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Title Analysis of Habitat Selection by Animals

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Description A collection of tools for the analysis of habitat selection.

VignetteBuilder utils

License GPL (>= 2)

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`bauges` *Census of chamois (Rupicapra rupicapra) in the Bauges mountains*

Description

This data set contains the relocations of 198 chamois groups in the Bauges mountains, as well as maps of 7 environmental variables on the study area.

Usage

```
data(bauges)
```

Details

This dataset contains a subsample of the data collected by volunteers and professionals working in various French wildlife and forest management, from 1994 to 2004 in the wildlife reserve of "les Bauges" (French Alps). Note that both the maps and the relocations have been slightly destroyed to preserve copyright on the data.

Source

Daniel Maillard, Office National de la chasse et de la faune sauvage, 95 rue Pierre Flourens, 34000 Montpellier, France

Examples

```
data(bauges)

mimage(bauges$map)
image(bauges$map, 1)
points(bauges$locs)
```

---

bighorn *Radio-Tracking of Bighorn Sheeps*

Description

This data set describes the habitat use and availability for 6 bighorn sheeps monitored by radio-tracking (Arnett et al. 1989, in Manly et al., 2003, p. 67-74). 10 habitat types are considered.

Usage

```
data(bighorn)
```

Details

The object `bighorn` is a list, with the following components:

`used` the number of resource units used by each animal (in rows) in each habitat category (in columns).

`availTrue` the availability of each habitat category.

`availEstimated` a sample of available resource units in each habitat category.

References

Manly, B.F.J., McDonald, L.L., Thomas, D.L., McDonald, T.L. & Erickson, W.P. (2003) *Resource selection by animals - Statistical design and Analysis for field studies. Second edition.* London: Kluwer academic publishers.

---

biv.test *Bivariate Test*

Description

`biv.plot` displays a bivariate plot. `biv.test` displays the results of a bivariate randomisation test.

Usage

```
biv.plot(dfxy, br = 10, points = TRUE, density = TRUE,
         kernel = TRUE, o.include = FALSE, pch, cex, col, h, sub,
         side = c("top", "bottom", "none"), ...)
biv.test(dfxy, point, br = 10, points = TRUE, density = TRUE,
         kernel = TRUE, o.include = FALSE, pch, cex, col, Pcol, h, sub,
         side = c("top", "bottom", "none"), ...)
```

Arguments

dfxy	a data frame with N lines (couples of values) and two columns
br	a parameter used to define the numbers of breaks of the histograms. A larger value leads to a larger number of breaks
points	logical. Whether the points should be displayed
density	logical. Whether the kernel density estimation should be displayed for the marginal histograms
kernel	logical. Whether the kernel density estimation should be displayed for the bivariate plot
o.include	logical. If TRUE, the origin is included in the plot
pch	plotting "character", i.e., symbol to use for the points. (see ?points)
cex	character expansion for the points
col	color code or name for the points, see ?par
h	vector of bandwidths for x and y directions, used in the function kde2d of the package MASS. Defaults to normal reference bandwidth (see ?kde2d)
sub	a character string to be inserted in the plot as a title
side	if "top", the x and y scales of the grid are upside, if "bottom" they are downside, if "none" no legend
point	a vector of length 2, representing the observation to be compared with the simulated values of the randomisation test
Pcol	color code or name for the observed point
...	further arguments passed to or from other methods

Details

biv.test is used to display the results of a bivariate randomisation test. An example of use of the function is provided in the function niche.test.

The x-axis of the main window corresponds to the first column of dfxy; the y-axis corresponds to the second column. Kernel density is estimated to indicate the contours of the distribution of randomised values. The two marginal histograms correspond to the univariate tests on each axis, for which the p-values are computed with as.randtest (package ade4, one-sided tests).

Warning

biv.plot and biv.test use the function kde2d of the package MASS.

Author(s)

Mathieu Basille <basille@ase-research.org>

See Also

as.randtest (package ade4)

Examples

```
x = rnorm(1000,2)
y = 2*x+rnorm(1000,2)
dfxy = data.frame(x, y)

biv.plot(dfxy)
biv.plot(dfxy, points=FALSE, col="lightblue", br=20)

p = c(3, 4)
biv.test(dfxy, p)
biv.test(dfxy, p, points=FALSE, Pcol="darkred", col="lightblue", br=20)
```

---

canomi *Canonical OMI analysis*

Description

This function performs a canonical OMI analysis (outlying mean index).

Usage

```
canomi(dudiX, Y, scannf = TRUE, nf = 2)
## S3 method for class 'canomi'
print(x, ...)
## S3 method for class 'canomi'
 plot(x, xax = 1, yax = 2, ...)
```

Arguments

dudiX	an object of class dudi
Y	a a data frame Resource units-animals according to dudiX$tab with no columns of zero
scannf	a logical value indicating whether the eigenvalues bar plot should be displayed
nf	if scannf FALSE, an integer indicating the number of kept axes
x	an object of class canomi returned by the function canomi
xax	the number of the x-axis
yax	the number of the x-axis
...	further arguments passed to or from other methods

Details

The canonical OMI analysis is similar to the function niche, from the package ade4. The principle of this analysis is the following. A set of N resource units (RUs) are available to the animals of the study. Each resource unit is described by P environmental variables. Therefore, the N resource units define a cloud of N points in the P-dimensionnal space defined by the P variables. We call this space "ecological space".

Moreover, the use of the N resource units is known (or sampled) for a sample of K animals (e.g., using radio-tracking). These utilization weights for each RU (rows) and each animal (column) define a table Y. For a given animal, the set of resource units used define the "niche" of the animal. The vector connecting the centroid (mean) of the available RUs to the centroid of the RUs used by this animal is named "marginality vector" (and its squared length is named "marginality" or "outlying mean index").

The canomi first distorts the ecological space so that the available resource units take a standard spherical shape (by first performing a principal component analysis). Then, in this distorted space, a non-centred principal component analysis of the marginality vectors is performed. The canonical OMI analysis finds the directions in the distorted ecological space where the marginality is, in average, the largest.

Value

canomi returns a list of the class canomi, with the following components:

call	original call.
rank	an integer indicating the rank of the studied matrix
nf	an integer indicating the number of kept axes
eig	a vector with all the eigenvalues of the analysis.
tab	a data frame with n rows (n animals) and p columns (p environmental variables).
li	animals coordinates, data frame with n rows and nf columns.
l1	animals normed coordinates, data frame with n rows and nf columns.
c1	column scores, data frame with p rows and nf columns.
cor	the correlation between the canomi axes and the original variables
ls	a data frame with the resource units coordinates
cm	The variables metric used in the analysis (e.g. ls = dudiX\$tab%*%cm%*%c1)
as	a data frame with the axis upon niche axis

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Chessel, D. 2006. Calcul de l'outlier mean index. Consultation statistique avec le logiciel R.

See Also

dudi for class dudi, niche for classical OMI analysis

Examples

```
## The data
data(puech)
locs <- puech$relocations
maps <- puech$maps

## the maps
mimage(maps)

## the relocations of the wild boar:
image(maps)
points(locs, col=as.numeric(slot(locs, "data")[,1]))


## count the number of relocations
## in each pixel of the maps
cp <- count.points(locs, maps)

## gets the data:
dfavail <- slot(maps, "data")
dfused <- slot(cp, "data")

## a preliminary principal component analysis of the data:
dud <- dudi.pca(dfavail, scannf=FALSE)

## The analysis:
nic <- canomi(dud, dfused, scannf=FALSE)
nic

## Plot the results:
plot(nic)
```

---

chamois *Location of Chamois Groups in the Chartreuse Mountains*

Description

This data set describes the habitat use and availability by the chamois of the Chartreuse mountains (Isere, France), in 1992 and 1997. These data have been gathered during the hunting season (Fall).

Usage

```
data(chamois)
```

Details

The object chamois is a list containing the following components:

locs is a data frame containing the x and y coordinates of 198 chamois groups.

map is a map of class kasc describing the vegetation (Forest or Open areas), the distance from the ecotone Open/Forest and the slopes on the area.

References

Federation Departementale des Chasseurs de l'Isere, 65 av Jean Jaures, 38320 Eybens. France.

---

compana *Compositional Analysis of Habitat Use*

Description

compana performs a classical compositional analysis of habitat use (Aebischer et al., 1993).

Usage

```
compana(used, avail, test = c("randomisation", "parametric"),
        rnv = 0.01, nrep = 500, alpha = 0.1)
```

Arguments

used	a matrix or a data frame describing the percentage of use of habitats (in columns) by animals (in rows).
avail	a matrix or a data frame describing the percentage of availability of habitats (in columns) by animals (in rows).
test	a character string. If "randomisation", randomisation tests are performed for both the habitat ranking and the test of habitat selection. If "parametric", usual parametric tests are performed (chi-square for the test of habitat selection and t-tests for habitat ranking).
rnv	the number replacing the 0 values occurring in the matrix used.
nrep	the number of repetitions in the randomisation tests.
alpha	the alpha level for the tests.

Details

The compositional analysis of habitat use has been recommended by Aebischer et al. (1993) for the analysis of habitat selection by several animals, when the resources are defined by several categories (e.g. vegetation types).

This analysis is carried out in two steps: first the significance of habitat selection is tested (using a Wilks lambda). Then, a ranking matrix is built, indicating whether the habitat type in row is significantly used more or less than the habitat type in column. When this analysis is performed on radio-tracking data, Aebischer et al. recommend to study habitat selection at two levels: (i)

selection of the home range within the study area, and (ii) selection of the relocations within the home range. The first level is termed second-order habitat selection on Johnson's scale (1980), and the second one, third-order habitat selection.

When zero values are found in the matrix of used habitats, they are replaced by a small value (by default, 0.01), according to the recommendations of Aebischer et al. (1993).

When zero values are found in the matrix of available habitats, the function `compana` uses the procedure termed "weighted mean lambda" described in Aebischer et al. (1993: Appendix 2), instead of the usual lambda (see examples). Zero values can be found in the matrix of available habitats when the third-order habitat selection is under focus. In this case, it may occur that some habitat types are available to some animals and not to the others.

Note that this method rely on the following hypotheses: (i) independence between animals, and (ii) all animals are selecting habitat in the same way (in addition to "traditional" hypotheses in these kinds of studies: no territoriality, all animals having equal access to all available resource units, etc.). The function `eisera` can be used as a preliminary to identify whether this is indeed the case (see examples).

Value

Returns a list of the class `compana`:

`used`	the matrix of used habitats
`avail`	the matrix of available habitats
`type.test`	a character string. Either `"randomisation"` or `"parametric"`
`test`	the results of the test of habitat selection
`rm`	the ranking matrix: a square matrix with `nh` rows and `nh` columns, where `nh` is the number of habitat types under study. At the intersection of the row `i` and of the column `j`, there is a `"+"` when the habitat `i` is more used than the habitat in column, and `"-"` otherwise. When the difference is significant, the sign is tripled.
`rmnb`	the matrix containing the number of animals used to perform the tests in `rm`.
`rank`	the rank of the habitat types. It is equal to the number of `"+"` for each habitat type in row of `rm`.
`rmv`	the matrix of statistics used to build `rm`. If `(test = "parametric")`, the matrix contains the values of `t`, in the t-test comparing the row and the column habitat. If `(test = "randomisation")`, the matrix contains the mean difference between the used and available log-ratios (see Aebischer et al., 1993).
`profile`	the profile of preferences: resource types are sorted so that the left type is the most preferred and the right type is the most avoided. Habitats for which the intensity of habitat selection is similar (no significant difference) are connected by a line.

Note

In the examples below, the results differ from those published in Aebischer et al. (squirrel example, selection of the relocations within the home range). In fact, there has been a confusion in the column names in the paper. Actually, Aebischer (pers. com.) indicated that the ranking matrix given in this example is correct.

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Aebischer, N. J. and Robertson, P. A. (1992) Practical aspects of compositional analysis as applied to pheasant habitat utilisation. pp. 285–293 In: Priede, G. and Swift, S. M. *Wildlife telemetry, remote monitoring and tracking of animals*.

Aebischer, N. J., Robertson, P. A. and Kenward, R. E. (1993) Compositional analysis of habitat use from animal radiotracking data. *Ecology*, **74**, 1313–1325.

Johnson, D. H. (1980) The comparison of usage and availability measurements for evaluating resource preference. *Ecology*, **61**, 65–71.

