Package 'RMacoqui'

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Type Package

Title Identifying and describing chorotypes based on similarity between species distributions

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Description RMacoqui develops a probability procedure for the identification of chorotypes, i.e. distribution patterns shared by a group of species, which can be operatively identified within an area.

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R topics documented:

`RMacoqui-package` *Identifying and describing chorotypes based on species distributions*

Description

RMacoqui develops a probability procedure for the identification of chorotypes, i.e. distribution patterns shared by a group of species, which can be operatively identified within an area (Baroni-Urbani et al., 1978). This method was first published by M<e1>rquez et al. (1997), based on a prior proposal for detecting biogeographic boundaries (Real et al., 1992), and with a mathematic rationale derived from McCoy et al. (1986). The method for chorotype identification was later enhanced by Mu<f1>oz et al. (2003) and Real et al. (2008), and was updated and contextualized under a fuzzy logic framework by Olivero et al. (2011). RMacoqui outputs are also useful as the basis for delimiting biogeographic regions and transition zones with the support of the fuzzy logic (Olivero et al. 2013).

Details

Package:	RMacoqui
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Date:	2014-04-04
License:	GPL-2

Author(s)

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References

Baroni-Urbani C., Rufo S., Vigna-Taglianti A. (1978) Materiali per una biogeografia italiana fondata su alcuni generi di Coleotteri, Cicindelidi, Carabidi e Crisomelidi. Estratto della Memorie della Societa Entomologica Italiana 56:35-92.

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Examples

```
## EXAMPLE 1: Basic usage of function macoqui
##
## If the data set is a presences/absences matrix:

data(amphib)
macoquires <- macoqui(amphib)


## If the data set is a similarity matrix:

data(simil)
macoquires <- macoqui(simil, nloc=273, isprox=1, vmax=0.553, vmin=0.445)


## Friendly 'macoqui' output:

ver.matRmacoqui(macoquires)


## EXAMPLE 2: Basic usage of function locCorot
##
## Parameters for chorotype mapping (only available if 'data' is a presences/absences matrix),
## and friendly output:

data(amphib)
macoquires <- macoqui(amphib)
locs <- locCorot(macoquires)
ver.matRmacoqui(locs)

## EXAMPLE 3: Basic usage of function fuzzy.Clusters
##
## Fuzzy-logic analysis of clusters selected by the researcher, and friendly output:

data(amphib)
macoquires <- macoqui(amphib)
grupos <- c(12,1,12,2,13,1,13,2,15,1,10,1,10,2,17,2)
fuzzyres <- fuzzy.Clusters(macoquires, grupos)
ver.matRmacoqui(fuzzyres)
```

```
## EXAMPLE 4: Basic usage of function locCorotGrupos
##
## Parameters for cluster mapping, and friendly output:

data(amphib)
macoquires <- macoqui(amphib)
grupos <- c(12,1,12,2,13,1,13,2,15,1,10,1,10,2,17,2)
fuzzyres <- fuzzy.Clusters(macoquires, grupos)
fuzzylocs <- locCorotGrupos(fuzzyres, grupos)
ver.matRmacoqui(fuzzylocs)
```

`amphib` *Amphibian presence/absence data*

Usage

```
data("amphib")
```

Format

A data frame with 273 rows (localities) and 18 columns (amphibian species), with values representing their presence (1) or absence (0).

Examples

```
data(amphib)
head(amphib)
```

`fuzzy.Clusters` *Fuzzy-logic analysis of dendrogram clusters selected by the researcher*

Description

This function provides fuzzy-logic descriptions and inter-relationships for all clusters in the dendrogram on which the analyst wishes to put the focus.

