Package ‘subniche’

February 26, 2021

Title Within Outlying Mean Indexes: Refining the OMI Analysis

Version 1.4

Date 2021-02-25

BugReports https://github.com/KarasiewiczStephane/WitOMI/issues

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. For details see Karasiewicz et al. (2017) <doi:10.7717/Peerj.3364>.

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

Depends ade4, siar, polyclip, wordcloud

License GPL (>= 2)

RoxygenNote 7.1.1

NeedsCompilation no

LazyData true

Author Stephane Karasiewicz [aut, cre] (<https://orcid.org/0000-0003-1652-9921>)

Maintainer Stephane Karasiewicz <skaraz.science@gmail.com>

Repository CRAN

Date/Publication 2021-02-26 13:30:03 UTC

R topics documented:

`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. doi: 10.1111/j.13652427.2004.01214.x.

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. doi: 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.doi: 10.2307/177351.

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.doi: 10.7717/peerj.3364.

`eigenbar` *The eigenvalue of the OMI analysis*

Description

The function plot the eigenvalues of the OMI analysis

Usage

```
eigenbar(
  subnic,
  col.sel = "black",
  col.unsel = "grey",
  ylab = "Eigen values in %",
  names.arg = NULL,
  main = NA,
  ...
)
```

Arguments

`subnic`	an object of class `subniche`.
`col.sel`	the color of the selected axes
`col.unsel`	the color of the other axes
`ylab`	label for y-axis, see title for more details.
`names.arg`	a vector of names to be plotted below each bar or group of bars. If this argument is omitted, then the names are taken from the names attribute of height if this is a vector, or the column names if it is a matrix.
`main`	a main title for the plot, see title for more details.
`...`	further arguments passed to or from other methods see barplot

Details

The black bars represents the selected axes for the OMI analysis See doi: 10.7717/peerj.3364 for more details on the subniche concept.

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)
eigenbar(subnic1)
```

`plot.subniche` *Summarizes the results of the species subniche*

Description

The function plot the resulting species subniche of the WitOMI calculation.

Usage

```
## S3 method for class 'subniche'
plot(
  x,
  xax = 1,
  yax = 2,
  ax.angle.arrow = 20,
  ax.col.arrow = "black",
  ax.length.arrow = 0.1,
  ax.lwd.arrow = 1,
  ax.leg.posi = "bottomleft",
  ax.leg.cex = 1.2,
  eig.col.chos = "black",
  eig.col.left = "gray",
  eig.leg.posi = "topright",
  eig.leg.cex = 1.2,
  su.leg.posi = "bottomleft",
  su.leg.cex = 1.2,
  col.axis = "azure3",
  lty.axis = 2,
  lwd.axis = 2,
  var.col.arrow = "black",
  var.length.arrow = 0.1,
  var.lwd.arrow = 1,
  var.angle.arrow = 20,
  var.leg.posi = "bottomleft",
  var.leg.cex = 1.2,
  fac.var.lab = 1.2,
  col.var = "black",
  col.su = "black",
  col.G_k = "red",
  nic.leg.posi = "bottomleft",
  nic.leg.cex = 1.2,
  sub.leg.cex = 1.2,
  sub.leg.posi = "bottomleft",
  pch.su = 16,
  cex.su = 1,
  border.E = "#92c5de",
  col.E = "#92c5de",
```

