

# Package ‘qrrc’

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**Title** Quick Read Quality Control

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**Imports** reshape, ggplot2, Biostrings, biovizBase, graphics, methods,plyr, stats

**Depends** reshape, ggplot2, Biostrings, biovizBase, brew, xtable,Rsamtools (>= 1.3.28), testthat

**LinkingTo** Rsamtools

**Description** Quickly scans reads and gathers statistics on base and quality frequencies, read length, k-mers by position, and frequent sequences. Produces graphical output of statistics for use in quality control pipelines, and an optional HTML quality report. S4 SequenceSummary objects allow specific tests and functionality to be written around the data collected.

**License** GPL (>=2)

**URL** <http://github.com/vsbuffalo/qrrc>

**biocViews** Sequencing, QualityControl, DataImport, Preprocessing,Visualization

## R topics documented:

|                               |    |
|-------------------------------|----|
| basePlot-methods . . . . .    | 2  |
| calcKL-methods . . . . .      | 4  |
| FASTASummary-class . . . . .  | 5  |
| FASTQSummary-class . . . . .  | 6  |
| gcPlot-methods . . . . .      | 7  |
| geom_qlinerange . . . . .     | 8  |
| getBase-methods . . . . .     | 9  |
| getBaseProp-methods . . . . . | 10 |

|                                   |    |
|-----------------------------------|----|
| getGC-methods . . . . .           | 11 |
| getKmer-methods . . . . .         | 12 |
| getMCQual-methods . . . . .       | 13 |
| getQual-methods . . . . .         | 14 |
| getSeqLen-methods . . . . .       | 15 |
| kmerEntropyPlot-methods . . . . . | 17 |
| kmerKLPlot-methods . . . . .      | 18 |
| list2df . . . . .                 | 19 |
| makeReport-methods . . . . .      | 20 |
| plotBases-methods . . . . .       | 21 |
| plotGC-methods . . . . .          | 22 |
| plotQuals-methods . . . . .       | 23 |
| plotSeqLengths-methods . . . . .  | 24 |
| qualPlot-methods . . . . .        | 25 |
| readSeqFile . . . . .             | 26 |
| scale_color_dna . . . . .         | 28 |
| scale_color_iupac . . . . .       | 29 |
| seqLenPlot-methods . . . . .      | 29 |
| SequenceSummary-class . . . . .   | 30 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>32</b> |
|--------------|-----------|

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|                  |  |
|------------------|--|
| basePlot-methods | <i>Plot Base Frequency or Proportion by Position</i> |
|------------------|--|

---

## Description

basePlot plots the frequency or proportion of bases by position in the read.

Specific bases (such as "N") can be plot alone with this function too.

## Usage

```
basePlot(x, geom=c("line", "bar", "dodge"),
         type=c("frequency", "proportion"), bases=DNA_BASES_N,
         colorvalues=getBioColor("DNA_BASES_N"))
```

## Arguments

|      |  |
|------|--|
| x    | an S4 object that inherits from <a href="#">SequenceSummary</a> from readSeqFile.  |
| geom | Either "line", "bar", or "dodge" indicating the geom to use when plotting the bases. "line" will plot base proportion of frequency with lines. "bar" and "dodge" will use bars; "bar" defaults to filling the bars with different colors to distinguish bases, "dodge" lays the bars side by side. |
| type | Either "frequency" or "proportion" indicating whether to use count data or the proportion per base.  |

|             |   |
|-------------|---|
| bases       | a character vector indicating which bases to include. By default, all bases in DNA_BASES_N. Another good option would be IUPAC_CODE_MAP, which is included in the Biostrings package. |
| colorvalues | a character vectors of colors to use; the names of the elements must map to the bases.  |

### Methods

signature(x = "FASTQSummary") basePlot will plot the base frequencies or proportions for a single object that inherits from SequenceSummary.

signature(x = "list") basePlot will plot the base frequencies or proportions for each of the SequenceSummary items in the list and display them in a series of panels.

### Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

### See Also

[getBase](#), [getBaseProp](#)

### Examples

```
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))

## Plot bases
basePlot(s.fastq)

## Plot bases with filled bars
basePlot(s.fastq, geom="bar")

## Plot bases with dodged bars
basePlot(s.fastq, geom="dodge")

## Plot bases with dodged bars
basePlot(s.fastq, geom="bar", bases=c("G", "T"))

## Plot multiple base plots
s.trimmed.fastq <- readSeqFile(system.file(extdata,
  test-trimmed.fastq, package=qrqc))
basePlot(list("not trimmed"=s.fastq, "trimmed"=s.trimmed.fastq))

## Graphical features can be added
basePlot(s.trimmed.fastq, type="proportion") +
  geom_hline(yintercept=0.25, color="purple")
```

---

|                |  |
|----------------|--|
| calcKL-methods | <i>Calculate the Kullback-Leibler Divergence Between the k-mer Distribution by Position and the k-mer Distribution Across All Positions.</i> |
|----------------|--|

---

### Description

calcKL takes in an object that inherits from [SequenceSummary](#) that has a kmers slot, and returns the terms of the K-L divergence sum (which correspond to items in the sample space, in this case, k-mers).

### Usage

```
calcKL(x)
```

### Arguments

x an S4 object a class that inherits from SequenceSummary.

### Value

calcKL returns a data.frame with columns:

|          |  |
|----------|--|
| kmer     | the k-mer sequence.  |
| position | the position in the read.  |
| kl       | the K-L term for this k-mer in the K-L sum, calculated as $p(i) \cdot \log_2(p(i)/q(i))$ . |
| p        | the probability for this k-mer, at this position.  |
| q        | the probability for this k-mer across all positions.                                       |

### Note

The K-L divergence calculation in calcKL uses base 2 in the log; the units are in bits.

### Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

### See Also

[kmerKLPlot](#), [getKmer](#)

**Examples**

```
## Load a somewhat contaminated FASTQ file
s.fastq <- readSeqFile(system.file(extdata, test.fastq,
  package=qrqc), hash.prop=1)

## As with getQual, this function is provided so custom graphics can
## be made easily. For example K-L divergence by position:
kld <- with(calcKL(s.fastq), aggregate(kl, list(position),
  sum))
colnames(kld) <- c("position", "KL")
p <- ggplot(kld) + geom_line(aes(x=position, y=KL), color="blue")
p + scale_y_continuous("K-L divergence")
```

---

FASTASummary-class      *FASTASummary class representing the summaries of a FASTA file*

---

**Description**

This class contains the same slots as the [SequenceSummary](#), but it is used to indicate the data originated from a FASTA file.

