Package 'speciesgeocodeR'

November 21, 2017

Type Package

Title Prepare Species Distributions for the Use in Phylogenetic
Analyses

Version 2.0-9

Date 2017-11-21

Description Facilitating the use of large scale species occurrence records in biogeographic analyses. Automated cleaning of geographic occurrence records, range size estimation, visualization of richness patterns and classifying occurrence data into discrete areas for historical biogeography. Data cleaning of species occurrence records by automated flagging of problems common to biodiversity data from biological collections. Range shape and range size estimation of species from geographic occurrences records based on convex hulls, area of occupancy, WWF ecoregions and various distance measures. Preparation of species occurrences and distribution data for the use in phylogenetic analyses. SpeciesgeocodeR is especially suited for biogeographical and ecological questions on large datasets. The package includes the easy creation of summary-tables and -graphs and geographical maps. See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

License GPL-3

Depends R (>= 3.0.0), sp

Imports stats, methods, utils, grDevices, graphics, raster, rgeos,
ggplot2, geosphere, rgdal, picante, viridis

Suggests ape, geiger, rgbif, maptools, rnaturalearth,
rnaturalearthdata

LazyData true

RoxygenNote 6.0.1

NeedsCompilation no

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R topics documented:

speciesgeocodeR-package

Prepare Species Distributions for the Use in Phylogenetic Analyses

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cleaning of geographic occurrence records, range size estimation, visualization of richness patterns
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Details

The DESCRIPTION file:

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Version:	2.0-9
Date:	2017-11-21
Authors@R:	c(person(given = "Alexander", family = "Zizka", email = "alexander.zizka@bioenv.gu.se", role = c("aut"
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Author:	Alexander Zizka [aut, cre], Ruud Scharn [ctb]
Maintainer:	Alexander Zizka <alexander.zizka@bioenv.gu.se>

Index of help topics:

Author(s)

NA

Maintainer: NA

CalcRange	*Range Polygons from Occurrence Points*

Description

Calculate range polygons based on convex hulls from occurrence points. Includes planar and a 'pseudospherical' method for lat/long geographic coordinates and can crop to terrestrial area.

Usage

```
CalcRange(x, method = "pseudospherical", terrestrial = F,
                        rare = "buffer", buffer.width = 10000)
```

Arguments

x	a data.frame of species occurrences, including the columns 'species', 'decimallongitude', 'decimallatitude' OR and object of the class spgeoOUT OR an object of the class SpatialPointsDataFrame, with at least one data column named 'species'.
method	character string. The method to calculate convex hull. One of 'euclidean' and 'pseudospherical'. See details.
terrestrial	logical. If TRUE the polygons are restriceted to terrestrial area as in [landmass](#)
rare	character string. Details how to deal with species with less <3 occurrence records. One of 'buffer' or 'drop'. If buffer a geographic buffer with width buffer.width around the occurrence records is used, if "drop", the respective species are dropped.
buffer.width	numeric. The size of the buffer for rare in meters. A cylindrical equal area projection is used for buffering. . Default is to 10000 meters.

Details

Be careful with polygons when using lat/long data, convex hulls on a sphere are not easily defined. The function is limited to occurrence records on one hemisphere, spanning less than 180 degrees longitude and not crossing the 180/0 boundary!

If method == 'euclidean', planar (projected, or local scale) coordinates are expected. If method == 'pseudospherical' the geosphere::makePoly is used to define the convex hull. In the latter case, to create the polygon intermediate points are added on a sphere between two coordinates.

Value

An object of the class SpatialPolygonsDataFrame.

Note

See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

Examples

```
occ.exmpl<- data.frame(species = sample(letters, size = 250, replace = TRUE),
                        decimallongitude = runif(n = 250, min = 42, max = 51),
                        decimallatitude = runif(n = 250, min = -26, max = -11))

CalcRange(occ.exmpl, method = "pseudospherical", terrestrial = FALSE)
```

Description

Approximate species range size from occurrence records. Implements various methods, including Extent of Occurrence (EOO) based on planar or spherical convex hulls, Area of Occupancy (AOO), maximum and quantile distance between occurrences as well as WWF ecoregions. Can be used to inform for criterion B of the IUCN red list classification using `IUCNest`.

