Package 'segRDA'

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Title Modeling Non-Continuous Linear Responses of Ecological Data

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Description Tools for modeling non-continuous linear responses of ecological communities to environmental data. The package is straightforward through three steps: (1) data ordering (function OrdData()), (2) split-moving-window analysis (function SMW()) and (3) piecewise redundancy analysis (function pwRDA()). Relevant references include Cornelius and Reynolds (1991) <doi:10.2307/1941559> and Legendre and Legendre (2012, ISBN: 9780444538697).

Depends R (>= 2.15), vegan (>= 2.4)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

URL https://github.com/DaniloCVieira/segRDA

BugReports https://github.com/DaniloCVieira/segRDA/issues

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NeedsCompilation no

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R **topics documented:**

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extract   *Extract results and breakpoints from a* smw *object*

Description

Functions to extract results and breakpoints from a smw object

Usage

```
## S3 method for class 'smw'
extract(smw, w = NULL, index = "dp", sig = "z",
  z = 1.85, BPs = "max", seq.sig = 3)

## S3 method for class 'dp'
bp(dp)
```

Arguments

smw   An object of class smw resulted from the [SMW](#) analysis.

w   Numeric. A "target" window size from which results will be extracted (see
            Details). Only effective if the smw object contains results from multiple window
            sizes.

index   The result to be extracted:

            - "dp": The dissimilarity profile (DP) table containing significant disconti-
              nuities and suggested breakpoints. The returned DP has class "dp", with
              an own generic print method. The print command prints and returns
              invisibly the DP.
            - "rdp": data frame containing the randomized DP;
            - "md": mean dissimilarity of the randomized DP;
            - "sd": standard deviation for each sample position;
            - "oem": overall expected mean dissimilarity;
            - "osd": average standard deviation for the dissimilarities;
            - "params": list with input arguments

sig	Significance test for detecting dissimilarity values that differs significantly from those appearing in a random pattern. The following tests are considered with default to sig.test="z":

- "dp" consider normalized dissimilarity (z-scores) discontinuities that exceed a "z" critical value;
- "sd" consider dissimilarity discontinuities that exceed mean plus one standard deviation;
- "SD2" consider dissimilarity discontinuities that exceed mean plus two standard deviation;
- "tail1" Consider dissimilarity discontinuities that exceed 95 percent confidence limits.

z	The critical value for the significance of z-values. Defaults to 'z=1.85' (Erdös et.al, 2014).
BPs	Defines if the breakpoints should be chosen as those sample positions corresponding to the maximum dissimilarity in a sequence of significant values ("max") or as those sample positions corresponding to the median position of the sequence ("median"). Defaults to BPs="max". If NULL the breakpoints are not computed.
seq.sig	The maximum length of consecutive, significant values of dissimilarity that will be considered in defining the community breakpoints. Defaults to seq.sig=3;
dp	An object of class dp (see Details).

Details

If the smw object contains results from multiple window sizes, the DP table will be based on the average Z-score over the set of analysed window sizes. Available methods for class "dp" are print, bp and plot.

The argument w is optional. If the smw object is length 1, w is ignored. If length(smw)>1 and w is NULL, the function will extract the dissimilarity profile averaged over the set of window sizes.

Value

- "extract" returns a result called by the argument index (see Details);
- "bp" returns the locations of the breakpoints.

See Also

plot.smw.

Examples

```
data(sim1)
sim1o<-OrdData(sim1$envi,sim1$comm)


ws50<-SMW(yo=sim1o$yo,ws=50)
ws50_dp<-extract(ws50)
```

```
head(ws50_dp)
```

---

nema   *Nematodes data from Araca Bay, Sao Sebastiao, Brazil.*

Description

A total of 37 sites arranged in an irregular grid were surveyed during four sampling campaigns at the Araçá Bay, southeastern Brazil. A total of 141 samples were collected for analyzing changes in nematodes assemblages along the environmental gradient of the bay.

Usage

```
data(nema)
```

Format

nema is a list with the following components:

envi a matrix with 141 sites and 9 environmental variables: chlorophyll a (mg.m-2), bathymetry (meters), percentage of total organic carbon, percentage of coarse sands (as the sum of pebbles, very coarse, coarse, and medium grains), percentage of fine sand, percentage of very fine sand, mean grain size, and sorting coefficient.

comm matrix with 141 sites of 194 nematodes species

References

- Checon, H. H., D. C. Vieira, G. N. Corte, E. C. P. M. Sousa, G. Fonseca, and A. C. Z. Amaral. 2018. Defining soft bottom habitats and potential indicator species as tools for monitoring coastal systems: A case study in a subtropical bay. Ocean & Coastal Management.

