

Package ‘ssviz’

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Type Package

Title A small RNA-seq visualizer and analysis toolkit

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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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| ssviz-package | <i>ssviz</i> |
|---------------|--------------|

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 | <i>counts data</i> |
|--------|--------------------|

Description

counts is an example total read count for bam reads

Usage

```
data(ssviz)
```

Source

internal

| | |
|---------|---------------------|
| ctrlbam | <i>ctrlbam data</i> |
|---------|---------------------|

Description

ctrlbam is an example control dataset from bam file read in with [readBam](#)

Usage

```
data(ssviz)
```

Source

internal

| | |
|----------------|-----------------------|
| getCountMatrix | <i>getCountMatrix</i> |
|----------------|-----------------------|

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

| | |
|-----------------------|---|
| <code>bam_file</code> | An object of class <code>DataFrame</code> (from <code>IRanges</code>). Can be generated from <code>readBam</code> . |
| <code>pseudo</code> | Logical. If <code>TRUE</code> , 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)
```

`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.

```
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 countcolumn and multiply the reads by its number of occurrence 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 | <i>ntfreq</i> |
|----------------|---------------|

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 frequencies along length of sequence provided.

Author(s)

Diana H.P. Low

| | |
|----------|----------------------|
| pctrlbam | <i>pctrlbam data</i> |
|----------|----------------------|

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, yname = "reads")
```

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, yna)
```

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 | <i>plotPP</i> |
|----------------|---------------|

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 | <i>plotRegion</i> |
|------------|-------------------|

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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