

# Package ‘bgafun’

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**Type** Package

**Title** BGAfun A method to identify specificity determining residues in protein families

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**Description** A method to identify specificity determining residues in protein families using Between Group Analysis

**License** Artistic-2.0

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convertAAP-package	<i>Converts an alignment into a matrix using the AAP encoding</i>
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### Description

Convert an alignment read in by seqinr into a matrix using the AAP encoding. this is suitable for BGA analysis using PCA

### Details

Package:	convertAAP
Type:	Package
Version:	1.0
Date:	2007-03-14
License:	Artistic License

### Author(s)

Iain Wallace

### References

BMC hopefully

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convert\_amino-package *The functions required to convert an alignment into a binary matrix suitable for BGA analysis*

---

### Description

The functions required to convert an alignment into a binary matrix suitable for BGA analysis

### Details

Read in the alignment, then convert into matrix

### Author(s)

Iain Wallace

### References

BMC hopefully

---

add\_pseudo\_counts *Add pseudo counts to amino acid matrix based on defined groups*

---

### Description

This function will add pseudo counts to binary amino acid matrix based on the defined groups. It is used to minimise the effect of small sample size. The method of Henikoff and Henikoff is used to calculate the pseudocounts An alternative method is to simply add 1 to the binary matrix

### Usage

```
add_pseudo_counts(amino, groups)
```

### Arguments

amino	Matrix representation of alignment generated by convert\_aln\_amino
groups	Vector or factor that shows the group representation for each sequence in the alignment

### Examples

```
library(bgafun)
data(LDH.amino.gapless)
data(LDH.groups)
LDH.pseudo=LDH.amino.gapless+1
#or use the function
LDH.pseudo=add_pseudo_counts(LDH.amino.gapless,LDH.groups)
```

---

amino_counts	<i>calculate count of amino acid types at each position</i>
--------------	---

---

### Description

Internal Function Calculate the counts of amino acid types at each position in an alignment from a binary amino acid matrix

---

average_cols_aap	<i>Replaces gaps with the average of the column</i>
------------------	---

---

### Description

This function will deal with gaps in the Amino Acid Property encoding scheme It replaces gaps with the average in the column for each group, provided the column is highly occupied for that group. It will only average out over columns that have high percentage of gaps It will remove all other columns containing gaps.

### Usage

```
average_cols_aap(x,y)
```

### Arguments

x	Matrix representation of alignment generated by <code>convert_aln_AAP</code>
y	Vector or factor that shows the group representation for each sequence in the alignment

### Examples

```
library(bgafun)
data(LDH)
data(LDH.groups)
LDH.aap=convert_aln_AAP(LDH)
LDH.aap.ave=average_cols_aap(LDH.aap,LDH.groups)
dim(LDH.aap.ave)
```

BGAFun

*BGAFun A method to identify specificity determining residues in protein families***Description**

This Package combines between group analysis with sequence alignments to identify specificity determining residues in protein families

**Author(s)**

Iain Wallace <iain.wallace@ucd.ie>

**References**

Wallace, I.M. and Higgins, D.G. (2007) Supervised multivariate analysis of sequence groups to identify specificity determining residues, BMC Bioinformatics, 8, 135.

**Examples**

```
library(bgafun)
#read in alignment
LDH <- read.alignment(file = system.file("sequences/LDH-MDH-PF00056.fasta", package = "bgafun"), format = "fasta")

#Assign into groups
LDH.amino=convert_aln_amino(LDH)
LDH.groups=rownames(LDH.amino)
LDH.groups[grep("LDH",LDH.groups)]= "LDH"
LDH.groups[grep("MDH",LDH.groups)]= "MDH"
LDH.groups=as.factor(LDH.groups)

#Convert to Amino Acid matrix (or Amino Acid properties matrix)
LDH.amino.gapless=remove_gaps_groups(LDH.amino,LDH.groups)
#Add Pseudo counts
LDH.pseudo=LDH.amino.gapless+1

LDH.binary.bga=bga(t(LDH.pseudo),LDH.groups)
plot(LDH.binary.bga)
```

calculate\_pseudo

*Calculates pseudo count for each column in the amino acid matrix***Description**

Internal function Calculates the pseudo count for each column in the amino acid matrix

---

Calculate\_Row\_Weights *Calculate the sequence weights for all the rows in my amino, using label as the grouping*

---

### Description

This will calculate the sequence weights for each group using the Henikoff and Henikoff method. Each residue in the sequence is assigned a weight depending on how unique it is in the column. The sequence weight is then the sum of these weights, and the total weight is the number of groups

### Usage

```
Calculate_Row_Weights(my_amino, label)
```

### Arguments

my_amino	Matrix representation of alignment generated by convert\_aln\_amino
label	Vector or factor that shows the group representation for each sequence in the alignment

### References

Henikoff, S. and J. G. Henikoff (1994). "Position-based sequence weights." J Mol Biol 243(4): 574-8.

