Package 'ConR'

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Type Package

Title Computation of Parameters Used in Preliminary Assessment of Conservation Status

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Maintainer Gilles Dauby <gildauby@gmail.com>

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, methods, rgdal, rgeos, tibble, writexl, snow, doSNOW, foreach, rnaturalearth, sf

LazyData true

Suggests rmarkdown, testthat, rnaturalearthdata, alphahull

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URL https://gdauby.github.io/ConR/

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

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Author Gilles Dauby [cre, aut] (<https://orcid.org/0000-0002-9498-413X>)

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R topics documented:

`.ahull_to_SPLDF` *Internal function*

Description

Alpha hull processing

Usage

```
.ahull_to_SPLDF(x)
```

Arguments

x	ahull class object

Details

The functions ahull_to_SPLDF and alpha.hull.poly were originally posted in the website https://casoilresource.lawr.ucdavis.e
advanced-statistical-package/working-spatial-data/converting-alpha-shapes-sp-objects/ in a now bro-
ken link. It is also used in functions written by David Bucklin, see https://github.com/dnbucklin/r_movement_homerange

.alpha.hull.poly *Internal function*

Description

Alpha hull process

Usage

```
.alpha.hull.poly(XY, alpha = 1, buff = 0.1)
```

Arguments

XY	data.frame coordinates
alpha	integer
buff	numeric

Details

The functions ahull_to_SPLDF and alpha.hull.poly were originally posted in the website https://casoilresource.lawr.ucdavis.e
advanced-statistical-package/working-spatial-data/converting-alpha-shapes-sp-objects/ in a now bro-
ken link. It is also used in functions written by David Bucklin, see https://github.com/dnbucklin/r_movement_homerange

.AOO.estimation *Internal function*

Description

AOO estimatiion

Usage

```
.AOO.estimation(coordEAC, cell_size = 2, nbe_rep = 0, export_shp = FALSE)
```

Arguments

coordEAC	data.frame
cell_size	integer
nbe_rep	integer
export_shp	logical

.cell.occupied *Internal function*

Description

Count number of occupied cells given resolution, projection

Usage

```
.cell.occupied(nbe_rep = 0, size = 4, coord, export_shp = TRUE)
```

Arguments

nbe_rep	integer
size	integer
coord	data.frame
export_shp	logical

Author(s)

Gilles Dauby, <gildauby@gmail.com>

.Convex.Hull.Poly *Internal function*

Description

Build convex hull polygon

Usage

```
.Convex.Hull.Poly(XY)
```

Arguments

XY	data.frame

Author(s)

Gilles Dauby, <gildauby@gmail.com>

.crop.poly *Internal function*

Description

Crop polygons

Usage

```
.crop.poly(poly, crop)
```

Arguments

poly	Spatial
crop	Spatial

.EOO.comp *Internal function*

Description

EOO estimation

Usage

```
.EOO.comp(
  XY,
  exclude.area = FALSE,
  buff_width = 0.1,
  country_map = NULL,
  Name_Sp = "tax",
  alpha.hull = FALSE,
  convex.hull = TRUE,
  alpha = 1,
  buff.alpha = 0.1,
  method.less.than3 = "not comp"
)
```

Arguments

XY	data.frame
exclude.area	logical
buff_width	numeric
country_map	SpatialPolygonDataframe

Name_Sp	string
alpha.hull	logical
convex.hull	logical
alpha	integer
buff.alpha	numeric
method.less.than3	string

