**rangemap R package functions**

**Functions**

* rangemap\_buff
* rangemap\_bound
* rangemap\_hull
* rangemap\_enm
* rangemap\_tsa
* rangemap\_fig
* ranges\_envcomp

**Schedule**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **May** | | **June** | | | | **July** | | | | **August** | |
| **S1** | **S2** | **S3** | **S4** | **S5** | **S6** | **S7** | **S8** | **S9** | **S10** | **S11** | **S12** |
| rangemap\_buff | **X** | **X** |  |  |  |  |  |  |  |  |  |  |
| rangemap\_bound |  | **X** | **X** |  |  |  |  |  |  |  |  |  |
| rangemap\_hull |  |  | **X** | **X** | **X** |  |  |  |  |  |  |  |
| rangemap\_enm |  |  |  |  | **X** | **X** |  |  |  |  |  |  |
| rangemap\_tsa |  |  |  |  |  | **X** | **X** | **X** |  |  |  |  |
| rangemap\_fig |  |  |  |  |  |  |  | **X** | **X** |  |  |  |
| ranges\_envcomp |  |  |  |  |  |  |  |  |  | **X** | **X** |  |
| Documentation | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** | **X** |
| Testing |  | **X** | **X** |  | **X** | **X** |  | **X** | **X** |  | **X** | **X** |

**Documentation**

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| rangemap\_buff {rangemap} | R Documentation |

Species distributional ranges based on buffered occurrences

**Description**

rangemap\_buff generates SpatialPolygonsDataFrame objects of a species range by buffering provided occurrences using a defined distance, and the species extent of occurrence and area of occupancy according to the UICN criteria. Shape files can be saved in the working directory if it is needed.

**Usage**

rangemap\_buff(occurrences, distance = 1e+05, polygons, save\_shp = FALSE,

name)

**Arguments**

|  |  |
| --- | --- |
| occurrences | a data.frame containing species occurrences, columns must be: Species, Longitude, and Latitude. Geographic coordinates must be in decimal degrees |
| distance | (numeric) distance, in meters, to be used for creating the buffer areas around occurrences, default = 100000. |
| polygons | (optional) a SpatialPolygon object that will be clipped with the buffer areas to create species ranges based on actual limits. Projection must be Geographic (longitude, latitude). If not defined, a default, simple world map will be used. |
| save\_shp | (logical) if TRUE shapefiles of the species range, extent of occurrence and area of occupancy will be written in the working directory. |
| name | (character) valid if save\_shp TRUE. The name of the shapefile to be exported. |

**Value**

A named list containing a data.frame with information about the species range and SpatialPolygonDataFrame objects of the species range, extent of occurrence, and area of occupancy; all in Azimuthal equal area projection. If save\_shp = TRUE, written shapefiles' projections will be the same as the SpatialPolygonDataFrame objects.

**Examples**

if(!require(rgbif)){

install.packages("rgbif")

library(rgbif)

}

# getting the data from GBIF

occ <- occ\_search(taxonKey = 2422480, return = "data")

# keeping only georeferenced records

occ\_g <- occ[!is.na(occ$decimalLatitude) & !is.na(occ$decimalLongitude),

c("name", "decimalLongitude", "decimalLatitude")]

# buffer distance

dist <- 100000

buff\_range <- rangemap\_buff(occurrences = occ\_g, distance = dist,

save\_shp = TRUE, name = "test")

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| rangemap\_bound {rangemap} | R Documentation |

## Species distributional ranges based on political boundaries

### Description

rangemap\_bound generates a species range polygon for a given species by considering all the polygons of political entities in which the species has been detected. Shape files can be saved in the working directory if it is needed.

### Usage

rangemap\_bound(occurrences, country\_code, boundary\_level = 0, polygons,

disolve = TRUE, save\_shp = FALSE, name)

### Arguments

|  |  |
| --- | --- |
| occurrences | a data.frame containing species occurrences, columns must be: Species, Longitude, and Latitude. |
| country\_code | (character) vector of country codes that will be considered when creating the species range. Codes follow the ISO-3166-1 norm as in function getData. |
| boundary\_level | (numeric) the level of the administrative boundaries from 0 to 5 (0 is the country and higher values equal finer divisions), default = 0. |
| polygons | (optional) a SpatialPolygon object that will be used instead of boundaries to create species ranges based on overlapping of species records with these layer. If defined, argument boundaries will not be considered. |
| disolve | (logical) if TRUE distint polygons selected as part of the species range will be disolved for creating simpler polygons, default = TRUE. |
| save\_shp | (logical) if TRUE shapefiles of the species range, extent of occurrence and area of occupancy will be written in the working directory. |
| name | (character) valid if save\_shp TRUE. The name of the shapefile to be exported. |

### Details

Boundaries used are loaded using the getData funcion.