Usage

```
fuzzy.Clusters(macoquires, grupos)
```

Arguments

`macoquires`	object resulting from function `macoqui`
`grupos`	dendrogram clusters -identified by the analyst- on which the analysis is focused

Details

Before applying `fuzzy.Clusters`, `macoqui` must be run, and outputs must be stored as object 'macoquires'.

grupos <- c(n, b, ...), where:

n dendrogram-node number (as in the dendrogram plot) b node-branch corresponding to the cluster (1 if left, 2 if right) ... idem for all clusters to be analized

Value

This function returns a list of 9 elements, some of which are shown in the console:

`ngrupos`	the input number of analysed groups
`grupos`	the input `groups` object
`desGrupos`	a description of the input groups, including their node and branch
`elementosGrupos1`	
`elementosGrupos2`	
`ldifusaGrupos`	parameters to compute cluster fuzzy entropy, fuzzy union of clusters, and fuzzy intersection between clusters
`mcardinales`	cardinals of fuzzy unions between clusters (top-right semi-matrix), and of fuzzy intersections between clusters (bottom-left semi-matrix)
`mentropia`	cluster fuzzy parameters (cardinal, entropy, height) and number of species in the cluster; fuzzy inclusion of the cluster in other clusters; fuzzy overlap between clusters
`datos`	the input species dataset

Author(s)

Jesus Olivero, Ramon Hidalgo, Ana L. Marquez, A. Marcia Barbosa, Raimundo Real

See Also

`macoqui`, `locCorotGrupos`, `ver.matRmacoqui`

Examples

```
data(amphib)
macoquires <- macoqui(amphib)
grupos <- c(12,1,12,2,13,1,13,2,15,1,10,1,10,2,17,2)
fuzzyres <- fuzzy.Clusters(macoquires, grupos)
```

`locCorot` *Parameters for chorotype mapping*

Description

This function provides ways for chorotype mapping. For each locality (rows in data), values of four parameters are given. Pi: Presence of chorotype i (presence/absence of at least one species of the chorotypical cluster); SRi: Species Richness of chorotype i (number of species of the chorotypical cluster); MMDi: Maximum Membership Degree-of any species-in chorotype i (fuzzy version of Pi); FSRi: Fuzzy Species Richness (fuzzy version of SRi, i.e sum of all species' degrees of membership in chorotype i).

Usage

```
locCorot(macoquires)
```

Arguments

`macoquires`	object resulting from function `macoqui`

Details

Before applying `locCorot`, `macoqui` must be run, and outputs stored as object 'macoquires'.

For `locCorot` to be run, function `macoqui` must be executed with a presences/absences data set.

Value

This function returns (invisibly) the `macoquires` input list with one added element, which is also shown in the console:

`locCorotipos`	locality identification (correlative numbers starting in 1 are given to lines in data); Pi, SRi, MMDi and FSRi values of every chorotype i in each locality

Note

This function can take some computing time.

Author(s)

Jesus Olivero, Ramon Hidalgo, Ana L. Marquez, A. Marcia Barbosa, Raimundo Real

See Also

`macoqui`, `ver.matRmacoqui`

Examples

```
data(amphib)
macoquires <- macoqui(amphib)
locs <- locCorot(macoquires)
```

`locCorotGrupos` *Parameters for cluster mapping*

Description

This function provides ways for cluster mapping. For each locality (lines in data), values of four parameters are given. Pi: Presence of the cluster i (presence/absence of at least one species of the cluster); SRi: Species Richness of the cluster i (number of species of the cluster); MMDi: Maximum Membership Degree-of any species-in the cluster i (fuzzy version of Pi); FSRi: Fuzzy Species Richness (fuzzy version of SRi, i.e sum of all species' degree of membership in the cluster i).

Usage

```
locCorotGrupos(fuzzyres, grupos)
```

Arguments

`fuzzyres`	object resulting from function `fuzzy.Clusters`
`grupos`	dendrogram clusters-identified by the analyst-on which the analysis is focused (see `fuzzy.Clusters`)

Details

Before applying `locCorotGrupos`, `fuzzy.Clusters` must be run, and outputs stored as object `fuzzyres`.

Function `locCorotGrupos` currently only works if `fuzzy.Clusters` was run with an object (`macoquires`) which resulted from executing `macoqui` with a presences/absences data set.

Value

This function returns the input list (invisibly), with one added element which is also shown in the console:

`locGrupos`	locality identification (correlative numbers starting in 1 are given to rows in data); Pi, SRi, MMDi and FSRi values of every cluster i in each locality

Note

This function can take some computing time for large data sets.

