

# Package ‘DiffLogo’

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**Type** Package

**Title** DiffLogo: A comparative visualisation of biooligomer motifs

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```

**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

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---

|              |                                |
|--------------|--------------------------------|
| alignPwmSets | <i>Multiple PWMs alignment</i> |
|--------------|--------------------------------|

---

**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 concatenation of left\_pwms\_set and right\_pwms\_set

**Author(s)**

Lando Andrey

---

|          |                       |
|----------|-----------------------|
| Alphabet | <i>built alphabet</i> |
|----------|-----------------------|

---

**Description**

builds 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 | <i>p-value that two PWM-positions are from the same distribution</i> |
|-----------------|----------------------------------------------------------------------|

---

**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 align 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 unaligned 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 | <i>normalized information content differences</i> |
|-----------------|---------------------------------------------------|

---

**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 | <i>Draw DiffLogo</i> |
|----------|----------------------|

---

## 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 | <i>Draw DiffLogo from PWM</i> |
|-----------------|-------------------------------|

---

**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 unaligned 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_pwm = FALSE, multiple_align_pwm = 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 reserved for labels                                                                                       |
| ratio                  | the ratio of the plot; this is needed to determine the margin sizes correctly                                       |
| align_pwm              | if True, will align and extend pwms in each cell of diffLogoTable independently.                                    |
| multiple_align_pwm     | 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 | <i>DNA alphabet</i> |
|-----|---------------------|

---

**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 | <i>Draws a table of DiffLogos</i> |
|-------------------|-----------------------------------|

---

**Description**

Draws a table of DiffLogos.

**Usage**

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

**Arguments**

|                  |                                                                        |
|------------------|------------------------------------------------------------------------|
| diffLogoTableObj | the diffLogoTable-Object created by function prepareDiffLogoTable(...) |
| ...              | optional parameters for function 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 | <i>Complete character alphabet</i> |
|---------------|------------------------------------|

---

**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 | <i>returns the alphabet which fits to the given characters</i> |
|---------------------------|----------------------------------------------------------------|

---

**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 | <i>generates a pwm from a file of different formats</i> |
|----------------|---------------------------------------------------------|

---

**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 | <i>generates a pwm from a homer file</i> |
|---------------------|------------------------------------------|

---

**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 | <i>information content</i> |
|--------------------|----------------------------|

---

**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 | <i>Align pwms</i> |
|-------------------|-------------------|

---

**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 similar. If you want to use non-uniform background distribution, provide your own function.                                                                                        |
| unaligned_penalty      | distance for unaligned columns at edges of matrixes. See divergencePenaltyForUnaligned 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 | <i>normalizes the given pwm</i> |
|--------------|---------------------------------|

---

**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 hierarchical 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);
```



**Value**

float - sum of divergences

---

|                    |                                |
|--------------------|--------------------------------|
| pwmsDistanceMatrix | <i>Multiple PWMs alignment</i> |
|--------------------|--------------------------------|

---

**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**

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

---

**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 | <i>sum of absolute information content differences</i> |
|-----------------------|--------------------------------------------------------|

---

**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 | <i>sum of probabilities, i.e. 1.0</i> |
|------------------|---------------------------------------|

---

**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 | <i>Switches between 'forward' and 'reverse'</i> |
|-----------------|-------------------------------------------------|

---

**Description**

Switches between 'forward' and 'reverse'

**Usage**

```
switchDirection(direction)
```

**Arguments**

direction      either 'forward' or 'reverse'

**Value**

either 'reverse' or 'forward'

---

|                                                |                                             |
|------------------------------------------------|---------------------------------------------|
| twoSetsAveragePwmDivergenceFromAlignmentVector | <i>Average divergence between two sets.</i> |
|------------------------------------------------|---------------------------------------------|

---

**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_pwm_list,
  left_pwm_alignment, right_pwm_list, right_pwm_alignment,
  divergence = shannonDivergence)
```

**Arguments**

left\_pwm\_list    is a list of matrixes  
left\_pwm\_alignment    is a list of shifts (\$shift) and orientations (\$direction)  
right\_pwm\_list    is a list of matrixes  
right\_pwm\_alignment    is a list of shifts (\$shift) and orientations (\$direction)  
divergence      divergence measure.

**Value**

float

**Author(s)**

Lando Andrey

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