Package 'Rfastp'

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Type Package

Title An Ultra-Fast and All-in-One Fastq Preprocessor (Quality Control, Adapter, low quality and polyX trimming) and UMI Sequence Parsing).

Version 1.7.0

Description Rfastp is an R wrapper of fastp developed in c++. fastp performs quality control for fastq files. including low quality bases trimming, polyX trimming, adapter auto-detection and trimming, paired-end reads merging, UMI sequence/id handling. Rfastp can concatenate multiple files into one file (like shell command cat) and accept multiple files as input.

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biocViews QualityControl, Sequencing, Preprocessing, Software

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Imports Rcpp, rjson, ggplot2, reshape2

Suggests BiocStyle, testthat, knitr, rmarkdown

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R topics documented:

`catfastq` *Concatenate Fastq Files.*

Description

concatenate multiple fastq files into a single file.

Usage

```
catfastq(output, inputFiles, append = FALSE, paired = FALSE, shuffled = FALSE)
```

Arguments

`output`	output file name [string]
`inputFiles`	a vector of input file names [vector]
`append`	a logical indicating append the files to a file already exists.
`paired`	a logical indicating split the input files into two halves. the first half merged into read1, the second half merged into read2.
`shuffled`	a logical indicating split the input file list into two halves. The R1/R2 files are inteleaved in the inputFiles vector.

Value

no returns.

Author(s)

Wei Wang

Examples

```
pe001_read1 <- system.file("extdata","splited_001_R1.fastq.gz",
     package="Rfastp")
pe002_read1 <- system.file("extdata","splited_002_R1.fastq.gz",
     package="Rfastp")
pe003_read1 <- system.file("extdata","splited_003_R1.fastq.gz",
     package="Rfastp")
pe004_read1 <- system.file("extdata","splited_004_R1.fastq.gz",
```

```
     package="Rfastp")

pe001_read2 <- system.file("extdata","splited_001_R2.fastq.gz",
     package="Rfastp")
pe002_read2 <- system.file("extdata","splited_002_R2.fastq.gz",
     package="Rfastp")
pe003_read2 <- system.file("extdata","splited_003_R2.fastq.gz",
     package="Rfastp")
pe004_read2 <- system.file("extdata","splited_004_R2.fastq.gz",
     package="Rfastp")

allR1 <- c(pe001_read1, pe002_read1, pe003_read1, pe004_read1)
allR2 <- c(pe001_read2, pe002_read2, pe003_read2, pe004_read2)

allreads <- c(allR1, allR2)
allreads_shuffled <- c(pe001_read1, pe001_read2, pe002_read1, pe002_read2,
               pe003_read1, pe003_read2, pe004_read1, pe004_read2)

outputPrefix <- tempfile(tmpdir = tempdir())
# a normal concatenation for single-end libraries.

catfastq(output = paste0(outputPrefix, "_R1.fastq.gz"), inputFiles = allR1)

# a normal concatenation for paired-end libraries.

catfastq(output = paste0(outputPrefix, "merged_paired"),
    inputFiles = allreads, paired=TRUE)

# Append to exist files (paired-end)

catfastq(output=paste0(outputPrefix,"append_paired"), inputFiles=allreads,
    append=TRUE, paired=TRUE)

# Input paired-end files are shuffled.

catfastq(output=paste0(outputPrefix,"_shuffled_paired"),
    inputFiles=allreads_shuffled, paired=TRUE, shuffled=TRUE)
```

`curvePlot` *Plot of Base Quality and GC Content.*

Description

generate a ggplot2 object of Base Quality/GC content before and after QC.

Usage

```
curvePlot(json, curves = "quality_curves")
```

Arguments

json	the output json of function rfastq. [json]
curves	plots for Base Quality("quality_curves") or GC content("content_curves"). default is "quality_curves"

Value

a ggplot2 object.

Author(s)

Wei Wang

Examples

```
outputPrefix <- tempfile(tmpdir = tempdir())
se_read1 <- system.file("extdata","Fox3_Std_small.fq.gz",package="Rfastp")
se_json_report <- rfastp(read1 = se_read1, outputFastq = outputPrefix,
   thread = 4)
# Base Quality plot is the default output:
p1 <- curvePlot(se_json_report)
p1

p2 <- curvePlot(se_json_report, curves = "content_curves")
```

---

qcSummary *Summary of Fastq Quality Control*

Description

generate a data frame of the Fastq QC summary.

