Package 'DiffLogo'

February 27, 2026

Type Package

Title DiffLogo: A comparative visualisation of biooligomer motifs

Version 2.34.0

Date 2015-02-12

Author c(
person(``Martin'', ``Nettling'', role = c(``aut'', ``cre''), email = ``martin.nettling@informatik.uni-halle.de''),
person(``Hendrik'', ``Treutler'', role = c(``aut'', ``cre''), email = ``hendrik.treutler@ipb-halle.de''),
person(``Jan'', ``Grau'', role = c(``aut'', ``ctb''), email = ``grau@informatik.uni-halle.de''),
person(``Andrey'', ``Lando'', role = c(``aut'', ``ctb''), email = ``dronte@autosome.ru''),
person(``Jens'', ``Keilwagen'', role = c(``aut'', ``ctb''), email = ``jens.keilwagen@julius-kuehn.de''),
person(``Stefan'', ``Posch'', role = ``aut'', email = ``posch@informatik.uni-halle.de''),
person(``Ivo'', ``Grosse'', role = ``aut'', email = ``grosse@informatik.uni-halle.de''))

Depends R (>= 3.4), stats, cba

Imports grDevices, graphics, utils, tools

Suggests knitr, testthat, seqLogo, MotifDb

Maintainer Hendrik Treutler<hendrik.treutler@gmail.com>

Description DiffLogo is an easy-to-use tool to visualize motif differences.

License GPL (>= 2)

URL https://github.com/mgledi/DiffLogo/

BugReports https://github.com/mgledi/DiffLogo/issues

biocViews Software, SequenceMatching, MultipleComparison, MotifAnnotation, Visualization, Alignment

Collate 'alphabet.R' 'baseDistrs.R' 'diffSeqLogo.R' 'preconditions.R' 'seqLogo.R' 'stackHeights.R' 'utilities.R' 'diffSeqLogoSupport.R' 'pwmAlignment.R'

RoxygenNote 6.1.1

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

git_branch RELEASE_3_22

git_last_commit 6dbe09c

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-02-27

Contents

alignPwmSets *Multiple PWMs alignment*

Description

Align two sets of pwms

Usage

```
alignPwmSets(left_pwms_set, left_alignment, right_pwms_set,
  right_alignment, try_reverse_complement)
```

Arguments

left_pwms_set   list of pwms(matrixes)

left_alignment   alignment of left_pwms_set.

right_pwms_set   list of pwms;

right_alignment
     alignment of right_pwms_set.

try_reverse_complement
     if true(default), also try reverse complement.

Value

list - alignment of concatination of left_pwms_set and right_pwms_set

Author(s)

Lando Andrey

Alphabet *built alphabet*

Description

builts an object of class Alphabet from the given set of symbols and colors

Usage

```
Alphabet(chars, cols, supportReverseComplement)
```

Arguments

chars   set of symbols

cols   set of colors; one for each symbol

supportReverseComplement
     boolean whether the alphabet supports reverse complementation (like DNA/RNA)
     or not (like ASN)

Value

the Alphabet object

Author(s)

Martin Nettling

Examples

```
DNA = Alphabet(c("A","C","G","T"),c("green4","blue","orange","red"),TRUE)
```

ASN   *ASN alphabet*

Description

the amino acid alphabet (20 symbols), i.e. A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y

Usage

```
ASN
```

Format

An object of class `Alphabet` of length 4.

Author(s)

Martin Nettling

Examples

```
ASN
```

---

baseDistributionPwm   *Generates a PWM*

Description

Generates a PWM consisting of only the uniform distribution or the given base_distribution (if defined).

Usage

```
baseDistributionPwm(pwm_length, alphabet_length,
  base_distribution = NULL)
```

Arguments

`pwm_length`	the number of positions
`alphabet_length`	
	the alphabet size
`base_distribution`	
	optional base distribution for each PWM position

Value

a PWM

`calculatePvalue`	*p-value that two PWM-positions are from the same distribution*

Description

Calculates the p-value for the null-hypothesis that two given probability vectors p1, p2 calculated from n1/n2 observations arise from the same distribution

Usage

```
calculatePvalue(p1, p2, n1, n2, stackHeight = shannonDivergence,
  numberOfPermutations = 100, plotGammaDistributionFit = FALSE)
```

