Package 'Weedmodels'

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Type Package

Title Classification of archaeobotanical data using linear discriminant analysis against modern models and plotting of the resultant discriminant scores

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Description This package contains functions which conduct linear discriminant analysis classification using one of three modern models (i.e., sets of discriminated modern arable fields) to classify archaeobotanical samples on the basis of relevant functional ecological attributes of weed species. Other functions include a data organisation function, as well as functions for plotting the results of the LDA.

License MIT

Depends dplyr, MASS, beeswarm

Encoding UTF-8

LazyData true

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

R topics documented:

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ave_wdata   *Function to average the functional trait data of a group of species*

Description

This function averages the functional trait data (SLA, ARNODE, LOGCANH, LOGCAND, VEG-PRO) of entered species. This should be used to average data of taxa whose identification is not to species level.

Usage

```
ave_wdata(newname, species1, species2, species3 = NULL, species4 = NULL, species5 =
NULL, species6 = NULL, species7 = NULL, species8 = NULL)
```

Arguments

newname	The code of the composite species to be created
species1	The four-three code of the first species to be averaged
species2	The four-three code of the second species to be averaged
species3	The four-three code of the third species to be averaged
species4	The four-three code of the fourth species to be averaged
species5	The four-three code of the fifth species to be averaged
species6	The four-three code of the sixth species to be averaged
species7	The four-three code of the seventh species to be averaged
species8	The four-three code of the eighth species to be averaged

Details

It is highly recommended that species are only averaged if their functional attributes are similar. MORE

Author(s)

Elizabeth Stroud

Examples

```
av_sp<-ave_wdata("bromahs", "bromarv","bromhor", "bromsec")
```

data_org	*Function for manipulating archaeobotanical scoresheets and obtaining functional trait data for* wmodel.LDA

Description

Changes archaeobotanical data into presence/absence data and extracts the functional data for the listed species, and calculates the average of the functional attributes for each sample.

Usage

```
data_org(abotdata, samples, codes, model, x)
```

Arguments

abotdata	The archaeobotanical data set. Data should be arranged with each sample as a column and each species as rows. One column needs to contain the species codes of the taxa (see X for list a taxa and codes).
samples	The column which the sample data starts
codes	The column which contains the species codes
model	The model being used; 1,2 or 3 - this will determine which functional attribute are used
x	The flowering period data for the species (needs to be set up as two columns: one of species codes and one of flowering data labelled FLOWPER)

Author(s)

Elizabeth Stroud

Examples

```
## Random data
species<-c("Chenopodium album" , "Anthemis cotula", "Brassica rapa ssp campestris",
"Raphanus raphanistrum", "Agrostemma githago" , "Poa annua" )
code<-c("chenalb", "anthcot", "brasrap","raphrap","agrogit", "poa_ann")
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,code,s.1246,s.46178,s.1,s.23,s.987)
code<-c("chenalb", "anthcot", "brasrap","raphrap","agrogit", "poa_ann")
FLOWPER<-sample(3:9, 6, replace=T)
x<-data.frame(code,FLOWPER)

## Use
results<-data_org(dataset, samples=3, codes=2, model=1, x=x)
```

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model1   *model1*

Description

The values of the five functional ecological attributes of the quadrats of modern arable fields from Asturias (study 1) and Haute Provence (study 2).

Usage

```
data("model1")
```

Format

A data frame with 121 observations on the following 6 variables.

SLA Mean specific leaf area

ARNODE Leaf area per node to fresh leaf thickness

LOGCANH Maximum canopy height converted to a log scale (base 2)

LOGCANH Maximum canopy diameter converted to a log scale (base 2)

FLOWPER Length of flowering period

Study Study location 1 (Asturias, Spain) and study location 2 (Haute Provence, France)

References

Bogaard, A., Hodgson, J., Nitsch, E., Jones, G., Styring, A., Diffey, C., Pouncett, J., Herbig, C., Charles, M., Ertuǧ, F., Tugay, O. Filipović, D. and Fraser, R. (2016) 'Combining functional weed ecology and crop stable isotope ratios to identify cultivation intensity: a comparison of cereal production regimes in Haute Provence, France and Asturias, Spain' *Vegetation History and Archaeobotany* 25, 57-73

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model2   *model2*

Description

The values of the four functional ecological attributes of the quadrats of modern arable fields from Asturias, Haute Provence, Evvia and Morocco.

