

Package ‘motifStack’

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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 <jianhong.ou@duke.edu>

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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)

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

browseMotifs	<i>browse motifs</i>
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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 pfm
phylog	layout type. see GraphvizLayouts
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

```
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 <- lapply(names(pfms), function(.ele, pfms){new("pfm",mat=pfms[[.ele]], name=.ele)},pfms)
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.

colorset *retrieve color setting for logo*

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")
```

DNAmotifAlignment *align DNA motifs*

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)
```

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()){
  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(1:length(pfms), 100)]
  jasper.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
                                                "extdata", "jaspar2010_PCC_SWU.scores"))
  d <- MotIV::motifDistances(lapply(pfms, pfm2pwm))
  hc <- MotIV::motifHclust(d, method="average")
  phylog <- hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  attr <- gsub("^(.*)_.*$", "\\1", leaves)
  getRankedUniqueMotifs(phylog, attr)
}
```

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 <code>colors()</code>), a hexadecimal string of the form "#rrggbb" or "#rrggbbaa" (see <code>rgb</code>), or a positive integer <code>i</code> meaning <code>palette()[i]</code> .
alpha	a value in <code>[0, 1]</code>

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	<i>import motifs from local files</i>
--------------	---------------------------------------

Description

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

Usage

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

Arguments

filenamees	filename to be imported.
format	file format
to	import to pcm-class or pfm-class

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))
```

mergeMotifs	<i>merge multiple motifs</i>
-------------	------------------------------

Description

merge multiple motifs by calculate mean of each position

Usage

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

Arguments

...	pcm or pfm 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 phylogenic tree and multiple color rings</i>
-------------	---

Description

plot sequence logo stacks with a radial phylogenic 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=";", rcprefix="(RC)",
motifScale=c("linear", "logarithmic", "none"), ic.scale=TRUE,
plotIndex=FALSE, IndexCol="black", IndexCex=.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	a 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
col.outer.label.circle	a vector of colors for outer circle of pfms

outer.label.circle.width	width for outer circle of pfms
draw.box	if TRUE draws a box around the current plot with the function box()
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/pfms2 contain multiple node of labels.leaves
rcpostfix	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.
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
plotAxis	logical. If TRUE, will plot distance axis.

Value

none

Author(s)

Jianhong Ou

See Also

[plotMotifStackWithRadialPhylog](#)

Examples

```
if(interactive()){
  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)
  jaspar.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
    "extdata", "jaspar2010_PCC_SWU.scores"))
  d <- MotIV::motifDistances(lapply(pfms, pfm2pwm))
  hc <- MotIV::motifHclust(d, method="average")
}
```

```

phylog <- hclust2phylog(hc)
leaves <- names(phylog$leaves)
pfms <- pfms[leaves]
pfms <- lapply(names(pfms), function(.ele, pfms){new("pfm",mat=pfms[[.ele]],
                                                    name=.ele)},pfms)

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, .5), rot.per=.1,
           draw.box=TRUE, draw.freq=TRUE,
           box.col="gray", freq.col="gray",
           group.col=NULL, groups=NULL, draw.legend=FALSE,
           font="Helvetica-Bold", ic.scale=TRUE, fontsize=12)

```

Arguments

motifSig	an object of class motifSig
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.
fontsize	font size of the template for grImport, default 12. Higher value make better quality figure, but also increase the file size.

Value

none

Examples

```

if(interactive()){
  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)
  jaspar.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
    "extdata", "jaspar2010_PCC_SWU.scores"))
  d <- MotIV::motifDistances(lapply(pfms, pfm2pwm))
  hc <- MotIV::motifHclust(d, method="average")
  phylog <- hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- lapply(names(pfms), function(.ele, pfms){new("pfm",mat=pfms[[.ele]],
    name=.ele)},pfms)
  motifSig <- motifSignature(pfms, phylog, groupDistance=0.1)
  motifCloud(motifSig)
}

```

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=.45, col.tree=NULL,
  cnodes=0, labels.nodes=names(phylog$nodes), clabel.nodes=0,
  cleaves=.2, labels.leaves=names(phylog$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=";", rcprefix="(RC)", ic.scale=TRUE,
plotIndex=FALSE, IndexCol="black", IndexCex=.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
rcprefix	the prefix 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()){
  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)
  jasper.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
    "extdata", "jaspar2010_PCC_SWU.scores"))
  d <- MotIV::motifDistances(lapply(pfms, pfm2pwm))
  hc <- MotIV::motifHclust(d, method="average")
  phylog <- hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- lapply(names(pfms), function(.ele, pfms){new("pfm",mat=pfms[[.ele]],
    name=.ele)},pfms)
  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](#)

Objects from the Class

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

Slots

`signatures` list object of class "pfm"
`freq` code"numeric" signature frequency
`nodelist` list object of class "ouNode"
`gpcol` code"character" signature group color sets

Methods

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

motifSig-methods	<i>"motifSig" methods</i>
------------------	---------------------------

Description

methods for motifSig objects.

Usage

