

Package ‘FastqCleaner’

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Type Package

Title A Shiny Application for Quality Control, Filtering and Trimming of FASTQ Files

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Description An interactive web application for quality control, filtering and trimming of FASTQ files. This user-friendly tool combines a pipeline for data processing based on Biostrings and ShortRead infrastructure, with a cutting-edge visual environment. Single-Read and Paired-End files can be locally processed. Diagnostic interactive plots (CG content, per-base sequence quality, etc.) are provided for both the input and output files.

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'complex_filter.R' 'adapter_filter.R' 'launch_fqc.R'
'length_filter.R' 'fixed_filter.R' 'trim3q_filter.R'
'unique_filter.R' 'plotObjects.R' 'qmean_filter.R' 'simulate.R'
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adapter_filter *Remove full and partial adapters from a ShortReadQ object*

Description

This program can remove adapters and partial adapters from 3' and 5', using the functions [trimLRPatterns](#). The program extends the methodology of the [trimLRPatterns](#) function of **Biostrings**, being also capable of removing adapters present within reads and with other additional options (e.g., threshold of minimum number of bases for trimming). For a given position in the read, the two **Biostrings** functions return TRUE when a match is present between a substring of the read and the adapter. As [trimLRPatterns](#), *adapter_filter* also selects region and goes up to the end of the sequence in the corresponding flank as the best match. The default error rate is 0.2. If several valid matches are found, the function removes the largest subsequence. Adapters can be anchored or not. When indels are allowed, the second method uses the 'edit distance' between the subsequences and the adapter

Usage

```
adapter_filter(  
  input,  
  Lpattern = "",  
  Rpattern = "",  
  rc.L = FALSE,  
  rc.R = FALSE,  
  first = c("R", "L"),  
  with_indels = FALSE,  
  error_rate = 0.2,  
  anchored = TRUE,  
  fixed = "subject",  
  remove_zero = TRUE,  
  checks = TRUE,  
  min_match_flank = 3L,  
  ...  
)
```

Arguments

| | |
|-----------------|--|
| <i>input</i> | ShortReadQ object |
| <i>Lpattern</i> | 5' pattern (character or DNASTring object) |
| <i>Rpattern</i> | 3' pattern (character or DNASTring object) |
| <i>rc.L</i> | Reverse complement <i>Lpattern</i> ? default FALSE |
| <i>rc.R</i> | Reverse complement <i>Rpattern</i> ? default FALSE |

| | |
|-----------------|--|
| first | trim first right('R') or left ('L') side of sequences when both Lpattern and Rpattern are passed |
| with_indels | Allow indels? This feature is available only when the error_rate is not null |
| error_rate | Error rate (value in the range [0, 1]) The error rate is the proportion of mismatches allowed between the adapter and the aligned portion of the subject. For a given adapter A, the number of allowed mismatches between each subsequence s of A and the subject is computed as: $error_rate * L_s$, where L_s is the length of the subsequence s |
| anchored | Adapter or partial adapter within sequence (anchored = FALSE, default) or only in 3' and 5' terminals? (anchored = TRUE) |
| fixed | Parameter passed to <code>trimLRPatterns</code> Default 'subject', ambiguities in the pattern only are interpreted as wildcard. See the argument fixed in <code>trimLRPatterns</code> |
| remove_zero | Remove zero-length sequences? Default TRUE |
| checks | Perform checks? Default TRUE |
| min_match_flank | Do not trim in flanks of the subject, if a match has min_match_flank of less length. Default 1L (only trim with ≥ 2 coincidences in a flank match) |
| ... | additional parameters passed to <code>trimLRPatterns</code> |

Value

Edited `DNASTring` or `DNASTringSet` object

Filtered `ShortReadQ` object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require('Biostrings')
require('ShortRead')

# create 6 sequences of width 43
set.seed(10)
input <- random_seq(6, 43)

# add adapter in 3'
adapter <- "ATCGACT"

input <- paste0(input, as.character(DNASTring(adapter)))
input <- DNASTringSet(input)

