

Package ‘Rqc’

May 11, 2024

Type Package

Title Quality Control Tool for High-Throughput Sequencing Data

Version 1.38.0

Author Welliton Souza, Benilton Carvalho <beniltoncarvalho@gmail.com>

Maintainer Welliton Souza <well309@gmail.com>

Description Rqc is an optimised tool designed for quality control and assessment of high-throughput sequencing data. It performs parallel processing of entire files and produces a report which contains a set of high-resolution graphics.

License GPL (>= 2)

Depends BiocParallel, ShortRead, ggplot2

Imports BiocGenerics (>= 0.25.1), Biostrings, IRanges, methods, S4Vectors, knitr (>= 1.7), BiocStyle, plyr, markdown, grid, reshape2, Rcpp (>= 0.11.6), biovizBase, shiny, Rsamtools, GenomicAlignments, GenomicFiles

LinkingTo Rcpp

Suggests rmarkdown, testthat

VignetteBuilder knitr

biocViews Sequencing, QualityControl, DataImport

URL <https://github.com/labbc/Rqc>

BugReports <https://github.com/labbc/Rqc/issues>

RoxygenNote 7.1.1

Encoding UTF-8

git_url <https://git.bioconductor.org/packages/Rqc>

git_branch RELEASE_3_19

git_last_commit 68a2092

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-10

Contents

Rqc-package	2
checkpoint	3
detectFileFormat	4
fromRRDNA	4
matdist	5
rqc	6
rqcCycleAverageQualityCalc	8
rqcCycleAverageQualityPcaCalc	9
rqcCycleBaseCallsCalc	10
rqcCycleGCCalc	11
rqcCycleQualityBoxCalc	12
rqcCycleQualityCalc	13
rqcFileHeatmap	14
rqcGroupCycleAverageQualityCalc	15
rqcQA	16
rqcReadFrequencyCalc	18
rqcReadQualityBoxCalc	19
rqcReadQualityCalc	20
rqcReadWidthCalc	21
rqcReport	22
RqcResultSet-class	23
rqcShinyReport	25
stats4trim	26
subsetByGroup	27
subsetByPair	27
toRRDNA	28
Index	30

Rqc-package

Quality Control Tool for High-Throughput Sequencing Data

Description

Rqc is an optimized tool designed for quality assessment of high-throughput sequencing data. It performs parallel processing of entire files and produces a report, which contains a set of high-resolution images that can be directly used on publications.

Author(s)

Welliton Souza, Benilton Carvalho

Maintainer: Welliton Souza <well309@gmail.com>

Examples

```
options(device.ask.default = FALSE)
folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
rqc(folder, ".fastq.gz", pair=c(1,1), workers=1)
```

checkpoint

Save time storing longer analysis step on disk

Description

This utility function can be used to save time on task that takes long time to complete. A Rda file are written on disk containing only objects setted to keep. If checkpoint function find related Rda file then this Rda will be loaded.

Usage

```
checkpoint(
  label,
  CODE,
  path = ".",
  overwrite = FALSE,
  verbose = FALSE,
  keep = NULL
)
```

Arguments

label	name of this code, will create a Rda file with the same name.
CODE	R code.
path	directory to write/load Rda file.
overwrite	Rerun CODE and replace Rda file.
verbose	argument passed to load function
keep	vector of object/variable name to keep. NULL means error.

Value

Nothing.

Note

Experimental function.

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
```

detectFileFormat	<i>Detect file format</i>
------------------	---------------------------

Description

Detect file format

Usage

```
detectFileFormat(file)
```

Arguments

file	file name
------	-----------

Value

FastqFile or BamFiles objects

Examples

```
folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
files <- list.files(full.names=TRUE, path=folder)
input <- lapply(files, detectFileFormat)
sapply(input, class)
```

fromRRDNA	<i>Revert codified DNA sequences to original DNA sequences.</i>
-----------	---

Description

This function receives a vector of strings containing codified DNA and returns a vector of string containing original DNA sequences.

Usage

```
fromRRDNA(rrdnas)
```

Arguments

rrdnas Vector of codified DNA (character vector).

Value

Vector of original DNA sequences (character vector).

Note

This function is used internally to restore original DNA sequences stored in RqcResultSet objects (per file top reads).

Author(s)

Welliton Souza

See Also

[perFileTopReads](#)

Examples