Usage

```
CalcRangeSize(x, method = "eoo_pseudospherical", terrestrial = F,
              biome = NULL, eco = NULL, convex.reps = 1,
              convex.repfrac = 1, convex.repsize = NULL,
              convex.rare = "buffer", convex.buffer.width = 10000,
              aoo.reps = 3, aoo.proj = NULL,
              aoo.gridsize = NULL, verbose = F)
```

Arguments

x	a `data.frame` of species occurrence records, including columns named 'species', 'decimallongitude', 'decimallatitude' OR and object of the class spgeoOUT OR an object of the class `SpatialPointDataFrame`, with at least one data column named 'species'.
method	a character string, defining the method for range size approximation one of 'eoo_euclidean', 'eoo_pseudospherical', 'aoo', 'maxdist', 'qdist', 'ecoregion'. See details.
terrestrial	logical. If TRUE the polygons are restricted to terrestrial area as in `landmass`
biome	A `SpatialPolygonsDataFrame` with a "BIOME" column. If provided, the extent of occurrence is intersected with the provided biome map and only areas in Biomes with at least one occurrence record are retained.
eco	A `SpatialPolygonsDataFrame` containing the WWF ecoregions. Only for `method == 'ecoregion'`.
convex.reps	numeric. The number of subsampling rounds for the convex hull calculation. See details.
convex.repfrac	numeric. The fraction of occurrence points (from the total number of occurrence points available in x for this species) to be used for convex hull calculation. See details.
convex.repsize	numeric. The number of occurrence points (from the total number of occurrence points available in x for this species) to be used for convex hull calculation. See details.
convex.rare	character string. Details how to deal with species with less <3 occurrence records for the convex hull methods. One of 'buffer' or 'drop'. If buffer a geographic buffer with width `convex.buffer.width` around the occurrence records is used, if "drop", the respective species are dropped.
convex.buffer.width	numeric. The size of the buffer for `rare` in meters. A cylindrical equal area projection is used for buffering. Default is to 10000 meters.

aoo.gridsize	numeric. The area of the grid cells used for the AOO calculation in units of aoo.proj or in meter if aoo.proj == NULL. Following the IUCN recommendations the default is to 4 square kilometres.
aoo.proj	A CRS object, indicating the projection used for AOO calculation. Should be a suitable equal area projection. See details.
aoo.reps	integer. The number of replicates for the AOO calculation. See details. Default = 3.
verbose	If TRUE, status will be reported.

Details

If method == 'eoo_euclidean', the range size is approximated as the area of a euclidean convex hull assuming planar coordinates in sqkm. The convex.reps option sets the number of replicates with convex.repfrac or convex.repsize points drawn randomly from the records available for each species. If convex.reps == 1 and convex.repfrac == 1 no replication is performed and all records are used for the convexhull. If convex.repfrac and convex.repsize are defined, convex.repfrac has priority. If method == 'eoo_pseudospherical', as above, except that a spherical convex hull is used, based on the geosphere package. If method == 'aoo' the area of occupancy is calculated using rasterization. If method == 'ecoregion', the ranges size is calculated as the total area of all WWF ecoregions with at least one occurrence of the species. If method == 'maxdist', the range size is approximated by the overall maximum distance (on a sphere) of all distances among the occurrence records per species in km. If method == 'qdist' the range size is approximated by the 25 and 75 quantiles of the maximum of all distances among the occurrence records per species in km. The default for aoo.proj is to CRS("+proj=cea +lon_0=0 +lat_ts=30 +x_0=0 +y_0=0 +a=6371228 +b=6371228 +units=m +no_defs")

Be careful with the polygons when using lat/long data, convex hulls on a sphere are not easily defined. The function is limited to occurrence records on one hemisphere, spanning less than 180 degrees longitude and not crossing the 180/0 boundary!

