Package ‘ngsReports’

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Title Load FastqQC reports and other NGS related files
Description This package provides methods and object classes for parsing FastQC reports and output summaries from other NGS tools into R. As well as parsing files, multiple plotting methods have been implemented for visualising the parsed data. Plots can be generated as static ggplot objects or interactive plotly objects.

URL https://github.com/smped/ngsReports

BugReports https://github.com/smped/ngsReports/issues

License file LICENSE

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Depends R (>= 4.2.0), BiocGenerics, ggplot2 (>= 3.4.0), patchwork (>= 1.1.1), tibble (>= 1.3.1)

Imports Biostrings, checkmate, dplyr (>= 1.1.0), DT, forcats, ggplot2, grDevices (>= 3.6.0), grid, jsonlite, lifecycle, lubridate, methods, pander, plotly (>= 4.9.4), readr, reshape2, rlang, rmarkdown, scales, stats, stringr, tidyselect (>= 0.2.3), utils, zoo

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Collate 'AllGenerics.R' 'validationFunctions.R' 'FastpData.R'
'FastpDataList.R' 'FastpFile.R' 'FastqcData.R'
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'importSJ.R' 'isCompressed.R' 'maxAdapterContent.R'
'ngsReports-package.R' 'overRep2Fasta.R' 'path.R'
'plotAdapterContent.R' 'plotAlignmentSummary.R'
'plotAssemblyStats.R' 'plotBaseQuals.R' 'plotDupLevels.R'
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- `plotGcContent.R`
- `plotInsertSize.R`
- `plotKmers.R`
- `plotNContent.R`
- `plotOverrep.R`
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- `pwf.R`
- `readTotals.R`
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.addPercent

Add a percentage sign to the end of a string

Usage

.addPercent(x)

Arguments

x Any vector

Value

character vector

Examples

x <- 1:10
ngsReports:::.addPercent(x)
**emptyPlot**

Create an empty plot with supplied text

**Description**

Create an empty plot with supplied text

**Usage**

```r
.emptyPlot(x)
```

**Details**

Create plot using `theme_void` and only with the supplied text

**Value**

A ggplot2 object

**Examples**

```r
ngsReports::emptyPlot("This is an empty plot")
```

---

**FastpFile-class**

The `.FastpFile Object Class`

**Description**

The `.FastpFile Object Class defines a path to the output from the standalone tool fastp. [Experimental]

**Arguments**

- `x` character(1) denoting a file.path

**Details**

This class simply refers to a fastp output file after checking for existence and validity (i.e. the correct internal structure). Underlying files are expected to be in json format

The helper function `.FastpFile()` is a simple constructor which checks validity and enables construction of other dependent classes.

**Value**

An object of class `.FastqcFile`
Slots

path  Character vector of length 1 which contains a valid file path.

Description

The .FastqcFile Object Class defines a path to the output from the standalone tool FastQC. [Stable]

Arguments

x character(1) denoting a file.path

Details

This class simply refers to a fastqc output file after checking for existence and validity (i.e. the correct internal structure). Underlying files can be zipped (*.fastqc.zip) or extracted directories.

The helper function .FastqcFile() is a simple constructor which checks validity and enables construction of other dependent classes.

Value

An object of class .FastqcFile

Slots

path  Character vector of length 1 which contains a valid file path.

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)[1]

# As this is the root structure, we can only call this
# function with an individual file
ff <- ngsReports:::.FastqcFile(fl)
.getToolName

Identify tool name

Description

Identify tool name for log files after reading in using readLines.

Usage

.getToolName(x, possTypes)

Arguments

x

Character vector as output when readLines to a supplied log file

Details

Checks for all the required fields in the lines provided

Value

logical(1)

.hidePWFRects

Hide PWF tooltips from line plots

Description

Hide tooltips from PWF rectangles in line plots

Usage

.hidePWFRects(x)

Arguments

x

plotlyObject$x$data

Value

plotlyObject$x$data
.isValidAdapterRemovalLog

*Check for a valid AdapterRemoval log*

**Description**

Checks internal structure of the parsed log file

**Usage**

`.isValidAdapterRemovalLog(x)`

**Arguments**

x Character vector containing parsed log file using the function `readLines`

**Value**

`logical(1)`

---

.isValidBowtieLog

*Check for correct structure of supplied Bowtie log files*

**Description**

Check for correct structure of supplied Bowtie log files after reading in using `readLines`.

**Usage**

`.isValidBowtieLog(x)`

**Arguments**

x Character vector as output when `readLines` to a supplied log file

**Details**

Checks for all the required fields in the lines provided

**Value**

`logical(1)`
.isValidBuscoLog

### Description

Check for correct structure of supplied BUSCO log files after reading in using readLines.

### Usage

```
.isValidBuscoLog(x)
```

### Arguments

x  
Character vector as output when readLines to a supplied log file

### Details

Checks for all the required fields in the lines provided

### Value

logical(1)

---

.isValidCutadaptLog  
Check for a valid cutadapt log

### Description

Checks internal structure of the parsed log file

### Usage

```
.isValidCutadaptLog(x)
```

### Arguments

x  
Character vector containing parsed log file using the function readLines

### Value

logical(1)
.isValidFeatureCountsLog

Description
Checks internal structure of the parsed log file

Usage
.isValidFeatureCountsLog(x)

Arguments
x
Character vector containing parsed log file using the function readLines

Value
logical(1)

.isValidDupplicationMetricsLog

Check for a valid Duplication Metrics log

Description
Checks internal structure of the parsed log file

Usage
.isValidDupplicationMetricsLog(x)

Arguments
x
Character vector containing parsed log file using the function readLines

Value
logical(1)
.isValidFlagstatLog

Check for correct structure of supplied flagstat

Description
Check for correct structure of supplied flagstat files

Usage
.isValidFlagstatLog(x)

Arguments
x Character vector as output when readLines to a supplied file

Details
Checks for all the required fields in the lines provided

Value
logical(1)

isValidHisat2Log

Check for a valid Hisat2 log

Description
Checks internal structure of the parsed log file

Usage
.isValidHisat2Log(x)

Arguments
x Character vector containing parsed log file using the function readLines

Value
logical(1)
.isValidMacs2CallpeakLog

*Check for correct structure of macs2 callpeak log*

**Description**
Check for correct structure of macs2 callpeak log

**Usage**
`isValidMacs2CallpeakLog(x)`

**Arguments**

- **x**
  Character vector as output when readLines to a supplied file

**Details**
Checks for all the required fields in the lines provided

**Value**
logical(1)

---

.isValidQuastLog

*Check for correct structure of supplied Quast log files*

**Description**
Check for correct structure of supplied Quast log files after reading in using readLines.

**Usage**
`isValidQuastLog(x)`

**Arguments**

- **x**
  Character vector as output when readLines to a supplied log file

**Details**
Checks for all the required fields in the lines provided

**Value**
logical(1)
isValidRnaseqcMetricsLog

Check for correct structure of rnaseqc metrics

Description
Check for correct structure of rnaseqc metrics files

Usage
.isValidRnaseqcMetricsLog(x)

Arguments
x Character vector as output when readLines to a supplied file

Details
Checks for all the required fields in the lines provided

Value
logical(1)

isValidStarLog

Check for a valid Star Alignment log

Description
Checks internal structure of the parsed log file

Usage
.isValidStarLog(x)

Arguments
x Character vector containing parsed log file using the function readLines

Value
logical(1)
.isValidTrimmomaticLog

*Check for correct structure of supplied Trimmomatic log files*

**Description**
Check for correct structure of supplied Trimmomatic log files after reading in using readLines.

**Usage**
```
.isValidTrimmomaticLog(x)
```

**Arguments**
- `x`: Character vector as output when readLines to a supplied log file

**Details**
Checks for all the required fields in the lines provided

**Value**
`logical(1)`

---

.isValidUmitoolsDedupLog

*Check for correct structure of umi_tools –dedup log*

**Description**
Check for correct structure of umi_tools –dedup log

**Usage**
```
.isValidUmitoolsDedupLog(x)
```

**Arguments**
- `x`: Character vector as output when readLines to a supplied file

**Details**
Checks for all the required fields in the lines provided

**Value**
`logical(1)`
.makeDendro

Make the dendrogram for heatmap-style plots

Description

Set the clusters for heatmap-style interactive plots

Usage

.makeDendro(df, rowVal, colVal, value)

Arguments

df           The data frame to be clustered
rowVal       The rows to be clustered
colVal       The value which will become column names
value        The value to use for the clustering

Value

A dendrogram

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fileList <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)
vals <- c("Filename", "Position", "Illumina_ Universal_Adapter")
ac <- getModule(fileList, "Adapter_Content")[[cols]]
ngsReports:::.makeDendro(df = ac,
                        rowVal = "Filename",
                        colVal = "Position",
                        value = "Illumina_ Universal_Adapter")

.makeLabels

Perform the checks and return the labels

Description

Checks for the presence of labels and returns defaults
Usage

```r
.makeLabels(
  x,
  labels,
  pattern = ".(fast|fq|bam|sam|cram).*",
  col = "Filename",
  ...
)
```

Arguments

- `x`: A data.frame with a column titled "Filename"
- `labels`: Named vector of labels for plotting
- `pattern`: character Regular expression to remove from filenames
- `col`: character Column to use for generating labels
- `...`: Not used

Details

Takes a named vector of labels and checks for the correct fields. If no vector is supplied, returns the file names missing the specified pattern, which defaults to removing the suffixes fastq(.gz), fq(.gz), bam, sam or cram.

Value

Named character vector

Examples

```r
f <- paste0(c("File1", "File2"), ".fastq")
df <- data.frame(Filename = f, stringsAsFactors = FALSE)
nsReports:::.makeLabels(df)
```

Description

Construct a gradient using PwfCols
Usage

```
.makePwfGradient(
  vals,
  pwfCols,
  breaks = c(0, 5, 10, 100),
  passLow = TRUE,
  na.value = "white"
)
```

Arguments

- **vals**: The values which need to have the scale generated
- **pwfCols**: An object of class PwfCols
- **breaks**: The breaks for the PWF bins
- **passLow**: Is the PASS category at the low or high end of the numeric range
- **na.value**: The colour to plot for missing values

Details

This constructs a list of arguments for passing to `scale_fill_gradientn()` using the values contained in the fill aesthetic and the supplied breaks for PASS/WARN/FAIL criteria.

Value

Returns a ggplot list

Description

Shortcut for making the status sidebar

Usage

```
.makeSidebar(status, key, pwfCols, usePlotly = TRUE)
```

Arguments

- **status**: A data.frame with columns 'Filename' & 'Status'
- **key**: A vector of values corresponding to the Filename column
- **pwfCols**: An object of class PwfCols
- **usePlotly**: If TRUE, output is a plotly panel
Value

if usePlotly = TRUE, a plotly object. The sidebar for an interactive plot showing PASS/WARN/FAIL status for each file. If usePlotly = FALSE the underlying ggplot object will be returned.

Description
Parse data from Adapter Removal log files

Usage
.parseAdapterRemovalLogs(data, which = 3)

Arguments

- `data`: List of lines read using readLines on one or more files
- `which`: which element of the log file to return. Can be 1:4, "sequences", "settings", "statistics" or "distribution"

Details
Checks for structure will have been performed

Value
tibble

Description
Parse data from Bowtie log files

Usage
.parseBowtieLogs(data, ...)

Arguments

- `data`: List of lines read using readLines on one or more files
- `...`: Not used
.parseBuscoLogs

Details
Checks for structure will have been performed

Value
data.frame

Description
Parse data from BUSCO log files

Usage
.parseBuscoLogs(data, ...)

