Package ‘EnvNicheR’

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Title Niche Estimation

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Description A plot overlying the niche of multiple species is obtained: 1) to determine the niche conditions which favor a higher species richness, 2) to create a box plot with the range of environmental variables of the species, 3) to obtain a list of species in an area of the niche selected by the user and, 4) to estimate niche overlap among the species.

License GPL (>= 2)

Encoding latin1

Depends R (>= 3.1.1), IDPmisc, stats, utils, graphics, grDevices

Repository CRAN

R topics documented:

`Carnivores` *Presence of terrestrial carnivores of the family Felidae and environmental variables.*

Description

Presence of terrestrial carnivores of the family Felidae and mean of environmental variables in cells of 1 degree x 1 degree around the world.

Usage

```
data(Carnivores)
```

Format

A matrix of the presence of terrestrial carnivores of the family Felidae and the mean altitude, mean annual temperature, isothermality, temperature seasonality and mean annual precipitation in cells of 1 degree x 1 degree around the world.

Source

The range maps of the species were obtained from the International Union for Conservation of Nature (IUCN) at the web page `http://www.iucn.org/`. The data of the mean annual temperature (BIO1), isothermality (BIO3), temperature seasonality (BIO4) and mean annual precipitation (BIO12) were downloaded from the web `http://www.worldclim.org/`. Both range maps and environmental variables were inputted into ModestR (`http://www.ipez.es/ModestR`) and the output file from ModestR is a CSV file that was converted to a RData file.

References

García-Roselló, E., Guisande, C., González-Dacosta, J., Heine, J., Pelayo-Villamil, P., Manjarrés-Hernández, A., Vaamonde, A. & Granado-Lorencio, C. (2013) ModestR: a software tool for managing and analyzing species distribution map databases. *Ecography*, 36, 1202-1207.

Hijmans, R.J., Cameron, S.E., Parra, J.L., Jones, P.G. and Jarvis, A. (2005) Very high resolution interpolated climate surfaces for global land areas. *International Journal of Climatology*, 25, 1965-1978.

IUCN (2012) The IUCN Red List of Threatened Species. Version 2012.2. `http://www.iucnredlist.org`. Downloaded on 17 October 2012.

Pelayo-Villamil, P., Guisande, C., González-Vilas. L., Carvajal-Quintero. J.D., Jiménez-Segura, L.F., García-Roselló, E., Heine, J., González-Dacosta, J., Manjarrés-Hernández, A., Vaamonde, A., Granado-Lorencio, C. (2012) ModestR: Una herramienta infromática para el estudio de los ecosistemas acuáticos de Colombia. *Actualidades Biológicas*, 34, 225-239.

`Niche` *Niche*

Description

This function allows to show a plot overlying the niche of multiple species, so it is possible to determine the niche conditions which favor a higher species richness and, to create boxplots with the range of environmental variables and list of species in an area of the niche selected by the user.

Usage

```
Niche(data, variables, Level="NULL", Taxon="NULL", cor=TRUE, d.main=0.5,
xlab="Polar coordinate X in pixels",ylab="Polar coordinate Y in pixels",
cex.labS=1.5, font.lab=1, main="", colramp = IDPcolorRamp, cex.main = 2,
font.main=2, nlab.xaxis = 5, nlab.yaxis = 5, minL.axis = 3, las = 1,
border = FALSE, tcl = -0.3, boxplot=TRUE, outline=FALSE, color="NULL",
range = 1.5, width = NULL, varwidth = FALSE, plot = TRUE,
pars = list(boxwex = 0.8, staplewex = 0.5, outwex = 0.5), cex.boxplot=1.5,
cex.labB=1.5, namesB, family="serif", line=1, file1 = "List of species.csv",
file2 = "Environmental variables.csv", file3 = "Polar coordinates.csv",
na = "NA", dec = ",", row.names = FALSE, fileEncoding = "")
```