Arguments

`p1`	first probability vector with one probability for each symbol of the alphabet
`p2`	second probability vector with one probability for each symbol of the alphabet
`n1`	number of observations for the calculation of p1
`n2`	number of observations for the calculation of p2
`stackHeight`	function for the calculation of a divergence measure for two probability vectors
`numberOfPermutations`	
	the number of permutations to perform for the calculation of stackHeights
`plotGammaDistributionFit`	
	if TRUE the fit of a gamma distribution to the sampled stackHeights is plotted

Value

a numeric p-value

Author(s)

Hendrik Treutler

Examples

```
p1 <- c(0.2, 0.3, 0.1, 0.4)
p2 <- c(0.2, 0.1, 0.3, 0.4)
n1 <- 100
n2 <- 200
numberOfPermutations = 100
plotGammaDistributionFit = TRUE

pValue <- calculatePvalue(p1 = p1, p2 = p2, n1 = n1, n2 = n2, stackHeight = shannonDivergence, numberOfPermutati
```

---

createDiffLogoObject   *DiffLogo object*

Description

Creates a DiffLogo object

Usage

```
createDiffLogoObject(pwm1, pwm2, stackHeight = shannonDivergence,
  baseDistribution = normalizedDifferenceOfProbabilities,
  alphabet = DNA, align_pwms = FALSE,
  unaligned_penalty = divergencePenaltyForUnaligned,
  try_reverse_complement = TRUE, base_distribution = NULL,
  length_normalization = FALSE, unaligned_from_left = 0,
  unaligned_from_right = 0)
```

Arguments

pwm1	representation of the first position weight matrix (PWM) of type pwm, data.frame, or matrix
pwm2	representation of the second position weight matrix (PWM) of type pwm, data.frame, or matrix
stackHeight	function for the height of a stack at position i
baseDistribution	function for the heights of the individual bases
alphabet	of type Alphabet
align_pwms	if True, will aling and extend pwms.
unaligned_penalty	is a function for localPwmAlignment.
try_reverse_complement	if True, alignment will try reverse complement pwms
base_distribution	is a vector of length nrow(pwm) that is added to unaligned columns of pwms for comparing. If NULL, uniform distribution is used
length_normalization	If true, will minimize the average divergence between PWMs. Otherwise will minimize the sum of divergences between positions. In both cases unalignes positions are compared to base_distribution and are counted when computing the alignment length.

```
unaligned_from_left
                the number of unaligned positions on the left
unaligned_from_right
                the number of unaligned positions on the right
```

Value

DiffLogo object

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoObj = createDiffLogoObject(pwm1 = pwm1, pwm2 = pwm2)
diffLogo(diffLogoObj)
```

---

differenceOfICs   *normalized information content differences*

Description

information content differences normalized by the sum of absolute information content differences
for the given pair of probability vectors

Usage

```
differenceOfICs(p1, p2)
```

Arguments

p1	probability vector representing the first symbol distribution
p2	probability vector representing the second symbol distribution

Value

a vector with one result for each symbol

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoFromPwm(pwm1 = pwm1, pwm2 = pwm2, baseDistribution = differenceOfICs)
```

---

diffLogo   *Draw DiffLogo*

Description

Draws the difference of two sequence logos.

Usage

```
diffLogo(diffLogoObj, ymin = 0, ymax = 0, sparse = FALSE,
  diffLogoConfiguration = list())
```

Arguments

diffLogoObj   a DiffLogoObject created by the function createDiffLogoObject

ymin   minimum value on the y-axis

ymax   maximum value on the y-axis

sparse   if TRUE margins are reduced and tickmarks are removed from the logo

diffLogoConfiguration
                     list of configuration parameters (see function diffLogoTableConfiguration(...))

Value

none (draws difference logo)

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoObj = createDiffLogoObject(pwm1 = pwm1, pwm2 = pwm2)
diffLogo(diffLogoObj)
```

---

diffLogoFromPwm *Draw DiffLogo from PWM*

Description

Draws the difference of two sequence logos.

Usage