# create qualities of width 50
set.seed(10)
input_q <- random_qual(c(30,40), slength = 6, swidth = 50,
  encod = 'Sanger')
```

```

# create names
input_names <- seq_names(length(input))

# create ShortReadQ object
my_read <- ShortReadQ(sread = input, quality = input_q, id = input_names)

# trim adapter
filtered <- adapter_filter(my_read, Rpattern = adapter)

# look at the filtered sequences
sread(filtered)

```

asc2int *ASCII to integer*

Description

ASCII to integer

Usage

```
asc2int(x)
```

Value

Integer

check_encoding *Check quality encoding*

Description

Check quality encoding

Usage

```
check_encoding(x = NULL, custom = NULL)
```

Arguments

| | |
|--------|--|
| x | Quality values |
| custom | custom encoding from the following: 'Sanger' ———> expected range: [0, 40] 'Illumina1.8' ———> expected range: [0, 41] 'Illumina1.5' ———> expected range: [0, 40] 'Illumina1.3' ———> expected range: [3, 40] 'Solexa' ———> expected range: [-5, 40] |

Value

List with encoding information

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require(Biostrings)

x <- list(PhredQuality(0:40), SolexaQuality(-5:40), IlluminaQuality(3:40))
x <- lapply(x, function(i)utf8ToInt(as.character(i)[1]))
lapply(x, check_encoding)

SolexaQuality(0:40)
IlluminaQuality(0:40)
```

| | |
|----------------|----------------------|
| check_onclick_ | <i>check onclick</i> |
|----------------|----------------------|

Description

Function to put a tickmark on click

Usage

```
check_onclick_(.menu_react, .butt_number, my_envir)
```

Value

Change value of reactive output, without return

| | |
|----------------|---|
| complex_filter | <i>Remove sequences with low complexity</i> |
|----------------|---|

Description

The program removes low complexity sequences, computing the entropy with the observed frequency of dinucleotides.

Usage

```
complex_filter(input, threshold = 0.5, referenceEntropy = 3.908135)
```

Arguments

| | |
|------------------|---|
| input | ShortReadQ object |
| threshold | A threshold value computed as the relation of the H of the sequences and the reference H. Default is 0.5 |
| referenceEntropy | Reference entropy. By default, the program uses a value of 3.908, that corresponds to the entropy of the human genome in bits |

Value

Filtered [ShortReadQ](#) object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require('Biostrings')
require('ShortRead')

# create sequences of different width
set.seed(10)
input <- lapply(c(0, 6, 10, 16, 20, 26, 30, 36, 40),
               function(x) random_seq(1, x))

# create repetitive 'CG' sequences with length adequate
# for a total length:
# input + CG = 40

set.seed(10)
CG <- lapply(c(20, 17, 15, 12, 10, 7, 5, 2, 0),
            function(x) paste(rep('CG', x), collapse = ''))

# concatenate input and CG
input <- mapply('paste', input, CG, sep = '')
input <- DNASTringSet(input)

# plot relative entropy (E, Shannon 1948)

freq <- dinucleotideFrequency(input)
freq <- freq / rowSums(freq)
H <- -rowSums(freq * log2(freq), na.rm = TRUE)
H_max <- 3.908135 # max entropy
plot(H/H_max, type='b', xlab = 'Sequence', ylab= 'E')

# create qualities of width 40
```

```

set.seed(10)
input_q <- random_qual(c(30,40), slength = 9, swidth = 40,
                      encod = 'Sanger')

# create names
input_names <- seq_names(9)

# create ShortReadQ object
my_read <- ShortReadQ(sread = input, quality = input_q, id = input_names)

# apply the filter
filtered <- complex_filter(my_read)

# look at the filtered sequences
sread(filtered)

```

create_cleanfunction_ *create_cleanfunction_*

Description

Create a function to process FASTQ files in function of the Shiny parameters selected by the user

Usage