.IUCN.comp *Internal function*

Description

Compute IUCN eval

Usage

```
.IUCN.comp(
  DATA,
  poly_borders = NULL,
  Cell_size_AOO = 2,
  Cell_size_locations = 10,
  Resol_sub_pop = 5,
  method_locations = c("fixed_grid"),
  Rel_cell_size = 0.05,
  protec.areas = NULL,
  exclude.area = FALSE,
  method_protected_area = "no_more_than_one",
  ID_shape_PA = "WDPA_PID",
  buff_width = 0.1,
  NamesSp = "species1",
  write_shp = FALSE,
  file_name = NULL,
  add.legend = TRUE,
  DrawMap = TRUE,
  map_pdf = FALSE,
  draw.poly.EOO = TRUE,
  SubPop = TRUE,
  MinMax,
  alpha = 1,
  buff.alpha = 0.1,
  method.range = "convex.hull",
  nbe.rep.rast.AOO = 0,
  verbose = TRUE,
  showWarnings = TRUE
)
```

Arguments

DATA	data.frame
poly_borders	SpatialPolygonDataFrame
Cell_size_AOO	integer
Cell_size_locations	integer
Resol_sub_pop	integer
method_locations	integer
Rel_cell_size	integer
protec.areas	SpatialPolygonDataFrame
exclude.area	logical
method_protected_area	string
ID_shape_PA	string
buff_width	numeric
NamesSp	string
write_shp	logical
file_name	string
add.legend	logical
DrawMap	logical
map_pdf	logical
draw.poly.EOO	logical
SubPop	logical
MinMax	numeric vector
alpha	integer
buff.alpha	numeric
method.range	string
nbe.rep.rast.AOO	integer
verbose	logical
showWarnings	logical

.proj_crs *Internal function*

Description

get proj CRS

Usage

```
.proj_crs()
```

.prop_threat *Internal function*

Description

Compute prop and nbr taxa per cell

Usage

```
.prop_threat(Cell_count, threshold)
```

Arguments

Cell_count	data.frame
threshold	integer

.subpop.comp *Internal function*

Description

subpopulations estimation

Usage

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

Arguments

XY	data.frame
Resol_sub_pop	integer

AOO.computing *Area of occupancy*

Description

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

Usage

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

Arguments

XY	"dataframe" see Details
Cell_size_AOO	numeric, value indicating the grid size in kilometers used for estimating Area of Occupancy. By default, equal to 2
nbe.rep.rast.AOO	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	logical, whether running in parallel. By default, it is FALSE
NbeCores	string integer, register the number of cores for parallel execution. By default, it is 2
show_progress	logical, whether a bar showing progress in computation should be shown. By default, it is TRUE
export_shp	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, taxa names

The argument of nbe.rep.rast.AOO ideally should be higher than 20 for increasing the chance to get the minimal number of occupied cell. Increasing nbe.rep.rast.AOO however also increase the computing time. So this is a trade-off that depend on the importance to get the minimal AOO and the sie of the dataset.

Value

If export_shp if FALSE a vector of AOO estimates for each taxa If export_shp if TRUE a list with two elements

1. a vector of AOO estimates for each taxa
2. a list of SpatialPolygonsDataFrame for each taxa

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:
AOO <- AOO.computing(dataset.ex)

## End(Not run)

# This would estimate AOO for all taxa by overlaying randomly a
# grid 100 times. For each taxa, the minimum value is kept
## Not run:
AOO <- AOO.computing(dataset.ex, nbe.rep.rast.AO = 100)

## End(Not run)
```

---

dataset.ex *Dataset of plant species distribution*

Description

A dataframe of three columns

Usage

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

Format

A dataframe

EOO.computing *Extent of Occurrences*

Description

Compute extent of occurrences (EOO) for multiple taxa in square kilometers 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 = TRUE
)
```

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 SpatialPolygonsl 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. 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	logical. Whether a progress bar should displayed. TRUE by default.