Arguments
data List of lines read using readLines on one or more files
... Not used

Details
Checks for structure will have been performed

Value
data.frame

.parseCutadaptLogs

Description
Parse data from cutadapt log files

Usage
.parseCutadaptLogs(data, which = 1)

Arguments
data List of lines read using readLines on one or more files
which which element of the log file to return. Can be summary, adapter1, adapter2, adapter3 or overview, or any integer in 1:5
Details
Checks for structure will have been performed

Value
tibble

---

`.parseDuplicationMetricsLogs`

*Parse data from Picard duplicationMetrics log files*

Description
Parse data from Picard duplicationMetrics log files

Usage
`.parseDuplicationMetricsLogs(data, which = 1)`

Arguments
- `data`: List of lines read using readLines on one or more files
- `which`: which element of the log file to return. Can be 1:2, "metrics" or "histogram"

Details
Checks for structure will have been performed

Value
tibble

---

`.parseFeatureCountsLogs`

*Parse data from featureCounts summary files*

Description
Parse data from featureCounts summary files

Usage
`.parseFeatureCountsLogs(data, ...)`
.parseFlagstatLogs

Arguments

  data      List of lines read using readLines on one or more files
  ...      Not used

Details

  Checks for structure will have been performed

Value

  tibble

Description

  Parse data from samtools flagstat files

Usage

  .parseFlagstatLogs(data, ...)

Arguments

  data      List of lines read using readLines on one or more files
  ...      Not used

Details

  Checks for structure will have been performed

Value

  data.frame
.parseHisat2Logs

**Parse data from HISAT2 log files**

**Description**
Parse data from HISAT2 log files

**Usage**
```
.parseHisat2Logs(data, ...)
```

**Arguments**
- `data` List of lines read using readLines on one or more files
- `...` Not used

**Details**
Checks for structure will have been performed

**Value**
data.frame

---

.parseMacs2CallpeaksLogs

**Parse data from macs2 callpeak log files**

**Description**
Parse data from macs2 callpeak log files

**Usage**
```
.parseMacs2CallpeaksLogs(data, ...)
```

**Arguments**
- `data` List of lines read using readLines on one or more files
- `...` Not used

**Details**
Checks for structure will have been performed

**Value**
data.frame
.parseQuastLogs

**Description**
Parse data from BUSCO log files

**Usage**
```
.parseQuastLogs(data, ...)
```

**Arguments**
- `data` List of lines read using readLines on one or more files
- `...` Not used

**Details**
Checks for structure will have been performed

**Value**
data.frame

---

.parseRnaseqcMetricsLogs

**Description**
Parse data from rnaseqc metrics files

**Usage**
```
.parseRnaseqcMetricsLogs(data, ...)
```

**Arguments**
- `data` List of lines read using readLines on one or more files
- `...` Not used

**Details**
Checks for structure will have been performed

**Value**
data.frame
.parseStarLogs  Parse data from STAR log files

Description
Parse data from STAR log files

Usage
.parseStarLogs(data, ...)

Arguments
data List of lines read using readLines on one or more files
... Not used

Details
Checks for structure will have been performed

Value
tibble

.parseTrimomaticLogs  Parse data from trimmomatic log files

Description
Parse data from trimmomatic log files

Usage
.parseTrimomaticLogs(data, ...)

Arguments
data List of lines read using readLines on one or more files
... not used

Details
Checks for structure will have been performed

Value
tibble
**Description**

Parse data from umi_tools dedup files

**Usage**

```r
.parseUmitoolsDedupLogs(data, ...)
```

**Arguments**

- `data`: List of lines read using readLines on one or more files
- `...`: Not used

**Details**

Checks for structure will have been performed

**Value**

data.frame

---

**Description**

Add dendrogram & status bar to ggplot2 heatmap

**Usage**

```r
.prepHeatmap(x, status, segments, usePlotly, heat_w = 8, pwf, hv = NULL)
```

**Arguments**

- `x`: a ggplot2 heatmap produced by ngsReports
- `status`: a tibble with the columns Filename and Status
- `segments`: a dendrogram produced during clustering of samples
- `usePlotly`: logical(1)
- `hv`: character vector of fields to include in hoverinfo

**Value**

Either a ggplot2 object assembled using patchwork, or an interactive plotly object
.renderDendro  
*Set up dendrograms for interactive plots*

**Description**
A commonly used (hidden) function for setting up dendrograms for interactive plots. Based on code found at https://plot.ly/ggplot2/ggdendro-dendrograms/

**Usage**
```r
.renderDendro(df)
```

**Arguments**
- `df`  A `data.frame` as required

**Details**
Create plot using `theme_dendro`

**Value**
A plotly object

---

.splitByTab  
*Split elements of a vector into a data.frame*

**Description**
Split elements of a character vector by the tab separator

**Usage**
```r
.splitByTab(x, firstRowToNames = TRUE, tab = "\t")
```

**Arguments**
- `x`  A character vector
- `firstRowToNames`  logical Should the first element be used for column names
- `tab`  character The string used to represent the tab symbol

**Details**
This will split a vector into a data.frame checking that every line has the same number of separators. By default the first element will be set as the column names. This is designed to take input from `readLines()`
**Value**

A data frame

**Examples**

```r
x <- c("ColA\tColB", "Value1\tValue2")
ngsReports:::splitByTab(x, firstRowToNames = TRUE)
ngsReports:::splitByTab(x, firstRowToNames = FALSE)
```

**Description**

Add custom theme elements from dotArgs

**Usage**

```
.updateThemeFromDots(p, ...)
```

**Arguments**

- `p` ggplot object
- `...` Standard dot arguments

**Value**

ggplot2 object

---

**estGcDistn**

*Estimate a GC Content Distribution From Sequences*

**Description**

Generate a GC content distribution from sequences for a given read length and fragment length

**Usage**

```
estGcDistn(x, n = 1e+06, rl = 100, fl = 200, fragSd = 30, bins = 101, ...)
```

### S4 method for signature 'ANY'

```
estGcDistn(x, n = 1e+06, rl = 100, fl = 200, fragSd = 30, bins = 101, ...)
```

### S4 method for signature 'character'

```
estGcDistn(x, n = 1e+06, rl = 100, fl = 200, fragSd = 30, bins = 101, ...)
```

### S4 method for signature 'DNAStringSet'

```
estGcDistn(x, n = 1e+06, rl = 100, fl = 200, fragSd = 30, bins = 101, ...)
```
Arguments

- **x**: DNAStringSet or path to a fasta file
- **n**: The number of reads to sample
- **rl**: Read Lengths to sample
- **fl**: The mean of the fragment lengths sequenced
- **fragSd**: The standard deviation of the fragment lengths being sequenced
- **bins**: The number of bins to estimate
- **...**: Not used

Details

The function takes the supplied object and returns the theoretical GC content distribution. Using a fixed read length essentially leads to a discrete distribution so the bins argument is used to define the number of bins returned. This defaults to 101 for 0 to 100% inclusive.

The returned values are obtained by interpolating the values obtained during sampling. This avoids returned distributions with gaps and jumps as would be obtained setting readLengths at values not in multiples of 100.

Based heavily on https://github.com/mikelove/fastqcTheoreticalGC

Value

A tibble with two columns: GC_Content and Freq denoting the proportion of GC and frequency of occurrence respectively

Examples

```r
faDir <- system.file("extdata", package = "ngsReports")
faFile <- list.files(faDir, pattern = "fasta", full.names = TRUE)
df <- estGcDistn(faFile, n = 200)
```

---

### FastpData-class

**The FastpData Object Class**

#### Description

The FastpData Object Class [Experimental]

#### Usage

```r
FastpData(x)
```

#### Arguments

- **x**: Path to a single zip archive or extracted folder for a individual fastp report.
Details
This object class is the main object required for generating plots and tables. Instantiation will first check for a .json file with the correct data structure, and will then parse all the data into R as a FastpData object. Fastp modules are contained as individual slots, which can be viewed using slotNames. Sub-modules are also contained within many larger modules with modules being based on the sections within a fastp html report.
Individual modules can be returned using the function getModule() and specifying which module/sub-module is required. See getModule() for more details.

Value
An object of class FastpData

Slots
Summary Contains three submodules 1) Before_filtering, 2) After_filtering and 3) Filtering_result. All values presented in the initial table for individual fastp reports are contained in other sections of the report.
Adapters Contains a tibble with all data from this module
Duplication Contains a tibble with all duplication results
Insert_size Contains a tibble with all insert size estimates
Before_filtering,After_filtering The modules can be selected for either Read1 or Read2 paired logical(1) indicating whether the file is from paired-end sequencing
command character(1) with the executed command
version character(1) with the fastp version being used
path Path to the Fastp report

FastpDataList-class The FastpDataList Object Class

Description
The FastpDataList Object Class [Stable]

Usage
FastpDataList(x)

Arguments
x Character vector of file paths specifying paths to fastp.json.gz output

Value
An object of class FastpDataList
FastqcData-class

Slots

... this can either be a single character vector of paths to fastp files, or several instances of .FastpFile objects

Description

The FastqcData Object Class [Stable]

Usage

FastqcData(x)

Arguments

x Path to a single zip archive or extracted folder for a individual FastQC report.

Details

This object class is the main object required for generating plots and tables. Instantiation will first test for a compressed file (or extracted directory) with the correct data structure, and will then parse all the data into R as a FastqcData object. FastQC modules are contained as individual slots, which can be viewed using slotNames.

Individual modules can be returned using the function getModule() and specifying which module is required. See getModule() for more details.

Value

An object of class FastqcData

Slots

Summary Summary of PASS/WARN/FAIL status for each module
Basic_Statistics The Basic_Statistics table from the top of a FastQC html report
Per_base_sequence_quality The underlying data from the Per_base_sequence_quality module
Per_sequence_quality_scores The underlying data from the Per_sequence_quality_scores module
Per_base_sequence_content The underlying data from the Per_base_sequence_content module
Per_sequence_GC_content The underlying data from the Per_sequence_GC_content module
Per_base_N_content The underlying data from the Per_base_N_content module
Sequence_Length_Distribution The underlying data from the Sequence_Length_Distribution module
Sequence_Duplication_Levels  The underlying data from the Sequence_Duplication_Levels module
Overrepresented_sequences  The underlying data from the Overrepresented_sequences module
Adapter_Content  The underlying data from the Adapter_Content module
Kmer_Content  The underlying data from the Kmer_Content module
Total_Deduplicated_Percentage  Estimate taken from the plot data for Sequence_Duplication_Levels.
  Only included in later versions of FastQC
version  The version of FastQC used for generation of the report (if available)
path  Path to the FastQC report

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)[1]

# Load the FASTQC data as a FastqcData object
fd <- FastqcData(fl)
fd

---

FastqcDataList-class  The FastqcDataList Object Class

Description

The FastqcDataList Object Class [Stable]

Usage

FastqcDataList(x)

Arguments

x  Character vector of file paths specifying paths to FastQC reports

Value

An object of class FastqcDataList

Slots

... this can either be a single character vector of paths to FASTQC files, or several instances of .FastqcFile objects
Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)
fdl

fqcVersion(FastqcData-method)

Get the FASTQC version

Description

Get the FASTQC version used to generate the initial files

Usage

## S4 method for signature 'FastqcData'
fqcVersion(object)

## S4 method for signature 'FastqcDataList'
fqcVersion(object)

## S4 method for signature 'ANY'
fqcVersion(object)

Arguments

object An object of class FastqcData or FastqcDataList

Value

A character vector (FastqcData), or tibble (FastqcDataList)

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Get the FASTQC version
fqcVersion(fdl)
fqName

Return the Underlying Fastq File Names from Fastqc/Fastp Objects

Description

Return the Underlying Fastq File Names from Fastqc/Fastp Objects

Usage

fqName(object)

fqName(object)

fqName(object)

fqName(object) <- value

Arguments

object An object able to extract an Fastq name from

value Replacement value for fqName

Value

Returns the names of the Fastq files the FastQC report was generated from, without any preceding directories.
Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)
fqName(fdl)

nm <- paste0(letters[seq_along(fdl)], ".fq")
fqName(fdl) <- nm
fqName(fdl)

---

gcAvail  
List Genomes or Transcriptomes with Theoretical GC Content

Description

List available genomes or transcriptomes in a TheoreticalGC object

Usage

gcAvail(object, type)

## S4 method for signature 'TheoreticalGC'
gcAvail(object, type)

Arguments

object  An object of class TheoreticalGC
type  character indicating either Genome or Transcriptome

Details

An object of class TheoreticalGC can hold the theoretical GC content for one or more species, for either the genome or transcriptome. This function checks which species are available in the given object, for either the genome or transcriptome, as supplied to the parameter type.