See Also

eisera to perform an eigenanalysis of selection ratios, preliminary to the use of compositional analysis.

Examples

```
## The examples presented here
## are the same as those presented in
## the paper of Aebischer et al. (1993)


##############################
## Pheasant dataset: first
## example in Aebischer et al.

data(pheasant)

## Second order habitat selection
## Selection of home range within the
## study area (example of parametric test)
pheana2 <- compana(pheasant$mcp, pheasant$studyarea,
                   test = "parametric")
pheana2

## The ranking matrix:
print(pheana2$rm, quote = FALSE)

## Third order habitat selection
## (relocation within home range)
## We remove the first pheasant of the analysis
## (as in the paper of Aebischer et al.)
## before the analysis
pheana3 <- compana(pheasant$locs[-1,], pheasant$mcp[-1,c(1,2,4)])
pheana3

## The ranking matrix:
```

```
print(pheana3$rm, quote = FALSE)



############################
## Squirrel data set: second
## example in Aebischer et al.

data(squirrel)

## Second order habitat selection
## Selection of home range within the
## study area
squiana2 <- compana(squirrel$mcp, squirrel$studyarea)
squiana2

## The ranking matrix:
print(squiana2$rm, quote = FALSE)


## However, note that here, the hypothesis of identical use
## on which this analysis relies is likely to be false.
## Indeed, an eisera indicates:

us <- round(30 * squirrel$locs / 100)
av <- squirrel$studyarea
ii <- eisera(us, av, scannf = FALSE)
scatter(ii, grid = FALSE, clab = 0.7)

## There are clearly two groups of animals.  In such cases,
## compositional analysis is to be avoided in this case.




## Third order habitat selection
## (relocation within home range)
## We remove the second column
## (as in the paper of Aebischer et al.)
squiana3 <- compana(squirrel$locs[,-2], squirrel$mcp[,-2])
squiana3

## The ranking matrix:
print(squiana3$rm, quote = FALSE)
```

Description

domain uses the DOMAIN algorithm to estimate the potential distribution of a species based on a list of species occurrences and on maps of the area.

Usage

```
domain(x, pts, type = c("value", "potential"), thresh = 0.95)
```

Arguments

x	an object of class SpatialPixelsDataFrame
pts	a data frame giving the x and y coordinates of the species occurrences.
type	a character string. The "value" of the suitability may be returned or the "potential" area of distribution
thresh	if value = "potential", a threshold value should be supplied for the suitability (by default 0.95)

Details

This function implements the DOMAIN algorithm described in Carpenter et al. (1993).

Value

Returns an object of class SpatialPixelsDataFrame.

Warning

domain is restricted to maps containing only numerical variables (i.e. no factors).

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Carpenter, G., Gillison, A.N. and Winter, J. (1993) DOMAIN: a flexible modelling procedure for mapping potential distributions of plants and animals. *Biodiversity and conservation*, **2**, 667–680.

See Also

mahasuhab

Examples

```
## Preparation of the data
data(lynxjura)
map <- lynxjura$map
pts <- lynxjura$locs

## View of the data
image(map)
title(main="Elevation")
points(pts, pch = 3)

## Estimation of habitat suitability map
hsm <- domain(map, pts)

image(hsm, col = grey((1:256)/256))
contour(hsm, add = TRUE)

## Lighter areas are the most used areas

## Potential distribution
hsm <- domain(map, pts, type = "potential", thresh = 0.98)
image(hsm, col = "orange")
title(main = "Habitat suitability map")
points(pts, pch = 3)
```

---

dunnfa *Factorial Analysis of the Specialization in Habitat Selection Studies. Unpublished Work of James Dunn (University of Arkansas)*

Description

dunnfa performs a factorial decomposition of the Mahalanobis distances in habitat selection studies (see details).

Usage

```
dunnfa(dudi, pr, scannf = TRUE, nf = 2)
## S3 method for class 'dunnfa'
print(x, ...)
```

Arguments

dudi	an object of class pca
pr	a vector giving the utilization weights associated to each unit
scannf	logical. Whether the eigenvalues barplot should be displayed
nf	an integer indicating the number of kept axes
x	an object of class dunnfa
...	additional arguments to be passed to the function print

Details

This analysis is in essence very similar to the MADIFA (see ?madifa). The Mahalanobis distances are often used in the context of niche-environment studies (Clark et al. 1993, see the function mahasuhab). Each resource unit takes a value on a set of environmental variables. Each environmental variable defines a dimension in a multidimensionnal space, namely the ecological space. A set of points (resource units) describes what is available to the species. For each point, a "utilization weight" measures the intensity of use of the point by the species. The set of points for which the utilization weight is greater than zero defines the "niche". The Mahalanobis distance between any resource unit in this space (e.g. the point defined by the values of environmental variables in a pixel of a raster map) and the centroid of the niche (the distribution of used resource units) can be used to give a value of eccentricity to this point.

For a given distribution of available resource units, for which a measure of Mahalanobis distances is desired, the MADIFA (MAhalanobis DIstances Factor Analysis) partitions the ecological space into a set of axes, so that the first axes maximises the average proportion of their squared Mahalanobis distances. James Dunn (formerly University of Arkansas) proposed the analysis programmed in the function dunnfa, as an alternative to the MADIFA (unpublished results). This analysis is closely related to both the ENFA (Ecological niche factor analysis, Hirzel et al. 2002) and the MADIFA.

The analysis proposed by James Dunn searches, in the multidimensional space defined by environmental variables, synthesis variables which maximise the ratio (variance of the scores of available resource units) / (variance of the scores of used resource units). This ratio is sometimes called "specialization" in the ecological literature (Hirzel et al. 2002). It is therefore very similar to the ENFA (which also maximises the specialization), except that the factorial axes returned by this analysis are not required to be *orthogonal to the marginality axis*.

James Dunn demonstrated that this analysis also partitions the Mahalanobis distances into uncorrelated axes, which makes it similar to the MADIFA (the difference is that the MADIFA maximises the mean squared Mahalanobis distances on the first axes, whereas the DUNNFA maximises the specialization on the first axes). Therefore, as for the MADIFA, the DUNNFA can be used to build reduced rank habitat suitability map.

Note that although this analysis could theoretically be used with all kinds of variables, it it currently implemented only for numeric variables.

Value

dunnfa returns a list of class dunnfa containing the following components:

call	original call.
tab	a data frame with n rows and p columns (original data frame centered by column for the uniform weighting).
pr	a vector of length n containing the number of points in each pixel of the map.
nf	the number of kept axes.
eig	a vector with all the eigenvalues of the analysis.
liA	row coordinates (centering on the centroid of the cloud of available points), data frame with n rows and nf columns.
liU	row coordinates (centering on the centroid of the cloud of available points), data frame with p rows and nf columns.

mahasu	a vector of length n containing the reduced-rank squared Mahalanobis distances for the n units.
co	column (environmental variables) coordinates, a data frame with p rows and nf columns
cor	the correlation between the DUNNFA axes and the original variable

Note

This analysis was developed by James Dunn during an e-mail discussion on the MADIFA, and is still unpublished work. Implemented in adehabitatHS with his autorization.

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Clark, J.D., Dunn, J.E. and Smith, K.G. (1993) A multivariate model of female black bear habitat use for a geographic information system. *Journal of Wildlife Management*, **57**, 519–526.

Hirzel, A.H., Hausser, J., Chessel, D. & Perrin, N. (2002) Ecological-niche factor analysis: How to compute habitat-suitability maps without absence data? *Ecology*, **83**, 2027–2036.

Calenge, C., Darmon, G., Basille, M., Loison, A. and Jullien J.M. (2008) The factorial decomposition of the Mahalanobis distances in habitat selection studies. *Ecology*, **89**, 555–566.

See Also

madifa, enfa and gnesfa for related methods. mahasuhab for details about the Mahalanobis distances.

Examples

```
## Not run:
data(bauges)

map <- bauges$map
locs <- bauges$loc

## We prepare the data for the analysis
tab <- slot(map, "data")
pr <- slot(count.points(locs, map), "data")[,1]

## We then perform the PCA before the analysis
pc <- dudi.pca(tab, scannf = FALSE)
(dun <- dunnfa(pc, pr, nf=2,
               scannf = FALSE))

## We should keep one axis:
barplot(dun$eig)
```

```
## The correlation of the variables with the first two axes:
s.arrow(dun$cor)

## A factorial map of the niche (centering on the available points)
scatterniche(dun$liA, dun$pr, pts=TRUE)

## a map of the reduced rank Mahalanobis distances
## (here, with one axis)
dun2 <- dunnfa(pc, pr, nf=1,
              scannf = FALSE)
df <- data.frame(MD=dun2$mahasu)
coordinates(df) <- coordinates(map)
gridded(df) <- TRUE
image(df)


## Compute the specialization on the row scores of
## the analysis:
apply(dun$liA, 2, function(x) {
   varav <- sum((x - mean(x))^2) / length(x)
   meanus <- sum(dun$pr*x)/sum(dun$pr)
   varus <- sum(dun$pr * (x - meanus )^2)/sum(dun$pr)
   return(varav/varus)
})
## The eigenvalues:
dun$eig


## End(Not run)
```

`eisera` *Eigenanalysis of Selection Ratios*

Description

Performs an eigenanalysis of selection ratios.

Usage

```
eisera(used, available, scannf = TRUE, nf = 2)
## S3 method for class 'esr'
print(x, ...)
## S3 method for class 'esr'
scatter(x, xax = 1, yax = 2,
            csub = 1, possub = "bottomleft", ...)
```

Arguments

used	a data frame containing the *number* of relocations of each animal (rows) in each habitat type (columns)
available	a data frame containing the *proportion* of availability of each habitat type (columns) to each animal (rows)
scannf	logical. Whether the eigenvalues bar plot should be displayed
nf	if scannf = FALSE, an integer indicating the number of kept axes
x	an object of class esr
xax	the column number for the x-axis
yax	the column number for the y-axis
csub	a character size for the legend, used with par("cex")*csub
possub	a string of characters indicating the sub-title position ("topleft", "topright", "bottomleft", "bottomright")
...	further arguments passed to or from other methods

Details

The eigenanalysis of selection ratios has been developped to explore habitat selection by animals monitored using radio-tracking, when habitat is defined by several categories (e.g. several vegetation types, see Calenge and Dufour 2006).

This analysis can be used for both designs II (same availability for all animals, e.g. selection of the home range within the study area) and designs III (different availability, e.g. selection of the sites within the home range). In the latter case, when some available proportions are equal to zero, the selection ratios are replaced by their expectation under random habitat use, following the recommendations of Calenge and Dufour (2006).

Value

A list of class esr and dudi containing also:

available	available proportions
used	number of relocations
wij	selection ratios

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Calenge, C. and Dufour, A.B. (2006) Eigenanalysis of selection ratios from animal radio-tracking data. *Ecology*. **87**, 2349–2355.

See Also

wi for further information about the selection ratios, compana for compositional analysis.

Examples

```
############################################################
############################################################
###
###  Example given in Calenge and Dufour 2006 (design II)


data(squirrel)

## computation of the number of relocations in each habitat type
## from the data given by Aebischer et al. (1993).
## squirrel$locs give the percentage of relocations in each habitat
## type, and Aebischer et al. (1993) indicate that there are 30
## relocations per animal.
## We therefore compute the number of relocations in each habitat type
## using:
us <- round(30 * squirrel$locs / 100)

## Habitat availability
av <- squirrel$studyarea

## Eigenanalysis of selection ratios
ii <- eisera(us, av, scannf = FALSE)

scatter(ii, grid = FALSE, clab = 0.7)


## The following graph may help the interpretation
## (see Calenge and Dufour 2006)
data(squirreloc)
locs <- squirreloc$locs
are <- squirreloc$map

ind <- levels(slot(locs, "data")$id)
opar <- par(mfrow=n2mfrow(length(ind)), mar=c(0,0,2,0))

tmp <- lapply(1:length(ind), function(i) {
     plot(are, col = as.data.frame(are)[,2])
     title(main = ind[i])
     points(locs[slot(locs, "data")[,1]==ind[i],], pch=16, cex=1.5)
box()
})
plot(0,0, axes=FALSE, ty="n", xlim=c(-1,1), asp=1)
legend(-0.8,0.8, unique(slot(are,"data")[,1]),
       fill=unique(slot(are,"data")[,2]))
par(opar)
```

```
############################################################
############################################################
###
###  Example of design III

iii <- eisera(us, squirrel$mcp, scannf = FALSE)
scatter(iii, grid = FALSE, clab = 0.7)
```

---

enfa *Ecological Niche Factor Analysis*

Description

enfa performs an Ecological Niche Factor Analysis. hist.enfa draws histograms of the row scores or of the initial variables of the ENFA.