Usage

```
data("model2")
```

Format

A data frame with 190 observations on the following 6 variables.

Study Grouping variable for type of farming regime (1 or 2)

SLA Mean specific leaf area

ARNODE Leaf area per node to fresh leaf thickness

LOGCANH Maximum canopy height converted to a log scale (base2)

LOGCAND Maximum canopy diameter converted to a log scale (base2)

husbandry Location of the modern arable fields

References

Bogaard, A., Styring, A., Ater, M., Hmimsa, Y., Green, L., Stroud, E., Whitlam, J., Diffey, C., Nitsch, E., Charles, M., Jones, G. and Hodgson, J.2018 'From traditional farming in Morocco to Early Urban Agroecology in northern Mesopotamia: combining Present-day Arable Weed Surveys and crop isotope analysis to reconstruct past Agrosystems in (Semi-)arid Regions' *Environmental Archaeology* 23, 303-322

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model3 *model3*

Description

The values of the two functional ecological attributes of the quadrats of modern arable fields from Highgrove and Laxton, UK.

Usage

    data("model3")

Format

A data frame with 36 observations on the following 4 variables.

Field Location of the modern arable fields

FLOWPER Length of flowering period

VEGPROP Vegetative propagation

Study Grouping variable for type of farming regime (1 or 2)

References

Bogaard, A., Hodgson, J., Kropp, C., McKerracher, M. and Stroud, E. (in press 2022). 'Lessons from Laxton, Highgrove and Lorsch: Building arable weed-based models for the investigation of early medieval agriculture in England', in M. McKerracher and H. Hamerow (eds) *New Perspectives on the Medieval 'Agricultural Revolution': Crop, Stock and Furrow* (Liverpool: Liverpool University Press).

trait_data	*trait data for X species including SLA, ARNODE, LOGCAHN, LOG-CADN, VEGPROP*

Usage

```
data("trait_data")
```

Format

A data frame with XXXX observations on the following 14? variables.

specices.and.subspecies column containing the full Latin name

species.code column containing the four-three species code

SLA Mean Specific leaf area

leaf.thick_new ???keep?

seedmass_germ ?Keep?

lifehist life history of the species - annual, biannual, perennial

LOGCANH Maximum canopy height converted to a log scale (base2)

LOGCAND Maximum canopy diameter converted to a log scale (base2)

VEGPRO vegetative propagation

lamax ???

ARNODE change to VOLNODE?

lvs_node leaves per node

leaf.width.class ???

varp ???

weed_data	*A function to extract the functional attributes of named species from the trait database.*

Description

A function which extracts the functional attributes of named species trait_data. This function extracts the SLA, ARNNODE, LOGCANH, LOGCAND and VEGPROP of a column of four-three coded species names.

Usage

```
weed_data(x)
```

Arguments

x   The column of a dataframe containing the four-three species codes

Note

The four-three codes should not have a space within them. Any species with a genus name less than four letters long (e.g. Poa) should be separated with a _. Full list of species and codes can be found at ?

Author(s)

Elizabeth Stroud

Examples

```
## Example data
species<-c("Chenopodium album" , "Anthemis cotula", "Brassica rapa ssp campestris",
"Raphanus raphanistrum", "Agrostemma githago" , "Poa annua" )
code<-c("chenalb", "anthcot", "brasrap","raphrap","agrogit", "poa_ann")
data<-as.data.frame(cbind(species, code))
## Usage
results<-weed_data(data$code)
```

---

wmodel.LDA	*Linear Discriminant Analysis based on Functional Ecological Attributes of Archaeological Weed Species*

Description

This function conducts linear discriminant analysis classification using one of three modern models (i.e. sets of discriminated modern arable fields) to classify archaeobotanical samples on the basis of relevant functional ecological attributes of weed species. The function provides the classification of each sample (class), as well as the discriminant scores of each sample (LD1) and the posterior probability 1 and 2 (posterior.1 and posterior.2)

Usage

```
wmodel.LDA(model,x)
```

Arguments

model	Either "model1", "model2" or "model3" (also 1, 2 or 3). This argument allows the choice between three modern models against which the archaeobotanical dataset is classified
x	The archaeobotanical data that will be compared against the model. Note data must be labelled with specific headers - see below.

