

Package ‘seqLogo’

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Title Sequence logos for DNA sequence alignments

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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

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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)
```

pwm-class

Class "pwm"

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.

Author(s)

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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

<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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