

Package ‘WEGE’

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Type Package

Title A Metric to Rank Locations for Biodiversity Conservation

Version 0.1.0

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Description Calculates the WEGE (Weighted Endemism including Global Endangerment index) index for a particular area. Additionally it also calculates rasters of KBA's (Key Biodiversity Area) criteria (A1a, A1b, A1e, and B1), Weighted endemism (WE), the EDGE (Evolutionarily Distinct and Globally Endangered) score, Evolutionary Distinctiveness (ED) and Extinction risk (ER). Farooq, H., Azevedo, J., Belluardo F., Nanvonamuquitxo, C., Bennett, D., Moat, J., Soares, A., Faurby, S. & Antonelli, A. (2020) <doi:10.1101/2020.01.17.910299>.

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Imports sf, sp, raster, stats, utils

NeedsCompilation no

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get_edge	<i>get_edge</i>
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Description

A function to get the WEGE index value for a provided polygon.

Usage

```
get_edge(
  target_area,
  input,
  x,
  y,
  species = "binomial",
  ed = "ED",
  category = "category",
  res = 1
)
```

Arguments

target_area	Either a sp or sf object to which to calculate the WEGE index.
input	Species ranges, either from a shapefile or from a georeferenced species list with a column for species, two columns for coordinates and one for the IUCN category.
x	name of the longitude column.
y	name of the latitude column.
species	name of the species column.
ed	name of the evolutionary distinctiveness column.
category	name of IUCN the category column. Terminology must be as follows: DD for Data Deficient, LC for Least Concern, NT for Near Threatened, EN, for Endangered, CR for Critically Endangered, EW for Extinct in the wild and EX for Extinct.
res	grid-cell size to use to calculate the range of the species in case a georeferenced species list was provided.

Value

a value corresponding to the EDGE score of the provided target_area

Examples

```
library(WEGE)
library(sp)
library(sf)

species <- letters[1:26]
range_list <- list()
for (i in seq_along(species)) {
  temp0 <- cbind(runif(3,1,50),runif(3,1,50))
  temp <- Polygon(rbind(temp0,temp0[1,]))
  range_list[[i]] <- Polygons(list(temp), ID = c(species[i]))
}
input <- st_as_sf(SpatialPolygons(range_list))
categories <- c('LC','NT','VU','EN','CR')
input$binomial <- species
input$category <- sample(size = nrow(input),x = categories,replace = TRUE)
input$ED <- runif(nrow(input),1,30)
temp0 <- cbind(runif(3,1,50),runif(3,1,50))
target_area <- Polygon(rbind(temp0,temp0[1,]))
target_area <- Polygons(list(target_area), ID = 'Target area')
target_area <- st_as_sf(SpatialPolygons(list(target_area)))

get_edge(target_area = target_area,input = input,species = 'binomial',category = 'category')
```

get_kba_criteria *Function to get the KBA criteria*

Description

A function to get the WEGE index value for a provided polygon.

Usage

```
get_kba_criteria(
  target_area,
  input,
  x,
  y,
  species = "binomial",
  category = "category",
  res = 1
)
```

Arguments

target_area	Either a sp or sf object to which to calculate the WEGE index.
input	Species ranges, either from a shapefile or from a georeferenced species list with a column for species, two columns for coordinates and one for the IUCN category.
x	name of the longitude column.
y	name of the latitude column.
species	name of the species column.
category	name of IUCN the category column. Terminology must be as follows: DD for Data Deficient, LC for Least Concern, NT for Near Threatened, EN, for Endangered, CR for Critically Endangered, EW for Extinct in the wild and EX for Extinct.
res	grid-cell size to use to calculate the range of the species in case a georeferenced species list was provided.

Value

a data.frame containing all the species that trigger KBA status as well as the criteria they trigger.

Examples

```
library(WEGE)
library(sp)
library(sf)

species <- letters[1:26]
range_list <- list()
for (i in seq_along(species)){
  temp0 <- cbind(runif(3,1,50),runif(3,1,50))
  temp <- Polygon(rbind(temp0,temp0[1,]))
  range_list[[i]] <- Polygons(list(temp), ID = c(species[i]))
}
input <- st_as_sf(SpatialPolygons(range_list))
categories <- c('LC','NT','VU','EN','CR')
input$binomial <- species
input$category <- sample(size = nrow(input),x = categories,replace = TRUE)

temp0 <- cbind(runif(3,1,50),runif(3,1,50))
target_area <- Polygon(rbind(temp0,temp0[1,]))
target_area <- Polygons(list(target_area), ID = 'Target area')
target_area <- st_as_sf(SpatialPolygons(list(target_area)))
get_kba_criteria(target_area,input)
```

get_wege	<i>get_wege</i>
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Description

A function to get the WEGE index value for a provided polygon.