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, 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 Dist*Dist*0.1 where Dist is the distance in kilometers 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 kilometers. 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 kilometers
2. `SpatialPolygons` used for EOO computation

Author(s)

Gilles Dauby

<gildauby@gmail.com>

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_AOO = 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.AOO = 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_AOO	a numeric, value indicating the grid size in kilometers used for estimating Area of Occupancy. By default, equal to 2
Cell_size_locations	a numeric, value indicating the grid size in kilometers used for estimating the number of location. By default, equal to 10
Resol_sub_pop	a numeric, value indicating the radius size in kilometers used for estimating the number of sub-population. By default, equal to 5

`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

`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

`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

`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

`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"

`ID_shape_PA`
: a character string, indicating the field name of `protec.areas` with ID of the `SpatialPolygonsDataFrame` of protected areas

`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

`SubPop`
: a logical. If TRUE, sub-populations will be estimated. By default, it is TRUE

`alpha`
: a numeric, if `method.range` is "alpha.hull", alpha value for the construction of alpha hull. By default, it is 1

`buff.alpha`
: a numeric, if `method.range` is "alpha.hull", indicate the buffer added to the alpha hull in decimal degree. By default, it is 0.1

`method.range` 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"

`nbe.rep.rast.AOO` 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

`showWarnings` a logical. Whether R should report warnings

`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"

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

`coly` and `family` are optional 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 single 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 descrived 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. a `dataframe` with results (see field description below)
2. a list of `SpatialPolygons` used for EOO computation
3. a list of `SpatialPolygons` used for subpopulations

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

[,1]	EOO	numeric, EOO (square kilometers)
[,2]	AOO	numeric, AOO (square kilometers)
[,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)

Gilles Dauby

<gildauby@gmail.com>

References

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

IUCN Standards and Petitions Subcommitte, 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_AOO = 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 *land*

Description

A SpatialPolygonDataFrame showing land cover

Usage

```
data(land)
```

Format

A dataframe

Source

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

locations.comp *Number of locations*

Description

Estimate the 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,
  show_progress = TRUE
)
```

Arguments

XY	data.frame, see details
method	string, indicating the method used for estimating the number of locations. Either "fixed_grid" or "sliding scale". See details. By default, it is "fixed_grid"
nbe_rep	numeric , indicate the number of raster with random starting position for estimating the number of locations By default, it is 0 but some minimal translation of the raster are still done
protec.areas	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	numeric, value indicating the grid size in kilometers used for estimating the number of location. By default, equal to 10
method_protected_area	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	string, indicating the field name of protec.areas with ID of the SpatialPolygonsDataFrame of protected areas
Rel_cell_size	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	logical, whether running in parallel. By default, it is FALSE
NbeCores	string integer, register the number of cores for parallel execution. By default, it is 2
show_progress	logical, whether a bar showing progress in computation should be shown. By default, it is TRUE

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, 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, <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:
locations <- locations.comp(dataset.ex)

## End(Not run)

# This would estimate the number of locations for all taxa by overlaying
# randomly a grid 100 times. For each taxa, the minimum value is kept
## Not run:
locations <- locations.comp(dataset.ex, nbe_rep = 100)

## 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 *Number of subpopulations*

Description

Estimate the number of locations following the method **circular buffer method**

Usage

```
subpop.comp(XY, Resol_sub_pop = 5)
```

Arguments

XY	string, indicating the method used for estimating the number of locations. Either "fixed_grid" or "sliding scale". See details. By default, it is "fixed_grid"
Resol_sub_pop	numeric. Defines in kilometers the radius of the circles around each occurrence

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, taxa names

Value

A list with one list for each taxa containing [[1]]Number of subpopulation and [[2]]SpatialPolygons.

Author(s)

Gilles Dauby, <gildauby@gmail.com>

References

Rivers MC, Bachman SP, Meagher TR, Lughadha EN, Brummitt NA (2010) Subpopulations, locations and fragmentation: applying IUCN red list criteria to herbarium specimen data. Biodiversity and Conservation 19: 2071-2085. doi: 10.1007/s10531-010-9826-9

Examples

```
data(dataset.ex)
## Not run:
subpop <- subpop.comp(dataset.ex, Resol_sub_pop = 5)

## End(Not run)
```

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