Usage

```
enfa(dudi, pr, scannf = TRUE, nf = 1)
## S3 method for class 'enfa'
hist(x, scores = TRUE, type = c("h", "l"), adjust = 1,
                    Acol, Ucol, Aborder, Uborder, Alwd = 1, Ulwd = 1, ...)
```

Arguments

dudi	a duality diagram, object of class dudi (see Details)
pr	a vector giving the utilization weights associated to each unit
scannf	logical. Whether the eigenvalues barplot should be displayed
nf	an integer indicating the number of kept specialization axes
x	an object of class enfa
scores	logical. If TRUE, the histograms display the row scores of the ENFA. If FALSE, they display the niche on the environmental variables (in this case, this is equivalent to histniche)
type	what type of plot should be drawn. Possible types are: "h" for histograms, "l" for kernel density estimates (see ?density). By default, type = "h" is used. If type = "l" is used, the position of the mean of each distribution is indicated by dotted lines
adjust	if type = "l", a parameter used to control the bandwidth of the density estimates (see ?density)
Acol	if type = "h", a color to be used to fill the histogram of the available pixels. if type = "l", a color to be used for the kernel density estimates of the available pixels

Ucol	if type = "h", a color to be used to fill the histogram of the used pixels. if type = "l", a color to be used for the kernel density estimates of the used pixels
Aborder	color for the border of the histograms of the available pixels
Uborder	color for the border of the histograms of the used pixels
Alwd	if type = "l", the line width of the kernel density estimates of the available pixels
Ulwd	if type = "l", the line width of the kernel density estimates of the used pixels
...	further arguments passed to or from other methods

Details

The niche concept, as defined by Hutchinson (1957), considers the ecological niche of a species as an hypervolume in the multidimensional space defined by environmental variables, within which the populations of a species can persist. The Ecological Niche Factor Analysis (ENFA) has been developped by Hirzel et al. (2002) to analyse the position of the niche in the ecological space. Nicolas Perrin (1984) described the position of the niche in the n-dimensional space using two measures: the M-specialization (hereafter termed marginality) and the S-specialization (hereafter termed specialization). The marginality represents the squared distance of the niche barycentre from the mean available habitat. A large specialization corresponds to a narrow niche relative to the habitat conditions available to the species.

The ENFA first extracts an axis of marginality (vector from the average of available habitat conditions to the average used habitat conditions). Then the analysis extracts successives orthogonal axes (i.e. uncorrelated), which maximises the specialization of the species. The calculations used in the function are described in Hirzel et al. (2002).

The function enfa can be used on both quantitative variables and qualitative variables (though the interpretation of the results of the ENFA for qualitative variables is still under research), provided that the table containing the values of habitat variables (columns) for each resource unit (rows) is correctly transformed (e.g. column-centered and standardised for tables containing only quantitative variables), and that appropriate column weights are given (e.g. the sum of the weights for the levels of a factor should be the same as the weight of one quantitative variable). Therefore, the function enfa requires that a preliminary multivariate analysis is performed on the table (using analysis of the family of duality diagram, e.g. principal component analysis or Hill and Smith analysis). The object returned by this preliminary analysis contains the appropriate weights and transformation of the original data frame. For example, the function dudi.mix can be used first on the data.frame containing the value of both quantitative (e.g. slope, elevation) and qualitative habitat variables (e.g. vegetation) for each pixel of a raster map. The result of this analysis can then be passed as argument to the function enfa (see examples below).

Value

enfa returns a list of class enfa containing the following components:

call	original call.
tab	a data frame with n rows and p columns.
pr	a vector of length n containing the number of points in each pixel of the map.

nf	the number of kept specialization axes.
m	the marginality (squared length of the marginality vector).
s	a vector with all the eigenvalues of the analysis.
lw	row weights, a vector with n components.
li	row coordinates, data frame with n rows and nf columns.
cw	column weights, a vector with p components.
co	column coordinates, data frame with p rows and nf columns.
mar	coordinates of the marginality vector.

Author(s)

Mathieu Basille <basille@ase-research.org>

References

Hutchinson, G.E. (1957) Concluding Remarks. *Cold Spring Harbor Symposium on Quantitative Biology*, **22**: 415–427.

Perrin, N. (1984) Contribution a l'ecologie du genre Cepaea (Gastropoda) : Approche descriptive et experimentale de l'habitat et de la niche ecologique. These de Doctorat. Universite de Lausanne, Lausanne.

Hirzel, A.H., Hausser, J., Chessel, D. and Perrin, N. (2002) Ecological-niche factor analysis: How to compute habitat-suitability maps without absence data? *Ecology*, **83**, 2027–2036.

Basille, M., Calenge, C., Marboutin, E., Andersen, R. and Gaillard, J.M. (2008) Assessing habitat selection using multivariate statistics: Some refinements of the ecological-niche factor analysis. *Ecological Modelling*, **211**, 233–240.

See Also

niche, kselect for other types of analysis of the niche, when several species are under studies, and scatter.enfa to have a graphical display of objects of class enfa. See madifa for another factorial analysis of the ecological niche.

Examples

```
data(lynxjura)

map <- lynxjura$map

## We keep only "wild" indices.
locs <- lynxjura$locs
locs <- locs[slot(locs, "data")[,2]!="D",]

hist(map, type = "l")
## The variable artif is far from symetric

## We perform a square root transformation
## of this variable
```

```
## We therefore normalize the variable 'artif'
slot(map,"data")[,4] <- sqrt(slot(map,"data")[,4])
hist(map, type = "l")

## We prepare the data for the ENFA
tab <- slot(map, "data")
pr <- slot(count.points(locs, map), "data")[,1]


## We then perform the PCA before the ENFA
pc <- dudi.pca(tab, scannf = FALSE)

## The object 'pc' contains the transformed table (i.e.
## centered so that all columns have a mean of 0
## and scaled so that all columns have a variance of 1
## 'pc' also contains the weights of the habitat variables,
## and the weights of the pixels in the analysis

(enfa1 <- enfa(pc, pr,
               scannf = FALSE))
hist(enfa1)
hist(enfa1, scores = FALSE, type = "l")


## scatterplot
scatter(enfa1)


## randomization test
## Not run:
(renfa <- randtest(enfa1))
plot(renfa)

## End(Not run)
```

---

engen2008II *Measuring Habitat Selection Using the Method of Engen et al. (2008)*

Description

These functions implements the method described by Engen et al. to measure the preference of animals for habitat variables in habitat selection studies.

Usage

```
engen2008II(us, av, id, nsim = 500, nsimra = 500)

engen2008I(us, av, nsimra=500)
```

```
## S3 method for class 'engenetalI'
print(x, ...)

## S3 method for class 'engenetalII'
print(x, ...)
```

Arguments

us	a data frame containing the value of numeric habitat variables (columns) in each site (rows) used by the animals.
av	a data frame containing the value of numeric habitat variables (columns) in each site (rows) available to the animals.
id	a factor with as many elements as there are rows in us, indicating the ID of the animal that used the corresponding rows in us.
nsim	the number of randomizations used in the calculation of the total variance.
nsimra	the number of random allocation of ranks used in the calculation of the normal score (see details).
x	an object of class engenetalI or engenetalII
...	additional arguments to be passed to other functions (currently unused)

Details

Engen et al. (2008) proposed an original approach to measure the preference of animals for values of each particular variable of a multivariate set of environmental variables. Their approach was originally developed for the case where there is a sample of used site is for each animal in a sample of identified animals (e.g. using radiotelemetry or GPS), with several sites per animal (i.e., design II according to the classification of Thomas and Taylor, 1990). However, we extended this approach to also include the case where habitat use is described by a sample of used site, with one site per unidentified animal (i.e., design I).

The original approach is the following: first, a normal score transformation of each habitat variable is performed: for each variable, the empirical cumulative distribution is computed, by dividing the rank of the value of each available site by the number of observations. Note that the ties are ranked randomly. Then, the inverse of the standard normal integral (see ?qnorm) of the cumulative distribution function is computed for all available sites: this results into a perfectly normal distribution of the habitat variables for the available sites. Then, the value of the cumulative distribution – estimated from the available sites – is computed for each used site. Then, the inverse of the standard normal integral is computed for each one.

Engen et al. (2008) suppose the following model describing how habitat use results from habitat availability. Let

$$Z_{ij}$$

be the value of a given habitat variable (transformed according to the normal score) for the j-th site used by the i-th animal. Then this value can be described by the model:

$$Z_{ij} = \mu + U_i + V_{ij}$$

where

$$\mu$$

is the preference for the habitat variable (0 indicates a non-preference),

$$U_i$$

and

$$V_{ij}$$

are normal distributions with means equal to zero and variances equal to

$$\sigma^2$$

and

$$\tau^2$$

respectively. Engen et al. give fomula for the estimation of these parameters. Their estimation is done by first estimating the total variance

$$\sigma^2 + \tau^2$$

(this variance is estimated by sampling randomly one observation per animal – the parameter `nsim` controls the number of samples used in this computation; see Engen et al. 2008). Note that the correlation between the value observed for two used units sampled from all the units used by a given animal is

$$\rho = \sigma^2/(\sigma^2 + \tau^2)$$

. A large value of rho indicates a large variation in the habitat used between animals (or a small within-animal variation). The main parameter of concern is here the preference. The function `engen2008II` allows to estimate these parameters.

The function `engen2008I` extends this model for design I studies (a sample of used sites and a sample of available sites, animals not identified), by considering the following model for these studies:

$$Z_{ij} = \mu + V_{ij}$$

where

$$\mu$$

is the preference for the habitat variable (0 indicates a non-preference), and

$$V_{ij}$$

are normal distributions with means equal to zero and variances equal to

$$\sigma^2$$

.

Note that the habitat variables may be correlated on the study area. In this case, observed preference for a given variable may be an artefact of other variables prefered by animals. Supposing that the data.frame containing the

$$Z_{ij}$$

's is a realization of a multivariate normal distribution, we can compute, for each habitat variable and each used site, the *conditional* mean

$$m_{ij}$$

and *conditional* standard deviation

$$s_{ij}$$

of this variable at this site, *given* the values of the other habitat variables at this site (this is done using the algorithm described by Ripley, 1987, p.98). We then compute the standardized values

$$P_{ij} = (Z_{ij} - m_{ij})/s_{ij}$$

. The preference is then computed using these standardized values.

Because there may be ties in the distribution of values of habitat variables, the results may vary depending on the random order chosen for ties when computing the normal scores. Engen et al. recommended to repeat the function a large number of times, and to use the mean values as estimates of the parameters. This is what the function does, and the number of randomization is controlled by the parameter `nsimra`.

Note that all these methods rely on the following hypotheses: (i) independence between animals, (ii) independence between sites, and (iii) all animals are selecting habitat in the same way (in addition to "traditional" hypotheses in these kinds of studies: no territoriality, all animals having equal access to all available resource units, etc., see Manly et al. 2002 for further details).

That the examples below provide an illustration and discussion of interesting and (at first sight) surprising properties of this method.

Value

`engen2008I` returns a list of class `engenetalI`, and `engen2008II` returns a list of class `engenetalII`. Both types of list contain two elements:

`raw`	this is a list containing one data frame per habitat variable, containing the value of the correlation rho (for `engenetalII` objects), mean preferences and standard error of these preferences (columns) for each randomization performed (rows);
`results`	a data frame containing the mean values over all the randomizations, of these parameters (columns) for each habitat variable (rows).

Note

Be patient! these functions can be very long (depending on the number of sites and on the value of `simra`)

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Engen, S., Grotan, V., Halley, D. and Nygard, T. (2008) An efficient multivariate approach for estimating preference when individual observations are dependent. *Journal of Animal Ecology*, **77**: 958–965.

Thomas, D. and Taylor, E. (1990) Study designs and tests for comparing resource use and availability. *Journal of Wildlife Management*, **54**, 322–330.