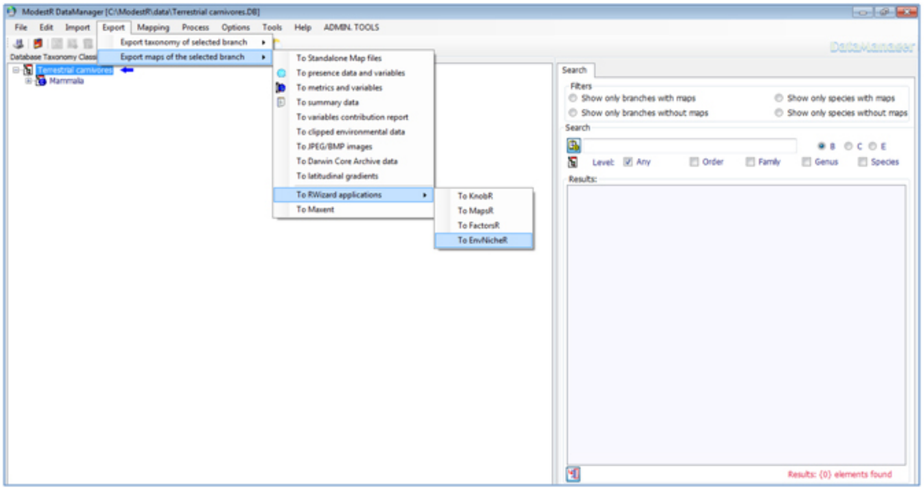
Arguments

`data`	A CSV file obtained from ModestR (García-Roselló et al., 2013) with data which show the presence of the species and abiotic and/or biotic factors.
`variables`	Selection of the variables for the estimation of the niche.
`Level`	Taxonomic level to be selected, i.e., Class, Family, Order, or Genus.
`Taxon`	Name of the taxon or taxa selected within the level, i.e., name of the Order, Family, etc. Can be a vector, so several taxa.
`cor`	If TRUE the variables are ordered according to the correlation between them. Therefore, the next variable to another variable is the one that has a greater positive correlation.
`d.main`	Scatter plot. Vertical distance between upper border of scatter plots and the title line in multiples of title height.
`xlab`	Scatter plot. Label for x-axis.
`ylab`	Scatter plot. Label for y-axis.
`cex.labS`	Scatter plot. Magnification used for text in axis labels relative to the current setting of cex.
`font.lab`	Scatter plot. The font to be used for x and y labels.
`main`	Scatter plot. Title of the plot.
`colramp`	Scatter plot. Color ramp to encode the number of counts within a pixel.
`cex.main`	Scatter plot. Magnification used for title relative to the current setting of cex.
`font.main`	Scatter plot. The font to be used for plot main titles.
`nlab.xaxis`	Scatter plot. Approximate number of labels on x-axes.
`nlab.yaxis`	Scatter plot. Approximate number of labels on y-axes.
`minL.axis`	Scatter plot. The minimum length of the abbreviations of factor levels, used to label the axes ticks.
`las`	Scatter plot. Orientation of labels on axes.
`border`	Scatter plot. Logical. When TRUE, a border is drawn around the individual colors in the legend.
`tcl`	Scatter plot. The length of tick marks as a fraction of the height of a line of text. The default value is -0.5; setting tcl = NA sets tck = -0.01 which is S' default.

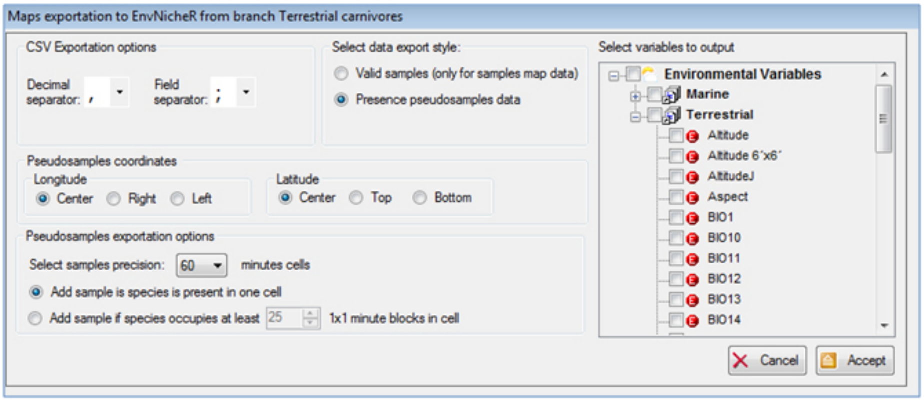
`boxplot`	If TRUE (the default) then a boxplot with the range of environmental variables in an area of the niche selected by the user is produced.
`outline`	Boxplot. If outline is not true, the outliers are not drawn (as points whereas S+ uses lines).
`color`	Boxplot. If col is non-null it is assumed to contain colors to be used to colour the bodies of the box plots.
`range`	Boxplot. This determines how far the plot whiskers extend out from the box. If the range is positive, the whiskers extend to the most extreme data point which is no more than range times the interquartile range from the box. A value of zero causes the whiskers to extend to the data extremes.
`width`	Boxplot. A vector giving the relative widths of the boxes making up the plot.
`varwidth`	Boxplot. If varwidth is TRUE, the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups.
`plot`	Boxplot. If TRUE (the default) then a boxplot is produced. If not, the summaries which the boxplots are based on are returned.
`pars`	Boxplot. A list of (potentially many) more graphical parameters, e.g., boxwex or outpch; these are passed to bxp (if plot is true).
`cex.boxplot`	Boxplot. Magnification used for axis annotation.
`cex.labB`	Boxplot. Magnification used for group labels which will be printed under each boxplot.
`namesB`	Boxplot. Group labels which will be printed under each boxplot. It can be a character vector.
`family`	The name of a font family for drawing text.
`line`	mtext. On which margin line, starting at 0 counting outwards.
`file1`	CSV file. A character string naming the file of the list of species.
`file2`	CSV file. A character string naming the file with the summary of the environmental variables.
`file3`	CSV file. A character string naming the file with the summary of the polar coordinates.
`na`	CSV files. The string to use for missing values in the data.
`dec`	CSV files. The string to use for decimal points in numeric or complex columns: must be a single character.
`row.names`	CSV files. Either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.
`fileEncoding`	CSV files. Character string: if non-empty declares the encoding to be used on a file (not a connection) so the character data can be re-encoded as they are written.