```
  lty.E = 1,
  border.K = "black",
  col.K = "#2c7fb8",
  lty.K = 1,
  show.lines = F,
  ...
)
```

Arguments

`x`	an object of class `subniche`.
`xax`	column for abscissas.
`yax`	column for ordinate.
`ax.angle.arrow`	arrow angle head for plot labeled "Axes", see arrows for more details.
`ax.col.arrow`	arrow color for plot labeled "Axes", see arrows for more details.
`ax.length.arrow`	arrow head length for plot labeled "Axes", see arrows for more details.
`ax.lwd.arrow`	arrow width for plot labeled "Axes", see arrows for more details.
`ax.leg.posi`	legend position for plot labeled "Axes", see legend for more details.
`ax.leg.cex`	legend size label for plot labeled "Axes", see legend for more details.
`eig.col.chos`	bar color for the selected components for plot labeled "Eigenvalues".
`eig.col.left`	bar color for the component leftover for plot labeled "Eigenvalues".
`eig.leg.posi`	legend position for plot labeled "Eigenvalues", see legend for more details.
`eig.leg.cex`	legend size label for plot labeled "Eigenvalues"", see legend for more details.
`su.leg.posi`	legend position for plot labeled "SU", see legend for more details.
`su.leg.cex`	legend size label for plot labeled "SU", see legend for more details.
`col.axis`	axis color, see par for more details.
`lty.axis`	axis line type, see par for more details.
`lwd.axis`	axis width, see par for more details.
`var.col.arrow`	variables arrow color for plot labeled "Variables and Species", see arrows for more details.
`var.length.arrow`	variables arrow length of the edges of the arrow head (in inches).
`var.lwd.arrow`	variables arrow width for plot labeled "Variables and Species", see arrows for more details.
`var.angle.arrow`	variables arrow angle head for plot labeled "Variables and Species", see arrows for more details.
`var.leg.posi`	legend position for plot labeled "Variables and Species", see legend for more details.
`var.leg.cex`	legend size label for plot labeled "Variables and Species", see legend for more details.

`fac.var.lab`	factor for moving the variable labels from its original coordinates for clarity, by defaults they are multiply 1.2
`col.var`	color variables labels, see textplot for more details.
`col.su`	color of sampling units, see points for more details.
`col.G_k`	color label G_k, see textplot for more details.
`nic.leg.posi`	legend position for plot labeled "Niches", see legend for more details.
`nic.leg.cex`	legend size label for plot labeled "Niches", see legend for more details.
`sub.leg.cex`	legend size label for plot labeled "Subsets"", see legend for more details.
`sub.leg.posi`	legend position for plot labeled "Subsets", see legend for more details.
`pch.su`	type of the points representing the sampling units (SU), see points for more details.
`cex.su`	size of the points representing the sampling units (SU), see points for more details.
`border.E`	color border of E polygon, see polygon for more details.
`col.E`	inside color of E polygon, see polygon for more details.
`lty.E`	line type for the E border, see polygon for more details.
`border.K`	color border of K polygon, see polygon for more details.
`col.K`	inside color of K polygon, see polygon for more details.
`lty.K`	line type for the K border, see polygon for more details.
`show.lines`	if true, then lines are plotted between x,y and the word, for those words not covering their x,y coordinates. See textplot for more details.
`...`	further arguments passed to or from other methods.

Details

The function illustrate the results of subniche calculation with a great deal of customization parameters.

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)
plot(subnic1)
```

`plot_dym` *Communities subniches dynamic*

Description

The function represents the species' subniches SR position within the environmental space E.

Usage

```
plot_dym(
  subnic,
  sig = NULL,
  sig_thres = 0.05,
  xlab = NULL,
  ylab = NULL,
  main = NA,
  col.axis = "azure3",
  lty.axis = 2,
  lwd.axis = 2,
  border.E = "black",
  col.E = "#92c5de",
  lty.E = 1,
  lwd.E = 1,
  pch.SR.pos = 21,
  cex.SR.pos = 1,
  col.SR.pos = "#ffa600",
  col.SR.pt = "black",
  col.SR.lab = "black",
  cex.SR.lab = NA,
  fac.SR.lab = 1.2,
  col.arrow = "black",
  angle.arrow = 20,
  lwd.arrow = 2,
  length.arrow = 0.1,
  font.sp = 2,
  leg = T,
  posi.leg = "topleft",
  bty.leg = "n",
  ...
)
```

Arguments

`subnic`	an object of class `subniche`.
`sig`	a factor defining the significance species, default NULL.
`sig_thres`	value for minimum significance, default 0.05

`xlab`	label for x-axis, see title for more details.
`ylab`	label for y-axis, see title for more details.
`main`	a main title for the plot, see title for more details.
`col.axis`	axis color, see par for more details.
`lty.axis`	axis line type, see par for more details.
`lwd.axis`	axis width, see par for more details.
`border.E`	color border of E polygon, see polygon for more details.
`col.E`	inside color of E polygon, see polygon for more details.
`lty.E`	line type for the E border, see polygon for more details.
`lwd.E`	line width for the E border, see polygon for more details.
`pch.SR.pos`	type of points representing the SR position, see points for more details.
`cex.SR.pos`	size of points representing the SR position, see points for more details.
`col.SR.pos`	color of points representing the SR position, see points for more details.
`col.SR.pt`	point color contour if pch=21:25.
`col.SR.lab`	color of the species labels, see see text for more details.
`cex.SR.lab`	size of the species labels defautls NA for no labels, see see text for more details.
`fac.SR.lab`	factor for moving the SR labels from its original coordinates for clarity, by defaults they are multiply 1.2
`col.arrow`	arrow color, see arrows for more details.
`angle.arrow`	arrow angle head, see arrows for more details.
`lwd.arrow`	arrow width, see arrows for more details.
`length.arrow`	arrow head length, see arrows for more details.
`font.sp`	An integer which specifies which font to use for species label. 1 corresponds to plain text (the default), 2 to bold face, 3 to italic and 4 to bold italic, see par for more details.
`leg`	a logical option for legend to be plotted or not, default leg=T.
`posi.leg`	setting legend positions with the following keywords "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center", see legend for more details.
`bty.leg`	the type of box to be drawn around the legend. The allowed values are "o" (the default) and "n", see legend for more details.
`...`	further arguments passed to or from other methods.