Author(s)

Jesus Olivero, Ramon Hidalgo, Ana L. Marquez, A. Marcia Barbosa, Raimundo Real

See Also

`fuzzy.Clusters`, `ver.matRmacoqui`

Examples

```
data(amphib)
macoquires <- macoqui(amphib)
grupos <- c(12,1,12,2,13,1,13,2,15,1,10,1,10,2,17,2)
fuzzyres <- fuzzy.Clusters(macoquires, grupos)
fuzzylocs <- locCorotGrupos(fuzzyres, grupos)
```

`macoqui` *Identify and describe chorotypes*

Description

A chorotype is a distribution pattern, shared by a group of species, which can be operatively identified within an area (Baroni-Urbani et al., 1978). The function 'macoqui' provides a set of outputs for the detection and description of chorotypes, based on similarities between species distributions. The most important outputs are: (1) a dendrogram showing a classification of species according to distribution similarities; (2) a 'chorotype report' that identifies chorotypical clusters (i.e. groups of species shaping each chorotype) with branches of the dendrogram. Other outputs describe chorotypes as fuzzy sets, and show the fuzzy relationships between all chorotypes.

Usage

```
macoqui(datos, lang = "en", isprox = 0, nloc = 0, vmax = 0, vmin = 0)
```

Arguments

`datos`	a matrix of data, which can be either presences/absences or similarities
`lang`	lang="en" provides outputs with labels in English language (default option); lang="es" provides outputs with labels in Spanish language
`isprox`	isprox=1 if data is a similarity (or proximity) matrix, and isprox=0 if data is a presence/absence matrix (isprox=0 by default)
`nloc`	number of localities considered for computing similarity (only required if isprox=1; otherwise nloc=0, which is the default value)
`vmax`	critical value above which similarity is significant (required if isprox=1, it can be specified if isprox=0 as well; by default, vmax automatically chooses critical values for the Baroni-Urbani & Buser index)
`vmin`	critical value below which dissimilarity is significant (required if isprox=1, it can be specified if isprox=0 as well; by default, vmin automatically chooses critical values for the Baroni-Urbani & Buser index)

Details

The 'data' set is, by default, a matrix of presences (1) and absences (0) of species (columns) in localities (rows). In this version, headers are only admitted in columns, and empty columns produce a function error. By default, 'macoqui' uses the Baroni-Urbani & Buser (1976) index to calculate similarities between distributions, and automatically estimates significant similarities (+) and differences (-), according to the table of critical values (vmax and vmin) of this index. For other indices, it is necessary to provide a similarity matrix (isprox=1), and values for nloc, vmax and vmin.

Value

This function returns a list of 30 elements, some of which are returned invisibly and some of which are also shown in the console:

`nvar`	number of species (number of columns in data)
`nval`	number of localities (number of rows in data, excluding header)
`extremos`	list of the 2 critical values, `vmax` and `vmin`
`metodo`	similarity index employed: Baroni-Urbani & Buser
`mprox`	similarity matrix, columns arranged as in data
`mproxOrdc`	similarity matrix, columns arranged as in the dendrogram
`msignosC`	significant similarity matrix; significant similarities represented as '+', significant dissimilarities represented as '-'
`dend`	a dendrogram in which species distributions are classified
`macdatos`	similarity values of each dendrogram node, and intermediate parameters for chorotype search
`macres`	Macoqui parameters for chorotype search in each dendrogram node
`ncor`	number of chorotypes identified
`CorElementos`	chorotype composition: species (numbered as arranged in data) and the chorotype of which they are chorotypical clusters (0 means "species not classified within any chorotype"); degree of membership of every species in each chorotype, as defined by fuzzy logic
`desCorotipos`	chorotype location in the dendrogram
`ldifusa`	parameters to compute chorotype fuzzy entropy, fuzzy union between chorotypes, and fuzzy intersection between chorotypes
`mcardinales`	cardinals of fuzzy unions between chorotypes (top-right semi-matrix), and of fuzzy intersections between chorotypes (bottom-left semi-matrix)
`mentropia`	chorotype fuzzy parameters (cardinal, entropy, height) and number of species in the chorotypical cluster; fuzzy inclusion of chorotypes in other chorotypes; fuzzy overlap between chorotypes
`isprox`	the input `isprox` value
`datos`	a data frame with the input data

Another output provided is a plot of the `dendrogram` in which species distributions are classified where nodes are identified with numbers, for interpretation of the elements `macdatos`, `macres` and `desCorotipos`.