Note that many accessor functions transform data in the slots into data frames. The data in the slots is mostly untransformed and less easy to work with directly, so using the accessor functions is recommended.

**Slots**

[FASTASummary](#) has the slots inherited from [SequenceSummary](#).

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[FASTQSummary](#) is the counterpart of this class for FASTQ data.

[readSeqFile](#) is the function that takes a FASTA file and returns a FASTASummary object.

[basePlot](#) is a function that plots the distribution of bases over sequence length for a particular FASTASummary object. [gcPlot](#) combines and plots the GC proportion.

[seqLenPlot](#) is a function that plots a histogram of sequence lengths for a particular FASTASummary object.

[kmerKLPlot](#) is a function that uses Kullback-Leibler divergence to make a plot that can aid in finding possible contamination (if [readSeqFile](#) had `kmer=TRUE`).

[kmerEntropyPlot](#) is a function that plots the Shannon entropy of k-mers per position.

There are accessor functions [getQual](#), [getBase](#), [getBaseProp](#), [getSeqLen](#), [getKmer](#), [getGC](#) for transforming the raw data in the object's slot (direct from the C call) to more usable data frames.

**Examples**

```
showClass("FASTASummary")
```

---

FASTQSummary-class      FASTQSummary class representing the summaries of a FASTQ file

---

**Description**

This class contains the same slots as the [SequenceSummary](#), as well as additional slots for quality information.

Note that many accessor functions transform data in the slots into data frames. The data in the slots is mostly untransformed and less easy to work with directly, so using the accessor functions is recommended.

**Slots**

In addition to the slots inherited from [SequenceSummary](#), [FASTQSummary](#) contains:

`quality` a string indicating the type of quality (used to convert ASCII characters to quality integers). Either "phred", "solexa", or "illumina".

`qual.freqs` a data frame of quality frequencies by position, if the file was a FASTQ file.

`mean.qual` a numeric that is the mean quality across all positions, weighted by the number of reads that extended to that position.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[FASTASummary](#) is the counterpart of this class for FASTA data.

[readSeqFile](#) is the function that takes a FASTQ file and returns a [FASTQSummary](#) object.

[basePlot](#) is a function that plots the distribution of bases over sequence length for a particular [FASTQSummary](#) object. [gcPlot](#) combines and plots the GC proportion.

[qualPlot](#) is a function that plots the distribution of qualities over sequence length for a particular [FASTQSummary](#) object.

[seqLenPlot](#) is a function that plots a histogram of sequence lengths for a particular [FASTQSummary](#) object.

[kmerKLPlot](#) is a function that uses Kullback-Leibler divergence to make a plot that can aid in finding possible contamination (if [readSeqFile](#) had `kmer=TRUE`).

[kmerEntropyPlot](#) is a function that plots the Shannon entropy of k-mers per position.

There are accessor functions [getQual](#), [getBase](#), [getBaseProp](#), [getSeqLen](#), [getKmer](#), [getGC](#) for transforming the raw data in the object's slot (direct from the C call) to more usable data frames.

## Examples

```
showClass("FASTQSummary")
```

---

gcPlot-methods      *Plot GC Content by Position*

---

## Description

gcPlot plots the GC content by position in the read.

## Usage

```
gcPlot(x, color="red")
```

## Arguments

x                    an S4 object that inherits from SequenceSummary from readSeqFile.  
color                the color to use for the GC content line.

## Methods

signature(x = "FASTQSummary") gcPlot will plot the GC content for a single object that inherits from SequenceSummary.

signature(x = "list") gcPlot will plot the GC content for each of the SequenceSummary items in the list and display them in a series of panels.

## Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

## See Also

[getBase](#), [getBaseProp](#)

## Examples

```
## Load a FASTQ file, with sequence hashing.  
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))  
  
## Plot GC content  
gcPlot(s.fastq)  
  
## Plot multiple GC content plots  
s.trimmed.fastq <- readSeqFile(system.file(extdata,  
  test-trimmed.fastq, package=qrqc))  
gcPlot(list("not trimmed"=s.fastq, "trimmed"=s.trimmed.fastq))  
  
## Graphical features can be added  
gcPlot(s.trimmed.fastq) + geom_hline(yintercept=0.5, color="purple")
```

---

|                 |  |
|-----------------|--|
| geom_qlinerange | <i>Use Line Segments and Points to Plot Quality Statistics by Position in the Read</i> |
|-----------------|--|

---

### Description

geom\_qlinerange uses multiple line segments and points to plot quality ranges. By default the 10% and 90% range is plotted in grey, the quartile range in orange, and the mean as a point in blue. It is used in [qualPlot](#).

### Usage

```
geom_qlinerange(extreme.color="grey", quartile.color="orange", mean.color="blue", median.color=NULL)
```

### Arguments

|                |   |
|----------------|---|
| extreme.color  | a character value indicating the color to use for the extreme values (the 10% and 90% quantiles). If NULL, these line segments will not be added. |
| quartile.color | a character value indicating the color to use for the quartiles. If NULL, these line segments will not be added.                                  |
| mean.color     | a character value indicating the color to use for the mean. If NULL, these line segments will not be added.                                       |
| median.color   | a character value indicating the color to use for the median. If NULL, these line segments will not be added.                                     |

### Value

A list of geoms from ggplot2 that this function put together, to be added to a call to ggplot which contains a data frame of quality data, i.e. from [getQual](#).

### Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

### See Also

[getQual](#), [qualPlot](#)



---

|                 |  |
|-----------------|--|
| getBase-methods | <i>Get a Data Frame of Base Frequency Data from a SequenceSummary Object</i> |
|-----------------|--|

---

### Description

An object that inherits from class [SequenceSummary](#) contains base frequency data by position gathered by [readSeqFile](#). [getBase](#) is an accessor function that reshapes the base frequency data by position into a data frame.

