Package ‘ConR’

October 12, 2022

Type Package

Title Computation of Parameters Used in Preliminary Assessment of Conservation Status

Version 1.3.0

Maintainer Gilles Dauby <gildauby@gmail.com>


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

Encoding UTF-8

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

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

RoxygenNote 7.1.0

NeedsCompilation no

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

Repository CRAN

Date/Publication 2020-05-18 13:40:06 UTC

R topics documented:

.ahull_to_SPLDF .......................................................... 2
.alpha.hull.poly .......................................................... 3
.AOO.estimation .......................................................... 3
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.edu/software/r-advanced-statistical-package/working-spatial-data/converting-alpha-shapes-sp-objects/](https://casoilresource.lawr.ucdavis.edu/software/r-advanced-statistical-package/working-spatial-data/converting-alpha-shapes-sp-objects/) in a now broken link. It is also used in functions written by David Bucklin, see [https://github.com/dnbucklin/r_movement_homerange](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.edu/software/r-advanced-statistical-package/working-spatial-data/converting-alpha-shapes-sp-objects/ in a now broken 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 estimation

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>


Internal function

Description
Build convex hull polygon

Usage

Arguments
- XY: data.frame

Author(s)
Gilles Dauby, <gildauby@gmail.com>
### .crop.poly

**Internal function**

**Description**

Crop polygons

**Usage**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>poly</td>
<td>Spatial</td>
</tr>
<tr>
<td>crop</td>
<td>Spatial</td>
</tr>
</tbody>
</table>

### .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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>XY</td>
<td>data.frame</td>
</tr>
<tr>
<td>exclude.area</td>
<td>logical</td>
</tr>
<tr>
<td>buff_width</td>
<td>numeric</td>
</tr>
<tr>
<td>country_map</td>
<td>SpatialPolygonDataframe</td>
</tr>
</tbody>
</table>
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
)
.proj_crs

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>DATA</td>
<td>data.frame</td>
</tr>
<tr>
<td>poly_borders</td>
<td>SpatialPolygonDataFrame</td>
</tr>
<tr>
<td>Cell_size_AOO</td>
<td>integer</td>
</tr>
<tr>
<td>Cell_size_locations</td>
<td>integer</td>
</tr>
<tr>
<td>Resol_sub_pop</td>
<td>integer</td>
</tr>
<tr>
<td>method_locations</td>
<td>integer</td>
</tr>
<tr>
<td>Rel_cell_size</td>
<td>integer</td>
</tr>
<tr>
<td>protec_areas</td>
<td>SpatialPolygonDataFrame</td>
</tr>
<tr>
<td>exclude.area</td>
<td>logical</td>
</tr>
<tr>
<td>method_protected_area</td>
<td>string</td>
</tr>
<tr>
<td>ID_shape_PA</td>
<td>string</td>
</tr>
<tr>
<td>buff_width</td>
<td>numeric</td>
</tr>
<tr>
<td>NamesSp</td>
<td>string</td>
</tr>
<tr>
<td>write_shp</td>
<td>logical</td>
</tr>
<tr>
<td>file_name</td>
<td>string</td>
</tr>
<tr>
<td>add.legend</td>
<td>logical</td>
</tr>
<tr>
<td>DrawMap</td>
<td>logical</td>
</tr>
<tr>
<td>map_pdf</td>
<td>logical</td>
</tr>
<tr>
<td>draw.poly.EOO</td>
<td>logical</td>
</tr>
<tr>
<td>SubPop</td>
<td>logical</td>
</tr>
<tr>
<td>MinMax</td>
<td>numeric vector</td>
</tr>
<tr>
<td>alpha</td>
<td>integer</td>
</tr>
<tr>
<td>buff.alpha</td>
<td>numeric</td>
</tr>
<tr>
<td>method.range</td>
<td>string</td>
</tr>
<tr>
<td>nbe.rep.rast.AOO</td>
<td>integer</td>
</tr>
<tr>
<td>verbose</td>
<td>logical</td>
</tr>
<tr>
<td>showWarnings</td>
<td>logical</td>
</tr>
</tbody>
</table>

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
**Description**

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

**Usage**

```r
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 size 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)

```r
## 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**

```r
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**

```r
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 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. 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

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>dlat</td>
<td>numeric, latitude (in decimal degrees)</td>
</tr>
<tr>
<td>2</td>
<td>dlon</td>
<td>numeric, longitude (in decimal degrees)</td>
</tr>
<tr>
<td>3</td>
<td>tax</td>
<td>character or factor, taxa names</td>
</tr>
</tbody>
</table>

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:
IUCN.eval

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

```r
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**

<p>| | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>[.1]</td>
<td>ddat</td>
<td>numeric, latitude (in decimal degrees)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>[.2]</td>
<td>ddlon</td>
<td>numeric, longitude (in decimal degrees)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>[.3]</td>
<td>tax</td>
<td>character or factor, taxa names</td>
<td></td>
<td></td>
</tr>
<tr>
<td>[.4]</td>
<td>family</td>
<td>character, optional field indicating higher taxonomic rank</td>
<td></td>
<td></td>
</tr>
<tr>
<td>[.5]</td>
<td>coly</td>
<td>numeric, optional field indicating collection year</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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 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:

