

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>

Imports stats4

Depends methods, grid

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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)

Oliver Bombom, <bombom@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

- | | | |
|------------------------|---------|---|
| <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 Bombom, <bombom@berkeley.edu>

Examples

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

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