Ripley, B. (1987) Stochastic Simulation. John Wiley and Sons.

See Also

niche, madifa, gnesfa for another approach to tackle the study of habitat selection. For categorical variables, see kselect

Examples

```
## Not run:

#################################
#################################
#################################

## Practical use of engen2008II

data(puechabonsp)
map <- puechabonsp$map

## Removes the aspect (no factor allowed in the function)
slot(map,"data")$Aspect <- NULL

## engen2008II:
avail <- slot(map, "data")
use <- join(puechabonsp$relocs, map)
id <- slot(puechabonsp$relocs, "data")$Name

## This function can be very long:
engen2008II(use, avail, id, nsimra=10)




## Practical use of engen2008I

data(lynxjura)
ma <- lynxjura$map
lo <- lynxjura$locs
av <- slot(ma, "data")
us <- join(lo, ma)
us <- us[!is.na(us[,1]),]

## Idem, be patient here:
engen2008I(us, av, nsimra=10)
```

```
#################################
#################################
#################################
##
##  For a deeper discussion on
##  this method... a simulation:



#################################
##
## First, simulation of a dataset
## copy and paste this part into R,
## but skip the reading of the
## comments if you are not interested
## into this simulation

## simulate the available points

suppressWarnings(RNGversion("3.5.0"))
set.seed(235)
av <- cbind(rnorm(1000, mean=0, sd=3), rnorm(1000, mean=0, sd=0.5))
tt <- cbind(c(cos(-pi/4),sin(-pi/4)),c(cos(pi/4), sin(pi/4)))
av <- as.data.frame(as.matrix(av)%*%tt)

## simulate the used points: we simulate a selection on the first
## principal component of the PCA of the data.frame describing the
## availability. In other words, we simulate the case where the
## habitat selection occurs on the "common part" of the two habitat
## variable (no preference for one particular variable).

us <- do.call("rbind", lapply(1:5, function(i) {
    us1 <- cbind(rnorm(30, mean=rnorm(1, -4, 1), sd=0.5),
                 rnorm(30, mean=rnorm(1, 0, 0.5), sd=0.2))

    return(us1%*%tt)
}))
colnames(us) <- colnames(av) <- c("var1", "var2")
id <- gl(5,30)


#################################
##
## Study of the habitat selection on these data
## The data are:
## - us: a matrix containing the used sites for two
##       habitat variables
## - av: a matrix containing the available sites for two
##       habitat variables
```

```
## - id: a vector containing the id of 5 animals

## First illustrate the use and availability of the two variables:

plot(av, xlab="Habitat variable 1", ylab="Habitat variable 2",
     col="grey", pch=16)
lius <- split(as.data.frame(us), id)
junk <- lapply(1:5, function(i) points(lius[[i]], pch=16, col=i))

## -----> ***It is very clear that there is a selection***:
## the animals select the low values of both habitat variables.
## (this is what we actually simulated)


## Now perform the method of Engen et al. (2008):
engen2008II(us, av, id)


## Surprisingly, the method seems to fail to identify the clear
## habitat selection identified graphically...
##
## In fact, it does not fail:
## this method identifies the part of habitat selection that is clearly
## attributable to a given variable.  Here the animals select the
## the common factor expressed in the two variables, and it is impossible
## to identify whether the selection is due only to the variable 1 or to
## the variable 2: it is caused by both variable simultaneously.
## Once the selection on the variable 2 (including the common part)
## has been removed, there is no longer appearant selection on
## variable 1.  Once the selection caused by the variable 1
## (including the common part) has been removed, there is no
## longer selection on variable 2...
##
## For this reason, Engen et al. recommended to use this method
## concurrently with other factor analyses of the habitat selection
## such as madifa, kselect, niche (in ade4 package), etc.
##
## Note also the strong correlation between the value of two random
## points used by a given animal. This indicates a strong variability
## among animals...




## End(Not run)
```

---

gnesfa *General Niche-Environment System Factor Analysis*

Description

The function gnesfa allows to perform a general niche-environment system factor analysis.

Usage

```
gnesfa(dudi, Focus, Reference,
       centering = c("single", "twice"),
       scannf = TRUE, nfFirst = 2, nfLast = 0)
## S3 method for class 'gnesfa'
print(x, ...)
```

Arguments

dudi	an object of class dudi
Focus	a vector containing the focus weights
Reference	a vector containing the reference weights
centering	a character string indicating the type of centering (see details)
scannf	a logical value indicating whether the eigenvalues bar plot should be displayed
nfFirst	the number of first axes to be kept
nfLast	the number of last axes to be kept
x	an object of class GNESFA
...	further arguments to be passed to other functions

Details

The GNESFA is an algorithm which generalises several factor analyses of the ecological niche. A table X gives the values of P environmental variables in N resource units (e.g. the pixels of a raster map). A distribution of weights D describes the availability of the resource units to the species (if not specified, these weights are considered to be uniform). Another distribution of weights Dp describes the use of the resource units by the species (for example the proportion of relocations in each pixel of a raster map).

Each environmental variable defines a dimension in a multidimensional space, the ecological space. The N resource units define a cloud of points in this space. Each point is associated to two weights. The GNESFA finds, in the ecological space, the directions on which these two distributions of weights are the most different.

The GNESFA relies on a choice of the analyst, followed by three steps. Before all, the analyst has to choose one distribution of weights as the Reference distribution, and the other one as the Focus distribution; (i) The first table X is centred on the centroid of the Reference distribution; (ii) a principal component analysis of this Reference distribution is performed; (iii) the cloud of points is distorted, so that the Reference distribution takes a standard spherical shape; (iv) a non centred principal component analysis of the Focus distribution allows to identify the directions of the ecological space where the two distributions are the most different.

Depending on the distribution chosen as Reference, this algorithm returns results with different meanings (see examples). This algorithm is closely related to several common analyses of habitat

selection/niche (ENFA, MADIFA, Mahalanobis distances, selection ratios, etc.). The examples below give some examples of the mathematical properties of this algorithm.

Note that the function takes a parameter named `centering`. Indeed, two types of centering can be performed prior to the GNESFA. The choice `"single"` consists in the centering of the cloud of point in the ecological space on the centroid of the Reference distribution. The choice `"twice"` consist to center the cloud of points on both the centroid of the Reference distribution and the centroid of the Focus distribution. This is done by projecting the cloud of points on the hyperplane orthogonal to the marginality vector (the vector connecting the two centroids. If this choice is done, the GNESFA is identical to the commonly used Ecological Niche Factor Analysis (see examples).

Value

`gnesfa` returns a list of class `gnesfa` containing the following components:

`call`	original call.
`centering`	The type of centering required.
`tab`	a data frame with n rows and p columns.
`Reference`	a vector of length n containing the Reference weights.
`Focus`	a vector of length n containing the Focus weights.
`nfFirst`	the number of kept first axes.
`nfLast`	the number of kept last axes.
`eig`	a vector with all the eigenvalues of the analysis.
`li`	row coordinates, data frame with n rows and nf columns.
`l1`	row normed coordinates, data frame with n rows and nf columns.
`co`	column scores, data frame with p rows and nf columns.
`cor`	the correlation between the GNESFA axes and the original variables

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Calenge, C. and Basille, M. (2008) A General Framework for the Statistical Exploration of the Ecological Niche. *Journal of Theoretical Biology*, **252**: 674-685.

Calenge, C., Darmon, G., Basille, M., Loison, A. and Jullien, J.M. (2008) The factorial decomposition of the Mahalanobis distances in habitat selection studies. *Ecology*, **89**, 555-566.

See Also

`madifa`, `mahasuhab`, `enfa`, `wi` for closely related methods (see Examples)

Examples

```
## Not run:

#################################################################
##
## Study of the habitat selection by the chamois in the French
## mountains of Les Bauges


## Loads the data
data(bauges)
names(bauges)
map <- bauges$map
locs <- bauges$locs


## displays the data
mimage(map)
image(map,1)
points(locs, pch = 3)


## Prepares the data for the GNESFA:
tab <- slot(map, "data")
Dp <- slot(count.points(locs,map), "data")[,1]
pc <- dudi.pca(tab, scannf = FALSE)


## Example of use with Dp = Reference
gn <- gnesfa(pc, Reference = Dp, scannf=FALSE)

## One main axis:
barplot(gn$eig)

## The correlation with variables indicate that
## the elevation, the proximity to grass and to
## deciduous forests:
s.arrow(gn$cor)

## The factorial map of the niche...
scatterniche(gn$li, Dp, pts = TRUE)

## The chamois is rather located at high elevation,
## in the grass, far from deciduous forests




#############################################################
#############################################################
##
##
```

```
##       Some interesting properties of the GNESFA
##
##
############################################################
############################################################



################################
################################
##
## Interesting properties of the
## choice: Dp as Reference
## identical to the MADIFA
## (Calenge et al. 2008),
## See the help page of the function madifa
## for other properties)

gn <- gnesfa(pc, Reference = Dp, scannf=FALSE,
             nfFirst = 7)
gn

## This is the same as the MADIFA:
mad <- madifa(pc, Dp, scannf=FALSE)

## Indeed:
plot(gn$li[,1], mad$li[,1])
cor(gn$li[,1], mad$li[,1])


## And consequently the sum of the squared scores,
## On the axes of the GNESFA...
su <- apply(gn$l1,1,function(x) sum(x^2))


## ... is equal to the Mahalanobis distances between
## the points and the centroid of the niche
## (Clark et al. 1993, see the help page of mahasuhab)

su2 <- slot(mahasuhab(map, locs), "data")[,1]


## Indeed:
all(su - su2 < 1e-7)
plot(su, su2)



################################
################################
##
## Centering twice is identical to
```

```
## the ENFA (Hirzel et al. 2002, see the help
## page of the function enfa)...


#######
##
## ... If Dp is the Reference:

gn <- gnesfa(pc, Reference = Dp, center = "twice", scannf = FALSE)
gn

enf <- enfa(pc, Dp, scannf = FALSE)
plot(enf$li[,2], gn$li[,1])
cor(enf$li[,2], gn$li[,1])

## The first specialization axis of the ENFA
## is the first axis of the GNESFA!


#######
##
## ... If Dp is the Focus:

gn <- gnesfa(pc, Focus = Dp, center = "twice",
             scannf = FALSE, nfFirst = 6)
plot(enf$li[,2], gn$li[,6])
cor(enf$li[,2], gn$li[,6])

## The first specialization axis of the ENFA
## is the last axis of the GNESFA!


#######
##
## Whatever the distribution chosen as Reference,
## projecting the cloud of points on the hyperplane
## orthogonal to the marginality axis, and performing
## a GNESFA in this subspace is identical to an ENFA!


## The marginality axis of the ENFA is identical
## to the component "projmar" of the GNESFA

plot(enf$li[,1],gn$projmar)
cor(enf$li[,1],gn$projmar)




################################
################################
##
## Interesting properties of the
```

```
## case: Dp as Focus, one categorical
## variable. Relationships with the selection
## ratios of Manly et al. (1972, see the
## help page of wi)


## For example, take the Elevation, and
## define a factor with 4 levels
elev <- data.frame(el = cut(slot(map, "data")$Elevation, 4))

## Now, compute the complete disjonctive table
dis <- acm.disjonctif(elev)
head(dis)

## Now perform the GNESFA with Dp as Focus:
pc <- dudi.pca(dis, scannf = FALSE)
gn <- gnesfa(pc, Dp, scannf = FALSE, nfFirst = 3)


#######
##
## This analysis is closely related to the concept of
## selection ratios

## Compute the percentage of use of each level:
us <- apply(dis, 2, function(x) sum(x*Dp)/sum(Dp))
av <- apply(dis, 2, function(x) sum(x)/length(x))

## The selection ratios
wi <- widesI(us, av)$wi

## Compute the sum of the eigenvalue
sum(gn$eig)

## Compute the sum of the selection ratios - 1
sum(wi) - 1

## In other words, when the GNESFA (Dp as Focus) is
## applied on only one categorical variable, this
## analysis finds a set of axes which partition the
## sum of the selection ratios so that it is maximum
## on the first axes!!



## End(Not run)
```

---

histniche *Histograms of the Ecological Niche*

Description

histniche draws histograms of the niche-environment system: an histogram of the available resource units (environment) is drawn on the same graph as an histogram of the used resource units (i.e. the niche), for comparison.

