

Package ‘ConR’

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Type Package

Title Computation of Parameters Used in Preliminary Assessment of Conservation Status

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Description Multi-species estimation of geographical range parameters for preliminary assessment of conservation status following Criterion B of the International Union for Conservation of Nature (IUCN, see <<http://www.iucnredlist.org>>).

Depends R (>= 3.3), raster, sp

License GPL-2

Imports fields, geosphere, grDevices, maptools, methods, rgdal, rgeos, spatstat, spatstat.utils, tibble, writexl, doParallel, foreach

LazyData true

Suggests knitr, rmarkdown, alphahull, testthat

VignetteBuilder knitr

URL <https://github.com/gdauby/ConR>

BugReports <https://github.com/gdauby/ConR/issues>

RoxygenNote 6.1.1

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ConR-package	<i>Computation of Parameters Used in Preliminary Assessment of Conservation Status</i>
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Description

R functions for calculating statistics used for a preliminary conservation assessment following Criterion B of the IUCN (Extent of Occurrence, Area of Occupancy, number of locations, number of sub-populations)

Details

Index of help topics:

A00.computing	Area of occupancy
ConR-package	Computation of Parameters Used in Preliminary Assessment of Conservation Status
EOO.computing	Extent of Occurrences
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Madagascar.protec	Dataset of Malagasy protected areas
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dataset.ex	Dataset of plant species distribution
land	land
locations.comp	Number of locations
map.res	Mapping in grid cell results of IUCN.eval
subpop.comp	Subpopulations computation following Circular buffer method

Author(s)

Gilles Dauby

Maintainer: Gilles Dauby <gildauby@gmail.com>

AOO.computing	<i>Area of occupancy</i>
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Description

Compute areas of occupancy (AOO) for multiple taxa in square kilometres

Usage

```
AOO.computing(XY, Cell_size_AOO = 2, nbe.rep.rast.AOO = 0,
  parallel = FALSE, NbeCores = 2, show_progress=FALSE, export_shp=FALSE)
```

Arguments

XY	dataframe see Details
Cell_size_AOO	a numeric, value indicating the grid size in kilometres used for estimating Area of Occupancy. By default, equal to 2
nbe.rep.rast.AOO	a numeric, indicate the number of raster with random starting position for estimating the AOO. By default, it is 0 but some minimal translation of the raster are still done
parallel	a logical. Whether running in parallel. By default, it is FALSE
NbeCores	an integer. Register the number of cores for parallel execution. By default, it is 2
show_progress	a logical. Whether a bar showing progress in computation should be shown. By default, it is FALSE
export_shp	a logical. Whether a shapefile of occupied cells should be exported. By default, it is FALSE

Details

Input as a dataframe should have the following structure:

It is mandatory to respect field positions, but field names do not matter

[,1]	ddlat	numeric, latitude (in decimal degrees)
[,2]	ddlon	numeric, longitude (in decimal degrees)
[,3]	tax	character or factor, optional field with taxa names

Value

A vector

Author(s)

Gilles Dauby
<gildauby@gmail.com>

References

Gaston & Fuller 2009 The sizes of species' geographic ranges, *Journal of Applied Ecology*, 49 1-9

Examples

```
data(dataset.ex)
## Not run:
A00 <- A00.computing(dataset.ex)

## End(Not run)
```

dataset.ex	<i>Dataset of plant species distribution</i>
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Description

A dataframe of three columns

Usage

```
data(dataset.ex)
```

Format

A dataframe

E00.computing	<i>Extent of Occurrences</i>
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Description

Compute extent of occurrences (EOO) for multiple taxa in square kilometres using [geosphere](#) package and provide SpatialPolygons used for EOO computation

Usage

```
EOO.computing(XY, exclude.area=FALSE, country_map=NULL, export_shp=FALSE, write_shp=FALSE,
alpha=1, buff.alpha=0.1, method.range="convex.hull",
Name_Sp="species1",
buff_width=0.1, method.less.than3="not comp",
write_results=TRUE,
file.name="EOO.results", parallel = FALSE, NbeCores = 2, show_progress=FALSE)
```