Details

The convex hulls measured is E is the environmental space. The arrows represent the species' subniche marginality from the origin G. See doi: 10.7717/peerj.3364 for more details on the subniche concept.

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$ls)[1]
#Create a factor which defines the subsets
fact <- factor(c(rep(1,N/2),rep(2,N/2)))
# nic1 will be use as reference and fact will be use to define the subniches environment
subnic1 <- subniche(nic1, fact)
sigg <- rtestrefor(subnic1,10)
sig = c(sigg$`1`$witomigtest$subni.pvalue[-28],sigg$`2`$witomigtest$subni.pvalue[-28])
plot_dym(subnic1, sig=sig, sig_thres= 0.1)
```

`plot_dym_sp` *Species subniches dynamic*

Description

The function represents the species' subniches SR within its realized niche NR.

Usage

```
plot_dym_sp(
  subnic,
  sp,
  xlab = NULL,
  ylab = NULL,
  main = NA,
  col.axis = "azure3",
  lty.axis = 2,
  lwd.axis = 2,
  border.E = "black",
  col.E = "#92c5de",
  lty.E = 1,
  lwd.E = 1,
  col.NR = "#fdb462",
  border.NR = "black",
  lty.NR = 1,
  lwd.NR = 1,
  col.NR.lab = "black",
  cex.NR.lab = 0.7,
  pch.NR.pos = 21,
  col.NR.pos = "black",
  col.NR.pt = "black",
  cex.NR.pos = 1,
```

```
    border.SR = "black",
    col.SR = "#a1d99b",
    lty.SR = 1,
    lwd.SR = 1,
    col.SR.lab = "black",
    cex.SR.lab = 0.7,
    fac.SR.lab = 1.2,
    pch.SR.pos = 21,
    col.SR.pos = "#ffa600",
    col.SR.pt = "black",
    cex.SR.pos = 1,
    col.arrow = "black",
    angle.arrow = 20,
    lwd.arrow = 2,
    length.arrow = 0.1,
    font.sp = 2,
    leg = T,
    posi.leg = "topleft",
    bty.leg = "n",
    ...
  )
```

Arguments

`subnic`	an object of class `subniche`.
`sp`	a character string of the species name.
`xlab`	label for x-axis, see title for more details.
`ylab`	label for y-axis, see title for more details.
`main`	a main title for the plot, see title for more details.
`col.axis`	axis color, see par for more details.
`lty.axis`	axis line type, see par for more details.
`lwd.axis`	axis width, see par for more details.
`border.E`	color border of E polygon, see polygon for more details.
`col.E`	inside color of E polygon, see polygon for more details.
`lty.E`	line type for the E border, see polygon for more details.
`lwd.E`	line width for the E border, see polygon for more details.
`col.NR`	inside color of NR polygon, see polygon for more details.
`border.NR`	color border of NR polygon, see polygon for more details.
`lty.NR`	line type for the NR border, see polygon for more details.
`lwd.NR`	line width for the NR border, see polygon for more details.
`col.NR.lab`	color of the species label representing the NR position, see textplot for more details.
`cex.NR.lab`	size of the species label representing the NR position, see textplot for more details.

`pch.NR.pos`	the type of points representing the NR position, see points for more details.
`col.NR.pos`	the color of points representing the NR position, see points for more details.
`col.NR.pt`	point color contour if pch=21:25.
`cex.NR.pos`	size of points representing the SR position, see points for more details.
`border.SR`	color border of SR polygon, see polygon for more details.
`col.SR`	inside color of SR polygon, see polygon for more details.
`lty.SR`	line type for the SR border, see polygon for more details.
`lwd.SR`	line width for the SR border, see polygon for more details.
`col.SR.lab`	color of the species label representing the SR position, see text for more details.
`cex.SR.lab`	size of the species label representing the SR position, see text for more details.
`fac.SR.lab`	factor for moving the SR labels from its original coordinates for clarity, by defaults they are multiply 1.2
`pch.SR.pos`	type of points representing the SR position, see points for more details.
`col.SR.pos`	color of points representing the SR position, see points for more details.
`col.SR.pt`	point color contour if pch=21:25.
`cex.SR.pos`	size of points representing the SR position, see points for more details.
`col.arrow`	arrow color, see arrows for more details.
`angle.arrow`	arrow angle head, see arrows for more details.
`lwd.arrow`	arrow width, see arrows for more details.
`length.arrow`	arrow head length, see arrows for more details.
`font.sp`	An integer which specifies which font to use for species label. 1 corresponds to plain text (the default), 2 to bold face, 3 to italic and 4 to bold italic, see par for more details.
`leg`	a logical option for legend to be plotted or not, default leg=T.
`posi.leg`	setting legend positions with the following keywords "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center", see legend for more details.
`bty.leg`	the type of box to be drawn around the legend. The allowed values are "o" (the default) and "n", see legend for more details.
`...`	further arguments passed to or from other methods.

Details

The convex hulls measured are :

1. E is the environmental space.
2. NR the realized subniche.
3. SR the species realized subniche.

The arrows represent the species' subniche marginality from the origin G. See doi: 10.7717/peerj.3364 for more details on the subniche concept.

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)
plot_dym_sp(subnic1, "Neba")
```