Author(s)

Jesus Olivero, Ramon Hidalgo, Ana L. Marquez, A. Marcia Barbosa, Raimundo Real

References

Baroni-Urbani C., Buser M.W. (1976) Similarity of binary data. Systematic Zoology 25:251-259.

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See Also

`ver.matRmacoqui`

Examples

```
## If the data set is a presences/absences matrix:

data(amphib)
macoquires <- macoqui(amphib)
macoquires


## If the data set is a similarity matrix:

data(simil)
macoquires <- macoqui(simil, nloc=273, isprox=1, vmax=0.553, vmin=0.445)
macoquires
```

`simil` *Similarity matrix among amphibian presence/absence patterns*

Usage

```
data("simil")
```

Format

A data frame with the similarity values among the presence/absence patterns of the 18 species of amphibians included in `amphib`.

Examples

```
data(simil)
```

`ver.matRmacoqui` *Friendly visualization of RMacoqui outputs*

Description

This function allows a user-friendly visualization of objects resulting from functions `macoqui`, codelocCorot, `fuzzy.Clusters` and `locCorotGrupos`. The results listed in these objects are visualized as tables, and are easily exportable as .txt files.

Usage

```
ver.matRmacoqui(x)
```

Arguments

`x`	object resulting from function `macoqui` or from function `fuzzy.Clusters`.

Value

The returned output is a Tcl/Tk interface (which appears in a separate window) with a menu of links.

The following links are provided in the menu after `ver.matRmacoqui(macoquires)`:

`Similarity Initial Order`

`Similarity Cluster Order`

`Significant Similarity`

`Intermediate MACOQUI Parameters`

`MACOQUI Parameters`

`Chorotype Report`

`Degree of Membership in Chorotypes`

`Intermediate Fuzzy Parameters`

`Cardinality Intersection-Union between Chorotypes`

`Fuzzy Parameters`

`Chorotypes in Localities`

The following links are provided in the menu after `ver.matRmacoqui(fuzzyres)`:

`Cluster Description`

`Species Presences in Clusters`

`Degree of Membership in Clusters`

`Intermediate Fuzzy Parameters`

`Cardinality Intersection-Union between Clusters`

`Fuzzy Parameters`

`Clusters in Localities`

Note

Before running `ver.matRmacoqui`, the **tcltk** package must be installed and loaded.

Author(s)

Jesus Olivero, Ramon Hidalgo, Ana L. Marquez, A. Marcia Barbosa, Raimundo Real

See Also

`macoqui`, `locCorot`, `fuzzy.Clusters`, `locCorotGrupos`

Examples

```
## ver.matRmacoqui for 'macoqui', not including link to 'Chorotypes in Localities':

data(amphib)
macoquires <- macoqui(amphib)
ver.matRmacoqui(macoquires)


## ver.matRmacoqui for 'macoqui', including link to 'Chorotypes in Localities':

data(amphib)
macoquires <- macoqui(amphib)
locs <- locCorot(macoquires)
ver.matRmacoqui(locs)


## ver.matRmacoqui for 'fuzzy.Clusters', not including link to 'Chorotypes in Localities':

data(amphib)
macoquires <- macoqui(amphib)
grupos <- c(12,1,12,2,13,1,13,2,15,1,10,1,10,2,17,2)
fuzzyres <- fuzzy.Clusters(macoquires, grupos)
ver.matRmacoqui(fuzzyres)
```

```
## ver.matRmacoqui for 'fuzzy.Clusters', including link to 'Chorotypes in Localities':

data(amphib)
macoquires <- macoqui(amphib)
grupos <- c(12,1,12,2,13,1,13,2,15,1,10,1,10,2,17,2)
fuzzyres <- fuzzy.Clusters(macoquires, grupos)
fuzzylocs <- locCorotGrupos(fuzzyres, grupos)
ver.matRmacoqui(fuzzylocs)
```

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