Usage

```
get_wege(  
  target_area,  
  input,  
  x,  
  y,  
  species = "binomial",  
  category = "category",  
  res = 1  
)
```

Arguments

target_area	Either a sp or sf object to which to calculate the WEGE index.
input	Species ranges, either from a shapefile or from a georeferenced species list with a column for species, two columns for coordinates and one for the IUCN category.
x	name of the longitude column.
y	name of the latitude column.
species	name of the species column.
category	name of IUCN the category column. Terminology must be as follows: DD for Data Deficient, LC for Least Concern, NT for Near Threatened, EN, for Endangered, CR for Critically Endangered, EW for Extinct in the wild and EX for Extinct.
res	grid-cell size to use to calculate the range of the species in case a georeferenced species list was provided.

Value

a value corresponding to the WEGE index value of the provided target_area

Examples

```
library(sp)  
library(sf)  
library(WEGE)  
  
species <- letters[1:26]
```

```

range_list <- list()
for (i in seq_along(species)){
  temp <- Polygon(cbind(runif(4,1,50),runif(4,1,50)))
  range_list[[i]] <- Polygons(list(temp), ID = c(species[i]))}
input <- st_as_sf(SpatialPolygons(range_list))
categories <- c('LC','NT','VU','EN','CR')
input$binomial <- species
input$category <- sample(size = nrow(input),x = categories,replace = TRUE)

target_area <- Polygon(cbind(runif(4,1,50),runif(4,1,50)))
target_area <- Polygons(list(target_area), ID = 'Target area')
target_area <- st_as_sf(SpatialPolygons(list(target_area)))
get_wege(target_area,input,species = 'binomial',category = 'category')

```

spat_ras

spat_ras

Description

A function to get the WEGE index value for a provided polygon.

Usage

```

spat_ras(
  target_area,
  input,
  x,
  y,
  species = "binomial",
  category = "category",
  show_progress = FALSE,
  ed,
  res = 1
)

```

Arguments

target_area	Either a sp or sf object to which to calculate the WEGE index.
input	Species ranges, either from a shapefile or from a georeferenced species list with a column for species, two columns for coordinates and one for the IUCN category.
x	name of the longitude column.
y	name of the latitude column.
species	name of the species column.
category	name of IUCN the category column. Terminology must be as follows: DD for Data Deficient, LC for Least Concern, NT for Near Threatened, EN, for Endangered, CR for Critically Endangered, EW for Extinct in the wild and EX for Extinct.

show_progress	Progress of the analysis by showing the number of the grid where the function is calculating the different indices.
ed	name of the evolutionary distinctiveness column.
res	grid-cell size to use to calculate the range of the species in case a georeferenced species list was provided.

Value

A RasterStack with rasters for each KBA criteria (A1a,A1b,A1e,B1) and indices calculated (GE,ED,EDGE,WEGE)

Examples

```
library(WEGE)
library(sp)
library(sf)
library(raster)

species <- sample(letters, 10)
range_list <- list()
for (i in seq_along(species)) {
  temp0 <- cbind(runif(3,1,50),runif(3,1,50))
  temp <- Polygon(rbind(temp0,temp0[1,]))
  range_list[[i]] <- Polygons(list(temp), ID = c(species[i]))
}
input <- st_as_sf(SpatialPolygons(range_list))
categories <- c('LC','NT','VU','EN','CR')
input$binomial <- species
input$category <- sample(size = nrow(input),x = categories,replace = TRUE)

input$ed <- runif(runif(10,1,50))
temp0 <- cbind(runif(3,1,50),runif(3,1,50))
target_area <- Polygon(rbind(temp0,temp0[1,]))
target_area <- Polygons(list(target_area), ID = 'Target area')
target_area <- st_as_sf(SpatialPolygons(list(target_area)))
spat_ras(target_area,input,species = 'binomial',ed='ed', res = 1)
```

WEGE

WEGE: A new metric for ranking locations for biodiversity conservation

Description

WEGE is an R package that allows the user to calculate the WEGE index for a particular area. Additionally it also calculates rasters of KBA criteria (A1a, A1b, A1e, and B1) Weighted endemism, the EDGE score, Evolutionary Distinctiveness and Extinction risk.

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