

seqLogo

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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

<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)

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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

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 $4 \times W$ 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>	<code>numeric</code>	The 4xW position weight matrix.
<code>ic.scale</code>	<code>logical</code>	If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
<code>xaxis</code>	<code>logical</code>	If TRUE, an X-axis will be plotted.
<code>yaxis</code>	<code>logical</code>	If TRUE, a Y-axis will be plotted.
<code>xfontsize</code>	<code>numeric</code>	Font size to be used for the X-axis.
<code>yfontsize</code>	<code>numeric</code>	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/pwml", package="seqLogo")
m <- read.table(mFile)
pwm <- makePWM(m)
seqLogo(pwm)
```

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