Details

The file required in the argument *data* may be obtained using ModestR (available at the web site `http://www.ipez.es/ModestR`), as it is shown in the following screenshot (Export/Export maps of the select branch/To RWizard Applications/To EnvNicheR).



The menu shown in the following screenshot is obtained, where it is possible to select several environmental variables. There is the option of exporting the data with the format of pseudosamples or all the valid samples. If the maps are areas, the proper way of exporting these data is to create a raster with grid cell for instance of 5´ x 5´, 30´ x 30´, 1° x 1°, etc. Therefore, the output of ModestR is a list of species within each of the grid cells with the size defined by the user. If the maps are records, it is possible to use pseudosamples or to select the option valid samples.


Maps exportation to EnvNicheR from branch Terrestrial carnivores

CSV Exportation options
Decimal separator: ,
Field separator: ;

Select data export style:
○ Valid samples (only for samples map data)
● Presence pseudosamples data

Pseudosamples coordinates
Longitude: ● Center ○ Right ○ Left
Latitude: ● Center ○ Top ○ Bottom

Pseudosamples exportation options
Select samples precision: 60 minutes cells
● Add sample is species is present in one cell
○ Add sample if species occupies at least 25 1x1 minute blocks in cell

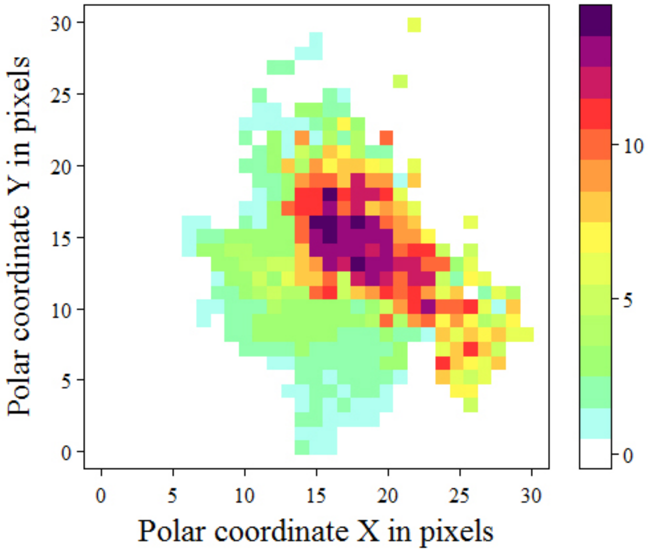
Select variables to output
☐ Environmental Variables
  ☐ Marine
  ☐ Terrestrial
    ☐ Altitude
    ☐ Altitude 6´x6´
    ☐ AltitudeJ
    ☐ Aspect
    ☐ BIO1
    ☐ BIO10
    ☐ BIO11
    ☐ BIO12
    ☐ BIO13
    ☐ BIO14

