

Package ‘subniche’

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Title Within Outlying Mean Indexes: Refining the OMI Analysis

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Description Complementary indexes calculation to the Outlying Mean Index analysis to explore niche shift of a community and biological constraint within an Euclidean space, with graphical displays.

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

Depends ade4

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ardecheinv

Temporal data

Description

The ardecheinv data are the temporal example used as an ecological application of the WitOMI calculations in Karasiewicz et al. (2017).

Usage

```
data(ardecheinv)
```

Format

The ardecheinv is a list of 3 components.

env is a dataframe of 67 rows with 5 environmental tables, collected in spring and autumn.

Invertebrates is a dataframe of 67 rows and 57 species of invertebrates.

code is a dataframe with 57 rows and 2 columns, the species scientific name and their respective code.

Source

Merigoux, S. and Doledec, S. (2004). Hydraulic requirements of stream communities: A case study on invertebrates. *Freshwater Biology*, **49**(5), 600-613.

References

Karasiewicz S.,Doledec S.and Lefebvre S. (2017). Within outlying mean indexes: refining the OMI analysis for the realized niche decomposition. *PeerJ* 5:e3364. <https://doi.org/10.7717/peerj.3364>.

drome

Spatial data

Description

The drome data are the spatial example used as an ecological application of the WitOMI calculations in Karasiewicz et al. (2017).

Usage

```
data(drome)
```

Format

The drome is a list of 3 components.

env is a dataframe with 64 rows with 6 environmental tables, collected in 10 different rivers.

fish is a dataframe with 64 rows and 13 columns (12 fish species, including young and older trouts).

code is a dataframe with 13 rows and 2 columns, the species, common and scientific, name and their respective code.

Source

Doledec S., Chessel D. and Gimaret C. (2000). Niche separation in community analysis: a new method. *Ecology*,**81**(10), 2914-1927.

References

Karasiewicz S.,Doledec S.and Lefebvre S. (2017). Within outlying mean indexes: refining the OMI analysis for the realized niche decomposition. *PeerJ* 5:e3364. <https://doi.org/10.7717/peerj.3364>.

sep.factor.row *A function to separate a matrix, by row, into submatrices.*

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 Indexes calculation

Description

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

Usage

```
subniche(nic, factor)

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

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

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

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

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

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

## 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)

subkrandtest(sim, obs, alter = "greater", call = match.call(),
             names = colnames(sim), p.adjust.method = "none")
```

```
subnikrandtest(sim, obs, alter = "greater", subpvalue, call = match.call(),
  names = colnames(sim), p.adjust.method = "none")
```

Arguments

nic	an object of class niche.
factor	a factor which will defined the subsets 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
colo	string of character specifying the subsets color. Default color is rezd.
object	an object of class subniche.
xtest	an object of class subniche.
nrepet	the number of permutations for the testing procedure
sim	a numeric vector of simulated values
obs	a numeric vector of an observed value
alter	a character string specifying the alternative hypothesis, must be one of "greater" (default), "less" or "two-sided".he length must be equal to the length of the vector obs, values are recycled if shorter.
call	a call order
names	a vector of names for tests
p.adjust.method	a string indicating a method for multiple adjustment, see p.adjust.methods for possible choices.
subpvalue	the subset pvalue resulting from subkrandtest function

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 subcales (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 subsets, 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_k , which corresponds to the suborigins. G is the graphical representation of the mean environmental conditions encountered over the full scale of the data.

G_k is the mean environmental conditions encountered at a subset defined by the factor. They are complementary as you can compare:

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

The subniches of a single species can only be compared to G as it is the common origin to all subsets. Whereas G_k is only common to the species found within the subset. So comparing different subniches of one species, found within different subsets, is only relevant to G . The community's subniches can be compared to both G and G_k , 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 subset. G_k , being the mean environmental conditions of the subset, will reflect the atypical value of the environmental condition, making the comparison of the community's subniches parameters more relevant. More information on the ecological concept can be found in Karasiewicz *et al.* 2017.

For more details description on the package use: <https://github.com/KarasiewiczStephane/WitOMI>.

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 submatrices.
 G_k a dataframe with the sub-origins, G_k .
 sub a dataframe with the species subniche coordinates

Author(s)

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References

- Karasiewicz S., Doledec S. and Lefebvre S. (2017). Within outlying mean indexes: refining the OMI analysis for the realized niche decomposition. *PeerJ* 5:e3364. <https://doi.org/10.7717/peerj.3364>.
- 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.
- Doledec S., Chessel D. and Gimaret C. (2000). Niche separation in community analysis: a new method. *Ecology*, **81**, 2914-1927.
- Thomas, D.L., Taylor, E.J. (1990). Study Designs and Tests for Comparing Resource Use and Availability II. *Natl. Wildl.* **54**(2), 322-330.

See Also

[niche niche.param](#)

Examples

```
library(subniche)
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 subsets
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 polygon, 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_k with the corresponding rtest
subparam.subor(subnic1)
rtestsubor(subnic1,10)
```

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