Package 'ssviz'

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Type Package

Title A small RNA-seq visualizer and analysis toolkit

Version 1.43.0

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Author Diana Low

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Description Small RNA sequencing viewer

License GPL-2

Depends R (>= 2.15.1),methods,Rsamtools,Biostrings,reshape,ggplot2,RColorBrewer,stats

biocViews ImmunoOncology, Sequencing,RNASeq,Visualization,MultipleComparison,Genetics

Collate AllClasses.R AllGenerics.R helper.R

VignetteBuilder knitr

Suggests knitr

RoxygenNote 6.0.1

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Contents

`ssviz-package` *ssviz*

Description

A package for short RNA seq visualization and quantification.

Details

Package:	ssviz
Type:	Package
Version:	0.99
Date:	2014-05-08
License:	GPL-2

Author(s)

Diana H.P. Low Maintainer: Diana Low <dlow@imcb.a-star.edu.sg>

counts *counts data*

Description

counts is an example total read count for bam reads

Usage

```
data(ssviz)
```

Source

internal

ctrlbam *ctrlbam data*

Description

ctrlbam is an example control dataset from bam file read in with readBam

Usage

```
data(ssviz)
```

Source

internal

getCountMatrix *getCountMatrix*

Description

returns the bam data.frame with an additional column counts. Only relevant if the fasta file used for mapping input was previously collapsed via fastx_toolkit to return a fasta read name in the format of readnumber-totalcounts

Usage

```
getCountMatrix(bam_file,pseudo=FALSE)
```

Arguments

bam_file	An object of class DataFrame (from IRanges). Can be generated from readBam.
pseudo	Logical. If TRUE, assume the reads in the bam file does not have a count record and sets all counts to 1.

Value

An object of class data.frame having the values from the original bam file with an additional 'count' column.

Author(s)

Diana H.P. Low

See Also

readBam

Examples

```
data(ssviz)
getCountMatrix(ctrlbam)
```

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getCountMatrix-methods

getCountMatrix

Description

returns the bam data.frame with an additional column counts. Only relevant if the fasta file used for mapping input was previously collapsed via fastx_toolkit to return a fasta read name in the format of `readnumber-totalcounts`

Methods

`signature(object="DataFrame")` Returns and object of class data.frame having the values from the original bam file with an additional 'count' column.

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logicalORmissing-class

Class "logicalORmissing"

Description

Class union of logical and missing object.

Author(s)

Diana H.P. Low

Examples

```
showClass("logicalORmissing")
```

ntfreq *ntfreq*

Description

Calculates nucleotide frequency of reads in bam file

Usage

```
ntfreq(bam_file, ntlength, toRNA = TRUE, count_type = "total")
```

Arguments

bam_file	An object of class data.frame or DataFrame
ntlength	An integer specifying the length of the sequence to quantify
toRNA	A logical value on whether to translate the DNA sequence to RNA
count_type	A character string on how to count the nucleotides. Can be either "total" or "unique". If `total` is selected, the function will look for the `count`column and multiply the reads by its number of occurence when calculating the frequency.

Value

Returns a data.frame of the frequency of nucleotides (either A/C/G/T or A/C/G/U) at each position up to the specified `ntlength`

Author(s)

Diana H.P. Low

Examples

```
data(ssviz)
freq<-ntfreq(pctrlbam,ntlength=10)
```

---

ntfreq-methods *ntfreq*

Description

Calculates nucleotide frequency of reads in bam file

Methods

`ntfreq(bam_file, ntlength, toRNA = TRUE, count_type = "total")` Returns a data frame of nucleotide frequences along length of sequence provided.

Author(s)

Diana H.P. Low

pctrlbam *pctrlbam data*

Description

pctrlbam is an example control dataset from bam file read in with readBam

Usage

```
data(ssviz)
```

Source

internal

pingpong *pingpong*

Description

piRNA ping-pong analysis of complementary sequences

Usage

```
pingpong(bam_file)
```

Arguments

bam_file	An object of class data.frame or DataFrame

Details

The ping-pong mechanism is a proposed method for the amplification of primary piRNAs, which leads to the production of new primary piRNAs from their precursor transcripts, which eventually amplifies the pool of both primary and secondary piRNAs. This positive feedback loop is a secondary biogenesis mechanism that requires complementary transcripts to a pre-existing pool of piRNAs.

Value

This function returns a data.frame object with frequency of overlapping complementary piRNAs.

Author(s)

Diana H.P. Low

References

Brennecke J. et al. Cell 128, 1089-1103, March 23, 2007

Examples

```
data(ssviz)
pp<-pingpong(pctrlbam)
```

`pingpong-methods` *pingpong*

Description

piRNA ping-pong analysis of complementary sequences

Methods

`pingpong(bam_file)` Returns a data.frame object with frequency of overlapping complementary piRNAs.