This accessor function is useful if you want to map variables to custom [ggplot2](#) aesthetics. Base proportions can be accessed with [getBaseProp](#).

### Usage

```
getBase(x, drop=TRUE)
```

### Arguments

|      |  |
|------|--|
| x    | an S4 object that inherits from <a href="#">SequenceSummary</a> from <a href="#">readSeqFile</a> . |
| drop | a logical value indicating whether to drop bases that don't have any counts.                       |

### Value

`getBase` returns a `data.frame` with columns:

|           |  |
|-----------|--|
| position  | the position in the read.                            |
| base      | the base.  |
| frequency | the number of a base found per position in the read. |

### Methods

signature(x = "SequenceSummary") `getBase` is an accessor function that works on any object read in with [readSeqFile](#); that is, objects that inherit from [SequenceSummary](#).

### Author(s)

Vince Buffalo <[vsbuffalo@ucdavis.edu](mailto:vsbuffalo@ucdavis.edu)>

### See Also

[getGC](#), [getSeqLen](#), [getBaseProp](#), [getQual](#), [getMCQual](#), [basePlot](#)

## Examples

```
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq,
  package=qrqc))

# A custom base plot
ggplot(getBase(s.fastq)) + geom_line(aes(x=position, y=frequency,
  color=base)) + facet_grid(. ~ base) + scale_color_dna()
```

---

getBaseProp-methods    *Get a Data Frame of Base Proportion Data from a SequenceSummary object*

---

## Description

An object that inherits from class `SequenceSummary` contains base frequency data by position gathered by `readSeqFile`. `getBaseProp` is an accessor function that reshapes the base frequency data by position into a data frame and calculates the proportions of each base per position.

This accessor function is useful if you want to map variables to custom `ggplot2` aesthetics. Base frequency be accessed with `getBase`.

## Usage

```
getBaseProp(x, drop=TRUE)
```

## Arguments

`x`                    an S4 object that inherits from `SequenceSummary` from `readSeqFile`.  
`drop`                a logical value indicating whether to drop bases that don't have any counts.

## Value

`getBaseProp` returns a `data.frame` with columns:

|                         |  |
|-------------------------|--|
| <code>position</code>   | the position in the read.                                |
| <code>base</code>       | the base.  |
| <code>proportion</code> | the proportion of a base found per position in the read. |

## Methods

`signature(x = "SequenceSummary")` `getBaseProp` is an accessor function that works on any object read in with `readSeqFile`; that is, objects that inherit from `SequenceSummary`.

## Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[getGC](#), [getSeqLen](#), [getBase](#), [getQual](#), [getMCQual](#), [basePlot](#)

**Examples**

```
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq,
  package=qrqc))

# A custom base plot
ggplot(getBaseProp(s.fastq)) + geom_line(aes(x=position, y=proportion,
  color=base)) + facet_grid(. ~ base) + scale_color_dna()
```

---

getGC-methods

*Get a Data Frame of GC Content from a SequenceSummary object*

---

**Description**

An object that inherits from class [SequenceSummary](#) contains base frequency data by position gathered by [readSeqFile](#). [getGC](#) is an accessor function that reshapes the base frequency data into a data frame and returns the GC content by position.

This accessor function is useful if you want to map variables to custom [ggplot2](#) aesthetics. Frequencies or proportions of all bases (not just GC) can be accessed with [getBase](#) and [getBaseProp](#) respectively.

**Usage**

```
getGC(x)
```

**Arguments**

x an S4 object that inherits from [SequenceSummary](#) from [readSeqFile](#).

**Value**

[getGC](#) returns a `data.frame` with columns:

|          |                                      |
|----------|--------------------------------------|
| position | the position in the read.            |
| gc       | GC content per position in the read. |

**Methods**

`signature(x = "SequenceSummary")` [getGC](#) is an accessor function that works on any object read in with [readSeqFile](#); that is, objects that inherit from [SequenceSummary](#).

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[getSeqLen](#), [getBase](#), [getBaseProp](#), [getQual](#), [getMCQual](#), [getKmer](#), [gcPlot](#)

**Examples**

```
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq,
  package=qrrc))

# A custom GC plot
d <- merge(getQual(s.fastq), getGC(s.fastq), by.x="position", by.y="position")
p <- ggplot(d) + geom_linerange(aes(x=position, ymin=lower,
  ymax=upper, color=gc)) + scale_color_gradient(low="red",
  high="blue") + scale_y_continuous("GC content")
p
```

---

getKmer-methods

*Get a Data Frame of k-mer Frequency by Position from a SequenceSummary Object*

---

**Description**

An object that inherits from class [SequenceSummary](#) contains k-mer frequency data by position gathered by [readSeqFile](#) when `kmer=TRUE`. [getKmer](#) is an accessor function that is useful for custom `ggplot2` aesthetics.

**Usage**

```
getKmer(x)
```

**Arguments**

`x` an S4 object that inherits from class `SequenceSummary` from, as returned from `readSeqFile`.

**Value**

`getKmer` returns a data.frame with columns:

|                       |  |
|-----------------------|--|
| <code>kmer</code>     | the k-mer sequence.                          |
| <code>position</code> | the position in the read.                    |
| <code>count</code>    | the frequency of the k-mer at this position. |

**Methods**

signature(x="SequenceSummary") `getKmer` is an accessor function that only works if there is k-mer data, thus it only works if `readSeqFile` was called with `kmer=TRUE` (and `hash.prop` is greater than 0).

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[getGC](#), [getSeqLen](#), [getBase](#), [getBaseProp](#), [getQual](#), [getMCQual](#), [kmerKLPlot](#), [kmerEntropyPlot](#)

**Examples**

```
## Load a FASTQ file, with sequence and k-mer hashing on by default.
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))

## plot counts of a subset of k-mers by position
s.kmers <- getKmer(s.fastq)
top.kmers <- s.kmers$kmer[order(s.kmers$count, decreasing=TRUE)[1:40]]
p <- ggplot(subset(s.kmers, kmer %in% top.kmers)) + geom_bar(aes(x=position, y=count,
  fill=kmer), stat="identity")
p
```

---

getMCQual-methods

*Get a Data Frame of Simulated Quality from a FASTQSummary object*

---

**Description**

An object that inherits from class [FASTQSummary](#) contains base quality data by position gathered by [readSeqFile](#). [getMCQual](#) generates simulated quality data for each base from this binned quality data that can be used for adding smoothed lines via lowess.

