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).
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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")
**pwm-class**

**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**

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

**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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