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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LazyData TRUE

Imports methods, shiny, stats, IRanges, Biostrings, ShortRead, DT, S4Vectors, graphics, htmltools, shinyBS, Rcpp (>= 0.12.12)

Suggests BiocStyle, testthat, knitr, rmarkdown

LinkingTo Rcpp

Collate 'roxygen_auxiliar.R' 'auxiliar.R' 'matching.R'
  'server_functions.R' 'in_filter.R' 'seq_filter.R'
  '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'
  'RcppExports.R'

biocViews QualityControl, Sequencing, Software, SangerSeq, SequenceMatching

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Contents

adapter_filter ........................................... 3
asc2int ..................................................... 5
check_encoding ........................................... 5
check_onclick_ ............................................ 6
complex_filter ........................................... 6
create_cleanfunction_ ................................. 8
create_uniform_width ................................ 8
cutRseq .................................................. 9
fixed_filter .............................................. 11
inject_letter_random .................................. 12
int2asc ................................................... 13
isNaturalNumber ......................................... 13
launch_fqc ............................................... 14
length_filter ............................................ 14
messageFun_ .............................................. 15
myPlot .................................................... 16
n_filter .................................................. 16
outputClean_ ............................................ 17
plotA ...................................................... 18
plotB ...................................................... 18
plotC ...................................................... 18
plotD ...................................................... 19
plotE ...................................................... 19
plotF ...................................................... 19
plotG ...................................................... 20
plotH ...................................................... 20
plotI ...................................................... 20
plotJ ...................................................... 21
plotObjects .............................................. 21
processingFunction_ ................................. 22
qmean_filter ........................................... 22
random_length .......................................... 23
random_qual ............................................. 25
random_seq .............................................. 26
seq_filter ............................................... 27
seq_names ............................................... 28
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

input ShortReadQ object
Lpattern 5' pattern (character or DNAString object)
Rpattern 3' pattern (character or DNAString object)
rc.L Reverse complement Lpattern? default FALSE
rc.R Reverse complement Rpattern? default FALSE
adapter_filter

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 trimLRPatterns Default 'subject', ambiguities in the pattern only are interpreted as wildcard. See the argument fixed in trimLRPatterns
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 trimLRPatterns

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

```r
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)
```

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

Description

Function to put a tickmark on click

Usage

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

Value

Change value of reactive output, without return

complex_filter

Remove sequences with low complexity

Description

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

Usage

```r
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

```r
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
```
```r
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_(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)
cutRseq

Value

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

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 adaptors. 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,
  checks = TRUE,
  min_match_flank = 3L,
  ...
)
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', 'AAAAA', '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,
fixed_filter

with.indels = TRUE)

fixed_filter          Remove a fixed number of bases of a ShortReadQ object from 3' or 5'

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 <learoser@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**          *Launch FastqCleaner application*

**Description**
Launch FastqCleaner application

**Usage**

```r
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**

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

NULL
```

---

**length_filter**          *Filter sequences of a FASTQ file by length*

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

**Usage**

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

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

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

# create ShortReadQ object width 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)
```

Description

messageFun

Usage

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

Value

Changes the state of reactive vector, without return.
myPlot

Description

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

Usage

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

Value

List with Highcharts plots

n_filter

Remove sequences with non-identified bases (Ns) from a ShortReadQ object

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

```r
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 = '')
```

Description

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

Usage

`outputClean_(.myFile, .lengthWidthVec, my_envir)`
Value
Vector with chunks length and width information

plotA

Description
plotA

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

Value
Per cycle quality plot

plotB

Description
plotB

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

Value
Per cycle mean base quality plot

plotC

Description
plotC

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

Value
Mean quality of reads distribution plot
plotD

Description
plotD

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

Value
percent of reads with quality > threshold plot

plotE

Description
plotE

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

Value
Per cycle base proportion plot

plotF

Description
plotF

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

Value
Per cycle base proportion plot (lineplot)
plotG

Description
plotG

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

Value
CG content distribution plot

plotH

Description
plotH

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

Value
Read length distribution

plotI

Description
plotI

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

Value
Read occurrence distribution plot
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

```r
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

```r
text = 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
random_qual

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

Create random qualities for a given encoding

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

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

random_seq  

Create random sequences

Description

Create a **DNAStringSet** object with random sequences

Usage

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

Remove a set of sequences

Description

Removes a set of sequences

Usage

seq_filter(input, rm.seq)
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: ")
trim3q_filter

Value

- BStringSet object

Examples

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

trim3q_filter

Filter sequences with low quality in 3' tails

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

```r
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

```r
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**

```r
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)))
```
Index

* internal
  
  asc2int, 5  
  check_onclick_, 6  
  create_cleanFunction_, 8  
  create_uniform_width, 8  
  cutRseq, 9  
  int2asc, 13  
  isNaturalNumber, 13  
  messageFun_, 15  
  myPlot, 16  
  outputClean_, 17  
  plotA, 18  
  plotB, 18  
  plotC, 18  
  plotD, 19  
  plotE, 19  
  plotF, 19  
  plotG, 20  
  plotH, 20  
  plotI, 20  
  plotJ, 21  
  plotObjects, 21  
  processingFunction_, 22

adapter_filter, 3  
asc2int, 5  
BStringSet, 25, 26, 28, 29

check_encoding, 5  
check_onclick_, 6  
complex_filter, 6  
create_cleanFunction_, 8  
create_uniform_width, 8  
cutLseq (cutRseq), 9  
cutRseq, 9

DNAString, 3, 4, 10  
DNAStringSet, 4, 10, 26, 27  
fixed_filter, 11

inject_letter_random, 12  
int2asc, 13  
isNaturalNumber, 13

launch_fqc, 14  
length_filter, 14  
messageFun_, 15  
myPlot, 16

n_filter, 16  
nFilter, 16

occurrenceFilter, 30  
outputClean_, 17

plotA, 18  
plotB, 18  
plotC, 18  
plotD, 19  
plotE, 19  
plotF, 19  
plotG, 20  
plotH, 20  
plotI, 20  
plotJ, 21  
plotObjects, 21  
processingFunction_, 22

qmean_filter, 22  
random_length, 23  
random_qual, 25  
random_seq, 26  
runApp, 14

seq_filter, 27  
seq_names, 28  
ShortReadQ, 3, 4, 7, 11, 15, 16, 22, 23, 25, 28, 29, 31

trim3q_filter, 29
INDEX

trimLRPatterns, 3, 4, 9, 10

unique_filter, 30