

# Package ‘dagLogo’

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**Type** Package

**Title** dagLogo

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**Description**

Visualize significant conserved amino acid sequence pattern in groups based on probability theory.

**License** GPL (>=2)

**Depends** R (>= 3.0.1), methods, biomaRt, grImport, grid, motifStack

**Imports** pheatmap, Biostrings

**Suggests** XML, UniProt.ws, RUnit, BiocGenerics, BiocStyle, knitr, rmarkdown

**biocViews** SequenceMatching, Visualization

**VignetteBuilder** knitr

**NeedsCompilation** no

## R topics documented:

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dagLogo-package	<i>Visualize significant conserved amino acid sequence pattern in groups based on probability theory</i>
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## Description

We implement iceLogo by R to visualize significant conserved amino acid sequence pattern based on probability theory. Compare to iceLogo, dagLogo can also visualize significant sequence patterns by clustering the peptides by groups such as charge, chemistry, hydrophobicity and etc.

## Details

Package: dagLogo  
 Type: Package  
 Version: 1.0  
 Date: 2013-09-31  
 License: GPL (>= 2)

DAG: Differential Amino acid Group

There are several differences between dagLogo from iceLogo:

1. The sequence patterns can be grouped by charge, chemistry, hydrophobicity and etc.
2. dagLogo accepts different length of aligned amino acid sequences.
3. Except Random, regional (called restricted in dagLogo) and terminal (called anchored) background model, the background sequence could be set to other regions of the genes in inputs and complementary set of the proteome.

## Author(s)

Jianhong Ou, Julie Lihua Zhu

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

## Examples

```
data("seq.example")
data("proteome.example")
bg <- buildBackgroundModel(seq.example, proteome=proteome.example, permutationSize=10L)
t <- testDAU(seq.example, bg)
dagLogo(t)
```

---

 buildBackgroundModel *build background model*


---

### Description

build background model for dag test

### Usage

```
buildBackgroundModel(dagPeptides,
                    bg=c("wholeGenome", "inputSet", "nonInputSet"),
                    model=c("any", "anchored"),
                    targetPosition=c("any", "Nterminus", "Cterminus"),
                    uniqueSeq=TRUE,
                    permutationSize=30L,
                    rand.seed=1,
                    replacement=FALSE,
                    proteome)
```

### Arguments

dagPeptides	an object of dagPeptides, output of <a href="#">fetchSequence</a> or <a href="#">formatSequence</a>
bg	could be "wholeGenome", "inputSet" or "nonInputSet"
model	could be "any" or "anchored"
targetPosition	could be "any", "Nterminus" or "Cterminus"
uniqueSeq	should the background sequence be unique?
permutationSize	how many times should it samples
rand.seed	random seed
replacement	Should sampling be with replacement?
proteome	an object of Proteome, output of <a href="#">prepareProteome</a>

### Details

The background could be generated from wholeGenome, inputSet or nonInputSet. whole genome: randomly select subsequences from the whole genome with each subsequence containing amino acids with same width of input sequences. anchored whole genome: randomly select subsequences from the whole genome with each subsequence containing amino acids with same width of input sequences where the middle amino acids must contain anchor amino acid, e.g., K, which is specified by user. input set: same to whole genome, but only use protein sequence from input id and not including the site specified in input sequences anchored input set: same to anchored whole genome, but only use protein sequences from input id, and not including the site specified in input sequences. non-input set: whole genome - input set. anchored non-input set: whole genome - input set and the middle amino acids must contain anchor amino acid.

**Value**

an object of `dagBackground` which contains `background` and `permutationSize`.

**Author(s)**

Jianhong Ou, Alexey Stukalov, Julie Zhu

**See Also**

[prepareProteome](#)

**Examples**

```
data("seq.example")
data("proteome.example")
bg <- buildBackgroundModel(seq.example, proteome=proteome.example)
```

---

colorsets

*retrieve color setting for logo*

---

**Description**

retrieve prepared color setting for logo

**Usage**

```
colorsets(colorScheme=c("null", "classic", "charge", "chemistry", "hydrophobicity"))
```

**Arguments**

`colorScheme` could be 'null', 'charge', 'chemistry', 'classic' or 'hydrophobicity'

**Value**

A character vector of color scheme

**Author(s)**

Jianhong Ou

**Examples**

```
col <- colorsets("hydrophobicity")
```

---

dagBackground-class    *Class "dagBackground"*

---

**Description**

An object of class "dagBackground" represents background model.