Value

A tibble object

Examples

gcAvail(gcTheoretical, "Genome")
Theoretical GC content

Description

This object contains the theoretical GC content for each provided species, for both the genome and transcriptome, where available.

Usage

gcTheoretical

Format

An object of class TheoreticalGC of length 1.

Details

The object is defined with the S4 class TheoreticalGC. Species for which information is available can be found using the command gcAvail(gcTheoretical) and selecting the appropriate type.

Metadata is accessible using mData(gcTheoretical).

All GC content was calculated using code from https://github.com/mikelove/fastqcTheoreticalGC using BSgenome packages. This provides a default set of GC content data for common organisms generated using 100bp reads/fragments and 1e6 reads.

See Also

gcAvail

Examples

```r
## Check which genomes are included
gcAvail(gcTheoretical, "Genome")

## Check which transcriptomes are included
gcAvail(gcTheoretical, "Transcriptome")
```
getColours

Work with objects of class PwfCols

Description

Get and modify colours from objects of class PwfCols

Usage

## S4 method for signature 'PwfCols'
getColours(object)

## S4 method for signature 'PwfCols'
setColours(object, PASS, WARN, FAIL, MAX)

## S4 method for signature 'PwfCols'
setAlpha(object, alpha)

Arguments

- object: An object of class PwfCols
- PASS: The colour denoting PASS on all plots, in rgb format
- WARN: The colour denoting WARN on all plots, in rgb format
- FAIL: The colour denoting FAIL on all plots, in rgb format
- MAX: The colour denoting the limit of values in rgb format
- alpha: Numeric(1). Ranges from 0 to 1 by default, but can also be on the range 0 to 255.

Details

Use getColours to obtain the colours in an object of class PwfCols. These can be modified using the functions setColours and setAlpha.

Value

- getColours will return a character vector of colours corresponding to PASS/WARN/FAIL
- setColours will return an object of class PwfCols
- setAlpha will return an object of class PwfCols

Examples

```
getColours(pwf)

# How to add transparency
pwf2 <- setAlpha(pwf, 0.1)
getColours(pwf2)
```
**getGC**

*Get Theoretical GC content*

**Description**

Get the GC content data from a TheoreticalGC object

**Usage**

```r
getGC(object, name, type)
```

## S4 method for signature 'ANY'
```
getGC(object, type)
```

## S4 method for signature 'TheoreticalGC'
```
getGC(object, name, type)
```

**Arguments**

- `object` An object of class Theoretical GC
- `name` The Name of the species in 'Gspecies' format, e.g. Hsapiens
- `type` The type of GC content. Can only be either "Genome" or "Transcriptome"

**Value**

A tibble object

**Examples**

```r
gcTheoretical, name = "Hsapiens", type = "Genome")
```

---

**getModule,FastqcData-method**

*Retrieve a given module from a Fastqc* Object

**Description**

Retrieve a specific module from a Fastqc* object as a data.frame
Usage

```r
## S4 method for signature 'FastqcData'
getMethod(object, module)

## S4 method for signature 'FastqcDataList'
getMethod(object, module)

## S4 method for signature 'ANY'
getMethod(object, module)

## S4 method for signature 'FastpData'
getMethod(object, module)

## S4 method for signature 'FastpDataList'
getMethod(object, module)
```

Arguments

- **object**: Can be a `FastqcData`, `fastqcDataList`, or simply a character vector of paths
- **module**: The requested module as contained in a FastQC report. Possible values are `Summary`, `Basic_Statistics`, `Per_base_sequence_quality`, `Per_tile_sequence_quality`, `Per_sequence_quality_scores`, `Per_base_sequence_content`, `Per_sequence_GC_content`, `Per_base_N_content`, `Sequence_Length_Distribution`, `Sequence_Duplication_Levels`, `Overrepresented_sequences`, `Adapter_Content`, `Kmer_Content`, `Total_Deduplicated_Percentage`. Note that spelling and capitalisation is exactly as contained within a FastQC report, with the exception that spaces have been converted to underscores. Partial matching is implemented for this argument.

Details

This function will return a given module from a Fastqc* object as a data.frame. Note that each module will be its own unique structure, although all will return a data.frame.

Value

A single tibble containing module-level information from all FastQC reports contained in the Fastqc* object.

Examples

```r
# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Extract the Summary module, which corresponds to the PASS/WARN/FAIL flags
getMethod(fdl, "Summary")
```
getSummary,.FastqcFile-method

# The Basic_Statistics module corresponds to the table at the top of each # FastQC report
getModule(fd1, "Basic_Statistics")

getSummary,.FastqcFile-method

Get the summary information from Fastqc Files

Description

Read the information from the summary.txt files in each .FastqcFile

Usage

## S4 method for signature '.FastqcFile'
getSummary(object)

## S4 method for signature 'ANY'
getSummary(object)

## S4 method for signature 'FastqcData'
getSummary(object)

## S4 method for signature 'FastqcDataList'
getSummary(object)

Arguments

object Can be a FastqcData, FastqcDataList object or a vector of paths to unparsed FastQC reports.

Details

This simply extracts the summary of PASS/WARN/FAIL status for every module as defined by the tool FastQC for each supplied file.

Value

A tibble containing the PASS/WARN/FAIL status for each module, as defined in a FastQC report.

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(f1)

# Return a tibble/tibble with the raw information
getSummary(fdl)

---

**importNgsLogs**  
Import Various NGS-related log files

**Description**

[Maturing] Imports NGS-related log files such as those generated from stderr.

**Usage**

```r
importNgsLogs(x, type = "auto", which, stripPaths = TRUE)
```

**Arguments**

- **x** character. Vector of filenames. All log files must be of the same type. Duplicate file paths will be silently ignored.
- **type** character. The type of file being imported. Can be one of bowtie, bowtie2, hisat2, star, flagstat, featureCounts, duplicationMetrics, cutadapt, umitoolsDedup, macs2Callpeak, adapterRemoval, rnaseqcMetrics, quast or busco. Defaults to type = "auto" which will automatically detect the file type for all implemented types.
- **which** Which element of the parsed object to return. Ignored in all file types except when type is set to duplicationMetrics, cutadapt or adapterRemoval. See details for possible values. To return all elements, set this value to 'all'
- **stripPaths** logical(1). Remove paths from the Filename column

**Details**

Imports one or more log files as output by tools such as: bowtie, bowtie2, featureCounts, Hisat2, STAR, picard MarkDuplicates, cutadapt, flagstat, macs2Callpeak Adapter Removal, trimmomatic, rnaseqcMetrics, quast or busco. autoDetect can be used to detect the log type by parsing the file.

The featureCounts log file corresponds to the counts.out.summary, not the main counts.out file. Whilst most log files return a single tibble, some are more complex with multiple modules.

adapterRemoval can return one of four modules (which = 1:4). When calling by name, the possible values are sequences, settings, statistics or distribution. Partial matching is implemented.

cutadapt can return one of five modules (which = 1:5). When calling by name the possible modules are summary, adapter1, adapter2, adapter3 or overview. Note that adapter2/3 may be missing from these files depending on the nature of your data. If cutadapt log files are obtained using report=minimal, all supplied log files must be of this format and no modules can be returned.
duplicatesMetrics will return either the metrics of histogram. These can be requested by setting which as 1 or 2, or naming either module.

Value

A tibble. Column names are broadly similar to the text in supplied files, but have been modified for easier handling under R naming conventions.

Examples

```r
f <- c("bowtiePE.txt", "bowtieSE.txt")
bowtieLogs <- system.file("extdata", f, package = "ngsReports")
df <- importNgsLogs(bowtieLogs, type = "bowtie")
```

---

**importSJ**  
**Import STAR Splice Junctions**

**Description**

Import the SJ.out.tab files produced by STAR

**Usage**

```r
importSJ(x, stripPaths = TRUE)
```

**Arguments**

- `x`: vector of file paths to SJ.out.tab files
- `stripPaths`: logical(1) Remove directory prefixes from the file paths in `x`

**Details**

Imports one or more splice-junction output files as produced by STAR. If all are located in separated directories with identical names, be sure to set the argument `stripPaths = FALSE`

All co-ordinates are 1-based, in keeping with the STAR manual

**Value**

A tibble

**Author(s)**

Stephen Pederson [stephen.pederson@adelaide.edu.au](mailto:stephen.pederson@adelaide.edu.au)
isCompressed

Description

Check to see if a file, or vector of files is compressed

Usage

isCompressed(path, type = c("zip", "gzip"), verbose = FALSE)

Arguments

path  
The path to one or more files

type  
The type of compression to check for. Currently only ZIP/GZIP files have been implemented.

verbose  
logical/integer Determine the level of output to show as messages

Details

Reads the first four bytes from the local file header. If the file is a .ZIP file, this should match the magic number PK\003\004.

This function assumes that the first thing in a zip archive is the .ZIP entry with the local file header signature. ZIP files containing a self-extracting archive may not exhibit this structure and will return FALSE.

Value

A logical vector

Examples

# Get the files included with the package
fileDir <- system.file("extdata", package = "ngsReports")
allFiles <- list.files(fileDir, pattern = "zip$", full.names = TRUE)
isCompressed(allFiles)
maxAdapterContent  

Get the maximum Adapter Content

Description

Get the maximum Adapter Content across one or more FASTQC reports

Usage

maxAdapterContent(x, asPercent = TRUE)

Arguments

x
  Can be a .FastqcFile, FastqcData, FastqcDataList or path

asPercent
  logical. Format the values as percentages with the added \% symbol

Details

This will extract the Adapter_Content module from the supplied object, and provide a tibble with the final value for each file.

Value

A tibble object containing the percent of reads with each adapter type at the final position

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Get the maxAdapterContent
maxAdapterContent(fdl)
mData

Extract Metadata for TheoreticalGC objects

Description

Extract Metadata for TheoreticalGC objects

Usage

mData(object)

## S4 method for signature 'TheoreticalGC'
mData(object)

Arguments

object An object of class Theoretical GC

Value

A tibble object

Examples

mData(gcTheoretical)

overRep2Fasta

Write fasta of Over-Represented sequences.

Description

Output overrepresented sequences to disk in fasta format.

Usage

overRep2Fasta(x, path, n = 10, labels, noAdapters = TRUE, ...)