```
create_cleanfunction_(my_envir, .which_read = c("FORWARD", "REVERSE"))
```

Value

Function with selected cleaning operations

create_uniform_width *Create fastq/sequences/qualities with uniform width*

Description

Create fastq/sequences/qualities with uniform width

Usage

```
create_uniform_width(input, type = c("fastq", "sequence", "quality"))
```

Arguments

| | |
|-------|--|
| input | input to edit |
| type | type of the input: 'fastq' (ShortReadQ), 'sequence' (DNASTringSet), 'quality' (BStringset) |

Value

ShortReadQ object or character vector with sequences or qualities, with uniform width (padded with Ns or })

cutRseq

Remove left and right full and partial patterns

Description

This set of programs are internal, and the function `adapter_filter` is recommended for trimming. The programs can remove adapters and partial adapters from 3' and 5'. The adapters can be anchored or not. When indels are allowed, the error rate consists in the edit distance. IUPAC symbols are allowed. The methods use the `trimLRPatterns` function of the **Biostrings** package, with some additions to take into account e.g., partial adapters. IUPAC symbols are allowed in all the cases. The present function also removes partial adapters, without the need of additional steps (for example, creating a padded adapter with 'Ns', etc). A similar result to the output of `trimLRPatterns` can be obtained with the option `anchored = TRUE`. When several matches are found, the function removes the subsequence that starts in the first match when `cutRseq` is used, or ends in the last match when `cutLseq` is used.

Usage

```
cutRseq(  
  subject,  
  Rpattern,  
  with.indels = FALSE,  
  fixed = "subject",  
  error_rate = 0.2,  
  anchored = TRUE,  
  ranges = FALSE,  
  checks = TRUE,  
  min_match_flank = 2L,  
  ...  
)
```

```
cutLseq(  
  subject,  
  Lpattern,  
  with.indels = FALSE,  
  fixed = "subject",  
  error_rate = 0.2,  
  anchored = TRUE,  
  ranges = FALSE,  
  min_match_flank = 3L,  
  checks = TRUE,  
  ...  
)
```

Arguments

| | |
|-----------------|--|
| subject | DNASTring or DNASTringSet object |
| Rpattern | 3' pattern, DNASTring object |
| with.indels | Allow indels? |
| fixed | Parameter passed to trimLRPatterns Default 'subject', ambiguities in the pattern only are interpreted as wildcard. See the argument fixed in trimLRPatterns |
| error_rate | Error rate (value in [0, 1]). The error rate is the proportion of mismatches allowed between the adapter and the aligned portion of the subject. For a given adapter A, the number of allowed mismatches between each subsequence s of A and the subject is computed as: $error_rate * L_s$, where L_s is the length of the subsequence s. |
| anchored | Can the adapter or partial adapter be within the sequence? (anchored = FALSE) or only in the terminal regions of the sequence? (anchored = TRUE). Default TRUE (trim only flanking regions) |
| ranges | Return ranges? Default FALSE |
| checks | Perform internal checks? Default TRUE |
| min_match_flank | Do not trim in flanks of the subject, if a match has min_match_flank of less length. Default 1L (only trim with ≥ 2 coincidences in a flank match) |
| ... | additional parameters passed to trimLRPatterns |
| Lpattern | 5' pattern, DNASTring object |

Value

Edited [DNASTring](#) or [DNASTringSet](#) object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
library(Biostrings)

subject <- DNASTringSet(c('ATCATGCCATCATGAT',
  'CATGATATTA', 'TCATG', 'AAAAAA', 'AGGTCATG'))

Lpattern <- Rpattern <- 'TCATG'

FastqCleaner:::cutLseq(subject, Lpattern)
FastqCleaner:::cutLseq(subject, Lpattern, ranges = TRUE)
FastqCleaner:::cutRseq(subject, Rpattern)

FastqCleaner:::cutLseq(subject, Lpattern, anchored = FALSE)
FastqCleaner:::cutLseq(subject, Lpattern, error_rate = 0.2)
FastqCleaner:::cutLseq(subject, Lpattern, error_rate = 0.2,
```

```
with.indels = TRUE)
```

| | |
|--------------|--|
| fixed_filter | <i>Remove a fixed number of bases of a ShortReadQ object from 3' or 5'</i> |
|--------------|--|

