Package 'seqLogo'

October 17, 2020

Title Sequence logos for DNA sequence alignments

Version 1.54.3

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).

Imports stats4

Depends methods, grid

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

License LGPL (>= 2)

LazyLoad yes

biocViews SequenceMatching

BugReports https://github.com/ivanek/seqLogo/issues

git_url https://git.bioconductor.org/packages/seqLogo

git_branch RELEASE_3_11

git_last_commit 1645eca

git_last_commit_date 2020-05-10

Date/Publication 2020-10-16

Author Oliver Bembom [aut],
Robert Ivanek [aut, cre] (<https://orcid.org/0000-0002-8403-056X>)

Maintainer Robert Ivanek <robert.ivanek@unibas.ch>

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)
```

Index