Details

wmodel.LDA requires the input dataset to have specific column names. The columns providing the values of the functional ecological attributes must be spelled as follows: SLA, ARNODE, LOGCANH, LOGCAND, FLOWPER, VEGPROP.

Value

The function prints an output table containing the samples classification, the posterior.1 and posterior.2 value (the posterior probabilities of the two linear discriminant function classifications as per Venables and Ripley (2003) and the MASS package), the linear discriminant function score (LD1), and the input functional ecological attributes of data x.

Author(s)

Elizabeth Stroud

References

model 1 - see Bogaard, A., Hodgson, J., Nitsch, E., Jones, G., Styring, A., Diffey, C., Pouncett, J., Herbig, C., Charles, M., Ertuğ, F., Tugay, O. Filipović, D. and Fraser, R. (2016) 'Combining functional weed ecology and crop stable isotope ratios to identify cultivation intensity: a comparison of cereal production regimes in Haute Provence, France and Asturias, Spain' *Vegetation History and Archaeobotany* 25, 57-73

model 2 - see Bogaard, A., Styring, A., Ater, M., Hmimsa, Y., Green, L., Stroud, E., Whitlam, J., Diffey, C., Nitsch, E., Charles, M., Jones, G. and Hodgson, J.2018 'From traditional farming in Morocco to Early Urban Agroecology in northern Mesopotamia: combining Present-day Arable Weed Surveys and crop isotope analysis to reconstruct past Agrosystems in (Semi-)arid Regions' *Environmental Archaeology* 23, 303-322

model 3 - see Bogaard, A., Hodgson, J., Kropp, C., McKerracher, M. and Stroud, E. (in press 2022). 'Lessons from Laxton, Highgrove and Lorsch: Building arable weed-based models for the investigation of early medieval agriculture in England', in M. McKerracher and H. Hamerow (eds) *New Perspectives on the Medieval 'Agricultural Revolution': Crop, Stock and Furrow* (Liverpool: Liverpool University Press).

Examples

```
wmodel.LDA ('model1', data)
##Create random dataset for examples
SLA<-runif(40, min=20, max=30)
ARNODE<-runif(40, min=3000, max=22000)
LOGCANH<-runif(40, min=5.5, max=6.5)
LOGCAND<-runif(40, min=5.5, max=7)
FLOWPER<-runif(40, min=3.5, max=7)
VEGPROP<-runif(40, min=0.15, max=0.8)
Study<-sample(1:3, 40, replace=T)
data<-as.data.frame(cbind(SLA,ARNODE,LOGCANH,LOGCAND,FLOWPER,VEGPROP,Study))
## Use of model 1 -  modern data from Asturias, Spain and Haute Provence, France
- see Bogaard et al. 2016
model<-wmodel.LDA("model1",data)
model<-wmodel.LDA(1,data)

##Use of model 2 - modern data from Evvia, Greece; Asturias, Spain; Haute Provence,
France; and oases and rain fed terraces in Morocco - see Bogaard et al. 2018
model<-wmodel.LDA("model2",data)
model<-wmodel.LDA(2,data)

##Use of model 3 - modern data from Highgrove and Laxton, UK - see Bogaard et al.2022
model<-wmodel.LDA("model3",data)
model<-wmodel.LDA(3,data)
```

| wplot_arch | *Function to plot the archaeobotanical samples' linear discriminant scores and model's centroids* |

Description

A function which plots the archaeobotanical samples linear discriminant scores from wmodel.LDA compared to the chosen modern model's group centroids

Usage

```
wplot_arch(model, x)

## Defaults
wplot_arch(model,x, xlims= NULL,ticks=NULL, col1 = "black",col3= "black", pch1 = 1,
pch3= 0,compact = FALSE, priority = "density", lines=TRUE, legend="split",site = "samples")
```