This accessor function is useful if you want to map variables to custom ggplot2 aesthetics.

**Usage**

```
getMCQual(x, n=100)
```

**Arguments**

x                    an S4 object that inherits from FASTQSummary from readSeqFile.  
n                    a numeric value indicating the number of quality values to draw per base.

**Value**

getMCQual returns a data.frame with columns:

position            the position in the read.  
quality             simulated quality scores.

## Methods

signature(x = "FASTQSummary") `getMCQual` is a function that works on any object with class `FASTQSummary` read in with `readSeqFile`.

## Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

## See Also

[getGC](#), [getSeqLen](#), [getBase](#), [getBaseProp](#), [getQual](#), [qualPlot](#)

## Examples

```
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq,
  package=qrqc))

# A custom quality plot
ggplot(getQual(s.fastq)) + geom_linerange(aes(x=position, ymin=lower,
  ymax=upper), color="grey") + geom_smooth(aes(x=position, y=quality),
  data=getMCQual(s.fastq), color="blue", se=FALSE)
```

---

getQual-methods

*Get a Data Frame of Quality Data from a FASTQSummary object*

---

## Description

An object of class `FASTQSummary` contains quality data (binned by `readSeqFile`). `getQual` is an accessor function that reshapes the data into a data frame.

This accessor function is useful if you want to map variables to custom `ggplot2` aesthetics.

## Usage

```
getQual(x)
```

## Arguments

`x` an S4 object of class `FASTQSummary` from `readSeqFile`.

## Value

`getQual` returns a data.frame with columns:

|                        |   |
|------------------------|---|
| <code>position</code>  | the position in the read.                             |
| <code>ymin</code>      | the minimum quality found per a position in the read. |
| <code>alt.lower</code> | the 10% quantile found per a position in the read.    |

|           |  |
|-----------|--|
| lower     | the 25% quartile found per a position in the read.   |
| middle    | the median found per a position in the read.   |
| upper     | the 75% quartile found per a position in the read.   |
| alt.upper | the 90% quartile found per a position in the read.   |
| ymax      | the maximum quality found per a position in the read.  |
| mean      | the mean quality (calculated from the binned data by using a weighted mean function) per the position in the read. |

## Methods

signature(x="FASTQSummary") getQual is an accessor function that only works if there is quality data, thus it only works with objects of class FASTQSummary.

## Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

## See Also

[getGC](#), [getSeqLen](#), [getBase](#), [getBaseProp](#), [getMCQual](#), [qualPlot](#)

## Examples

```
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))

## Mean quality by position
p <- ggplot(getQual(s.fastq)) + geom_line(aes(x=position, y=mean), color="blue")
p <- p + scale_y_continuous(limits=c(0, 42))
p

## A different type of quality plot
p <- ggplot(getQual(s.fastq)) + geom_linerange(aes(x=position,
  ymin=lower, ymax=upper, color=mean))
p <- p + scale_color_gradient("mean quality", low="red", high="green")
p + scale_y_continuous("quality")
```

---

getSeqLen-methods      *Get a Data Frame of Sequence Lengths from a SequenceSummary object*

---

## Description

An object that inherits from class SequenceSummary contains sequence length data by position gathered by readSeqFile. getSeqLen is an accessor function that returns the sequence length data.

This accessor function is useful if you want to map variables to custom ggplot2 aesthetics.

**Usage**

```
getSeqLen(x)
```

**Arguments**

x an S4 object that inherits from SequenceSummary from readSeqFile.

**Value**

getSeqLen returns a data.frame with columns:

length the sequence length.

count the number of reads with this sequence length.

**Methods**

signature(x = "SequenceSummary") getSeqLen is an accessor function that works on any object read in with readSeqFile; that is, objects that inherit from SequenceSummary.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[getGC](#), [getBase](#), [getBaseProp](#), [getQual](#), [getMCQual](#), [seqLenPlot](#)

**Examples**

```
library(ggplot2)

## Load a FASTQ file, with sequence hashing.
s.trimmed.fastq <- readSeqFile(system.file("extdata", "test-trimmed.fastq",
  package="qrrc"))

# A custom plot - a bit contrived, but should show power
d <- merge(getSeqLen(s.trimmed.fastq), getQual(s.trimmed.fastq),
  by.x="length", by.y="position")
ggplot(d) + geom_linerange(aes(x=length, ymin=0, ymax=count),
  color="grey") + geom_linerange(aes(x=length, ymin=lower, ymax=upper),
  color="blue") + scale_y_continuous("quality/count") + theme_bw()
```



---

kmerEntropyPlot-methods

*Plot Entropy of k-mers by Position*

---

## Description

kmerEntropyPlot plots the Shannon entropy per position of k-mers. Lower Shannon entropy implies that the distribution of k-mers is non-random and could indicate bias.

## Usage

```
kmerEntropyPlot(x)
```

## Arguments

x an S4 object a class that inherits from SequenceSummary from readSeqFile or a list of objects that inherit from SequenceSummary with names.

## Methods

signature(x = "SequenceSummary") kmerEntropyPlot will plot Shannon entropy per position for an object that inherits from SequenceSummary.

signature(x = "list") kmerEntropyPlot will plot the Shannon entropy per position for each of the objects that inherit from SequenceSummary in the list and display them in a series of panels.

## Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

## See Also

[getKmer](#), [calcKL](#), [kmerKLPlot](#)

## Examples

```
## Load a somewhat contaminated FASTQ file
s.fastq <- readSeqFile(system.file(extdata, test.fastq,
  package=qrqc), hash.prop=1)

## Load a really contaminated FASTQ file
s.contam.fastq <- readSeqFile(system.file(extdata,
  test-contam.fastq, package=qrqc), hash.prop=1)

## Load a random (equal base frequency) FASTA file
s.random.fasta <- readSeqFile(system.file(extdata,
  random.fasta, package=qrqc), type="fasta", hash.prop=1)
```

```
## Plot the Shannon entropy for a single file
kmerEntropyPlot(s.fastq)

## Plot the Shannon entropy for many files
kmerEntropyPlot(list("highly contaminated"=s.contam.fastq, "less
  contaminated"=s.fastq, "random"=s.random.fasta))
```

---

kmerKLPlot-methods      *Plot K-L Divergence Components for a Subset of k-mers to Inspect for Contamination*

---

## Description

kmerKLPlot calls `calckL`, which calculates the Kullback-Leibler divergence between the k-mer distribution at each position compared to the k-mer distribution across all positions. kmerKLPlot then plots each k-mer's contribution to the total K-L divergence by stack bars, for a *subset* of the k-mers. Since there are  $4^k$  possible k-mers for some value k-mers, plotting each often dilutes the interpretation; however one can increase `n.kmers` to a number greater than the possible number of k-mers to force kmerKLPlot to plot the entire K-L divergence and all terms (which are k-mers) in the sum.

If a `x` is a list, the K-L k-mer plots are faceted by sample; this allows comparison to a FASTA file of random reads.

Again, please note that this is *not* the total K-L divergence, but rather the K-L divergence calculated on a subset of the sample space (those of the top `n.kmers` k-mers selected).

## Usage

```
kmerKLPlot(x, n.kmers=20)
```

## Arguments

|                      |  |
|----------------------|--|
| <code>x</code>       | an S4 object a class that inherits from <code>SequenceSummary</code> from <code>readSeqFile</code> or a list of objects that inherit from <code>SequenceSummary</code> with names. |
| <code>n.kmers</code> | a integer value indicating the size of top k-mers to include.  |

## Methods

`signature(x = "SequenceSummary")` kmerKLPlot will plot the K-L divergence for a subset of k-mers for a single object that inherits from `SequenceSummary`.

`signature(x = "list")` kmerKLPlot will plot the K-L divergence for a subset of k-mers for each of the objects that inherit from `SequenceSummary` in the list and display them in a series of panels.

**Note**

The K-L divergence calculation in `calcKL` uses base 2 in the log; the units are in bits.

Also, note that `ggplot2` warns that "Stacking is not well defined when `ymin != 0`". This occurs when some k-mers are less frequent in the positional distribution than the distribution across all positions, and the term of the K-L sum is negative (producing a bar below zero). This does not appear to affect the plot much. In examples below, warnings are suppressed, but the given this is a valid concern from `ggplot2`, warnings are not suppressed in the function itself.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[getKmer](#), [calcKL](#), [kmerEntropyPlot](#)

**Examples**

```
## Load a somewhat contaminated FASTQ file
s.fastq <- readSeqFile(system.file(extdata, test.fastq,
  package=qrqc), hash.prop=1)

## Load a really contaminated FASTQ file
s.contam.fastq <- readSeqFile(system.file(extdata,
  test-contam.fastq, package=qrqc), hash.prop=1)

## Load a random (equal base frequency) FASTA file
s.random.fasta <- readSeqFile(system.file(extdata,
  random.fasta, package=qrqc), type="fasta", hash.prop=1)

## Make K-L divergence plot - shows slight 5-end bias. Note units
## (bits)
suppressWarnings(kmerKLPlot(s.fastq))

## Plot multiple K-L divergence plots
suppressWarnings(kmerKLPlot(list("highly contaminated"=s.contam.fastq, "less
  contaminated"=s.fastq, "random"=s.random.fasta)))
```

---

list2df

*Apply a function to items in list and combine into data frame*

---

**Description**

`list2df` is a helper function that takes a named list and applies a function to each element, and combines the resulting data frames into a single data frame. The output data frame will have an additional column named `sample` indicating which element the data came from.

**Usage**

```
list2df(x, fun)
```

**Arguments**

x                    a named list of objects.  
fun                  a function that takes in the elements of x and outputs a data frame.

**Value**

A data frame made by applying fun to each element of the list x. An additional column named sample will indicate which element the data came from.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**Examples**

```
## Get some sequence files
sq.files = list.files(system.file(extdata, package=qrqc),
  pattern="test.*fastq", full.names=TRUE)
names(sq.files) <- gsub("(.)\\.fastq", "\\1", basename(sq.files))
sq <- lapply(sq.files, readSeqFile)

## Take the FASTQSummary objects, extract quality data from each of
## the, and combine.
d <- list2df(sq, getQual)

## Look at difference in average quality
aggregate(d$mean, list(sample=d$sample), mean)

## Look at difference in variance - this is where we really see a
## change.
aggregate(d$mean, list(sample=d$sample), var)
```

---

makeReport-methods      *Make an HTML report from a FASTASummary of FASTQSummary object*

---

**Description**

makeReport takes a [FASTQSummary](#) or [FASTASummary](#) object, creates an HTML report, and writes it to a file within a directory. The directory naming is incremental so past reports will not be overwritten.

**Usage**

```
makeReport(x, outputDir=".")
```

**Arguments**

x an object that is either FASTQSummary or FASTASummary.  
outputDir an optional character argument to indicate the report output directory. By default, the current directory.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**Examples**

```
## Load a FASTQ file  
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))  
  
## Make and save a report  
makeReport(s.fastq)
```

---

plotBases-methods      *Plot Bases by Position*

---

**Description**

plotBases plots the frequency or proportion of bases by position in the read.

plotBases uses the Sanger base color scheme: blue is Cytosine, green is Adenine, black is Guanine, red is Thymine, and purple in N (any base). Other IUPAC nucleotides are colored using **RColorBrewer**.

**Usage**

```
plotBases(obj, type="freq", bases=NULL, legend=TRUE)
```

**Arguments**

obj an S4 object of class that inherits from [SequenceSummary](#) (either [FASTASummary](#) or [FASTQSummary](#)) from readSeqFile.  
type a character string that is either "freq" or "prop" indicating whether to plot frequencies or proportions on the y-axis.  
bases a vector of characters indicating which bases to include. The default value NULL indicates to plot `_all_` bases.  
legend a logical value indicating whether to include a legend on the top right.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[basePlot](#)

**Examples**

```
## Not run:
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrgc))

## Plot base frequencies
plotBases(s.fastq, type="freq")

## Plot base proportions
plotBases(s.fastq, type="prop")

## End(Not run)
```

---

plotGC-methods

*Plot per Base GC Content by Position*

---

**Description**

plotGC plots the GC proportion by position.