`plot_NR` *Community niche distribution*

Description

The function represents the species' niche NR position within the environmental space E.

Usage

```
plot_NR(
  subnic,
  sig = NULL,
  sig_thres = 0.05,
  xlab = NULL,
  ylab = NULL,
  main = NA,
  col.axis = "azure3",
  lty.axis = 2,
  lwd.axis = 2,
  border.E = "black",
  col.E = "#92c5de",
  lty.E = 1,
  lwd.E = 1,
  pch.NR.pos = 21,
  cex.NR.pos = 1,
  col.NR.pos = "#a1d99b",
  col.NR.pt = "black",
  col.NR.lab = "black",
  cex.NR.lab = NA,
  fac.NR.lab = 1.2,
  col.arrow = "black",
  angle.arrow = 20,
  lwd.arrow = 2,
  length.arrow = 0.1,
```

```
    font.sp = 2,
    leg = T,
    posi.leg = "topleft",
    bty.leg = "n",
    ...
  )
```

Arguments

`subnic`	an object of class `subniche`.
`sig`	a factor defining the significance species, default NULL.
`sig_thres`	value for minimum significance, default 0.05
`xlab`	label for x-axis, see title for more details.
`ylab`	label for y-axis, see title for more details.
`main`	a main title for the plot, see title for more details.
`col.axis`	axis color, see par for more details.
`lty.axis`	axis line type, see par for more details.
`lwd.axis`	axis width, see par for more details.
`border.E`	color border of E polygon, see polygon for more details.
`col.E`	inside color of E polygon, see polygon for more details.
`lty.E`	line type for the E border, see polygon for more details.
`lwd.E`	line width for the E border, see polygon for more details.
`pch.NR.pos`	type of points representing the NR position, see points for more details.
`cex.NR.pos`	size of points representing the NR position, see points for more details.
`col.NR.pos`	color of points representing the NR position, see points for more details.
`col.NR.pt`	point color contour if pch=21:25.
`col.NR.lab`	color of the species labels, see see text for more details.
`cex.NR.lab`	size of the species labels defautls NA for no labels, see see text for more details.
`fac.NR.lab`	factor for moving the NR labels from its original coordinates for clarity, by defaults they are multiply 1.2
`col.arrow`	arrow color, see arrows for more details.
`angle.arrow`	arrow angle head, see arrows for more details.
`lwd.arrow`	arrow width, see arrows for more details.
`length.arrow`	arrow head length, see arrows for more details.
`font.sp`	An integer which specifies which font to use for species label. 1 corresponds to plain text (the default), 2 to bold face, 3 to italic and 4 to bold italic, see par for more details.
`leg`	a logical option for legend to be plotted or not, default leg=T.
`posi.leg`	setting legend positions with the following keywords "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center", see legend for more details.
`bty.leg`	the type of box to be drawn around the legend. The allowed values are "o" (the default) and "n", see legend for more details.
`...`	further arguments passed to or from other methods.

Details

The convex hulls measured is E is the environmental space. The arrows represent the species' NR marginality from the origin G. See doi: 10.7717/peerj.3364 for more details on the subniche concept.

