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 positon 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

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)

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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)

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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