## S4 method for signature 'ANY'
overRep2Fasta(x, path, n = 10, labels, noAdapters = TRUE, ...)

## S4 method for signature 'FastqcData'
overRep2Fasta(x, path, n = 10, labels, noAdapters = TRUE, ...)

## S4 method for signature 'FastqcDataList'
overRep2Fasta(x, path, n = 10, labels, noAdapters = TRUE, ...)
path

Arguments

- `x` Can be a FastqcData or FastqcDataList
- `path` Path to export the fasta file to. Reverts to a default in the working directory if not supplied
- `n` The number of sequences to output
- `labels` An optional named factor of labels for the file names. All filenames must be present in the names. File extensions are dropped by default.
- `noAdapters` logical. Remove any sequences identified as possible adapters or primers by FastQC
- `...` Used to pass any alternative patterns to remove from the end of filenames

Details

Fasta will contain Filename, Possible Source, Percent of total reads

Value

Exports to a fasta file, and returns the fasta information invisibly

Examples

```r
# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Export the top10 Overrepresented Sequences as a single fasta file
faOut <- file.path(tempdir(), "top10.fa")
overRep2Fasta(fdl, path = faOut)
```

path

Return the File Paths from an object

Description

Return the File Paths from an object
Usage

```r
## S4 method for signature '.FastqcFile'
path(object)

## S4 method for signature 'FastqcData'
path(object)

## S4 method for signature 'FastqcDataList'
path(object)

## S4 method for signature '.FastpFile'
path(object)

## S4 method for signature 'FastpData'
path(object)

## S4 method for signature 'FastpDataList'
path(object)
```

Arguments

- `object` An object of class `.FastqcFile`

Details

Obtains the file.path for objects of multiple classes

Value

A character vector of the file paths to the underlying FastQC reports

Examples

```r
# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)
path(fdl)
```

---

**plotAdapterContent**

*Draw an Adapter Content Plot*

Description

Draw an Adapter Content Plot across one or more FASTQC reports
plotAdapterContent

Usage

plotAdapterContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  ...
)

## S4 method for signature 'ANY'
plotAdapterContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  ...
)

## S4 method for signature 'FastqcData'
plotAdapterContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  pwfCols,
  showPwf = TRUE,
  warn = 5,
  fail = 10,
  scaleColour = NULL,
  plotlyLegend = FALSE,
  ...
)

## S4 method for signature 'FastqcDataList'
plotAdapterContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  pwfCols,
  showPwf = TRUE,
  warn = 5,
  fail = 10,
  plotType = c("heatmap", "line"),
  adapterType = "Total",
  cluster = FALSE,
  dendrogram = FALSE,
  heat_w = 8L,
scaleFill = NULL,
scaleColour = NULL,
plotlyLegend = FALSE,
...
)

## S4 method for signature 'FastpData'
plotAdapterContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".*(fast|fq|bam).*",
  scaleFill = NULL,
  plotlyLegend = FALSE,
  plotTheme = theme(),
  ...
)

## S4 method for signature 'FastpDataList'
plotAdapterContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".*(fast|fq|bam).*",
  pwfCols,
  showPwf = FALSE,
  warn = 5,
  fail = 10,
  cluster = FALSE,
  dendrogram = FALSE,
  scaleFill = NULL,
  plotTheme = theme(),
  heat_w = 8L,
  ...
)

Arguments

x Can be a `FastqcData`, a `FastqcDataList` or character vector of file paths
usePlotly logical. Output as ggplot2 (default) or plotly object.
labels An optional named vector of labels for the file names. All filenames must be present in the names.
pattern regex used to trim the ends of all filenames for plotting
... Used to pass additional attributes to theme() for FastQC objects and geoms for Fastp objects
pwfCols Object of class `PwfCols()` containing the colours for PASS/WARN/FAIL
showPwf logical(1) Show PASS/WARN/FAIL status as would be included in a standard FastQC report
plotAdapterContent

warn, fail
The default values for warn and fail are 5 and 10 respectively (i.e. percentages)

plotlyLegend
logical(1) Show legend when choosing interactive plots. Ignored for heatmaps

plotType
character. Can only take the values plotType = "heatmap" or plotType = "line"

adapterType
A regular expression matching the adapter(s) to be plotted. To plot all adapters summed, specify adapterType = "Total". This is the default behaviour.

cluster
logical default FALSE. If set to TRUE, fastqc data will be clustered using hierarchical clustering

dendrogram
logical redundant if cluster is FALSE if both cluster and dendrogram are specified as TRUE then the dendrogram will be displayed.

heat_w
Width of the heatmap relative to other plot components

scaleFill, scaleColour
scale_fill* and scale_colour_* objects

plotTheme
Set theme elements by passing a theme

Details
This extracts the Adapter_Content module from the supplied object and generates a ggplot2 object, with a set of minimal defaults. The output of this function can be further modified using the standard ggplot2 methods.

When x is a single or FastqcData object line plots will always be drawn for all adapters. Otherwise, users can select line plots or heatmaps. When plotting more than one fastqc file, any undetected adapters will not be shown.

An interactive version of the plot can be made by setting usePlotly as TRUE

Value
A standard ggplot2 object, or an interactive plotly object

Examples
# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# The default plot
plotAdapterContent(fdl)

# Also subset the reads to just the R1 files
r1 <- grepl("R1", fqName(fdl))
plotAdapterContent(fdl[r1])

# Plot just the Universal Adapter
# and change the y-axis using ggplot2::scale_y_continuous
plotAdapterContent(fdl, adapterType ="Illumina_Universal", plotType = "line") +
```
facet_wrap(~Filename) +
guides(colour = "none")

# For FastpData object, the plots are slightly different
fp <- FastpData(system.file("extdata/fastp.json.gz", package = "ngsReports"))
plotAdapterContent(fp, scaleFill = scale_fill_brewer(palette = "Set1"))
```

---

**plotAlignmentSummary**  
*Plot a summary of alignments*

**Description**  
Plot a summary of alignments from a set of log files

**Usage**
```
plotAlignmentSummary(
  x,
  type = c("star", "bowtie", "bowtie2", "hisat2"),
  usePlotly = FALSE,
  stripPaths = TRUE,
  asPercent = FALSE,
  ...,
  fill = c("red", "yellow", "blue", rgb(0, 0.5, 1))
)
```

**Arguments**
- `x` Paths to one or more alignment log files
- `type` The aligner used. Can be one of star, bowtie, bowtie2 or hisat2
- `usePlotly` logical. If TRUE an interactive plot will be generated.
- `stripPaths` logical(1). Remove paths from the Filename column
- `asPercent` Show alignments as percentages, with the alternative (FALSE) being the total number of reads If FALSE a ggplot object will be output
- `...` Used to pass additional attributes to theme() and between methods
- `fill` Colours used to fill the bars. Passed to scale_fill_manual.

**Details**  
Loads a set of alignment log files and creates a default plot. Implemented aligners are bowtie, bowtie2, Hisat2 and STAR.

**Value**  
A ggplot2 object, or a plotly object
plotAssemblyStats

Examples

f <- c("bowtie2PE.txt", "bowtie2SE.txt")
bowtie2logs <- system.file("extdata", f, package = "ngsReports")
plotAlignmentSummary(bowtie2logs, "bowtie2")

plotAssemblyStats
Plot a summary of assembly logs

Description

Plot a summary of assembly stats from a set of log files

Usage

plotAssemblyStats(
  x,
  type = c("quast", "busco"),
  usePlotly = FALSE,
  plotType = c("bar", "paracoord"),
  ...
)

Arguments

  x          Paths to one or more log files
  type       The tool used. Can be one of quast or busco
  usePlotly  logical. If TRUE an interactive plot will be generated. If FALSE a ggplot object will be output
  plotType   character. Plot type to output, one of bar or paracoord.
  ...        Used to pass additional attributes to theme() and between methods

Details

Loads a set of assembly log files and creates a default plot. Implemented tools are quast and BUSCO. quast will plot a parallele coordinate plot of some assembly statistics BUSCO will plot a stacked barplot of completeness statistics

Value

A ggplot2 object, or a plotly object
Examples

# getquast log filenames
quastFiles <- system.file("extdata",
c("quast1.tsv", "quast2.tsv"), package = "ngsReports")

# The default plot
plotAssemblyStats(quastFiles)

plotBaseQuals

Plot the Base Qualities for each file

Description

Plot the Base Qualities for each file as separate plots

Usage

plotBaseQuals(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'ANY'
plotBaseQuals(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'FastqcData'
plotBaseQuals(
x,
usePlotly = FALSE,
labels,
pattern = ".(fast|fq|bam).*",
pwfCols,
warn = 25,
fail = 20,
boxWidth = 0.8,
showPwf = TRUE,
plotlyLegend = FALSE,
...)

## S4 method for signature 'FastqcDataList'
plotBaseQuals(
x,
usePlotly = FALSE,
labels,
pattern = ".(fast|fq|bam).*",
pwfCols,
warn = 25,
fail = 20,
showPwf = TRUE,
boxWidth = 0.8,
plotType = c("heatmap", "boxplot"),
plotValue = "Mean",
cluster = FALSE,
dendrogram = FALSE,
nc = 2,
heat_w = 8L,
... 
)

## S4 method for signature 'FastpData'
plotBaseQuals(
x,
usePlotly = FALSE,
labels,
pattern = ".(fast|fq|bam).*",
pwfCols,
warn = 25,
fail = 20,
showPwf = FALSE,
module = c("Before_filtering", "After_filtering"),
reads = c("read1", "read2"),
readsBy = c("facet", "linetype"),
bases = c("A", "T", "C", "G", "mean"),
scaleColour = NULL,
plotTheme = theme(),
plotlyLegend = FALSE,
... 
)

## S4 method for signature 'FastpDataList'
plotBaseQuals(
x,
usePlotly = FALSE,
labels,
pattern = ".(fast|fq|bam).*",
pwfCols,
warn = 25,
fail = 20,
showPwf = FALSE,
module = c("Before_filtering", "After_filtering"),
plotType = "heatmap",
plotValue = c("mean", "A", "T", "C", "G"),
scaleFill = NULL,
plotTheme = theme(),
cluster = FALSE,
dendrogram = FALSE,
plotBaseQuals

heat_w = 8L,
...
)

Arguments

x Can be a FastqcData, FastqcDataList or character vector of file paths
usePlotly logical Default FALSE will render using ggplot. If TRUE plot will be rendered with plotly
labels An optional named vector of labels for the file names. All filenames must be present in the names.
pattern Regex to remove from the end of the Fastp report and Fastq file names
... Used to pass additional attributes to theme() and between methods
pwfCols Object of class PwfCols() to give colours for pass, warning, and fail values in plot
warn, fail The default values for warn and fail are 30 and 20 respectively (i.e. percentages)
boxWidth set the width of boxes when using a boxplot
showPwf Include the Pwf status colours
plotlyLegend logical(1) Show legend for interactive plots. Only called when drawing line plots
plotType character Can be either "boxplot" or "heatmap"
plotValue character Type of data to be presented. Can be any of the columns returned by the appropriate call to getModule()
cluster logical default FALSE. If set to TRUE, fastqc data will be clustered using hierarchical clustering
dendrogram logical redundant if cluster is FALSE if both cluster and dendrogram are specified as TRUE then the dendrogram will be displayed.
nc numeric. The number of columns to create in the plot layout. Only used if drawing boxplots for multiple files in a FastqcDataList
heat_w Relative width of any heatmap plot components
module Select Before and After filtering when using a FastpDataList
reads Create plots for read1, read2 or all when using a FastpDataList
readsBy If paired reads are present, separate using either linetype or by facet
bases Which bases to include on the plot
scaleColour ggplot discrete colour scale, passed to lines
plotTheme theme object
scaleFill ggplot2 continuous scale. Passed to heatmap cells
Details

When acting on a `FastqcDataList`, this defaults to a heatmap using the mean `Per_base_sequence_quality` score. A set of plots which replicate those obtained through a standard FastQC html report can be obtained by setting `plotType = "boxplot"`, which uses `facet_wrap` to provide the layout as a single `ggplot` object.