```
dna <- "ATCG"  
dna.converted <- toRRDNA(dna)  
dna.reverted <- fromRRDNA(dna.converted)  
all.equal(dna, dna.reverted)
```

matdist

Distance matrix of the similarity between the DNA sequences.

Description

This function receives a vector of strings representing codified DNA sequences and returns a integer matrix representing the similarities between all sequences from input vectors.

Usage

```
matdist(rrdnas)
```

Arguments

rrdnas Vector of codified DNA sequences (character vector).

Value

Matrix $n \times n$, where n is the length of the largest original DNA sequence.

Note

This function is used internally to compute data for `rqcFileHeatmap` function.

Author(s)

Welliton Souza

See Also

[rqcFileHeatmap](#)

Examples

```
dna1 <- toRRDNA("atcgn")
dna2 <- toRRDNA("atcga")
matdist(c(dna1, dna2))
```

rqc

Main Rqc function

Description

Rqc is an optimized tool designed for quality assessment of high-throughput sequencing data. It performs parallel processing of entire files and produces an HTML report, which contains a set of high-resolution images that can be directly used on publications.

Usage

```
rqc(
  path = ".",
  pattern,
  sample = TRUE,
  n = 1e+06,
  group = NULL,
  top = 10,
  pair = NULL,
  outdir = tempdir(),
  file = "rqc_report",
  openBrowser = TRUE,
  workers = multicoreWorkers()
)
```

Arguments

path	directory path that contains input files.
pattern	a regex expression that matches to input file names
sample	it reads a random sample from files if this parameter is TRUE.
n	number of sequences to read from each input file. This represents sample size if 'sample' parameter is TRUE, if not represents the chunk size to read on each iteration. By default, it reads a sample of one million sequences from each input file.
group	group name for each input file.
top	number of top over-represented reads. Default is 10 reads.
pair	combination of files for paired-end reads. By default, all input files are treated as single-end. For paired-end, please define a vector of numbers where two index with the same value represent a pair. Examples, single-end c(1,2,3,4) and paired-end c(1,1,2,2).
outdir	output directory path. Is created a temporary directory by default.
file	output file name.
openBrowser	if TRUE opens report file on default Internet Browser.
workers	Number of parallel workers. Set 1 to serial. Default value from multicoreWorkers .

Value

A invisible named list of RqcResultSet objects, each one represents a file.

Author(s)

Welliton Souza

See Also

[rqcQA](#)

Examples

```
options(device.ask.default = FALSE)
folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
rqc(folder, ".fastq.gz", pair=c(1,1), workers=1, openBrowser=FALSE)
```

`rqcCycleAverageQualityCalc`*Per cycle average quality by files*

Description

This function plots line graph of per cycle average quality.

Usage

```
rqcCycleAverageQualityCalc(rqcResultSet)
```

```
rqcCycleAverageQualityPlot(rqcResultSet)
```

Arguments

`rqcResultSet` list of `RqcResultSet` objects created by `rqc` and `rqcQA` functions.

Value

ggplot2 object

Functions

- `rqcCycleAverageQualityCalc`: calculates necessary statistics

Author(s)

Welliton Souza

See Also

[rqcGroupCycleAverageQualityPlot](#) plots cycle-specific quality by groups

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)  
}, keep="rqcResultSet")  
rqcCycleAverageQualityPlot(rqcResultSet)
```

`rqcCycleAverageQualityPcaCalc`*Biplot of PCA of per cycle read average quality*

Description

This function creates a Biplot of PCA of per cycle read average quality

Usage

```
rqcCycleAverageQualityPcaCalc(rqcResultSet)
```

```
rqcCycleAverageQualityPcaPlot(rqcResultSet)
```

Arguments

`rqcResultSet` list of `RqcResultSet` objects created by `rqc` and `rqcQA` functions.

Value

Plot object from `ggplot` function.