**Objects from the Class**

Objects can be created by calls of the form `new("dagBackground", background, permutationSize)`.

**Slots**

background    Object of class "list" records the background model  
permutationSize    code"integer" permutation size of background

---

dagHeatmap                    *plot heatmap for test results*

---

**Description**

plot heatmap for test results

**Usage**

```
dagHeatmap(testDAUresults, type=c("diff", "zscore"), ...)
```

**Arguments**

testDAUresults    output of `testDAU`, should be an object of testDAUresults  
type                    "diff" or "zscore"  
...                    parameter could be passed to pheatmap

**Value**

none

**Author(s)**

Jianhong Ou

**Examples**

```
data("seq.example")
data("proteome.example")
bg <- buildBackgroundModel(seq.example, proteome=proteome.example, permutationSize=10)
t <- testDAU(seq.example, bg)
dagHeatmap(t)
```

---

dagLogo *plot sequence logo for test results*

---

**Description**

plot sequence logo for test results

**Usage**

```
dagLogo(testDAUresults, type=c("diff", "zscore"), pvalueCutoff=0.05, namehash=NULL,
        font="Helvetica-Bold", textgp=gpar(), legend=FALSE,
        labelRelativeToAnchor=FALSE,
        labels=NULL)
```

**Arguments**

testDAUresults	output of <code>testDAU</code> , should be an object of testDAUresults
type	"diff" or "zscore"
pvalueCutoff	pvalue cutoff for logo plot
namehash	the hash table to convert rownames of test results to a single letter to be plotted in the logo
font	font for logo symbol
textgp	text parameter
legend	plot legend or not, default false.
labelRelativeToAnchor	plot label relative to anchor or not, default false.
labels	the labels in each position.

**Value**

none

**Author(s)**

Jianhong Ou

**See Also**

[nameHash](#)

**Examples**

```
data("seq.example")
data("proteome.example")
bg <- buildBackgroundModel(seq.example, proteome=proteome.example, permutationSize=10)
t <- testDAU(seq.example, bg)
dagLogo(t)
```

---

dagPeptides-class	Class "dagPeptides"
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---

### Description

An object of class "dagPeptides" represents the information of peptides.

### Objects from the Class

Objects can be created by calls of the form `new("dagPeptides", data, peptides, upstreamOffset, downstreamOffset)`

### Slots

`data` Object of class "data.frame" The details of the input sequences. It includes the columns: IDs, anchorAA (anchor Amino Acid), anchorPos (anchor Position), peptide (protein peptide), anchor, upstream, downstream (peptides in given upstream and downstream offset from anchor)

`peptides` code"matrix" The input peptides. Each column contains one peptide in that position

`upstreamOffset` "numeric" The upstream offset from anchor

`downstreamOffset` "numeric" The downstream offset from anchor

`type` "character" ID type of inputs

---

ecoli.proteome	<i>the subset proteome of Escherichia coli</i>
----------------	--

---

### Description

the subset proteome of Escherichia coli

### Usage

```
data(ecoli.proteome)
```

### Format

An object of Proteome for Escherichia coli proteome. The format is: A list with one data frame and an character.

proteome 'data.frame': obs. of 4 variables

type 'character': "UniProt"

The format of proteome is

ENTREZ\_GENE a character vector, records entrez gene id

SEQUENCE a character vector, peptide sequences

ID a character vector, Uniprot ID

LEN a character vector, length of peptides

**Details**

used in the examples Annotation data obtained by: `library(UniProt.ws) taxId(UniProt.ws) <- 562`  
`proteome <- prepareProteome(UniProt.ws, species="Escherichia coli")`

**Examples**

```
data(ecoli.proteome)
head(ecoli.proteome@proteome)
ecoli.proteome@type
```

---

fetchSequence	<i>fetch sequence by id</i>
---------------	-----------------------------

