

Package ‘seqLogo’

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Title Sequence logos for DNA sequence alignments

Version 1.77.0

Description seqLogo takes the position weight matrix of a DNA sequence motif and plots the corresponding sequence logo as introduced by Schneider and Stephens (1990).

LazyLoad yes

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Imports stats4, grDevices

Depends R (>= 4.2), methods, grid

Suggests knitr, BiocStyle, rmarkdown, testthat

BugReports <https://github.com/ivanek/seqLogo/issues>

VignetteBuilder knitr

Collate AllClasses.R AllGenerics.R pwm.R seqLogo.R

License LGPL (>= 2)

biocViews SequenceMatching

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makePWM	<i>Constructing a pwm object</i>
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Description

This function constructs an object of class `pwm` from a matrix. It checks that the matrix has correct dimensions and that columns add up to 1.0.

Usage

```
makePWM(pwm, alphabet = "DNA")
```

Arguments

<code>pwm</code>	matrix. Numerical matrix representing the position weight matrix.
<code>alphabet</code>	character. The alphabet making up the sequence. Currently, only 'DNA' and 'RNA' is supported.

Value

An object of class `pwm`.

Author(s)

Oliver Bembom

Examples

```
mFile <- system.file("extdata/pwm1", package = "seqLogo")
m <- read.table(mFile)
pwm <- makePWM(m)
```

pwm-class	<i>An S4 class to represent a PWM matrix.</i>
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Description

An object of class 'pwm' represents the alphabet*width position weight matrix of a sequence motif. In case of DNA sequence motif, the entry in row `i`, column `j` gives the probability of observing nucleotide `c('A', 'C', 'G', 'T')[i]` in position `j` of the motif.

Usage

```
## S4 method for signature 'pwm'  
show(object)  
  
## S4 method for signature 'pwm'  
summary(object, ...)  
  
## S4 method for signature 'pwm,ANY'  
plot(x, y = "missing", ...)  
  
## S4 method for signature 'pwm'  
pwm(pwm)  
  
## S4 method for signature 'pwm'  
ic(pwm)  
  
## S4 method for signature 'pwm'  
consensus(pwm)
```

Arguments

object	object of pwm-class
...	additional parameters for plot function
x	object of pwm-class
y	default (missing) for plot function
pwm	object of pwm-class

Value

pwm-class object with slots: pwm, width, ic and alphabet.

Functions

- `show, pwm-method`: Shows the position weight matrix.
- `summary, pwm-method`: Prints the summary information about position weight matrix.
- `plot, pwm, ANY-method`: Plots the sequence logo of the position weight matrix.
- `pwm, pwm-method`: Access to 'pwm' slot
- `ic, pwm-method`: Access to 'ic' slot
- `consensus, pwm-method`: Access to 'consensus' slot

Slots

`pwm` matrix. The position weight matrix.

`width` numeric. The width of the motif.

`ic` numeric. The information content (IC).

`alphabet` character. The sequence alphabet. Currently, only 'DNA' and 'RNA' is supported.

`consensus` character. The consensus sequence.

Author(s)

Oliver Bembom

Examples

```
mFile <- system.file("extdata/pwm1", package = "seqLogo")
m <- read.table(mFile)
p <- makePWM(m)
#
# slot access
pwm(p)
ic(p)
consensus(p)
```

`seqLogo`*Plot a sequence logo for a given position weight matrix*

Description

This function takes the alphabet*width position weight matrix of a sequence motif and plots the corresponding sequence logo.

Usage

```
seqLogo(pwm, ic.scale=TRUE, xaxis=TRUE, yaxis=TRUE, xfontsize=15, yfontsize=15,
        fill=c(A='#61D04F', C='#2297E6', G='#F5C710', T='#DF536B'))
```

Arguments

<code>pwm</code>	numeric. The alphabet*width position weight matrix.
<code>ic.scale</code>	logical. If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
<code>xaxis</code>	logical. If TRUE, an X-axis will be plotted.
<code>yaxis</code>	logical. If TRUE, a Y-axis will be plotted.
<code>xfontsize</code>	numeric. Font size to be used for the X-axis.
<code>yfontsize</code>	numeric. Font size to be used for the Y-axis.
<code>fill</code>	character. Fill color to be used for the letters. Must be a named character vector of length equal to number of rows in <code>pwm</code> slot and names identical to its row-names.

Value

NULL.

Author(s)

Oliver Bembom

Examples

```
mFile <- system.file("extdata/pwm1", package = "seqLogo")  
m <- read.table(mFile)  
p <- makePWM(m)  
seqLogo(p)
```

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