Package 'CropPro'

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Type Package

Title Classification using discriminant analysis of archaeobotanical
datasets against ethnographic data to understand crop
processing stages

Version 0.1.0

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Description This package contains functions for the linear discriminant analysis of ethno-
graphic data against which archaeobotanical data can be classified. The package contains func-
tions to transform archaeobotanical datasets, conduct LDA and then plot the archaeobotani-
cal data against the ethnographic data as 2D or 3D plots. The package contains two LDA func-
tions which allows the archaeobotanical samples to be classified as one of four crop process-
ing stages, or one of five classes (four crop processing stages and the archaeological group)

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Depends dplyr, MASS, rgl

Encoding UTF-8

LazyData true

R topics documented:

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crop.plot2d   *Plotting the output of the* LDAcrop.pro *as a 2D graph*

Description

This function plots the output of LDAcrop.pro as a 2D graph showing LD1 and LD2

Usage

```
crop.plot2d(x, y, ylims=NULL, xlims=NULL, gcols=NULL, gpchs=NULL, col ='black', pch=15,
site="Site")
```

Arguments

x	The first linear discriminant function. If using the output of LDAcrop.pro then this will be called x.LD1
y	The second linear discriminant function. If using the output of LDAcrop.pro then this will be called x.LD2
ylims	The limits of the y axis (expressed as c(min, max))
xlims	The limits of the x axis (expressed as c(min, max))
gcols	Symbol colours of the ethnographical crop processing groups written as c("red", "green"...) etc
gpchs	The symbols of the ethnographical crop processing groups (expressed as c(1, 2, 3, 14, 18))
col	Symbol colour for archaeobotanical data
pch	Symbol of the archaeobotanical data
site	The name the archaeobotanical data will be labelled as in key

Author(s)

Elizabeth Stroud

Examples

```
##Example dataset
LD1<-runif(40, min= -0, max=3)
LD2<-runif(40, min = -2, 4)
Study<-sample(1:3, 40, replace=T)
data<-data.frame(Study,LD1)

###Use with defaults (will return a black and white graph)
crop.plot2d(data$LD1, data$LD2)

##Use with variables
crop.plot2d(data$LD1,data$LD2, xlims = c(-5, 5), ylims =c(-5,5), gcols =c("forestgreen", "blue",
"skyblue", "orange"), gpch=c(6,7,8,9), col = "darkred", pch = 20 , site ="Example")
```

| crop.plot3d | *plotting the results of* LDAcrop.pro *as a 3d object* |

Usage

```
crop.plot3d(x, y, z, col, gcol, site)
```

Arguments

x	Column of the dataframe containing the discriminant scores of function 1 (if results from LDAcrop.pro it will be called x.LD1)
y	Column of the dataframe containing the discriminant scores of function 2 (if results from LDAcrop.pro it will be called x.LD2)
z	Column of the dataframe containing the discriminant scores of function 3 (if results from LDAcrop.pro it will be called x.LD3)
col	Symbol colour of archaeobotanical data
gcol	Symbol colours of the ethnographical crop processing groups written as c("red", "green"...) etc
site	The name the archaeobotanical data will be labelled as in key

Author(s)

Elizabeth Stroud

Examples

```
##example dataset

LD1<-runif(40, min= -0, max=3)
LD2<-runif(40, min = -2, max=4)
LD3<-runif(40, min =-4, max=-1)
Study<-sample(1:3, 40, replace=T)
data<-data.frame(Study,LD1, LD2, LD3)

## use

crop.plot3d(data$LD1, data$LD2, data$LD3)

## without defaults

crop.plot3d(data$LD1, data$LD2, data$LD3, gcol = c("black", "grey", "grey48", "grey100"),
col = "red", site = "Example")
```

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data.model   *The ethnobotanical dataset*

Description

The attributes of the weed seeds classified under the 5 different seed attribute groupings

Usage

```
data("data.model")
```

See what Glynis wants to call
them
?seed attribute categories
?seed size, weight and aerodynamic
attributes categories

Format

A data frame with 216 observations on the following 8 variables.

