

# Package ‘motifStack’

April 9, 2025

**Type** Package

**Version** 1.51.1

**Title** Plot stacked logos for single or multiple DNA, RNA and amino acid sequence

**Author** Jianhong Ou, Michael Brodsky, Scot Wolfe and Lihua Julie Zhu

**Maintainer** Jianhong Ou <jou@morgridge.org>

**Depends** R (>= 2.15.1), methods, grid

**Imports** ade4, Biostrings, ggplot2, grDevices, graphics, htmlwidgets, stats, stats4, utils, XML, TFBSTools

**Suggests** Cairo, grImport, grImport2, BiocGenerics, MotifDb, RColorBrewer, BiocStyle, knitr, RUnit, rmarkdown, JASPAR2020

**biocViews** SequenceMatching, Visualization, Sequencing, Microarray, Alignment, ChIPchip, ChIPSeq, MotifAnnotation, DataImport

**Description** The motifStack package is designed for graphic representation of multiple motifs with different similarity scores. It works with both DNA/RNA sequence motif and amino acid sequence motif. In addition, it provides the flexibility for users to customize the graphic parameters such as the font type and symbol colors.

**License** GPL (>= 2)

**Lazyload** yes

**VignetteBuilder** knitr

**RoxygenNote** 7.3.1

**Encoding** UTF-8

**git\_url** <https://git.bioconductor.org/packages/motifStack>

**git\_branch** devel

**git\_last\_commit** a56a420

**git\_last\_commit\_date** 2025-01-03

**Repository** Bioconductor 3.21

**Date/Publication** 2025-04-08

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---

motifStack-package	<i>Plot stacked logos for single or multiple DNA, RNA and amino acid sequence</i>
--------------------	---

---

## Description

motifStack is a package that is able to draw amino acid sequence as easy as to draw DNA/RNA sequence. motifStack provides the flexibility for users to select the font type and symbol colors. motifStack is designed for graphical representation of multiple motifs.

## Author(s)

Jianhong Ou and Lihua Julie Zhu

Maintainer: Jianhong Ou <jianhong.ou@umassmed.edu>

---

AAmotifAlignment	<i>align AA motifs</i>
------------------	------------------------

---

## Description

align AA motifs for plotting motifs stack

## Usage

```
AAmotifAlignment(pcms, threshold = 0.4, minimalConsensus = 0)
```

## Arguments

pcms	a list of position frequency matrices, pfms must be a list of class pcm
threshold	information content cutoff threshold for useful postions
minimalConsensus	minimal length of consensus for alignment

## Value

a list of aligned motifs

**Examples**

```
pcms<-importMatrix(system.file("extdata", "prot.meme", package="motifStack"),
                   format="meme", to="pfm")
motifs<-AAMotifAlignment(pcms)
```

---

browseMotifs	<i>browse motifs</i>
--------------	----------------------

---

**Description**

browse motifs in a web browser

**Usage**

```
browseMotifs(
  pfms,
  phylog,
  layout = c("tree", "cluster", "radialPhylog"),
  nodeRadius = 2.5,
  baseWidth = 12,
  baseHeight = 30,
  xaxis = TRUE,
  yaxis = TRUE,
  width = NULL,
  height = NULL,
  ...
)
```

**Arguments**

pfms	a list of <a href="#">pfm</a>
phylog	layout type. see <a href="#">GraphvizLayouts</a>
layout	layout type. Could be tree, cluster or radialPhylog.
nodeRadius	node radius, default 2.5px.
baseWidth, baseHeight	width and height of each alphabet of the motif logo.
xaxis, yaxis	plot x-axis or y-axis or not in the motifs.
width	width of the figure
height	height of the figure
...	parameters not used

**Value**

An object of class `htmlwidget` that will intelligently print itself into HTML in a variety of contexts including the R console, within R Markdown documents, and within Shiny output bindings.

**Examples**

```

if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  motifs <- as.list(matrix.fly)
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-",
                        names(motifs), fixed=TRUE)]
  names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
                      gsub("_FBgn[0-9]+$", "",
                           gsub("[^a-zA-Z0-9]", "_",
                                   gsub("(_[0-9]+)$", "", names(motifs))))))
  motifs <- motifs[unique(names(motifs))]
  pfms <- sample(motifs, 10)
  pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
    new("pfm",mat=.ele, name=.name)})
  browseMotifs(pfms)
}

```

---

browseMotifs-shiny      *Shiny bindings for browseMotifs*

---

**Description**

Output and render functions for using browseMotifs within Shiny applications and interactive Rmd documents.

**Usage**

```
browseMotifsOutput(outputId, width = "100%", height = "400px")
```

```
renderbrowseMotifs(expr, env = parent.frame(), quoted = FALSE)
```

**Arguments**

outputId	output variable to read from
width, height	Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended.
expr	An expression that generates a browseMotifs
env	The environment in which to evaluate expr.
quoted	Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable.

---

calF *calculate frequency*

---

**Description**

calculate frequency

**Usage**

```
calF(count, P = rep(1/length(count), length(count)), pseudo = 1)
```

**Arguments**

count	position counts
P	background probability
pseudo	pseudocount

**Value**

numeric(1)

---

calI *calculate I'*

---

**Description**

calculate I'

**Usage**

```
calI(freq1, freq2, P)
```

**Arguments**

freq1	position frequency for matrix 1 position j
freq2	position frequency for matrix 2 position j
P	background of profile1

**Value**

numeric(1)

---

clusterMotifs	<i>cluster motifs</i>
---------------	-----------------------

---

**Description**

A help function to do matalign and motifHclust in one function.

**Usage**

```
clusterMotifs(motifs, ...)
```

**Arguments**

motifs	A list of pcms of pfms.
...	parameter to be passed to <a href="#">matalign</a> function.

**Value**

An object of hclust.

**Examples**

```
if(interactive() || Sys.getenv("USER")=="jianhongou"){  
  fp <- system.file("extdata", package="motifStack")  
  fs <- dir(fp, "pcm$")  
  pcms <- importMatrix(file.path(fp, fs), format="pcm")  
  hc <- clusterMotifs(pcms)  
}
```

---

colorset	<i>retrieve color setting for logo</i>
----------	--

---

**Description**

retrieve color setting for logo

**Usage**

```
colorset(alphabet = "DNA", colorScheme = "auto")
```

**Arguments**

alphabet	character, 'DNA', 'RNA' or 'AA'
colorScheme	'auto', 'charge', 'chemistry', 'classic' or 'hydrophobicity' for AA, 'auto', 'base-pairing', or 'blindnessSafe' for DNA ro RNA

**Value**

A character vector of color scheme

**Examples**

```
col <- colorset("AA", "hydrophobicity")
```

---

compare2profiles	<i>compare two profiles</i>
------------------	-----------------------------

---

**Description**

compare two pcm object

**Usage**

```
compare2profiles(  
  pcm1,  
  pcm2,  
  method = c("Smith-Waterman", "Needleman-Wunsch"),  
  pseudo = 1  
)
```

**Arguments**

pcm1, pcm2	object of pcm
method	Alignment method. "Smith-Waterman" or "Needleman-Wunsch". Default is "Smith-Waterma"
pseudo	pseudocount

**Value**

a list with names: motif1, motif2, alignmentScore, startPos1, startPos2, endPos1, endPos2, alignmentLength.



---

compareProfiles	<i>comapre w pcm</i>
-----------------	----------------------

---

**Description**

compare two pcm objects

**Usage**

```
compareProfiles(  
  pcm1,  
  pcm2,  
  method = c("Smith-Waterman", "Needleman-Wunsch"),  
  pseudo = 1,  
  revcomp = TRUE  
)
```

**Arguments**

pcm1, pcm2	object of pcm
method	Alignment method. "Smith-Waterman" or "Needleman-Wunsch". Default is "Smith-Waterma"
pseudo	pseudocount
revcomp	Check reverseComplement or not.

**Value**

a list with names: motif1, motif2, alignmentScore, startPos1, startPos2, endPos1, endPos2, alignmentLength.