```r
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:

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>[1] EOO</td>
<td>numeric, EOO (square kilometers)</td>
</tr>
<tr>
<td>[2] AOO</td>
<td>numeric, AOO (square kilometers)</td>
</tr>
<tr>
<td>[3] Nbe_unique_occ.</td>
<td>numeric, Number of unique occurrences</td>
</tr>
<tr>
<td>[4] Nbe_subPop</td>
<td>numeric, Number of subpopulations</td>
</tr>
<tr>
<td>[5] Nbe_loc</td>
<td>numeric, Number of locations</td>
</tr>
<tr>
<td>[6] Category_CriteriaB</td>
<td>character, IUCN threat category according to Criterion B</td>
</tr>
<tr>
<td>[7] Category_code</td>
<td>character, IUCN annotation</td>
</tr>
<tr>
<td>[8] Category_AOO</td>
<td>character, IUCN threat category according to Criterion B ignoring EOO</td>
</tr>
<tr>
<td>[9] Category_EOO</td>
<td>character, IUCN threat category according to Criterion B ignoring AOO</td>
</tr>
</tbody>
</table>
Author(s)

Gilles Dauby
<gildauby@gmail.com>

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

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)
Description

A SpatialPolygonDataFrame showing land cover

Usage

data(land)

Format

A dataframe

Source

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

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>XY</td>
<td>data.frame, see details</td>
</tr>
<tr>
<td>method</td>
<td>string, indicating the method used for estimating the number of locations. Either &quot;fixed_grid&quot; or &quot;sliding scale&quot;. See details. By default, it is &quot;fixed_grid&quot;</td>
</tr>
<tr>
<td>nbe_rep</td>
<td>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</td>
</tr>
<tr>
<td>protec_areas</td>
<td>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</td>
</tr>
<tr>
<td>Cell_size_locations</td>
<td>numeric, value indicating the grid size in kilometers used for estimating the number of location. By default, equal to 10</td>
</tr>
<tr>
<td>method_protected_area</td>
<td>string, by default is &quot;no_more_than_one&quot;&quot;, 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 &quot;no_more_than_one&quot;</td>
</tr>
<tr>
<td>ID_shape_PA</td>
<td>string, indicating the field name of protec_areas with ID of the SpatialPolygonsDataFrame of protected areas</td>
</tr>
<tr>
<td>Rel_cell_size</td>
<td>numeric, if method_locations=&quot;sliding scale&quot;, 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</td>
</tr>
<tr>
<td>parallel</td>
<td>logical, whether running in parallel. By default, it is FALSE</td>
</tr>
<tr>
<td>NbeCores</td>
<td>string integer, register the number of cores for parallel execution. By default, it is 2</td>
</tr>
<tr>
<td>show_progress</td>
<td>logical, whether a bar showing progress in computation should be shown. By default, it is TRUE</td>
</tr>
</tbody>
</table>

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] dllon     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.
**Madagascar.protec**

**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**

```r
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**

```r
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**

```r
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](http://doi.org/10.15468/dl.2tkoae)

**References**

Download Information: DOI: [http://doi.org/10.15468/dl.2tkoae](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](http://doi.org/10.15468/dl.2tkoae).
map.res

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] dlat  numeric, latitude (in decimal degrees)
[,2] dlon  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

<p>| | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>.1</td>
<td>X</td>
<td>numeric, x coordinates of cell</td>
<td>.2</td>
<td>Y</td>
</tr>
<tr>
<td>.3</td>
<td>meanLat</td>
<td>numeric, mean longitude of occurrences within cell</td>
<td>.4</td>
<td>NbeRec</td>
</tr>
<tr>
<td>.5</td>
<td>NbeEsp</td>
<td>numeric, Number of species</td>
<td>.6</td>
<td>meanLat</td>
</tr>
<tr>
<td>.7</td>
<td>NbeThreatened</td>
<td>numeric, Number of threatened species</td>
<td>.8</td>
<td>PropThreatened</td>
</tr>
</tbody>
</table>

Author(s)

Gilles Dauby

See Also

package fields function quilt.plot

Examples

```r
## 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)
```
subpop.comp

    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)

<table>
<thead>
<tr>
<th>subpop.comp</th>
<th>Number of subpopulations</th>
</tr>
</thead>
</table>

### 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] `dlon` 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


Examples

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

## End(Not run)
```
Index

* datasets
  * dataset.ex, 10
  * land, 19
  * Madagascar.protec, 21
  * Malagasy.amphibian, 22
  * AOO.estimation, 3
  * Convex.Hull.Poly, 4
  * EOO.comp, 5
  * IUCN.comp, 6
  * ahull_to_SPLDF, 2
  * alpha.hull.poly, 3
  * cell.occupied, 4
  * crop.poly, 5
  * proj_crs, 7
  * prop_threat, 8
  * subpop.comp, 8

ahull, 11, 13

AOOcomputing, 9

dataset.ex, 10

EOO.comp, 11

geosphere, 11

IUCN.eval, 13, 23

land, 19

locations.comp, 19

Madagascar.protec, 21

Malagasy.amphibian, 22

map.res, 22

quilt.plot, 22

subpop.comp, 25