Description

The program removes a given number of bases from the 3' or 5' regions of the sequences contained in a ShortReadQ object

Usage

```
fixed_filter(input, trim3 = NA, trim5 = NA)
```

Arguments

| | |
|-------|-----------------------------------|
| input | ShortReadQ object |
| trim3 | Number of bases to remove from 3' |
| trim5 | Number of bases to remove from 5' |

Value

Filtered ShortReadQ object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require('Biostrings')
require('ShortRead')

# create 6 sequences of width 20

set.seed(10)
input <- random_seq(6, 20)

# create qualities of width 20

set.seed(10)
input_q <- random_qual(c(30,40), slength = 6, swidth = 20,
  encod = 'Sanger')

# create names
input_names <- seq_names(6)
```

```
# create ShortReadQ object
my_read <- ShortReadQ(sread = input, quality = input_q, id = input_names)

# apply the filter
filtered3 <- fixed_filter(my_read, trim5 = 5)

filtered5 <- fixed_filter(my_read, trim3 = 5)

filtered3and5 <- fixed_filter(my_read, trim3 = 10, trim5 = 5)

# look at the trimmed sequences
sread(filtered3)
sread(filtered5)
sread(filtered3and5)
```

inject_letter_random *Inject a letter in a set of sequences at random positions*

Description

Inject a letter in a set of sequences at random positions

Usage

```
inject_letter_random(  
  my_seq,  
  how_many_seqs = NULL,  
  how_many_letters = NULL,  
  letter = "N"  
)
```

Arguments

| | |
|------------------|--|
| my_seq | character vector with sequences to inject |
| how_many_seqs | How many sequences pick to inject Ns. An interval [min_s, max_s] with min_s minimum and max_s maximum sequences can be passed. In this case, a value is picked from the interval. If NULL, a random value within the interval [1, length(my_seq)] is picked. |
| how_many_letters | How many times inject the letter in the i sequences that are going to be injected. An interval [min_i max_i] can be passed. In this case, a value is randomly picked for each sequence i. This value represents the number of times that the letter will be injected in the sequence i. If NULL, a random value within the interval [1, width(my_seq[i])] is picked for each sequence i. |
| letter | Letter to inject. Default: 'N' |

Value

character vector

Author(s)

Leandro Roser <learosier@gmail.com>

Examples

```
# For reproducible examples, make a call to set.seed before
# running each random function

set.seed(10)
s <- random_seq(slength = 10, swidth = 20)

set.seed(10)
s <- inject_letter_random(s, how_many_seqs = 1:30, how_many= 2:10)
```

int2asc

Integer to ASCII

Description

Integer to ASCII

Usage

int2asc(n)

Value

ASCII character

isNaturalNumber

Is natural number

Description

Is natural number

Usage

isNaturalNumber(x)

Value

Logical

| | |
|------------|--|
| launch_fqc | <i>Launch FastqCleaner application</i> |
|------------|--|

Description

Launch FastqCleaner application

Usage

```
launch_fqc(launch.browser = TRUE, ...)
```

Arguments

launch.browser Launch in browser? Default TRUE
... Additional parameters passed to [runApp](#)

Value

Launch the application, without return value

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
# Uncomment and paste in te console to launch the application:  
# launch_fqc()  
  
NULL
```

| | |
|---------------|---|
| length_filter | <i>Filter sequences of a FASTQ file by length</i> |
|---------------|---|

Description

The program removes from a ShortReadQ object those sequences with a length lower than rm.min or/and higher than rm.max