Functions

- `rqcCycleAverageQualityPcaCalc`: calculates necessary statistics

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)  
}, keep="rqcResultSet")  
rqcCycleAverageQualityPcaPlot(rqcResultSet)
```

`rqcCycleBaseCallsCalc` *Per cycle base calls plot*

Description

Creates a bar graph of per cycle base calls.

Usage

```
rqcCycleBaseCallsCalc(rqcResultSet)

rqcCycleBaseCallsLinePlot(rqcResultSet)

rqcCycleBaseCallsPlot(rqcResultSet)
```

Arguments

`rqcResultSet` list of `RqcResultSet` objects created by `rqc` and `rqcQA` functions.

Value

Plot object from `ggplot` function.

Functions

- `rqcCycleBaseCallsCalc`: calculates necessary statistics
- `rqcCycleBaseCallsLinePlot`: creates a line graph

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
rqcCycleBaseCallsPlot(rqcResultSet)
```

rqcCycleGCCalc	<i>Per cycle percentual GC plot</i>
----------------	-------------------------------------

Description

Creates a line graph of per cycle percentual GC.

Usage

```
rqcCycleGCCalc(rqcResultSet)
```

```
rqcCycleGCPlot(rqcResultSet)
```

Arguments

`rqcResultSet` list of `RqcResultSet` objects created by `rqc` and `rqcQA` functions.

Value

Plot object from `ggplot` function.

Functions

- `rqcCycleGCCalc`: calculates necessary statistics

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
rqcCycleGCPlot(rqcResultSet)
```

rqcCycleQualityBoxCalc

Per cycle quality box plot

Description

Plots per cycle quality box plot.

Usage

```
rqcCycleQualityBoxCalc(rqcResultSet)
```

```
rqcCycleQualityBoxPlot(rqcResultSet)
```

Arguments

rqcResultSet list of RqcResultSet objects created by [rqc](#) and [rqcQA](#) functions.

Value

Plot object from [ggplot](#) function.

Functions

- [rqcCycleQualityBoxCalc](#): calculates necessary statistics

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)  
}, keep="rqcResultSet")  
rqcCycleQualityBoxPlot(rqcResultSet)
```

`rqcCycleQualityCalc` *Per cycle quality plot*

Description

Creates a graph of per cycle quality.

Usage

```
rqcCycleQualityCalc(rqcResultSet)
```

```
rqcCycleQualityPlot(rqcResultSet)
```

Arguments

`rqcResultSet` list of `RqcResultSet` objects created by `rqc` and `rqcQA` functions.

Value

Plot object from `ggplot` function.

Functions

- `rqcCycleQualityCalc`: calculates necessary statistics

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, workers=1)  
}, keep="rqcResultSet")  
rqcCycleQualityPlot(rqcResultSet)
```

rqcFileHeatmap	<i>Heatmap of distance matrix of top over-represented reads</i>
----------------	---

Description

This function plots a heatmap of distance matrix of top over-represented reads. This function does not work with list of RqcResultSet objects, only with one RqcResultSet object.

Usage

```
rqcFileHeatmap(  
  rqcResultSet,  
  dist.method = "euclidean",  
  hclust.method = "ward.D"  
)
```

Arguments

`rqcResultSet` RqcResultSet object created by `rqc` and `rqcQA` functions.
`dist.method` the distance measure to be used by `dist` function.
`hclust.method` the agglomeration method to be used by `hclust` function.

Value

Plot object from `ggplot` function.

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)  
}, keep="rqcResultSet")  
rqcFileHeatmap(rqcResultSet[[1]])
```

`rqcGroupCycleAverageQualityCalc`*Per group average quality across cycles*

Description

This function plots cycle-specific quality by groups

Usage

```
rqcGroupCycleAverageQualityCalc(rqcResultSet)
```

```
rqcGroupCycleAverageQualityPlot(rqcResultSet)
```

Arguments

`rqcResultSet` list of `RqcResultSet` objects created by `rqc` and `rqcQA` functions.

Value

ggplot2 object

Functions

- `rqcGroupCycleAverageQualityCalc`: calculates necessary statistics

Author(s)

Welliton Souza

See Also

[rqcCycleAverageQualityPlot](#) plots cycle-specific quality by files

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
rqcGroupCycleAverageQualityPlot(rqcResultSet)
```

rqcQA

Quality Assessment Rqc function

Description

Process a set of files and returns a list of quality control data. Files must be FASTQ format, compressed or not.

Usage

```

rqcQA(
  x,
  sample = TRUE,
  n = 1e+06,
  group = rep("None", length(x)),
  top = 10,
  pair = seq_along(x),
  ...
)

## S4 method for signature 'list'
rqcQA(x, sample, n, group, top, pair, workers = multicoreWorkers())

## S4 method for signature 'character'
rqcQA(
  x,
  sample = TRUE,
  n = 1e+06,
  group = rep("None", length(x)),
  top = 10,
  pair = seq_along(x),
  workers = multicoreWorkers()
)