When acting an a `FastqcData` object, this replicates the `Per base sequence quality` plots from FastQC with no faceting.

For large datasets, subsetting by R1 or R2 reads may be helpful.

An interactive plot can be obtained by setting `usePlotly = TRUE`.

Value

A standard `ggplot2` object or an interactive `plotly` object

Examples

```r
# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a `FastqcDataList` object
fdl <- FastqcDataList(fl)

# The default plot for multiple libraries is a heatmap
plotBaseQuals(fdl)

# The default plot for a single library is the standard boxplot
plotBaseQuals(fdl[[1]])

# `FastpData` objects have qualities by base
fp <- FastpData(system.file("extdata/fastp.json.gz", package = "ngsReports"))
plotBaseQuals(
  fp, plotTheme = theme(plot.title = element_text(hjust = 0.5))
)
```

---

**plotDupLevels**  
*Plot the combined Sequence_Duplication_Levels information*

Description

Plot the Sequence_Duplication_Levels information for a set of FASTQC reports
Usage

plotDupLevels(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'ANY'
plotDupLevels(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'FastqcData'
plotDupLevels(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
  warn = 20,
  fail = 50,
  showPwf = TRUE,
  plotlyLegend = FALSE,
  lineCol = c("red", "blue"),
  lineWidth = 1,
  ...
)

## S4 method for signature 'FastqcDataList'
plotDupLevels(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
  warn = 20,
  fail = 50,
  showPwf = TRUE,
  plotlyLegend = FALSE,
  lineCol = c("red", "blue"),
  lineWidth = 1,
  ...
)

## S4 method for signature 'FastpData'
plotDupLevels(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  ...
plotDupLevels

pwfCols,
warn = 20,
fail = 50,
showPwf = FALSE,
maxLevel = 10,
lineCol = "red",
barFill = "dodgerblue4",
barCol = barFill,
plotlyLegend = FALSE,
plotTheme = theme(),
...
)

## S4 method for signature 'FastpDataList'
plotDupLevels(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
pwfCols,
warn = 20,
fail = 50,
showPwf = FALSE,
plotlyLegend = FALSE,
plotType = c("bar", "heatmap"),
barFill = "blue",
barCol = "blue",
cluster = FALSE,
dendrogram = FALSE,
scaleFill = NULL,
plotTheme = theme(),
heat_w = 8,
maxLevel = 10,
...
)

Arguments

x
  Can be a FastqcData, FastqcDataList or file path
usePlotly
  logical Default FALSE will render using ggplot. If TRUE plot will be rendered with plotly
labels
  An optional named vector of labels for the file names. All filenames must be present in the names. File extensions are dropped by default.
pattern
  regex to remove from the end of fastp & fastq file names
...
  Used to pass additional attributes to theme() and between methods
pwfCols
  Object of class PwfCols() to give colours for pass, warning, and fail values in the plot
plotDupLevels

warn, fail The default values for warn and fail are 20 and 50 respectively (i.e. percentages) showPwf logical(1) Show PWF rectangles in the background plotlyLegend logical(1) Show legend for line plots when using interactive plots lineCol, lineWidth Colours and width of lines drawn deduplication Plot Duplication levels 'pre' or 'post' deduplication. Can only take values "pre" and "post" plotType Choose between "heatmap" and "line" cluster logical default FALSE. If set to TRUE, fastqc data will be clustered using hierarchical clustering dendrogram logical Plot will automatically be clustered if TRUE. heatCol Colour palette used for the heatmap heat_w Relative width of the heatmap relative to other plot components maxLevel The maximum duplication level to plot. Beyond this level, all values will be summed barFill, barCol Colours for bars when calling geom_col() plotTheme theme object. Applied after a call to theme_bw() scaleFill Discrete scale used to fill heatmap cells

Details

This extracts the Sequence_Duplication_Levels from the supplied object and generates a ggplot2 object, with a set of minimal defaults. For multiple reports, this defaults to a heatmap with block sizes proportional to the percentage of reads belonging to that duplication category.

If setting usePlotly = FALSE, the output of this function can be further modified using standard ggplot2 syntax. If setting usePlotly = TRUE an interactive plotly object will be produced.

Value

A standard ggplot2 or plotly object

Examples

```
# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Draw the default plot for a single file
plotDupLevels(fdl[[1]])
plotDupLevels(fdl)
```
plotFastqcPCA

plotFastqcPCA

Draw a PCA plot for Fast QC modules

Description

Draw a PCA plot for Fast QC modules across multiple samples [Experimental]

Usage

plotFastqcPCA(
  x,
  module = "Per_sequence_GC_content",
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  sz = 4,
  groups,
  ...
)

## S4 method for signature 'ANY'
plotFastqcPCA(
  x,
  module = "Per_sequence_GC_content",
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  sz = 4,
  groups,
  ...
)

## S4 method for signature 'character'
plotFastqcPCA(
  x,
  module = "Per_sequence_GC_content",
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  sz = 4,
  groups,
  ...
)

## S4 method for signature 'FastqcDataList'
plotFastqcPCA(
  x,
module = "Per_sequence_GC_content",
usePlotly = FALSE,
labels,
pattern = ".(fast|fq|bam).*",
sz = 4,
groups,
pc = 1:2,
...)

Arguments

x Can be a FastqcDataList or character vector of file paths
module character vector containing the desired FastQC module (eg. c("Per_base_sequence_quality",
"Per_base_sequence_content"))
usePlotly logical. Output as ggplot2 (default) or plotly object.
labels An optional named vector of labels for the file names. All file names must be
present in the names of the vector.
pattern Regex to remove from the end of any filenames
sz The size of the text labels
groups Optional factor of the same length as x. If provided, the plot will be coloured
using this factor as the defined groups. Ellipses will also be added to the final
plot.
... Used to pass additional attributes to theme() and between methods
pc The two components to be plotted

Details

This carries out PCA on a single FastQC module and plots the output using either ggplot or
plotly. Current modules for PCA are Per_base_sequence_quality, Per_sequence_quality_scores,
Per_sequence_GC_content, Per_base_sequence_content, and Sequence_Length_Distribution.

If a factor is provided in the groups argument, this will be applied to the plotting colours and ellipses
will be drawn using these groups. Only the labels will be plotted using geom_text()

Value

A standard ggplot2 object, or an interactive plotly object

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)
grp <- as.factor(gsub(".+\([12]\).+", "\1", fqName(fdl)))
plotFastqcPCA(fdl, module = "Per_sequence_GC_content", groups = grp)

plotGcContent  Plot the Per Sequence GC Content

Description

Plot the Per Sequence GC Content for a set of FASTQC files

Usage

plotGcContent(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'ANY'
plotGcContent(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'FastqcData'
plotGcContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  theoreticalGC = TRUE,
  gcType = c("Genome", "Transcriptome"),
  species = "Hsapiens",
  GCobject,
  plotlyLegend = FALSE,
  Fastafile,
  n = 1e+06,
  counts = FALSE,
  scaleColour = NULL,
  lineCols = c("red3", "black"),
  linetype = 1,
  linewidth = 0.5,
  ...
)

## S4 method for signature 'FastqcDataList'
plotGcContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  theoreticalGC = TRUE,
  gcType = c("Genome", "Transcriptome"),
  ...)
species = "Hsapiens",
GCobject,
Fastfile,
n = 1e+06,
plotType = c("heatmap", "line", "cdf"),
cluster = FALSE,
dendrogram = FALSE,
heat_w = 8,
pwfCols,
showPwf = TRUE,
scaleFill = NULL,
scaleColour = NULL,
plotlyLegend = FALSE,
lineCols = RColorBrewer::brewer.pal(12, "Paired"),
linetype = 1,
linewidth = 0.5,
... )

## S4 method for signature 'FastpData'
plotGcContent(
x,
usePlotly = FALSE,
labels,
pattern = ".(fast|fq|bam).\*",
theoreticalGC = TRUE,
gcType = c("Genome", "Transcriptome"),
species = "Hsapiens",
GCobject,
Fastfile,
n = 1e+06,
plotType = "bar",
scaleFill = NULL,
plotlyLegend = FALSE,
plotTheme = theme(),
... )

## S4 method for signature 'FastpDataList'
plotGcContent(
x,
usePlotly = FALSE,
labels,
pattern = ".(fast|fq|bam).\*",
theoreticalGC = TRUE,
gcType = c("Genome", "Transcriptome"),
species = "Hsapiens",
GCobject,
plotGcContent

Fastafile,
  n = 1e+06,
plotType = "bar",
scaleFill = NULL,
plotTheme = theme(),
plotlyLegend = FALSE,
...
)

Arguments

x Can be a FastqcData, FastqcDataList or character vector of file paths
usePlotly logical Default FALSE will render using ggplot. If TRUE plot will be rendered
  with plotly
labels An optional named vector of labels for the file names.
pattern Pattern to remove from the end of filenames
... Used to pass various potting parameters to themes and geoms.
thoreticalGC logical default is FALSE to give the true GC content, set to TRUE to normalize
  values of GC_Content by the theoretical values using gcTheoretical(). species must be specified. For Fastqc* objects, the entire distributions will be
  used, whereas for the Fastp* objects, only the expected mean value is shown as a
  horizontal line
gcType character Select type of data to normalize GC content against. Accepts either
  "Genome" (default) or "Transcriptome".
species character if gcTheory is TRUE it must be accompanied by a species. Species
  currently supported can be obtained using mData(gcTheoretical)
GCObject an object of class GCTheoretical. Defaults to the gcTheoretical object supplied
  with the package
plotlyLegend logical(1) Show legend on interactive line plots
Fastafile a fasta file contains DNA sequences to generate theoretical GC content
n number of simulated reads to generate theoretical GC content from Fastafile
counts logical. Plot the counts from each file if counts = TRUE, otherwise frequencies
  will be plotted. Ignored if calling the function on a FastqcDataList.
scaleColour ggplot2 scale for line colours
lineCols, linetype, linewidth Line colour type and width for observed and theoretical GC lines
plotType Takes values "line", "heatmap" or "cdf"
cluster logical default FALSE. If set to TRUE, fastqc data will be clustered using hier-
  archical clustering
dendrogram logical redundant if cluster is FALSE if both cluster and dendrogram are
  specified as TRUE then the dendrogram will be displayed.
heat_w Relative width of any heatmap plot components
plotInsertSize

Description

Plot the insert size distribution from one of Fastp reports

plotInsertSize

Object of class \texttt{PwfCols()} to give colours for pass, warning, and fail values in plot

\texttt{showPwf} logical(1) Show Pwf Status on the plot

\texttt{scaleFill} ggplot2 scale for filling heatmap cells or bars

\texttt{plotTheme} theme object

Details

Makes plots for GC\_Content. When applied to a single FastqcData object a simple line plot will be
drawn, with Theoretical GC content overlaid if desired.

When applied to multiple FastQC reports, the density at each GC content bin can be shown as a
heatmap by setting \texttt{theoreticalGC} = \texttt{FALSE}. By default the difference in observed and expected
theoretical GC is shown. Species and genome/transcriptome should also be set if utilising the
theoretical GC content.

As an alternative to a heatmap, a series of overlaid distributions can be shown by setting \texttt{plotType} = "line".

Can produce a static ggplot2 object or an interactive plotly object.