Usage

```
length_filter(input, rm.min = NA, rm.max = NA)
```

Arguments

| | |
|--------|---|
| input | ShortReadQ object |
| rm.min | Threshold value for the minimum number of bases |
| rm.max | Threshold value for the maximum number of bases |

Value

Filtered ShortReadQ object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require('Biostrings')
require('ShortRead')

# create ShortReadQ object with widths between 1 and 100

set.seed(10)
input <- random_length(100, widths = 1:100)

# apply the filter, removing sequences length < 10 or length > 80
filtered <- length_filter(input, rm.min = 10, rm.max = 80)

# look at the filtered sequences
sread(filtered)
```

messageFun_

messageFun_

Description

messageFun_

Usage

```
messageFun_(.who, .chunk, .which_read, my_envir)
```

Value

Changes the state of reactive vector, without return

| | |
|--------|---------------|
| myPlot | <i>myPlot</i> |
|--------|---------------|

Description

Construction of diagnostic plots. The function depends of the values created by plotObject

Usage

```
myPlot(isPaired, location, sampleSize, kmerLength, theFile, maxFreq)
```

Value

List with Highcharts plots

| | |
|----------|---|
| n_filter | <i>Remove sequences with non-identified bases (Ns) from a ShortReadQ object</i> |
|----------|---|

Description

This program is a wrapper to [nFilter](#). It removes the sequences with a number of N's above a threshold value 'rm.N'. All the sequences with a number of N > rm.N (N >= rm.N) will be removed

Usage

```
n_filter(input, rm.N)
```

Arguments

| | |
|-------|--|
| input | ShortReadQ object |
| rm.N | Threshold value of N's to remove a sequence from the output (sequences with number of Ns > threshold are removed) For example, if rm.N is 3, all the sequences with a number of Ns > 3 (Ns >= 4) will be removed |

Value

Filtered [ShortReadQ](#) object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require('Biostrings')
require('ShortRead')

# create 6 sequences of width 20
set.seed(10)
input <- random_seq(50, 20)

# inject N's
set.seed(10)
input <- inject_letter_random(input, how_many_seqs = 1:30,
how_many = 1:10)

input <- DNASTringSet(input)

# watch the N's frequency
hist(letterFrequency(input, 'N'), breaks = 0:10,
main = 'Ns Frequency', xlab = '# Ns')

# create qualities of width 20
set.seed(10)
input_q <- random_qual(50, 20)

# create names
input_names <- seq_names(50)

# create ShortReadQ object
my_read <- ShortReadQ(sread = input, quality = input_q, id = input_names)

# apply the filter
filtered <- n_filter(my_read, rm.N = 3)

# watch the filtered sequences
sread(filtered)

# watch the N's frequency
hist(letterFrequency(sread(filtered), 'N'),
main = 'Ns distribution', xlab = '')
```

outputClean_

outputClean_

Description

outputClean_

Usage

```
outputClean_(.myFile, .lengthWidthVec, my_envir)
```

Value

Vector with chunks length and width information

| | |
|-------|--------------|
| plotA | <i>plotA</i> |
|-------|--------------|

Description

plotA

Usage

```
plotA(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

Per cycle quality plot

| | |
|-------|--------------|
| plotB | <i>plotB</i> |
|-------|--------------|

Description

plotB

Usage

```
plotB(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

Per cycle mean base quality plot

| | |
|-------|--------------|
| plotC | <i>plotC</i> |
|-------|--------------|

Description

plotC

Usage

```
plotC(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

Mean quality of reads distribution plot

| | |
|-------|--------------|
| plotD | <i>plotD</i> |
|-------|--------------|

Description

plotD

Usage

```
plotD(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

percent of reads with quality > threshold plot

| | |
|-------|--------------|
| plotE | <i>plotE</i> |
|-------|--------------|

Description

plotE

Usage

```
plotE(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

Per cycle base proportion plot

| | |
|-------|--------------|
| plotF | <i>plotF</i> |
|-------|--------------|

Description

plotF

Usage