- Corte, G. N., H. H. Checon, G. Fonseca, D. C. Vieira, F. Gallucci, M. Di Domenico, and A. C. Z. Amaral. 2017. Cross-taxon congruence in benthic communities: Searching for surrogates in marine sediments. Ecological Indicators 78:173–182.

OrdData   *Data ordering*

Description

Ordinates both community and explanatory matrices based on the first RDA score.

Usage

```
OrdData(x, y, axis = 1, method = NA, ...)
```

Arguments

x	explanatory matrix;
y	community matrix;
axis	the RDA axis in which the ordering should be based. Defaults to axis=1
method	standardization method (described in decostand) to be applied on y before the RDA analysis. If NA (default), no transformation is performed.
...	furhter parameters passed to decostand and vegan::rda;

Value

An object of class "ord", which is a list consisting of:

1. xo: the ordered explanatory matrix
2. yo: the ordered community matrix (non-transformed)
3. x: the original explanatory matrix
4. y: the original community matrix

Author(s)

Danilo Candido Vieira

Examples

```
data(sim1)
sim1.o<-OrdData(x=sim1$envi, y=sim1$comm)
sim1.o<-OrdData(x=sim1$envi, y=sim1$comm, method="hellinger")
```

---

plot.smw   *Plot the dissimilarity profiles*

Description

Plot results from smw and dp objects. The command is a shortcut for extracting and plotting SMW resuts. Auxiliary arguments from extract (i.e. sig, z, BPs and seq.sig) can be passed to plot.smw. The auxilary method bgDP is available for the returned dp object when the argument bg is not NULL (see Details).

Usage

```
## S3 method for class 'smw'
plot(x, w = NULL, sig = "z", z = 1.85, BPs = "max",
  seq.sig = 3, w.effect = F, values = c("zscore", "diss"),
  pchs = c(16, 16, 17), cols = c("black", "red", "blue"), bg = NULL,
  bg_alpha = 0.1, wcols = "rainbow", legend = TRUE, ...)

## S3 method for class 'dp'
bgDP(dp)
```

Arguments

x	An object of class `"smw"` resulted from the function [SMW](#).
w	The window size from which results will be plotted. Only effective if length(smw)>1.
sig	Significance test for detecting dissimilarity values that differs significantly from those appearing in a random pattern. If NULL the significance test is ommited from the plot.The following tests are considered with default to sig.test="z":

- `'z'` consider normalized dissimilarity (z-scores) discontinuities that exceed a "z" critical value;
- `'sd'` consider dissimilarity discontinuities that exceed mean plus one standard deviation;
- `'SD2'` consider dissimilarity discontinuities that exceed mean plus two standard deviation;
- `'tail1'` Consider dissimilarity discontinuities that exceed 95 percent confidence limits.

z	The critical value for the significance of z-values. Defaults to `'z=1.85'` (Erdös et.al, 2014).
BPs	Defines if the breakpoints should be chosen as those sample positions corresponding to the maximum dissimilarity in a sequence of significant values (`"max"`) or as those sample positions corresponding to the median position of the sequence (`"median"`). Defaults to BPs=`"max"`. If NULL the breakpoints are not computed.
seq.sig	The maximum length of consecutive, significant values of dissimilarity that will be considered in defining the community breakpoints. Defaults to seq.sig=3;
w.effect	Logical, if TRUE draws a dissimilarity profile using different windows sizes and returns an invisible data.frame with the breakpoint frequencies. Only effective if length(smw)>1. The function uses [extract](#) with defaults parameters to define the breakpoint positions for each of the evaluated window sizes.
values	Character. `"zscore"` for plotting z-scores, `"diss"` for plotting dissimilarity values.
pchs	A numerical vector of the form c(d,s,b) which modifies the default symbols of the plot. The default pch = c(16,16,17) describes respectively the dissimilarity values, significant dissimilarity values and breakpoints.
cols	Vector of length 3 specifying the colors of the plot in the same way as the pch argument. Defaults to colors=c("black","red","blue").
bg	Optional. Sets background colors according to the breakpoints. It can be expressed either by a vector of colors or by the name of a pallet function (e.g. `"rainbow"`).
bg_alpha	Factor modifying the opacity alpha of the backgroud [0,1].
wcols	Sets the colors for the window sizes (lines) when w.effect=TRUE. It can be expressed by a vector of colors or by the name of a pallet function. Defaults to wcol="rainbow" which uses the colour palette rainbow from R stats.
legend	Logical. Should a default legend appear?
...	Further graphical parameters.
dp	An object of class dp.

