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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**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**

```r
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**

```r
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", ...).`
seqLogo

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

  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)

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Examples

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