---

DNAmotifAlignment	<i>align DNA motifs</i>
-------------------	-------------------------

---

**Description**

align DNA motifs for plotting motifs stack

**Usage**

```
DNAmotifAlignment(  
  pfms,  
  threshold = 0.4,  
  minimalConsensus = 0,  
  rcpostfix = "(RC)",  
  revcomp = rep(TRUE, length(pfms))  
)
```

**Arguments**

pfms	a list of position frequency matrices, pfms must be a list of class pfm or psam
threshold	information content cutoff threshold for useful postions
minimalConsensus	minimal length of consensus for alignment
rcpostfix	the postfix for reverse complements
revcomp	a logical vector to indicates whether the reverse complemet should be involved into alignment

**Value**

a list of aligned motifs

**Examples**

```
pcms<-readPCM(file.path(find.package("motifStack"), "extdata"),"pcm$")
motifs<-lapply(pcms,pcm2pfm)
motifs<-DNAmotifAlignment(motifs)
```

---

DNAmotifToRNAmotif      *convert DNA motif into RNA motif*

---

**Description**

convert DNA motif into RNA motif

**Usage**

```
DNAmotifToRNAmotif(pfm)
```

**Arguments**

pfm                    An object of "pcm" or "pfm"

**Value**

An object of "pcm" or "pfm" of RNA motif

**Examples**

```
motifs<-importMatrix(dir(file.path(find.package("motifStack"),
                               "extdata"),"pcm$", full.names = TRUE))
rnaMotifs <- DNAmotifToRNAmotif(motifs)
```

---

dpGlobal                      *Global alignment version*

---

**Description**

Global alignment version

**Usage**

dpGlobal(score, m, n)

**Arguments**

score	ALLR scores, m x n matrix
m, n	matrix width

**Value**

score matrix

---

dpLocal                      *Dynamic programming function, local version*

---

**Description**

Dynamic programming function, local version

**Usage**

dpLocal(score, m, n)

**Arguments**

score	ALLR scores, m x n matrix
m, n	matrix width

**Value**

score matrix

---

GeomMotif

*GeomMotif object*

---

## Description

GeomMotif object is a ggproto object.

## Usage

GeomMotif

## Format

The format is: Classes 'GeomMotif', 'Geom', 'ggproto', 'gg' <ggproto object: Class GeomMotif, Geom, gg> aesthetics: function default\_aes: uneval draw\_group: function draw\_key: function draw\_layer: function draw\_panel: function extra\_params: na.rm handle\_na: function non\_missing\_aes: optional\_aes: parameters: function required\_aes: xmin ymin xmax ymax motif setup\_data: function use\_defaults: function super: <ggproto object: Class Geom, gg>

## See Also

geom\_motif

## Examples

```
pcm <- read.table(file.path(find.package("motifStack"),
                           "extdata", "bin_SOLEXA.pcm"))
pcm <- pcm[,3:ncol(pcm)]
rownames(pcm) <- c("A", "C", "G", "T")
motif <- new("pcm", mat=as.matrix(pcm), name="bin_SOLEXA")

df <- data.frame(xmin=c(.25, .25), ymin=c(.25, .75), xmax=c(.75, .75), ymax=c(.5, 1))
df$motif <- list(pcm2pfm(motif), pcm2pfm(motif))

library(ggplot2)

ggplot(df, aes(xmin=xmin, ymin=ymin, xmax=xmax, ymax=ymax, motif=motif)) +
  geom_motif() + theme_bw() + ylim(0, 1) + xlim(0, 1)
```

---

 geom\_motif

*geom\_motif*


---

## Description

geom\_motif uses the locations of the four corners (xmin, xmax, ymin and ymax) to plot motifs.

## Usage

```
geom_motif(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  ic.scale = TRUE,
  use.xy = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

## Arguments

mapping	Set of aesthetic mappings created by aes() or aes_(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	The data to be displayed in this layer.
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	Other arguments passed on to layer().
ic.scale	logical If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
use.xy	logical If TRUE, the required aesthetics will be x, y, width, height, and motif. Otherwise, xmin, ymin, xmax, ymax and motif.
show.legend	Not used.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them.

## Value

a layer that contains GeomMotif object.

## Aesthetics

geom\_motif() understands the following aesthetics (required aesthetics are in bold):

- xmin
- xmax
- ymin
- ymax
- motif
- angle
- fontfamily
- fontface

OR

- x
- y
- width
- height
- motif
- angle
- fontfamily
- fontface

## Author(s)

Jianhong Ou

## Examples

```
pcm <- read.table(file.path(find.package("motifStack"),
                           "extdata", "bin_SOLEXA.pcm"))
pcm <- pcm[,3:ncol(pcm)]
rownames(pcm) <- c("A", "C", "G", "T")
motif <- new("pcm", mat=as.matrix(pcm), name="bin_SOLEXA")

df <- data.frame(xmin=c(.25, .25), ymin=c(.25, .75), xmax=c(.75, .75), ymax=c(.5, 1))
df$motif <- list(pcm2pfm(motif), pcm2pfm(motif))

library(ggplot2)
ggplot(df, aes(xmin=xmin, ymin=ymin, xmax=xmax, ymax=ymax, motif=motif)) +
  geom_motif() + theme_bw() + ylim(0, 1) + xlim(0, 1)
```

---

getALLRscoreFromCounts  
*calculate ALLR from counts*

---

**Description**

calculate ALLR from counts

**Usage**

getALLRscoreFromCounts(count1, count2, P1, P2, pseudo)

**Arguments**

count1, count2    count in position j for matrix 1 or 2  
P1, P2            background for matrix 1 or 2  
pseudo            pseudocount

**Value**

numeric(1) of ALLR

---

getDistance            *Calculate distances between two profiles*

---

**Description**

Calculate distances between two profiles

**Usage**

getDistance(hsp, count1, count2, P1, P2, pseudo)

**Arguments**

hsp                output of traceBack function  
count1, count2    motif profile 1 or 2  
P1, P2            background of profile 1 or 2  
pseudo            pseudocount

**Value**

full distance and aligned distance.

---

getRankedUniqueMotifs *get the unique motif in each category grouped by distance*

---

### Description

to get the unique motif in a given category, eg by species.

### Usage

```
getRankedUniqueMotifs(phylog, attr)
```

### Arguments

phylog	an object of class phylog
attr	attribute used for category of motifs

### Value

return a list:

uni.rank	unique motif ranks
uni.length	length of unique motif grouped by distance
uni.list	unique motif names grouped by distance

### Author(s)

Jianhong Ou

### Examples

```
if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  matrix.human <- query(MotifDb, "Hsapiens")
  pfms <- c(as.list(matrix.fly), as.list(matrix.human))
  pfms <- pfms[sample(seq_along(pfms), 100)]
  hc <- clusterMotifs(pfms)
  library(ade4)
  phylog <- ade4::hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  attr <- gsub("^(.*)_*.*$", "\\1", leaves)
  getRankedUniqueMotifs(phylog, attr)
}
```



---

getScore	<i>Calculate pair_wise position score</i>
----------	---

---

**Description**

Calculate pair\_wise position score

**Usage**

```
getScore(pcm1, pcm2, pseudo = 1)
```

**Arguments**

pcm1, pcm2	object of pcm
pseudo	pseudocount

**Value**

A score matrix with nrow of ncol of pcm1 and ncol of ncol of pcm2.

---

highlightCol	<i>add alpha transparency value to a color</i>
--------------	--

---

**Description**

An alpha transparency value can be specified to a color, in order to get better color for background.

**Usage**

```
highlightCol(col, alpha = 0.5)
```

**Arguments**

col	vector of any of the three kinds of R color specifications, i.e., either a color name (as listed by <a href="#">colors()</a> ), a hexadecimal string of the form "#rrggbb" or "#rrggbbaa" (see <a href="#">rgb</a> ), or a positive integer i meaning <a href="#">palette()[i]</a> .
alpha	a value in [0, 1]

**Value**

a vector of colors in hexadecimal string of the form "#rrggbbaa".

**Author(s)**

Jianhong Ou

## Examples

```
highlightCol(1:5, 0.3)
highlightCol(c("red", "green", "blue"), 0.3)
```

---

importMatrix

*import motifs from local files*

---

## Description

Import the motifs into [pcm-class](#) or [pfm-class](#) from files exported from Transfac, CisBP, and JASPAR.

## Usage

```
importMatrix(
  filenames,
  format = c("auto", "pfm", "cm", "pcm", "meme", "transfac", "jaspar", "scpd", "cisbp",
    "psam", "xmatrix"),
  to = c("auto", "pcm", "pfm", "pssm", "psam")
)
```

## Arguments

filenames	filename, an <a href="#">XMatrixList</a> object, or an <a href="#">XMatrix</a> object to be imported.
format	file format
to	import to <a href="#">pcm-class</a> or <a href="#">pfm-class</a>

## Value

a list of object [pcm-class](#) or [pfm-class](#)

## Author(s)

Jianhong Ou

## Examples

```
path <- system.file("extdata", package = "motifStack")
importMatrix(dir(path, "*.pcm", full.names = TRUE))
```

---

marker-class	<i>Class marker</i>
--------------	---------------------

---

**Description**

An object of class "marker" represents a marker in a motif

**Usage**