Arguments

XY	dataframe see Details
exclude.area	a logical, if TRUE, areas outside of country_map are cropped of SpatialPolygons used for calculating EOO. By default is FALSE
country_map	a SpatialPolygonsDataFrame or SpatialPolygons showing for example countries or continent borders. This shapefile will be used for cropping the SpatialPolygons if exclude.area is TRUE
export_shp	a logical, whether shapefiles should be exported or not, see Value. By default is FALSE
write_shp	a logical, if TRUE, export SpatialPolygons used for EOO computation as ESRI shapefiles in the working directory. By default is FALSE
alpha	a numeric, if method.range is "alpha.hull", value of alpha of the alpha hull, see ahull . By default is 1
buff.alpha	a numeric, if method.range is "alpha.hull", define the buffer in decimal degree added to alpha hull. By default is 0.1
method.range	a character string, "convex.hull" or "alpha.hull". By default is "convex.hull"
Name_Sp	a character string, if XY is for one taxon and field containing taxon names is not provided, this item provide taxon name. By default is "Species1"
buff_width	a numeric. For a specific case where all points of a taxa are on a straight line, see Details. By default is 0.1
method.less.than3	a character string. If equal to "arbitrary", will give a value to species with two unique occurrences, see Details. By default is "not comp"
write_results	a logical. If TRUE, results will be exported in the working environment as a csv file. By default is TRUE
file.name	a character string. Name file for exported results in csv file. By default is "EOO.results"
parallel	a logical. Wether running in parallel. By default, it is FALSE
NbeCores	an integer. Register the number of cores for parallel execution. By default, it is 2
show_progress	a logical. Whether a bar showing progress in computation should be shown. By default, it is FALSE

Details

Input as a dataframe should have the following structure:

It is mandatory to respect field positions, but field names do not matter

[,1]	ddlat	numeric, latitude (in decimal degrees)
[,2]	ddl lon	numeric, longitude (in decimal degrees)
[,3]	tax	character or factor, optional field with taxa names

Important notes:

EOO will only be computed if there is at least three unique occurrences unless `method.less.than3` is put to "arbitrary". In that specific case, EOO for species with two unique occurrences will be equal to $\text{Dist} \times \text{Dist} \times 0.1$ where Dist is the distance in kilometres separating the two points.

For the very specific (and infrequent) case where all occurrences are localized on a straight line (in which case EOO would be null), EOO is estimated by the area of polygon surrounding this straight line with a buffer of `buff.alpha` decimal degree. There is a warning when this happen.

Limitation

For a species whose occurrences span more than 180 degrees, EOO is not computed. This is the case for example for species whose distribution span the 180th meridian.

Value

If `export_shp` is FALSE, a dataframe with one field containing EOO in square kilometres. NA is given when EOO could not be computed because there is less than three unique occurrences (or two if `method.less.than3` is put to "arbitrary").

If `export_shp` is TRUE, a list with:

1. EOO in square kilometres
2. SpatialPolygons used for EOO computation

Author(s)

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References

Gaston & Fuller 2009 The sizes of species' geographic ranges, *Journal of Applied Ecology*, 49 1-9

See Also

[ahull](#)

<https://github.com/azizka/speciesgeocodeR>

Examples

```
data(dataset.ex)
data(land)
## Not run:
EOO <- EOO.computing(dataset.ex)
```

```
## This exclude areas outside of land (i.e. ocean) for EOO computation
EOO <- EOO.computing(dataset.ex,
  exclude.area=TRUE, country_map=land)

## End(Not run)
```

IUCN.eval

Preliminary conservation status assessment following IUCN Criterion B

Description

Given a dataframe of georeferenced occurrences of one, or more, taxa, this function provide statistics values (Extent of Occurrence, Area of Occupancy, number of locations, number of subpopulations) and provide a preliminary conservation status following Criterion B of IUCN. A graphical map output is also available.