```
plotF(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

Per cycle base proportion plot (lineplot)

plotG *plotG*

Description

plotG

Usage

```
plotG(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

CG content distribution plot

plotH *plotH*

Description

plotH

Usage

```
plotH(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

Read length distribution

plotI *plotI*

Description

plotI

Usage

```
plotI(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

Read occurrence distribution plot

plotJ

plotJ

Description

plotJ

Usage

```
plotJ(x, nplots = 1, theFile = c("input", "output"), sampleSize)
```

Value

Relative kmer diversity plot

plotObjects

plotObjects Create the information required to construct the plots. This is the input of myplot, which uses the values created for this function to construct the plots

Description

plotObjects Create the information required to construct the plots. This is the input of myplot, which uses the values created for this function to construct the plots

Usage

```
plotObjects(fq, klength, basename, maxFreq, sampleSize)
```

Value

List with information to construct the diagnostic plots

processingFunction_ *processingFunction_*

Description

This function is the core of the application. It is used for the program to process the FASTQ file/s in the environment of the Shiny app. Note that this program makes a call to create_cleanfunction

Usage

```
processingFunction_(my_envir)
```

Value

Processes the input FASTQ file, without return

qmean_filter *Filter sequences by their average quality*

Description

The program removes the sequences with a quality lower the 'minq' threshold

Usage

```
qmean_filter(input, minq, q_format = NULL, check.encod = TRUE)
```

Arguments

| | |
|-------------|---|
| input | ShortReadQ object |
| minq | Quality threshold |
| q_format | Quality format used for the file, as returned by check.encoding |
| check.encod | Check the encoding of the sequence? This argument is incompatible with q_format |

Value

Filtered [ShortReadQ](#) object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require(ShortRead)

set.seed(10)
# create 30 sequences of width 20
input <- random_seq(30, 20)

# create qualities of width 20
## high quality (15 sequences)
set.seed(10)
my_qual <- random_qual(c(30,40), slength = 15, swidth = 20,
                      encod = 'Sanger')
## low quality (15 sequences)
set.seed(10)
my_qual_2 <- random_qual(c(5,30), slength = 15, swidth = 20,
                        encod = 'Sanger')

# concatenate vectors
input_q<- c(my_qual, my_qual_2)

# create names
input_names <- seq_names(30)

# create ShortReadQ object
my_read <- ShortReadQ(sread = input, quality = input_q, id = input_names)

# watch the average qualities
alphabetScore(my_read) / width(my_read)

# apply the filter
filtered <- qmean_filter(my_read, minq = 30)

# watch the average qualities
alphabetScore(my_read) / width(my_read)

# watch the filtered sequences
sread(filtered)
```

random_length

Create a named object with random sequences and qualities

Description

Create a [ShortReadQ](#) object with random sequences and qualities

Usage

```

random_length(
  n,
  widths,
  random_widths = TRUE,
  replace = TRUE,
  len_prob = NULL,
  seq_prob = c(0.25, 0.25, 0.25, 0.25),
  q_prob = NULL,
  nuc = c("DNA", "RNA"),
  qual = NULL,
  encod = c("Sanger", "Illumina1.8", "Illumina1.5", "Illumina1.3", "Solexa"),
  base_name = "s",
  sep = "_"
)

