Package 'CropPro'

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Type Package

Title Discriminant anaylsis classification of archaebotanical datasets
against ethnographic data to understand crop processing stages

Version 0.1.0

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Description Discriminant anaylsis classification of archaebotanical datasets against ethno-
graphic data to understand crop processing stages.
The package contains functions to transform archaeobotanical datasets, con-
duct LDA and then plot the data against the ethnographic data as 2D or 3D plots

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Depends dplyr, MASS, rgl

Encoding UTF-8

LazyData true

R topics documented:

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crop.plot3d   *ploting the results of the LDA as a 3 d object*

Usage

```
cropplot3dpoints(x, y, z, col, gcol, site)
```

Arguments

x	Function 1
y	Function 2
z	Function 3
col	colour of archaeobotanical data
gcol	group colour
site	name of archaeobotanical data

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
cropplot3dpoints(data$LD1, data$LD2, data$LD3)

## without defaults
cropplot3dpoints(data$LD1, data$LD2, data$LD3, gcol = c("black", "grey", "grey48", "grey100"), col = "red", si
```

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cropplot2d	*Ploting the output of the LDAcrop.pro as a 2d graph*

Description

This function plots the output of LDAcrop.pro as a 2d graphshowing LD1 and LD2

Usage

```
cropplot2d(x, y, ylims = ylims, xlims = xlims, gcols = NULL, gpchs = NULL, col = "black", pch = 23, si
```

Arguments

x	The first linear discriminant function
y	the second linear discriminant 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 for the symbols of the modern crop processing groups (expressed as c("pink", "red", etc))
gpchs	the symbols of the modern crop processing groups (expressed as c(1,2,3,14,18))
col	The colour of the archaeobotanical data's symbol
pch	the symbol of the archaebotanical data
site	the name of the archaeobotanical data showing in the legend

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)
cropplot2d(data$LD1, data$LD2)

##Use with variables
cropplot2d(data$LD1,data$LD2, xlims = c(-5, 5), ylims =c(-5,5), gcols =c("forestgreen", "blue", "skyblue", "or
```

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data.model	*test 2*

Description

test 2

Usage

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

Format

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

NO 1

PROC 2a numeric vector

BHH a 3numeric vector

BFH a numeric vector

SHH a n4umeric vector

SHL a nu5meric vector

SFH a num6eric vector

SFL a nume6ric vector

Examples

```
data(data.model)
## maybe str(data.model) ; plot(data.model) ...
```

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dataorg   *function to transform raw archaeobotanical data into the form required for LDAcrop.pro.*

Description

the function transforms raw archaeobotnical data, calculating the squareroot of each species number muliplited by 100, divided by the total weed species within the sample

Usage

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

Arguments

dataframe   the data to be entered

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

Author(s)

Elizabeth Stroud

References

see - references

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==>  Define data, use random,
##--or do  help(data=index)  for the standard data sets.

## The function is currently defined as
function (x)
{
  }
```

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dungplot2d   *Ploting the output of the LDAcrop.dung as a 2d graph showing LD1 and LD2*

Description

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

Usage

```
dungplot2d(data, ylims = NULL, xlims = NULL, gcols = NULL, gpchs = NULL, col = "black", pch = 15, site
```

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 archaeobotnical samples to appear in the legend

Author(s)

Elizabeth Stroud

See Also

LDAcrop.dung

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dungplot3d	*3d plot for the results of the LDA anaylsis where the archaeobotanical samples are entred at the discrimination point.*

Description

3d plot for the results of the LDA anaylsis where the archaeobotanical samples are entred at the discrimination point.

Usage

```
dungplot3d(x,y,z, gcol=NULL, col="black", site="site", forth=3)
```

Arguments

data	the output of LDAcrop.dung
gcol	the colour of the crop processing stages
col	the colour of the archaeobotanical samples
site	the name to appear on the legend for the archaebotanical samples
LD	whether using the first three discriminant functions or subsituting the 3rd or for the 4th (response is LD=4)

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==>  Define data, use random,
##--or do  help(data=index)  for the standard data sets.

## The function is currently defined as
function (x)
{
  }
```

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

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. This function is a modification of LDAcrop.pro, in that it uses the entered archaeobotncial data as well as the ethnographic data to create the model. The archaeobotanical data is then reclassified angainst that. 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: Archaeological, Winnowing by-products, Coarse sieve by-products, Fine sieve by-products, Fine sieve products

Usage

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

Arguments

x	archaeobotanical dataset

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   archaeobotanical dataset

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)
```