FUNCTIONS

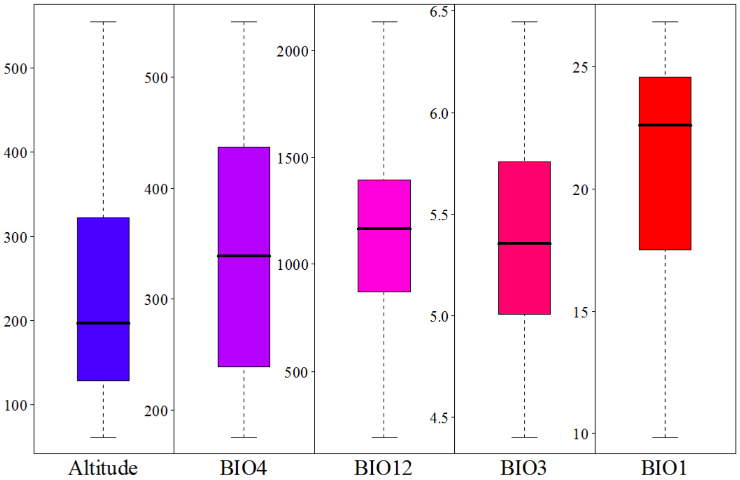
The scatter plot is performed with the function iplot of the package IDPmisc (Locher & Ruckstuhl, 2014).

EXAMPLE

The dataset of the example is Carnivores that was described above. The first plot shows the polar coordinates using the environmental variables selected by the user in the file obtained from ModestR (in the example BIO1, BIO3, BIO4 and BIO12 and altitude). In this first plot, a darker color of the square indicates a higher number of species in the cell. In this plot it is necessary to click four times with the mouse to select one or several cells.



The second plot shows a boxplot with the median and range of the environmental variables and/or latitude and longitude, in the cells selected with the mouse in the first plot.



Value

A list of the species present in the cells selected by the user with the mouse, a summary of the environmental variables and the polar coordinates are saved in three CSV files.

Author(s)

Cástor Guisande González, Universidad de Vigo, Spain.

References

García-Roselló, E., Guisande, C., González-Dacosta, J., Heine, J., Pelayo-Villamil, P., Manjarrés-Hernández, A., Vaamonde, A. & Granado-Lorencio, C. (2013) ModestR: a software tool for managing and analyzing species distribution map databases. *Ecography*, 36, 1202-1207.

Hijmans, R.J., Cameron, S.E., Parra, J.L., Jones, P.G. and Jarvis, A. (2005)Very high resolution interpolated climate surfaces for global land areas. *International Journal of Climatology*, 25, 1965-1978.

IUCN (2012) The IUCN Red List of Threatened Species. Version 2012.2. `http://www.iucnredlist.org`. Downloaded on 17 October 2012.

Locher, R. & Ruckstuhl, A. (2014) Utilities of Institute of Data Analyses and Process Design. R package version 1.1.17. Available at: http://CRAN.R-project.org/package=IDPmisc.

Examples

```
## Not run:
data(Carnivores)

Niche(data=Carnivores, variables= c("Altitude", "BIO1", "BIO3",
"BIO4", "BIO12"), Level="Genus", Taxon= c("Leopardus", "Puma", "Panthera"),
cex.boxplot=1.7)

#Remove the data set
rm(Carnivores)

## End(Not run)
```

`NicheOverlap` *Niche overlap between two taxa*

Description

This function shows in a plot the niche overlap between two taxa, at any level of the taxonomy (order, family, genus or species), using the file *Polar coordinates.CSV* obtained from the function Niche.

Usage

```
NicheOverlap(data, Level1, Taxon1, Level2=Level1, Taxon2,
colA=hsv(h=0,s=1,v=1,alpha=0.4), colB=hsv(h=0.7,s=1,v=1, alpha=0.4),
xlab="Polar coordinate X in pixel", ylab="Polar coordinate Y in pixels",
cex=1.57, cex.lab=1.5,font.lab=1, main="", cex.main = 2, font.main=2,
family="serif", digits =2, xlegend="topleft", ylegend=NULL, pch=15, bty="n",
text.font=3, cex.legend=1.2, ncol=1, x.intersp=1, y.intersp=1, legend=TRUE)
```