Arguments

model	Either "model1", "model2" or "model3" - following wmodel.LDA
x	The LD1 column from the results dataframe of wmodel.LDA
xlims	The x limits
ticks	The location of the x axis labels
col1	The colour of the centroids of the selected model
col3	The colour of the archaeobotanical samples
pch1	The symbol of the model's centroids
pch3	The symbol of the archaeobotanical samples
compact	Follows swarmy from the beeswarm package
priority	Follows the swarmy function relating to the method of point layout
lines	Adds lines from group centroid to x-axis
legend	Adds a legend showing the symbols used to denote group centroids and archaeology sample. Options are "right" (located on the right- hand side), "left" (located on the left-hand side of the graph), and "split" (located on the right-hand side, with labels aligning with the graphed data)
site	Name of the archaeobotanical data to appear on legend

Author(s)

Elizabeth Stroud

References

model 1 - see Bogaard, A., Hodgson, J., Nitsch, E., Jones, G., Styring, A., Diffey, C., Pouncett, J., Herbig, C., Charles, M., Ertuǧ, F., Tugay, O. Filipović, D. and Fraser, R. (2016) 'Combining functional weed ecology and crop stable isotope ratios to identify cultivation intensity: a comparison of cereal production regimes in Haute Provence, France and Asturias, Spain' *Vegetation History and Archaeobotany* 25, 57-73

model 2 - see Bogaard, A., Styring, A., Ater, M., Hmimsa, Y., Green, L., Stroud, E., Whitlam, J., Diffey, C., Nitsch, E., Charles, M., Jones, G. and Hodgson, J.2018 'From traditional farming in Morocco to Early Urban Agroecology in northern Mesopotamia: combining Present-day Arable Weed Surveys and crop isotope analysis to reconstruct past Agrosystems in (Semi-)arid Regions' *Environmental Archaeology* 23, 303-322

model 3 - see Bogaard, A., Hodgson, J., Kropp, C., McKerracher, M. and Stroud, E. (in press 2022). 'Lessons from Laxton, Highgrove and Lorsch: Building arable weed-based models for the investigation of early medieval agriculture in England', in M. McKerracher and H. Hamerow (eds) *New Perspectives on the Medieval 'Agricultural Revolution': Crop, Stock and Furrow* (Liverpool: Liverpool University Press).

See Also

wmodel.LDA, wplot_geog, wplot_basic

Examples

```
## Example dataset
LD1<-runif(40, min=-6.6, max=6)
Study<-sample(1:3, 40, replace=T)
data<-data.frame(Study,LD1)

## If using defaults
wplot_arch( "model1", data$LD1)
wplot_arch( 1, data$LD1)

## Use of model1 -  modern data from Asturias, Spain and Haute Provence,
France (Boggard et al. 2016)
wplot_arch("model1",data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green",col3="purple",
pch1=1,  pch3=19, compact =F, priority = "ascending", lines=T, site="example")

## Use of model2 - modern data from Evvia, Greece; Asturias, Spain; HauteProvence,
France; and oases and rain fed terraces in Morocco (Bogaard et al. 2018)
wplot_arch("model2",data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col3="purple",
pch1=1,pch3=19, compact =F, priority = "ascending", lines=T, site= "example")

## Use of model3 - modern data from Highgrove and Laxton, UK- (Bogaard et al.2022)
wplot_arch("model3", data$LD1, xlims=c(-7,7),ticks=-7:7, col1="green",  col3="purple",
pch1=1,pch3=19, compact =F, priority = "ascending", lines=T, site="example")


## Different legend options
wplot_arch(1,data$LD1, legend = "right")

wplot_arch(1,data$LD1, legend = "left")

wplot_arch(1,data$LD1,legend = "split")

## Different priority options using "ascending", "descending", "density",
"random","none"
par(mfrow=c(3,2),
    oma=c(2,0,0,0),
    mar=c(0,0,0,0))
wplot_arch(1,data$LD1, compact =F, priority = "ascending")
mtext("ascending", 3,-2)
wplot_arch(1,data$LD1, compact =F, priority = "descending")
```

```
mtext("descending", 3, -2)
wplot_arch(1,data$LD1,compact =F, priority = "density")
mtext("density",3, -2)
wplot_arch(1,data$LD1, compact =F, priority = "random")
mtext("random",3,-2)
wplot_arch(1,data$LD1, compact =F, priority = "none")
mtext("none",3, -2)

## Options with compact TRUE and FALSE while using ascending or descending priority
par(mfrow=c(2,2),
    oma=c(2,0,0,0),
    mar=c(0,0,0,0))
wplot_arch(1,data$LD1, compact =F, priority = "ascending")
mtext("ascending, TRUE", 3,-3)
wplot_arch(1,data$LD1, compact =T, priority = "ascending")
mtext("ascending, FALSE", 3,-3)
wplot_arch(1,data$LD1,compact =F, priority = "descending")
mtext("descending, TRUE", 3,-3)
wplot_arch(1,data$LD1, compact =T, priority = "descending")
mtext("descending, FALSE", 3,-3)
```

