

Package ‘motifStack’

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Type Package

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

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Imports XML, scales, htmlwidgets, grDevices, stats, stats4, graphics, utils

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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

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| | |
|------------------------------|---|
| motifStack-package | 2 |
| browseMotifs | 3 |
| browseMotifs-shiny | 4 |
| colorset | 4 |

| | |
|--|-----------|
| DNAmotifAlignment | 5 |
| getRankedUniqueMotifs | 5 |
| highlightCol | 6 |
| importMatrix | 7 |
| mergeMotifs | 8 |
| motifCircos | 8 |
| motifCloud | 11 |
| motifPiles | 12 |
| motifSig-class | 14 |
| motifSig-methods | 15 |
| motifSignature | 16 |
| motifStack | 17 |
| ouNode-class | 17 |
| pcm-class | 18 |
| pcm-methods | 19 |
| pfm-class | 20 |
| pfm-methods | 21 |
| pfm2pwm | 22 |
| plotAffinityLogo | 23 |
| plotMotifLogo | 24 |
| plotMotifLogoA | 25 |
| plotMotifLogoStack | 25 |
| plotMotifLogoStackWithTree | 26 |
| plotMotifOverMotif | 27 |
| plotMotifStackWithPhylog | 28 |
| plotMotifStackWithRadialPhylog | 29 |
| plotXaxis | 32 |
| plotYaxis | 32 |
| psam-class | 33 |
| psam-methods | 33 |
| readPCM | 34 |
| reorderUPGMAtree | 35 |
| Index | 36 |

| | |
|--------------------|---|
| 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>

| | |
|--------------|----------------------|
| 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 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)
```

| | |
|---------------------------|---------------------------------------|
| <code>importMatrix</code> | <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

| | |
|-------------------------|--|
| <code>filenamees</code> | filename to be imported. |
| <code>format</code> | file format |
| <code>to</code> | 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)
  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")
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
sizel: numeric indicates the size of left leave
sizer: 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, sizel=1, sizer=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> | a 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)
}
```

Index

*Topic **classes**

- motifSig-class, 14
- motifSig-methods, 15
- ouNode-class, 17
- pcm-class, 18
- pcm-methods, 19
- pfm-class, 20
- pfm-methods, 21
- psam-class, 33
- psam-methods, 33

*Topic **misc**

- getRankedUniqueMotifs, 5
- highlightCol, 6
- importMatrix, 7
- mergeMotifs, 8
- motifCircos, 8
- motifPiles, 12
- pfm2pwm, 22
- reorderUPGMAtree, 35

*Topic **package**

- motifStack-package, 2

*Topic **plot**

- browseMotifs, 3

\$, motifSig-method (motifSig-methods), 15

\$, ouNode-method (ouNode-class), 17

\$, pcm-method (pcm-methods), 19

\$, pfm-method (pfm-methods), 21

\$, psam-method (psam-methods), 33

\$<-, motifSig-method (motifSig-methods), 15

\$<-, ouNode-method (ouNode-class), 17

\$<-, pcm-method (pcm-methods), 19

\$<-, pfm-method (pfm-methods), 21

\$<-, psam-method (psam-methods), 33

addBlank (pfm-methods), 21

addBlank, pcm, numeric, logical-method (pcm-methods), 19

addBlank, pfm, numeric, logical-method (pfm-methods), 21

addBlank, psam, numeric, logical-method (psam-methods), 33

browseMotifs, 3

browseMotifs-shiny, 4

browseMotifsOutput (browseMotifs-shiny), 4

colors, 6

colorset, 4

DNAmotifAlignment, 5

frequence (motifSig-methods), 15

frequence, motifSig-method (motifSig-methods), 15

getIC (pfm-methods), 21

getIC, matrix, matrix-method (pfm-methods), 21

getIC, matrix, numeric-method (pfm-methods), 21

getIC, pcm, ANY-method (pcm-methods), 19

getIC, pfm, ANY-method (pfm-methods), 21

getRankedUniqueMotifs, 5

GraphvizLayouts, 3

highlightCol, 6

importMatrix, 7

matrixReverseComplement (pfm-methods), 21

matrixReverseComplement, pcm-method (pcm-methods), 19

matrixReverseComplement, pfm-method (pfm-methods), 21

matrixReverseComplement, psam-method (psam-methods), 33

mergeMotifs, 8

motifCircos, 8, 14

motifCloud, 11

motifPiles, 12

motifSig, 11, 15, 16

motifSig (motifSig-methods), 15

motifSig-class, 14

motifSig-methods, 15

motifSignature, 14, 16

motifStack, 17

- motifStack-package, 2
- nodelist (motifSig-methods), 15
- nodelist, motifSig-method
(motifSig-methods), 15
- ouNode, 15, 18
- ouNode (ouNode-class), 17
- ouNode-class, 17
- palette, 6
- pcm, 8, 23, 27, 34
- pcm (pcm-methods), 19
- pcm-class, 7, 18
- pcm-methods, 19
- pcm2pfm (pcm-methods), 19
- pcm2pfm, data.frame, ANY-method
(pcm-methods), 19
- pcm2pfm, data.frame, numeric-method
(pcm-methods), 19
- pcm2pfm, matrix, ANY-method
(pcm-methods), 19
- pcm2pfm, matrix, numeric-method
(pcm-methods), 19
- pcm2pfm, pcm, ANY-method (pcm-methods), 19
- pfm, 3, 8, 17, 23, 27
- pfm (pfm-methods), 21
- pfm-class, 7, 20
- pfm-methods, 21
- pfm2pwm, 22
- plot, pcm, ANY-method (pcm-methods), 19
- plot, pfm, ANY-method (pfm-methods), 21
- plot, psam, ANY-method (psam-methods), 33
- plot.phylog, 29, 31
- plotAffinityLogo, 23
- plotMotifLogo, 24
- plotMotifLogoA, 25
- plotMotifLogoStack, 17, 25
- plotMotifLogoStackWithTree, 17, 26
- plotMotifOverMotif, 27
- plotMotifStackWithPhylog, 17, 28
- plotMotifStackWithRadialPhylog, 10, 17,
29
- plotXaxis, 32
- plotYaxis, 32
- psam (psam-methods), 33
- psam-class, 33
- psam-methods, 33
- PWM, 23
- readPCM, 34
- renderbrowseMotifs
(browseMotifs-shiny), 4
- reorderUPGMAtree, 35
- rgb, 6
- sigColor (motifSig-methods), 15
- sigColor, motifSig-method
(motifSig-methods), 15
- signatures (motifSig-methods), 15
- signatures, motifSig-method
(motifSig-methods), 15
- trimMotif (pcm-methods), 19
- trimMotif, pcm, numeric-method
(pcm-methods), 19
- trimMotif, pfm, numeric-method
(pfm-methods), 21