**Usage**

```
plotGC(obj)
```

**Arguments**

obj                    an S4 object of class that inherits from [SequenceSummary](#) (either [FASTASummary](#) or [FASTQSummary](#)) from readSeqFile.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[gcPlot](#)

## Examples

```
## Not run:
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qraqc))

## Plot Qualities
plotGC(s.fastq)

## End(Not run)
```

---

plotQuals-methods      *Plot a Base Quality Boxplot by Position*

---

## Description

plotQuals plots quality statistics by position. Optionally, it adds a lowess curve through the qualities, which is fit with data randomly drawn from the distribution of qualities at each position. A histogram of the sequence length distribution is plotted above the quality plot when histogram is TRUE.

A legend is plotted on the bottom left if legend is TRUE (this location is used because this where the bases are likely to be of highest quality, and thus not overlap the legend). The grey lines indicate the range of the 10% and 90% quantiles, the orange lines indicate the range of the 25% and 75% quartiles, the blue point is the median, the green dash is the mean, and the purple line is the lowess curve if lowess is TRUE.

## Usage

```
plotQuals(obj, ylim=relative, lowess=TRUE, histogram=TRUE, legend=TRUE)
```

## Arguments

|           |  |
|-----------|--|
| obj       | an S4 object of class FASTQSummary from readSeqFile.   |
| ylim      | either 'relative' or 'fixed', which will scale the y axis to either the relative range (from the data) or absolute range of qualities. |
| lowess    | a logical value indicating whether to fit a lowess curve through the quality plot.   |
| histogram | a logical value indicating whether to add a histogram of the sequence length distribution above the quality plot.                      |
| legend    | a logical value indicating whether a legend is to be included.   |

## Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

## See Also

[qualPlot](#)

**Examples**

```
## Not run:
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrc))

## Plot Qualities
plotQuals(s.fastq)

## End(Not run)
```

---

plotSeqLengths-methods

*Plot Histogram of Sequence Lengths*

---

**Description**

plotSeqLengths plots histogram of sequence lengths.

**Usage**

```
plotSeqLengths(obj)
```

**Arguments**

obj            an S4 object of class that inherits from [SequenceSummary](#) (either [FASTASummary](#) or [FASTQSummary](#)) from readSeqFile.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[seqLenPlot](#)

**Examples**

```
## Not run:
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrc))

## Plot Qualities
plotSeqLengths(s.fastq)

## End(Not run)
```



**Description**

basePlot plots quality statistics by position. Optionally, it adds a smoothed curve through the qualities, which is fit with data randomly drawn from the distribution of qualities at each position.

The grey lines indicate the range of the 10% and 90% quantiles, the orange lines indicate the range of the 25% and 75% quartiles, the blue point is the mean. Optionally, one can plot the median as well.

**Usage**

```
qualPlot(x, smooth=TRUE, extreme.color="grey", quartile.color="orange", mean.color="blue", median.co
```

**Arguments**

|                |   |
|----------------|---|
| x              | an S4 object of class FASTQSummary from readSeqFile or a list of FASTQSummary objects with names.   |
| smooth         | a logical value indicating whether to add a smooth curve.   |
| extreme.color  | a character value indicating the color to use for the extreme values (the 10% and 90% quantiles). If NULL, these line segments will not be added. |
| quartile.color | a character value indicating the color to use for the quartiles. If NULL, these line segments will not be added.                                  |
| mean.color     | a character value indicating the color to use for the mean. If NULL, these line segments will not be added.                                       |
| median.color   | a character value indicating the color to use for the median. If NULL, these line segments will not be added.                                     |

**Methods**

signature(x = "FASTQSummary") qualPlot will plot the qualities for a single object of class FASTQSummary.

signature(x = "list") qualPlot will plot the qualities for each of the FASTQSummary items in the list and display them in a series of panels.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[getQual](#)

**Examples**

```
## Load a FASTQ file
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))

## Plot qualities
qualPlot(s.fastq)

## Combine with ggplot2 to produce custom graphics
p <- qualPlot(s.fastq, smooth=FALSE)
p <- p + geom_smooth(aes(x=position, y=quality),
  data=getMCQual(s.fastq), method="lm", color="green", se=FALSE)
p <- p + theme_bw()
p

## Plot multiple quality plots
s.trimmed.fastq <- readSeqFile(system.file(extdata,
  test-trimmed.fastq, package=qrqc))
qualPlot(list("not trimmed"=s.fastq, "trimmed"=s.trimmed.fastq))
```

---

readSeqFile

*Read and Summarize a Sequence (FASTA or FASTQ) File*


---

**Description**

readSeqFile reads a FASTQ or FASTA file, summarizing the nucleotide distribution across position (cycles) and the sequence length distributions. If type is 'fastq', the distribution of qualities across position will also be recorded. If hash is TRUE, the unique sequences will be hashed with counts of their frequency. By default, only 10% of the reads will be hashed; this proportion can be controlled with hash.prop. If kmer=TRUE, k-mers of length k will be hashed by position, also with the sampling proportion controlled by hash.prop.

**Usage**

```
readSeqFile(filename, type=c("fastq", "fasta"), max.length=1000,
  quality=c("sanger", "solexa", "illumina"), hash=TRUE,
  hash.prop=0.1, kmer=TRUE, k=6L, verbose=FALSE)
```

**Arguments**

|            |  |
|------------|--|
| filename   | the name of the file which the sequences are to be read from.  |
| type       | either 'fastq' or 'fasta', representing the type of the file. FASTQ files will have the quality distribution by position summarized.   |
| max.length | the largest sequence length likely to be encountered. For efficiency, a matrix larger than the largest sequence is allocated to <i>this</i> size in C, populated, and then trimmed in R. Specifying a value too small will lead to an error and the function will need to be re-run. |

|           |  |
|-----------|--|
| quality   | either 'illumina', 'sanger', or 'solexa', this determines the quality offsets and range. See the values of QUALITY.CONSTANTS for more information. |
| hash      | a logical value indicating whether to hash sequences   |
| hash.prop | a numeric value in (0, 1] that functions as the proportion of reads to hash.   |
| kmer      | a logical value indicating whether to hash k-mers by position.   |
| k         | an integer value indicating the k-mer size.  |
| verbose   | a logical value indicating whether be verbose (in the C backend).  |

### Value

An S4 object of [FASTQSummary](#) or [FASTASummary](#) containing the summary statistics.