If method == euclidean, planar (projected, or local scale) coordinates are expected. If method == 'pseudospherical' the geosphere::makePoly is used to define the convex hull. In the latter case, to create the polygon intermediate points are added on a sphere between two coordinates.

Value

A data.frame of range sizes in skqm, or distance in km (for methods 'qdist' and 'maxdist').

Note

See https://github.com/azizka/speciesgeocodeR/wiki for more details and tutorials.

Examples

```
occ.exmpl<- data.frame(species = sample(letters, size = 250, replace = TRUE),
                       decimallongitude = runif(n = 250, min = 42, max = 51),
                       decimallatitude = runif(n = 250, min = -26, max = -11))

CalcRangeSize(occ.exmpl, method = 'eoo_pseudospherical', terrestrial = FALSE,
                 convex.reps = 2)
CalcRangeSize(occ.exmpl, method = 'maxdist', terrestrial = FALSE)
```

CladeByTrait *Extract Clades Based on Trait Values*

Description

Extract clades from a larger phylogeny based on a binary trait, with options to choose minimum and maximum clade size as well as the fraction of species sharing the trait

Usage

```
CladeByTrait(x, tree, prefix, min_clade_size, max_clade_size,
             monophyly_threshold, summary = F)
```

Arguments

x	a data.frame, with two columns: species, and the binary trait of interest (1 = present, 0 = absent, NA values permitted).
tree	a phylo object. The phylogenetic tree from which the clades shall be extracted.
prefix	a character string. A prefix for the output file names.
min_clade_size	numeric. The minimum number of tips in the resulting clades.
max_clade_size	numeric. The maximum number of tips in the resulting clades.
monophyly_threshold	
	numeric. The number of species in a clade permitted not to exhibit the trait of interest.
summary	logical. If TRUE a summary file is written to disk.

Value

A set of nexus files and plots in the working directory

Note

See https://github.com/azizka/speciesgeocodeR/wiki for more details and tutorials.

Author(s)

Alexander Zizka, Ruud Scharn

Examples

```
sp.nam <-  unique(paste(sample(letters, size = 250, replace = TRUE),
                        sample(letters, size = 250, replace = TRUE),
                  sep = ""))
tr.dat <- sample(c(0,1), size = length(sp.nam), replace = TRUE)
trait <- data.frame(species = sp.nam, trait = tr.dat)
```

DESin   *Create Input Files for DES-PyRate*

Description

Create the input for the DES model implemented in PyRate from tables of fossil and current species distributions.

Usage

```
DESin(x, recent, bin.size, reps = 3, verbose = F)
```

Arguments

x   a data.frame or the path to a tab delimited table with the fossil data. Column
             names follow the darwinCore standard: scientificName, earlistAge, latestAge,
             higherGeography. Each row represents a single fossil with scientificName =
             taxon name, earliestAge = maximum fossil age, latestAge = minimum fossil
             age, higherGeography = the area of interest for the DES analyses.

recent   a data.frame or the path to a tab delimited table with the recent distribution
             data. Column names follow the darwinCore standard: scientificName, higher-
             Geography. Each row represents a taxon with scientificName = taxon name and
             higherGeography = the area of interest for the DES analyses. If a taxon occurs
             in both areas, two separated rows are needed, one for each area.

bin.size   numeric. The size of the DES-time bins in the same unit as fossil ages, but
             usually million years.

reps   numeric. The number of replicated output files. Replication arises from the
             uncertainty in fossil age. For each replicate the age of the fossil is sampled from
             a uniform distribution between the earliestAge and the latestAge.

verbose   logical. If TRUE, the progress is reported

Value

An object of the class DESin, which is a list containing the input and output data

Note

See https://github.com/azizka/speciesgeocodeR/wiki for more details and tutorials and