### Examples

```
library("bgafun")
data(LDH.amino.gapless)
data(LDH.groups)
LDH.weights=Calculate_Row_Weights(LDH.amino.gapless,LDH.groups)
sum(LDH.weights)
```

---

convert\_aln\_AAP *Converts alignment into a matrix using the amino acid property encoding*

---

### Description

Each residue in the alignment is represented by a vector of five continuous variables as given by Atchley et al They applied a multivariate statistic approach to reduce the information in 494 amino acid attributes into a set of five factors for each amino acid. Factor A is termed the polarity index. It correlates well with a large variety of descriptors including the number of hydrogen bond donors, polarity versus nonpolarity, and hydrophobicity versus hydrophilicity. Factor B is a secondary structure index. It represents the propensity of an amino acid to be in a particular type of secondary structure, such as a coil, turn or bend versus the frequency of it in an a-helix. Factor C is correlated with molecular size, volume and molecular weight. Factor D reflects the number of codons coding for an amino acid and amino acid composition. These attributes are related to various physical properties including refractivity and heat capacity. Factor E is related to the electrostatic charge. Gaps are represented by five zeros and should be either removed or replaced by the average of the column for a particular group.

**Usage**

```
convert_aln_AAP(Alignment)
```

**Arguments**

Alignment      Alignment object read in using read.alignment function in seqinr

**References**

Atchley, W. R., J. Zhao, et al. (2005). "Solving the protein sequence metric problem." Proc Natl Acad Sci U S A 102(18): 6395-400.

**Examples**

```
library(bgafun)
data(LDH)
data(LDH.groups)
LDH.aap=convert_aln_AAP(LDH)
dim(LDH.aap)
LDH.aap.ave=average_cols_aap(LDH.aap,LDH.groups)
dim(LDH.aap.ave)
```

---

convert_aln_amino	<i>Converts an alignment object into binary amino matrix</i>
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---

**Description**

Converts an alignment object, read in by the seqinr package, into a binary matrix. The binary matrix represents the absence or presence of amino acids at each position in the alignment

**Usage**

```
convert_aln_amino(Alignment)
```

**Arguments**

Alignment      Alignment object read in using read.alignment function in seqinr

**Examples**

```
library(bgafun)
LDH <- read.alignment(file = system.file("sequences/LDH-MDH-PF00056.fasta", package = "bgafun"), format = "fasta")
LDH.amino=convert_aln_amino(LDH)
dim(LDH.amino)
```

---

convert_seq_amino	<i>Converts a single sequence into a binary string</i>
-------------------	--

---

**Description**

Internal Function Converts a single sequence from an alignment object into a binary string

---

create\_colnames\_amino    *Creates the column names for the binary matrix*

---

### Description

Internal Function Creates the column names for the matrix in the form "Position" "Amino Acid Letter"

---

create\_probab                      *Generates probability matrix for pseudocounts calculation*

---

### Description

Internal function. Generates an amino acid probability matrix which is based on BLOSUM 62, and is used to calculate how many pseudo counts should be added

---

create\_profile                      *Creates a sequence profile for an binary amino acid matrix*

---

### Description

Internal Function Returns a profile matrix, which show how many of each type of amino acids are in each position in an alignment It takes in a binary amino acid matrix

---

create\_profile\_strings                      *Create a profile string for each group in an alignment*

---

### Description

This function is used to analysis the amino acids at each position in the alignment. It can be used to analysis the columns that the bga analysis identified as interesting It creates a profile string, 1D vector which shows the number of amino acids at each position in an alignment for each group that has been defined

### Usage

```
create_profile_strings(x,y)
```

### Arguments

x	Matrix representation of alignment generated by convert\_aln\_amino
y	Vector or factor that shows the group representation for each sequence in the alignment



**Examples**

```

library(bgafun)
data(LDH.groups)
data(LDH.amino.gapless)
#run the analysis
LDH.binary.bga=bga(t(LDH.amino.gapless+1),LDH.groups)
#Get the important residues
top_res=top_residues_2_groups(LDH.binary.bga)
#To tidy up the results
names(top_res)=sub("X","",names(top_res))
# and now look at the amino acid content in the alignment
LDH.profiles=create_profile_strings(LDH.amino.gapless,LDH.groups)
# and now look at only those columns that are identified by BGA
#LDH.profiles[, (colnames(LDH.profiles) %in% names(top_res))]

```

---

Henikoff_weights	<i>Calculates Henikoff weights for each sequence in a binary amino acid matrix</i>
------------------	--

---

**Description**

Internal Function Calculates a sequence weight for each sequence in an alignment using the Henikoff method.

**References**

Henikoff, S. and J. G. Henikoff (1994). "Position-based sequence weights." J Mol Biol 243(4): 574-8.

---

LDH	<i>LDH alignment read in from a file</i>
-----	--

---

**Description**

Seqinr representation of the LDH example alignment.