```
diffLogoFromPwm(pwm1, pwm2, ymin = 0, ymax = 0,
  stackHeight = shannonDivergence,
  baseDistribution = normalizedDifferenceOfProbabilities,
  sparse = FALSE, alphabet = DNA, align_pwms = FALSE,
  unaligned_penalty = divergencePenaltyForUnaligned,
  try_reverse_complement = TRUE, base_distribution = NULL,
  length_normalization = FALSE)
```

Arguments

pwm1	representation of the first position weight matrix (PWM) of type pwm, data.frame, or matrix
pwm2	representation of the second position weight matrix (PWM) of type pwm, data.frame, or matrix
ymin	minimum value on the y-axis
ymax	maximum value on the y-axis
stackHeight	function for the height of a stack at position i
baseDistribution	
	function for the heights of the individual bases
sparse	if TRUE margins are reduced and tickmarks are removed from the logo
alphabet	of type Alphabet
align_pwms	if true, DiffLogo will align pwms before plotting
unaligned_penalty	
	is a function for localPwmAlignment.

`try_reverse_complement`

        if True, alignment will try reverse complement pwms

`base_distribution`

        is a vector of length nrow(pwm) that is added to unaligned columns of pwms for comparing. If NULL, uniform distribution is used

`length_normalization`

        If true, will minimize the average divergence between PWMs. Otherwise will minimize the sum of divergences between positions. In both cases unalignes positions are compared to base_distribution and are counted when computing the alignment length.

Value

none (draws difference logo)

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoFromPwm(pwm1 = pwm1, pwm2 = pwm2)
```

---

diffLogoTable   *Draw DiffLogo-table*

Description

Draws a table of DiffLogos.

Usage

```
diffLogoTable(PWMs, sampleSizes = NULL, alphabet = DNA,
  configuration = list(), ...)
```

Arguments

PWMs	a list/vector of position weight matrices (PWMs) each of type pwm, data.frame, or matrix
sampleSizes	the number of sequences behind each PWM
alphabet	the alphabet of the given PWMs
configuration	list of (probably part of) of configuration options. See diffLogoTableConfiguration.
...	set of parameters passed to the function 'axis' for plotting

Value

none (draws table of difference logos)

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

diffLogoTable(motifs)
```

---

diffLogoTableConfiguration

Configuration object for diffLogoTable

Description

Default configuration list for diffLogoTable

Usage

```
diffLogoTableConfiguration(alphabet, stackHeight = shannonDivergence,
  baseDistribution = normalizedDifferenceOfProbabilities,
  uniformYaxis = TRUE, sparse = TRUE, showSequenceLogosTop = TRUE,
  enableClustering = TRUE, treeHeight = 0.5, margin = 0.02,
  ratio = 1, align_pwms = FALSE, multiple_align_pwms = TRUE,
  unaligned_penalty = divergencePenaltyForUnaligned,
  try_reverse_complement = TRUE, length_normalization = FALSE,
  numberOfPermutations = 100)
```

Arguments

`alphabet`	used alphabet of type Alphabet
`stackHeight`	function for the height of a stack at position i
`baseDistribution`	
	function for the heights of the individual bases
`uniformYaxis`	if TRUE each DiffLogo is plotted with the same scaling of the y-axis
`sparse`	if TRUE margins are reduced and tickmarks are removed from the logo
`showSequenceLogosTop`	
	if TRUE the classical sequence logos are drawn above each column of the table
`enableClustering`	
	if TRUE the motifs are reordered, so that similar motifs have a small vertical and horizontal distance in the table
`treeHeight`	the height of the plotted cluster tree above the columns of the table; set equal to zero to omit the cluster tree
`margin`	the space reseverved for labels
`ratio`	the ratio of the plot; this is needed to determine the margin sizes correctly
`align_pwms`	if True, will align and extend pwms in each cell of diffLogoTable independently.
`multiple_align_pwms`	
	if True, will align and extend pwms in the diffLogoTable jointly.
`unaligned_penalty`	
	is a function for localPwmAlignment.
`try_reverse_complement`	
	if True, alignment will try reverse complement pwms
`length_normalization`	
	if True, divergence between pwms is divided by length of pwms.
`numberOfPermutations`	
	number of permutations for the permutation test for the calculation of p-values

Value

list of parameters

Author(s)

Lando Andrey

Examples

```
diffLogoTableConfiguration(DNA)
```

DNA *DNA alphabet*

Description

the DNA alphabet, i.e. A, C, G, T

Usage

```
DNA
```

Format

An object of class `Alphabet` of length 4.

Author(s)

Martin Nettling

Examples

```
DNA
```

---

drawDiffLogoTable *Draws a table of DiffLogos*

Description

Draws a table of DiffLogos.

Usage