Details

If bg is not NULL, the attribute `params$bg` is added to the returned dp. This attribute contains the sample colors used by the argument bg. The auxilary method bgDP can be used for accessing this color vector.

Value

The function returns invisibly an object of class "dp" (see Details).

Author(s)

Danilo Candido Vieira

See Also

SMW, extract.

Examples

```
data(sim1)
sim1o<-OrdData(sim1$envi,sim1$comm)


ws20<-SMW(yo=sim1o$yo,ws=20)
pool<-SMW(yo=sim1o$yo,ws=c(20,30,40))
plot(ws20)
plot(pool, w.effect=TRUE)
```

---

pwRDA   *Piecewise redundancy analysis (pwRDA)*

Description

Perform a pwRDA using the specified breakpoints

Usage

```
pwRDA(x.ord, y.ord, BPs, n.rand = 99)
```

Arguments

x.ord	ordered explanatory matrix
y.ord	ordered community matrix
BPs	community breakpoints
n.rand	The number of randomizations for significance computation

Value

Returns an invisible list of length 4:

1. `..$summ`: summary statistics of the pwRDA analysis;
2. `..$rda.0`: full model cca object, which is described separately in vegan::`cca.object`
3. `..$rda.pw`: pw model cca object, which is described separately in vegan::`cca.object`

Author(s)

Danilo Candido Vieira

Examples

```
data(sim1)
sim1o<-OrdData(sim1$envi,sim1$comm)


w50<-SMW(sim1o$yo, ws=50)
sim1.pw<-pwRDA(sim1o$xo,sim1o$yo, BPs=bp(extract(w50)))
```

---

sim1   *Simulated datasets*

Description

Simulated datasets for testing **segRDA** package

Usage

```
data(sim1)

data(sim2)

data(sim3)
```

Format

Each data set is a list with the following components:

envi environmental matrix

comm community matrix

Description

Function `SMW` performs split moving window analysis (SMW) with randomizations tests. It may compute dissimilarities for a single window size or for several windows sizes.

Usage

```
SMW(yo, ws, dist = "bray", rand = c("shift", "plot"), n.rand = 99)
```

Arguments

yo	The ordered community matrix.
ws	The window sizes to be analyzed. Either a single value or a vector of values.
dist	The dissimilarity index used in vegan::`vegdist`. Defaults to `'bray'`.
rand	The type of randomization for significance computation (Erdös et.al, 2014):

- `"shift"`: restricted randomization in which data belonging to the same species are randomly shifted along the data series ("Random shift");
- `"plot"`: unrestricted randomization: each sample is randomly repositioned along the data series ("Random plot").

n.rand	The number of randomizations.

Value

A two-level list object (class `smw`) describing the SMW results for each window w analyzed. The smw object is of length ws, and each of the w slots is a list of SMW results:

- `..$dp`: The raw dissimilarity profile (DP). The DP is a data frame giving the positions, labels, values of dissimilarity and z-scores for each sample;
- `..$rdp`: data frame containing the randomized DP;
- `..$md`: mean dissimilarity of the randomized DP;
- `..$sd`: standard deviation for each sample position;
- `..$oem`: overall expected mean dissimilarity;
- `..$osd`: average standard deviation for the dissimilarities;
- `..$params`: list with input arguments

Available methods for class `"smw"` are `print`, `extract` and `plot`.

Author(s)

Danilo Candido Vieira

References

- Erdos, L., Z. Bátori, C. S. Tölgyesi, and L. Körmöczi. 2014. The moving split window (MSW) analysis in vegetation science - An overview. Applied Ecology and Environmental Research 12:787–805.

- Cornelius, J. M., and J. F. Reynolds. 1991. On Determining the Statistical Significance of Discontinuities with Ordered Ecological Data. Ecology 72:2057–2070.

See Also

plot.smw, extract.

Examples

```
data(sim1)
sim1o<-OrdData(sim1$envi,sim1$comm)


ws20<-SMW(yo=sim1o$yo,ws=20)
pool<-SMW(yo=sim1o$yo,ws=c(20,30,40))
```

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