Usage

```
histniche(x, pr, type = c("h", "l"), adjust = 1,
          Acol, Ucol, Aborder, Uborder, Alwd = 1,
          Ulwd = 1, ylim, ncla = 15, ...)
```

Arguments

x	a data frame giving the value of environmental variables (columns) in resource units (rows, e.g. the pixels of a raster map)
pr	a vector of integers with the same length as nrow(x) (giving for example the number of detections in the pixels)
type	what type of plot should be drawn. Possible types are: * "h" for histograms, * "l" for kernel density estimates (see ?density). By default, type = "h" is used. If type = "l" is used, the position of the mean of each distribution is indicated by dotted lines
adjust	if type = "l", a parameter used to control the bandwidth of the density estimate (see ?density)
Acol	color for the histograms of the available pixels
Ucol	color for the histograms of the used pixels
Aborder	if type = "h", color for the border of the histograms of the available pixels (see help(hist.default))
Uborder	if type = "h", color for the border of the histograms of the used pixels (see help(hist.default))
Alwd	if type = "l", line width for the density estimate of the available pixels
Ulwd	if type = "l", line width for the density estimate of the used pixels
ylim	the limits for the y axis
ncla	The number of classes of the histogram
...	further arguments passed to or from other methods

Author(s)

Mathieu Basille <basille@ase-research.org>

Examples

```
## Not run:

data(puechabonsp)
```

```
cp <- count.points(puechabonsp$relocs, puechabonsp$map)
puechabonsp$map

histniche(slot(puechabonsp$map, "data"), slot(cp, "data")[,1])
histniche(slot(puechabonsp$map, "data"), slot(cp, "data")[,1],
          ty="l")


## End(Not run)
```

---

kselect *K-Select Analysis: a Method to Analyse the Habitat Selection by Animals*

Description

Performs a multivariate analysis of ecological data (K-select analysis).

Usage

```
kselect(dudi, factor, weight, scannf = TRUE, nf = 2, ewa = FALSE)
## S3 method for class 'kselect'
print(x, ...)
## S3 method for class 'kselect'
kplot(object, xax = 1, yax = 2, csub = 2, possub = c("topleft",
              "bottomleft", "bottomright", "topright"),
              addval = TRUE, cpoint = 1, csize = 1, clegend = 2, ...)
## S3 method for class 'kselect'
hist(x, xax = 1, mar=c(0.1,0.1,0.1,0.1),
             ncell=TRUE, csub=2,
             possub=c("bottomleft", "topleft",
                      "bottomright", "topright"),
             ncla=15, ...)
## S3 method for class 'kselect'
plot(x, xax = 1, yax = 2, ...)
prepksel(sa, hr, locs)
```

Arguments

dudi	an object of class dudi
factor	a factor with the same length as nrow(dudi$tab)
weight	a numeric vector of integer values giving the weight associated to the rows of dudi$tab
scannf	logical. Whether the eigenvalues bar plot should be displayed
nf	if scannf = FALSE, an integer indicating the number of kept axes

ewa	logical. If TRUE, uniform weights are given to all animals in the analysis. If FALSE, animal weights are given by the proportion of relocations of each animal (i.e. an animal with 10 relocations has a weight 10 times lower than an animal with 100 relocations)
x, object	an object of class kselect
xax	the column number for the x-axis
yax	the column number for the y-axis
addval	logical. If TRUE, the frequency of the relocations per animal is displayed (see examples)
cpoint	the size of the points (if 0, the points where no relocations are found are not displayed)
mar	the margin parameter (see help(par))
ncell	logical. If TRUE, the histogram shows the distribution of the cells of the raster map where at least one relocation is found. If FALSE, the histogram shows the distribution of the relocations
csub	the character size for the legend, used with par("cex")*csub
csize	the size coefficient for the points
clegend	the character size for the legend used by par("cex")*clegend
possub	a character string indicating the sub-title position ("topleft", "topright", "bottomleft", "bottomright")
ncla	the number of classes of the histograms
sa	an object of class SpatialPixelsDataFrame containing the values of the environmental variables on the study area
hr	an object of class SpatialPixelsDataFrame with the same number of rows as sa, for which the pixels contain 1 inside the home ranges of the animals (one animal per column) and NA otherwise
locs	an object of class SpatialPixelsDataFrame with the same dimensions as hr, containing the number of relocations of the animals (columns) in each pixel of sa (rows)
...	additional arguments to be passed to the generic function histniche, print or, in the case of plot.kselect, s.distri

Details

The K-select analysis is intended for hindcasting studies of habitat selection by animals using radio-tracking data. Each habitat variable defines one dimension in the ecological space. For each animal, the difference between the vector of average available habitat conditions and the vector of average used conditions defines the marginality vector. Its size is proportional to the importance of habitat selection, and its direction indicates which variables are selected. By performing a non-centered principal component analysis of the table containing the coordinates of the marginality vectors of each animal (row) on the habitat variables (column), the K-select analysis returns a linear combination of habitat variables for which the average marginality is greatest. It is a synthesis of variables which contributes the most to the habitat selection. As with principal component analysis, the biological significance of the factorial axes is deduced from the loading of variables.

prepksel allows to prepare the data for the kselect analysis (see examples).

plot.kselect returns a summary of the analysis: it displays (i) a graph of the correlations between the principal axes of the PCA of the objects of class dudi passed as argument and the factorial axes of the K-select analysis; (ii) a graph giving the scores of the habitat variables on the factorial axes of the K-select analysis; (iii) the barplot of the eigenvalues of the analysis (each eigenvalue measure the mean marginality explained by the axis; (iv) the projection of the non-recentred marginality vectors on the factorial plane (the origin of the arrow indicates the average available habitat conditions, and the end of the arrow indicates the average used conditions); (v) the projection of the resource units available to each animal on the first factorial plane and (vi) the coordinates of the recentred marginality vectors (i.e. recentred so that they have a common origin) on the first factorial plane.

kplot.kselect returns one graph per animal showing the projections of the available resource units on the factorial plane, as well as their use by the animal. hist.kselect does the same thing, but on one dimension instead of two.

Value

kselect returns a list of the class kselect and dudi (see dudi).

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Calenge, C., Dufour, A.B. and Maillard, D. (2005) K-select analysis: a new method to analyse habitat selection in radio-tracking studies. *Ecological modelling*, **186**, 143–153.

See Also

s.distri, and dudi for class dudi.

Examples

```
## Not run:
## Load the data
data(puechabonsp)

locs <- puechabonsp$relocs
map <- puechabonsp$map


## compute the home range of animals (e.g. using the minimum convex
## polygon)
pc <- mcp(locs[,"Name"])

## rasterize it
hr <- hr.rast(pc, map)


## Compute the number of relocation in each pixel of the map
```

```
cp <- count.points(locs[,"Name"], map)

## prepares the data for the kselect analysis
x <- prepksel(map, hr, cp)
tab <- x$tab

## Example of analysis with two variables: the slope and the elevation.
## Have a look at the use and availability of the two variables
## for the 4 animals
tab <- tab[,((names(tab) == "Slope")|(names(tab) == "Elevation"))]
tab <- scale(tab)
tmp <- split.data.frame(tab, x$factor)
wg <- split(x$weight, x$factor)
opar <- par(mfrow = n2mfrow(nlevels(x$factor)))
for (i in names(tmp))
  s.distri(scale(tmp[[i]]), wg[[i]])
par(opar)

## We call a new graphic window
x11()
## A K-select analysis
acp <- dudi.pca(tab, scannf = FALSE, nf = 2)
kn <- kselect(acp, x$factor, x$weight,
 scannf = FALSE, nf = 2)

# use of the generic function scatter
scatter(kn)

# Displays the first factorial plane
kplot(kn)
kplot(kn, cellipse = 0, cpoint = 0)
kplot(kn, addval = FALSE, cstar = 0)

# this factorial plane can be compared with
# the other graph to see the rotation proposed by
# the analysis
graphics.off()

# Displays the first factorial axis
hist(kn)

# Displays the second factorial axis
hist(kn, xax = 2)

# Summary of the analysis
plot(kn)

## End(Not run)
```

---

madifa *The MADIFA: a Factorial Decomposition of the Mahalanobis Distances*

Description

The MADIFA allows a factorial decomposition of the Mahalanobis distances. This method is presented here in the framework of niche-environment studies.

`predict.madifa` allows the computation of the Mahalanobis Distances based on a restricted number of factorial axes.
All other functions allow various graphical displays of the results of the MADIFA.

Usage

```
madifa(dudi, pr, scannf = TRUE, nf = 2)
## S3 method for class 'madifa'
print(x, ...)
## S3 method for class 'madifa'
scatter(x, xax = 1, yax = 2, pts = FALSE, percent = 95,
               clabel = 1, side = c("top", "bottom", "none"),
               Adensity, Udensity, Aangle, Uangle, Aborder,
               Uborder, Acol, Ucol, Alty,
               Ulty, Abg, Ubg, Ainch, Uinch, ...)
## S3 method for class 'madifa'
hist(x, scores = TRUE, type = c("h", "l"), adjust = 1, Acol,
           Ucol, Aborder, Uborder, Alwd = 1, Ulwd = 1, ...)
## S3 method for class 'madifa'
predict(object, map, nf, ...)
s.madifa(x, xax = 1, yax = 2, cgrid = 1, clab = 1, ...)
## S3 method for class 'madifa'
plot(x, map, xax = 1, yax = 2, cont = FALSE, ...)
```

Arguments

`dudi`	a duality diagram, an object of class `dudi`
`pr`	a vector giving the utilization weights associated to each unit
`scannf`	logical. Whether the eigenvalues barplot should be displayed
`nf`	an integer indicating the number of kept factorial axes
`x, object`	an object of class `madifa`
`xax`	the column number for the x-axis
`yax`	the column number for the y-axis
`pts`	logical. Whether the points should be drawn. If `FALSE`, minimum convex polygons are displayed
`percent`	100 minus the proportion of outliers to be excluded from the computation of the minimum convex polygons
`clabel`	a character size for the columns
`side`	if `"top"`, the legend of the kept axis is upside, if `"bottom"` it is downside, if `"none"` no legend
`Adensity`	the density of shading lines, in lines per inch, for the available pixels polygon. See `polygon` for more details

Udensity	the density of shading lines, in lines per inch, for the used pixels polygon. See polygon for more details
Aangle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the available pixels polygon
Uangle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the used pixels polygon
Aborder	the color for drawing the border of the available pixels polygon (or of the bars of the histogram) . See polygon for more details
Uborder	the color for drawing the border of the used pixels polygon (or of the bars of the histogram). See polygon for more details
Acol	the color for filling the available pixels polygon. if pts == FALSE, the color for the points corresponding to available pixels
Ucol	the color for filling the used pixels polygon. if pts == FALSE, the color for the points corresponding to used pixels
Alty	the line type for the available pixels polygon, as in par
Ulty	the line type for the used pixels polygon, as in par
Abg	if pts == TRUE, background color for open plot symbols of available pixels
Ubg	if pts == TRUE, background color for open plot symbols of used pixels
Ainch	if pts == TRUE, heigth in inches of the available pixels
Uinch	if pts == TRUE, heigth in inches of the largest used pixels
scores	logical. If TRUE, the histograms display the row scores of the MADIFA. If FALSE, they display the niche on the environmental variables (in this case, this is equivalent to histniche)
type	what type of plot should be drawn. Possible types are: * "h" for histograms, * "l" for kernel density estimates (see ?density). By default, type = "h" is used. If type = "l" is used, the position of the mean of each distribution is indicated by dotted lines
adjust	if type = "l", a parameter used to control the bandwidth of the density estimates (see ?density)
Alwd	if type = "l", the line width of the kernel density estimates of the available pixels
Ulwd	if type = "l", the line width of the kernel density estimates of the used pixels
cgrid	a character size, parameter used with par("cex")* cgrid to indicate the mesh of the grid
clab	if not NULL, a character size for the labels, used with par("cex")*clab
map	an object of class SpatialPixelsDataFrame
cont	logical. Whether contour lines should be added to the maps
...	additional arguments to be passed to the functions print, scatter, and plot

Details

The Mahalanobis distances are often used in the context of niche-environment studies (Clark et al. 1993, see the function `mahasuhab`). Each environmental variable defines a dimension in a multidimensionnal space, namely the ecological space. The Mahalanobis distance between any resource unit in this space (e.g. the point defined by the values of environmental variables in a pixel of a raster map) and the centroid of the niche (the distribution of used resource units) can be used to give a value of eccentricity to this point.