Author(s)

Diana H.P. Low

`plotDistro` *plotDistro*

Description

Plots distribution of reads in the bam file based on length, direction (strand) or location (rname)

Usage

```
plotDistro(bamlist, type = "qwidth", samplenames = NULL, unique = FALSE, ncounts = NULL, norm = FALSE
```

Arguments

`bamlist`	An object of type list, giving a list of bam files. If you only have 1 file, use `list(bam_file)`
`type`	An object of type character. Can be `qwidth`,`rname` or `strand`. In theory, any column property existing in the bam file can be used, but these 3 would be most meaningful.
`samplenames`	Labels for the plot.
`unique`	Logical value to use unique reads (`TRUE`) or all reads (`FALSE`)
`ncounts`	Number of total counts in the bam file, used if `unique` is set to `FALSE`.
`norm`	Logical value to determine if plot will be normalised.
`yname`	y axis label.

Author(s)

Diana H.P. Low

Examples

```
data(ssviz)
plotDistro(list(ctrlbam))
```

`plotDistro-methods` *plotDistro*

Description

Plots distribution of reads in the bam file based on length, direction (strand) or location (rname)

Methods

`plotDistro(bamlist, type = "qwidth", samplenames = NULL, unique = FALSE, ncounts = 1e+06, norm = FALSE,`
Returns a distribution plot.

Author(s)

Diana H.P. Low

`plotFreq` *plotFreq*

Description

Plots nucleotide frequency generated by `ntfreq`

Usage

```
plotFreq(freqvector, percentage = TRUE)
```

Arguments

`freqvector`	`data.frame` object generated by `ntfreq`
`percentage`	Logical value to represent y-axis as percentage or frequency.

Author(s)

Diana H.P. Low

See Also

`ntfreq`

Examples

```
data(ssviz)
freq<-ntfreq(pctrlbam,ntlength=10)
plotFreq(freq)
```

plotFreq-methods *plotFreq*

Description

Plots nucleotide frequency generated by ntfreq

Methods

plotFreq(freqvector, percentage = TRUE) Returns a frequency bar plot.

Author(s)

Diana H.P. Low

plotPP *plotPP*

Description

Plots the ping-pong frequency of piRNA amplification

Usage

```
plotPP(pout, samplenames = NULL)
```

Arguments

pout	An object of type data.frame generated by pingpong
samplenames	An object of type character for sample labels.

Author(s)

Diana H.P. Low

References

Brennecke J. et al. Cell 128, 1089-1103, March 23, 2007

See Also

pingpong

Examples

```
data(ssviz)
pp<-pingpong(pctrlbam)
plotPP(list(pp))
```

plotPP-methods *plotPP*

Description

Plots the ping-pong frequency of piRNA amplification

Methods

`plotPP(pout, samplenames = NULL)` Returns the pingpong amplification plot.

Author(s)

Diana H.P. Low

plotRegion *plotRegion*

Description

Plots the read density given a chromosome region.

Usage

```
plotRegion(bamlist, region, howsmooth = 2, ncounts = NULL, samplenames = NULL)
```

Arguments

`bamlist`	An object of type list, giving a list of bam files. If you only have 1 file, use `list(bam_file)`
`region`	An object of type character defining the region to plot. Eg. `chr1:1000-2000`
`howsmooth`	Numeric value controlling smoothness of the plot.
`ncounts`	Total number of reads for plot normalization.
`samplenames`	Sample names

Value

Returns the x and y components of the region's reads and plots the density.

Author(s)

Diana H.P. Low

Examples

```
data(ssviz)
region<-'chr1:3015526-3080526'
plotRegion(list(ctrlbam), region=region)
```

plotRegion-methods *plotRegion*

Description

Plots the read density given a chromosome region.

Methods

`plotRegion(bamlist, region, howsmooth = 2, ncounts = NULL, samplenames = NULL)` Returns the x and y components of the region's reads and plots the density.

Author(s)

Diana H.P. Low

ptreatbam *ptreatbam data*

Description

`ptreatbam` is an example treatment dataset from bam file read in with `readBam`

Usage

```
data(ssviz)
```

Source

internal

readBam *readBam*

Description

Reads a bam file through RSamtools, and converts it into a data frame of class `DataFrame`

Usage

```
readBam(file_name, tags = character(0))
```

Arguments

`file_name`	Character string of bam file location
`tags`	Bam tags to import into the data frame. By default it only takes the standard values if none are given.

Details

This function formalizes what had been described in the RSamtools documentation and makes it easier to compute the downstream functions in this package.

Value

Returns the bam file contents in a readable dataframe format.

Author(s)

Diana H.P. Low

References

RSamtools package

Examples

```
bam.files <- dir(system.file("extdata", package = "ssviz"), full = TRUE, patt = "bam$")
ctrlbam <- readBam(bam.files[1])
```

---

readBam-methods *readBam*

Description

Reads a bam file through RSamtools, and converts it into a data frame of class `DataFrame`

Methods

`readBam(bam_file, tags = character(0))` Returns the bam file contents in a readable dataframe format.

Author(s)

Diana H.P. Low

---

treatbam *treatbam data*

Description

`treatbam` is an example treatment dataset from bam file read in with `readBam`

Usage

```
data(ssviz)
```

Source

internal

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