Usage

```
qcSummary(json)
```

Arguments

json	the output json of function rfastq. [json]

Value

a data frame.

Author(s)

Wei Wang

Examples

```
outputPrefix <- tempfile(tmpdir = tempdir())
se_read1 <- system.file("extdata","Fox3_Std_small.fq.gz",package="Rfastp")
se_json_report <- rfastp(read1 = se_read1, outputFastq = outputPrefix,
   thread = 4)
df_summary <- qcSummary(se_json_report)
```

`rfastp` *R wrap of fastp*

Description

Quality control (Cut adapter, low quality trimming, polyX trimming, UMI handling, and etc.) of fastq files.

Usage

```
rfastp(
  read1,
  read2 = "",
  outputFastq,
  unpaired = "",
  failedOut = "",
  merge = FALSE,
  mergeOut = "",
  phred64 = FALSE,
  interleaved = FALSE,
  fixMGIid = FALSE,
  adapterTrimming = TRUE,
  adapterSequenceRead1 = "auto",
  adapterSequenceRead2 = "auto",
  adapterFasta = "",
  trimFrontRead1 = 0,
  trimTailRead1 = 0,
  trimFrontRead2 = 0,
  trimTailRead2 = 0,
  maxLengthRead1 = 0,
  maxLengthRead2 = 0,
  forceTrimPolyG = FALSE,
  disableTrimPolyG = FALSE,
  minLengthPolyG = 10,
  trimPolyX = FALSE,
  minLengthPolyX = 10,
  cutWindowSize = 4,
  cutLowQualTail = FALSE,
  cutSlideWindowRight = FALSE,
```

```
  cutLowQualFront = FALSE,
  cutMeanQual = 20,
  cutFrontWindowSize = 4,
  cutFrontMeanQual = 20,
  cutTailWindowSize = 4,
  cutTailMeanQual = 20,
  cutSlideWindowSize = 4,
  cutSlideWindowQual = 20,
  qualityFiltering = TRUE,
  qualityFilterPhred = 15,
  qualityFilterPercent = 40,
  maxNfilter = 5,
  averageQualFilter = 0,
  lengthFiltering = TRUE,
  minReadLength = 15,
  maxReadLength = 0,
  lowComplexityFiltering = FALSE,
  minComplexity = 30,
  index1Filter = "",
  index2Filter = "",
  maxIndexMismatch = 0,
  correctionOverlap = FALSE,
  minOverlapLength = 30,
  maxOverlapMismatch = 5,
  maxOverlapMismatchPercentage = 20,
  umi = FALSE,
  umiLoc = "",
  umiLength = 0,
  umiPrefix = "",
  umiSkipBaseLength = 0,
  umiNoConnection = FALSE,
  umiIgnoreSeqNameSpace = FALSE,
  overrepresentationAnalysis = FALSE,
  overrepresentationSampling = 20,
  splitOutput = 0,
  splitByLines = 0,
  thread = 2,
  verbose = TRUE
)
```

Arguments

read1	read1 input file name(s). [vector]
read2	read2 input file name(s). [vector]
outputFastq	string of /path/prefix for output fastq [string]
unpaired	for PE input, output file name for reads which the mate reads failed to pass the QC [string], default NULL, discard it. [string]
failedOut	file to store reads that cannot pass the filters default NULL, discard it. [string]

`merge` for PE input, A logical(1) indicating whether merge each pair of reads into a single read if they are overlaped, unmerged reads will be write to 'output' file. Default is FALSE. the 'mergeOut' must be set if TRUE.

`mergeOut` under 'merge' mode, file to store the merged reads. [string]

`phred64` A logical indicating whether the input is using phred64 scoring (it will be converted to phred33, so the output will still be . phred33)

`interleaved` A logical indicating whether <read1> is an interleaved FASTQ which contains both read1 and read2. Default is FALSE.

`fixMGIid` the MGI FASTQ ID format is not compatible with many BAM operation tools, enable this option to fix it. Default is FALSE

`adapterTrimming`
A logical indicating whether run adapter trimming. Default is 'TRUE'

`adapterSequenceRead1`
the adapter for read1. For SE data, if not specified, the adapter will be auto-detected. For PE data, this is used if R1/R2 are found not overlapped.

`adapterSequenceRead2`
the adapter for read2 (PE data only). This is used if R1/R2 are found not overlapped. If not specified, it will be the same as <adapterSequenceRead1>

`adapterFasta` specify a FASTA file to trim both read1 and read2 (if PE) by all the sequences in this FASTA file.

