

Package ‘sdStaf’

October 4, 2018

Type Package

Title Species Distribution and Stability Future Models

Version 1.0.0

Date 2018-10-03

Maintainer P. Joser Atauchi <patauchi@gmail.com>

Description Functions for post processing the outcomes of ecological niche models. It further include methods to build stability maps based on species distribution models under climate change projections and to reduce environmental data.

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

Depends methods, stats, dplyr, ggplot2, R (>= 2.10)

Imports sp, rgdal, rgeos, rasterVis, tidyr, raster, dismo

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author P. Joser Atauchi [aut, cre]

Repository CRAN

Date/Publication 2018-10-03 22:00:03 UTC

R topics documented:

cor.show	2
EnvimRed-class	2
phytotoma	3
reduce.env	3
StabEcodist-class	5
stability	5
stim.M	6
Index	8

<code>cor.show</code>	<i>Correlogram plot</i>
-----------------------	-------------------------

Description

Returns plot with correlation values among predicted variables.

Usage

```
cor.show(r, rm = FALSE, var.rm)
```

Arguments

<code>r</code>	EnvimRed-class.
<code>rm</code>	logical. If TRUE, allows remove some variables from input data set. (default = FALSE)
<code>var.rm</code>	variables names of input data set. Using <code>colnames(RasterStick)</code> , Where RasterStick is RasterStack* object.

Details

Correlation matrix based on pearson.

Value

Correlogram plot

See Also

[reduce.env](#)

EnvimRed-class	<i>myRefClass</i>
----------------	-------------------

Description

myRefClass

Slots

<code>cropla</code>	A RasterBrinck
<code>m.env</code>	A Matrix
<code>project</code>	A List

phytotoma

Peruvian Plantcutter Occurrence Data

Description

A dataset containing occurrence record locations of Peruvian plantcutter (*Phytoma raimondii*), endemic species of Dry forest in northern Peru. These records have been examined to check for accurate species identification.

Usage

```
data(phytotoma)
```

Format

A data frame with 50 rows and 3 columns

Details

- sp.name species name
- x Longitude
- y Latitude

reduce.env

Reduce environmental data

Description

This function allows reduce environmental data clipping by mask or buffer area

Usage

```
reduce.env(env, transfer = NULL, occ_data, mask)
```

Arguments

env	RasterStack* objet.
transfer	List of rasterstack object
occ_data	A data.frame of occurrence records. It must include two column based on latitude and longitude.
mask	Cropped mask, must be shapefile (.shp), readOGR.

Details

Reduce the correlation among predicted variables either buffer zone, or clipping mask.

Provide reduce objet with cut predicted variables and data.frame for the values of each point of occurrence of them.

Value

@crop RasterStack* Objet

@m.env data.frame of environmental values to occurrence localities.

See Also

[cor.show](#)

Examples

```
# Phytotoma occurrence data
data(phytotoma)

# Complement
library(dismo)
predictor <- stack(list.files(path=paste(system.file(package="dismo"),'/ex', sep=''),
  pattern='grd', full.names=TRUE ))

maskM <- stim.M(phytotoma[,2:3], 131)

reduce_cut <- reduce.env(env = predictor, occ_data = phytotoma[,2:3], mask=maskM)

# Plot reduce_cut
plot(reduce_cut@cropla$bio1)

# Add points
points(phytotoma[,2:3], pch=16,col='blue')

# Correlogram
cor.show(reduce_cut)
rd <- c('bio1','bio12','bio16','biome','bio8')

# Removing rd-variables on correlogram
cor.show(reduce_cut, rm=TRUE, var.rm = rd)

# Remove rd-variables
var_reduce <- dropLayer(reduce_cut@cropla, rd)

# summary
var_reduce
```

StabEcodist-class	<i>StabEcodist</i>
-------------------	--------------------

Description

StabEcodist

Slots

df A RasterBrinck

map A Matrix

stability	<i>Stability of ecological niche models</i>
-----------	---

Description

Returns stability niche based on species distribution models and their projections.

Usage

```
stability(current = NULL, future = NULL, thr.value = NULL,
          charname = NULL)
```

Arguments

current	Raster* objet of present distribution. Raster has continue values.
future	RasterStack* object of future distributions. Must have three models with continue values.
thr.value	Cut value (0 — 1) of threshold in order to species distribution.
charname	character-Class, name of the species. (default = NULL).

Value

An object of class 'StabEcodist'

Method S4 print

Return table with these features: Models and nPixel (frequency of pixel with that feature).

1. Lost area

code Models:

code 0 mention the area with species absence.

code 14 mention the lost area current in the future projections

2. Gain area

code Models:

code 1 mention the gain area according with one model.

code 2 according with two models.

code 3 according with three models.

3. Stable

code Models:

code 15 mention the stable area with one model.

code 16 mention the stable area with two models

code 17 mention the stable area with three models.

Method S4 plot

Return maps of stability niche

References

Peterson et al., (2017) Influences of climate change on the potential distribution of *Lutzomyia longipalpis* sensu lato (Psychodidae: Phlebotominae). *International Journal for Parasitology*. 47(10–11):667–74.

stim.M

Build buffer zone to M

Description

Returns buffer zone based on occurrence data

Usage

```
stim.M(occs, radio, bgeo = NULL, ...)
```

Arguments

occs	data.frame of occurrence data (longitude/latitude).
radio	radio of buffer.
bgeo	Biogeographical layer. Categorical values.
...	Optional features of buffer

Details

To define calibration area is crucial step (Barve et al., 2011), even more with incomplete sample data sometime is complicated, because to get complete sample within geography space is difficult, in these cases is appropriate define M with buffer zone (Peterson et al., 2017); and in other cases it helps to cut the ends of the calibration area based on the maximum dispersion capacity (Atauchi et al., 2018).

Value

SpatialPolygons* object

References

Atauchi et al. (2018). Species distribution models for Peruvian Plantcutter improve with consideration of biotic interactions. *J. avian biology* 2018: e01617. <doi:http://10.1111/jav.01617.>

Barve et al. (2011) The crucial role of the accessible area in ecological niche modeling and species distribution modeling. *Ecol. Mod.* 222:1810–1819.

Peterson et al.(2017) Influences of climate change on the potential distribution of *Lutzomyia longipalpis* sensu lato (Psychodidae: Phlebotominae). *International journal for parasitology.* 45(10-11): 667–674.

Examples

```
# Phytotoma occurrence data
data(phytotoma)

# Build buffer zone
buf_M <- stim.M(occs=phytotoma[,2:3], 100)

# Add points
points(phytotoma[,2:3])
```

Index

*Topic **datasets**

phytotoma, [3](#)

cor.show, [2](#), [4](#)

EnvimRed (EnvimRed-class), [2](#)

EnvimRed-class, [2](#)

phytotoma, [3](#)

reduce.env, [2](#), [3](#)

StabEcodist-class, [5](#)

stability, [5](#)

stim.M, [6](#)