```
drawDiffLogoTable(diffLogoTableObj, ...)
```

Arguments

diffLogoTableObj

the diffLogoTable-Object created by function prepareDiffLogoTable(...)

... optional parameters for functon axis

Value

none (draws difference logo)

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

diffLogoTableObj = prepareDiffLogoTable(motifs)
drawDiffLogoTable(diffLogoTableObj)
```

---

enrichDiffLogoObjectWithPvalues

Enriches a difflogo object with p-values

Description

Enriches a difflogo object with p-values which quantifies the probability that two PWM-positions are from the same distribution

Usage

```
enrichDiffLogoObjectWithPvalues(diffLogoObj, n1, n2,
  stackHeight = shannonDivergence, numberOfPermutations = 100)
```

Arguments

`diffLogoObj`	matrix of difflogo objects
`n1`	the number of sequences behind the first pwm behind the given difflogo object
`n2`	the number of sequences behind the second pwm behind the given difflogo object
`stackHeight`	function for the calculation of a divergence measure for two probability vectors
`numberOfPermutations`	
	the number of permutations to perform for the calculation of stackHeights

Value

enriched difflogo object

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}
```

```
pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]
n1 <- 100
n2 <- 100
diffLogoObj = createDiffLogoObject(pwm1 = pwm1, pwm2 = pwm2)
diffLogoObj = enrichDiffLogoObjectWithPvalues(diffLogoObj, n1, n2)
```

---

enrichDiffLogoTableWithPvalues

Enriches a matrix of difflogo objects with p-values

Description

Enriches a matrix of difflogo objects with p-values which quantifies the probability that two PWM-positions are from the same distribution

Usage

```
enrichDiffLogoTableWithPvalues(diffLogoObjMatrix, sampleSizes,
    stackHeight = shannonDivergence, numberOfPermutations = 100)
```

Arguments

diffLogoObjMatrix

matrix of difflogo objects

sampleSizes   number of sequences behind the pwms behind the given difflogo objects

stackHeight   function for the calculation of a divergence measure for two probability vectors

numberOfPermutations

the number of permutations to perform for the calculation of stackHeights

Value

matrix of difflogo objects enriched with p-values

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}
sampleSizes <- c(100, 150, 200, 250)
names(sampleSizes) <- motif_names

diffLogoTableObj = prepareDiffLogoTable(motifs);
diffLogoTableObj$diffLogoObjMatrix = enrichDiffLogoTableWithPvalues(diffLogoTableObj$diffLogoObjMatrix, samp
```

---

extendPwmsFromAlignmentVector

Extend pwms with respect to alignment

Description

Extends pwms by adding base_distribution to both sides, so that they keep aligned, but have equal length.

Usage

```
extendPwmsFromAlignmentVector(pwms, alignment_vector,
  base_distribution = NULL)
```

Arguments

pwms   is a list of matrixes

alignment_vector
                    is a list of shifts ($shift) and orientations ($direction)

base_distribution
                    is a vector of length nrow(pwm) that is added to unaligned columns of pwms for
                    comparing. If NULL, uniform distribution is used

Value

extended pwms

Author(s)

Lando Andrey

Examples

```
file1 = system.file("extdata/homer/Max.motif",   package = "DiffLogo")
file2 = system.file("extdata/homer/c-Myc.motif", package = "DiffLogo")
pwm1 = getPwmFromFile(file1)
pwm2 = getPwmFromFile(file2)

pwms <- list(pwm1, pwm2)
multiple_pwms_alignment = multipleLocalPwmsAlignment(pwms)
aligned_pwms = extendPwmsFromAlignmentVector(pwms, multiple_pwms_alignment$alignment$vector)
```

FULL_ALPHABET   *Complete character alphabet*

Description

the alphabet of all 26 characters

Usage

```
FULL_ALPHABET
```

Format

An object of class `Alphabet` of length 4.