Value

A ggplot2 or plotly object

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# The default plot for a FastqcDataList
plotGcContent(fdl)

# Plot a single FastqcData object
plotGcContent(fdl[[1]])
### Usage

```
plotInsertSize(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).\*", ...)
```

#### S4 method for signature 'FastpData'

```
plotInsertSize(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  plotType = c("histogram", "cumulative"),
  counts = FALSE,
  plotTheme = theme(),
  expand.x = 0.01,
  expand.y = c(0, 0.05),
  ...)
```

#### S4 method for signature 'FastpDataList'

```
plotInsertSize(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  plotType = c("heatmap"),
  plotTheme = theme(),
  scaleFill = NULL,
  cluster = FALSE,
  dendrogram = FALSE,
  heat_w = 8,
  ...
)
```

### Arguments

- **x** A FastpData or FastpDataList object
- **usePlotly** logical. Generate an interactive plot using plotly
- **labels** An optional named vector of labels for the file names. All file names must be present in the names of the vector.
- **pattern** Regex to remove from the end of any filenames
- **plotType** Determine the plot type. Options vary with the input structure
- **counts** logical(1) Plot read counts, or percentages (default)
- **plotTheme** a theme object
- **expand.x, expand.y** Axis expansions
- **scaleFill** Continuous scale used to fill heatmap cells. Defaults to the "inferno" palette
plotKmers

Description

Plot Overrepresented Kmers

Usage

plotKmers(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'ANY'
plotKmers(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'FastqcData'
plotKmers(
  x,
  usePlotly = FALSE,
  labels,

cluster logical default FALSE. If set to TRUE, data will be clustered using hierarchical clustering

dendrogram logical redundant if cluster is FALSE if both cluster and dendrogram are specified as TRUE the dendrogram will be displayed.

heat_w Width of the heatmap relative to other plot components

Details

Takes a Fastp or a set of Fastp reports and plot insert size distributions. Plots can be drawn as cumulative totals or the default histograms for a single report, and as boxplots or heatmaps for a set of reports

Value

A ggplot or plotly object

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastp.json.gz", full.names = TRUE)
fp <- FastpData(fl)
plotInsertSize(
  fp, counts = TRUE, fill = "steelblue4",
  plotTheme = theme(plot.title = element_text(hjust = 0.5))
)
plotInsertSize(fp, plotType = "cumulative")

plotKmers

Plot Overrepresented Kmers

Description

Plot Overrepresented Kmers

Usage

plotKmers(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'ANY'
plotKmers(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'FastqcData'
plotKmers(
  x,
  usePlotly = FALSE,
  labels,
plotKmers

pattern = ".(fast|fq|bam).*",
  n = 6,
  linewidth = 0.5,
  plotlyLegend = FALSE,
  scaleColour = NULL,
  pal = c("red", "blue", "green", "black", "magenta", "yellow"),
  ...
)

## S4 method for signature 'FastqcDataList'
plotKmers(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  cluster = FALSE,
  dendrogram = FALSE,
  pwfCols,
  showPwf = TRUE,
  scaleFill = NULL,
  heatCol = hcl.colors(50, "inferno"),
  heat_w = 8,
  ...
)

## S4 method for signature 'FastpData'
plotKmers(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  module = c("Before_filtering", "After_filtering"),
  reads = c("read1", "read2"),
  readsBy = c("facet", "mean", "diff"),
  trans = "log2",
  scaleFill = NULL,
  plotTheme = theme(),
  plotlyLegend = FALSE,
  ...
)

**Arguments**

*x* Can be a FastqcData, FastqcDataList or file paths

*usePlotly* logical Default FALSE will render using ggplot. If TRUE plot will be rendered with plotly

*labels* An optional named vector of labels for the file names. All filenames must be present in the names.
pattern regex to drop from the end of filenames

... Used to pass parameters to theme for FastqcData objects and to geoms for Fast-
pData objects

n numeric. The number of Kmers to show.

linewidth Passed to geom_line()

plotlyLegend Show legend for interactive plots

pal The colour palette. If the vector supplied is less than n, grDevices::colorRampPalette() will be used

cluster logical default FALSE. If set to TRUE, fastqc data will be clustered using hier-
archical clustering

dendrogram logical redundant if cluster is FALSE if both cluster and dendrogram are
specifed as TRUE then the dendrogram will be displayed.

pwfCols Object of class PwfCols() to give colours for pass, warning, and fail values in
the plot

showPwf Show the PASS/WARN/FAIL status

scaleFill, scaleColour ggplot2 scales to be used for colour palettes

heatCol Colour palette used for the heatmap. Default is inferno from the viridis set of
palettes

heat_w Relative width of any heatmap plot components

module The module to obtain data from when using a FastpData object

reads Either read1 or read2. Only used when using a FastpData object

readsBy Strategy for visualising both read1 and read2. Can be set to show each set of
reads by facet, or within the same plot taking the mean of the enrichment above
mean, or the difference in the enrichment above mean

trans Function for transforming the count/mean ratio. Set as NULL to use the ratio
without transformation

plotTheme theme object

Details

As the Kmer Content module present in FastQC reports is relatively uninformative, and omitted by
default in later versions of FastQC, these are rudimentary plots.

Plots for FastqcData objects replicate those contained in a FastQC report, whilst the heatmap gen-
erated from FastqcDataList objects simply show the location and abundance of over-represented
Kmers.

Value

A standard ggplot2 object or an interactive plotly object
Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)
plotKmers(fd1[[1]])

# Use a FastpData object
fl <- system.file("extdata", "fastp.json.gz", package = "ngsReports")
fp <- FastpData(fl)
plotKmers(fp, size = 2)
plotKmers(
  fp, reads = "read1", size = 2, trans = NULL,
  scaleFill = scale_fill_gradient(low = "white", high = "black")
)

plotNContent

Draw an N Content Plot

Description

Draw an N Content Plot across one or more FastQC reports

Usage

plotNContent(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'ANY'
plotNContent(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'FastqcData'
plotNContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
  warn = 5,
  fail = 20,
  showPwf = TRUE,
  ...,
  lineCol = "red"
)

## S4 method for signature 'FastqcDataList'
plotNContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  pwfCols,
  warn = 5,
  fail = 20,
  showPwf = TRUE,
  cluster = FALSE,
  dendrogram = FALSE,
  heat_w = 8,
  scaleFill = NULL,
  ...
)

## S4 method for signature 'FastpData'
plotNContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  module = c("Before_filtering", "After_filtering"),
  moduleBy = c("facet", "colour", "linetype"),
  reads = c("read1", "read2"),
  readsBy = c("facet", "colour", "linetype"),
  scaleColour = NULL,
  scaleLine = NULL,
  plotTheme = theme(),
  plotlyLegend = FALSE,
  ...
)

## S4 method for signature 'FastpDataList'
plotNContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).\*",
  module = c("Before_filtering", "After_filtering"),
  reads = c("read1", "read2"),
  scaleFill = NULL,
  plotTheme = theme(),
  cluster = FALSE,
  dendrogram = FALSE,
  heat_w = 8,
  ...
)
plotNContent

Arguments

x Can be a FastqcData, FastqcDataList or file paths
usePlotly logical. Output as ggplot2 (default) or plotly object.
labels An optional named vector of labels for the file names. All filenames must be present in the names.
pattern Regex used to trim the end of filenames
... Used to pass additional attributes to theme() for FastqcData objects and to geom* calls for FastpData-based objects
pwfCols Object of class PwfCols() containing the colours for PASS/WARN/FAIL
warn, fail The default values for warn and fail are 5 and 10 respectively (i.e. percentages)
showPwf logical(1) Show the PASS/WARN/FAIL status
lineCol Line colours
cluster logical default FALSE. If set to TRUE, fastqc data will be clustered using hierarchical clustering
dendrogram logical redundant if cluster is FALSE if both cluster and dendrogram are specified as TRUE then the dendrogram will be displayed.
heat_w Relative width of any heatmap plot components
scaleFill, scaleColour, scaleLine ggplot2 scale objects
module Used for Fastp* structures to show results before or after filtering
moduleBy, readsBy How to show each module or set of reads on the plot
reads Show plots for read1, read2 or both.
plotTheme theme object
plotlyLegend logical(1) Show legend on interactive plots

Details

This extracts the N_Content from the supplied object and generates a ggplot2 object, with a set of minimal defaults. The output of this function can be further modified using the standard ggplot2 methods.

When x is a single FastqcData object line plots will always be drawn for all Ns. Otherwise, users can select line plots or heatmaps.

Value

A standard ggplot2 object, or an interactive plotly object
Examples

## Using a Fastp Data object
fl <- system.file("extdata/fastp.json.gz", package = "ngsReports")
fp <- FastpData(fl)
plotNContent(fp)
plotNContent(
  fp, pattern = "_.001.+",
  moduleBy = "colour", scaleColour = scale_colour_brewer(palette = "Set1"),
  plotTheme = theme(
    legend.position = c(0.99, 0.99), legend.justification = c(1, 1),
    plot.title = element_text(hjust = 0.5)
  )
)

plotOverrep

Plot a summary of Over-represented Sequences

Description

Plot a summary of Over-represented Sequences for a set of FASTQC reports

Usage

plotOverrep(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
  ...
)

## S4 method for signature 'ANY'
plotOverrep(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
  ...
)

## S4 method for signature 'character'
plotOverrep(
  x,
  usePlotly = FALSE,
plotOverrep

labels,
pattern = ",(fast|fq|bam)\.*",
pwfCols,
...
)

## S4 method for signature 'FastqcData'
plotOverrep(
  x,
  usePlotly = FALSE,
  labels,
pattern = ",(fast|fq|bam)\.*",
pwfCols,
  n = 10,
  expand.x = c(0, 0, 0.05, 0),
  expand.y = c(0, 0.6, 0, 0.6),
  plotlyLegend = FALSE,
...
)

## S4 method for signature 'FastqcDataList'
plotOverrep(
  x,
  usePlotly = FALSE,
  labels,
pattern = ",(fast|fq|bam)\.*",
pwfCols,
  showPwf = TRUE,
  cluster = FALSE,
  dendrogram = FALSE,
  scalefill = NULL,
  paletteName = "Set1",
  panel_w = 8,
  expand.x = c(0, 0, 0.05, 0),
  expand.y = rep(0, 4),
...
)

Arguments

x Can be a FastqcData, FastqcDataList or file paths

usePlotly logical Default FALSE will render using ggplot. If TRUE plot will be rendered with plotly

labels An optional named factor of labels for the file names. All filenames must be present in the names.

pattern Regex to remove from the end of any filenames

pwfCols Object of class PwfCols() containing the colours for PASS/WARN/FAIL
... Used to pass additional attributes to theme() and between methods

n The number of sequences to plot from an individual file

expand.x, expand.y Output from expansion() or numeric vectors of length 4. Passed to scale_*_continuous()

plotlyLegend Show legend on interactive plots

showPwf Show PASS/WARN/FAIL status on the plot

cluster logical default FALSE. If set to TRUE, fastqc data will be clustered using hierarchical clustering

dendrogram logical redundant if cluster is FALSE if both cluster and dendrogram are specified as TRUE then the dendrogram will be displayed.

scaleFill ggplot scale object

paletteName Name of the palette for colouring the possible sources of the overrepresented sequences. Must be a palette name from RColorBrewer. Ignored if specifying the scaleFill separately

panel_w Width of main panel on output

Details

Percentages are obtained by simply summing those within a report. Any possible double counting by FastQC is ignored for the purposes of a simple approximation.

Plots generated from a FastqcData object will show the top n sequences grouped by their predicted source & coloured by whether the individual sequence would cause a WARN/FAIL.

Plots generated from a FastqcDataList group sequences by predicted source and summarise as a percentage of the total reads.