### Note

Identifying the correct quality can be difficult. `readSeqFile` will error out if it a base quality outside of the range of a known quality type, but it is possible one could have reads with a different quality type that won't fall outside of the another type.

Here is a bit more about quality:

**phred** PHRED quality scores (e.g. from Roche 454). ASCII with no offset, range: [4, 60]. This has been removed as an option since sequence reads with this type are very, very uncommon.

**sanger** Sanger are PHRED ASCII qualities with an offset of 33, range: [0, 93]. From NCBI SRA, or Illumina pipeline 1.8+.

**solexa** Solexa (also very early Illumina - pipeline < 1.3). ASCII offset of 64, range: [-5, 62]. Uses a different quality-to-probabilities conversion than other schemes.

**illumina** Illumina output from pipeline versions between 1.3 and 1.7. ASCII offset of 64, range: [0, 62].

### Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

### See Also

[FASTQSummary](#) and [FASTASummary](#) are the classes of the objects returned by `readSeqFile`.

[basePlot](#) is a function that plots the distribution of bases over sequence length for a particular [FASTASummary](#) or [FASTQSummary](#) object. [gcPlot](#) combines and plots the GC proportion.

[qualPlot](#) is a function that plots the distribution of qualities over sequence length for a particular [FASTASummary](#) or [FASTQSummary](#) object.

[seqLenPlot](#) is a function that plots a histogram of sequence lengths for a particular [FASTASummary](#) or [FASTQSummary](#) object.

[kmerKLPlot](#) is a function that plots K-L divergence of k-mers to look for possible bias in reads.

## Examples

```
## Load a FASTQ file, with sequence hashing.
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))

## Load a FASTA file, without sequence hashing.
s.fasta <- readSeqFile(system.file(extdata, test.fasta, package=qrqc),
                      type=fasta, hash=FALSE)
```

---

|                 |   |
|-----------------|---|
| scale_color_dna | <i>Set the color scheme to biovizBase's for DNA</i> |
|-----------------|---|

---

## Description

This wraps ggplot2's `scale_color_manual` to use biovizBase's scheme for DNA (with N).

## Usage

```
scale_color_dna()
```

## Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

## See Also

[scale\\_color\\_iupac](#), [basePlot](#)

## Examples

```
## Load a FASTQ file
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))

## Plot qualities with the DNA color scheme
ggplot(getBase(s.fastq)) + geom_line(aes(x=position, y=frequency,
    color=base)) + scale_color_dna()
```

---

scale\_color\_iupac      *Set the color scheme to biovizBase's for IUPAC codes*

---

**Description**

This wraps ggplot2's scale\_color\_manual to use biovizBase's scheme IUPAC nucleotides codes.

**Usage**

```
scale_color_iupac()
```

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[scale\\_color\\_dna](#), [basePlot](#)

**Examples**

```
## Load a FASTQ file
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))

## Plot qualities with the DNA color scheme
ggplot(getBase(s.fastq)) + geom_line(aes(x=position, y=frequency,
color=base)) + scale_color_iupac()
```

---

seqLenPlot-methods      *Plot a Histogram of Sequence Lengths*

---

**Description**

seqLenPlot plots a histogram of sequence lengths.

**Usage**

```
seqLenPlot(x)
```

**Arguments**

x                      an S4 object that inherits from SequenceSummary from readSeqFile.

## Methods

signature(x = "FASTQSummary") seqLenPlot will plot a histogram of a single object that inherits from SequenceSummary.

signature(x = "list") seqLenPlot will plot a histogram for each of the SequenceSummary items in the list and display them in a series of panels.

## Author(s)

Vince Buffalo <vsbuffalo@ucdavis.edu>

## See Also

[getSeqLen](#)

## Examples

```
## Load a FASTQ file
s.fastq <- readSeqFile(system.file(extdata, test.fastq, package=qrqc))

## Plot sequence lengths
seqLenPlot(s.fastq)

## Plot sequence lengths before and after trimming
s.trimmed.fastq <- readSeqFile(system.file(extdata,
  test-trimmed.fastq, package=qrqc))
seqLenPlot(list("not trimmed"=s.fastq, "trimmed"=s.trimmed.fastq))
```

---

SequenceSummary-class *SequenceSummary class representing the summaries of a sequence file*

---

## Description

A sequence file read in with readSeqFile is summarized by a C call. This is a base class with slots common to both [FASTQSummary](#) and [FASTASummary](#). This is not usually instantiated directly.

Note that many accessor functions transform data in the slots into data frames. The data in the slots is mostly untransformed and less easy to work with directly, so using the accessor functions is recommended.

## Slots

filename the filename processed by readSeqFile.

base.freqs a data frame of base frequencies by position. Each column is a nucleotide (there is a column for position too), and each row contains the count frequencies of bases for that position.

seq.lengths a numeric vector of the number of sequences of a particular length (the length is the position in the vector).

hash a numeric vector of the count frequencies of sequences (the sequences are in the name attribute).

hash.prop a numeric value indicating the proportion of sequences that were sampled for hashing.

kmer a data frame of k-mer frequency by position.

k an integer indicating the length of k-mers hashed.

hashed a logical indicating whether the sequences were hashed in readSeqFile.

kmers.hashed a logical indicating whether the k-mers were hashed in readSeqFile.

**Author(s)**

Vince Buffalo <vsbuffalo@ucdavis.edu>

**See Also**

[FASTQSummary](#) and [FASTASummary](#) are the classes that inherit from SequenceSummary.

[readSeqFile](#) is the function that takes a FASTQ or FASTA file and returns a FASTQSummary object or FASTASummary object.