Author(s)

Hendrik Treutler

Examples

```
FULL_ALPHABET
```

---

getAlphabetFromCharacters

returns the alphabet which fits to the given characters

Description

returns the alphabet which fits to the given characters

Usage

```
getAlphabetFromCharacters(characters)
```

Arguments

characters   a character vector of characters

Value

an alphabet of type Alphabet

Examples

```
alphabet = getAlphabetFromSequences(c("A","A","C","C","G","G","T","T"))
```

---

getAlphabetFromSequences

returns the alphabet which fits to the given sequences

Description

returns the alphabet which fits to the given sequences

Usage

```
getAlphabetFromSequences(sequences)
```

Arguments

sequences   a character vector of sequences

Value

an alphabet of type Alphabet

Examples

```
alphabet = getAlphabetFromSequences("AACCGGTT")
```

---

getPwmFromAlignment   *Create PWM from alignment*

Description

Creates a matrix-representation of a PWM from a set of sequences

Usage

```
getPwmFromAlignment(alignment, alphabet = NULL, pseudoCount = 0)
```

Arguments

alignment   a vector or list of sequences each with equal length

alphabet   of type Alphabet

pseudoCount   the number of pseudo-observations for each character in the alphabet

Value

PWM as matrix

Author(s)

Hendrik Treutler

Examples

```
motif_folder= "extdata/alignments"
motif_name = "calamodulin_1"
fileName = paste(motif_folder,"/",motif_name,".txt",sep="")
file = system.file(fileName, package = "DiffLogo")
motif = getPwmFromAlignment(readLines(file), ASN, 1)
seqLogo(pwm = motif, alphabet=ASN)
```

---

getPwmFromAlignmentFile
generates a pwm from an alignment file

Description

generates a pwm from an alignment file

Usage

```
getPwmFromAlignmentFile(filename, alphabet = NULL)
```

Arguments

filename	the alignment file
alphabet	the desired alphabet of type Alphabet

Value

a pwm

Examples

```
fileName = "extdata/alignments/calamodulin_1.txt"
file = system.file(fileName, package = "DiffLogo")
pwm = getPwmFromAlignmentFile(file)
```

---

getPwmFromFastaFile   *generates a pwm from a FASTA file*

Description

generates a pwm from a FASTA file

Usage

```
getPwmFromFastaFile(filename, alphabet = NULL)
```

Arguments

filename	the FASTA file
alphabet	the desired alphabet of type Alphabet

Value

a pwm

Examples

```
fileName = "extdata/alignments/F-box_bacteria.seq.fa"
file = system.file(fileName, package = "DiffLogo")
pwm = getPwmFromFastaFile(file)
```

---

getPwmFromFile *generates a pwm from a file of different formats*

Description

Generates a pwm from a file of different formats. Supported formats are FASTA files (.fa, .fasta), alignment files (.txt, .text, .al, .alignment), PWM files (.pwm), JASPAR / Position Frequency Matrix files (.pfm), and homer files (.motif).

Usage

```
getPwmFromFile(filename)
```

Arguments

filename   the file

Value

a pwm

Examples

```
fileName = "extdata/pwm/H1-hESC.pwm"
file = system.file(fileName, package = "DiffLogo")
pwm = getPwmFromFile(file)
```

---

getPwmFromHomerFile *generates a pwm from a homer file*

Description

generates a pwm from a homer file

Usage

```
getPwmFromHomerFile(filename)
```

Arguments

filename   the homer file

Value

a pwm

Examples

```
fileName = "extdata/homer/CTCF_Zf_CD4.motif"
file = system.file(fileName, package = "DiffLogo")
pwm = getPwmFromHomerFile(file)
```

getPwmFromPfmOrJasparFile

generates a pwm from a jaspar file

Description

generates a pwm from a jaspar file

Usage

```
getPwmFromPfmOrJasparFile(filename)
```

Arguments

filename   the jaspar file

Value

a pwm

Examples

```
fileName = "extdata/pfm/ctcf_jaspar.pfm"
file = system.file(fileName, package = "DiffLogo")
pwm = getPwmFromPfmOrJasparFile(file)
```

getPwmFromPwmFile   *generates a pwm from a pwm file*

Description

generates a pwm from a pwm file

Usage

```
getPwmFromPwmFile(filename)
```

Arguments

filename   the pwm file

Value

a pwm

Examples

```
fileName = "extdata/pwm/H1-hESC.pwm"
file = system.file(fileName, package = "DiffLogo")
pwm = getPwmFromPwmFile(file)
```

---

getSequencesFromAlignmentFile

extracts the sequences from an alignment file

Description

extracts the sequences from an alignment file

Usage

```
getSequencesFromAlignmentFile(filename)
```

Arguments

filename   the alignment file

Value

a vector of sequences

Examples

```
fileName = "extdata/alignments/calamodulin_1.txt"
file = system.file(fileName, package = "DiffLogo")
sequences = getSequencesFromAlignmentFile(file)
```