```
## S4 method for signature 'marker'  
x$name
```

**Arguments**

x	A marker object
name	slot name of marker object

**Objects from the Class**

Objects can be created by calls of the form `new("marker", type, start, stop, label, gp)`.

**Examples**

```
new("marker", type="rect", start=c(2, 4), gp=gpar(lty=3))
```

---

malign	<i>Matrix Aligner</i>
--------	-----------------------

---

**Description**

Matrix Aligner is modified from Malign-v4a. Malign-v4a is a program to compare two positional specific matrices. The author of Malign-v4a is Ting Wang and Gary Stormo.

**Usage**

```
malign(  
  pcms,  
  method = c("Smith-Waterman", "Needleman-Wunsch"),  
  pseudo = 1,  
  revcomp = TRUE,  
  ...  
)
```

**Arguments**

pcms	A list of <a href="#">pcm</a>
method	Alignment method. "Smith-Waterman" or "Needleman-Wunsch". Default is "Smith-Waterma"
pseudo	pseudocount
revcomp	Check reverseComplement or not.
...	Not use.

**Value**

A data frame with alignment information. The column names are motif1, motif2, alignmentScore, startPos1, startPos2, endPos1, endPos2, alignmentLength.

**Examples**

```
if(interactive() || Sys.getenv("USER")=="jianhongou"){
  fp <- system.file("extdata", package="motifStack")
  fs <- dir(fp, "pcm$")
  pcms <- importMatrix(file.path(fp, fs), format="pcm")
  matalign(pcms)
}
```

---

mergeMotifs

*merge multiple motifs*


---

**Description**

merge multiple motifs by calculate mean of each position

**Usage**

```
mergeMotifs(..., bgNoise = NA)
```

**Arguments**

...	<a href="#">pcm</a> or <a href="#">pfm</a> objects
bgNoise	if it is not NA, test will using a background by Dirichlet(1)-distributed random frequencies with weight bg.noise. The value of bgNoise should be a number in the range of 0 to 1, eg. 0.05

**Value**

a [pfm](#) object

**Author(s)**

Jianhong Ou

**Examples**

```
pcms<-readPCM(file.path(find.package("motifStack"), "extdata"),"pcm$")
mergeMotifs(pcms)
```

---

motifCircos	<i>plot sequence logo stacks with a radial phylogenetic tree and multiple color rings</i>
-------------	---

---

**Description**

plot sequence logo stacks with a radial phylogenetic tree and multiple color rings. The difference from plotMotifStackWithRadialPhylog is that it has more color setting and one more group of pfms.

**Usage**

```
motifCircos(
  phylog,
  pfms = NULL,
  pfms2 = NULL,
  R = 2.5,
  r.tree = 1,
  col.tree.bg = NULL,
  col.tree.bg.alpha = 1,
  cnodes = 0,
  labels.nodes = names(phylog$nodes),
  clabel.nodes = 0,
  r.leaves = NA,
  cleaves = 1,
  labels.leaves = names(phylog$leaves),
  clabel.leaves = 1,
  col.leaves = rep("black", length(labels.leaves)),
  col.leaves.bg = NULL,
  col.leaves.bg.alpha = 1,
  r.pfms = NA,
  r.pfms2 = NA,
  r.rings = 0,
  col.rings = list(),
  col.inner.label.circle = NULL,
  inner.label.circle.width = 0.02,
  col.outer.label.circle = NULL,
  outer.label.circle.width = 0.02,
  draw.box = FALSE,
  clockwise = FALSE,
  init.angle = if (clockwise) 90 else 0,
  angle = 360,
  pfmNameSplitter = ";",
```

```

rcpostfix = "(RC)",
motifScale = c("linear", "logarithmic", "none"),
ic.scale = TRUE,
plotIndex = FALSE,
IndexCol = "black",
IndexCex = 0.8,
groupDistance = NA,
groupDistanceLineCol = "red",
plotAxis = FALSE
)

```

### Arguments

phylog	an object of class phylog
pfms	a list of objects of class pfm
pfms2	a list of objects of class pfm
R	radius of canvas
r.tree	half width of the tree
col.tree.bg	a vector of colors for tree background
col.tree.bg.alpha	alpha value [0, 1] of colors for tree background
cnodes	a character size for plotting the points that represent the nodes, used with par("cex")*cnodes. If zero, no points are drawn
labels.nodes	a vector of strings of characters for the nodes labels
clabel.nodes	a character size for the nodes labels, used with par("cex")*clabel.nodes. If zero, no nodes labels are drawn
r.leaves	width of the leaves
cleaves	a character size for plotting the points that represent the leaves, used with par("cex")*cleaves. If zero, no points are drawn
labels.leaves	a vector of strings of characters for the leaves labels
clabel.leaves	a character size for the leaves labels, used with par("cex")*clabel.leaves
col.leaves	a vector of colors for leaves labels
col.leaves.bg	a vector of colors for background of leaves labels
col.leaves.bg.alpha	alpha value [0, 1] for the colors of background of leaves labels
r.pfms	width of the pfms
r.pfms2	width of the pfms2
r.rings	a vector of width of color rings
col.rings	a list of color rings
col.inner.label.circle	a vector of colors for inner circle of pfms
inner.label.circle.width	width for inner circle of pfms

<code>col.outer.label.circle</code>	a vector of colors for outer circle of pfms
<code>outer.label.circle.width</code>	width for outer circle of pfms
<code>draw.box</code>	if TRUE draws a box around the current plot with the function <code>box()</code>
<code>clockwise</code>	a logical value indicating if slices are drawn clockwise or counter clockwise
<code>init.angle</code>	number specifying the starting angle (in degrees) for the slices. Defaults to 0 (i.e., '3 o'clock') unless <code>clockwise</code> is true where <code>init.angle</code> defaults to 90 (degrees), (i.e., '12 o'clock')
<code>angle</code>	number specifying the angle (in degrees) for phylogenetic tree. Defaults 360
<code>pfmNameSplitter</code>	splitter when name of pfms/pfms2 contain multiple node of labels.leaves
<code>rcpostfix</code>	the postfix for reverse complements
<code>motifScale</code>	the scale of logo size
<code>ic.scale</code>	logical. If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
<code>plotIndex</code>	logical. If TRUE, will plot index number in the motifLogo which can help user to describe the motifLogo
<code>IndexCol</code>	The color of the index number when <code>plotIndex</code> is TRUE.
<code>IndexCex</code>	The cex of the index number when <code>plotIndex</code> is TRUE.
<code>groupDistance</code>	show <code>groupDistance</code> on the draw
<code>groupDistanceLineCol</code>	<code>groupDistance</code> line color, default: red
<code>plotAxis</code>	logical. If TRUE, will plot distance axis.

**Value**

none

**Author(s)**

Jianhong Ou

**See Also**

[plotMotifStackWithRadialPhylog](#)

**Examples**

```
if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  motifs <- as.list(matrix.fly)
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-",
                        names(motifs), fixed=TRUE)]
  names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
                      gsub("_FBgn[0-9]+$", "",
```

```

        gsub("[^a-zA-Z0-9]", "_",
            gsub("(_[0-9]+)$", "", names(motifs))))
motifs <- motifs[unique(names(motifs))]
pfms <- sample(motifs, 50)
hc <- clusterMotifs(pfms)
library(ade4)
phylog <- ade4::hclust2phylog(hc)
leaves <- names(phylog$leaves)
pfms <- pfms[leaves]
pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
    new("pfm",mat=.ele, name=.name)})
pfms <- DNAmotifAlignment(pfms, minimalConsensus=3)
library(RColorBrewer)
color <- brewer.pal(12, "Set3")
motifCircos(phylog, pfms, cleaves = 0.5, clabel.leaves = 0.7,
            col.tree.bg=rep(color, each=5),
            col.leaves=rep(color, each=5),
            r.rings=c(0.02, 0.03, 0.04),
            col.rings=list(sample(colors(), 50),
                            sample(colors(), 50),
                            sample(colors(), 50)))
}

```

---

motifCloud

*plot a DNA sequence logo cloud*


---

## Description

Plot a DNA sequence logo cloud

## Usage