### Value

A named list containing a data.frame with information about the species range, a SpatialPolygon object of the species range in Geographic projection, and the same SpatialPolygon object projected to the Azimuthal equal area projection.

### Examples

if(!require(rgbif)){

install.packages("rgbif")

library(rgbif)

}

# getting the data from GBIF

occ <- occ\_search(taxonKey = 2440788, return = "data")

# keeping only georeferenced records

occ\_g <- occ[!is.na(occ$decimalLatitude) & !is.na(occ$decimalLongitude),

c("name", "decimalLongitude", "decimalLatitude")]

level <- 0

disolve <- TRUE

save <- TRUE

name <- "test"

countries <- c("PER", "BRA", "COL", "VEN", "ECU", "GUF", "GUY", "SUR")

bound\_range <- rangemap\_bound(occurrences = occ\_g, country\_code = countries, boundary\_level = level,

disolve = disolve, save\_shp = save, name = name)

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| rangemap\_hull {rangemap} | R Documentation |

Species distributional ranges based on distinct hull polygons

**Description**

rangemap\_hull generates a species range polygon for a given species by considering all the polygons of political entities in which the species has been detected.

**Usage**

rangemap\_hull(occurrences, hull\_type = "concave", distance = 0.5,

split\_distance = 2, export = FALSE)

**Arguments**

|  |  |
| --- | --- |
| occurrences | a data.frame containing species occurrences, columns must be: Species, Longitude, and Latitude. |
| hull\_type | (character) type of hull polygons to be created. Available options are: "convex", "concave", and "alpha" hulls. |
| distance | (numeric) distance in decimal degrees to be used for creating a buffer area around the hull polygons, default = 0.5. |
| split\_distance | (numeric) distance in decimal degrees that will limit connectivity among hull polygons created with chunks of points separated by long distances, , default = 2. |
| export | (logical) if TRUE a shapefile of the species range will be written in the working directory, appart of the returned object. |

**Value**

A named list containing a data.frame with information about the species range, a SpatialPolygon object of the species range in Geographic projection, and the same SpatialPolygon object projected to the Azimuthal equal area projection.

**Examples**

if(!require(rgbif)){

install.packages("rgbif")

library(rgbif)

}

# getting the data from GBIF

occ <- occ\_search(taxonKey = 5219426, return = "data", limit = 1000)

# keeping only georeferenced records

occ\_g <- occ[!is.na(occ$decimalLatitude) & !is.na(occ$decimalLongitude),]

disolve <- TRUE

hull <- "convex"

split <- 4

hull\_range <- rangemap\_hull(occurrences = occ\_g, hull\_type = hull, distance = dist, split\_distance = split)

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| rangemap\_enm {rangemap} | R Documentation |

## Species distributional ranges based on ecological niche models

### Description

rangemap\_enm generates species range polygons for a given species using a continuous raster layer produced with an ecological niche modeling tool. This function split the model in suitable and unsuitable habitats using a user specified level of error or a given threshold value. Shape files can be saved in the working directory if it is needed.

### Usage

rangemap\_enm(occurrences, model, threshold\_value, threshold, export = FALSE)

### Arguments

|  |  |
| --- | --- |
| occurrences | a data.frame containing species occurrences, columns must be: Species, Longitude, and Latitude. |
| model | a RasterLayer object that will binarized using the threshold value defined by the user or a value calculated based on a threshold (from 0 - 100) defined in threshold. |
| threshold\_value | (numeric) decimal value used for reclasifying the model. This value will be the lowest considered as suitable for the species. |
| threshold | (numeric) percentage of occurrence records to be excluded from suitable areas considering their values of suitability in the continuous model (e.g., 0, 5, or 10). |
| export | (logical) if TRUE a shapefile of the species range will be written in the working directory, appart of the returned object. |

### Details

If threshold\_value is provided, argument threshold is ignored.

### Value

A named list containing a data.frame with information about the species range, a SpatialPolygon object of the species range in Geographic projection, and the same SpatialPolygon object projected to the Azimuthal equal area projection.

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| rangemap\_tsa {rangemap} | R Documentation |

## Species distributional ranges based on a trend surface analysis

### Description

rangemap\_tsa generates species range polygons for a given species using .