See Also

plot.DESin, summary.DESin, write.DESin

Examples

```
fos <- data.frame(species= rep(letters[1:4],25),
                  earliestAge = runif(100, min = 60, max = 100),
                  latestAge = runif(100, min = 0, max = 60),
                  area = sort(rep(c("A", "B"), 50)))

rec <- data.frame(species = c(letters[1:4], letters[1:2]),
```

```
                    area = c(rep("A",4), rep("B", 2)))

exp1 <- DESin(fos, rec, bin.size = 2, reps = 3)

summary(exp1)
#plot(exp1)

## Not run:
write.DES.in(exp1, file = "Example1_DES_in")

## End(Not run)
```

IUCNest   *Convert Range Sizes to IUCN Assessment*

Description

The function converts range sizes (Area of Occupancy and Extent of Occurrence), as calculated by `CalcRange` to conservation assessments based on IUCN criterion B and extinction probabilities following Mooers et al. (2008).

Usage

```
IUCNest(x, value = "all",
        NT.thresh = c(30000, 3000), VU.thresh = c(20000, 2000),
        EN.thresh = c(5000, 500), CR.thresh = c(100, 10))
```

Arguments

x	an object of the class range.sizes, as produced by `CalcRange`.
value	a character string. Defining the output value, see details. One of "all", "AOO", "EOO", "IUCN50", "IUCN100", "IUCN500" Default = "all".
NT.thresh	numeric. Thresholds for categorization to near threatened, in the form (EOO, AOO). Defaults from IUCN Standards and Petitions (Subcommittee 2014).
VU.thresh	numeric. Thresholds for categorization to vulnerable, in the form (EOO, AOO). Defaults from IUCN Standards and Petitions (Subcommittee 2014).
EN.thresh	numeric. Thresholds for categorization to endangered, in the form (EOO, AOO). Defaults from IUCN Standards and Petitions Subcommittee (2014).
CR.thresh	numeric. Thresholds for categorization to critically endangered, in the form (EOO, AOO). Defaults from IUCN Standards and Petitions Subcommittee (2014).

Details

The value argument defines the type of assessment in the output: "AOO" = assessment based on the AOO, "EOO" = assessment based on the EOO, "both" = assessment based on AOO and EOO, "IUCN50" = a extra column where the assessment is converted into a probability of extinction within the next 50 years, "IUCN100" = a extra column where the assessment is converted into a probability of extinction within the next 100 years, "IUCN500" = a extra column where the assessment is converted into a probability of extinction within the next 500 years. See Mooers et al. 2008 for reference on the conversion.

Value

a `data.frame`, the number of columns depend on the value argument (see details).

Note

See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

References

IUCN Standards and Petitions Subcommittee (2014) Guidelines for using the IUCN Red List categories and criteria. Version 11. Prepared by the Standards and Petitions Subcommittee. Downloadable from: http://www.iucnredlist.org/documents/RedListGuidelines.pdf.

Mooers, A.O., Faith D.P. & Maddison W. P. (2008) Converting Endangered Species Categories to Probabilities if Extinction for Phylogenetic Conservation Prioritization. *PLOSone*, **3**(11)

Examples

```
occ.exmpl<- data.frame(species = sample(letters, size = 250, replace = TRUE),
                       decimallongitude = runif(n = 250, min = 42, max = 51),
                       decimallatitude = runif(n = 250, min = -26, max = -11))

rang <- CalcRange(occ.exmpl, method = 'pseudospherical', terrestrial = FALSE)
IUCNest(rang)
```

---

landmass   *Global Coastlines*

Description

A `SpatialPolygonsDataFrame` with global coastlines.

Usage

```
data("landmass")
```

Note

Most of the times it might be desirable to only flag records far away from the coast as problematic rather than those close to the coastline (which might be due to disagreements in coastlines, or low gps uncertainty). For these cases, there is a alternative coastline reference buffered by one degree available at <https://github.com/azizka/CoordinateCleaner/tree/master/extra_gazetteers>.

Source

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

Examples

```
data("landmass")
## Not run:
plot(landmass)

## End(Not run)
```

---

lemurs   *Distribution of Lemur Species*

Description

A `data.frame` with point occurrences of 17 Lemur species from Madagascar. The data is from <www.gbif.org>.