Arguments

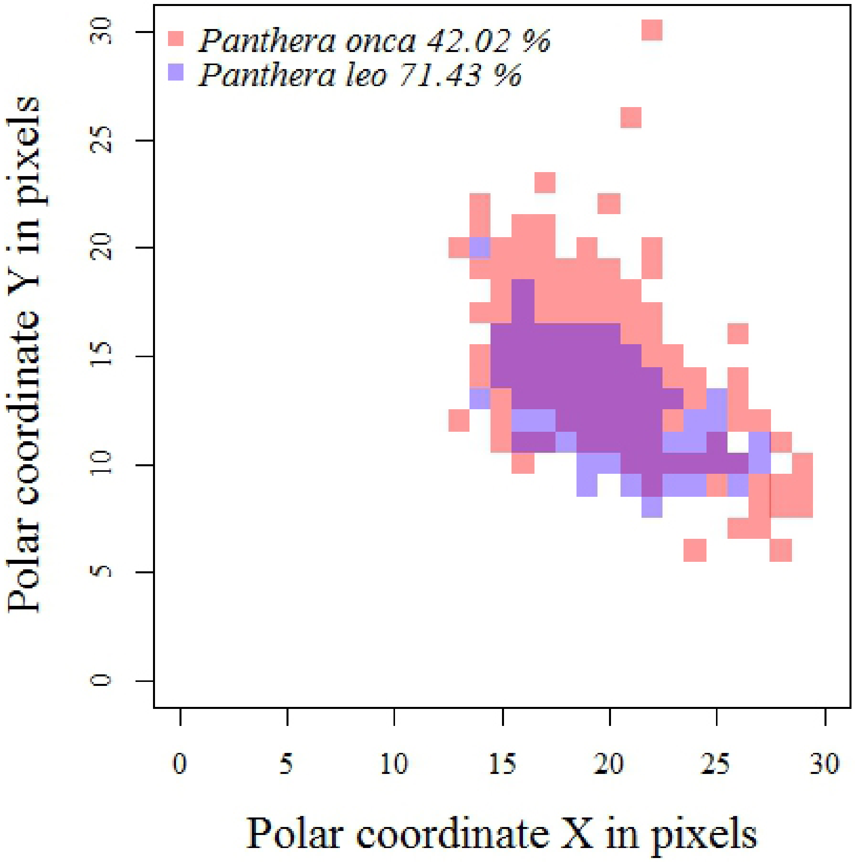
`data`	The file *Polar coodinates.CSV* obtained from the function Niche.
`Level1`	Taxonomic level to be selected, i.e., Class, Order, Family or Genus, of the first taxon.
`Taxon1`	Name of the taxon of the first taxonomic level.
`Level2`	Taxonomic level to be selected, i.e., Class, Order, Family or Genus, of the second taxon. If missing the default value is Level1.
`Taxon2`	Name of the taxon of the second taxonomic level.
`colA`	Color of Taxon1.
`colB`	Color of Taxon2.
`xlab`	Label for x-axis.
`ylab`	Label for y-axis.
`cex`	Size of the symbols.This argument and the argument *omi* of the function par are useful to adjust the overlap among symbols and to avoid white lines.
`cex.lab`	Magnification used for text in axis labels relative to the current setting of cex.
`font.lab`	The font to be used for x and y labels.
`main`	Title of the plot.
`cex.main`	Magnification used for title relative to the current setting of cex.
`font.main`	The font to be used for plot main titles.
`family`	The name of a font family for drawing text.
`digits`	Integer indicating the number of decimal places of the overlap values.
`xlegend`	The x co-ordinates to be used to position the legend.
`ylegend`	The y co-ordinates to be used to position the legend.
`pch`	The plotting symbols appearing in the plot and in the legend.
`bty`	The type of box to be drawn around the legend. The allowed values are "o" and "n" (the default).
`text.font`	The font used for the legend text, see text.
`cex.legend`	Character expansion factor relative to current par("cex") of the legend.
`ncol`	The number of columns in which to set the legend items.
`x.intersp`	Character interspacing factor for horizontal (x) spacing of the legend.
`y.intersp`	Character interspacing factor for vertical (y) spacing of the legend.
`legend`	If TRUE the legend is shown.

Details

This function uses the file *Polar coordinates.CSV* obtained from the function Niche. It is necessary to select two taxa of the same level (order, family, genus or species).

EXAMPLE

In the example, the niche overlap between the species *Panthera onca* and *Panthera leo* is estimated. The overlap is estimated counting the overlapping pixels.



Value

A plot shows the values of niche overlap for both taxa and the overlapping area.

Author(s)

Cástor Guisande González, Universidad de Vigo, Spain.