---

wplot_basic	*Plotting function to display functional ecological model centroids, the model's linear discriminant scores and the archaeological samples' linear discriminant scores from* wmodel.LDA

Description

A function which plots the linear discriminant scores of the modern models based on arable fields from wmodel.LDA, their group centroids and the archaeobotanical data's discriminant scores.

Usage

```
wplot_basic(model, x)

## Defaults
wplot_basic (model, x, xlims= NULL,ticks = NULL,col1 = "black",col2 = "black",
col3 = "black", pch1 = 1,pch2 = 2,pch3 = 0,compact =  FALSE, priority = "density",
lines = TRUE, legend = "split", site = "samples")
```

Arguments

model	the modern model to be plotted – either "model1", "model2", or "model3" - use the model against which the archaeobotanical samples have a been classified against, using wmodel.LDA.
x	the column x from the data frame which contains the linear discriminant scores of the archaeobotanical data - if using data from wmodel.LDA, such column will be called LD1
xlims	The limits of the x axis

ticks	The location of the x axis labels along the x axis
col1	The colour of the modern model's centroids
col2	The colour of the modern model's datapoints
col3	The colour of the archaeobotanical datapoints
pch1	The symbol of the modern model's centroids - must be between 0 and 2
pch2	The symbol of the modern model's datapoints - must be between 0 and 2
pch3	The symbol of the archaeobotanical datapoints
compact	Follows swarmy from the beeswarm package
priority	Follows the swarmy function relating to the method of point layout
lines	Adds lines from group centroid to x-axis
legend	Adds a legend showing the symbols used to denote group centroids and archaeobotanical samples. Options are "right" (located on the right-hand side), "left" (located on the left-hand side of the graph), and "split" (located on the right-hand side, with labels aligning with the graphed data)
site	Add labels in the legend for the archaeobotanical data

Author(s)

Elizabeth Stroud

References

model 1 - see Bogaard, A., Hodgson, J., Nitsch, E., Jones, G., Styring, A., Diffey, C., Pouncett, J., Herbig, C., Charles, M., Ertuğ, F., Tugay, O. Filipović, D. and Fraser, R. (2016) 'Combining functional weed ecology and crop stable isotope ratios to identify cultivation intensity: a comparison of cereal production regimes in Haute Provence, France and Asturias, Spain' *Vegetation History and Archaeobotany* 25, 57-73

model 2 - see Bogaard, A., Styring, A., Ater, M., Hmimsa, Y., Green, L., Stroud, E., Whitlam, J., Diffey, C., Nitsch, E., Charles, M., Jones, G. and Hodgson, J.2018 'From traditional farming in Morocco to Early Urban Agroecology in northern Mesopotamia: combining Present-day Arable Weed Surveys and crop isotope analysis to reconstruct past Agrosystems in (Semi-)arid Regions' *Environmental Archaeology* 23, 303-322

model 3 - see Bogaard, A., Hodgson, J., Kropp, C., McKerracher, M. and Stroud, E. (in press 2022). 'Lessons from Laxton, Highgrove and Lorsch: Building arable weed-based models for the investigation of early medieval agriculture in England', in M. McKerracher and H. Hamerow (eds) *New Perspectives on the Medieval 'Agricultural Revolution': Crop, Stock and Furrow* (Liverpool: Liverpool University Press).

