

# Package ‘seqLogo’

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**Title** Sequence logos for DNA sequence alignments

**Version** 1.44.0

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**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).

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**Imports** stats4

**Depends** methods, grid

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

**License** LGPL (>= 2)

**LazyLoad** yes

**biocViews** SequenceMatching

**NeedsCompilation** no

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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**

**pwm** matrix representing the position weight matrix  
**alphabet** character the alphabet making up the sequence. Currently, only "DNA" is supported.

**Value**

An object of class `pwm`.

**Author(s)**

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**Examples**

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

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pwm-class

*Class "pwm"*

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**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>

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

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**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**

<code>pwm</code>	numeric	The 4xW 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.

**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)
```

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