Examples

```
## Not run:
data(Polar.coordinates)

NicheOverlap(Polar.coordinates, Level1="Species", Taxon1="Panthera onca",
Taxon2="Panthera leo")

#Remove the data set
rm(Polar.coordinates)

## End(Not run)
```

`OverlapTaxa` *Niche overlap among all species within a taxa*

Description

Estimation of the niche overlap among all species within a taxa of a taxonomic level selected by the user (order, family or genus), using the file Polar coordinates.CSV obtained from the function Niche.

Usage

```
OverlapTaxa(data, Level, digits =2, file1 = "Overlap among taxa.csv",
file2 = "Mean overlap among taxa.csv", na = "NA", dec = ",", row.names = FALSE,
fileEncoding = "")
```

Arguments

`data`	The file Polar coodinates.CSV obtained from the function Niche.
`Level`	Taxonomic level to be selected, i.e., Class, Order, Family or Genus
`digits`	Integer indicating the number of decimal places of the overlap values.
`file1`	CSV file. A character string naming the file with the overllap among species.
`file2`	CSV file. A character string naming the file with mean and standard deviation of the overlap for each taxonomic level selected by the user.
`na`	CSV files. The string to use for missing values in the data.
`dec`	CSV files. The string to use for decimal points in numeric or complex columns: must be a single character.
`row.names`	CSV files. Either a logical value indicating whether the row names of x are to be written along with x, or a character vector of row names to be written.
`fileEncoding`	CSV files. Character string: if non-empty declares the encoding to be used on a file (not a connection) so the character data can be re-encoded as they are written.

Details

In the first CSV file *Overlap among taxa.CSV*, this function estimates the niche overlap, using the file *Polar coordinates.CSV* obtained from the function Niche, among all species within the taxonomic level selected by the user. In the second CSV file *Mean overlap among taxa.CSV*, the function estimates the mean overlap within the taxonomic level selected by the user. If there are many species, e.g. over 5000, the process can take several hours.

Value

Two CSV files with the overlap among species and the mean overlap among the species for the taxonomic level selected by the user.

Author(s)

Cástor Guisande González, Universidad de Vigo, Spain.

Examples

```
## Not run:
data(Polar.coordinates)

OverlapTaxa(data=Polar.coordinates, Level="Genus")

#Remove the data set
rm(Polar.coordinates)

## End(Not run)
```

`Polar.coordinates` *Polar cooordinates obtained from the function Niche*

Description

Polar cooordinates.CSV file obtained from the function Niche using presence data of terrestrial carnivores of the family Felidae and mean of environmental variables in cells of 1 degree x 1 degree around the world.

Usage

```
data(Polar.coordinates)
```

Format

A matrix with the taxonomy, polar coordinates and mean values of the environemntal variables for each polar coordinate.

Source

The range maps of the species were obtained from the International Union for Conservation of Nature (IUCN) at the web page `http://www.iucn.org/`. The data of the mean annual temperature (BIO1), isothermality (BIO3), temperature seasonality (BIO4) and mean annual precipitation (BIO12) were downloaded from the web `http://www.worldclim.org/`. Both range maps and environmental variables were inputted into ModestR (`http://www.ipez.es/ModestR`) and the output file was used in the function Niche() and the file Polar coordinates.CSV obtained was converted to a RData file.

References

García-Roselló, E., Guisande, C., González-Dacosta, J., Heine, J., Pelayo-Villamil, P., Manjarrés-Hernández, A., Vaamonde, A. & Granado-Lorencio, C. (2013) ModestR: a software tool for managing and analyzing species distribution map databases. *Ecography*, 36, 1202-1207.

Hijmans, R.J., Cameron, S.E., Parra, J.L., Jones, P.G. and Jarvis, A. (2005) Very high resolution interpolated climate surfaces for global land areas. *International Journal of Climatology*, 25, 1965-1978.

IUCN (2012) The IUCN Red List of Threatened Species. Version 2012.2. `http://www.iucnredlist.org`. Downloaded on 17 October 2012.

Pelayo-Villamil, P., Guisande, C., González-Vilas. L., Carvajal-Quintero. J.D., Jiménez-Segura, L.F., García-Roselló, E., Heine, J., González-Dacosta, J., Manjarrés-Hernández, A., Vaamonde, A., Granado-Lorencio, C. (2012) ModestR: Una herramienta infromática para el estudio de los ecosistemas acuáticos de Colombia. *Actualidades Biológicas*, 34, 225-239.

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