---

**Description**

fetch amino acid sequence by given identifiers via biomaRt or proteome prepared by [prepareProteome](#)

**Usage**

```
fetchSequence(IDs, type="entrezgene", anchorAA=NULL, anchorPos,
              mart, proteome, upstreamOffset, downstreamOffset)
```

**Arguments**

IDs	A vector of Identifiers to retrieve peptides
type	type of identifiers
anchorAA	a vector of character, anchor Amino Acid
anchorPos	a vector of character or numeric, anchor position, for example, K121
mart	an object of Mart
proteome	an object of Proteome, output of <a href="#">prepareProteome</a>
upstreamOffset	an integer, upstream offset position
downstreamOffset	an integer, downstream offset position

**Value**

return an object of [dagPeptides](#)

**Author(s)**

Jianhong Ou, Alexey Stukalov, Julie Zhu

**See Also**

[formatSequence](#)



## Examples

```
mart <- useMart("ensembl", "dmelanogaster_gene_ensembl")
dat <- read.csv(system.file("extdata", "dagLogoTestData.csv", package="dagLogo"))
seq <- fetchSequence(as.character(dat$entrez_geneid[1:5]),
                    anchorPos=as.character(dat$NCBI_site[1:5]),
                    mart=mart,
                    upstreamOffset=7,
                    downstreamOffset=7)
```

---

formatSequence	<i>prepare an object of dagPeptides from sequences</i>
----------------	--

---

## Description

prepare an object of dagPeptides from sequences

## Usage

```
formatSequence(seq, proteome, upstreamOffset, downstreamOffset)
```

## Arguments

seq                    a vector of character, amino acid sequences  
proteome               an object of Proteome, output of [prepareProteome](#)  
upstreamOffset        an integer, upstream offset position  
downstreamOffset     an integer, downstream offset position

## Value

return an object of dagPeptides, which is a list contains: data, peptides, upstreamOffset, downstreamOffset and type information

## Author(s)

Jianhong Ou, Julie Zhu

## See Also

[fetchSequence](#)

**Examples**

```
if(interactive()){
  dat <- unlist(read.delim(system.file("extdata",
    "grB.txt", package="dagLogo"),
    header=F, as.is=TRUE))
  proteome <- prepareProteome(fasta=system.file("extdata",
    "HUMAN.fasta",
    package="dagLogo"))
  seq <- formatSequence(dat, proteome)
}
```

---

nameHash	<i>convert group name to a single character</i>
----------	---

---

**Description**

convert group name to a single character to shown in a logo

**Usage**

```
nameHash(nameScheme=c("classic", "charge", "chemistry", "hydrophobicity"))
```

**Arguments**

nameScheme      could be "classic", "charge", "chemistry", "hydrophobicity"

**Value**

A character vector of name scheme

**Author(s)**

Jianhong Ou

**Examples**

```
nameHash("charge")
```

---

prepareProteome	<i>prepare proteome for background building</i>
-----------------	---

---

## Description

prepare proteome from UniProt webservice or a fasta file

## Usage

```
prepareProteome(UniProt.ws, fasta, species="unknown")
```

## Arguments

UniProt.ws	an object of UniProt.ws
fasta	fasta file name or an object of AAStringSet
species	an character to assign the species of the proteome

## Value

an object of Proteome which contain protein sequence information

## Author(s)

Jianhong Ou

## See Also

[formatSequence](#), [buildBackgroundModel](#)

## Examples

```
if(interactive()){  
  library(UniProt.ws)  
  taxId(UniProt.ws) <- 7227  
  proteome <- prepareProteome(UniProt.ws, species="Drosophila melanogaster")  
}
```

---

Proteome-class	<i>Class "Proteome"</i>
----------------	-------------------------

---

**Description**

An object of class "Proteome" represents proteome of a given species.

**Objects from the Class**

Objects can be created by calls of the form `new("Proteome", proteome, type, species)`.

**Slots**

`proteome` Object of class "data.frame" the proteome of a given species, should include ids and peptide sequences.