NO Running number of samples

PROC The crop proccessing stage written as a number and used as the grouping factor in `LDAcrop.pro` and `LDAcrop.dung`. 1= Winnowing by-products, 2= Coarse-sieving by-products, 3= Fine-sieving by-products, 4 =Fine-sieving products

BHH Big, headed and heavy

BFH Big, free and heavy

SHH Small, headed and heavy

SHL Small, headed and light

SFH Small, free and heavy

SFL Small, free and light

References

Jones, G., 1987. A statistical approach to the archaeological identification of crop processing. Journal of archaeological science, 14(3), pp.311-323.

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dataorg   *Function to transform raw archaeobotanical data into the form required for* `LDAcrop.pro` *and* `LDAcrop.dung`.

Description

The function transforms raw archaeobotanical data, calculating the squareroot of each species number multiplied by 100, divided by the total weed species within the sample

Usage

```
dataorg(dataframe, groupcol)
```

Arguments

dataframe   The dataframe with the archaeobotanical samples

groupcol   The column containing the grouping variables of the different species (BHH, BFH etc)

Author(s)

Elizabeth Stroud

References

see - Jones, G., 1987. A statistical approach to the archaeological identification of crop processing. Journal of archaeological science, 14(3), pp.311-323.

Examples

```
# Example data
species<-c("Chenopodium album" , "Anthemis cotula", "Brassica rapa ssp campestris",
"Raphanus raphanistrum", "Agrostemma githago" , "Poa annua" )
category<-c("SFH", "BHH","SFH","BHH","BFH", "SFL" )
s.1246<-sample(1:3, 6, replace=T)
s.46178<-sample(1:5, 6, replace=T)
s.1<-sample(0:8, 6, replace=T)
s.23<-sample(0:3, 6, replace=T)
s.987<-sample(3:9, 6, replace=T)
dataset<-data.frame(species,category,s.1246,s.46178,s.1,s.23,s.987))

# Usage

data<-dataorg(dataset, groupcol=2)
```

---

dung.plot2d   *Plotting the output of the* LDAcrop.dung *as a 2D graph*

Description

This function plots the output of LDAcrop.dung as a 2D graph showing function1 (LD1) and function 2 (LD2)

Usage

```
dung.plot2d(data, ylims = NULL, xlims = NULL, gcols = NULL, gpchs = NULL, col = "black",
pch = 15, site = "Archaeological")
```

Arguments

data	The dataframe containing the results of the LDAcrop.dung function
ylims	The limits of the y axis expressed as c(min, max)
xlims	The limits of the x axis expressed as c(min, max)
gcols	The colours of the symbols of the modern crop processing groups expressed as for example c("pink", "red", etc)
gpchs	The symbols of the modern crop processing groups expressed as for example c(1,2,3,4)
col	The colour of the archaeobotanical samples
pch	The symbol of the archaeobotanical samples
site	The name of the archaeobotanical samples to appear in the legend

Author(s)

Elizabeth Stroud

See Also

LDAcrop.dung

Examples

```
# Random data
BHH<-runif(40, min=0, max=7)
BFH<-runif(40, min=0, max=24)
SHH<-runif(40, min=1, max=13)
SHL<-runif(40, min=0.5, max=17)
SFH<-runif(40, min=1, max=22)
SFL<-runif(40, min=1, max=8)
NO<-sample(1:40, 40, replace=F)
PROC<-runif(40,min=0,max=0)
data<-as.data.frame(cbind(NO,PROC,BHH,BFH,SHH,SHL,SFH,SFL))
results<-LDAcrop.dung(results)
# Use
dung.plot2d(results)
```

---

dung.plot3d   *3D plot for the results of* LDAcrop.dung *where the archaeobotanical*
                           samples are entered at the discrimination point.