## S4 method for signature 'BamFile'
rqcQA(x, sample, n, group, top, pair)

## S4 method for signature 'FastqFile'
rqcQA(x, sample, n, group, top, pair)

```

Arguments

x	input file(s)
sample	It reads a random sample from files if this parameter is TRUE.
n	Number of sequences to read from each input file. This represents sample size if 'sample' parameter is TRUE, if not represents the chunk size to read on each iteration. Default is read a sample of one million sequences from each input file.

group	group name for each input file.
top	number of top over-represented reads. Default is 10 reads.
pair	combination of files for paired-end reads. By default, all input files are treated as single-end. For paired-end, please define a vector of numbers where two index with the same value represent a pair. Examples, single-end c(1,2,3,4) and paired-end c(1,1,2,2).
...	other parameters
workers	number of parallel workers

Details

Input files are read using `FastStreamer` and `FastSampler` classes of `ShortRead` package. Process multiple files in parallel using `bplapply` function of `BiocParallel` package.

Value

A named list of `RqcResultSet` objects, each one represents a file.

Methods (by class)

- `list`: process a list of `FastqFile` and `BamFile` objects.
- `character`: automatically detects file format (using `detectFileFormat` function) of input files then process.
- `BamFile`: process only one BAM file.
- `FastqFile`: process only one FASTQ file.

Author(s)

Welliton Souza

See Also

[rqc](#)

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
rqcReadQualityPlot(rqcResultSet)
```

rqcReadFrequencyCalc *Read frequency plot*

Description

This function creates a bar graph of read frequency (in percentage).

Usage

```
rqcReadFrequencyCalc(rqcResultSet)
```

```
rqcReadFrequencyPlot(rqcResultSet)
```

Arguments

`rqcResultSet` list of `RqcResultSet` objects created by `rqc` and `rqcQA` functions.

Value

Plot object from `ggplot` function.

Functions

- `rqcReadFrequencyCalc`: calculates necessary statistics

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)  
}, keep="rqcResultSet")  
rqcReadFrequencyPlot(rqcResultSet)
```

`rqcReadQualityBoxCalc` *Per read mean quality box plot*

Description

This function creates a graphic chart with box plots describing per read mean quality distribution for each input file

Usage

```
rqcReadQualityBoxCalc(rqcResultSet)
```

```
rqcReadQualityBoxPlot(rqcResultSet)
```

Arguments

`rqcResultSet` list of `RqcResultSet` objects created by `rqc` and `rqcQA` functions.

Value

Plot object from `ggplot` function.

Functions

- `rqcReadQualityBoxCalc`: calculates necessary statistics

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)  
}, keep="rqcResultSet")  
rqcReadQualityBoxPlot(rqcResultSet)
```

rqcReadQualityCalc *Per read quality plot*

Description

Plots the quality of all the files by read.

Usage

```
rqcReadQualityCalc(rqcResultSet)
```

```
rqcReadQualityPlot(rqcResultSet)
```

Arguments

rqcResultSet list of RqcResultSet objects created by [rqc](#) and [rqcQA](#) functions.

Value

Plot object from [ggplot](#) function.

Functions

- [rqcReadQualityCalc](#): calculates necessary statistics

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
rqcReadQualityPlot(rqcResultSet)
```

rqcReadWidthCalc	<i>Per read width plot</i>
------------------	----------------------------

Description

Creates bar graph of per read width from all elements of input list.

Usage

```
rqcReadWidthCalc(rqcResultSet)
```

```
rqcReadWidthPlot(rqcResultSet)
```

Arguments

rqcResultSet list of RqcResultSet objects created by [rqc](#) and [rqcQA](#) functions.

Value

Plot object from [ggplot](#) function.

Functions

- rqcReadWidthCalc: calculates necessary statistics

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)  
}, keep="rqcResultSet")  
rqcReadWidthPlot(rqcResultSet)
```

`rqcReport`*Quality Control HTML Report*

Description

Generates an HTML report file.