### Usage

rangemap\_tsa(occurrences, variables, threshold = 5, export = FALSE)

### Arguments

|  |  |
| --- | --- |
| occurrences | a data.frame containing species occurrences, columns must be: Species, Longitude, and Latitude. |
| variables | a RasterStack object of environmental variables that will be used for performing the trend surface analysis. |
| threshold | (numeric) percentage of occurrence records to be excluded when deciding the minimum surface value to be considered part of the species range, default = 5. |
| export | (logical) if TRUE a shapefile of the species range will be written in the working directory, appart of the returned object. |

### Details

Trend surface analysis Is a method based on low-order polynomials of spatial coordinates for estimating a regular grid of points from scattered observations.

### Value

A named list containing a data.frame with information about the species range, a SpatialPolygon object of the species range in Geographic projection, and the same SpatialPolygon object projected to the Azimuthal equal area projection.

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| rangemap\_fig {rangemap} | R Documentation |

## Figures of species range maps

### Description

rangemap\_fig generates customizable figures of species range maps using the objects produced by other function of this package.

### Usage

rangemap\_fig(range, polygon, xlim, ylim, grid = "measured",

appearance = "labels", sides = "bottomleft", north = FALSE,

north\_position = "topleft", scalebar = FALSE,

scalebar\_position = "bottomleft", export = FALSE, format = "png", ...)

### Arguments

|  |  |
| --- | --- |
| range | an object produced with any of the following functions:rangemap\_buff, rangemap\_bound, rangemap\_hull,rangemap\_enm, and rangemap\_tsa. |
| polygon | a SpatialPolygon object to be used as base map for plotting the species range. |
| xlim | two element numeric vector giving a range of longitudes, expressed in degrees, to which drawing should be restricted. Longitude is measured in degrees east of Greenwich, so that, in particular, locations in the USA have negative longitude. If fill = TRUE, polygons selected by region must be entirely inside the xlim range. The default value of this argument spans the entire longitude range of the database. |
| ylim | two element numeric vector giving a range of latitudes, expressed in degrees, to which drawing should be restricted. Latitude is measured in degrees north of the equator, so that, in particular, locations in the USA have positive latitude. If fill = TRUE, polygons selected by region must be entirely inside the ylim range. The default value of this argument spans the entire latitude range of the database. |
| grid | (character) units to be used in the grid. It can be "null", "measured", or "graticules". |
| appearance | (character) type of grid if grid is different than "null". It can be "labels", "grids", or "ticks". |
| sides | (character) sides in which the labels will be placed in the figure. |
| north | (logical) if TRUE, a simple north arrow will be placed in north\_position. |
| north\_position | (character) site in the figure where the north arrow will be placed. |
| scalebar | (logical) if TRUE a simple scale bar will be inserted in scalebar\_position. |
| scalebar\_position | (character) place for the scale bar insertion. |
| export | (logical) if TRUE a figure in format = format will be written in the working directory, appart of the returned object. |
| format | (character) format of the figure that will be written in the working directory if export = TRUE. |
| ... | other arguments from function plot. |

### Details

Position of distinct elements depend on the spatial configuration of the species range. Therefore, their positiuon may need to be changed if the elements are needed. Position options are the same than in keywords for representing x and y in the function plot

### Value

A figure of the species distributional range in a geographical context, with the map components defined by the user.

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| ranges\_envcomp {rangemap} | R Documentation |

## Comparison of species ranges in environmental space

### Description

ranges\_envcomp generates a two dimensional comparison of a species' ranges created using distinct algortihms, to visualize implications of selecting one of them if environmental conditions are considered.

### Usage

ranges\_envcomp(occurrences, variables, ranges, export = FALSE,

format = "png", ...)

### Arguments

|  |  |
| --- | --- |
| occurrences | a data.frame containing species occurrences, columns must be: Species, Longitude, and Latitude. |
| variables | a RasterStack object of environmental variables that will be used for performing the trend surface analysis. |
| ranges | a list of objects produced with any of the following functions:rangemap\_buff, rangemap\_bound, rangemap\_hull,rangemap\_enm, and rangemap\_tsa. |
| export | (logical) if TRUE a figure in format = format will be written in the working directory, appart of the returned object. |
| format | (character) format of the figure that will be written in the working directory if export = TRUE. |
| ... | other arguments from function plot. |

### Details

Trend surface analysis Is a method based on low-order polynomials of spatial coordinates for estimating a regular grid of points from scattered observations.

### Value

A figure showing, in the environmental space, the species ranges generated with any of the functions: rangemap\_buff, rangemap\_bound, rangemap\_hull, rangemap\_enm, andrangemap\_tsa.