Usage

```
IUCN.eval(DATA, country_map = NULL, Cell_size_A00 = 2, Cell_size_locations = 10,
  Resol_sub_pop = 5, method_locations = "fixed_grid", Rel_cell_size = 0.05,
  DrawMap = FALSE, add.legend = TRUE,
  file_name = NULL, export_shp = FALSE, write_shp = FALSE,
  write_results=TRUE, protec_areas = NULL, map_pdf = FALSE, draw.poly.EOO=TRUE,
  exclude.area = FALSE, method_protected_area = "no_more_than_one",
  ID_shape_PA = "WDPA_PID",
  buff_width = 0.1, SubPop=TRUE, alpha=1, buff.alpha=0.1,
  method.range="convex.hull", nbe.rep.rast.A00=0,
  showWarnings=TRUE, write_file_option="excel",
  parallel=FALSE, NbeCores=2)
```

Arguments

DATA	a dataframe or an object of class spgeoIN see https://github.com/azizka/speciesgeocodeR . See Details
country_map	a SpatialPolygonsDataFrame or SpatialPolygons showing for example countries or continent borders. This shapefile will be used for cropping the SpatialPolygons used for EOO computation if exclude.area is TRUE. By default, it is land
Cell_size_A00	a numeric, value indicating the grid size in kilometres used for estimating Area of Occupancy. By default, equal to 2
Cell_size_locations	a numeric, value indicating the grid size in kilometres used for estimating the number of location. By default, equal to 10
Resol_sub_pop	a numeric, value indicating the radius size in kilometres used for estimating the number of sub-population. By default, equal to 5

DrawMap	a logical, if TRUE a map is produced for each species in png format, unless map_pdf is TRUE. By default, it is FALSE
add.legend	a logical, if TRUE a legend and a submap showing distribution in 'country_map' are displayed for each map. By default, it is TRUE
method_locations	a character string, indicating the method used for estimating the number of locations. "fixed_grid" or "sliding scale". See details. By default, it is "fixed_grid"
Rel_cell_size	a numeric, if method_locations="sliding scale", Cell_size_locations is ignored and the resolution is given by the maximum distance separating two occurrences multiplied by Rel_cell_size. By default, it is 0.05
file_name	a character string. Name of the file. By default, it is "IUCN_"
export_shp	a logical, if TRUE, shapefiles of SpatialPolygons used for EOO computation are exported. By default, it is FALSE
write_shp	a logical, if TRUE, shapefiles of SpatialPolygons used for EOO computation are written as ESRI shapefiles in a sub-directory in the working directory. By default, it is FALSE
write_results	a logical, if TRUE, results are exported in a file which can csv or excel, see write_file_option. By default, it is TRUE
write_file_option	a character, if "excel", results are exported in excel file, if "csv", results are exported in csv. By default, it is "excel"
protec_areas	a SpatialPolygonsDataFrame, shapefile with protected areas. If provided, this will be taken into account for calculating number of location (see Details and method_protected_area). By default, no shapefile is provided
ID_shape_PA	a character string, indicating the field name of protec_areas with ID of the SpatialPolygonsDataFrame of protected areas
map_pdf	a logical, if TRUE, maps are exported in one pdf file. Otherwise, each species map is exported in png. By default, it is FALSE
draw.poly.EOO	a logical, if TRUE, the polygon used for estimating EOO is drawn. By default, it is TRUE
exclude_area	a logical, if TRUE, areas outside of country_map are cropped of SpatialPolygons used for EOO computation. By default, it is FALSE
method_protected_area	a character string. By default is "no_more_than_one", which means occurrences within protected areas (if provided) will not be taken into account for estimating the number of locations following the grid system, see Details. By default, it is "no_more_than_one"
SubPop	a logical. If TRUE, sub-populations will be estimated. By default, it is TRUE
buff_width	a numeric. For a specific case where all points of a species are on a straight line, EOO is computed by first drawing this straight line and adding a buffer of buff_width decimal degrees around this line. By default, it is 0.1
alpha	a numeric, if method.range is "alpha.hull", alpha value for the construction of alpha hull. By default, it is 1

