Package ‘seqLogo’

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Title Sequence logos for DNA sequence alignments

Version 1.74.0

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

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

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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Author Oliver Bembom [aut],
Robert Ivanek [aut, cre] (ORCID:
<`https://orcid.org/0000-0002-8403-056X`>)

Maintainer Robert Ivanek <`robert.ivanek@unibas.ch`>

Contents

`makePWM` *Constructing a pwm object*

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

`pwm`	matrix. Numerical matrix representing the position weight matrix.
`alphabet`	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)
```

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pwm-class *An S4 class to represent a PWM matrix.*

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

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

Value

NULL.

Author(s)

Oliver Bembom

Examples

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

Index