Usage

```
data("lemurs")
```

Format

A data frame with 282 observations on the following 3 variables.

`species` species name

`decimallongitude` longitude

`decimallatitude` latitude

Source

<www.gbif.org>, doi: 10.15468/dl.9ctrmi.

Examples

```
data(lemurs)
str(lemurs)
```

MapRichness   *Plotting Species Richness in a Set of Polygons*

Description

Illustrates the species number per polygon, based on and object of the class spgeoOUT (created by SpGeoCod).

Usage

```
MapRichness(x, buffer = 1, show.occ = F)
```

Arguments

x	an object of the class 'spgeoOUT'.
buffer	numeric. Indicating the buffer around the the data rectangle when plotting the map.
show.occ	logical. Defines if the occurrence points should be added to the plot (default = F).

Value

A plotted map.

Note

See https://github.com/azizka/speciesgeocodeR/wiki for more details and tutorials.

See Also

RichnessGrid, RangeRichness.

Examples

```
data(lemurs)
data(mdg_biomes)

outp <- SpGeoCod(lemurs, mdg_biomes, areanames = 'name')
## Not run:
MapRichness(outp)

## End(Not run)
```

---

mdg_biomes	*WWF Biomes of Madagascar*

Description

A `SpatialPolygonsDataFrame` of a simplified version of the WWF biomes of Madagascar.

Usage

```
data("mdg_biomes")
```

References

Olson, D. M., Dinerstein, E., Wikramanayake, E. D., Burgess, N. D., Powel, G. V. N., Underwood, E. C., Damico, J. A.,Itoua, I., Strand, H. E., Morrison, J. C., Loucks, C. J., Ricketts, T. H., Kura, Y., Lamoreux, J. F., Wettengel, W. W., Hedao, P., and Kassem, K.R. 2001 Terrestrial ecoregions of the world: A new map of life on earth. *BioScience*, **51**(11):933–938.

http://www.worldwildlife.org/publications/terrestrial-ecoregions-of-the-world

Examples

```
data(mdg_biomes)
str(mdg_biomes)
```

---

plot.DESin   *Plot Method for DESin*

Description

Plotting method for class DESin. Plots the number of species through time, after randomization.

Usage

```
## S3 method for class 'DESin'
plot(x, ribbon = TRUE, ...)
```

Arguments

x	an object of the class DESin.
ribbon	logical. If TRUE, the minimum and maximum species numbers per timebin over all replicates are shown as a ribbon around the mean.
...	other arguments passed to plot

Value

a plot showing the mean species number per timebin over all replicates.

See Also

DESin, summary.DESin,write.DESin

Examples

```
fos <- data.frame(species = rep(letters[1:4],25),
                  earliestAge = runif(100, min = 60, max = 100),
                  latestAge = runif(100, min = 0, max = 60),
                  area = sort(rep(c("A", "B"), 50)))

rec <- data.frame(species = c(letters[1:4], letters[1:2]),
                  area = c(rep("A",4), rep("B", 2)))

exp1 <- DESin(fos, rec, bin.size = 2, reps = 3)

plot(exp1)
```

---

plot.spgeoOUT *Plot Method for SpgeoOUT Objects*

Description

The plotting method for objects of the class spgeoOUT. Depending on the type argument the function can be used to get an overview over the data or plot all elements of the object.

Usage

```
## S3 method for class 'spgeoOUT'
plot(x,  type = "summary", mode = "percent", ...)
```

Arguments

x   an object of the class spgeoOUT.

type   a character string. Controls which data shall be plotted. Default is to "summary". See details for more information.

mode   a character string. Can be "percent" or "total" controls if percentage or total is shown for type = "species". Default is "percent".