---

getSequencesFromFastaFile

extracts the sequences from a FASTA file

Description

extracts the sequences from a FASTA file

Usage

```
getSequencesFromFastaFile(filename)
```

Arguments

filename   the FASTA file

Value

a vector of sequences

Examples

```
fileName = "extdata/alignments/F-box_bacteria.seq.fa"
file = system.file(fileName, package = "DiffLogo")
sequences = getSequencesFromFastaFile(file)
```

---

informationContent *information content*

Description

the information content for the given probability vector

Usage

```
informationContent(p)
```

Arguments

p   probability vector representing the symbol distribution

Value

an object consisting of height a ylab

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_name = "HepG2"
fileName = paste(motif_folder,"/",motif_name,".pwm",sep="")
file = system.file(fileName, package = "DiffLogo")
motif = getPwmFromPwmFile(file)
seqLogo(pwm = motif, stackHeight = informationContent)
```

---

localPwmAlignment   *Align pwms*

Description

Finds best local alignment for two PWMs.

Usage

```
localPwmAlignment(pwm_left, pwm_right, divergence = shannonDivergence,
  unaligned_penalty = divergencePenaltyForUnaligned,
  try_reverse_complement = TRUE, base_distribution = NULL,
  length_normalization = FALSE)
```

Arguments

pwm_left   first PWM, a matrix of type matrix

pwm_right   first PWM, a matrix of type matrix

divergence   is a measure of difference between two pwm columns. Smaller is more simi-
                  lar. If you want to use non-uniform background distribution, provide your own
                  function.

unaligned_penalty
                  distance for unaligned columns at edges of matrixes. See divergencePenalty-
                  ForUnaligned as an example for providing your own function

try_reverse_complement
                  If false the alignment will not be performed on reverse complements. If true, the
                  input pwms should have column order of ACTG/ACGU.

base_distribution
                  is a vector of length nrow(pwm) that is added to unaligned columns of pwms for
                  comparing. If NULL, uniform distribution is used

length_normalization
                  If true, will minimize the average divergence between PWMs. Otherwise will
                  minimize the sum of divergences between positions. In both cases unalignes
                  positions are compared to base_distribution and are counted when computing
                  the alignment length.

Value

list of length two containing the alignment and the divergence

Author(s)

Lando Andrey

lossOfAbsICDifferences

the change of information content

Description

the change of information content for the given probability vectors

Usage

```
lossOfAbsICDifferences(p1, p2)
```

Arguments

p1	probability vector representing the first symbol distribution
p2	probability vector representing the second symbol distribution

Value

an object consisting of height and ylab

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoFromPwm(pwm1 = pwm1, pwm2 = pwm2, stackHeight = lossOfAbsICDifferences)
```

multipleLocalPwmsAlignment

Multiple PWMs alignment

Description

Creates a multiple alignment of pwms

Usage

```
multipleLocalPwmsAlignment(pwms, divergence = shannonDivergence,
  unaligned_penalty = divergencePenaltyForUnaligned,
  try_reverse_complement = TRUE, base_distribution = NULL,
  length_normalization = FALSE)
```

Arguments

pwms   list of pwms

divergence   Divergence measure.

unaligned_penalty
                  is a function for localPwmAlignment.

try_reverse_complement
                  if True, alignment will try reverse complement pwms

base_distribution
                  is a vector of length nrow(pwm) that is added to unaligned columns of pwms for comparing. If NULL, uniform distribution is used

length_normalization
                  If true, will minimize the average divergence between PWMs. Otherwise will minimize the sum of divergences between positions. In both cases unalignes positions are compared to base_distribution and are counted when computing the alignment length.