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$ls)[1]
#Create a factor which defines the subsets
fact <- factor(c(rep(1,N/2),rep(2,N/2)))
# nic1 will be use as reference and fact will be use to define the subniches environment
subnic1 <- subniche(nic1, fact)
sigi <- rtest(nic1,10)
M <- length(sigi$pvalue)
plot_NR(subnic1, sig=sigi$pvalue[-M], sig_thres= 0.1)
```

`plot_NR_sp` *Species niche*

Description

The function represents the species' niche NR within the environmental space E.

Usage

```
plot_NR_sp(
  subnic,
  sp,
  xlab = NULL,
  ylab = NULL,
  main = NA,
  col.axis = "azure3",
  lty.axis = 2,
  lwd.axis = 2,
  border.E = "black",
  col.E = "#92c5de",
  lty.E = 1,
  lwd.E = 1,
  border.NR = "black",
  col.NR = "#fdb462",
  lty.NR = 1,
  lwd.NR = 1,
  pch.NR.pos = 21,
```

```
    cex.NR.pos = 1,
    col.NR.pos = "#a1d99b",
    col.NR.pt = "black",
    col.NR.lab = "black",
    cex.NR.lab = NA,
    fac.NR.lab = 1.2,
    col.arrow = "black",
    angle.arrow = 20,
    lwd.arrow = 2,
    length.arrow = 0.1,
    font.sp = 2,
    leg = T,
    posi.leg = "topleft",
    bty.leg = "n",
    ...
  )
```

Arguments

`subnic`	an object of class `subniche`.
`sp`	a character string of the species name, default rownames(subnic$li)
`xlab`	label for x-axis, see title for more details.
`ylab`	label for y-axis, see title for more details.
`main`	a main title for the plot, see title for more details.
`col.axis`	axis color, see par for more details.
`lty.axis`	axis line type, see par for more details.
`lwd.axis`	axis width, see par for more details.
`border.E`	color border of E polygon, see polygon for more details.
`col.E`	inside color of E polygon, see polygon for more details.
`lty.E`	line type for the E border, see polygon for more details.
`lwd.E`	line width for the E border, see polygon for more details.
`border.NR`	color border of NR polygon, see polygon for more details.
`col.NR`	inside color of NR polygon, see polygon for more details.
`lty.NR`	line type for the NR border, see polygon for more details.
`lwd.NR`	line width for the NR border, see polygon for more details.
`pch.NR.pos`	type of points representing the NR position, see points for more details.
`cex.NR.pos`	size of points representing the NR position, see points for more details.
`col.NR.pos`	color of points representing the NR position, see points for more details.
`col.NR.pt`	point color contour if pch=21:25.
`col.NR.lab`	color of the species labels, see see text for more details.
`cex.NR.lab`	size of the species labels defaults NA for no labels, see see text for more details.

`fac.NR.lab`	factor for moving the NR labels from its original coordinates for clarity, by defaults they are multiply 1.2
`col.arrow`	arrow color, see arrows for more details.
`angle.arrow`	arrow angle head, see arrows for more details.
`lwd.arrow`	arrow width, see arrows for more details.
`length.arrow`	arrow head length, see arrows for more details.
`font.sp`	An integer which specifies which font to use for species label. 1 corresponds to plain text (the default), 2 to bold face, 3 to italic and 4 to bold italic, see par for more details.
`leg`	a logical option for legend to be plotted or not, default leg=T.
`posi.leg`	setting legend positions with the following keywords "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center", see legend for more details.
`bty.leg`	the type of box to be drawn around the legend. The allowed values are "o" (the default) and "n", see legend for more details.
`...`	further arguments passed to or from other methods.

Details

The convex hulls measured is E is the environmental space. The arrows represent the species' NR marginality from the origin G. See doi: 10.7717/peerj.3364 for more details on the subniche concept.

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)
plot_NR_sp(subnic1, "Neba")
```

`sep.factor.row` *A function to seperate 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

`subarea` *Convex hull decomposition*

Description

The function is used to calculate the coordinates and area of each convex hull from E environmental space to SR subniche.

Usage

```
subarea(subnic)
```

Arguments

`subnic`	an object of class `subniche`.

Details

The convex hulls measured are :

1. E is the environmental space.
2. K the sub-environmental space.
3. NR the realized subniche.
4. SP the existing fundamental subniche.
5. SB the area of the biological constraint reducing SP.
6. SR the species realized subniche.

See doi: 10.7717/peerj.3364 for more details on the subniche concept.

Value

A list containing the coordinates and area of each convex hulls

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. doi: 10.7717/peerj.3364.

