Package 'seqLogo'

November 12, 2026

Title Sequence logos for DNA sequence alignments

Version 1.78.0

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

git_url https://git.bioconductor.org/packages/seqLogo

git_branch RELEASE_3_23

git_last_commit a7902a4

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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`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)
```

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 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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