`trimFrontRead1` trimming how many bases in front for read1, default is 0.

`trimTailRead1` trimming how many bases in tail for read1, default is 0'

`trimFrontRead2` trimming how many bases in front for read2. If it's not specified, it will follow read1's settings

`trimTailRead2` trimming how many bases in tail for read2. If it's not specified, it will follow read1's settings

`maxLengthRead1` if read1 is longer than maxLengthRead1, then trim read1 at its tail to make it as long as maxLengthRead1 Default 0 means no limitation.

`maxLengthRead2` if read2 is longer than maxLengthRead2, then trim read2 at its tail to make it as long as maxLengthRead2. Default 0 means no limitation. If it's not specified, it will follow read1's settings.

`forceTrimPolyG` A logical indicating force polyG tail trimming, trimming is only automatically enabled for Illumina NextSeq/NovaSeq . data.

`disableTrimPolyG`
A logical indicating disable polyG tail trimming.

`minLengthPolyG` the minimum length to detect polyG in the read tail. 10 by default.

`trimPolyX` A logical indicating force polyX tail trimming.

`minLengthPolyX` the minimum length to detect polyX in the read tail. 10 by default.

`cutWindowSize` the window size option shared by cutLowQualFront, cutLowQualTail, or cutSlideWindowRight. Range: 1~1000, default: 4

`cutLowQualTail` A logical indiccating move a sliding window from tail (3') to front, drop the bases in the window if its mean quality < threshold, stop otherwise. Default is 'FALSE'

`cutSlideWindowRight`
: A logical indicating move a sliding window from front to tail, if meet one window with mean quality < threshold, drop the bases in the window and the right part, and then stop. Default is 'FALSE'

`cutLowQualFront`
: A logical indiccating move a sliding window from front (5') to tail, drop the bases in the window if its mean quality < threshold, stop otherwise. Default is 'FALSE'

`cutMeanQual`
: the mean quality requirement option shared by cutLowQualFront, cutLowQualTail or cutSlideWindowRight. Range: 1~36, default: 20

`cutFrontWindowSize`
: the window size option of cutLowQualFront, default to cutWindowSize if not specified. default: 4

`cutFrontMeanQual`
: the mean quality requirement option for cutLowQualFront, default to cutMeanQual if not specified. default: 20

`cutTailWindowSize`
: the window size option of cutLowQualTail, default to cutWindowSize if not specified. default: 4

`cutTailMeanQual`
: the mean quality requirement option for cutLowQualTail, default to cutMeanQual if not specified. default: 20

`cutSlideWindowSize`
: the window size option of cutSlideWindowRight, default to cutWindowSize if not specified. default: 4

`cutSlideWindowQual`
: the mean quality requirement option for cutSlideWindowRight, default to cutMeanQual if not specified. default: 20

`qualityFiltering`
: A logical indicating run quality filtering. Default is 'TRUE'.

`qualityFilterPhred`
: the minimum quality value that a base is qualified. Default 15 means phred quality >=Q15 is qualified.

`qualityFilterPercent`
: Maximum percents of bases are allowed to be unqualified (0~100). Default 40 means 40%

`maxNfilter`
: maximum number of N allowed in the sequence. read/pair is discarded if failed to pass this filter. Default is 5

`averageQualFilter`
: if one read's average quality score < 'averageQualFilter', then this read/pair is discarded. Default 0 means no requirement.

`lengthFiltering`
: A logical indicating whether run lenght filtering. Default: TRUE

`minReadLength`
: reads shorter than minReadLength will be discarded, default is 15.

`maxReadLength`
: reads longer than maxReadLength will be discarded, default 0 means no limitation.

`lowComplexityFiltering`
: A logical indicating whethere run low complexity filter. The complexity is defined as the percentage of base that is different from its next base (base[i] != base[i+1]). Default is 'FALSE'

`minComplexity`
: the threshold for low complexity filter (0~100). Default is 30, which means 30% complexity is required. (int [=30])

`index1Filter`
: specify a file contains a list of barcodes of index1 to be filtered out, one barcode per line.

`index2Filter`
: specify a file contains a list of barcodes of index2 to be filtered out, one barcode per line.

`maxIndexMismatch`
: the allowed difference of index barcode for index filtering, default 0 means completely identical.