```
## S4 method for signature 'motifSig'
signatures(object)
## S4 method for signature 'motifSig'
frequency(object)
## S4 method for signature 'motifSig'
nodelist(object)
## S4 method for signature 'motifSig'
sigColor(object)
```

Arguments

`object` An object of class motifSig.

Methods

signatures signature(object = "motifSig") return the signatures of motifSig
frequency 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, groupDistance, rcprefix="(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
groupDistance	maximal distance of motifs in the same group
rcprefix	prefix 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()){
  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)
  jaspar.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
    "extdata", "jaspar2010_PCC_SWU.scores"))
  d <- MotIV::motifDistances(lapply(pfms, pfm2pwm))
  hc <- MotIV::motifHclust(d, method="average")
  phylog <- hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- lapply(names(pfms), function(.ele, pfms){new("pfm",mat=pfms[[.ele]],
    name=.ele)},pfms)
  motifSig <- motifSignature(pfms, phylog, groupDistance=0.1)
}
```

motifStack	<i>plot a DNA sequence logo stack</i>
------------	---------------------------------------

Description

Plot a DNA sequence logo stack

Usage

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

Arguments

pfms	a list of objects of class pfm
layout	layout of the logo stack, stack, treeview or radialPhylog
...	any parameters could to pass to plotMotifLogoStack , plotMotifLogoStackWithTree , plotMotifStackWithPhylog or plotMotifStackWithRadialPhylog

Value

return a list contains pfms and phylog

Examples

```
if(interactive()){
  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 <- lapply(names(pfms), function(.ele, pfms){new("pfm", mat=pfms[[.ele]], name=.ele)}, pfms)
  motifStack(pfms, "radialPhylog")
}
```

ouNode-class	<i>Class ouNode</i>
--------------	---------------------

Description

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

Objects from the Class

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

Slots

left: character indicates the name of left leave
right: character indicates the name of right leave
parent: character indicates the name of parent node
distl: numeric indicates the distance of left leave
distr: numeric indicates the distance of right leave
size1: numeric indicates the size of left leave
size2: numeric indicates the size of right leave

Methods

\$, \$<- Get or set the slot of `ouNode`

Examples

```
new("ouNode", left="A", right="B", parent="Root", distl=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.

Objects from the Class

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

Slots

mat Object of class "matrix" The position count matrix
name code"character" The motif name
alphabet "character" The sequence alphabet. "DNA", "RNA", "AA" or "others".
color a "character" vector. The color setting for each symbol
background a "numeric" vector. The background frequency.

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.
trimMotif signature(`x = "pcm"`, `t= "numeric"`) trim motif by information content.
plot signature(`x = "pcm"`) Plots the sequence logo of the position count matrix.

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)

```

pcm-methods

*"pcm" methods***Description**

methods for pcm objects.

Usage

```

## S4 method for signature 'pcm,numeric,logical'
addBlank(x,n,b)
## S4 method for signature 'pcm,ANY'
getIC(x,p="missing")
## S4 method for signature 'pcm'
matrixReverseComplement(x)
## S4 method for signature 'pcm,ANY'
plot(x,y="missing",...)
## S4 method for signature 'pcm,ANY'
pcm2pfm(x,background="missing")
## S4 method for signature 'matrix,ANY'
pcm2pfm(x,background="missing")
## S4 method for signature 'matrix,numeric'
pcm2pfm(x,background)
## S4 method for signature 'data.frame,ANY'
pcm2pfm(x,background="missing")
## S4 method for signature 'data.frame,numeric'
pcm2pfm(x,background)
## S4 method for signature 'pcm,numeric'
trimMotif(x,t)

```

Arguments

x	An object of class pcm. For getIC, if parameter p is followed, x should be an object of matrix. For pcm2pfm, x also could be an object of matrix.
y	Not use.
p	p is the background frequency.
n	how many spaces should be added.
b	logical value to indicate where the space should be added.
background	a "numeric" vector. The background frequency.
t	numeric value of information content threshold for trimming.
...	Further potential arguments passed to plotMotifLogo.