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)
area_sub <- subarea(subnic1)
```

`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'
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
`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 has 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)

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

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. doi: 10.7717/peerj.3364.

Calenge C., Dufour A.B. and Maillard D. (2005). K-select analysis: a new method to analyze habitat selection in radio-tracking studies. *Ecological modelling*, **186**, 143-153. doi: 10.1016/j.ecolmodel.2004.12.005.

Doledec S., Chessel D. and Gimaret C. (2000). Niche separation in community analysis: a new method. *Ecology*,**81**, 2914-1927. doi: 10.2307/177351

Thomas, D.L., Taylor, E.J. (1990). Study Designs and Tests for Comparing Resource Use and Availability II. *Natl. Widl.* **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
#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)
```

`subplot` *Sub-community plot under each sub-environmental space K*

Description

The function to represent the community subniche position under each subenvironment K with their respective marginality from Gk.

Usage

```
subplot(
  subnic,
  main = NULL,
  sig = NULL,
  sig_thres = 0.05,
  xlab = NULL,
  ylab = NULL,
  col.axis = "azure3",
  lty.axis = 2,
  lwd.axis = 2,
  pch.SR.pos = 21,
  cex.SR.pos = 1,
  col.SR.pt = "black",
  col.SR.pos = "#ffa600",
  col.SR.lab = "black",
  cex.SR.lab = NA,
  fac.SR.lab = 1.2,
  border.E = "black",
  col.E = "#92c5de",
  lty.E = 1,
  lwd.E = 1,
  border.K = "black",
  col.K = "#2c7fb8",
  lty.K = 1,
  lwd.K = 1,
  col.arrow = "black",
  angle.arrow = 20,
  lwd.arrow = 2,
  length.arrow = 0.1,
  col.Gk.pos = "red",
  col.Gk.pt = "black",
  cex.Gk.pos = 1,
  pch.Gk.pos = 21,
  col.su = "#b35806",
  pt.su = "black",
  cex.su = 0.7,
  pch.su = 1,
  font.sp = 2,
  leg = T,
  posi.leg = "topleft",
  bty.leg = "n",
  ...
```

```
)
```

Arguments

`subnic`	an object of class `subniche`.
`main`	a main title for the plot, see title for more details.
`sig`	a factor defining the significance species, default NULL.
`sig_thres`	value for minimum significance, default 0.05
`xlab`	a label for the x axis, defaults to a description of x, see title for more details.
`ylab`	a label for the y axis, defaults to a description of y, see title for more details.
`col.axis`	axis color, see par for more details.
`lty.axis`	axis line type, see par for more details.
`lwd.axis`	axis width, see par for more details.
`pch.SR.pos`	type of the point representing SR position, see points for more details.
`cex.SR.pos`	size of the point representing SR position, see points for more details.
`col.SR.pt`	point color contour if pch=21:25.
`col.SR.pos`	color of the point representing SR position, see points for more details.
`col.SR.lab`	color of the species labels, see see text for more details.
`cex.SR.lab`	size of the species labels defautls NA for no labels, see see text for more details.
`fac.SR.lab`	factor for moving the SR labels from its original coordinates for clarity, by defaults they are multiply 1.2
`border.E`	color border of E polygon, see polygon for more details.
`col.E`	inside color of E polygon, see polygon for more details.
`lty.E`	line type for the E border, see polygon for more details.
`lwd.E`	line width for the E border, see polygon for more details.
`border.K`	color border of K polygon, see polygon for more details.
`col.K`	inside color of K polygon, see polygon for more details.
`lty.K`	line type for the K border, see polygon for more details.
`lwd.K`	line width for the K border, see polygon for more details.
`col.arrow`	arrow color, see arrows for more details.
`angle.arrow`	arrow angle head, see arrows for more details.
`lwd.arrow`	arrow width, see arrows for more details.
`length.arrow`	arrow head length, see arrows for more details.
`col.Gk.pos`	color of the point representing Gk, see points for more details.
`col.Gk.pt`	point color contour if pch=21:25.
`cex.Gk.pos`	size of the point representing Gk, see points for more details.
`pch.Gk.pos`	type of the point representing Gk, see points for more details.
`col.su`	color of the points representing the sampling units (SU), see points for more details.