...   additional arguments passed to other methods

Details

The output will be different depending on the type argument. type = "summary": a map with all occurrence points and polygons (red points not classified to any polygon), the species number for all polygons, and if available, a heatplot visualizing the coexistence matrix; type = "species": a bar chart for each input species showing the number of occurrences in each polygon; type = "polygons": a bar chart for each input-polygon showing the number of occurrences for each species in the polygon; type = "speciesrichness": a bar chart showing species number per polygon; type = "mapspecies": one map per species showing all occurrence points in all polygons; type = "mappolygons": a series of maps, showing each polygon and its close environment, with all samples classified to this polygon. Species are color-coded; type = "mapunclassified": a map with all sample points that could not be classified to any polygon; type = "mapall": a map of all occurrence points in the object.

See Also

[summary.spgeoOUT](#)

Examples

```
#simulate example occurrences
data(lemurs)
data(mdg_biomes)

outp <- SpGeoCod(lemurs, mdg_biomes, areanames = 'name')
## Not run:
plot(outp)
plot(outp, type = "speciesrichness")
plot(outp, type = "mapall")
```

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

PlotHull   *Plotting Species Ranges*

Description

Plots species distribution ranges approximated with [CalcRange](#) in the geographic context.

Usage

```
PlotHull(dat, select = "all", buffer = 1, bgmap,
         col = rgb(255, 0, 0, 10, maxColorValue = 255))
```

Arguments

dat	a list of 'SpatialPolygons' objects created with [CalcRange](#).
select	a character string indicating which elements of the list to plot. Can be one or multiple species names. Default = "all".
buffer	numerical. The buffer around the polygon extent when plotting the map.
bgmap	a SpatialPolygonsDataFrame as background map for the plots. Default = [landmass](#).
col	a character string indicating the colour of the polygons. Default is to transparent red.

Details

If type is set to "separate", set par(ask = T) to see all maps.

Value

A plot or a set of plots.

Note

See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

Examples

```
#simulate example occurrences
occ.exmpl<- data.frame(species = sample(letters, size = 250, replace = TRUE),
                       decimallongitude = runif(n = 250, min = 42, max = 51),
                       decimallatitude = runif(n = 250, min = -26, max = -11))


dat <- CalcRange(occ.exmpl, method = "pseudospherical", terrestrial = FALSE)
## Not run:
PlotHull(dat)

## End(Not run)
```

---

print.summary.spgeoOUT

Printing method for spgeoOUT summary object

Description

Prints the summary to screen.

Usage

```
## S3 method for class 'summary.spgeoOUT'
print(x, ...)
```

Arguments

x	summary of an spgeoOUT object.
...	arguments passed to other methods.

See Also

[plot.spgeoOUT](), [summary.spgeoOUT]()

RangeRichness   *Species Richness Raster from Range Polygons*

Description

Calculate species richness for the specified grid based on an list of range polygons, as derived from
[CalcRange]().

Usage

```
RangeRichness(x, ras, reso = 1, buffer = 1, terrestrial = FALSE)
```

Arguments

x	a list of SpatialPolygons with species ranges.
ras	template raster to rasterize x. If missing, the raster is constructed using the data extent and reso.
reso	numeric. Resolution of the raster in decimal degree. Only if ras is missing.
buffer	numerical. The buffer around the polygon extent when plotting the map.
terrestrial	logical. If TRUE, oceans are omitted.

Value

a [raster]() object with species number per gridcell.

Note

See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

Examples

```
#simulate example occurrences
occ.exmpl<- data.frame(species = sample(letters, size = 250, replace = TRUE),
                       decimallongitude = runif(n = 250, min = 42, max = 51),
                       decimallatitude = runif(n = 250, min = -26, max = -11))

rang <- CalcRange(occ.exmpl, method = 'pseudospherical')
sprich <- RangeRichness(rang)
plot(sprich)
```

RichnessGrid   *Species Richness and Abundance Grids from Point Records*

Description

A species richness or record abundance grid.