```

motifCloud(
  motifSig,
  rcpostfix = "(RC)",
  layout = c("rectangles", "cloud", "tree"),
  scale = c(6, 0.5),
  rot.per = 0.1,
  draw.box = TRUE,
  draw.freq = TRUE,
  box.col = "gray",
  freq.col = "gray",
  group.col = NULL,
  groups = NULL,
  draw.legend = FALSE,
  font = "sans",
  ic.scale = TRUE
)

```



**Arguments**

motifSig	an object of class <a href="#">motifSig</a>
rcpostfix	postfix for reverse-complement motif names, default: (RC)
layout	layout of the logo cloud, rectangles, cloud or tree
scale	A vector of length 2 indicating the range of the size of the sequence logo.
rot.per	proportion sequence logo with 90 degree rotation. Only work for "cloud" layout
draw.box	draw box for each sequence logo or not
draw.freq	label frequency of each signature or not
box.col	color of box for each sequence logo
freq.col	color of frequency label
group.col	color setting for groups
groups	a named vectors of motif groups
draw.legend	draw group color legend or not
font	font of logo
ic.scale	logical If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.

**Value**

none

**Examples**

```

if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  motifs <- as.list(matrix.fly)
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-",
                        names(motifs), fixed=TRUE)]
  names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
                      gsub("_FBgn[0-9]+$", "",
                           gsub("[^a-zA-Z0-9]", "_",
                                   gsub("(_[0-9]+)$", "", names(motifs))))))
  motifs <- motifs[unique(names(motifs))]
  pfms <- sample(motifs, 50)
  hc <- clusterMotifs(pfms)
  library(ade4)
  phylog <- ade4::hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
    new("pfm",mat=.ele, name=.name)})
  motifSig <- motifSignature(pfms, phylog, cutoffPval=0.0001)
  motifCloud(motifSig)
}

```

---

 motifGrob
 

---

*Motif Grob***Description**

This function create a motif grob.

**Usage**

```
motifGrob(
  pfm,
  x = unit(0.5, "npc"),
  y = unit(0.5, "npc"),
  width = unit(1, "npc"),
  height = unit(1, "npc"),
  angle = 0,
  ic.scale = TRUE,
  default.units = "native",
  name = NULL,
  gp = gpar(fontfamily = "sans", fontface = "bold")
)
```

**Arguments**

pfm	an object of pfm
x	A numeric vector or unit object specifying x-values.
y	A numeric vector or unit object specifying y-values.
width	A numeric vector or unit object specifying width.
height	A numeric vector or unit object specifying height.
angle	A numeric value indicating the angle of rotation of the motif. Positive values indicate the amount of rotation, in degrees, anticlockwise from the positive x-axis.
ic.scale	logical If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
default.units	A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
name	A character value to uniquely identify the motifGrob once it has been pushed onto the grob tree.
gp	A gpar object, typically the output from a call to the function gpar. The list will be used as parameter of plotMotifLogoA.

**Value**

An gTree object.

**Author(s)**

Jianhong Ou

**Examples**

```
pcm<-matrix(runif(40,0,100),nrow=4,ncol=10)
pfm<-pcm2pfm(pcm)
rownames(pfm)<-c("A","C","G","T")
motif <- new("pfm", mat=pfm, name="bin_SOLEXA")
motifGrob(motif)
```

---

motifHclust

*Hierarchical Clustering motifs*

---

**Description**

functions to perform clustering of output of matalign

**Usage**

```
motifHclust(align, ...)
```

**Arguments**

`align` output of matalign, used to generate distance matrix.  
`...` parameter to pass to the [hclust](#).

**Value**

An object of `hclust`.

**Examples**

```
if(interactive() || Sys.getenv("USER")=="jianhongou"){
  fp <- system.file("extdata", package="motifStack")
  fs <- dir(fp, "pcm$")
  pcms <- importMatrix(file.path(fp, fs), format="pcm")
  align <- matalign(pcms)
  hc <- motifHclust(align, method="average")
}
```

---

motifPiles	<i>plot sequence logo stacks with a linear phylogenetic tree and multiple color sets</i>
------------	--

---

### Description

plot sequence logo stacks with a linear phylogenetic tree and multiple color sets.

### Usage

```
motifPiles(
  phylog,
  pfms = NULL,
  pfms2 = NULL,
  r.tree = 0.45,
  col.tree = NULL,
  cnodes = 0,
  labels.nodes = names(phylog$nodes),
  clabel.nodes = 0,
  cleaves = 0.2,
  labels.leaves = names(phylog$leaves),
  clabel.leaves = 1,
  col.leaves = rep("black", length(labels.leaves)),
  col.leaves.bg = NULL,
  col.leaves.bg.alpha = 1,
  r.pfms = NA,
  r.pfms2 = NA,
  motifScale = c("logarithmic", "linear", "none"),
  col.pfms = NULL,
  col.pfms.width = 0.02,
  col.pfms2 = NULL,
  col.pfms2.width = 0.02,
  r.anno = 0,
  col.anno = list(),
  pfmNameSplitter = ";",
  rcpostfix = "(RC)",
  ic.scale = TRUE,
  plotIndex = FALSE,
  IndexCol = "black",
  IndexCex = 0.8,
  groupDistance = NA,
  groupDistanceLineCol = "red"
)
```

### Arguments

phylog            an object of class phylog

pfms	a list of objects of class pfm
pfms2	a list of objects of class pfm
r.tree	width of the tree
col.tree	a vector of colors for tree
cnodes	a character size for plotting the points that represent the nodes, used with <code>par("cex")*cnodes</code> . If zero, no points are drawn
labels.nodes	a vector of strings of characters for the nodes labels
clabel.nodes	a character size for the nodes labels, used with <code>par("cex")*clabel.nodes</code> . If zero, no nodes labels are drawn
cleaves	a character size for plotting the points that represent the leaves, used with <code>par("cex")*cleaves</code> . If zero, no points are drawn
labels.leaves	a vector of strings of characters for the leaves labels
clabel.leaves	a character size for the leaves labels, used with <code>par("cex")*clabel.leaves</code>
col.leaves	a vector of colors for leaves labels
col.leaves.bg	a vector of colors for background of leaves labels
col.leaves.bg.alpha	alpha value [0, 1] for the colors of background of leaves labels
r.pfms	width of the pfms
r.pfms2	width of the pfms2
motifScale	the scale of logo size
col.pfms	a vector of colors for inner pile of pfms
col.pfms.width	width for inner pile of pfms
col.pfms2	a vector of colors for outer pile of pfms
col.pfms2.width	width for outer pile of pfms
r.anno	a vector of width of color sets
col.anno	a list of color sets
pfmNameSplitter	splitter when name of pfms/pfms2 contain multiple node of labels.leaves
rpostfix	the postfix for reverse complements
ic.scale	logical. If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
plotIndex	logical. If TRUE, will plot index number in the motifLogo which can help user to describe the motifLogo
IndexCol	The color of the index number when plotIndex is TRUE.
IndexCex	The cex of the index number when plotIndex is TRUE.
groupDistance	show groupDistance on the draw
groupDistanceLineCol	groupDistance line color, default: red

**Value**

none

**Author(s)**

Jianhong Ou

**See Also**

[motifCircos](#)

**Examples**

```
if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  motifs <- as.list(matrix.fly)
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-",
                        names(motifs), fixed=TRUE)]
  names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
                      gsub("_FBgn[0-9]+$", "",
                          gsub("[^a-zA-Z0-9]", "_",
                              gsub("(_[0-9]+)$", "", names(motifs))))))
  motifs <- motifs[unique(names(motifs))]
  pfms <- sample(motifs, 50)
  hc <- clusterMotifs(pfms)
  library(ade4)
  phylog <- ade4::hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
    new("pfm",mat=.ele, name=.name)})
  pfms <- DNAmotifAlignment(pfms, minimalConsensus=3)
  library(RColorBrewer)
  color <- brewer.pal(12, "Set3")
  motifPiles(phylog, pfms, cleaves = 0.5, clabel.leaves = 0.7,
             col.leaves=rep(color, each=5),
             col.leaves.bg = sample(colors(), 50),
             col.tree=rep(color, each=5),
             r.anno=c(0.02, 0.03, 0.04),
             col.anno=list(sample(colors(), 50),
                           sample(colors(), 50),
                           sample(colors(), 50)))
}
```

---

motifSig-class	Class "motifSig"
----------------	------------------

---

### Description

An object of class "motifSig" represents the output of function [motifSignature](#) methods for motifSig objects.

### Usage