See Also

wmodel.LDA, wplot_arch, wplot_geog

Examples

```
##Example dataset
LD1<-runif(40, min=-6.6, max=6)
Study<-sample(1:3, 40, replace=T)
data<-data.frame(Study,LD1)

##Usage with defaults
```

```
wplot_basic("model1", data$LD1)
wplot_basic("model2", data$LD1)
wplot_basic("model3", data$LD1)

## Use of model 1 - modern data from Asturias, Spain and Haute Provence, France
(Bogaard et al. 2016)

wplot_basic("model1",data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1, pch2=2, pch3=19, compact =F, priority = "ascending", lines=T, site="example")

##Use of model2 - modern data from Evvia, Greece; Asturias, Spain; Haute Provence, France;
and oases and rainfed terraces in Morocco (Bogaard et al. 2018)

wplot_basic("model2", data$LD1, xlims=c(-7,7),ticks=-7:7, col1="green",  col2="red",col3="purple",
pch1=1, pch2=2,pch3=19, compact =F, priority = "ascending", lines=T, site="example")

##Use of model3 - modern data from Highgrove and Laxton, UK- see Bogaard \emph{et al.} 2022

wplot_basic("model3", data$LD1, xlims=c(-7,7),ticks=-7:7, col1="green",  col2="red",col3="purple",
pch1=1,pch2=2, pch3=19, compact =F, priority = "ascending", lines=T, site="example")

## Options with different colours and symbols for different archaeological sites
wplot_basic("model1", data$LD1, col3=data$Study,pch3=data$Study, site=c("Site 1","Site 2","Site 3"))

##Different priority options using "ascending", "descending", "density", "random", "none"
par(mfrow=c(3,2),
    oma=c(0,0,0,0),
    mar=c(0,0,0,0))
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =F, priority = "ascending")
mtext("ascending", 3,-1.5)
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =F, priority = "descending")
mtext("descending", 3, -1.5)
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =F, priority = "density")
mtext("density",3, -1.5)
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =F, priority = "random")
mtext("random",3,-1.5)
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =F, priority = "none")
mtext("none",3, -1.5)

## Grpah options using compact TRUE and FALSE as well as ascending and descending priority
par(mfrow=c(2,2),
    oma=c(0,0,0,0),
    mar=c(0,0,0,0))
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =F, priority = "ascending")
mtext("ascending, TRUE", 3,-1.5)
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =T, priority = "ascending")
mtext("ascending, FALSE", 3,-1.5)
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =F, priority = "descending")
mtext("descending, TRUE", 3,-1.5)
```

```
wplot_basic(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple", pch1=1,
pch2=2, pch3=19, compact =T, priority = "descending")
mtext("descending, FALSE", 3,-1.5)
```

---

wplot_geog	*Plotting function for displaying the output of* wmodel.LDA*, plotting the archaeobotanical samples linear discriminant scores, the chosen model's centroids, and the model's discriminant scores with separate symbols for the different modern study's arable fields.*

Description

A function which plots the archaeobotanical samples linear discriminant scores from following wmodel.LDA compared to with the chosen modern model's centroids, and the model's discriminant scores separated according to modern study location

Usage

```
wplot_geog(model, x)

#defaults
wplot_geog(model,
  x,
  xlims= NULL,
  ticks= NULL,
  col1= "black",
  col2= "black",
  col3= "black",
  pch1= 1,
  pch3= 5,
  compact= F,
  priority= "descending",
  site= "samples",
  lines= F,
  legend= F)
```

Arguments

model	The modern model to be plotted – either "model1", "model3" or "model3" following wmodel.LDA
x	The LD1 column from the results dataframe of wmodel.LDA. Can also use linear discriminant score from other sources.
xlims	The limits of the x axis
ticks	The location of the x axis labels
col1	The colour of the modern model's centroids
col2	The colour of the modern model's datapoints
col3	The colour of the archaeobotanical datapoints

pch1	The symbol of the modern model's centroids- must be between 0 and 2
pch3	The symbol of the archaeobotanical datapoints
compact	Follows the beeswarm package's [swarmy](#) compact variable
priority	Follows [swarmy](#) priority regarding the method of point layout
lines	Adds lines from group centroid to x-axis
site	Adds the name of the archaeobotanical data to be shown in the legend
legend	Adds a legend to the plot

Author(s)

