Package ‘dynRB’

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Type Package

Title Dynamic Range Boxes

Version 0.19

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Description Improves the concept of multivariate range boxes, which is highly susceptible for outliers and does not consider the distribution of the data. The package uses dynamic range boxes to overcome these problems.

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Contents

`dynRB-package` *Dynamic Range Boxes*

Description

The package DynRB improves the concept of multivariate range boxes, which is highly susceptible for outlines and does not consider the distribution of the data. The package uses dynamic range boxes to overcome these problems.

Details

Package:	dynRB
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References

Junker RR, Kuppler J, Bathke AC, Schreyer ML, Trutschnig W (2016) Dynamic range boxes - A robust non-parametric approach to quantify size and overlap of n-dimensional hypervolumes. Methods in Ecology and Evolution doi: 10.1111/2041-210X.12611

Judith H. Parkinson, Raoul Kutil, Jonas Kuppler, Robert R. Junker, Wolfgang Trutschnig, Arne C. Bathke: A Fast and Robust Way to Estimate Overlap of Niches and Draw Inference, International Journal of Biostatistics (2018)

Examples

```
# example function dynRB_VPa
# for reliable results use steps = 201
data(finch2)
r<-dynRB_VPa(finch2, steps = 101)
r$result
```

`dynRB_Pn` *Pairwise overlaps for each dimension*

Description

Function returns pairwise overlaps for each dimension n. Number of dynamic range boxes (`steps`) can be adjusted. Default: `steps = 201`

Usage

```
dynRB_Pn(A = A, steps = 201, correlogram = FALSE, row_col = c(2, 2))
```

Arguments

`A`	Data frame, where the first column is a character vector containing the objects (e.g. species) and the other columns are numeric vectors (containing measurements).
`steps`	Number of range boxes. Default: `steps = 201`
`correlogram`	If `TRUE`, the correlogram for each species is shown. If `FALSE`, no correlogram is shown. Default: `correlogram = FALSE`
`row_col`	Number of rows and columns of the figures (correlogram for each species). Default: `row_col = c(2, 2)`

Value

Data frame containing the summarized overlaps for each pair of objects and dimension.

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References

Junker RR, Kuppler J, Bathke AC, Schreyer ML, Trutschnig W (2016) Dynamic range boxes - A robust non-parametric approach to quantify size and overlap of n-dimensional hypervolumes. Methods in Ecology and Evolution doi: 10.1111/2041-210X.12611

Examples

```
# example function dynRB_Pn
# for reliable results use steps = 201
data(finch2)
r<-dynRB_Pn(finch2, steps = 101)
```

`dynRB_Vn` *Relative Dynamic Range Box size per dimension and object*

Description

Function returns Dynamic Range Box size of each dimension n. Number of dynamic range boxes (`steps`) can be adjusted. Default: `steps = 201`

Usage

```
dynRB_Vn(A = A, steps = 201, correlogram = FALSE, row_col = c(2, 2))
```

Arguments

`A`	Data frame, where the first column is a character vector and the other columns are numeric vectors.
`steps`	Number of range boxes. Default: `steps = 201`
`correlogram`	If `TRUE`, the correlogram for each species is shown. If `FALSE`, no correlogram is shown. Default: `correlogram = FALSE`
`row_col`	Number of rows and columns of the figures (correlogram for each species). Default: `row_col = c(2, 2)`

Value

Data frame containing the summarized niche length for each object and dimension.

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References

Junker RR, Kuppler J, Bathke AC, Schreyer ML, Trutschnig W (2016) Dynamic range boxes - A robust non-parametric approach to quantify size and overlap of n-dimensional hypervolumes. Methods in Ecology and Evolution doi: 10.1111/2041-210X.12611

Examples

```
# example function dynRB_Vn
# for reliable results use steps = 201
data(finch2)
r<-dynRB_Vn(finch2, steps = 101)
```

`dynRB_VPa` *Size and pairwise overlap*

Description

Function returns size and pairwise overlaps of niches or trait-spaces. Size or overlaps of dimensions can be aggregated by using either "product", "mean" or "geometric mean" as aggregation method. The results obtained by using the product are automatically printed. Number of dynamic range boxes (`steps`) can be adjusted. Default: `steps = 201`

Usage

```
dynRB_VPa(A = A, steps = 201, correlogram = FALSE, row_col = c(2, 2),
          pca.corr = FALSE, var.thres = 0.9)
```

Arguments

`A`	Data frame, where the first column is a character vector and the other columns are numeric vectors.
`steps`	Number of range boxes. Default: `steps = 201`
`correlogram`	If `TRUE`, the correlogram for each species is shown. If `FALSE`, no correlogram is shown. Default: `correlogram = FALSE`
`row_col`	Number of rows and columns of the figures (correlogram for each species). Default: `row_col = c(2, 2)`
`pca.corr`	If `TRUE`, a principal components analysis is performed.
`var.thres`	Variance predicted by the PCA-axes, if `pca.corr = TRUE`.