```
signatures(object)
```

```
frequence(object)
```

```
nodelist(object)
```

```
sigColor(object)
```

```
## S4 method for signature 'motifSig'  
x$name
```

### Arguments

object	An object of class motifSig.
x	A motifSig object
name	slot name of motifSig object

### Objects from the Class

Objects can be created by calls of the form `new("motifSig", signature, freq, nodelist, gpcol)`.

### Methods

**signatures** signature(object = "motifSig") return the signatures of motifSig

**frequence** signature(object = "motifSig") return the frequency of motifSig

**nodelist** signature(object = "motifSig") return the nodelist of motifSig

**sigColor** signature(object = "motifSig") return the group color sets of motifSig

**\$, \$<-** Get or set the slot of [motifSig](#)

motifSignature      *get signatures from motifs*

---

### Description

extract signatures from multiple motifs by distance calculated from STAMP

### Usage

```
motifSignature(  
  pfms,  
  phylog,  
  cutoffPval,  
  groupDistance,  
  rcpostfix = "(RC)",  
  min.freq = 2,  
  trim = 0.2,  
  families = list(),  
  sort = TRUE  
)
```

### Arguments

pfms	a list of objects of class pfm
phylog	an object of class phylog
cutoffPval	pvalue for motifs to merge.
groupDistance	maximal distance of motifs in the same group
rcpostfix	postfix for reverse-complement motif names, default: (RC)
min.freq	signatures with frequency below min.freq will not be plotted
trim	minimal information content for each position of signature
families	for each family, the motif number in one signature should only count as 1
sort	sort the signatures by frequency or not.

### Value

an Object of class [motifSig](#)

### Examples

```
if(interactive() || Sys.getenv("USER")=="jianhongou"){  
  library("MotifDb")  
  matrix.fly <- query(MotifDb, "Dmelanogaster")  
  motifs <- as.list(matrix.fly)  
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-",  
                        names(motifs), fixed=TRUE)]
```



```

names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
                    gsub("_FBgn[0-9]+$", "",
                          gsub("[^a-zA-Z0-9]", "_",
                                gsub("(_[0-9]+)$", "", names(motifs))))))
motifs <- motifs[unique(names(motifs))]
pfms <- sample(motifs, 50)
hc <- clusterMotifs(pfms)
library(ade4)
phylog <- ade4::hclust2phylog(hc)
leaves <- names(phylog$leaves)
pfms <- pfms[leaves]
pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
  new("pfm",mat=.ele, name=.name)})
motifSig <- motifSignature(pfms, phylog, cutoffPval=0.0001)
}

```

---

motifStack

*plot a DNA sequence logo stack*


---

### Description

Plot a DNA sequence logo stack

### Usage

```

motifStack(
  pfms,
  layout = c("stack", "treeview", "phylog", "radialPhylog"),
  reorder = TRUE,
  ...
)

```

### Arguments

pfms	a list of objects of class <a href="#">pfm</a>
layout	layout of the logo stack, stack, treeview or radialPhylog
reorder	logical(1). Default TRUE. Set to FALSE will do alignment but keep the order of the pfms. This parameter only work for stack layout.
...	any parameters could to pass to <a href="#">plotMotifLogoStack</a> , <a href="#">plotMotifLogoStackWithTree</a> , <a href="#">plotMotifStackWithPhylog</a> or <a href="#">plotMotifStackWithRadialPhylog</a> . And the ‘revcomp’ parameter for <a href="#">DNAmotifAlignment</a> .

### Value

return a list contains pfms and phylog

**Examples**

```

if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  motifs <- as.list(matrix.fly)
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-",
                        names(motifs), fixed=TRUE)]
  names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
                      gsub("_FBgn[0-9]+$", "",
                           gsub("[^a-zA-Z0-9]", "_",
                                 gsub("(_[0-9]+)$", "", names(motifs))))))
  motifs <- motifs[unique(names(motifs))]
  pfms <- sample(motifs, 50)
  pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
    new("pfm",mat=.ele, name=.name)})
  motifStack(pfms, "radialPhylog")

  ## AA motifs
  pcms<-importMatrix(system.file("extdata", "prot.meme",
                                package="motifStack"),
                    format="meme", to="pfm")
  motifStack(pcms[1:5])
  motifStack(pcms[1:5], reorder=FALSE)
}

```

ouNode-class

*Class* ouNode**Description**

An object of class "ouNode" represents a motif node in a cluster tree

**Usage**

```
## S4 method for signature 'ouNode'
x$name
```

**Arguments**

x	A ouNode object
name	slot name of ouNode object

**Objects from the Class**

Objects can be created by calls of the form `new("ouNode", left, right, parent, distl, distr, sizel, sizer)`.

**Examples**

```
new("ouNode", left="A", right="B", parent="Root", dist1=1, distr=2, size1=1, size2=1)
```

---

 pcm-class

 Class "pcm"
 

---

**Description**

An object of class "pcm" represents the position count matrix of a DNA/RNA/amino-acid sequence motif. The entry stores a matrix, which in row *i*, column *j* gives the counts of observing nucleotide/or amino acid *i* in position *j* of the motif.

methods for pcm objects.

**Usage**

```
## S4 method for signature 'pcm'
x$name

## S4 method for signature 'pcm,ANY'
plot(x, y = "missing", ...)

trimMotif(x, t)

matrixReverseComplement(x)

addBlank(x, n, b)

getIC(x, p)

pcm2pfm(x, background)

pcm2pssm(x, background)

## S4 method for signature 'pcm'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S4 method for signature 'pcm'
format(x, ...)
```

**Arguments**

<code>x</code>	An object of class pcm. For getIC, if parameter <code>p</code> is followed, <code>x</code> should be an object of matrix. For pcm2pfm, <code>x</code> also could be an object of matrix.
<code>name</code>	slot name of pcm object.
<code>y</code>	Not use.

... Further potential arguments passed to plotMotifLogo.  
 t numeric value of information content threshold for trimming.  
 n how many spaces should be added.  
 b logical value to indicate where the space should be added.  
 p p is the background frequency.  
 background a "numeric" vector. The background frequency.  
 row.names, optional  
     see as.data.frame

### Objects from the Class

Objects can be created by calls of the form `new("pcm", mat, name, alphabet, color, background)`.

### Methods

**addBlank** signature(x="pcm", n="numeric", b="logical") add space into the position count matrix for alignment. b is a bool value, if TRUE, add space to the 3' end, else add space to the 5' end. n indicates how many spaces should be added.  
**coerce** signature(from = "pcm", to = "matrix"): convert object pcm to matrix  
**getIC** signature(x = "pcm", ) Calculate information content profile for position frequency matrix.  
**matrixReverseComplement** signature(x = "pcm") get the reverse complement of position frequency matrix.  
**plot** signature(x = "pcm") Plots the sequence logo of the position count matrix.  
**trimMotif** signature(x = "pcm", t= "numeric") trim motif by information content.  
**\$, \$<-** Get or set the slot of `pcm-class`  
**as.data.frame** convert `pcm-class` to a data.frame  
**format** return the name\_pcm of `pcm-class`

### Examples

```
pcm <- read.table(file.path(find.package("motifStack"), "extdata", "bin_SOLEXA.pcm"))
pcm <- pcm[,3:ncol(pcm)]
rownames(pcm) <- c("A", "C", "G", "T")
motif <- new("pcm", mat=as.matrix(pcm), name="bin_SOLEXA")
plot(motif)
pcm2pfm(pcm)
pcm2pssm(pcm)

pcm <- read.table(file.path(find.package("motifStack"), "extdata", "bin_SOLEXA.pcm"))
pcm <- pcm[,3:ncol(pcm)]
rownames(pcm) <- c("A", "C", "G", "T")
motif <- new("pcm", mat=as.matrix(pcm), name="bin_SOLEXA")
getIC(motif)
matrixReverseComplement(motif)
as(motif, "matrix")
```

```

pcm2pfm(motif)
as.data.frame(motif)
format(motif)

```

---

pfm-class

*Class "pfm"*


---

## Description

An object of class "pfm" represents the position frequency matrix of a DNA/RNA/amino-acid sequence motif. The entry stores a matrix, which in row *i*, column *j* gives the frequency of observing nucleotide/or amino acid *i* in position *j* of the motif.

methods for pfm objects.

## Usage