Usage

```
rqcReport(  
  rqcResultSet,  
  outdir = tempdir(),  
  file = "rqc_report",  
  keepMD = FALSE,  
  templateFile = system.file("templates", package = "Rqc", "rqc_report.Rmd")  
)
```

Arguments

<code>rqcResultSet</code>	list of <code>RqcResultSet</code> objects created by <code>rqc</code> and <code>rqcQA</code> functions.
<code>outdir</code>	output directory path. It is created a temporary directory by default.
<code>file</code>	output file name.
<code>keepMD</code>	If true <code>Rqc</code> does not delete markdown file. <code>knit</code> function takes RMarkdown template file (within package) and generates a temporary Markdown file. Next <code>markdownToHTML</code> function takes this markdown file and creates final HTML file.
<code>templateFile</code>	Path of Rmarkdown file as <code>Rqc</code> web report template.

Details

Also creates a directory called "figure" in `outdir` path.

Value

Report file path.

Author(s)

Welliton Souza

See Also

[rqc](#)
[rqcQA](#)

Examples

```

options(device.ask.default = FALSE)
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
reportFile <- rqcReport(rqcResultSet)
browseURL(reportFile)

```

RqcResultSet-class *Class RqcResultSet*

Description

Class RqcResultSet
 Frequency distribution of cycle-specific base call
 Frequency distribution of cycle-specific quality
 File information
 Top over-represented sequencing reads
 Read frequency table
 Frequency distribution of per read mean quality
 Frequency distribution of read width

Usage

```

perCycleBasecall(x)

## S4 method for signature 'RqcResultSet'
perCycleBasecall(x)

## S4 method for signature 'list'
perCycleBasecall(x)

perCycleQuality(x)

## S4 method for signature 'RqcResultSet'
perCycleQuality(x)

## S4 method for signature 'list'
perCycleQuality(x)

perFileInformation(x)

```

```
## S4 method for signature 'RqcResultSet'  
perFileInformation(x)  
  
## S4 method for signature 'list'  
perFileInformation(x)  
  
perFileTopReads(x)  
  
## S4 method for signature 'RqcResultSet'  
perFileTopReads(x)  
  
## S4 method for signature 'list'  
perFileTopReads(x)  
  
perReadFrequency(x)  
  
## S4 method for signature 'RqcResultSet'  
perReadFrequency(x)  
  
## S4 method for signature 'list'  
perReadFrequency(x)  
  
perReadQuality(x)  
  
## S4 method for signature 'RqcResultSet'  
perReadQuality(x)  
  
## S4 method for signature 'list'  
perReadQuality(x)  
  
perReadWidth(x)  
  
## S4 method for signature 'RqcResultSet'  
perReadWidth(x)  
  
## S4 method for signature 'list'  
perReadWidth(x)
```

Arguments

x RqcResultSet object or list of RqcResultSet objects

Value

data frame
data frame
data frame
data frame

data frame

data frame

data frame

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
head(perCycleBasecall(rqcResultSet))
head(perCycleQuality(rqcResultSet))
head(perReadFrequency(rqcResultSet))
head(perReadQuality(rqcResultSet))
head(perReadWidth(rqcResultSet))
perFileInformation(rqcResultSet)
perFileTopReads(rqcResultSet)
```

rqcShinyReport

Interactive Quality Control Report

Description

This function runs a Shiny web application of interactive Rqc report. This is useful for large amount of files and sample groups.

Usage

```
rqcShinyReport(rqcResultSet)
```

Arguments

rqcResultSet list of [RqcResultSet-class](#) objects

Value

function

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
# rqcShinyReport(rqcResultSet)
```

stats4trim

Minimum read mean quality and maximum percentage loss of reads estimations for trimming step.

Description

This function estimates how many reads would be lost if the sequences are filtered by a minimum read mean quality value. Also this function estimates what is the minimum read mean quality value for filtering and lose max percentage defined.

Usage

```
stats4trim(rqcResultSet, qmin, pmax)
```

Arguments

rqcResultSet list of RqcResultSet objects created by `rqc` and `rqcQA` functions.
qmin Minimum read mean quality value (between 0 and 41).
pmax Maximum percentage of reads permitted been lost during trimming step.

Value

A data frame containg estimated minimum quality and maximum percentage for each input file.