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](#)

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")
getIC(motif)
matrixReverseComplement(motif)
as(motif, "matrix")
pcm2pfm(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.

Objects from the Class

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

Slots

mat Object of class "matrix" The position frequency matrix

name code"character" The motif name

alphabet "character" The sequence alphabet. "DNA", "RNA", "AA" or "others".

color a "character" vector. The color setting for each symbol

background a "numeric" vector. The background frequency.

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.

coerce signature(from = "pfm", to = "matrix"): convert object pfm to matrix

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.

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

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

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)
```

pfm-methods

"pfm" methods

Description

methods for pfm objects.

Usage

```
## S4 method for signature 'pfm,numeric,logical'
addBlank(x,n,b)
## S4 method for signature 'pfm,ANY'
getIC(x,p="missing")
## S4 method for signature 'matrix,numeric'
getIC(x,p)
## S4 method for signature 'pfm'
matrixReverseComplement(x)
## S4 method for signature 'pfm,ANY'
plot(x,y="missing",...)
## S4 method for signature 'pfm,numeric'
trimMotif(x,t)
```

Arguments

x	An object of class pfm. For getIC, if parameter p is followed, x should be an object of matrix.
y	Not use.
p	p is the background frequency.
n	how many spaces should be added.
b	logical value to indicate where the space should be added.
t	numeric value of information content threshold for trimming.
...	Further potential arguments passed to plotMotifLogo.

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](#)

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")
getIC(motif)
matrixReverseComplement(motif)
addBlank(motif, 1, FALSE)
addBlank(motif, 3, TRUE)
as(motif,"matrix")
```

pfm2pwm

convert pfm object to PWM

Description

convert pfm object to PWM

Usage

```
pfm2pwm(x)
```

Arguments

x an object of `pfm` or `pcm` or matrix

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="Helvetica-Bold",
                 colset=c("#00811B", "#2000C7", "#FFB32C", "#D00001"),
                 alpha=0.5, newpage=TRUE, fontsize=12)
```

Arguments

psam	a position-specific affinity matrix
motifName	motif name
font	font 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.
fontsize	font size of the template for <code>grImport</code> , default 12. Higher value make better quality figure, but also increase the file size.

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	<i>plot sequence logo</i>
---------------	---------------------------

Description

plot amino acid or DNA sequence logo

Usage

```
plotMotifLogo(pfm, motifName, p=rep(0.25, 4), font="Helvetica-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, fontsize=12)
```

Arguments

pfm	a position frequency matrices
motifName	motif name
p	background possibility
font	font of logo
colset	color setting for each logo letter
xaxis	draw x-axis or not
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.
fontsize	font size of the template for grImport, default 12. Higher value make better quality figure, but also increase the file size.

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="Helvetica-Bold", ic.scale=TRUE, fontsize=12)
```

Arguments

pfm	an object of pfm
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.
fontsize	font size of the template for grImport, default 12. Higher value make better quality figure, but also increase the file size.

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$")
motifs<-lapply(pcms, pcm2pfm)

#####Clustering#####
jaspar.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
                                             "extdata", "jaspar2010_PCC_SWU.scores"))
d <- MotIV::motifDistances(lapply(motifs, pfm2pwm))
hc <- MotIV::motifHclust(d, method="average")

##reorder the motifs for plotMotifLogoStack
motifs<-motifs[hc$order]
##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="Helvetica-Bold", textgp=gpar())
```

Arguments

motif	an object of pcm or pfm
backgroundMotif	an object of pcm or pfm
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
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="Helvetica-Bold", ic.scale=TRUE, fontsize=12)
```

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.
fontsize	font size of the template for grImport, default 12. Higher value make better quality figure, but also increase the file size.

Value

none

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

```

if(interactive()){
  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)
  jasper.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
    "extdata", "jaspar2010_PCC_SWU.scores"))
  d <- MotIV::motifDistances(lapply(pfms, pfm2pwm))
  hc <- MotIV::motifHclust(d, method="average")
  phylog <- hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- lapply(names(pfms), function(.ele, pfms){new("pfm",mat=pfms[[.ele]],
    name=.ele)},pfms)

  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=";", rcprefix = "(RC)",
  motifScale=c("linear","logarithmic"), ic.scale=TRUE,

```

```
plotIndex=FALSE, IndexCol="black", IndexCex=.8,
groupDistance=NA, groupDistanceLineCol="red",
plotAxis=FALSE, font="Helvetica-Bold", fontsize=12)
```

