanges additional methods, 19
- getBM, 7, 9
- GRanges, 19
- GRangesList, 5, 18–20
- hist, 13
- IRanges, 15, 20
- IRanges additional methods, 20
- islandCounts (easyRNASeq summarization  
methods), 16
- islandCounts,RNAseq-method (RNAseq  
class), 22
- knownOrganisms (easyRNASeq annotation  
methods), 9
- knownOrganisms,missing-method  
(easyRNASeq annotation  
methods), 9

- librarySize (easyRNASeq accessors), 8
- librarySize,RNAseq-method (RNAseq class), 22
- librarySize<- (easyRNASeq accessors), 8
- librarySize<-,RNAseq-method (RNAseq class), 22
- list.files, 7
- listDatasets, 9
  
- makePSOCKcluster, 21
- multivariateConditions (DESeq additional methods), 3
- multivariateConditions,CountDataSet-method (DESeq additional methods), 3
  
- naPositionFilter (ShortRead additional methods), 23
- naPositionFilter,SRFilter-method (ShortRead additional methods), 23
  
- organismName (easyRNASeq accessors), 8
- organismName,RNAseq-method (RNAseq class), 22
- organismName<- (easyRNASeq accessors), 8
- organismName<-,RNAseq-method (RNAseq class), 22
  
- parallel, 15
- parallel additional methods, 21
- parallelize (parallel additional methods), 21
- parallelize,GRangesList,function-method (parallel additional methods), 21
- parallelize,list,function-method (parallel additional methods), 21
- parallelize,vector,function-method (parallel additional methods), 21
- plotDispersionEstimates (DESeq and edgeR common methods), 4
- plotDispersionEstimates,CountDataSet-method (DESeq and edgeR common methods), 4
- plotDispersionEstimates,DGEList-method (DESeq and edgeR common methods), 4
- plotNormalizationFactors (edgeR additional methods), 17
- plotNormalizationFactors,DGEList,character,character-method (edgeR additional methods), 17
- print, 22
  
- print (print methods), 21
- print methods, 21
- print,RNAseq-method (RNAseq class), 22
  
- RangedData, 5, 10, 18, 20, 22
- ranges (IRanges additional methods), 20
- ranges,RNAseq-method (IRanges additional methods), 20
- readCounts, 11
- readCounts (easyRNASeq accessors), 8
- readCounts,RNAseq-method (RNAseq class), 22
- readCounts<- (easyRNASeq accessors), 8
- readCounts<-,RNAseq-method (RNAseq class), 22
- readCoverage (easyRNASeq accessors), 8
- readCoverage,RNAseq-method (RNAseq class), 22
- readCoverage<- (easyRNASeq accessors), 8
- readCoverage<-,RNAseq-method (RNAseq class), 22
- readGff3, 9
- readGffGtf, 7, 9
- readIslands (easyRNASeq accessors), 8
- readIslands,RNAseq-method (RNAseq class), 22
- readIslands<- (easyRNASeq accessors), 8
- readIslands<-,RNAseq-method (RNAseq class), 22
- readLength (easyRNASeq accessors), 8
- readLength,RNAseq-method (RNAseq class), 22
- readLength<- (easyRNASeq accessors), 8
- readLength<-,RNAseq-method (RNAseq class), 22
  
- Rle, 13
- RleList, 22
- RNAseq, 2, 3, 7, 9, 10, 12, 15, 16, 20–22, 25
- RNAseq (RNAseq class), 22
- RNAseq class, 22
- RNAseq-class (RNAseq class), 22
- RPKM (easyRNASeq correction methods), 10
- RPKM,matrix,ANY,vector,vector-method (easyRNASeq correction methods), 10
- RPKM,RNAseq,ANY,ANY,ANY-method (easyRNASeq correction methods), 10
- RPKM,RNAseq-method (RNAseq class), 22
- Rsamtools, 15
  
- ShortRead, 15

ShortRead additional methods, [23](#)  
ShortRead methods, [15](#)  
ShortRead:readAligned, [3](#), [7](#), [13](#)  
show methods, [25](#)  
show,RNAseq-method (RNAseq class), [22](#)  
SRFilter, [23](#), [24](#)  
stopCluster, [21](#)  
SummarizedExperiment, [2](#), [3](#), [6](#), [7](#), [15](#)

transcriptCounts (easyRNASeq  
    summarization methods), [16](#)  
transcriptCounts,RNAseq-method  
    (RNAseq class), [22](#)  
type,Genome\_intervals-method  
    (genomeIntervals additional  
    methods), [18](#)