

Package ‘seqLogo’

January 20, 2026

Title Sequence logos for DNA sequence alignments
Version 1.76.0
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_22
git_last_commit 5d40dcb
git_last_commit_date 2025-10-29
Repository Bioconductor 3.22
Date/Publication 2026-01-19
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 | 2 |
| pwm-class | 2 |
| seqLogo | 4 |

Index**6**

| | |
|---------|----------------------------------|
| makePWM | <i>Constructing a pwm object</i> |
|---------|----------------------------------|

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> |
|-----------|---|

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)
```

Index

alphabet (pwm-class), [2](#)
consensus (pwm-class), [2](#)
consensus, pwm-method (pwm-class), [2](#)
ic (pwm-class), [2](#)
ic, pwm-method (pwm-class), [2](#)
makePWM, [2](#)
plot, pwm, ANY-method (pwm-class), [2](#)
pwm (pwm-class), [2](#)
pwm, pwm-method (pwm-class), [2](#)
pwm-class, [2](#)
seqLogo, [4](#)
show, pwm-method (pwm-class), [2](#)
summary, pwm-method (pwm-class), [2](#)