

Package ‘subniche’

November 19, 2016

Title Within Outlying Mean Index Analysis: Exploratory Niche Methods

Version 0.9.1

Date 2016-11-19

Author Stephane Karasiewicz

Maintainer Stephane Karasiewicz <stephane.karasiewicz@wanadoo.fr>

Description Complementary multivariate analysis to the Outlying Mean Index analysis to explore niche shift of a community within an Euclidean space, with graphical displays.

Suggests ade4TkGUI, adegraphics, ape, CircStats, deldir, lattice, maptools, MASS, pixmap, spdep, splancs, waveslim

Depends ade4

License GPL (>= 2)

RoxygenNote 5.0.1

NeedsCompilation no

Repository CRAN

Date/Publication 2016-11-19 16:52:58

R topics documented:

sep.factor.row	1
subniche	2

Index	6
--------------	----------

sep.factor.row	<i>A function to seperate a matrix, by row, into submatrices.</i>
----------------	---

Description

separate matrix by rows into submatrices

Usage

```
sep.factor.row (x, factor)
```

Arguments

x a matrix.
factor a factor of the same length as the number of row in the matrix.

Value

list of submatrices

subniche

The Within Outlying Mean Index analysis

Description

The analysis allows to divide the reference niche, estimated from the [niche](#) function in the [ade4](#) package into subniches defined by a factor, which creates the subscales. See details for more information.

Usage

```
subniche(nic, factor)

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

## S3 method for class 'subniche'
plot(x, xax = 1, yax = 2, ...)

margvect(x, xax = 1, yax = 2, ...)

subplot(x, xax = 1, yax = 2, ...)

## S3 method for class 'subniche'
summary(object, ...)

refparam(x)

## S3 method for class 'subniche'
rtest(xtest, nrepet = 99, ...)

subparam.refor(x)

rtestrefor(x, nrepet)
```

```
subparam.subor(x)
```

```
rtestsubor(x, nrepet)
```

Arguments

nic	an object of class niche.
factor	a factor which will defined the subscales within which the subniches will be calculated (the same length of the number of sites)
x	an object of class subniche.
...	further arguments passed to or from other methods
xax	specify the x column in your matrix
yax	specify the y column in your matrix
object	an object of class subniche.
xtest	an object of class subniche.
nrepet	the number of permutations for the testing procedure

Details

The Within Outlying Mean Index analysis is a statistical exploratory niche analysis which provides observation of niche shift and/or conservatism, of an entire community, at different subscales (temporal, spatial and/or finer biological organisation level), and comparable under the same environmental gradients. This hindcasting multivariate analysis is based on the OMI analysis (Doledec *et al.* 2000) which is used as reference. The niches refinement is inspired by the K-select (Calenge *et al.* 2005) which emphasizes the limiting factors in habitat use in design II and III (Thomas and Taylor, 1990). The different estimations should help understand:

1. the environmental factors defining a species' reference niche, under on the full scale, within a community.
2. the environmental factors defining a species' subniches, under each subscales, within a community.

The subniches parameters can be calculated from both the reference origin, G , which corresponds to the reference plan origin, and from G' , which corresponds to the suborigins. G is the graphical representation of the mean environmental conditions encountered over the full scale of the data. G' is the mean environmental conditions encountered at a subscale defined by the factor. They are complementary has you can compare:

1. a single species' subniches to G .
2. the community' subniches to G' at a specific subscale.

The subniches of a single species can only be compared to G as it is the common origin to all subscales. Whereas G' is only common to the species found within the subscale. So comparing different subniches of one species, found within different subscales, is only relevant to G . The community's subniches can be compared to both G and G' , but G , being the mean environmental conditions found within the full scale, will not express the specificity of the environmental conditions that the species encountered at the subscale. G' , being the mean environmental conditions of the subscale, will reflect the atypical value of the environmental condition, making the comparison of the community's subniches parameters more relevant.

Value

Adds items in the niche list and changing the class into subniche containing:
 factor the factor use to divide the environmental and species matrix into subscale.
 mav a dataframe with the subscale origins, G' .
 mus a dataframe with the subscale species niche coordinates

Author(s)

Stephane Karasiewicz, <stephane.karasiewicz@wanadoo.fr>

References

- Doledec S., Chessel D. and Gimaret C. (2000). Niche separation in community analysis: a new method. *Ecology*, **81**, 2914-1927.
- 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.
- Thomas D.L., Taylor E.J., (1990). Study designs and tests for comparing resource use and availability. *J. Wildl. Manage.*, **54**, 322-330.
- Karasiewicz S.,Doledec S.and Lefebvre S. (submitted). Within Outlying Mean Index analysis: combining OMI and K-select analysis for the realized niche decomposition.

See Also

[niche niche.param](#)

Examples

```
library(ade4)
data(doubs)
dudi1 <- dudi.pca(doubs$env, scale = TRUE, scan = FALSE, nf = 3)
nic1 <- niche(dudi1, doubs$fish, scann = FALSE)
# number of sites
N <- dim(nic1$ls)[1]
#Create a factor which defines the subscales
fact <- factor(c(rep(1,N/2),rep(2,N/2)))
# nic1 will be use as reference and fact will be use to define the subniches environment
subnic1 <- subniche(nic1, fact)
# the following two functions do the same display, plot.refniche is adapted to subniche objects
plot(nic1)
plot(subnic1)
#Display the marginality vector of the suborigins and the species subniche
margvect(subnic1)
#Display the subset's chull, found within the overall environment's chull,
#and the corresponding species positions
subplot(subnic1)
# The following two functions do the same display, refparam is adapted to subniche objects
niche.param(nic1)
refparam(subnic1)
# The following two functions do the same display, rtest is adapted to subniche objects
```

```
rtest(nic1,10)
rtest(subnic1,10)
#Calculates the subniches' parameters from G with the corresponding rtest
subparam.refor(subnic1)
rtestrefor(subnic1,10)
#Calculates the subniches' parameters from G' with the corresponding rtest
subparam.subor(subnic1)
rtestsubor(subnic1,10)
```

Index

*Topic **subniche**

subniche, [2](#)

ade4, [2](#)

margvect (subniche), [2](#)

niche, [2](#), [4](#)

niche.param, [4](#)

plot.subniche (subniche), [2](#)

print.subniche (subniche), [2](#)

refparam (subniche), [2](#)

rtest.subniche (subniche), [2](#)

rtestrefor (subniche), [2](#)

rtestsubor (subniche), [2](#)

sep.factor.row, [1](#)

subniche, [2](#)

subparam.refor (subniche), [2](#)

subparam.subor (subniche), [2](#)

subplot (subniche), [2](#)

summary.subniche (subniche), [2](#)