Package ‘seqLogo’

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Title Sequence logos for DNA sequence alignments

Version 1.32.1

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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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Depends methods, grid

Imports stats4

Collate AllClasses.R AllGenerics.R pwm.R seqLogo.R zzz.R

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LazyLoad yes

biocViews SequenceMatching

R topics documented:

`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

`pwm`	`matrix` representing the positon weight matrix
`alphabet`	`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 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)

Oliver Bembom, `<bembom@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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