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
  files <- list.files(full.names=TRUE, path=folder)
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)
}, keep="rqcResultSet")
stats4trim(rqcResultSet, qmin=20)
stats4trim(rqcResultSet, pmax=10)
```

subsetByGroup	<i>Subset RqcResultSet object by group name.</i>
---------------	--

Description

This function subsets RqcResultSet object function by group name.

Usage

```
subsetByGroup(rqcResultSet, group)
```

Arguments

rqcResultSet	list of RqcResultSet objects created by rqc and rqcQA functions.
group	Name of the group to subset

Value

list of RqcResultSet objects from only one group.

Author(s)

Welliton Souza

Examples

```
folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")
files <- list.files(full.names=TRUE, path=folder)
rqcResultSet <- rqcQA(files, workers=1, group=c("a", "b"))
perFileInformation(subsetByGroup(rqcResultSet, "a"))
```

subsetByPair	<i>Subset RqcResultSet object by pair files.</i>
--------------	--

Description

This function subsets RqcResultSet object function by pair files.

Usage

```
subsetByPair(rqcResultSet, pair)
```

Arguments

rqcResultSet	list of RqcResultSet objects created by rqc and rqcQA functions.
pair	index of the pair

Value

list of RqcResultSet objects from only one pair.

Author(s)

Welliton Souza

Examples

```
checkpoint("Rqc", path=system.file(package="Rqc", "extdata"), {  
  folder <- system.file(package="ShortRead", "extdata/E-MTAB-1147")  
  files <- list.files(full.names=TRUE, path=folder)  
  rqcResultSet <- rqcQA(files, pair=c(1,1), workers=1)  
}, keep="rqcResultSet")  
perFileInformation(subsetByPair(rqcResultSet, 1))
```

toRRDNA

Title: Convert DNA sequences to Reduced Representation format

Description

This function receives a vector of strings (character vector) containing DNA sequences and returns a vector of strings containing codified DNA.

Usage

```
toRRDNA(dnas)
```

Arguments

dnas Vector of DNA sequences (character vector).

Value

Vector of DNA converted to reduced representation format (character vector).

Note

This function is used internally to compute top over-represented reads and to store in RqcResultSet objects (per file top reads).

Author(s)

Welliton Souza

See Also

[perFileTopReads](#)

Examples