`pt.su`	point color contour if pch=21:25.
`cex.su`	size of the points representing the sampling units (SU), see points for more details.
`pch.su`	type of the points representing the sampling units (SU), see points for more details.
`font.sp`	font of the species labels, see see text for more details.
`leg`	a logical option for legend to be plotted or not, default leg=T.
`posi.leg`	legend location in the graph, see legend for more details.
`bty.leg`	the type of box to be drawn around the legends. The allowed values are "o" (the default) and "n". See legend for more details
`...`	further arguments passed to or from other methods.

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$ls)[1]
#Create a factor which defines the subsets
fact <- factor(c(rep(1,N/2),rep(2,N/2)))
# nic1 will be use as reference and fact will be use to define the subniches environment
subnic1 <- subniche(nic1, fact)
#Two graphs are drawn one after the other
siggk <- rtestsubor(subnic1,10)
sig = c(siggk$`1`$witomigktest$subni.pvalue[-28],siggk$`2`$witomigktest$subni.pvalue[-28])
subplot(subnic1, sig = sig, sig_thres= 0.1)
```

`subplot_K` *Plot sub-environmental space K in E*

Description

The function to represent the sub-environment K in E.

Usage

```
subplot_K(
  subnic,
  main = NULL,
  xlab = NULL,
  ylab = NULL,
  col.axis = "azure3",
  lty.axis = 2,
```

```
    lwd.axis = 2,
    border.E = "black",
    col.E = "#92c5de",
    lty.E = 1,
    lwd.E = 1,
    border.K = "black",
    col.K = "#2c7fb8",
    lty.K = 1,
    lwd.K = 1,
    col.Gk.pos = "red",
    col.Gk.pt = "black",
    cex.Gk.pos = 1,
    pch.Gk.pos = 21,
    col.Gk.lab = "black",
    cex.Gk.lab = 0.8,
    fac.Gk.lab = 1.5,
    col.su = "#b35806",
    pt.su = "black",
    cex.su = 0.7,
    pch.su = 1,
    leg = T,
    posi.leg = "topleft",
    bty.leg = "n",
    ...
)
```

Arguments

`subnic`	an object of class `subniche`.
`main`	a main title for the plot, see title for more details.
`xlab`	label for x-axis, see title for more details.
`ylab`	label for y-axis, see title for more details.
`col.axis`	axis color, see par for more details.
`lty.axis`	axis line type, see par for more details.
`lwd.axis`	axis width, see par for more details.
`border.E`	color border of E polygon, see polygon for more details.
`col.E`	inside color of E polygon, see polygon for more details.
`lty.E`	line type for the E border, see polygon for more details.
`lwd.E`	line width for the E border, see polygon for more details.
`border.K`	color border of K polygon, see polygon for more details.
`col.K`	inside color of K polygon, see polygon for more details.
`lty.K`	line type for the K border, see polygon for more details.
`lwd.K`	line width for the K border, see polygon for more details.
`col.Gk.pos`	color of the point representing Gk, see points for more details.

`col.Gk.pt`	point color contour if pch=21:25.
`cex.Gk.pos`	size of the point representing Gk, see points for more details.
`pch.Gk.pos`	type of the point representing Gk, see points for more details.
`col.Gk.lab`	color of the Gk labels, see see text for more details.
`cex.Gk.lab`	size of the Gk labels defaults NA for no labels, see see text for more details.
`fac.Gk.lab`	factor for moving the Gk labels from its original coordinates for clarity, by defaults they are multiply 1.2
`col.su`	color of the points representing the sampling units (SU), see points for more details.
`pt.su`	point color contour if pch=21:25.
`cex.su`	size of the points representing the sampling units (SU), see points for more details.
`pch.su`	type of the points representing the sampling units (SU), see points for more details.
`leg`	a logical option for legend to be plotted or not, default leg=T.
`posi.leg`	legend location in the graph, see legend for more details.
`bty.leg`	the type of box to be drawn around the legends. The allowed values are "o" (the default) and "n". See legend for more details
`...`	further arguments passed to or from other methods.

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)
#Plot K in E
subplot_K(subnic1)
```

`subplot_sp` *Plot a species subniche under each sub-environmental space K*

Description

The function to represent the species subniche under each subenvironment K with their respective marginality from G_K.