Value

Data frame containing the summarized niche overlap (and volume) for each pair of objects aggregated by all three possible choices (i.e. product, mean, geometric mean).

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References

Junker RR, Kuppler J, Bathke AC, Schreyer ML, Trutschnig W (2016) Dynamic range boxes - A robust non-parametric approach to quantify size and overlap of n-dimensional hypervolumes. Methods in Ecology and Evolution doi: 10.1111/2041-210X.12611

Examples

```
# example function dynRB_VPa
# for reliable results use steps = 201
data(finch2)
r<-dynRB_VPa(finch2, steps = 101, correlogram = TRUE, row_col = c(1,1))
r$result
```

`finch` *Data set finch*

Description

To demonstrate the application of the functions for real world data, we used existing data sets on niches and trait-spaces and quantified their sizes and overlaps. The data set finch is a data set on morphological measurements of Darwin finches. The data set comprises quantitative measurements of nine traits characterizing five species of finches, each trait was measured at least in 10 individuals per species.

Usage

```
data("finch")
```

Format

A data frame with 146 observations on the following 10 variables.

`Species` a character vector of the Species Geospiza heliobates, Geospiza prosthemelas prosthemelas, Geospiza fuliginosa parvula, Geospiza fortis fortis and Geospiza fortis platyrhyncha

`BodyL` a numeric vector

`WingL` a numeric vector

`TailL` a numeric vector

`BeakW` a numeric vector

`BeakH` a numeric vector

`LBeakL` a numeric vector

`UBeakL` a numeric vector

`N.UBkL` a numeric vector

`TarsusL` a numeric vector

Source

Snodgrass R and Heller E (1904) Papers from the Hopkins-Stanford Galapagos Expedition, 1898-99. XVI. Birds. Proceedings of the Washington Academy of Sciences 5: 231-372.

Examples

```
data(finch)
## quick overview
head(finch)
```

`finch2` *Subset of data set finch*

Description

To demonstrate the application of the functions for real world data, we used existing data sets on niches and trait-spaces and quantified their sizes and overlaps. The data set finch2 is a data set on morphological measurements of three Darwin finches. The data set comprises quantitative measurements of nine traits characterizing two species of finches, each trait was measured at least in 10 individuals per species.

Usage

```
data("finch2")
```

Format

A data frame with 103 observations on the following 10 variables.

`Species`	a character vector of the Species Geospiza fuliginosa parvula and Geospiza fortis fortis
`BodyL`	a numeric vector
`WingL`	a numeric vector
`TailL`	a numeric vector
`BeakW`	a numeric vector
`BeakH`	a numeric vector
`LBeakL`	a numeric vector
`UBeakL`	a numeric vector
`N.UBkL`	a numeric vector
`TarsusL`	a numeric vector

Source

Snodgrass R and Heller E (1904) Papers from the Hopkins-Stanford Galapagos Expedition, 1898-99. XVI. Birds. Proceedings of the Washington Academy of Sciences 5: 231-372.

Examples

```
data(finch2)
## quick overview
head(finch2)
```

`overview` *Overview function*

Description

This functions can be used to show the graphics generated by the functions dynRB_Pn,dynRB_Vn and dynRB_VPa.

Usage

```
overview(r, row_col = c(3, 3))
```

Arguments

`r`	Output of the function dynRB_Pn,dynRB_Vn or dynRB_VPa.
`row_col`	Number of rows and columns of the figures. Default: `row_col = c(3, 3)`

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Examples

```
# example for the function dynRB_Pn
# for reliable results use steps = 201
data(finch2)
r<-dynRB_Pn(finch2, steps = 101)
overview(r)
```

`ranks_OV` *Overlaps for each dimension using ranks*

Description

Function returns the asymmetric overlaps for each dimension, calculated by the method published by Parkinson et al. (2018) using ranks. Further two confidence intervals are returned for each estimate. The confidence level, as well as the repetitions for bootstrap can be adjusted.

Usage

```
ranks_OV(A = A, alpha = 0.05, reps4boot = 1000, digit = 3)
```

Arguments

`A`	Data frame, where the first column contains two objects (e.g. species) and the other columns are numeric vectors (containing measurments).
`alpha`	The confidence level. Default: `alpha = 0.05`
`reps4boot`	Number of repetitions for the bootstrap. . Default: `reps4boot = 1000`
`digit`	Number of digits after which the results are cut off. Default: `digit = 3`

Value

Data Frame containing the two asymmetric overlaps for each dimension together with their confidence intervals. The last row contains the d-dimensional asymmetric overlaps.

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References

Judith H. Parkinson, Raoul Kutil, Jonas Kuppler, Robert R. Junker, Wolfgang Trutschnig, Arne C. Bathke: A Fast and Robust Way to Estimate Overlap of Niches and Draw Inference, International Journal of Biostatistics (2018)

Examples

```
# example function ranks_OV
data(finch2)
head(finch2)
ranks_OV(finch2[1:4], alpha = 0.05)
```

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