Value

list

Author(s)

Lando Andrey

Examples

```
file1 = system.file("extdata/homer/Max.motif",   package = "DiffLogo")
file2 = system.file("extdata/homer/c-Myc.motif", package = "DiffLogo")
pwm1 = getPwmFromFile(file1)
pwm2 = getPwmFromFile(file2)

multiple_pwms_alignment = multipleLocalPwmsAlignment(list(pwm1, pwm2))
```

---

normalizedDifferenceOfProbabilities
normalized probability differences

Description

probability differences normalized by the sum of absolute probability differences for the given pair of probability vectors

Usage

```
normalizedDifferenceOfProbabilities(p1, p2)
```

Arguments

p1   probability vector representing the first symbol distribution

p2   probability vector representing the second symbol distribution

Value

a vector with one result for each symbol

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoFromPwm(pwm1 = pwm1, pwm2 = pwm2, baseDistribution = normalizedDifferenceOfProbabilities)
```

---

normalizePWM   *normalizes the given pwm*

Description

normalizes the given pwm to column-sums of 1.0

Usage

```
normalizePWM(pwm)
```

Arguments

pwm   a pwm

Value

a normalized pwm

Examples

```
pwm = matrix(1:40, nrow = 4, dimnames = list(c("A","C","G","T"), 1:10))
pwm = normalizePWM(pwm)
```

---

prepareDiffLogoTable   *Prepare a table of difflogo objects*

Description

Prepares a DiffLogoTable and generates an object that contains the hirarchical clustering and a matrix of prepared difference logos.

Usage

```
prepareDiffLogoTable(PWMs, alphabet = DNA, configuration = list())
```

Arguments

PWMs	a list/vector of position weight matrices (PWMs) each of type pwm, data.frame, or matrix
alphabet	the alphabet of the given PWMs
configuration	list of (probably part of) of configuration options. See diffLogoTableConfiguration.

Value

matrix of difference logos

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}
sampleSizes <- c(100, 150, 200, 250)

diffLogoTableObj = prepareDiffLogoTable(motifs);
```

---

probabilities   *probabilities*

Description

the given probabilities

Usage

```
probabilities(p)
```

Arguments

p   probability vector representing the symbol distribution

Value

the given vector

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_name = "HepG2"
fileName = paste(motif_folder,"/",motif_name,".pwm",sep="")
file = system.file(fileName, package = "DiffLogo")
motif = getPwmFromPwmFile(file)
seqLogo(pwm = motif, baseDistribution = probabilities)
```

---

pwmDivergence   *PWM divergence*

Description

Counts PWM divergence as sum of divergencies of their columns.

Usage

```
pwmDivergence(pwm_left, pwm_right, divergence = shannonDivergence)
```

Arguments

pwm_left   is a PWM representation in type of matrix

pwm_right   is a PWM representation in type of matrix. The result is symmetric on pwm_left
                    and pwm_right

divergence   is a Divergence function on columns.

Value

float - sum of divergences

---

pwmsDistanceMatrix   *Multiple PWMs alignment*

Description

Creates a distance matrix for pwms

Usage

```
pwmsDistanceMatrix(pwms, diagonal_value = 0,
  bottom_default_value = NULL, divergence = shannonDivergence,
  unaligned_penalty = divergencePenaltyForUnaligned,
  try_reverse_complement = TRUE, base_distribution = NULL,
  length_normalization = FALSE)
```

Arguments

pwms   list of pwms

diagonal_value   value to put on diagonal.

bottom_default_value

                        value to put on bottom triangle. Set to NULL to get symmetric distance matrix.

divergence   divergence measure.

unaligned_penalty

                        is a function for localPwmAlignment.

try_reverse_complement

                        if True, alignment will try reverse complement pwms

base_distribution

                        is a vector of length nrow(pwm) that is added to unaligned columns of pwms for
                        comparing. If NULL, uniform distribution is used

length_normalization

                        is a vector of length nrow(pwm) that is added to unaligned columns of pwms for
                        comparing. If NULL, uniform distribution is used

Value

list

Author(s)

Lando Andrey

reverseAlignmentVector

Reverse for alignment vector

Description

Returns alignment vector as if all pwm were reverted.

Usage

```
reverseAlignmentVector(alignment_vector, pwms)
```

Arguments

alignment_vector
 list of list which $shift and $orientation

pwms list of matrixes.

Value

list - reversed alignment vector

Author(s)

Lando Andrey

RNA *RNA alphabet*

Description

the RNA alphabet, i.e. A, C, G, U

Usage

```
RNA
```

Format

An object of class `Alphabet` of length 4.

Author(s)

Martin Nettling

Examples

```
RNA
```

---

seqLogo   *Draw sequence logo*

Description

Draws the classic sequence logo.

Usage