Usage

```
RichnessGrid(x, ras, reso = 1, type = "spnum")
```

Arguments

x	an object of the class spgeoOUT or a data.frame. If x is a data.frame, it must comprise three columns,: 'species', 'longitude' and 'latitude'.
ras	an object of the class raster defining the extent and resolution for the richness grid. If missing, estimated from the data.
reso	numeric. resolution of the raster in decimal degree, only specify if ras is missing.
type	character string indicating the type of data displayed: "spnum" = number of species per grid cell, "abu" = the number of occurrence points per grid cell.

Value

a raster object.

Note

See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

See Also

MapRichness, RangeRichness.

Examples

```
# for x = data.frame
data(lemurs)
dat <- RichnessGrid(lemurs, reso = 1, type = "spnum")
```

---

speciesgeocodeR-defunct

Defunct functions in package 'speciesgeocodeR'

Description

These functions are no longer available. Type FUNCTIONNAME() to see replacement.

Details

Defunct functions as of v.2.0-1 are: GeoClean, CoExClass, GetElevation, MapGrid, ReadPoints, SpeciesGeoCodeR, SpGeoCodH and WwfLoad

---

Spgc2BioGeoBEARS   *Geography Input for BioGeoBEARS*

Description

Convert an object of the class spgeoOUT in the format to be used as geography input for BioGeo-BEARS.

Usage

```
Spgc2BioGeoBEARS(x, phyl = NULL, file = NULL, true.areas = T, true.species = T)
```

Arguments

x	an object of the class 'spgeoOUT'
phyl	an object of the class phylo. An optional phylogeny to be used with BioGeo-BEARS, to align species.
file	character. The complete path and filename to the outputfile.
true.areas	logical. If TRUE, areas with 0 species are removed from the matrix. Default = TRUE.
true.species	logical. If TRUE, species not occurring in any area are removed from the matrix. Default = TRUE.

Details

This will create a file in the working directory.

Value

A file in the working directory and a list.

Note

See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

Author(s)

Alexander Zizka, Ruud Scharn

Examples

```
## Not run:
data(lemurs)
data(mdg_poly)

outp <- SpGeoCod(lemurs, mdg_poly)
conv <- Spgc2BioGeoBEARS(outp)

## End(Not run)
```

SpGeoCod   *Point to Polygon Classification*

Description

Classifying point occurrences to polygons for the use in phylogenetic analysis.

Usage

```
SpGeoCod(x, y, areanames, occ.thresh = 0, elevation, threshold)
```

Arguments

x	a `data.frame` with three columns named: species, decimallongitude, decimallatitude OR a `character string` with the path to a text file containing the coordinates of points of interest (tab delimited, three columns with header: species, decimallongitude, decimallatitude) OR a `character string` giving species names, to download from GBIF.
y	an `SpatialPolygonsDataframe` OR a `character string` with the path to a shape file containing the polygons of interest OR the path to a text file containing the polygons of interest (tab delimited, three columns with header: species, decimallongitude, decimallatitude) OR an object of the class SpatialPolygons .
areanames	a `character string`. If y is a `SpatialPolygonsDataFrame` or the path to a shape file, this column indicates the column with the area names. If the polygon input file is a text file leave as default (Default = "").
occ.thresh	numerical. Threshold for the minimum number of occurrences necessary in a polygon to be counted as present (in percent of the total occurrences of the species). Default = 0.
elevation	logical. Should the results be split by elevation class? (default = FALSE)
threshold	numeric vector. Indicating the elevation thresholds.

Value

An object of the class spgeoOUT.

Note

See https://github.com/azizka/speciesgeocodeR/wiki for more details and tutorials.

Examples

```
data(lemurs)
data(mdg_biomes)

outp <- SpGeoCod(lemurs, mdg_biomes, areanames = "name")
```

---

summary.DESin   *Summary Method for DESin*

Description

Summarizes the content of a DESin object.

Usage

```
## S3 method for class 'DESin'
summary(object, ...)
```

Arguments

object   an object of the class DESin.

...   arguments passed to other methods.