```
dna <- "ATCGNATCGTA"  
dna.converted <- toRRDNA(dna)  
nchar(dna)  
nchar(dna.converted)
```

Index

* **graphics**

- [rqc](#), [6](#)
- [rqcCycleAverageQualityCalc](#), [8](#)
- [rqcCycleAverageQualityPcaCalc](#), [9](#)
- [rqcCycleBaseCallsCalc](#), [10](#)
- [rqcCycleGCCalc](#), [11](#)
- [rqcCycleQualityBoxCalc](#), [12](#)
- [rqcCycleQualityCalc](#), [13](#)
- [rqcFileHeatmap](#), [14](#)
- [rqcGroupCycleAverageQualityCalc](#),
[15](#)
- [rqcReadFrequencyCalc](#), [18](#)
- [rqcReadQualityBoxCalc](#), [19](#)
- [rqcReadQualityCalc](#), [20](#)
- [rqcReadWidthCalc](#), [21](#)

* **package**

- [Rqc-package](#), [2](#)

* **qc**

- [rqc](#), [6](#)
- [rqcCycleAverageQualityCalc](#), [8](#)
- [rqcCycleAverageQualityPcaCalc](#), [9](#)
- [rqcCycleBaseCallsCalc](#), [10](#)
- [rqcCycleGCCalc](#), [11](#)
- [rqcCycleQualityBoxCalc](#), [12](#)
- [rqcCycleQualityCalc](#), [13](#)
- [rqcFileHeatmap](#), [14](#)
- [rqcGroupCycleAverageQualityCalc](#),
[15](#)
- [rqcReadFrequencyCalc](#), [18](#)
- [rqcReadQualityBoxCalc](#), [19](#)
- [rqcReadQualityCalc](#), [20](#)
- [rqcReadWidthCalc](#), [21](#)
- [stats4trim](#), [26](#)
- [subsetByGroup](#), [27](#)
- [subsetByPair](#), [27](#)

* **trimming**

- [stats4trim](#), [26](#)

[BamFile](#), [17](#)

[BiocParallel](#), [17](#)

[bplapply](#), [17](#)

[checkpoint](#), [3](#)

[detectFileFormat](#), [4](#), [17](#)

[dist](#), [14](#)

[FastqFile](#), [17](#)

[fromRRDNA](#), [4](#)

[ggplot](#), [9–14](#), [18–21](#)

[hclust](#), [14](#)

[knit](#), [22](#)

[markdownToHTML](#), [22](#)

[matdist](#), [5](#)

[multicoreWorkers](#), [7](#)

[perCycleBasecall](#) ([RqcResultSet-class](#)),
[23](#)

[perCycleBasecall](#), list-method
([RqcResultSet-class](#)), [23](#)

[perCycleBasecall](#), [RqcResultSet-method](#)
([RqcResultSet-class](#)), [23](#)

[perCycleQuality](#) ([RqcResultSet-class](#)), [23](#)

[perCycleQuality](#), list-method
([RqcResultSet-class](#)), [23](#)

[perCycleQuality](#), [RqcResultSet-method](#)
([RqcResultSet-class](#)), [23](#)

[perFileInformation](#)
([RqcResultSet-class](#)), [23](#)

[perFileInformation](#), list-method
([RqcResultSet-class](#)), [23](#)

[perFileInformation](#), [RqcResultSet-method](#)
([RqcResultSet-class](#)), [23](#)

[perFileTopReads](#), [5](#), [28](#)

[perFileTopReads](#) ([RqcResultSet-class](#)), [23](#)

[perFileTopReads](#), list-method
([RqcResultSet-class](#)), [23](#)

- perFileTopReads, RqcResultSet-method
(RqcResultSet-class), 23
- perReadFrequency (RqcResultSet-class),
23
- perReadFrequency, list-method
(RqcResultSet-class), 23
- perReadFrequency, RqcResultSet-method
(RqcResultSet-class), 23
- perReadQuality (RqcResultSet-class), 23
- perReadQuality, list-method
(RqcResultSet-class), 23
- perReadQuality, RqcResultSet-method
(RqcResultSet-class), 23
- perReadWidth (RqcResultSet-class), 23
- perReadWidth, list-method
(RqcResultSet-class), 23
- perReadWidth, RqcResultSet-method
(RqcResultSet-class), 23

- Rqc (Rqc-package), 2
- rqc, 6, 8–15, 17–22, 26, 27
- Rqc-package, 2
- rqcCycleAverageQualityCalc, 8
- rqcCycleAverageQualityPcaCalc, 9
- rqcCycleAverageQualityPcaPlot
(rqcCycleAverageQualityPcaCalc),
9
- rqcCycleAverageQualityPlot, 15
- rqcCycleAverageQualityPlot
(rqcCycleAverageQualityCalc), 8
- rqcCycleBaseCallsCalc, 10
- rqcCycleBaseCallsLinePlot
(rqcCycleBaseCallsCalc), 10
- rqcCycleBaseCallsPlot
(rqcCycleBaseCallsCalc), 10
- rqcCycleGCCalc, 11
- rqcCycleGCPlot (rqcCycleGCCalc), 11
- rqcCycleQualityBoxCalc, 12
- rqcCycleQualityBoxPlot
(rqcCycleQualityBoxCalc), 12
- rqcCycleQualityCalc, 13
- rqcCycleQualityPlot
(rqcCycleQualityCalc), 13
- rqcFileHeatmap, 6, 14
- rqcGroupCycleAverageQualityCalc, 15
- rqcGroupCycleAverageQualityPlot, 8
- rqcGroupCycleAverageQualityPlot
(rqcGroupCycleAverageQualityCalc),
15
- rqcQA, 7–15, 16, 18–22, 26, 27
- rqcQA, BamFile-method (rqcQA), 16
- rqcQA, character-method (rqcQA), 16
- rqcQA, FastqFile-method (rqcQA), 16
- rqcQA, list-method (rqcQA), 16
- rqcReadFrequencyCalc, 18
- rqcReadFrequencyPlot
(rqcReadFrequencyCalc), 18
- rqcReadQualityBoxCalc, 19
- rqcReadQualityBoxPlot
(rqcReadQualityBoxCalc), 19
- rqcReadQualityCalc, 20
- rqcReadQualityPlot
(rqcReadQualityCalc), 20
- rqcReadWidthCalc, 21
- rqcReadWidthPlot (rqcReadWidthCalc), 21
- rqcReport, 22
- RqcResultSet-class, 23
- rqcShinyReport, 25

- ShortRead, 17
- stats4trim, 26
- subsetByGroup, 27
- subsetByPair, 27

- toRRDNA, 28