<code>buff.alpha</code>	a numeric, if <code>method.range</code> is "alpha.hull", indicate the buffer added to the alpha hull in decimal degree. By default, it is 0.1
<code>method.range</code>	a character string, if "convex.hull", EOO is based on a convex hull. if "alpha.hull", EOO is based on alpha hull of alpha value. By default, it is "convex.hull"
<code>nbe.rep.rast.AOO</code>	a numeric, indicate the number of raster with random starting position for estimating the AOO. By default, it is NULL but some minimal translation of the raster are still done
<code>showWarnings</code>	a logical. Wether R should report warnings
<code>parallel</code>	a logical. Wether running in parallel. By default, it is FALSE
<code>NbeCores</code>	an integer. Register the number of cores for parallel execution. By default, it is 2

Details

Input as a dataframe should have the following structure:

It is mandatory to respect field positions, but field names do not matter

[,1]	<code>ddlat</code>	numeric, latitude (in decimal degrees)
[,2]	<code>ddlon</code>	numeric, longitude (in decimal degrees)
[,3]	<code>tax</code>	character or factor, taxa names
[,4]	<code>family</code>	character, optional field indicating higher taxonomic rank
[,5]	<code>coly</code>	numeric, optional field indicating collection year

`coly` and `family` are optinal fields

If the optional field named 'family' is provided, indicating higher taxonomic rank, this will be displayed in the title of the map if `DrawMap` is 'TRUE'.

If the optional field named 'coly' is provided, indicating collection year, a sub-graph in the map will be displayed (if `DrawMap` and `add.legend` are both TRUE) showing a barplot of collection year

Starting position of the raster used for estimating the Area Of Occupancy

Different starting position of the raster used for estimate the AOO may provide different number of occupied cells. Hence, by default, 4 different translations of the raster is done (fixed increment of 1/4 resolution north and east) and the minimum number of occupied cells is used for estimating AOO. It is also possible to define a given number of random starting position of the raster using the argument `nbe.rep.rast.AOO`

Estimating number of locations

Locations are estimated by overlaying a grid of a given resolution (see `Cell_size_locations` for specifying the resolution). The number of locations is simply the number of occupied locations. Note that the grid position is overlaid in order to minimize the number of locations (several translation of the grid are performed and the one providing the minimum number of occupied cells is provided).

Taking into account protected area for estimating the number of locations

A location is defined by the IUCN as a "geographically or ecologically distinct area in which a sin-

gle threatening event can affect all individuals of the taxon". A simple way to include threat level is to rely on a map of protected areas and assume that populations within and outside protected areas are under different threat level.

If a map of protected area is provided, this one is used for estimating the number of locations by the following procedure:

- if `method_protected_area` is "no_more_than_one", all occurrences within a given protected area will be considered as one location. Occurrences outside protected area will be used for estimating the number of locations using overlaying grid as described above. See the vignette for illustration.
- if `method_protected_area` is NOT "no_more_than_one", number of locations will be estimated by the overlaying grid as described above, but by considering differently occurrences outside and inside protected area. See the vignette for illustration.

The protected areas layers should be given as as `SpatialPolygonsDataFrame` in `protec_areas`. The `ID_shape_PA` should also be given and should represent the unique ID of each protected area in the provided shapefile. This can be checked by the following code:

```
colnames(ProtectedAreas@data) Where ProtectedAreas is the name of your shapefile.
```

Limitation in the estimations of EOO

For a species whose occurrences span more than 180 degrees, EOO is not computed. This is the case for example for species whose distribution span the 180th meridian.

Value

A dataframe if 'export_shp' is FALSE. A list if 'export_shp' is TRUE.