---

LDH.aap	<i>AAP matrix</i>
---------	-------------------

---

**Description**

Amino Acid Propties representation of LDH alignment

---

 LDH.aap.ave

*AAP matrix*


---

**Description**

Amino Acid Properties Matrix after averaging out gaps

---

LDH.amino

*Binary amino acid matrix after converting the Lactate alignment*


---

**Description**

Binary amino acid matrix after converting the Lactate alignment

---

LDH.amino.gapless

*Amino acid matrix after removing gaps*


---

**Description**

The amino acid matrix for the lactate example, after removing gappy positions

---

LDH.amino.pseudo

*Amino acid matrix after adding pseudo counts*


---

**Description**

Amino acid matrix after adding pseudo counts to the LDH.amino.gapless matrix

**Usage**

```
data(LDH.amino.pseudo)
```

---

LDH.groups

*Groups in the LDH alignment*


---

**Description**

Factor assigning the sequences in the LDH alignment into one of two groups

---

pseudo_counts	<i>Calculate pseudo counts for a profile</i>
---------------	--

---

**Description**

Internal function that is used to calculate pseudo counts for an amino acid profile. The Henikoff method is used.

---

remove_gaps	<i>Removes gaps from a amino binary matrix</i>
-------------	--

---

**Description**

Internal Function This removes gappy positions from an alignment represented in a binary matrix.

---

remove_gaps_groups	<i>remove gaps from a binary amino matrix</i>
--------------------	---

---

**Description**

This function is used to deal with gaps in the binary amino acid encoding. It will remove positions from a binary amino matrix that contain more a certain fraction of gaps for any group in a column, in the alignment The gap fraction should be between 0 and 1, and can be changed with the `gap\_fraction` variable.

**Usage**

```
remove_gaps_groups(x,z,gap_fraction=0.6)
```

**Arguments**

x	Matrix representation of alignment generated by <code>convert\_aln\_amino</code>
z	Vector or factor that shows the group representation for each sequence in the alignment
gap_fraction	Float between 0 and 1 indicating the fraction of gaps in a column before it should be removed

**Examples**

```
library(bgafun)
data(LDH)
data(LDH.groups)
LDH.amino=convert_aln_amino(LDH)
dim(LDH.amino)
LDH.amino.gapless=remove_gaps_groups(LDH.amino,LDH.groups,gap_fraction=0.6)
dim(LDH.amino.gapless)
```

---

run_between_pca	<i>run PCA to identify functional positions in an alignment</i>
-----------------	---

---

### Description

This is a cover function that runs supervised PCA on a matrix that represents an alignment. The matrix can either be a binary matrix (with or without pseudocounts) or one that represents the properties at each position of the alignment

### Usage

```
run_between_pca(x, z, y)
```

### Arguments

x	Matrix representation of alignment generated by <code>convert_aln\amino</code>
z	Matrix representation of alignment generated by <code>convert_aln\amino</code> or <code>convert_aln\AAP</code>
y	Vector or factor that shows the group representation for each sequence in the alignment

### Examples

```
library(bgafun)
data(LDH)
data(LDH.groups)
#Used to calculate the sequence weights
data(LDH.amino.gapless)
data(LDH.aap.ave)
#Run the analysis
LDH.aap.ave.bga=run_between_pca(LDH.amino.gapless,LDH.aap.ave,LDH.groups)
class(LDH.aap.ave.bga)
#to visualise the results
plot(LDH.aap.ave.bga)
```

---

sum_20_aln	<i>Calculates number of amino acids in each group of 20 columns (1 column in an alignment)</i>
------------	--

---

### Description

Internal Function Calculates number of amino acids in each group of 20 columns which corresponds to 1 column in an alignment It takes in an binary amino acid matrix.

sum\_20\_cols

*Calculate number of amino acids in a column of an alignment***Description**

Internal Function Sum up 20 columns in an amino acid matrix which corresponds to one column in an alignment

sum\_aln

*Calculate number of amino acids in each position in an alignment***Description**

Internal Function Calculates the total number of amino acids in each position. It is used to identify positions with a high percentage of gaps It works on an amino acid matrix

top\_residues\_2\_groups *Return a list of the top residues at either end of the axis***Description**

This will identify the residues that are most discriminating between the two groups, and as such are most likely to be specificity determining residues It will return a list of the residues at the end of the axis in a bga analysis. It is used when there are two groups. The function create\_profile\_strings can be used to look at the amino acid content in the column that the analysis identifies

**Usage**

```
top_residues_2_groups(bga_results, residue_number=20)
```

**Arguments**

bga\_results Results of BGA analysis, either from BGA or run\_between\_pca function  
 residue\_number Number of positions at each end of the axis to return

**Examples**

```
library(bgafun)
data(LDH.groups)
data(LDH.amino.gapless)
LDH.binary.bga=bga(t(LDH.amino.gapless+1),LDH.groups)
top_res=top_residues_2_groups(LDH.binary.bga)
#To tidy up the results
names(top_res)=sub("X","",names(top_res))
# to look at the amino acid content in the alignment
LDH.profiles=create_profile_strings(LDH.amino.gapless,LDH.groups)
LDH.profiles[, colnames(LDH.profiles) %in% names(top_res)]
```

---

Weight_Amino	<i>Calculates sequence weight for each sequence in an amino acid matrix</i>
--------------	---

---

**Description**

Internal Function Calculates sequence weight for each sequence, and multiplies the matrix by this weight. It returns a weighted amino acid matrix.

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