**Examples**

```
showClass("SequenceSummary")
```

# Index

- \*Topic **accessor**
  - getBase-methods, 9
  - getBaseProp-methods, 10
  - getGC-methods, 11
  - getKmer-methods, 12
  - getMCQual-methods, 13
  - getQual-methods, 14
  - getSeqLen-methods, 15
- \*Topic **classes**
  - FASTASummary-class, 5
  - FASTQSummary-class, 6
  - SequenceSummary-class, 30
- \*Topic **file**
  - makeReport-methods, 20
  - readSeqFile, 26
- \*Topic **graphics**
  - basePlot-methods, 2
  - calcKL-methods, 4
  - gcPlot-methods, 7
  - geom\_qlinerange, 8
  - kmerEntropyPlot-methods, 17
  - kmerKLPlot-methods, 18
  - plotBases-methods, 21
  - plotGC-methods, 22
  - plotQuals-methods, 23
  - plotSeqLengths-methods, 24
  - qualPlot-methods, 25
  - scale\_color\_dna, 28
  - scale\_color\_iupac, 29
  - seqLenPlot-methods, 29
- \*Topic **methods**
  - basePlot-methods, 2
  - calcKL-methods, 4
  - gcPlot-methods, 7
  - geom\_qlinerange, 8
  - getBase-methods, 9
  - getBaseProp-methods, 10
  - getGC-methods, 11
  - getKmer-methods, 12
  - getMCQual-methods, 13
  - getQual-methods, 14
  - getSeqLen-methods, 15
  - kmerEntropyPlot-methods, 17
  - kmerKLPlot-methods, 18
  - plotQuals-methods, 23
  - qualPlot-methods, 25
  - seqLenPlot-methods, 29
- basePlot, 5, 6, 9, 11, 22, 27–29
- basePlot (basePlot-methods), 2
- basePlot, list-method
  - (basePlot-methods), 2
- basePlot, SequenceSummary-method
  - (basePlot-methods), 2
- basePlot-methods, 2
- calcKL, 17–19
- calcKL (calcKL-methods), 4
- calcKL, SequenceSummary-method
  - (calcKL-methods), 4
- calcKL-methods, 4
- FASTASummary, 5, 6, 20–22, 24, 27, 30, 31
- FASTASummary-class, 5
- FASTQSummary, 5, 6, 13, 14, 20–22, 24, 27, 30, 31
- FASTQSummary-class, 6
- gcPlot, 5, 6, 12, 22, 27
- gcPlot (gcPlot-methods), 7
- gcPlot, list-method (gcPlot-methods), 7
- gcPlot, SequenceSummary-method
  - (gcPlot-methods), 7
- gcPlot-methods, 7
- geom\_qlinerange, 8
- getBase, 3, 5–7, 9, 11–16
- getBase (getBase-methods), 9
- getBase, SequenceSummary-method
  - (getBase-methods), 9



- getBase-methods, 9
- getBaseProp, 3, 5–7, 9, 11–16
- getBaseProp (getBaseProp-methods), 10
- getBaseProp, SequenceSummary-method (getBaseProp-methods), 10
- getBaseProp-methods, 10
- getGC, 5, 6, 9, 11, 13–16
- getGC (getGC-methods), 11
- getGC, SequenceSummary-method (getGC-methods), 11
- getGC-methods, 11
- getKmer, 4–6, 12, 17, 19
- getKmer (getKmer-methods), 12
- getKmer, SequenceSummary-method (getKmer-methods), 12
- getKmer-methods, 12
- getMCQual, 9, 11–13, 15, 16
- getMCQual (getMCQual-methods), 13
- getMCQual, FASTQSummary-method (getMCQual-methods), 13
- getMCQual-methods, 13
- getQual, 5, 6, 8, 9, 11–14, 16, 25
- getQual (getQual-methods), 14
- getQual, FASTQSummary-method (getQual-methods), 14
- getQual-methods, 14
- getSeqLen, 5, 6, 9, 11–15, 30
- getSeqLen (getSeqLen-methods), 15
- getSeqLen, SequenceSummary-method (getSeqLen-methods), 15
- getSeqLen-methods, 15
- kmerEntropyPlot, 5, 6, 13, 19
- kmerEntropyPlot (kmerEntropyPlot-methods), 17
- kmerEntropyPlot, list-method (kmerEntropyPlot-methods), 17
- kmerEntropyPlot, SequenceSummary-method (kmerEntropyPlot-methods), 17
- kmerEntropyPlot-methods, 17
- kmerKLPlot, 4–6, 13, 17, 27
- kmerKLPlot (kmerKLPlot-methods), 18
- kmerKLPlot, list-method (kmerKLPlot-methods), 18
- kmerKLPlot, SequenceSummary-method (kmerKLPlot-methods), 18
- kmerKLPlot-methods, 18
- list2df, 19
- makeReport (makeReport-methods), 20
- makeReport, FASTASummary-method (FASTASummary-class), 5
- makeReport, FASTQSummary-method (FASTQSummary-class), 6
- makeReport-methods, 20
- plotBases (plotBases-methods), 21
- plotBases, SequenceSummary-method (SequenceSummary-class), 30
- plotBases-methods, 21
- plotGC (plotGC-methods), 22
- plotGC, SequenceSummary-method (SequenceSummary-class), 30
- plotGC-methods, 22
- plotQuals (plotQuals-methods), 23
- plotQuals, FASTQSummary-method (FASTQSummary-class), 6
- plotQuals-methods, 23
- plotSeqLengths (plotSeqLengths-methods), 24
- plotSeqLengths, SequenceSummary-method (SequenceSummary-class), 30
- plotSeqLengths-methods, 24
- qualPlot, 6, 8, 14, 15, 23, 27
- qualPlot (qualPlot-methods), 25
- qualPlot, FASTQSummary-method (qualPlot-methods), 25
- qualPlot, list-method (qualPlot-methods), 25
- qualPlot-methods, 25
- readSeqFile, 5, 6, 9, 11–14, 26, 31
- scale\_color\_dna, 28, 29
- scale\_color\_iupac, 28, 29
- seqLenPlot, 5, 6, 16, 24, 27
- seqLenPlot (seqLenPlot-methods), 29
- seqLenPlot, list-method (seqLenPlot-methods), 29
- seqLenPlot, SequenceSummary-method (seqLenPlot-methods), 29
- seqLenPlot-methods, 29
- SequenceSummary, 2, 4–6, 9, 11, 12, 21, 22, 24
- SequenceSummary-class, 30