If a list, three elements are provided:

1. first element a dataframe with results (see field description below)
2. second element `SpatialPolygons` used for EOO computation
3. third element `SpatialPolygons` used for subpopulations

The dataframe has as many rows as taxa and the following fields:

[,1]	EOO	numeric, EOO (square kilometres)
[,2]	AOO	numeric, AOO (square kilometres)
[,3]	Nbe_unique_occ.	numeric, Number of unique occurrences
[,4]	Nbe_subPop	numeric, Number of subpopulations
[,5]	Nbe_loc	numeric, Number of locations
[,6]	Category_CriteriaB	character, IUCN threat category according to Criterion B
[,7]	Category_code	character, IUCN annotation
[,8]	Category_AOO	character, IUCN threat category according to Criterion B ignoring EOO
[,9]	Category_EOO	character, IUCN threat category according to Criterion B ignoring AOO

Author(s)

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References

Gaston KJ & Fuller AF, 2009, The sizes of species' geographic ranges, *Journal of Applied Ecology*, 49 1-9

IUCN Standards and Petitions Subcommittee, 2010, Guidelines for Using the IUCN Red List Categories and Criteria. <https://www.iucnredlist.org/resources/categories-and-criteria>

Rivers CM, Bachman SP & Meagher TR, 2010, Subpopulations, locations and fragmentation: applying IUCN red list criteria to herbarium specimen data, *Biodiversity Conservation* 19:2071-2085

See Also

<https://CRAN.R-project.org/package=biogeo>

<https://github.com/azizka/speciesgeocodeR>

Examples

```
data(dataset.ex)
data(land)
## Not run:
Results <- IUCN.eval(dataset.ex, country_map=land)
## A directory has been created in your working directory
and maps for each species has been produced

### The method for computing locations is a sliding scale:
## the grid resolution will be 0.05*the maximum distance separating occurrences
Results <- IUCN.eval(dataset.ex,
                    country_map=land, Cell_size_locations=10,
                    Resol_sub_pop = 5, Cell_size_A00 = 4, method_locations="sliding scale")

## End(Not run)
## Not run:
## Install speciesgeocodeR package for an example with their lemurs dataset
library(speciesgeocodeR)
data("lemurs_in")

Results <- IUCN.eval(lemurs_in, DrawMap=FALSE, country_map=land, SubPop=FALSE)

## End(Not run)
```

land	<i>land</i>
------	-------------

Description

A SpatialPolygonDataFrame showing land cover

Usage

```
data(land)
```

Format

A dataframe

Source

<http://www.naturalearthdata.com/downloads/10m-physical-vectors/>

locations.comp	<i>Number of locations</i>
----------------	----------------------------

Description

Compute number of locations for multiple taxa

Usage

```
locations.comp(XY, method = "fixed_grid",
              nbe_rep = 0,
              protec_areas = NULL,
              Cell_size_locations = 10,
              method_protected_area="no_more_than_one",
              ID_shape_PA="WDPA_PID",
              Rel_cell_size=0.05,
              parallel=FALSE,
              NbeCores=2)
```

Arguments

XY	dataframe see Details
method	a character string, indicating the method used for estimating the number of locations. "fixed_grid" or "sliding scale". See details. By default, it is "fixed_grid"
nbe_rep	a numeric, indicate the number of raster with random starting position for estimating the number of location. By default, it is 0 but some minimal translation of the raster are still done

protec_areas	a SpatialPolygonsDataFrame, shapefile with protected areas. If provided, this will be taken into account for calculating number of location (see Details and method_protected_area). By default, no shapefile is provided
Cell_size_locations	a numeric, value indicating the grid size in kilometres used for estimating the number of location. By default, equal to 10
method_protected_area	a character string. By default is "no_more_than_one", which means occurrences within protected areas (if provided) will not be taken into account for estimating the number of locations following the grid system, see Details. By default, it is "no_more_than_one"
ID_shape_PA	a character string, indicating the field name of protec_areas with ID of the SpatialPolygonsDataFrame of protected areas
Rel_cell_size	a numeric, if method_locations="sliding scale", Cell_size_locations is ignored and the resolution is given by the maximum distance separating two occurrences multiplied by Rel_cell_size. By default, it is 0.05
parallel	a logical. Whether running in parallel. By default, it is FALSE
NbeCores	an integer. Register the number of cores for parallel execution. By default, it is 2