```
seqLogo(pwm, sparse = FALSE, drawLines = 0.5,
  stackHeight = informationContent, baseDistribution = probabilities,
  alphabet = DNA, main = NULL)
```

Arguments

pwm	representation of a position weight matrix (PWM) of type pwm, data.frame, or matrix
sparse	if TRUE margins are reduced and tickmarks are removed from the logo
drawLines	distance between background lines
stackHeight	function for the height of a stack at position i
baseDistribution	
	function for the heights of the individual bases
alphabet	of type Alphabet
main	the main title for the plot

Value

none (draws sequence logo)

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_name = "HepG2"
fileName = paste(motif_folder,"/",motif_name,".pwm",sep="")
file = system.file(fileName, package = "DiffLogo")
motif = getPwmFromPwmFile(file)
seqLogo(pwm = motif)
```

---

shannonDivergence   *shannon divergence*

Description

the shannon divergence for the given pair of probability vectors

Usage

```
shannonDivergence(p1, p2)
```

Arguments

p1	probability vector representing the first symbol distribution
p2	probability vector representing the second symbol distribution

Value

an object consisting of height and ylab

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoFromPwm(pwm1 = pwm1, pwm2 = pwm2, stackHeight = shannonDivergence)
```

---

sumOfAbsICDifferences   *sum of absolute information content differences*

Description

the sum of absolute information content differences for the given pair of probability vectors

Usage

```
sumOfAbsICDifferences(p1, p2)
```

Arguments

p1	probability vector representing the first symbol distribution
p2	probability vector representing the second symbol distribution

Value

an object consisting of height and ylab

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoFromPwm(pwm1 = pwm1, pwm2 = pwm2, stackHeight = sumOfAbsICDifferences)
```

---

sumOfAbsProbabilityDifferences
                          sum of absolute probability differences

---

Description

the sum of absolute probability differences for the given pair of probability vectors

Usage

```
sumOfAbsProbabilityDifferences(p1, p2)
```

Arguments

p1	probability vector representing the first symbol distribution
p2	probability vector representing the second symbol distribution

Value

an object consisting of height and ylab

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_names = c("HepG2","MCF7","HUVEC","ProgFib")
motifs = list()
for (name in motif_names) {
  fileName = paste(motif_folder,"/",name,".pwm",sep="")
  file = system.file(fileName, package = "DiffLogo")
  motifs[[name]] = getPwmFromPwmFile(file)
}

pwm1 = motifs[[motif_names[[1]]]]
pwm2 = motifs[[motif_names[[2]]]]

diffLogoFromPwm(pwm1 = pwm1, pwm2 = pwm2, stackHeight = sumOfAbsProbabilityDifferences)
```

---

sumProbabilities	*sum of probabilities, i.e. 1.0*

Description

the sum of probabilities for the given probability vector, i.e. 1.0

Usage

```
sumProbabilities(p)
```

Arguments

p   probability vector representing the symbol distribution

Value

an object consisting of height and ylab

Author(s)

Martin Nettling

Examples

```
motif_folder= "extdata/pwm"
motif_name = "HepG2"
fileName = paste(motif_folder,"/",motif_name,".pwm",sep="")
file = system.file(fileName, package = "DiffLogo")
motif = getPwmFromPwmFile(file)
seqLogo(pwm = motif, stackHeight = sumProbabilities)
```

---

switchDirection   *Switches between 'forward' and 'reverse'*

Description

Switches between 'forward' and 'reverse'

Usage

```
switchDirection(direction)
```

Arguments

direction   either 'forward' or 'reverse'

Value

either 'reverse' or 'forward'

---

twoSetsAveragePwmDivergenceFromAlignmentVector
Average divergence between two sets.

Description

Computes average pwm divergence from alignment vector for two datasets. This equals to average divergence between all pairs where one pwm comes from left set, and other comes from right

Usage

```
twoSetsAveragePwmDivergenceFromAlignmentVector(left_pwms_list,
  left_pwms_alignment, right_pwms_list, right_pwms_alignment,
  divergence = shannonDivergence)
```

Arguments

left_pwms_list is a list of matrixes
left_pwms_alignment
                is a list of shifts ($shift) and orientations ($direction)
right_pwms_list
                is a list of matrixes
right_pwms_alignment
                is a list of shifts ($shift) and orientations ($direction)
divergence   divergence measure.

Value

float

Author(s)

Lando Andrey

Index