```

## S4 method for signature 'pfm'
x$name

## S4 method for signature 'pfm,ANY'
plot(x, y = "missing", ...)

## S4 method for signature 'pfm,ANY'
getIC(x, p = "missing")

## S4 method for signature 'pfm,numeric'
trimMotif(x, t)

## S4 method for signature 'pfm'
matrixReverseComplement(x)

## S4 method for signature 'pfm,numeric,logical'
addBlank(x, n, b)

## S4 method for signature 'pfm'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S4 method for signature 'pfm'
format(x, ...)

```

## Arguments

<code>x</code>	An object of class pfm. For getIC, if parameter <i>p</i> is followed, <i>x</i> should be an object of matrix.
<code>name</code>	Slot name.
<code>y</code>	Not use.

... Further potential arguments passed to plotMotifLogo.  
 p p is the background frequency.  
 t numeric value of information content threshold for trimming.  
 n how many spaces should be added.  
 b logical value to indicate where the space should be added.  
 row.names, optional  
     see as.data.frame

### Objects from the Class

Objects can be created by calls of the form `new("pfm", mat, name, alphabet, color, background)`.

### Methods

**addBlank** signature(x="pfm",n="numeric", b="logical") add space into the position frequency matrix for alignment. b is a bool value, if TRUE, add space to the 3' end, else add space to the 5' end. n indicates how many spaces should be added.

**getIC** signature(x = "pfm",) Calculate information content profile for position frequency matrix.

**getIC** signature(x = "matrix", p = "numeric") Calculate information content profile for matrix. p is the background frequency

**matrixReverseComplement** signature(x = "pfm") get the reverse complement of position frequency matrix.

**plot** signature(x = "pfm") Plots the sequence logo of the position frequency matrix.

**trimMotif** signature(x = "pfm", t = "numeric") trim motif by information content.

**\$, \$<-** Get or set the slot of [pfm-class](#)

**as.data.frame** convert [pfm-class](#) to a data.frame

**format** return the name\_pfm of [pfm-class](#)

### Examples

```
pcm <- read.table(file.path(find.package("motifStack"), "extdata", "bin_SOLEXA.pcm"))
pcm <- pcm[,3:ncol(pcm)]
rownames(pcm) <- c("A", "C", "G", "T")
motif <- pcm2pfm(pcm)
motif <- new("pfm", mat=motif, name="bin_SOLEXA")
plot(motif)
```

```
pcm <- read.table(file.path(find.package("motifStack"), "extdata", "bin_SOLEXA.pcm"))
pcm <- pcm[,3:ncol(pcm)]
rownames(pcm) <- c("A", "C", "G", "T")
motif <- pcm2pfm(pcm)
motif <- new("pfm", mat=motif, name="bin_SOLEXA")
getIC(motif)
matrixReverseComplement(motif)
addBlank(motif, 1, FALSE)
```

```
addBlank(motif, 3, TRUE)
as(motif, "matrix")
as.data.frame(motif)
format(motif)
```

---

pfm2pwm

*convert pfm object to PWM*

---

### Description

convert pfm object to PWM

### Usage

```
pfm2pwm(x, N = 10000)
```

### Arguments

x                    an object of [pfm](#) or [pcm](#) or matrix  
N                    Total number of event counts used for pfm generation.

### Value

A numeric matrix representing the Position Weight Matrix for PWM.

### Author(s)

Jianhong Ou

### See Also

[PWM](#)

### Examples

```
library("MotifDb")
matrix.fly <- query(MotifDb, "Dmelanogaster")
pfm2pwm(matrix.fly[[1]])
```

---

plotAffinityLogo      *plot affinity logo*

---

**Description**

plot affinity logo

**Usage**

```
plotAffinityLogo(  
  psam,  
  motifName,  
  font = "sans",  
  fontface = "bold",  
  colset = c("#00811B", "#2000C7", "#FFB32C", "#D00001"),  
  alpha = 0.5,  
  newpage = TRUE,  
  draw = TRUE  
)
```

**Arguments**

psam	a position-specific affinity matrix
motifName	motif name
font	font of logo
fontface	fontface of logo
colset	color setting for each logo letter
alpha	Alpha channel for transparency of low affinity letters.
newpage	plot in a new canvas or not.
draw	Vector (logical(1)). TRUE to plot. FALSE, return a gList

**Value**

none

**References**

Barrett C. Foat, Alexandre V. Morozov, Harmen J. Bussemaker; Statistical mechanical modeling of genome-wide transcription factor occupancy data by MatrixREDUCE, *Bioinformatics*, Volume 22, Issue 14, 15 July 2006, Pages e141-e149, <https://doi.org/10.1093/bioinformatics/btl223>

**Examples**

```
psam <- importMatrix(file.path(find.package("motifStack"), "extdata", "PSAM.mxr"),  
  format="psam")[[1]]  
plotAffinityLogo(psam)
```



---

plotMotifLogo                    *plot sequence logo*

---

### Description

plot amino acid or DNA sequence logo

### Usage

```
plotMotifLogo(  
  pfm,  
  motifName,  
  p = rep(0.25, 4),  
  font = "sans",  
  fontface = "bold",  
  colset = c("#00811B", "#2000C7", "#FFB32C", "#D00001"),  
  xaxis = TRUE,  
  yaxis = TRUE,  
  xlab = "position",  
  ylab = "bits",  
  xlcex = 1.2,  
  ylcex = 1.2,  
  ncex = 1.2,  
  ic.scale = TRUE,  
  newpage = TRUE,  
  margins = c(4.1, 4.1, 2.1, 0.1),  
  draw = TRUE,  
  ...  
)
```

### Arguments

pfm	a position frequency matrices
motifName	motif name
p	background possibility
font	font of logo
fontface	fontface of logo
colset	color setting for each logo letter
xaxis	draw x-axis or not. If a vector of character or numeric is provided, the function will try to plot the x-axis by setting the labels as the vectors.
yaxis	draw y-axis or not
xlab	x-label, do nothing if set xlab as NA
ylab	y-label, do nothing if set ylab as NA
xlcex	cex value for x-label

ylcex	cex value for y-label
ncex	cex value for motif name
ic.scale	logical If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height. It will also can be set as FALSE followed by a numeric vectors. The format is c(FALSE, scale). If it is FALSE followed by a number (eg c(FALSE, 100)), the y axis labels will be re-scaled by 100.
newpage	logical If TRUE, plot it in a new page.
margins	A numeric vector interpreted in the same way as par(mar) in base graphics.
draw	Vector (logical(1)). TRUE to plot. FALSE, return a gList
...	Not used.

**Value**

none

**Examples**

```
pcm<-matrix(runif(40,0,100),nrow=4,ncol=10)
pfm<-pcm2pfm(pcm)
rownames(pfm)<-c("A","C","G","T")
plotMotifLogo(pfm)
```

---

plotMotifLogoA

*plot sequence logo without plot.new*

---

**Description**

plot amino acid or DNA sequence logo in a given canvas

**Usage**

```
plotMotifLogoA(
  pfm,
  font = "sans",
  fontface = "bold",
  ic.scale = TRUE,
  draw = TRUE
)
```

**Arguments**

pfm	an object of pfm
font	font of logo
fontface	fontface of logo
ic.scale	logical If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
draw	Vector (logical(1)). TRUE to plot. FALSE, return a gList

**Value**

none

**Examples**

```
pcm<-matrix(runif(40,0,100),nrow=4,ncol=10)
pfm<-pcm2pfm(pcm)
rownames(pfm)<-c("A","C","G","T")
motif <- new("pfm", mat=pfm, name="bin_SOLEXA")
plotMotifLogoA(motif)
```

---

plotMotifLogoStack     *plot sequence logos stack*

---

**Description**

plot sequence logos stack

**Usage**

```
plotMotifLogoStack(pfms, ...)
```

**Arguments**

pfms	a list of position frequency matrices, pfms must be a list of class pfm
...	other parameters can be passed to plotMotifLogo function

**Value**

none

**Examples**

```

pcm1<-matrix(c(0,50,0,50,
              100,0,0,0,
              0,100,0,0,
              0,0,100,0,
              0,0,0,100,
              50,50,0,0,
              0,0,50,50), nrow=4)
pcm2<-matrix(c(50,50,0,0,
              0,100,0,0,
              0,50,50,0,
              0,0,0,100,
              50,50,0,0,
              0,0,50,50), nrow=4)
rownames(pcm1)<-c("A","C","G","T")
rownames(pcm2)<-c("A","C","G","T")
pfms<-list(p1=new("pfm",mat=pcm2pfm(pcm1),name="m1"),
           p2=new("pfm",mat=pcm2pfm(pcm2),name="m2"))
pfms<-DNAMotifAlignment(pfms)
plotMotifLogoStack(pfms)

```

---

plotMotifLogoStackWithTree

*plot sequence logos stack with hierarchical cluster tree*

---

**Description**

plot sequence logos stack with hierarchical cluster tree

**Usage**

```
plotMotifLogoStackWithTree(pfms, hc, treewidth = 1/8, trueDist = FALSE, ...)
```

**Arguments**

pfms	a list of position frequency matrices, pfms must be a list of class pfm
hc	an object of the type produced by stats::hclust
treewidth	the width to show tree
trueDist	logical flags to use hclust height or not.
...	other parameters can be passed to plotMotifLogo function

**Value**

none

## Examples