For a given distribution of available resource units, for which a measure of Mahalanobis distances is desired, the MADIFA (MAhalanobis DIstances Factor Analysis) partitions the ecological space into a set of axes, so that the first axes maximises the average proportion of their squared Mahalanobis distances. Note that the sum of the squared scores of any resource unit on all the axes of the analysis is equal to the squared Mahalanobis distances for this resource unit. Thus, the MADIFA partitions the Mahalanobis distances into several axes of biological meaning (see examples). `predict.madifa` allows to compute approximate Mahalanobis distances from the axes of the MADIFA.

`plot.madifa` returns a graphical summary of the analysis: it returns graphs of (i) the eigenvalues of the analysis (each eigenvalue measures the average Mahalanobis distance explained by each factorial axis); (ii) the scores of the habitat variables (i.e. the coefficients associated to each environmental variable in the linear combination defining the axes) - note that as the ecological space is distorted to "sphericize" the niche, the factorial axes are no longer orthogonals, and the scores of the variables are distributed within an ellipsoid instead of an hypersphere of radius equal to one in classical PCA. The limits of this ellipsoid is displayed on this graph, to see the amount of distortion done by the analysis (further research needs yet to be done on this graph); (iii) The projection of the available and used points on the factorial plane of the MADIFA; (iv) The map of the Mahalanobis distances computed from the original environmental variables; (v) the map of the approximated Mahalanobis distances computed from the two axes displayed in this plot; the correlations between the original environmental variables and the factorial axes; (v) the map of the first factorial axis and (vi) the map of the second factorial axis.

`hist.madifa` returns a graph of the niche and the available resource units on the factorial axes of the analysis.

Value

`madifa` returns a list of class `madifa` containing the following components:

`call`	original call.
`tab`	a data frame with n rows and p columns.
`pr`	a vector of length n containing the number of points in each pixel of the map.
`nf`	the number of kept factorial axes.
`eig`	a vector with all the eigenvalues of the analysis.
`lw`	row weights, a vector with n components.
`li`	row coordinates, data frame with n rows and nf columns.
`l1`	row normed coordinates, data frame with n rows and nf columns.
`cw`	column weights, a vector with p components.
`co`	column coordinates, data frame with p rows and nf columns.

mahasu	a vector of length n containing the squared Mahalanobis distances for the n units.
cor	the correlation between the MADIFA axes and the original variable

predict.madifa returns a matrix of class SpatialPixelsDataFrame.

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Clark, J.D., Dunn, J.E. and Smith, K.G. (1993) A multivariate model of female black bear habitat use for a geographic information system. *Journal of Wildlife Management*, **57**, 519–526.

Calenge, C., Darmon, G., Basille, M., Loison, A. and Jullien J.M. (2008) The factorial decomposition of the Mahalanobis distances in habitat selection studies. *Ecology*, **89**, 555–566.

See Also

mahasuhab for a detailed description of the Mahalanobis distances, enfa and gnesfa for closely related methods.

Examples

```
## Not run:

data(bauges)

map <- bauges$map
locs <- bauges$loc

## We prepare the data for the MADIFA
tab <- slot(map, "data")
pr <- slot(count.points(locs, map), "data")[,1]


## We then perform the PCA before the MADIFA
pc <- dudi.pca(tab, scannf = FALSE)
(mad <- madifa(pc, pr, nf=7,
               scannf = FALSE))

########################################
##                                    ##
## Graphical exploration of the MADIFA ##
##                                    ##
########################################

hist(mad)

plot(mad, map)

## this plot represents:
```

```
##  - the eigenvalues diagram
##  - the scores of the columns on the axes
##  - a graph of the niche in the available space
##  - a map of the Mahalanobis distances computed
##    using all environmental variables
##  - a map of the Mahalanobis distances computed
##    using the two factorial axes used in the
##    previous graphs
##  - the correlation between habitat variables
##    and factorial axes
##  - the geographical maps of the two
##    factorial axes

## predict with just the first axis
pred <- predict(mad, map, nf=1)
image(pred)



########################################
##                                    ##
## Mathematical properties of  MADIFA  ##
##                                    ##
########################################

## mad$li is equal to mad$l1, up to a constant (mad$l1 is normed)
plot(mad$li[,1],mad$l1[,1])

## This constant is the square root of the corresponding eigenvalue:
## the variance of mad$l1 is equal to the eigenvalue
apply(mad$l1,2,function(x) sum(x^2))/nrow(mad$li)

## the variance of mad$l1 weighted by pr is equal to 1
apply(mad$l1,2,function(x) sum(mad$pr*x^2)/sum(mad$pr))

## Therefore, the eigenvalues are equal to the average of Mahalanobis
## distance for the available resource units on each axis
mean(mahalanobis(matrix(mad$l1[,1], ncol=1), 0, 1))
mad$eig[1]

## Computation of the Mahalanobis distances
ma1 <- mahasuhab(map, locs)

## The sum of squared scores for a given Resource unit is equal to the
## Mahalanobis distances
ma2 <- apply(mad$l1,1, function(x) sum(x^2))
plot(ma2, slot(ma1, "data")[,1])


## End(Not run)
```

mahasuhab *Habitat Suitability Mapping with Mahalanobis Distances.*

Description

This function computes the habitat suitability map of an area for a species, given a set of locations of the species occurences (Clark et al. 1993). This function is to be used in habitat selection studies, when animals are not identified.

Usage

```
mahasuhab(x, pts, type = c("distance", "probability"))
```

Arguments

x	a raster map of class SpatialPixelsDataFrame
pts	a data frame with two columns, giving the coordinates of the species locations
type	a character string. Whether the raw "distance" should be returned, or rather the "probability" (see details).

Details

Let assume that a set of locations of the species on an area is available (gathered on transects, or during the monitoring of the population, etc.). If we assume that the probability of detecting an individual is independent from the habitat variables, then we can consider that the habitat found at these sites reflects the habitat use by the animals.

The Mahalanobis distances method has become more and more popular during the past few years to derive habitat suitability maps. The niche of a species is defined as the probability density function of presence of a species in the multidimensionnal space defined by the habitat variables. If this function can be assumed to be multivariate normal, then the mean vector of this distribution corresponds to the optimum for the species.

The function mahasuhab first computes this mean vector as well as the variance-covariance matrix of the niche density function, based on the value of habitat variables in the sample of locations. Then, the *squared* Mahalanobis distance from this optimum is computed for each pixel of the map. Thus, the smaller this squared distance is for a given pixel, and the better is the habitat in this pixel.

Assuming multivariate normality, squared Mahalanobis distances are approximately distributed as Chi-square with n degrees of freedom, where n equals the number of habitat characteristics (see the section note below on this question). If the argument type = "probability", maps of these p-values are returned by the function. As such these are the probabilities of a larger squared Mahalanobis distance than that observed when x is sampled from the niche.

Value

Returns a raster map of class SpatialPixelsDataFrame.

Note

The computation of the squared Mahalanobis distances inverts the variance-covariance matrix of the niche density function (see ?mahalanobis). It is therefore important that the habitat variables considered are not too correlated among each other. When the habitat variables are too correlated, the variance-covariance matrix is singular and cannot be inverted.

Note also that it is recommended to scale the variables before the computation, so that they all have the same variance, and therefore the same weight in the analysis (see examples below).

Finally, note that in versions of adehabitatHS prior to 0.3.16, mahasuhab incorrectly calculated the probability, when type = "probability", based on a Chi-square with (n-1) degrees of freedom instead of n degrees of freedom (see Etherington 2019 on this issue).

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Clark, J.D., Dunn, J.E. and Smith, K.G. (1993) A multivariate model of female black bear habitat use for a geographic information system. *Journal of Wildlife Management*, **57**, 519–526.

Etherington, T.R. (2019) Mahalanobis distances and ecological niche modelling: correcting a chi-squared probability error. *Peer J*, **7**, e6678.

See Also

madifa and dunnfa for factor analyses of the Mahalanobis distances, domain for another method of habitat suitability mapping, mahalanobis for information on the computation of Mahalanobis distances.

Examples

```
## loads the data
data(lynxjura)
ma <- lynxjura$map
lo <- lynxjura$locs[,1:2]

## We first scale the maps
slot(ma, "data") <- dudi.pca(slot(ma, "data"), scannf=FALSE)$tab

## habitat suitability mapping
hsm <- mahasuhab(ma, lo, type = "probability")
image(hsm)
title(main = "Habitat suitability map for the Lynx")
points(lo, pch = 3)
```

niche.test *Monte-Carlo Test on Parameters of the Ecological Niche*

Description

niche.test tests for the significance of two parameters of the ecological niche of a species (marginality and tolerance), using Monte-Carlo methods. This is a bivariate test.

Usage

```
niche.test(x, pts, nrep = 999, o.include = TRUE, ...)
```

Arguments

x	a raster map of class SpatialPixelsDataFrame
pts	an object inheriting the class SpatialPoints
nrep	the number of permutations
o.include	logical, passed to biv.test. If TRUE, the origin is included in the plot
...	further arguments passed to biv.test

Details

niche.test tests the significance of two parameters describing the ecological niche: the marginality (squared length of the vector linking the average available habitat conditions to the average used habitat conditions in the ecological space defined by the habitat variables), and the tolerance (inertia of the niche in the ecological space, i.e. the sum over all variables of the variance of used pixels).

At each step of the randomisation procedure, the test randomly allocates the n points in the pixels of the map. The marginality and the tolerance are then recomputed on this randomised data set.

Actual values are compared to random values with the help of the function biv.test.

Value

Returns a list containing the following components:

dfxy	a data frame with the randomized values of marginality (first column) and tolerance (second column).
obs	the actual value of marginality and tolerance.

Warning

biv.test uses the function kde2d of the package MASS.

Author(s)

Mathieu Basille <basille@ase-research.org>
Clement Calenge <clement.calenge@ofb.gouv.fr>

See Also

biv.test for more details on bivariate tests. histniche for the histograms of the variables of the niche.

Examples

```
## Not run:
data(chamois)

niche <- niche.test(chamois$map,
                    chamois$locs,
                    side = "bottom")
names(niche)

## End(Not run)
```

---

pheasant *Radio-Tracking of Pheasants*

Description

This data set describes the use and availability of 5 habitat types for 13 pheasants monitored using radio-tracking.

Usage

```
data(pheasant)
```

Format

This list has three components:

`studyarea` a data frame giving the proportion of each habitat type (columns) on the study area. These habitat types are `Scrub`, `Broadleaf`, `Coniferous`, `Grassland` and `Crop`. These proportions are repeated by rows, for all animals (rows)

`mcp` a data frame giving the proportion of each habitat type (columns) in the home range of each animal (rows)

`locs` a data frame giving the proportion of relocations of each animal (rows) reported in 3 of the 5 habitat types (columns). Indeed, `Coniferous` and `Crops` were not used by most of the animals.

Source

Aebischer, N. J., Robertson, P. A. and Kenward, R. E. (1993) Compositional analysis of habitat use from animal radiotracking data. *Ecology*, **74**, 1313–1325.

predict.enfa *Habitat Suitability Maps Built from the ENFA*

Description

predict.enfa computes habitat suitability maps using the Ecological-Niche Factor Analysis and the Mahalanobis distances method.

Usage

```
## S3 method for class 'enfa'
predict(object, map, nf, ...)
```

Arguments

object	an object of class enfa
map	an object of class SpatialPixelsDataFrame.
nf	the number of axes of specialization kept for the predictions. By default, all axes kept in object are used
...	further arguments passed to or from other methods

Details

The predictions are based on the position of the niche defined by the ENFA within the multidimensional space of environmental variables. The ENFA produces row coordinates for each pixel, which are used with the function mahalanobis. For each pixel, this function computes the Mahalanobis distances from the barycentre of the niche.

Actually, the function predict.enfa is identical to the function mahasuhab, except that the habitat suitability map is computed using the axes of the ENFA, instead of the raw data.

Note that the MADIFA allows a more consistent factorial decomposition of the Mahalanobis distances.

Value

Returns a raster map of class SpatialPixelsDataFrame.

