

# Package ‘seqLogo’

April 5, 2014

**Title** Sequence logos for DNA sequence alignments

**Version** 1.28.0

**Author** Oliver Bembom

**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).

**Maintainer** Oliver Bembom <oliver.bembom@gmail.com>

**Depends** methods, grid

**Collate** AllClasses.R AllGenerics.R pwm.R seqLogo.R zzz.R

**License** LGPL (>= 2)

**LazyLoad** yes

**biocViews** SequenceMatching

## R topics documented:

makePWM . . . . .	2
pwm-class . . . . .	2
seqLogo . . . . .	3

<b>Index</b>	<b>5</b>
--------------	----------

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**

<code>pwm</code>	matrix representing the position weight matrix
<code>alphabet</code>	character the alphabet making up the sequence. Currently, only "DNA" is supported.

**Value**

An object of class `pwm`.

**Author(s)**

Oliver Bembom, <bembom@berkeley.edu>

**Examples**

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

---

`pwm-class`*Class "pwm"*

---

**Description**

An object of class `"pwm"` represents the  $4 \times W$  position weight matrix of a 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.

**Objects from the Class**

Objects can be created by calls of the form `new("pwm", ...)`.

**Slots**

consensus Object of class "character"  
 ic Object of class "numeric"  
 pwm Object of class "matrix" The position weight matrix.  
 width: "numeric" The width of the motif.  
 alphabet: "character" The sequence alphabet. Currently, only "DNA" is supported.

**Methods**

**summary** signature(object = "pwm", ...) Prints the position weight matrix.  
**print** signature(x = "pwm", ...) Prints the position weight matrix.  
**show** signature(object = "pwm") Prints the position weight matrix.  
**plot** signature(x = "pwm") Plots the sequence logo of the position weight matrix.

**Author(s)**

Oliver Bombom, <bombom@berkeley.edu>

---

 seqLogo

---

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


---

**Description**

This function takes the 4xW position weight matrix of a DNA sequence motif and plots the corresponding sequence logo.

**Usage**

```
seqLogo(pwm, ic.scale=TRUE, xaxis=TRUE, yaxis=TRUE, xfontsize=15, yfontsize=15)
```

**Arguments**

pwm	numeric	The 4xW 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.

**Details**

Within each column, the height of a given letter is proportional to its frequency at that position. If ic.scale is TRUE, the height of each column in the plot indicates the information content at that position of the motif. Otherwise, the height of all columns are identical.

**Value**

None.

**Author(s)**

Oliver Bembom, <bembom@berkeley.edu>

**Examples**

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

# Index

\*Topic **classes**

pwm-class, [2](#)

\*Topic **misc**

makePWM, [2](#)

seqLogo, [3](#)

makePWM, [2](#)

plot, pwm-method (pwm-class), [2](#)

print, pwm-method (pwm-class), [2](#)

pwm-class, [2](#)

seqLogo, [3](#)

show, pwm-method (pwm-class), [2](#)

summary, pwm-method (pwm-class), [2](#)