```
#####Input#####
pcms<-readPCM(file.path(find.package("motifStack"), "extdata"),"pcm$")

#####Clustering#####
hc <- clusterMotifs(pcms)

##reorder the motifs for plotMotifLogoStack
motifs<-pcms[hc$order]
motifs <- lapply(motifs, pcm2pfm)
##do alignment
motifs<-DNAmotifAlignment(motifs)
##plot stacks
plotMotifLogoStack(motifs, ncex=1.0)
plotMotifLogoStackWithTree(motifs, hc=hc)
```

---

plotMotifOverMotif      *plot motif over another motif*

---

## Description

plot motif over another motif to emphasize the difference.

## Usage

```
plotMotifOverMotif(
  motif,
  backgroundMotif,
  bgNoise = NA,
  font = "sans",
  textgp = gpar()
)
```

## Arguments

motif	an object of <code>pcm</code> or <code>pfm</code>
backgroundMotif	an object of <code>pcm</code> or <code>pfm</code>
bgNoise	if it is not NA, test will using a background by Dirichlet(1)-distributed random frequencies with weight <code>bg.noise</code> . The value of <code>bgNoise</code> should be a number in the range of 0 to 1, eg. 0.05
font	font for logo symbol
textgp	text parameter

## Value

none

**Examples**

```
pcms <- readPCM(file.path(find.package("motifStack"), "extdata"), "pcm$")
len <- sapply(pcms, function(.ele) ncol(.ele$mat))
pcms <- pcms[len==7]
plotMotifOverMotif(pcms[[1]], pcms[[2]], bgNoise=0.05)
```

---

```
plotMotifStackWithPhylog
```

*plot sequence logo stacks with a ape4-style phylogenetic tree*

---

**Description**

plot sequence logo stacks with a ape4-style phylogenetic tree

**Usage**

```
plotMotifStackWithPhylog(
  phylog,
  pfms = NULL,
  f.phylog = 0.3,
  f.logo = NULL,
  cleaves = 1,
  cnodes = 0,
  labels.leaves = names(phylog$leaves),
  clabel.leaves = 1,
  labels.nodes = names(phylog$nodes),
  clabel.nodes = 0,
  font = "sans",
  ic.scale = TRUE,
  ...
)
```

**Arguments**

phylog	an object of class phylog
pfms	a list of objects of class pfm
f.phylog	a size coefficient for tree size (a parameter to draw the tree in proportion to leaves label)
f.logo	a size coefficient for the motif
cleaves	a character size for plotting the points that represent the leaves, used with par("cex")*cleaves. If zero, no points are drawn
cnodes	a character size for plotting the points that represent the nodes, used with par("cex")*cnodes. If zero, no points are drawn
labels.leaves	a vector of strings of characters for the leaves labels

clabel.leaves	a character size for the leaves labels, used with par("cex")*clabel.leaves
labels.nodes	a vector of strings of characters for the nodes labels
clabel.nodes	a character size for the nodes labels, used with par("cex")*clabel.nodes. If zero, no nodes labels are drawn
font	font of logo
ic.scale	logical If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.
...	not used.

**Value**

none

**See Also**[plot.phylog](#)**Examples**

```

if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  motifs <- as.list(matrix.fly)
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-", names(motifs), fixed=TRUE)]
  names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
    gsub("_FBgn[0-9]+$", "",
      gsub("[^a-zA-Z0-9]", "_",
        gsub("(_[0-9]+)$", "", names(motifs))))))
  motifs <- motifs[unique(names(motifs))]
  pfms <- sample(motifs, 50)
  hc <- clusterMotifs(pfms)
  library(ade4)
  phylog <- ade4::hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
    new("pfm",mat=.ele, name=.name)})
  pfms <- DNAmotifAlignment(pfms, minimalConsensus=3)
  plotMotifStackWithPhylog(phylog, pfms, f.phylog=0.3,
    cleaves = 0.5, clabel.leaves = 0.7)
}

```

---

```
plotMotifStackWithRadialPhylog
```

*plot sequence logo stacks with a radial phylogenetic tree*

---

### Description

plot sequence logo stacks with a radial phylogenetic tree

### Usage

```
plotMotifStackWithRadialPhylog(
  phylog,
  pfms = NULL,
  circle = 0.75,
  circle.motif = NA,
  cleaves = 1,
  cnodes = 0,
  labels.leaves = names(phylog$leaves),
  clabel.leaves = 1,
  labels.nodes = names(phylog$nodes),
  clabel.nodes = 0,
  draw.box = FALSE,
  col.leaves = rep("black", length(labels.leaves)),
  col.leaves.bg = NULL,
  col.leaves.bg.alpha = 1,
  col.bg = NULL,
  col.bg.alpha = 1,
  col.inner.label.circle = NULL,
  inner.label.circle.width = "default",
  col.outer.label.circle = NULL,
  outer.label.circle.width = "default",
  clockwise = FALSE,
  init.angle = if (clockwise) 90 else 0,
  angle = 360,
  pfmNameSplitter = ";",
  rcpostfix = "(RC)",
  motifScale = c("linear", "logarithmic"),
  ic.scale = TRUE,
  plotIndex = FALSE,
  IndexCol = "black",
  IndexCex = 0.8,
  groupDistance = NA,
  groupDistanceLineCol = "red",
  plotAxis = FALSE,
  font = "sans",
  ...
)
```



**Arguments**

phylog	an object of class phylog
pfms	a list of objects of class pfm
circle	a size coefficient for the outer circle of the labels. Please note this is the position of inner.label.cirle.
circle.motif	a size coefficient for the motif circle
cleaves	a character size for plotting the points that represent the leaves, used with par("cex")*cleaves. If zero, no points are drawn
cnodes	a character size for plotting the points that represent the nodes, used with par("cex")*cnodes. If zero, no points are drawn
labels.leaves	a vector of strings of characters for the leaves labels
clabel.leaves	a character size for the leaves labels, used with par("cex")*clabel.leaves
labels.nodes	a vector of strings of characters for the nodes labels
clabel.nodes	a character size for the nodes labels, used with par("cex")*clabel.nodes. If zero, no nodes labels are drawn
draw.box	if TRUE draws a box around the current plot with the function box()
col.leaves	a vector of colors for leaves labels
col.leaves.bg	a vector of colors for background of leaves labels
col.leaves.bg.alpha	alpha value [0, 1] for the colors of backgroud of leaves labels
col.bg	a vector of colors for tree background
col.bg.alpha	a alpha value [0, 1] of colors for tree background
col.inner.label.circle	a vector of colors for inner circlce of pfms
inner.label.circle.width	width for inner circle of pfms
col.outer.label.circle	a vector of colors for outer circle of pfms
outer.label.circle.width	width for outer circle of pfms
clockwise	a logical value indicating if slices are drawn clockwise or counter clockwise
init.angle	number specifying the starting angle (in degrees) for the slices. Defaults to 0 (i.e., '3 o'clock') unless clockwise is true where init.angle defaults to 90 (degrees), (i.e., '12 o'clock')
angle	number specifying the angle (in degrees) for phylogenetic tree. Defaults 360
pfmNameSplitter	splitter when name of pfms contain multiple node of labels.leaves
rpostfix	the postfix for reverse complements
motifScale	the scale of logo size
ic.scale	logical. If TRUE, the height of each column is proportional to its information content. Otherwise, all columns have the same height.

<code>plotIndex</code>	logical. If TRUE, will plot index number in the motifLogo which can help user to describe the motifLogo
<code>IndexCol</code>	The color of the index number when <code>plotIndex</code> is TRUE.
<code>IndexCex</code>	The cex of the index number when <code>plotIndex</code> is TRUE.
<code>groupDistance</code>	show <code>groupDistance</code> on the draw
<code>groupDistanceLineCol</code>	<code>groupDistance</code> line color, default: red
<code>plotAxis</code>	logical. If TRUE, will plot distance axis.
<code>font</code>	font of logo
<code>...</code>	not used.

**Value**

none

**See Also**

[plot.phylog](#)

**Examples**