Details

Input as a dataframe should have the following structure:

It is mandatory to respect field positions, but field names do not matter

[,1]	ddlats	numeric, latitude (in decimal degrees)
[,2]	ddlons	numeric, longitude (in decimal degrees)
[,3]	tax	character or factor, optional field with taxa names

Value

A list with one list for each species containing [[1]]SpatialPolygonDataframe and [[2]]vector of the number of location.

Author(s)

Gilles Dauby
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Examples

```
data(dataset.ex)
## Not run:
locations <- locations.comp(dataset.ex)
```

```
## End(Not run)
```

Madagascar.protec *Dataset of Malagasy protected areas*

Description

A SpatialPolygonDataFrame showing Malagasy protected areas

Usage

```
data(Madagascar.protec)
```

Format

A SpatialPolygonDataFrame

Source

World Database on Protected Areas <http://protectedplanet.net/country/MG>

References

<http://protectedplanet.net/country/MG>

Malagasy.amphibian *Dataset of Malagasy Amphibian occurrences*

Description

A SpatialPolygonDataFrame showing land cover

Usage

```
data(Malagasy.amphibian)
```

Format

A dataframe

Details

This dataset was further filtered out for keeping only species that have at least one occurrence in Madagascar

Source

GBIF.org (9th February 2016) GBIF Occurrence Download <http://doi.org/10.15468/dl.2tkoae>

References

Download Information: DOI: <http://doi.org/10.15468/dl.2tkoae> (may take some hours before being active) Creation Date: Tuesday, February 9, 2016 9:31:26 PM CET Records included: 74352 records from 50 published datasets Data size: 4.6 MB Download format: SIMPLE_CSV Filter used: TaxonKey: Amphibia Linnaeus, 1758 Geometry: POLYGON((-17.578125 33.724339,-17.578125 -36.597889,56.953125 -36.597889,56.953125 33.724339,-17.578125 33.724339)) HasCoordinate: true HasGeospatialIssue: false BasisOfRecord: Human Observation or Observation or Living Specimen or Literature Occurrence or Specimen

map.res

Mapping in grid cell results of IUCN.eval

Description

Provides four maps showing in grid cells of a given resolution : number of records, species richness, number of threatened species (CR+EN+VU) and proportion of threatened species. Based on [quilt.plot](#).

Usage

```
map.res(Results, Occurrences, country_map=NULL, Resol=1, threshold=0,
        LatMin=NULL, LatMax=NULL, LongMin=NULL,
        LongMax=NULL, export_map=FALSE, file_name=NULL, export_data=FALSE)
```

Arguments

Results	The default output of IUCN.eval applied to multiple species
Occurrences	A dataframe, see Details
country_map	A SpatialPolygonsDataFrame or SpatialPolygons showing for example countries or continent borders
Resol	numeric , resolution in decimal degrees
threshold	numeric, only grid cells with at least this number of records will be shown
LatMin	numeric, minimum latitude for the map
LatMax	numeric, maximum latitude for the map
LongMin	numeric, minimum longitude for the map
LongMax	numeric, maximum longitude for the map
export_map	logical, if TRUE, four maps in png will be created in the working directory if FALSE, maps will be displayed in the R session
file_name	character string. Name of the file
export_data	logical. If TRUE, a dataframe containing all information on the grid cell mapped is exported

Details

Input Occurrences as a dataframe should have the following structure:

