**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**

|  |  |
| --- | --- |
| rangemap {rangemap} | R Documentation |

rangemap: A package for construction of species distributional range maps.

**Description**

rangemap helps This package presents various tools to create species range maps based on occurrence data, statistics, and distinct shapefiles. Other tools of this package can be used to analyze environmental characteristics of the species ranges and to create high quality figures for publication.

**rangemap functions**

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

|  |  |
| --- | --- |
| rangemap\_buff {rangemap} | R Documentation |

Species range maps based on buffered occurrences

**Description**

rangemap\_buff generates a species range polygon for a given species by buffering provided occurrences using a defined distance. Shape files can be saved in the working directory if it is needed.

**Usage**

rangemap\_buff(occurrences, distance = 1, polygons, export = FALSE)

**Arguments**

|  |  |
| --- | --- |
| occurrences | a data.frame containing species occurrences, columns must be: Species, Longitude, and Latitude. |
| distance | (numeric) distance in decimal degrees to be used for creating the buffer areas around occurrences, default = 1. |
| polygons | (optional) a SpatialPolygon object that will be clipped with the buffer areas to create species ranges based on actual limits. If not defined, a default world map will be used. |
| 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 latlong 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 = pek[1], return = "data")

# keeping only georeferenced records

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

# buffer distance

dist <- 0.5

|  |  |
| --- | --- |
| 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.

**Usage**

rangemap\_bound(occurrences, boundaries = "countries", polygons,

disolve = TRUE, export = FALSE)

**Arguments**

|  |  |
| --- | --- |
| occurrences | a data.frame containing species occurrences, columns must be: Species, Longitude, and Latitude. |
| boundaries | (character) type of boundaries to use from the available: "countries", "states" for USA and CAN only, "counties" for USA, "departments" and "provinces" for other countries; default = "countries". |
| 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. |
| export | (logical) if TRUE a shapefile of the species range will be written in the working directory, appart of the returned object. |

**Details**

Boundaries used are loaded using the gadm.loadCountries 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),]

disolve <- TRUE

bound\_range <- rangemap\_bound(occurrences = occ\_g, boundaries = "countries", disolve = disolve)

|  |  |
| --- | --- |
| 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)