```

Arguments

| | |
|---------------|--|
| n | number of sequences |
| widths | width of the sequences |
| random_widths | width must be picked at random from the passed parameter 'widths', considering the value as an interval where any integer can be picked. Default TRUE. Otherwise, widths are picked only from the vector passed. |
| replace | sample widths with replacement? Default TRUE. |
| len_prob | vector with probabilities for each width value. Default NULL (equiprobability) |
| seq_prob | a vector of four probabilities values to set the frequency of the nucleotides 'A', 'C', 'G', 'T', for DNA, or 'A', 'C', 'G', 'U', for RNA. For example = c(0.25, 0.25, 0.5, 0). Default is = c(0.25, 0.25, 0.25, 0.25) (equiprobability for the 4 bases). If the sum of the probabilities is > 1, the values will be normalized to the range [0, 1]. |
| q_prob | a vector of range = range(qual), with probabilities to set the frequency of each quality value. Default is equiprobability. If the sum of the probabilities is > 1, the values will be normalized to the range [0, 1]. |
| nuc | create sequences of DNA (nucleotides = c('A', 'C', 'G', 'T')) or RNA (nucleotides = c('A', 'C', 'G', 'U'))?. Default: 'DNA' |
| qual | quality range for the sequences. It must be a range included in the selected encoding: 'Sanger' = [0, 40] 'Illumina1.8' = [0, 41] 'Illumina1.5' = [0, 40] 'Illumina1.3' = [3, 40] 'Solexa' = [-5, 40] example: for a range from 20 to 30 in Sanger encoding, pass the argument = c(20, 30) |
| encod | sequence encoding |

| | |
|-----------|---|
| base_name | Base name for strings |
| sep | Character separating base names and the read number. Default: '_' |

Value

ShortReadQ object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
# For reproducible examples, make a call to set.seed before
# running each random function

set.seed(10)
s1 <- random_seq(slength = 10, swidth = 20)
s1

set.seed(10)
s2 <- random_seq(slength = 10, swidth = 20,
prob = c(0.6, 0.1, 0.3, 0))
s2
```

| | |
|-------------|---|
| random_qual | <i>Create random qualities for a given encoding</i> |
|-------------|---|

Description

Create a [BStringSet](#) object with random qualities

Usage

```
random_qual(
  slength,
  swidth,
  qual = NULL,
  encod = c("Sanger", "Illumina1.8", "Illumina1.5", "Illumina1.3", "Solexa"),
  prob = NULL
)
```

Arguments

| | |
|---------|--|
| slength | number of sequences |
| swidth | width of the sequences |
| qual | quality range for the sequences. It must be a range included in the selected encoding: 'Sanger' = [0, 40] 'Illumina1.8' = [0, 41] 'Illumina1.5' = [0, 40] 'Illumina1.3' = [3, 40] 'Solexa' = [-5, 40] example: for a range from 20 to 30 in Sanger encoding, pass the argument = c(20, 30) |
| encod | sequence encoding |
| prob | a vector of range = range(qual), with probabilities to set the frequency of each quality value. Default is equiprobability. If the sum of the probabilities is > 1, the values will be normalized to the range [0, 1]. |

Value

[BStringSet](#) object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
q <- random_qual(30, 20)
q
```

random_seq

Create random sequences

Description

Create a [DNAStringSet](#) object with random sequences

Usage

```
random_seq(  
  slength,  
  swidth,  
  nuc = c("DNA", "RNA"),  
  prob = c(0.25, 0.25, 0.25, 0.25)  
)
```

Arguments

| | |
|--------|---|
| length | Number of sequences |
| width | Width of the sequences |
| nuc | Create sequences of DNA (nucleotides = c('A', 'C', 'G', 'T')) or RNA (nucleotides = c('A', 'C', 'G', 'U'))?. Default: 'DNA' |
| prob | A vector of four probability values used to set the frequency of the nucleotides 'A', 'C', 'G', 'T', for DNA, or 'A', 'C', 'G', 'U', for RNA. For example = c(0.25, 0.25, 0.5, 0). Default is = c(0.25, 0.25, 0.25, 0.25) (equiprobability for the 4 bases). If the sum of the probabilities is > 1, the values will be normalized to the range [0, 1]. |

Value

DNAStrngSet object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
# For reproducible examples, make a call to set.seed before
# running each random function

set.seed(10)
s1 <- random_seq(length = 10, width = 20)
s1

set.seed(10)
s2 <- random_seq(length = 10, width = 20,
prob = c(0.6, 0.1, 0.3, 0))
s2
```

seq_filter

Remove a set of sequences

Description

Removes a set of sequences

Usage