`correctionOverlap`
: A logical indicating run base correction in overlapped regions (only for PE data), default is 'FALSE'

`minOverlapLength`
: the minimum length to detect overlapped region of PE reads. This will affect overlap analysis based PE merge, adapter trimming and correction. 30 by default.

`maxOverlapMismatch`
: the maximum number of mismatched bases to detect overlapped region of PE reads. This will affect overlap analysis based PE merge, adapter trimming and correction. 5 by default.

`maxOverlapMismatchPercentage`
: the maximum percentage of mismatched bases to detect overlapped region of PE reads. This will affect overlap analysis based PE merge, adapter trimming and correction. Default 20 means 20%

`umi`
: A logical indicating whethere preprocessing unique molecular identifier (UMI). Default: 'FALSE'

`umiLoc`
: specify the location of UMI, can be (index1/index2/read1/read2/per_index/per_read)

`umiLength`
: length of UMI if the UMI is in read1/read2.

`umiPrefix`
: an string indication the following string is UMI (i.e. prefix=UMI, UMI=AATTCG, final=UMIAATTCG). Only letters, numbers, and '#" allowed. No prefix by default.

`umiSkipBaseLength`
: if the UMI is in read1/read2, skip 'umiSkipBaseLength' bases following UMI, default is 0.

`umiNoConnection`
: an logical indicating remove "_" between the UMI prefix string and the UMI string. Default is FALSE.

`umiIgnoreSeqNameSpace`
: an logical indicating ignore the space in the sequence name. Default is FALSE, the umi tag will be inserted into the sequence name before the first SPACE.

`overrepresentationAnalysis`
: A logical indicating overrepresentation analysis. Default is 'FALSE'

overrepresentationSampling
: one in 'overrepresentationSampling' reads will be computed for overrepresentation analysis (1~10000), smaller is slower, default is 20.

splitOutput
: number of files to be splitted (2~999). a sequential number prefix will be added to output name. Default is 0 (no split)

splitByLines
: split output by limiting lines of each file(>=1000), a sequential number prefix will be added to output name (0001.out.fq, 0002.out.fq...), default is 0 (disabled).

thread
: owrker thread number, default is 2

verbose
: output verbose log information

Value

returns a json object of the report.

Author(s)

Thomas Carroll, Wei Wang

Examples

```
# preprare for the input and output files.
# if the output file exists, it will be OVERWRITEN.

se_read1 <- system.file("extdata","Fox3_Std_small.fq.gz",package="Rfastp")
pe_read1 <- system.file("extdata","reads1.fastq.gz",package="Rfastp")
pe_read2 <- system.file("extdata","reads2.fastq.gz",package="Rfastp")
outputPrefix <- tempfile(tmpdir = tempdir())


# a normal single-end file

se_json_report <- rfastp(read1 = se_read1,
    outputFastq=paste0(outputPrefix, "_se"), thread = 4)


# merge paired-end data by overlap:

pe_json_report <- rfastp(read1 = pe_read1, read2 = pe_read2, merge = TRUE,
    outputFastq = paste0(outputPrefix, '_unpaired'),
    mergeOut = paste0(outputPrefix, '_merged.fastq.gz'))


# a clipr example

clipr_json_report <- rfastp(read1 = se_read1,
   outputFastq = paste0(outputPrefix, '_clipr'),
   disableTrimPolyG = TRUE,
   cutLowQualFront = TRUE,
   cutFrontWindowSize = 29,
   cutFrontMeanQual = 20,
```

```
   cutLowQualTail = TRUE,
   cutTailWindowSize = 1,
   cutTailMeanQual = 5,
   minReadLength = 29,
   adapterSequenceRead1 = 'GTGTCAGTCACTTCCAGCGG'
)
```

`trimSummary` *Summary of Fastq adapter and low quality trimming*

Description

generate a data frame of the Fastq trim summary.

Usage

```
trimSummary(json)
```

Arguments

`json`	the output json of function rfastq. [json]

Value

a data frame.

Author(s)

Wei Wang

Examples

```
outputPrefix <- tempfile(tmpdir = tempdir())
se_read1 <- system.file("extdata","Fox3_Std_small.fq.gz",package="Rfastp")
se_json_report <- rfastp(read1 = se_read1, outputFastq = outputPrefix,
   thread = 4, adapterSequenceRead1 = 'GTGTCAGTCACTTCCAGCGG')
trim_summary <- trimSummary(se_json_report)
```

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