It is mandatory to respect field positions, but field names do not matter

[,1]	ddlat	numeric, latitude (in decimal degrees)
[,2]	ddlon	numeric, longitude (in decimal degrees)
[,3]	tax	character or factor, taxa names

Value

Produce four maps either in the R session (if `export_map` is FALSE) or in png format in the working directory (if `export_map` is TRUE)

If `export_data` is TRUE

Output

[,1]	X	numeric, x coordinates of cell	[,2]	Y	numeric, y coordinates of cell	[,3]	mean
[,4]	meanLat	numeric, mean longitude of occurrences within cell					
[,5]	NbeRec	numeric, Number of records					
[,6]	NbeEsp	numeric, Number of species					
[,7]	NbeThreatened	numeric, Number of threatened species					
[,8]	PropThreatened	numeric, Proportion of threatened species					

Author(s)

Gilles Dauby

See Also

package fields function quilt.plot

Examples

```
## Not run:
data(land)
data(Malagasy_amphibian)
Results <- IUCN.eval(Malagasy_amphibian, DrawMap=FALSE, country_map=land, SubPop=FALSE)
### This should run for 3 to 6 minutes depending of the computer.

### Maps covering the whole dataset with a minimum of 5 records in each cell
map.res(Results=Results, Occurrences=Malagasy_amphibian, country_map=land,
export_map=FALSE, threshold=5)

## Maps focusing on Madagascar with a minimum of 5 records in each cell
map.res(Results=Results, Occurrences=Malagasy_amphibian, country_map=land, export_map=FALSE,
threshold=5, LatMin=-25, LatMax=-12, LongMin=42, LongMax=52)

## Maps focusing on Madagascar at half degree resolution with a minimum of 5 records in each cell
```

```

map.res(Results=Results, Occurrences=Malagasy_amphibian, country_map=land,
export_map=FALSE,Resol=0.5,
threshold=5, LatMin=-25,LatMax=-12,LongMin=42, LongMax=52)

## Maps have been exported in the directory IUCN__results_map
map.res(Results=Results, Occurrences=Malagasy_amphibian, country_map=land, export_map=TRUE,
threshold=5, LatMin=-25,LatMax=-12,LongMin=42, LongMax=52)

## Install speciesgeocodeR package for an example with their lemurs dataset
library(speciesgeocodeR)
data("lemurs_in")

Results <- IUCN.eval(lemurs_in, DrawMap=FALSE, country_map=land, SubPop=FALSE)

map.res(Results=Results, Occurrences=lemurs_in, country_map=land, export_map=FALSE, threshold=3,
LatMin=-25,LatMax=-12,LongMin=42, LongMax=52, Resol=1)

## End(Not run)

```

subpop.comp

Subpopulations computation following Circular buffer method

Description

Compute subpopulations following the Circular buffer method (see reference)

Usage

```
subpop.comp(XY, Resol_sub_pop)
```

Arguments

XY	Dataframe, coordinates in decimal degrees of one species, latitude in first column, longitude in second column
Resol_sub_pop	Numeric, radius of circles in kilometres

Details

Circular buffer method of Rivers et al. 2010 Each unique occurrence is buffered with a circle of a radius of Resol_sub_pop km. Overlapping circles are merged to form a single subpopulation, while non-overlapping circles are considered as separate subpopulations.

Value

A list, two elements:

1. first element The number of subpopulation
2. second element A shapefile of the subpopulations

Author(s)

Gilles Dauby

References

Rivers CM, Bachman SP & Meagher TR, 2010, Subpopulations, locations and fragmentation: applying IUCN red list criteria to herbarium specimen data, *Biodiversity Conservation* 19:2071-2085

Examples

```
## Not run:  
data(dataset.ex)  
data(land)  
  
SUB <- subpop.comp(dataset.ex, Resol_sub_pop=25)  
plot(SUB[["Platycoryne guingangae"]][["subpop.poly"]], col="red")  
plot(land, add=TRUE)  
  
## End(Not run)
```

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