```
seq_filter(input, rm.seq)
```

Arguments

input [ShortReadQ](#) object
 rm.seq Ccharacter vector with sequences to remove

Value

Filtered [ShortReadQ](#) object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require(ShortRead)

set.seed(10)
input <- random_length(30, 3:7)
rm.seq = c('TGGTC', 'CGGT', 'GTTCT', 'ATA')

# verify that some sequences match
match_before <- unlist(lapply(rm.seq,
  function(x) grep(x, as.character(sread(input)))))

filtered <- seq_filter(input, rm.seq = rm.seq)

# verify that matching sequences were removed
match_after <- unlist(lapply(rm.seq,
  function(x) grep(x, as.character(sread(filtered)))))
```

seq_names

Create sequences names

Description

Create [BStringSet](#) object with names

Usage

```
seq_names(n, base_name = "s", sep = "_")
```

Arguments

n Number of reads
 base_name Base name for strings
 sep Character separating base names and the read number. Default: '_'

Value

BStringSet object

Examples

```
snames <- seq_names(10)
snames
snames2 <- seq_names(10, base_name = 's', sep = '.')
snames2
```

| | |
|---------------|--|
| trim3q_filter | <i>Filter sequences with low quality in 3' tails</i> |
|---------------|--|

Description

The program removes from the 3' tails of the sequences a set of nucleotides showing a quality < a threshold value in a ShortReadQ object

Usage

```
trim3q_filter(
  input,
  rm.3qual,
  q_format = NULL,
  check.encod = TRUE,
  remove_zero = TRUE
)
```

Arguments

| | |
|-------------|--|
| input | ShortReadQ object |
| rm.3qual | Quality threshold for 3' tails |
| q_format | Quality format used for the file, as returned by check_encoding |
| check.encod | Check the encoding of the sequence? This argument is incompatible with q_format. Default TRUE |
| remove_zero | Remove zero-length sequences? |

Value

Filtered ShortReadQ object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require('Biostrings')
require('ShortRead')

# create 6 sequences of width 20
set.seed(10)
input <- random_seq(6, 20)

# create qualities of width 15 and paste to qualities
# of length 5 used for the tails.
# for two of the sequences, put low qualities in tails

set.seed(10)
my_qual <- random_qual(c(30,40), slength = 6, swidth = 15,
  encod = 'Sanger')

set.seed(10)
tails <- random_qual(c(30,40), slength = 6, swidth = 5,
  encod = 'Sanger')

set.seed(10)
tails[2:3] <- random_qual(c(3, 20), slength = 2,
  swidth = 5, encod = 'Sanger')
my_qual <- paste0(my_qual, tails)
input_q <- BStringSet(my_qual)
# create names
input_names <- seq_names(6)

# create ShortReadQ object
my_read <- ShortReadQ(sread = input,
  quality = input_q, id = input_names)

# apply the filter
filtered <- trim3q_filter(my_read, rm.3qual = 28)

# look at the trimmed sequences
sread(filtered)
```

unique_filter

Remove duplicated sequences in a FASTQ file

Description

This program is a wrapper to [occurrenceFilter](#). It removes the duplicated sequences of a FASTQ file.

Usage

```
unique_filter(input)
```

Arguments

input [ShortReadQ](#) object

Value

Filtered [ShortReadQ](#) object

Author(s)

Leandro Roser <learoser@gmail.com>

Examples

```
require('Biostrings')
require('ShortRead')

set.seed(10)
s <- random_seq(10, 10)
s <- sample(s, 30, replace = TRUE)
q <- random_qual(30, 10)
n <- seq_names(30)

my_read <- ShortReadQ(sread = s, quality = q, id = n)

# check presence of duplicates
isUnique(as.character(sread(my_read)))

# apply the filter
filtered <- unique_filter(my_read)

isUnique(as.character(sread(filtered)))
```

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