**Package ‘seqLogo’**

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**Title**  Sequence logos for DNA sequence alignments

**Version**  1.40.0

**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).

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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

**R topics documented:**

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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**

```r
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

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

Description

An object of class "pwm" represents the 4xW 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.

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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)

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Examples

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