`type` "character" indicates how the object is prepared, could be "fasta" or "UniProt"

`species` "character" the species

---

<code>proteome.example</code>	<i>the subset proteome of fruit fly</i>
-------------------------------	---

---

**Description**

the subset proteome of fruit fly

**Usage**

```
data(proteome.example)
```

**Format**

An object of Proteome for fly subset proteome. The format is: A list with one data frame and an character.

`proteome` 'data.frame': 1406 obs. of 4 variables

`type` 'character': "UniProt"

The format of proteome is

`ENTREZ_GENE` a character vector, records entrez gene id

`SEQUENCE` a character vector, peptide sequences

`ID` a character vector, Uniprot ID

`LEN` a character vector, length of peptides

**Details**

```
used in the examples Annotation data obtained by: library(UniProt.ws) taxId(UniProt.ws) <- 7227
proteome <- prepareProteome(UniProt.ws) proteome@proteome <- proteome@proteome[sample(1:19902,
1406), ]
```

**Examples**

```
data(proteome.example)
head(proteome.example@proteome)
proteome.example@type
```

---

seq.example

*example object of dagPeptides*


---

**Description**

example object of dagPeptides

**Usage**

```
data(seq.example)
```

**Format**

An object of dagPeptides. The format is: A list.

data 'data.frame': 732 obs. of 7 variables

peptides 'matrix': amino acid in each position

upstreamOffset an integer, upstream offset position

downstreamOffset an integer, downstream offset position

type "character", type of identifiers

The format of data is

IDs a character vector, input identifiers

anchorAA a character vector, anchor amino acid provided in inputs

anchorPos a numeric vector, anchor position in the protein

peptide a character vector, peptide sequences

anchor a character vector, anchor amino acid in the protein

upstream a character vector, upstream peptides

downstream a character vector, downstream peptides

**Details**

```
used in the examples seq obtained by: mart <- useMart("ensembl", "dmelanogaster_gene_ensembl")
dat <- read.csv(system.file("extdata", "dagLogoTestData.csv", package="dagLogo")) seq <- fetchSequence(as.character(dat$entrez_geneid), anchorPos=as.character(dat$NCBI_site), mart=mart, upstreamOffset=7, downstreamOffset=7)
```

**Examples**

```
data(seq.example)
head(seq.example@peptides)
seq.example@upstreamOffset
seq.example@downstreamOffset
```

---

testDAU	<i>DAU test</i>
---------	-----------------

---

**Description**

Performs DAU test

**Usage**

```
testDAU(dagPeptides, dagBackground,
        group=c("null", "classic", "charge", "chemistry", "hydrophobicity"),
        bgNoise=NA)
```

**Arguments**

dagPeptides	an object of dagPeptides, output of <a href="#">fetchSequence</a> or <a href="#">fformatSequence</a>
dagBackground	an object of dagBackground, output of <a href="#">buildBackgroundModel</a>
group	could be "null", "classic", "charge", "chemistry", "hydrophobicity"
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**

an object of testDAUresults ready for plotting

**Author(s)**

Jianhong Ou, Alexey Stukalov, Julie Zhu

**Examples**

```
data("seq.example")
data("proteome.example")
bg <- buildBackgroundModel(seq.example, proteome=proteome.example)
t <- testDAU(seq.example, bg, bgNoise=0.05)
```

---

testDAUresults-class    *Class* "testDAUresults"

---

**Description**

An object of class "testDAUresults" represents background model.

**Objects from the Class**

Objects can be created by calls of the form `new("dagBackground", group="character",`

differen

**Slots**

`group` Object of class "character" could be "null", "classic", "charge", "chemistry", "hydrophobicity"

`difference` code"matrix" the difference of inputs from background for each amino acid in each position

`zscore` code"matrix" z score for each amino acid in each position

`pvalue` code"matrix" pvalue for each amino acid in each position

`background` code"matrix" background frequencies for each amino acid in each position

`motif` code"matrix" inputs frequencies for each amino acid in each position

`upstream` "numeric" The upstream offset from anchor

`downstream` "numeric" The downstream offset from anchor

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