Usage

```
subplot_sp(
  subnic,
  sp,
  main = NULL,
  col.axis = "azure3",
  lty.axis = 2,
  lwd.axis = 2,
  xlab = NULL,
  ylab = NULL,
  border.E = "black",
  col.E = "#92c5de",
  lty.E = 1,
  lwd.E = 1,
  border.K = "black",
  lwd.K = 1,
  col.K = "#2c7fb8",
  lty.K = 1,
  col.Gk.pos = "red",
  col.Gk.pt = "black",
  cex.Gk.pos = 1,
  pch.Gk.pos = 21,
  border.SP = "#bc5090",
  col.SB = "#ffff99",
  lty.SP = 1,
  lwd.SP = 2,
  border.NR = "#fdb462",
  col.NR = NA,
  lty.NR = 1,
  lwd.NR = 2,
  border.SR = "#a1d99b",
  col.SR = "#a1d99b",
  lty.SR = 1,
  lwd.SR = 1,
  pch.SR.pos = 19,
  cex.SR.pos = 1,
  col.SR.pt = "black",
  col.SR.pos = "black",
  cex.SR.lab = 0.7,
  col.SR.lab = "black",
  fac.SR.lab = 1.2,
  font.sp = 2,
  col.arrow = "black",
  angle.arrow = 20,
  lwd.arrow = 2,
  length.arrow = 0.1,
  leg = T,
  posi.leg = "topleft",
```

```
  bty.leg = "n",
  ...
)
```

Arguments

`subnic`	an object of class `subniche`.
`sp`	a character string of the species name.
`main`	a main title for the plot, see title for more details.
`col.axis`	axis color, see par for more details.
`lty.axis`	axis line type, see par for more details.
`lwd.axis`	axis width, see par for more details.
`xlab`	label for x-axis, see title for more details.
`ylab`	label for y-axis, see title for more details.
`border.E`	color border of E polygon, see polygon for more details.
`col.E`	inside color of E polygon, see polygon for more details.
`lty.E`	line type for the E border, see polygon for more details.
`lwd.E`	line width for the E border, see polygon for more details.
`border.K`	color border of K polygon, see polygon for more details.
`lwd.K`	line width for the K border, see polygon for more details.
`col.K`	inside color of K polygon, see polygon for more details.
`lty.K`	line type for the K border, see polygon for more details.
`col.Gk.pos`	color of the point representing G_k, see points for more details.
`col.Gk.pt`	point color contour if pch=21:25.
`cex.Gk.pos`	size of the point representing G_k, see points for more details.
`pch.Gk.pos`	type of the point representing G_k, see points for more details.
`border.SP`	color border of species subniche polygon, see polygon for more details.
`col.SB`	color of the SB area.
`lty.SP`	line type for the SP border, see polygon for more details.
`lwd.SP`	line width for the SP border, see polygon for more details.
`border.NR`	color border of NR polygon, see polygon for more details.
`col.NR`	inside color of NR polygon, see polygon for more details.
`lty.NR`	line type for the NR border, see polygon for more details.
`lwd.NR`	line width for the NR border, see polygon for more details.
`border.SR`	color border of SR polygon, see polygon for more details.
`col.SR`	inside color of SR polygon, see polygon for more details.
`lty.SR`	line type for the SR border, see polygon for more details.
`lwd.SR`	line width for the SR border, see polygon for more details.
`pch.SR.pos`	type of points representing the SR position, see points for more details.

`cex.SR.pos`	size of points representing the SR position, see points for more details.
`col.SR.pt`	point color contour if pch=21:25.
`col.SR.pos`	color of points representing the SR position, see points for more details.
`cex.SR.lab`	size of the species label representing the SR position, see text for more details.
`col.SR.lab`	color of the species label representing the SR position, see text for more details.
`fac.SR.lab`	factor for moving the SR labels from its original coordinates for clarity, by defaults they are multiply 1.2
`font.sp`	An integer which specifies which font to use for species label. 1 corresponds to plain text (the default), 2 to bold face, 3 to italic and 4 to bold italic, see par for more details.
`col.arrow`	arrow color, see arrows for more details.
`angle.arrow`	arrow angle head, see arrows for more details.
`lwd.arrow`	arrow width, see arrows for more details.
`length.arrow`	arrow head length, see arrows for more details.
`leg`	a logical option for legend to be plotted or not, default leg=T.
`posi.leg`	legend location in the graph, see legend for more details.
`bty.leg`	the type of box to be drawn around the legends. The allowed values are "o" (the default) and "n". See legend for more details
`...`	further arguments passed to or from other methods.

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$ls)[1]
#Create a factor which defines the subsets
fact <- factor(c(rep(1,N/2),rep(2,N/2)))
# nic1 will be use as reference and fact will be use to define the subniches environment
subnic1 <- subniche(nic1, fact)
eig <- round(subnic1$eig/sum(subnic1$eig)*100,2)[1:2]
#Two graphs are drawn one after the other
subplot_sp(subnic1,"Neba")
```

Index