Value

A standard ggplot2 object

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# A brief summary across all FastQC reports
plotOverrep(fdl)
plotReadTotals  

**Description**

Draw a barplot of read totals

**Usage**

```r
plotReadTotals(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)
```

**S4 method for signature 'ANY'**

```r
plotReadTotals(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)
```

**S4 method for signature 'FastqcDataList'**

```r
plotReadTotals(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  duplicated = TRUE,
  bars = c("stacked", "adjacent"),
  vertBars = TRUE,
  divBy = 1,
  barCols = c("red", "blue"),
  expand.y = c(0, 0.02),
  plotlyLegend = FALSE,
  ...
)
```

**S4 method for signature 'FastpDataList'**

```r
plotReadTotals(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  adjPaired = TRUE,
  divBy = 1e+06,
  scaleFill = NULL,
  labMin = 0.05,
  status = TRUE,
  labelVJ = 0.5,
  labelFill = "white",
  plotTheme = theme(),
  vertBars = FALSE,
  plotlyLegend = FALSE,
  expand.y = c(0, 0.05),
)"
Arguments

- **x**: Can be a FastqcData, FastqcDataList or file paths
- **usePlotly**: logical. Default FALSE will render using ggplot. If TRUE plot will be rendered with plotly
- **labels**: An optional named vector of labels for the file names. All filenames must be present in the names.
- **pattern**: Regex used to trim the end of filenames
- **...**: Used to pass additional attributes to theme()
- **duplicated**: logical(1). Include deduplicated read total estimates to plot charts
- **bars**: If duplicated = TRUE, show unique and deduplicated reads as "stacked" or "adjacent".
- **vertBars**: logical(1) Show bars as vertical or horizontal
- **divBy**: Scale read totals by this value. The default shows the y-axis in millions for FastpDataList objects, but does not scale FastQC objects, for the sake of backwards compatability
- **barCols**: Colours for duplicated and unique reads.
- **expand.y**: Passed to ggplot2::expansion for the axis showing totals
- **plotlyLegend**: logical(1) Show legend on interactive plots
- **adjPaired**: Scale read totals by 0.5 when paired
- **scaleFill**: ScaleDiscrete function to be applied to the plot
- **labMin**: Only show labels for filtering categories higher than this values as a proportion of reads. Set to any number > 1 to turn off labels
- **status**: logical(1) Include read status in the plot
- **labelVJ**: Relative vertical position to labels within each bar.
- **labelFill**: Passed to geom_label
- **plotTheme**: theme to be added to the plot

Details

Draw a barplot of read totals using the standard ggplot2 syntax. The raw data from readTotals() can otherwise be used to manually create a plot.

Duplication levels are based on the value shown on FASTQC reports at the top of the DeDuplicated-Totals plot, which is known to be inaccurate. As it still gives a good guide as to sequence diversity it is included as the default. This can be turned off by setting duplicated = FALSE.

For FastpDataList objects, duplication statistics are not part of the default module containing ReadTotals. However, the status of reads and the reason for being retained or filtered is, and as such these are shown instead of duplication statistics.
plotSeqContent

Value

Returns a ggplot or plotly object

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Plot the Read Totals showing estimated duplicates
plotReadTotals(fdl)

# Plot the Read Totals without estimated duplicates
plotReadTotals(fdl, duplicated = FALSE)

plotSeqContent

Plot the per base content as a heatmap

Description

Plot the Per Base content for a set of FASTQC files.

Usage

plotSeqContent(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'ANY'
plotSeqContent(x, usePlotly = FALSE, labels, pattern = ".(fast|fq|bam).*", ...)

## S4 method for signature 'FastqcData'
plotSeqContent(
    x,
    usePlotly = FALSE,
    labels,
    pattern = ".(fast|fq|bam).*",
    bases = c("A", "T", "C", "G"),
    scaleColour = NULL,
    plotTheme = theme(),
    plotlyLegend = FALSE,
    expand.x = 0.02,
    expand.y = c(0, 0.05),
    ...
)
## S4 method for signature 'FastqcDataList'
plotSeqContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = "\.(fast|fq|bam)\.*,",
  pwfCols,
  showPwf = TRUE,
  plotType = c("heatmap", "line", "residuals"),
  scaleColour = NULL,
  plotTheme = theme(),
  cluster = FALSE,
  dendrogram = FALSE,
  heat_w = 8,
  plotlyLegend = FALSE,
  nc = 2,
  ...
)

## S4 method for signature 'FastpData'
plotSeqContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = "\.(fast|fq|bam)\.*,",
  module = c("Before_filtering", "After_filtering"),
  reads = c("read1", "read2"),
  readsBy = c("facet", "linetype"),
  moduleBy = c("facet", "linetype"),
  bases = c("A", "T", "C", "G", "N", "GC"),
  scaleColour = NULL,
  scaleLine = NULL,
  plotlyLegend = FALSE,
  plotTheme = theme(),
  expand.x = 0.02,
  expand.y = c(0, 0.05),
  ...
)

## S4 method for signature 'FastpDataList'
plotSeqContent(
  x,
  usePlotly = FALSE,
  labels,
  pattern = "\.(fast|fq|bam)\.*,",
  module = c("Before_filtering", "After_filtering"),
  moduleBy = c("facet", "linetype"),
  reads = c("read1", "read2"),
readsBy = c("facet", "linetype"),
bases = c("A", "T", "C", "G", "N", "GC"),
showPwf = FALSE,
pwfCols,
warn = 10,
fail = 20,
plotType = c("heatmap", "line", "residuals"),
plotlyLegend = FALSE,
scaleColour = NULL,
scaleLine = NULL,
plotTheme = theme(),
cluster = FALSE,
dendrogram = FALSE,
heat_w = 8,
expand.x = c(0.01),
expand.y = c(0, 0.05),
nc = 2,
...
)

Arguments

\textbf{x} \quad \text{Can be a} \texttt{FastqcData, FastqcDataList} \text{or file paths}

\textbf{usePlotly} \quad \text{logical. Generate an interactive plot using plotly}

\textbf{labels} \quad \text{An optional named vector of labels for the file names. All file names must be present in the names of the vector.}

\textbf{pattern} \quad \text{Regex to remove from the end of any filenames}

\textbf{...} \quad \text{Used to pass additional attributes to plotting geoms}

\textbf{bases} \quad \text{Which bases to draw on the plot. Also becomes the default plotting order by setting these as factor levels}

\textbf{scaleColour} \quad \text{Discrete colour scale as a ggplot ScaleDiscrete object. If not provided, will default to \texttt{scale_colour_manual}}

\textbf{plotTheme} \quad \text{theme object to be applied. Note that all plots will have \texttt{theme\_bw} theme applied by default, as well as any additional themes supplied here}

\textbf{plotlyLegend} \quad \text{logical(1). Show legends for interactive plots. Ignored for heatmaps}

\textbf{expand.x, expand.y} \quad \text{Passed to \texttt{expansion} in the x- and y-axis scales respectively}

\textbf{pwfCols} \quad \text{Object of class \texttt{PwfCols()} to give colours for pass, warning, and fail values in plot}

\textbf{showPwf} \quad \text{Show PASS/WARN/FAIL categories as would be defined in a FastQC report}

\textbf{plotType} \quad \text{character. Type of plot to generate. Must be "line", "heatmap" or "residuals"}

\textbf{cluster} \quad \text{logical default FALSE. If set to \texttt{TRUE}, fastqc data will be clustered using hierarchical clustering}

\textbf{dendrogram} \quad \text{logical redundant if \texttt{cluster} is \texttt{FALSE} if both \texttt{cluster} and \texttt{dendrogram} are specified as \texttt{TRUE} then the dendrogram will be displayed.}
plotSeqContent

heat_w  Relative width of any heatmap plot components

nc  Specify the number of columns if plotting a FastqcDataList as line plots. Passed to facet_wrap.

module  Fastp Module to show. Can only be Before/After_filtering

reads  Which set of reads to show

readsBy, moduleBy  When plotting both R1 & R2 and both modules, separate by either linetype or linetype

scaleLine  Discrete scale_linetype object. Only relevant if plotting values by linetype

warn, fail  Default values for WARN and FAIL based on FastQC reports. Only applied to heatmaps for FastpDataList objects

Details

Per base sequence content (%A, %T, %G, %C), is shown as four overlaid heatmap colours when plotting from multiple reports. The individual line plots are able to be generated by setting plotType = "line", and the layout is determined by facet_wrap from ggplot2.

Individual line plots are also generated when plotting from a single FastqcData object.

If setting usePlotly = TRUE for a large number of reports, the plot can be slow to render. An alternative may be to produce a plot of residuals for each base, produced by taking the position-specific mean for each base.

Value

A ggplot2 object or an interactive plotly object

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# The default plot
plotSeqContent(fdl)

fp <- FastpData(system.file("extdata/fastp.json.gz", package = "ngsReports"))
plotSeqContent(fp)
plotSeqContent(fp, moduleBy = "linetype", bases = c("A", "C", "G", "T"))
plotSeqLengthDistn  

**Plot the Sequence Length Distribution**

**Description**

Plot the Sequence Length Distribution across one or more FASTQC reports

**Usage**

```r
plotSeqLengthDistn(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  ...
)
```

## S4 method for signature 'ANY'
```r
plotSeqLengthDistn(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  ...
)
```

## S4 method for signature 'character'
```r
plotSeqLengthDistn(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  ...
)
```

## S4 method for signature 'FastqcData'
```r
plotSeqLengthDistn(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  counts = TRUE,
  plotType = c("line", "cdf"),
  expand.x = c(0, 0.2, 0, 0.2),
  plotlyLegend = FALSE,
  colour = "red",
  ...
)```
plotSeqLengthDistn

## S4 method for signature 'FastqcDataList'

plotSeqLengthDistn(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".\.(fast|fq|bam).\*",
  counts = FALSE,
  plotType = c("heatmap", "line", "cdf"),
  cluster = FALSE,
  dendrogram = FALSE,
  heat_w = 8,
  pwfCols,
  showPwf = TRUE,
  scaleFill = NULL,
  scaleColour = NULL,
  heatCol = hcl.colors(50, "inferno"),
  plotlyLegend = FALSE,
  ...
)

Arguments

x Can be a FastqcData, FastqcDataList or file paths

usePlotly logical. Output as ggplot2 or plotly object.

labels An optional named vector of labels for the file names. All filenames must be present in the names.

pattern Regex to remove from the end of any filenames

... Used to pass additional attributes to theme()

counts logical Should distributions be shown as counts or frequencies (percentages)

plotType character. Can only take the values plotType = "heatmap" plotType = "line" or plotType = "cdf"

expand.x Output from expansion() or numeric vector of length 4. Passed to scale_x_discrete

plotlyLegend logical(1) Show legend for interactive line plots

colour Line colour

cluster logical default FALSE. If set to TRUE, fastqc data will be clustered using hierarchical clustering

dendrogram logical redundant if cluster and usePlotly are FALSE. If both cluster and dendrogram are specified as TRUE then the dendrogram will be displayed.

heat_w Relative width of any heatmap plot components

pwfCols Object of class PwfCols() to give colours for pass, warning, and fail values in plot

showPwf logical(1) Show PASS/WARN/FAIL status
plotSeqQuals

scaleFill, scaleColour
  Optional ggplot scale objects
heatCol
  The colour scheme for the heatmap

Details

This extracts the Sequence Length Distribution from the supplied object and generates a ggplot2 object, with a set of minimal defaults. The output of this function can be further modified using the standard ggplot2 methods.