Author(s)

Mathieu Basille <basille@ase-research.org>

References

Clark, J.D., Dunn, J.E. and Smith, K.G. (1993) A multivariate model of female black bear habitat use for a geographic information system. *Journal of Wildlife Management*, **57**, 519–526.

Hirzel, A.H., Hausser, J., Chessel, D. & Perrin, N. (2002) Ecological-niche factor analysis: How to compute habitat-suitability maps without absence data? *Ecology*, **83**, 2027–2036.

See Also

mahalanobis for information on the computation of Mahalanobis distances. mahasuhab for more details on the computation of habitat suitability maps using the Mahalanobis distances. madifa for a more consistent factorial decomposition of the Mahalanobis distances

Examples

```
## Not run:
data(lynxjura)

map <- lynxjura$map

## We keep only "wild" indices.
locs <- lynxjura$locs
locs <- locs[slot(locs, "data")[,2]!="D",]

pr <- slot(count.points(locs, map), "data")[,1]

(enfa1 <- enfa(dudi.pca(slot(map, "data"), scannf=FALSE),
               pr, scannf = FALSE))

## Compute the prediction
pred <- predict(enfa1, map)
image(pred)
contour(pred, col="green", add=TRUE)
points(locs, pch = 3)


## End(Not run)
```

---

puech *Radio-Tracking Data of Wild Boar (2)*

Description

This data set stores the results of the monitoring of 6 wild boar at Puechabon (Mediterranean habitat, South of France). These data have been collected by Daniel Maillard (Office national de la chasse et de la faune sauvage).

Usage

```
data(puech)
```

Details

The list puech has two components:

puech$relocations is an object of class SpatialPixelsDataFrame containing the relocations of the wild boar resting sites in summer. It contains the coordinates of the relocations and the name of the corresponding wild boar.

puech$map is n object of class SpatialPixelsDataFrame that describe nine environmental variables on the study area (the elevation, the tree cover, the shrub cover, the distance to recreational trails, the distance to crops, the distance to water points, the grass cover, the slope and the sunshine).

Note that both the maps and the relocations have been slightly "damaged" to preserve the copyright on the data.

References

Maillard, D. (1996). *Occupation et utilisation de la garrigue et du vignoble mediterraneens par le Sanglier*. Universite d'Aix-Marseille III: PhD thesis.

---

puechdesIII *Habitat Selection by the Wild Boar at Puechabon*

Description

This data set contains two data frames describing the use and the availability of 3 elevation classes for 6 wild boars (*Sus scrofa* L.) monitored using radio-tracking at Puechabon (South of France). These data have been collected by Daniel Maillard (Office national de la chasse et de la faune sauvage).

Usage

```
data(puechdesIII)
```

Details

The list puechdesIII has two components:
The data frame used describes the number of telemetry relocations for each of the 6 animals in each of the three elevation classes.
The data frame available describes a sample of random points placed in the areas available to these wild boars (a buffer area of 200 m around the relocations).

Source

Maillard, D. (1996) *Occupation et utilisation de la garrigue et du vignoble mediterraneens par le Sanglier*. Universite d'Aix-Marseille III: PhD thesis.

`rand.kselect` *Test of the Third-Order Habitat Selection*

Description

`rand.kselect` tests whether the marginality vector of animals is significantly larger than what is expected under the hypothesis of random habitat use (third-order habitat selection: selection by the animals of the relocations within their home range; the habitat availability is measured for each animal). The effect of each variable on individual marginality is also tested. Finally, the pertinence of a K-select analysis is also tested. This is a randomisation test. The alpha-level of the tests is ajusted using the Bonferroni inequality.

Usage

```
rand.kselect(dudi, factor, weight, nrep = 200, alpha = 0.05, ewa = FALSE)
## S3 method for class 'rand.kselect'
print(x, ...)
```

Arguments

`dudi`	an object of class `dudi`.
`factor`	a factor defining the animals identity
`weight`	a weight vector of integer values (number of relocations counted in each resource unit in row of the object dudi)
`nrep`	the number of repetitions of the test
`alpha`	the alpha level for the tests.
`ewa`	logical. If `TRUE`, uniform weights are given to all animals in the analysis. If `FALSE`, animal weights are given by the proportion of relocations of each animal (i.e. an animal with 10 relocations has a weight 10 times lower than an animal with 100 relocations)
`x`	an object of the class `rand.kselect`.
`...`	further arguments to be passed to the generic function `print`

Details

This test is carried out by simulating a random use of space by animals. `rand.kselect` is closely related to the function `kselect` (same arguments).

At each step of the randomisation procedure, and for each animal, the test randomly allocates the nk relocations (where nk is the sum of the weight vector for the animal k) in the Ik pixels available to this animal (where Ik is the length of the weight vector for animal k).

The length of the marginality vector is recomputed at each step of the randomisation procedure and for each animal. The effect of each variable on the use of pixels by each animal is measured by the criterion "(average habitat variable j used by animal i) minus (average habitat variable j available to animal i)". Finally the value of the first eigenvalue of the K-select analysis provides a criterion to test the pertinence of the K-select analysis.

All these values are then compared to the observed values to assess the significance of theses effects.

Value

Returns an object of class `rand.kselect`. This list has three components:

`global`	a vector of length 2 giving the results of the randomisation procedure for the first eigenvalue of the K-select analysis.
`marg`	a matrix giving the significance of the marginality of each animal.
`per.ind`	a list giving the results of the randomisation test for the coordinates of the marginality vector for each animal on each habitat variable.
`alpha`	the alpha level of the tests.

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Calenge, C., Dufour, A.B. and Maillard, D. (2005) K-select analysis: a new method to analyse habitat selection in radio-tracking studies. *Ecological modelling*, **186**, 143–153.

See Also

`kselect` to perform a K-select analysis.

Examples

```
## Not run:
## Loads the data
data(puechabonsp)

locs <- puechabonsp$relocs
map <- puechabonsp$map


## compute the home range of animals (e.g. using the minimum convex
## polygon)
pc <- mcp(locs[,"Name"])

## rasterize it
hr <- do.call("data.frame", lapply(1:nrow(pc), function(i) {
    sp::over(map, geometry(pc[i,]))
}))
names(hr) <- slot(pc, "data")$id
coordinates(hr) <- coordinates(map)
gridded(hr) <- TRUE


## Compute the number of relocation in each pixel of the map
cp <- count.points(locs[,"Name"], map)

## prepares the data for the kselect analysis
```

```
x <- prepksel(map, hr, cp)
tab <- x$tab
dud <- dudi.mix(tab, scannf = FALSE, nf = 2)

## the randomisation tests
## be patient, this can be very long on some machines
(te <- rand.kselect(dud, x$factor, x$weight, nrep = 500))


## End(Not run)
```

`randtest.enfa` *Randomisation Test for the Ecological Niche Factor Analysis*

Description

`randtest.enfa` performs a randomisation test for the Ecological Niche Factor analysis (ENFA).

Usage

```
## S3 method for class 'enfa'
randtest(xtest, nrepet = 999, ...)
```

Arguments

`xtest`	an object of class `enfa`
`nrepet`	the number of iterations for the randomisation test
`...`	further arguments to be passed to the generic function `randtest`

Details

This test is carried out by simulating a random distribution of the species occurrences in the pixels of a map.

At each step of the randomisation procedure, the test randomly allocates the nk occurrences (where nk is the sum of the occurrence vector `pr` of the object of class `enfa`) in the Ik pixels of the focus area (where Ik is the length of this occurrence vector).

At each step of the procedure, the first eigenvalue of the ENFA performed on the randomised data set is recomputed. This value provides a criterion to test the pertinence of the ENFA analysis.

Value

returns a list of class `randtest`

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Manly, B.F.J. (1997) *Randomization, Bootstrap and Monte Carlo Methods in Biology*. London: Chapman & Hall.

Hirzel, A.H., Hausser, J., Chessel, D. and Perrin, N. (2002) Ecological-niche factor analysis: How to compute habitat suitability maps without absence data? *Ecology*, **83**, 2027–2036.

See Also

enfa

Examples

```
## Not run:
data(chamois)
locs <- chamois$locs
map <- chamois$map

## prepare the data
tab <- slot(map, "data")
tab$Vegetation <- NULL
pr <- slot(count.points(locs, map), "data")[,1]

en <- enfa(dudi.pca(tab, scannf=FALSE), pr, scannf = FALSE)
(tutu <- randtest(en, nrepet = 100))
plot(tutu)


## End(Not run)
```

---

scatter.enfa *Scatter Plot of the Results of the ENFA*

Description

Performs the scatter diagrams of objects of class enfa.

Usage

```
## S3 method for class 'enfa'
scatter(x, xax = 1, yax = 2, pts = FALSE, nc = TRUE,
             percent = 95, clabel = 1, side = c("top", "bottom", "none"),
             Adensity, Udensity, Aangle, Uangle, Aborder, Uborder,
             Acol, Ucol, Alty, Ulty, Abg, Ubg, Ainch, Uinch, ...)
```

Arguments

x	an object of class enfa
xax	the column number for the x-axis
yax	the column number for the y-axis
pts	logical. Whether the points should be drawn. If FALSE, minimum convex polygons are displayed
nc	whether or not the niche center should be displayed
percent	100 minus the proportion of outliers to be excluded from the computation of the minimum convex polygons
clabel	a character size for the columns
side	if "top", the legend of the kept axis is upside, if "bottom" it is downside, if "none" no legend
Adensity	the density of shading lines, in lines per inch, for the available pixels polygon. See polygon for more details
Udensity	the density of shading lines, in lines per inch, for the used pixels polygon. See polygon for more details
Aangle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the available pixels polygon
Uangle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the used pixels polygon
Aborder	the color for drawing the border of the available pixels polygon. See polygon for more details
Uborder	the color for drawing the border of the used pixels polygon. See polygon for more details
Acol	the color for filling the available pixels polygon. if pts == FALSE, the color for the points corresponding to available pixels
Ucol	the color for filling the used pixels polygon. if pts == FALSE, the color for the points corresponding to used pixels
Alty	the line type for the available pixels polygon, as in par
Ulty	the line type for the used pixels polygon, as in par
Abg	if pts == TRUE, background color for open plot symbols of available pixels
Ubg	if pts == TRUE, background color for open plot symbols of used pixels
Ainch	if pts == TRUE, heigth in inches of the available pixels
Uinch	if pts == TRUE, heigth in inches of the largest used pixels
...	further arguments passed to or from other methods

Details

scatter.enfa displays a factorial map of pixels, as well as the projection of the vectors of the canonical basis multiplied by a constant of rescaling. The kept axes for the plot are specified in a corner.

Author(s)

Mathieu Basille <basille@ase-research.org>

References

Basille, M., Calenge, C., Marboutin, E., Andersen, R. & Gaillard, J.M. (2008) Assessing habitat selection using multivariate statistics: Some refinements of the ecological-niche factor analysis. *Ecological Modelling*, **211**, 233–240.

See Also

enfa, scatter

Examples

```
data(lynxjura)

map <- lynxjura$map

## We keep only "wild" indices.
locs <- lynxjura$locs
locs <- locs[slot(locs, "data")[,2]!="D",]

hist(map, type = "l")
## The variable artif is far from symetric

## We perform a square root transformation
## of this variable
## We therefore normalize the variable 'artif'
slot(map,"data")[,4] <- sqrt(slot(map,"data")[,4])
hist(map, type = "l")

## We prepare the data for the ENFA
tab <- slot(map, "data")
pr <- slot(count.points(locs, map), "data")[,1]


## We then perform the PCA before the ENFA
pc <- dudi.pca(tab, scannf = FALSE)

## We perform the ENFA
(enfa1 <- enfa(pc, pr, scannf = FALSE))

scatter(enfa1)
```

scatterniche *Display the Niche in the Ecological Space*

Description

scatterniche displays the niche in the Ecological space (multidimensional space defined by habitat variables).