Description

3D plot for the results of LDAcrop.dung where the archaeobotanical samples are entered at the discrimination point and then everything is classified as either the crop processing stages or as an archaeological sample

Usage

```
dung.plot3d(data, gcol=NULL, col="black", site="site", LD=3)
```

Arguments

data	The output of LDAcrop.dung
gcol	The colour of the crop processing stages symbols
col	The colour of the archaeobotanical samples symbols
site	The name for the archaeobotanical samples - to appear in the legend
LD	Whether using the first three discriminant functions or the 4th has been substituted for the 3rd function (response is LD=4)

Author(s)

Elizabeth Stroud

Examples

```
##Random data
BHH<-runif(40, min=0, max=7)
BFH<-runif(40, min=0, max=24)
SHH<-runif(40, min=1, max=13)
SHL<-runif(40, min=0.5, max=17)
SFH<-runif(40, min=1, max=22)
SFL<-runif(40, min=1, max=8)
NO<-sample(1:40, 40, replace=F)
PROC<-runif(40,min=0,max=0)
data<-as.data.frame(cbind(NO,PROC,BHH,BFH,SHH,SHL,SFH,SFL))
results<-LDAcrop.dung(results)
## Usage
dung.plot3d(results)
dung.plot3d(results, LD=4)
```

LDAcrop.dung	*Linear discriminant analysis based on attributes of weed seeds to classify taphonomic pathway (processing vs dung)*

Description

This function conducts linear discriminant analysis classification using ethnographic data of crop processing sequence to classify archaeobotanical samples on the basis of weed seeds attributes. This function is a modification of `LDAcrop.pro`, in that it uses the entered archaeobotanical data as well as the ethnographic data to create the model. Data is then reclassified against that model, allowing the archaeobotanical samples to be classified as 1 of five groups: archaeological, winnowing by-products, coarse sieve by-products, fine sieve by-products, fine sieve products. The function provides the classification of each sample (class), as well as the discriminant scores of each sample (LD1, LD2, LD3) and the posterior probabilities. The function also produces a classification table showing the classification results and the percentage of samples classified for each group.

Usage

```
LDAcrop.dung(x)
```

Arguments

x   The archaeobotanical dataset

Details

The dataset needs to be organised in the way described in `LDAcrop.pro` or as the output of `dataorg`

Author(s)

Elizabeth Stroud

Examples

```
## Create random dataset for example
BHH<-runif(40, min=0, max=7)
BFH<-runif(40, min=0, max=24)
SHH<-runif(40, min=1, max=13)
SHL<-runif(40, min=0.5, max=17)
SFH<-runif(40, min=1, max=22)
SFL<-runif(40, min=1, max=8)
NO<-sample(1:40, 40, replace=F)
PROC<-runif(40,min=0,max=0)
data<-as.data.frame(cbind(NO, PROC,BHH,BFH,SHH,SHL,SFH,SFL))

## function usage
LDAcrop.dung(data)
```

LDAcrop.pro   *Linear discriminant analysis based on attributes of weed seeds*

Description

This function conducts linear discriminant analysis classification using ethnographic data of crop processing to classify archaeobotanical samples on the basis of attributes of weed seeds. The function provides the classification of each sample (class), as well as the discriminant scores of each sample (LD1, LD2, LD3) and the posterior probabilities. The function also produces a classification table showing the classification results and the percentage of samples classified as either: winnowing by-products, coarse sieve by-products, fine sieve by-products, fine sieve products

Usage

```
LDAcrop.pro(x)
```

Arguments

x   The archaeobotanical dataset

Details

The archaeobotanical dataset needs to have been transformed and organised with columns labelled and in the order of: BHH,BFH,SHH,SHL,SFH,SFL. Transformation can be done manually following (insert reference) or through the use of dataorg which can transform a raw archaeobotanical dataset.

Author(s)

Eizabeth Stroud

Examples

```
##Create random dataset for examples
BHH<-runif(40, min=0, max=7)
BFH<-runif(40, min=0, max=24)
SHH<-runif(40, min=1, max=13)
SHL<-runif(40, min=0.5, max=17)
SFH<-runif(40, min=1, max=22)
SFL<-runif(40, min=1, max=8)
Sample<-sample(1:40, 40, replace=F)
data<-as.data.frame(cbind(BHH, BFH, SHH, SHL, SFH, SFL, Sample))

#Use
LDAcrop.pro(data)
```