A cdf plot can also be generated to provide guidance for minimum read length in some NGS workflows, by setting `plotType = "cdf"`. If all libraries have reads of identical lengths, these plots may be less informative.

An alternative interactive plot is available by setting the argument `usePlotly = TRUE`.

Value

A standard ggplot2 object, or an interactive plotly object

Examples

```r
# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Plot as a frequency plot using lines
plotSeqLengthDistn(fdl)

# Or plot the cdf
plotSeqLengthDistn(fdl, plotType = "cdf")
```

plotSeqQuals

Plot the Per Sequence Quality Scores

Description

Plot the Per Sequence Quality Scores for a set of FASTQC reports

Usage

```r
plotSeqQuals(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
```
plotSeqQuals

## S4 method for signature 'ANY'
plotSeqQuals(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
  ...
)

## S4 method for signature 'character'
plotSeqQuals(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
  ...
)

## S4 method for signature 'FastqcData'
plotSeqQuals(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
  showPwf = TRUE,
  counts = FALSE,
  alpha = 0.1,
  warn = 30,
  fail = 20,
  colour = "red",
  plotlyLegend = FALSE,
  ...
)

## S4 method for signature 'FastqcDataList'
plotSeqQuals(
  x,
  usePlotly = FALSE,
  labels,
  pattern = ".(fast|fq|bam).*",
  pwfCols,
counts = FALSE,
alpha = 0.1,
warn = 30,
fail = 20,
showPwf = TRUE,
plotType = c("heatmap", "line"),
dendrogram = FALSE,
cluster = FALSE,
scaleFill = NULL,
heatCols = hcl.colors(100, "inferno"),
heat_w = 8,
scaleColour = NULL,
plotlyLegend = FALSE,
...)

Arguments

x Can be a FastqcData, FastqcDataList or path
usePlotly logical Default FALSE will render using ggplot. If TRUE plot will be rendered with plotly
labels An optional named vector of labels for the file names. All file names must be present in the names of the vector.
pattern Regex to remove from the end of any filenames
pwfCols Object of class PwfCols() containing the colours for PASS/WARN/FAIL
... Used to pass various potting parameters to theme. Can also be used to set size and colour for box outlines.
showPwf logical(1) Show PASS/WARN/FAIL status
counts logical. Plot the counts from each file if counts = TRUE, otherwise the frequencies will be plotted
alpha set alpha for line graph bounds
warn, fail The default values for warn and fail are 5 and 10 respectively (i.e. percentages)
colour Colour for single line plots
plotlyLegend logical(1) Show legend for interactive line plots
plotType character. Can only take the values plotType = "heatmap" or plotType = "line"
dendrogram logical redundant if cluster is FALSE if both cluster and dendrogram are specified as TRUE then the dendrogram will be displayed.
cluster logical default FALSE. If set to TRUE, fastqc data will be clustered using hierarchical clustering
scaleFill, scaleColour ggplot2 scales
heatCols Colour palette for the heatmap
heat_w Relative width of any heatmap plot components
plotSummary

Details

Plots the distribution of average sequence quality scores across the set of files. Values can be plotted either as counts (counts = TRUE) or as frequencies (counts = FALSE).

Any faceting or scale adjustment can be performed after generation of the initial plot, using the standard methods of ggplot2 as desired.

Value

A standard ggplot2 object, or an interactive plotly object

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# The default plot
plotSeqQuals(fdl)

# Also subset the reads to just the R1 files
r1 <- grepl("R1", fqName(fdl))
plotSeqQuals(fdl[r1])

plotSummary

Plot the PASS/WARN/FAIL information

Description

Extract the PASS/WARN/FAIL summaries and plot them

Usage

plotSummary(
  x,
  usePlotly = FALSE,
  labels,
  pwfCols,
  cluster = FALSE,
  dendrogram = FALSE,
  ...
)

## S4 method for signature 'ANY'
plotSummary(
  ...
plotSummary

x,
usePlotly = FALSE,
labels,
pwfCols,
cluster = FALSE,
dendrogram = FALSE,
... 
)

## S4 method for signature 'character'
plotSummary(
  x,
  usePlotly = FALSE,
  labels,
pwfCols,
cluster = FALSE,
dendrogram = FALSE,
...
)

## S4 method for signature 'FastqcDataList'
plotSummary(
  x,
  usePlotly = FALSE,
  labels,
pwfCols,
cluster = FALSE,
dendrogram = FALSE,
...,
gridlineWidth = 0.2,
gridlineCol = "grey20"
)

Arguments

x
  Can be a FastqcData, FastqcDataList or character vector of file paths
usePlotly
  logical. Generate an interactive plot using plotly
labels
  An optional named vector of labels for the file names. All filenames must be present in the names. File extensions are dropped by default.
pwfCols
  Object of class PwfCols() containing the colours for PASS/WARN/FAIL
cluster
  logical default FALSE. If set to TRUE, fastqc data will be clustered using hierarchical clustering
dendrogram
  logical redundant if cluster is FALSE if both cluster and dendrogram are specified as TRUE then the dendrogram will be displayed.
...,
  Used to pass various potting parameters to theme.
gridlineWidth, gridlineCol
  Passed to geom_hline and geom_vline to determine width and colour of gridlines
Details

This uses the standard ggplot2 syntax to create a three colour plot. The output of this function can be further modified using the standard ggplot2 methods if required.

Value

A ggplot2 object (usePlotly = FALSE) or an interactive plotly object (usePlotly = TRUE)

Examples

# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Check the overall PASS/WARN/FAIL status
plotSummary(fdl)

---

pwf

Colours for PASS/WARN/FAIL

Description

Default colours for PASS/WARN/FAIL

Usage

pwf

Format

An object of class PwfCols of length 1.

Details

pwf is an object of class PwfCols supplied with the package and used as the default colouring. Colours correspond approximately to PASS, WARN and FAIL from the FASTQC reports, with the additional colour (MAX) included to indicate an extreme FAIL. In order, these colours in the default vector are green (rgb(0, 0.8, 0)), yellow (rgb(0.9, 0.9, 0.2)), red (rgb(0.8, 0.2, 0.2)) and white (rgb(1, 1, 1))

Examples

# Make a pie chart showing the default colours
pie(rep(1,4), labels = names(pwf), col = getColours(pwf))
The PwfCols class and associated methods

Description
Define the PwfCols class and associated methods

Details
This is an object of with four colours in components named PASS, WARN, FAIL and MAX. Used to indicate these categories as defined on the standard plots from fastqc.

Slots
PASS  A vector of length 1, defining the colour for PASS in rgb format. Defaults to rgb(0, 0.8, 0)
WARN  A vector of length 1, defining the colour for WARN in rgb format. Defaults to rgb(0.9, 0.9, 0.2)
FAIL  A vector of length 1, defining the colour for FAIL in rgb format. Defaults to rgb(0.8, 0.2, 0.2)
MAX   A vector of length 1, defining the colour for an extreme FAIL or NA in rgb format. Defaults to rgb(1, 1, 1)

readTotals  Get the read totals

Description
Get the read totals from one or more FASTQC reports

Usage
readTotals(x)

Arguments
x  Can be a FastqcData, FastqcDataList, FastpData, FastpDataList or file paths

Value
A tibble with the columns Filename and Total_Sequences
TheoreticalGC-class

The TheoreticalGC Object Class

Description

Contains Theoretical GC content for a selection of species

Details

Estimates are able to be retained for genomic and transcriptomic sequences. Values are stored as frequencies.

Value

An object of class TheoreticalGC

Slots

Genome  A data.frame containing theoretical GC content for genomic sequences

Transcriptome  A data.frame containing theoretical GC content for transcriptomic sequences

mData  A data.frame containing metadata about all species in the object

Examples

## How to form an object using your own fasta file
faDir <- system.file("extdata", package = "ngsReports")
faFile <- list.files(faDir, pattern = "fasta", full.names = TRUE)
gen_df <- estGcDistn(faFile, n = 200)
gen_df <- dplyr::rename(gen_df, Athaliana = Freq)
mData_df <-
data.frame(Name = "Athaliana", Genome = TRUE, Transcriptome = FALSE)
tr_df <- data.frame()
myGC <- new("TheoreticalGC", Genome = gen_df, Transcriptome = tr_df, mData = mData_df)
**writeHtmlReport**

**Write an HTML Summary Report**

**Description**

Compiles an HTML report using a supplied template

**Usage**

```r
writeHtmlReport(
  fastqcDir,  # A directory containing zipped, or extracted FastQC reports
  template,    # The template file which will be copied into `fastqcDir`
  outDir,      # The directory to write the compiled document to
  usePlotly = TRUE,  # Generate interactive plots?
  species = "Hsapiens",  # Species/closely related species of sequenced samples
  gcType = c("Genome", "Transcriptome"),  # Is the data "Transcriptomic" or "Genomic" in nature?
  nOver = 30,  # The maximum number of Overrepresented Sequences to show
  targetsDF,  # A data.frame with at least two columns named `Filename` and `Label`. The filenames should match the original fastq files, and the labels should be simply alternative labels for these files for convenience.
  overwrite = FALSE,  # logical. Overwrite any previous copies of the template file in the destination directory
  quiet = TRUE  # logical. Show or hide markdown output in the Console.
)
```

**Arguments**

- `fastqcDir`  
  A directory containing zipped, or extracted FastQC reports

- `template`  
  The template file which will be copied into `fastqcDir`

- `outDir`  
  The directory to write the compiled document to

- `usePlotly`  
  Generate interactive plots?

- `species`  
  Species/closely related species of sequenced samples

- `gcType`  
  Is the data "Transcriptomic" or "Genomic" in nature?

- `nOver`  
  The maximum number of Overrepresented Sequences to show

- `targetsDF`  
  A data.frame with at least two columns named `Filename` and `Label`. The filenames should match the original fastq files, and the labels should be simply alternative labels for these files for convenience.

- `overwrite`  
  logical. Overwrite any previous copies of the template file in the destination directory

- `quiet`  
  logical. Show or hide markdown output in the Console.

**Details**

This will take a user supplied template, or the file supplied with the package and create an HTML summary of all standard FASTQC plots for all files in the supplied directory.
Value

Silently returns TRUE and will output a compiled HTML file from the supplied Rmarkdown template file.

Examples

```r
## Not run:
packageDir <- system.file("extdata", package = "ngsReports")
fileList <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)
# Copy these files to tempdir() to avoid overwriting
# any files in the package directory
file.copy(fileList, tempdir(), overwrite = TRUE)
writeHtmlReport(fastqcDir = tempdir())

## End(Not run)
```

Description

Extract elements from FastqcDataList Object

Usage

```r
## S4 method for signature 'FastqcDataList,numeric,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'FastqcDataList,character,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'FastqcDataList,logical,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'FastqcDataList,ANY,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'FastpDataList,numeric,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'FastpDataList,character,missing'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'FastpDataList,logical,missing'
x[i, j, ..., drop = TRUE]
```
## S4 method for signature 'FastqcDataList,ANY,missing'
x[i, j, ..., drop = TRUE]

### Arguments

- **x**: A FastqcDataList or FastpDataList
- **i**: character, logical or integer vector
- **j**: not used
- **...**: not used
- **drop**: not used

### Details

Extract elements in a consistent manner with R conventions

### Value

Will return a subset of the original object following the standard rules for subsetting objects

### Examples

```r
# Get the files included with the package
packageDir <- system.file("extdata", package = "ngsReports")
fl <- list.files(packageDir, pattern = "fastqc.zip", full.names = TRUE)

# Load the FASTQC data as a FastqcDataList object
fdl <- FastqcDataList(fl)

# Subsetting using the standard methods
fdl[[1]]
fdl[[1]]
```
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