See Also

plot.DESin, write.DESin

Examples

```
fos <- data.frame(species = rep(letters[1:4],25),
                  earliestAge = runif(100, min = 60, max = 100),
                  latestAge = runif(100, min = 0, max = 60),
                  area = sort(rep(c("A", "B"), 50)))

rec <- data.frame(species = c(letters[1:4], letters[1:2]),
                  area = c(rep("A",4), rep("B", 2)))

exp1 <- DESin(fos, rec, bin.size = 2, reps = 3)

summary(exp1)
```

---

write.DESin *Write Method for DESin*

Description

Writes out objects of the class DESin to the working directory in a format suitable as direct input for PyRate-DES.

Usage

```
## S3 method for class 'DESin'
write(x, file)
```

Arguments

x	an object of the class DESin.
file	character. Path to where the files shall be written.

Value

a set of replicate tables in the working directory.

See Also

DESin, summary.DESin,plot.DESin

Examples

```
## Not run:
fos <- data.frame(species = rep(letters[1:4],25),
                  earliestAge = runif(100, min = 60, max = 100),
                  latestAge = runif(100, min = 0, max = 60),
                  area = sort(rep(c("A", "B"), 50)))

rec <- data.frame(species = c(letters[1:4], letters[1:2]),
                  area = c(rep("A",4), rep("B", 2)))

exp1 <- DESin(fos, rec, bin.size = 2, reps = 3)

write(exp1)

## End(Not run)
```

WriteOut   *Write spgeoOUT Objects to the Working Directory*

Description

Writes objects of the class 'spgeoOUT' (as generated by SpGeoCod) to the working directory. Output statistics as .txt files, maps and plots as .pdf and a nexus file for use in phylogenetic analyses.

Usage

```
WriteOut(x, type = "all")
```

Arguments

x   an object of the class spgeoOUT

type   a character string. Defines which results should be written to disk. One of "all", "BioGeoBEARS", "BayArea", "graphs", "maps", "nexus", "stats". Default is to "all".

Details

There are different options for the `writetype` argument: "all" = all summary tables, plots and maps; "BioGeoBEARS" = a text file in the geography input format of BioGeoBEARS; "BayArea" = two text files in the input format of BayArea; "graphs" = summary graphs as pdf files; "maps" = summary maps as .pdf file; "nexus" = the species to area classification as nexus file; "stats" = the summary tables as .txt files.

Value

a set of files in the working directory

Note

See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

See Also

[SpGeoCod](#)

Examples

```
## Not run:
data(lemurs)
data(mdg_biomes)

outp <- SpGeoCodH(lemurs, mdg_biomes, areanames = 'name')
WriteOut(outp)
WriteOut(outp, writetype = "graphs")
WriteOut(outp, writetype = "statistics")
WriteOut(outp, writetype = "nexus")

## End(Not run)
```

WWFload   *Download the WWF Terrestrial Ecoregions*

Description

Downloads a shape-file containing the terrestrial ecoregions as defined by Olson et al. 2001 from
<www.worldwildlife.org/publications/terrestrial-ecoregions-of-the-world>, unpacks them
and loads the into R.

Usage

```
WWFload(x = "")
```

Arguments

x   the path to the folder where the shapes should be saved. If set to " " the files are
                    saved to the working directory.

Value

A `SpatialPolygonsDataframe` with global biomes and ecoregions.

Note

See <https://github.com/azizka/speciesgeocodeR/wiki> for more details and tutorials.

References

Olson, D. M., Dinerstein, E. ,Wikramanayake, E. D., Burgess, N. D., Powel, G. V. N., Underwood,
E. C., Damico, J. A., Itoua, I., Strand, H. E., Morrison, J. C., Loucks, C. J., Ricketts, T. H., Kura,
Y., Lamoreux, J. F., Wettengel, W. W., Hedao, P., and Kassem, K.R. 2001 Terrestrial ecoregions of
the world: A new map of life on earth. *BioScience*, **51**(11):933–938.

<http://www.worldwildlife.org/publications/terrestrial-ecoregions-of-the-world>

Examples

```
## Not run:
wwf_eco <- WWFload()
plot(wwf_eco)
names(wwf_eco)

## End(Not run)
```

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