Usage

```
scatterniche(x, pr, xax = 1, yax = 2, pts = FALSE,
             percent = 95, clabel = 1,
             side = c("top", "bottom", "none"),
             Adensity, Udensity, Aangle, Uangle, Aborder,
             Uborder, Acol, Ucol, Alty, Ulty, Abg,
             Ubg, Ainch, Uinch, ...)
```

Arguments

x	a data frame giving the value of environmental variables (columns) in resource units (rows, e.g. the pixels of a raster map)
pr	a vector giving the utilisation weight for each resource unit
xax	the column number for the x-axis
yax	the column number for the y-axis
pts	logical. Whether the points should be drawn. If FALSE, minimum convex polygons are displayed
percent	100 minus the proportion of outliers to be excluded from the computation of the minimum convex polygons
clabel	a character size for the columns
side	if "top", the legend of the kept axis is upside, if "bottom" it is downside, if "none" no legend
Adensity	the density of shading lines, in lines per inch, for the available pixels polygon. See polygon for more details
Udensity	the density of shading lines, in lines per inch, for the used pixels polygon. See polygon for more details
Aangle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the available pixels polygon
Uangle	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the used pixels polygon
Aborder	the color to draw the border of the available pixels polygon. See polygon for more details
Uborder	the color to draw the border of the used pixels polygon. See polygon for more details

Acol	the color for filling the available pixels polygon. if pts==FALSE, the color for the points corresponding to available pixels
Ucol	the color for filling the used pixels polygon. if pts==FALSE, the color for the points corresponding to used pixels
Alty	the line type for the available pixels polygon, as in par.
Ulty	the line type for the used pixels polygon, as in par.
Abg	if pts==TRUE, background color for open plot symbols of available pixels
Ubg	if pts==TRUE, background color for open plot symbols of used pixels
Ainch	if pts==TRUE, heigth in inches of the available pixels
Uinch	if pts==TRUE, heigth in inches of the largest used pixels
...	further arguments passed to or from other methods

Author(s)

Mathieu Basille <basille@ase-research.org>
Clement Calenge <clement.calenge@ofb.gouv.fr>

Examples

```
data(chamois)
cpi <- slot(count.points(chamois$locs, chamois$map),"data")[,1]
chamois$map

tab <- slot(chamois$map, "data")

## we focus on the distance to ecotone and on the slope,
## after centring and scaling (with the help of a PCA)
scatterniche(dudi.pca(tab[,2:3], scannf=FALSE)$tab, cpi)
scatterniche(dudi.pca(tab[,2:3], scannf=FALSE)$tab, cpi, pts=TRUE)
```

---

squirrel *Radio-Tracking Data of Squirrels*

Description

This data set describes the use and availability of 5 habitat types for 17 squirrels monitored using radio-tracking. See also the dataset squirreloc.

Usage

```
data(squirrel)
```

Format

This list has three components:

`studyarea` a data frame giving the proportion of each habitat type (columns) on the study area. These proportions are repeated by rows, for all animals

`mcp` a data frame giving the proportion of each habitat type (columns) in the home range of each animal (rows)

`locs` a data frame giving the proportion of relocations of each animal (rows) reported in each habitat type (columns).

Source

Aebischer, N. J., Robertson, P. A. and Kenward, R. E. (1993) Compositional analysis of habitat use from animal radiotracking data. *Ecology*, **74**, 1313–1325.

`squirreloc` *Radio-tracking of squirrels*

Description

This data set contains the trajectories of 15 radio-monitored squirrels, as well as the vector maps of habitat composition.

Usage

```
data(squirreloc)
```

Format

This data set is a list of two objects: `locs` is a `SpatialPointsDataFrame` containing the relocations of 15 squirrels

`map` is an object of class `SpatialPolygonsDataFrame` containing the habitat composition of the area. The habitat types and colour coding are stored in the data.frame

Details

The dataset `squirreloc` comes from the Ranges VI software. It has been used to illustrate the compositional analysis (see `?compana`) and the eigenanalysis of selection ratios (see `?eisera`). See also the dataset `squirrel`.

Source

Kenward, R.E., South, A.B. and Walls, S.S. (2003). Ranges6 v1.2 : For the analysis of tracking and location data. Online manual. Anatrack Ltd. Wareham, UK. ISBN 0-9546327-0-2.

vanoise — *Habitat Use by Three Species of Galliformes in the Vanoise National Parc*

Description

This data frame describes the habitat use by the Black Grouse (*Tetrao tetrix*), the Rock Partridge (*Alectoris graeca*) and the Rock Ptarmigan (*Lagopus mutus*), in the Vanoise National Park (French Alps), from 1990 to 2000.

Usage

```
data(vanoise)
```

Format

This data frame has 3110 rows and eight columns describing the habitat composition for each occurrence of three species of Galliformes. For each located occurrence (in rows), the employees of the national park have noted: the species, the elevation (in metres), the aspect (8 classes), the habitat type (7 categories, `FR` means "fallen rocks") and the date (season, day, month and year).

Source

Calenge, C., Martinot, J.P. and Lebreton, P. (2003) Ecological niche separation among mountain Galliformes in the Vanoise National Parc. *Game and Wildlife Science*, 20, 259-285.

wi — *Computation of Selection Ratios for Habitat Selection Studies.*

Description

These functions compute the resource selection ratios (wi) for design I, II and III data types, with resources defined by several categories. Basic tests are also provided.

Usage

```
widesI(u, a, avknown = TRUE, alpha = 0.05)
widesII(u, a, avknown = TRUE, alpha = 0.05)
widesIII(u, a, avknown = TRUE, alpha = 0.05)
## S3 method for class 'wiI'
print(x, ...)
## S3 method for class 'wiII'
print(x, ...)
## S3 method for class 'wiIII'
print(x, ...)
## S3 method for class 'wi'
plot(x, caxis = 0.7, clab = 1, ylog = FALSE, errbar = c("CI", "SE"),
        main = "Manly selectivity measure", noorder = TRUE, ...)
```

Arguments

u	for widesI, a vector with named elements describing the sample of used resource units. For widesII and widesIII a matrix or a data frame giving the number of used resource units for each animal (in rows) in each resource category (in columns)
a	for widesI and widesII, a vector with named elements describing the sample or the proportion of available resource units. For widesIII a matrix or a data frame giving the number or the proportion of available resource units for each animal (in rows) in each resource category (in columns)
avknown	logical. TRUE if the available proportions are known, and FALSE if they are estimated
alpha	the threshold value for the tests and confidence intervals
x	an object of class wi
caxis	character size on axes to be passed to par("cex.axis")
clab	character size of axes labels to be passed to par("cex.lab")
ylog	logical. If TRUE, the selection ratios are plotted on a log scale
errbar	a character string. Type of error bars: either "CI" for confidence intervals or "SE" for standard errors
main	a character string. The title of the graph
noorder	logical. If TRUE, the habitat categories are ordered on the graph in decreasing order of their preference. If FALSE, they are not ordered (i.e. they are in the same order as the columns in used and available
...	additionnal arguments to be passed to the function plot

Details

widesI may be used to explore resource selection by animals, when designs I are involved (habitat use and availability are measured at the population level - animals are not identified). The function tests habitat selection with the Khi2 of Pearson and log-likelihood Khi2 (recommended, see Manly et al. 2003). The Manly selectivity measure (selection ratio = used/available) is computed, the preference / avoidance is tested for each habitat, and the differences between selection ratios are computed and tested.

widesII computes the selection ratios with design II data (same availability for all animals, but use measured for each one). Tests of identical habitat use for all animals, and of habitat selection are also provided.

widesIII computes the selection ratios for design III data (when the use and the availability are measured for each animal - see examples on the wild boar below). Habitat selection is tested using a Chi-square for each animal, and the overall habitat selection is also tested.

Note that all these methods rely on the following hypotheses: (i) independence between animals, and (ii) all animals are selecting habitat in the same way (in addition to "traditional" hypotheses in these kinds of studies: no territoriality, all animals having equal access to all available resource units, etc., see Manly et al. 2002 for further details).

Value

widesI returns a list of the class wiI. widesII returns a list of class wiII. widesIII returns a list of class wiIII. These objects are all inheriting from the class wi. They have the following components:

used.prop	the proportion of use for each resource type.
avail.prop	the proportion of available resources.
wi	the Manly selectivity measure (selection ratio: used/available).
se.wi	the standard error of the selection ratios.
comparisons	a list with the following components: diffwi a matrix with the differences of the selection ratios for each pair of resource type. ICdiffupper a matrix containing the upper limit of confidence interval on the differences of the selection ratios between each pair of resource type. ICdifflower a matrix containing the lower limit of confidence interval on the differences of the selection ratios between each pair of resource type. signif the ranking matrix, with the sign of the differences between the resource type in row and the resource type in column. When the difference is significant, the sign is tripled.
profile	the profile of preferences: resource types are sorted so that the left type is the most preferred and the right type is the most avoided. Habitats for which the selection ratios are not significant are connected by a line.
alpha	the parameter alpha of this function.
avknown	the parameter avknown of this function.
se.used	only for designs I, the standard error of the proportion of use.
se.avail	only for designs I, the standard error of the available proportion.
chisquwi	only for designs I, the results of Chi-Square tests of the hypothesis that the selection ratios are in average equals to zero.
Bi	only for designs I, equals to wi/sum(wi).
Khi2P	only for designs I, test of random resource use (Pearson statistic).
Khi2L	For designs I, test of random resource use (Log-likelihood statistic). For design III, global test of random resource use (Log-likelihood statistic)
Khi2L1	only for designs II, test of identical use of habitat by all animals.
Khi2L2	only for designs II, test of overall habitat selection.
Khi2L2MinusL1	only for designs II, test of hypothesis that animals are on average using resources in proportion to availability, irrespective of whether they are the same or not (= Khi2L2 - Khi2L1).
wij	only for designs II and III, a matrix with the selection ratios for all animals and all resource categories.
ICwiupper	only for designs II and III, the upper limit of the confidence intervals on the selection ratios.
ICwilower	only for designs II and III, the lower limit of the confidence intervals on the selection ratios.
Khi2Lj	only for designs III, the test of habitat selection for each animal.

Author(s)

Clement Calenge <clement.calenge@ofb.gouv.fr>

References

Manly B.F.J., McDonald L.L., Thomas, D.L., McDonald, T.L. & Erickson, W.P. (2003) *Resource selection by animals - Statistical design and Analysis for field studies. Second edition* London: Kluwer academic publishers.

Thomas D. L. and Taylor E. J. (1990) Study designs and tests for comparing resource use and availability. *Journal of Wildlife Management*, **54**, 322–330.

See Also

compana for compositional analysis, and eisera to perform an eigenanalysis of selection ratios.

Examples

```
############################
## Example of moose (Manly et al., 2003, p.52)
## Known available proportions on design I data
moose.avail <- c(0.34, 0.101, 0.104, 0.455)
moose.used <- c(25, 22, 30, 40)
names(moose.used) <- c("InBurnInterior",
                       "InBurnEdge",
                       "OutOfBurnEdge",
                       "OutOfBurnFurther")
names(moose.avail) <- names(moose.used)
## Computation of wi
(wiRatio <- widesI(moose.used, moose.avail))

## plot the values of the selection ratios
opar <- par(mfrow=c(2,2))
plot(wiRatio)

par(opar)



############################
## Example of Elk (Manly et al., 2003, p.62)
## Estimated available proportions on design I data
elk.avail <- c(15, 61, 84, 40)
elk.used <- c(3, 90, 181, 51)
names(elk.used) <- c("0%", "1-25%", "26-75%", ">75%")
names(elk.avail) <- names(elk.used)
## Computation of wi
(wiRatio <- widesI(elk.used, elk.avail, avknown=FALSE))

## plot the values of the selection ratios
opar <- par(mfrow=c(2,2))
```

```
plot(wiRatio)

par(opar)



############################
## Example of Bighorn (Manly et al., 2003, p.67)
## Known available proportions on design II data
data(bighorn)
## Computation of wi
(wi <- widesII(bighorn$used, bighorn$availT, alpha = 0.1))

## plot the values of the selection ratios
opar <- par(mfrow=c(2,2))
plot(wi)



############################
## Example of Bighorn (Manly et al., 2003, p.74)
## Estimated available proportions on design II data
## Computation of wi
(wi <- widesII(bighorn$used, bighorn$availE, avknown = FALSE, alpha = 0.1))

## plot the values of the selection ratios
plot(wi)

par(opar)


############################
## Example of Wild boar
## Estimated available proportions on design III data
data(puechdesIII)
used <- puechdesIII$used
available <- puechdesIII$available

## calculation of the selectio ratios
## with sampled availability
(i <- widesIII(used,available, avknown = FALSE, alpha = 0.1))

opar <- par(mfrow = c(2,2))
plot(i)

par(opar)
```

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