

Package ‘seqLogo’

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Title Sequence logos for DNA sequence alignments

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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

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LazyLoad yes

biocViews SequenceMatching

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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)

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)
```

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