```

if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  motifs <- as.list(matrix.fly)
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-",
                        names(motifs), fixed=TRUE)]
  names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
                      gsub("_FBgn[0-9]+$", "",
                          gsub("[^a-zA-Z0-9]", "_",
                              gsub("(_[0-9]+)$", "", names(motifs))))))
  motifs <- motifs[unique(names(motifs))]
  pfms <- sample(motifs, 50)
  hc <- clusterMotifs(pfms)
  library(ade4)
  phylog <- ade4::hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
    new("pfm",mat=.ele, name=.name)})
  pfms <- DNAmotifAlignment(pfms, minimalConsensus=3)
  library(RColorBrewer)
  color <- brewer.pal(12, "Set3")
  plotMotifStackWithRadialPhylog(phylog, pfms, circle=0.9,
                                cleaves = 0.5, clabel.leaves = 0.7,
                                col.bg=rep(color, each=5), col.leaves=rep(color, each=5))
}

```

---

plotXaxis	<i>plot x-axis</i>
-----------	--------------------

---

**Description**

plot x-axis for the sequence logo

**Usage**

```
plotXaxis(pfm, p = rep(0.25, 4), label = NULL)
```

**Arguments**

pfm	position frequency matrices
p	background possibility
label	x-axis labels

**Value**

none

---

plotYaxis	<i>plot y-axis</i>
-----------	--------------------

---

**Description**

plot y-axis for the sequence logo

**Usage**

```
plotYaxis(ymax, ic.scale)
```

**Arguments**

ymax	max value of y axis
ic.scale	Use IC scale or not. See plotMotifLogo for help.

**Value**

none

psam-class

Class "psam"

**Description**

An object of class "psam" represents the position specific affinity matrix (PSAM) of a DNA/RNA/amino-acid sequence motif. The entry stores a matrix, which in row *i*, column *j* gives the affinity of observing nucleotide/or amino acid *i* in position *j* of the motif.

methods for psam objects.

**Usage**

```
## S4 method for signature 'psam'
x$name

## S4 method for signature 'psam,ANY'
plot(x, y = "missing", ...)

## S4 method for signature 'psam'
matrixReverseComplement(x)

## S4 method for signature 'psam,numeric,logical'
addBlank(x, n, b)

## S4 method for signature 'psam'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S4 method for signature 'psam'
format(x, ...)
```

**Arguments**

<code>x</code>	An object of class psam.
<code>name</code>	Slot name.
<code>y</code>	Not use.
<code>...</code>	Further potential arguments passed to plotAffinityLogo.
<code>n</code>	how many spaces should be added.
<code>b</code>	logical value to indicate where the space should be added.
<code>row.names, optional</code>	see as.data.frame

**Objects from the Class**

Objects can be created by calls of the form `new("psam", mat, name, alphabet, color)`.

## Methods

**addBlank** signature(x="psam",n="numeric", b="logical") add space into the position specific affinity matrix for alignment. b is a bool value, if TRUE, add space to the 3' end, else add space to the 5' end. n indicates how many spaces should be added.

**matrixReverseComplement** signature(x = "psam") get the reverse complement of position specific affinity matrix.

**plot** signature(x = "psam") Plots the affinity logo of the position specific affinity matrix.

**\$, \$<-** Get or set the slot of [psam-class](#)

**as.data.frame** convert [psam-class](#) to a data.frame

**format** return the name\_pfm of [psam-class](#)

## Examples

```
motif <- importMatrix(file.path(find.package("motifStack"), "extdata", "PSAM.mxr"),
                      format="psam")[[1]]
plot(motif)
```

```
motif <- importMatrix(file.path(find.package("motifStack"), "extdata", "PSAM.mxr"),
                      format="psam")[[1]]
matrixReverseComplement(motif)
addBlank(motif, 1, FALSE)
addBlank(motif, 3, TRUE)
as(motif, "matrix")
as.data.frame(motif)
format(motif)
```

---

pssm-class

*Class "pssm"*

---

## Description

An object of class "pssm" represents the position specific score matrix of a DNA/RNA/amino-acid sequence motif. The entry stores a matrix, which in row i, column j gives the log-odds probability of nucleotide/or amino acid i in position j of the motif.

methods for pssm objects.

## Usage

```
## S4 method for signature 'pssm'
```

```
x$name
```

```
## S4 method for signature 'pssm,ANY'
```

```
plot(x, y = "missing", ...)
```

```
## S4 method for signature 'pssm'
matrixReverseComplement(x)

## S4 method for signature 'pssm,numeric,logical'
addBlank(x, n, b)

## S4 method for signature 'pssm'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S4 method for signature 'pssm'
format(x, ...)
```

### Arguments

x	An object of class pssm. For getIC, if parameter p is followed, x should be an object of matrix.
name	Slot name.
y	Not use.
...	Further potential arguments passed to plotMotifLogo.
n	how many spaces should be added.
b	logical value to indicate where the space should be added.
row.names, optional	see as.data.frame

### Objects from the Class

Objects can be created by calls of the form `new("pssm", mat, name, alphabet, color, background)`.

### Methods

**addBlank** signature(x="pssm",n="numeric", b="logical") add space into the position frequency matrix for alignment. b is a bool value, if TRUE, add space to the 3' end, else add space to the 5' end. n indicates how many spaces should be added.

**matrixReverseComplement** signature(x = "pssm") get the reverse complement of position frequency matrix.

**plot** signature(x = "pssm") Plots the sequence logo of the position frequency matrix.

**\$, \$<-** Get or set the slot of [pssm-class](#)

**as.data.frame** convert [pssm-class](#) to a data.frame

**format** return the name\_pssm of [pssm-class](#)

### Examples

```
pcm <- read.table(file.path(find.package("motifStack"),
                           "extdata", "bin_SOLEXA.pcm"))
pcm <- pcm[,3:ncol(pcm)]
rownames(pcm) <- c("A", "C", "G", "T")
```

```
motif <- pcm2pssm(pcm)
motif <- new("pssm", mat=motif, name="bin_SOLEXA")
plot(motif)

pcm <- read.table(file.path(find.package("motifStack"),
                           "extdata", "bin_SOLEXA.pcm"))
pcm <- pcm[,3:ncol(pcm)]
rownames(pcm) <- c("A","C","G","T")
motif <- pcm2pssm(pcm)
motif <- new("pssm", mat=motif, name="bin_SOLEXA")
matrixReverseComplement(motif)
addBlank(motif, 1, FALSE)
addBlank(motif, 3, TRUE)
as(motif,"matrix")
as.data.frame(motif)
format(motif)
```

---

readPCM

*read pcm from a path*

---

## Description

read position count matrix from a path

## Usage

```
readPCM(path = ".", pattern = NULL)
```

## Arguments

path	a character vector of full path names
pattern	an optional regular expression

## Value

A list of `pcm` objects

## Examples

```
pcms<-readPCM(file.path(find.package("motifStack"), "extdata"),"pcm$")
```

---

reorderUPGMAtree	<i>re-order UPGMA tree</i>
------------------	----------------------------

---

**Description**

re-order the UPGMA tree by adjacent motif distance

**Usage**

```
reorderUPGMAtree(phylog, motifs, rcpostfix = "(RC)")
```

**Arguments**

phylog	an object of phylog
motifs	a list of objects of pfm
rcpostfix	the postfix for reverse complements

**Value**

an object of phylog

**Author(s)**

Jianhong Ou

**Examples**

```
if(interactive() || Sys.getenv("USER")=="jianhongou"){
  library("MotifDb")
  matrix.fly <- query(MotifDb, "Dmelanogaster")
  motifs <- as.list(matrix.fly)
  motifs <- motifs[grepl("Dmelanogaster-FlyFactorSurvey-", names(motifs), fixed=TRUE)]
  names(motifs) <- gsub("Dmelanogaster_FlyFactorSurvey_", "",
    gsub("_FBgn[0-9]+$", "",
      gsub("[^a-zA-Z0-9]", "_",
        gsub("(_[0-9]+)$", "", names(motifs))))))
  motifs <- motifs[unique(names(motifs))]
  pfms <- sample(motifs, 50)
  hc <- clusterMotifs(pfms)
  library(ade4)
  phylog <- ade4::hclust2phylog(hc)
  pfms <- mapply(pfms, names(pfms), FUN=function(.ele, .name){
    new("pfm",mat=.ele, name=.name)})
  reorderUPGMAtree(phylog, pfms)
}
```



---

traceBackGlobal	<i>traceback global</i>
-----------------	-------------------------

---

**Description**

traceback global

**Usage**

```
traceBackGlobal(dpScore, score, m, n)
```

**Arguments**

dpScore	Dynamic programming score
score	ALLR scores
m, n	matrix width

**Value**

a data.frame

---

traceBackLocal	<i>traceback local</i>
----------------	------------------------

---

**Description**

traceback local

**Usage**

```
traceBackLocal(dpScore, score, m, n)
```

**Arguments**

dpScore	Dynamic programming score matrix
score	ALLR scores, m x n matrix
m, n	matrix width

**Value**

a data.frame

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