Arguments

<code>phylog</code>	an object of class <code>phylog</code>
<code>pfms</code>	a list of objects of class <code>pfm</code>
<code>circle</code>	a size coefficient for the outer circle of the labels. Please note this is the position of <code>inner.label.cirle</code> .
<code>circle.motif</code>	a size coefficient for the motif circle
<code>cleaves</code>	a character size for plotting the points that represent the leaves, used with <code>par("cex")*cleaves</code> . If zero, no points are drawn
<code>cnodes</code>	a character size for plotting the points that represent the nodes, used with <code>par("cex")*cnodes</code> . If zero, no points are drawn
<code>labels.leaves</code>	a vector of strings of characters for the leaves labels
<code>clabel.leaves</code>	a character size for the leaves labels, used with <code>par("cex")*clabel.leaves</code>
<code>labels.nodes</code>	a vector of strings of characters for the nodes labels
<code>clabel.nodes</code>	a character size for the nodes labels, used with <code>par("cex")*clabel.nodes</code> . If zero, no nodes labels are drawn
<code>draw.box</code>	if TRUE draws a box around the current plot with the function <code>box()</code>
<code>col.leaves</code>	a vector of colors for leaves labels
<code>col.leaves.bg</code>	a vector of colors for background of leaves labels
<code>col.leaves.bg.alpha</code>	alpha value [0, 1] for the colors of background of leaves labels
<code>col.bg</code>	a vector of colors for tree background
<code>col.bg.alpha</code>	alpha value [0, 1] of colors for tree background
<code>col.inner.label.circle</code>	a vector of colors for inner circle of <code>pfms</code>
<code>inner.label.circle.width</code>	width for inner circle of <code>pfms</code>
<code>col.outer.label.circle</code>	a vector of colors for outer circle of <code>pfms</code>
<code>outer.label.circle.width</code>	width for outer circle of <code>pfms</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 <code>pfms</code> contain multiple node of <code>labels.leaves</code>
<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.

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
plotAxis	logical. If TRUE, will plot distance axis.
font	font of logo
fontsize	font size of the template for grImport, default 12. Higher value make better quality figure, but also increase the file size.

Value

none

See Also

[plot.phylog](#)

Examples

```

if(interactive()){
  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)
  jasper.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
    "extdata", "jaspar2010_PCC_SWU.scores"))
  d <- MotIV::motifDistances(pfms)
  hc <- MotIV::motifHclust(d, method="average")
  phylog <- hclust2phylog(hc)
  leaves <- names(phylog$leaves)
  pfms <- pfms[leaves]
  pfms <- lapply(names(pfms), function(.ele, pfms){new("pfm",mat=pfms[[.ele]],
    name=.ele)},pfms)
  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 *plot x-axis*

Description

plot x-axis for the sequence logo

Usage

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

Arguments

pfm position frequency matrices
p background possibility

Value

none

plotYaxis *plot y-axis*

Description

plot y-axis for the sequence logo

Usage

```
plotYaxis(ymax)
```

Arguments

ymax max value of y axis

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.

Objects from the Class

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

Slots

`mat` Object of class "matrix" The position specific affinity matrix
`name` code"character" The motif name
`alphabet` "character" The sequence alphabet. "DNA", "RNA", "AA" or "others".
`color` a "character" vector. The color setting for each symbol

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.
coerce signature(from = "psam", to = "matrix"): convert object psam to matrix
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.

Examples

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

psam-methods	"psam" methods
--------------	----------------

Description

methods for psam objects.

Usage

```
## S4 method for signature 'psam,numeric,logical'
addBlank(x,n,b)
## S4 method for signature 'psam'
matrixReverseComplement(x)
## S4 method for signature 'psam,ANY'
plot(x,y="missing",...)
```

Arguments

x	An object of class psam.
y	Not use.
n	how many spaces should be added.
b	logical value to indicate where the space should be added.
...	Further potential arguments passed to plotAffinityLogo.

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](#)

Examples

```
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")
```

readPCM	<i>read pcm from a path</i>
---------	-----------------------------

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()){
  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)
  jasper.scores <- MotIV::readDBScores(file.path(find.package("MotIV"),
    "extdata", "jaspar2010_PCC_SWU.scores"))
  d <- MotIV::motifDistances(pfms)
  hc <- MotIV::motifHclust(d, method="average")
  phylog <- hclust2phylog(hc)
  reorderUPGMAtree(phylog, pfms)
}
```

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