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References

model 1 - see Bogaard, A., Hodgson, J., Nitsch, E., Jones, G., Styring, A., Diffey, C., Pouncett, J., Herbig, C., Charles, M., Ertuğ, F., Tugay, O. Filipović, D. and Fraser, R. (2016) 'Combining functional weed ecology and crop stable isotope ratios to identify cultivation intensity: a comparison of cereal production regimes in Haute Provence, France and Asturias, Spain' *Vegetation History and Archaeobotany* 25, 57-73

model 2 - see Bogaard, A., Styring, A., Ater, M., Hmimsa, Y., Green, L., Stroud, E., Whitlam, J., Diffey, C., Nitsch, E., Charles, M., Jones, G. and Hodgson, J.2018 'From traditional farming in Morocco to Early Urban Agroecology in northern Mesopotamia: combining Present-day Arable Weed Surveys and crop isotope analysis to reconstruct past Agrosystems in (Semi-)arid Regions' *Environmental Archaeology* 23, 303-322

model 3 - see Bogaard, A., Hodgson, J., Kropp, C., McKerracher, M. and Stroud, E. (in press 2022). 'Lessons from Laxton, Highgrove and Lorsch: Building arable weed-based models for the investigation of early medieval agriculture in England', in M. McKerracher and H. Hamerow (eds) *New Perspectives on the Medieval 'Agricultural Revolution': Crop, Stock and Furrow* (Liverpool: Liverpool University Press).

See Also

[wmodel.LDA](#), [wplot_arch](#), [wplot_basic](#)

Examples

```
##example dataset
LD1<-runif(40, min=-6.6, max=6)
Study<-sample(1:3, 40, replace=T)
data<-data.frame(Study,LD1)

##If using with defaults
wplot_geog("model1", data$LD1)
wplot_geog("model2", data$LD1)
wplot_geog("model3", data$LD1)

##Use of model 1 -  modern data from Asturias, Spain and Haute Provence, France
- see Bogaard et al. 2016

wplot_geog("model1",data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",
col3="purple", pch1=1, pch3=19, compact =F, priority = "ascending", lines=T, site="example")
```

```
##Use of model 2 - modern data from Evvia, Greece; Asturias, Spain; Haute Provence,
France; and oases and rain fed terraces in Morocco - see Bogaard et al. 2018

wplot_geog("model2", data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green",  col2="red",
col3="purple", pch1=1, pch3=19, compact =F, priority = "ascending", lines=T, site="example")

##Use of model 3 - modern data from Highgrove and Laxton, UK- see Bogaard et al. 2022

wplot_geog("model3", data$LD1, xlims=c(-7,7),ticks=-7:7, col1="green",  col2="red",
col3="purple", pch1=1, pch3=19, compact =F, priority = "ascending", lines=T, site="example")


##Different priority options using "ascending", "descending", "density", "random", "none"
par(mfrow=c(3,2),
    oma=c(0,0,0,0),
    mar=c(0,0,0,0))
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1,  pch3=19,compact =F, priority = "ascending")
mtext("ascending", 3,-1.5)
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1,  pch3=19,compact =F, priority = "descending")
mtext("descending", 3, -1.5)
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1,  pch3=19,compact =F, priority = "density")
mtext("density",3, -1.5)
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1,  pch3=19,compact =F, priority = "random")
mtext("random",3,-1.5)
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1,  pch3=19,compact =F, priority = "none")
mtext("none",3, -1.5)

## options with compact T and F using ascending and descending priority
par(mfrow=c(2,2),
    oma=c(0,0,0,0),
    mar=c(0,0,0,0))
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1, pch3=19,
compact =F, priority = "ascending")
mtext("ascending, TRUE", 3,-1.5)
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1, pch3=19,compact =T, priority = "ascending")
mtext("ascending, FALSE", 3,-1.5)
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1, pch3=19, compact =F, priority = "descending")
mtext("descending, TRUE", 3,-1.5)
wplot_geog(1,data$LD1,xlims=c(-7,7),ticks=-7:7, col1="green", col2="red",col3="purple",
pch1=1, pch3=19,compact =T, priority = "descending")
mtext("descending, FALSE", 3,-1.5)

## options with different col and pch for different archaeobotanical sites or different phases
wplot_geog("model2", data$LD1, col3=data$Study,pch3=data$Study, legend=T, site=c("Site 1",
"Site 2","Site 3"))
```