

# Package ‘bRacatus’

May 28, 2021

**Title** A Method to Estimate the Accuracy and Biogeographical Status of Georeferenced Biological Data

**Version** 1.0.4

**Language** en-GB

**Description** Automated assessment of accuracy and geographical status of georeferenced biological data. The methods rely on reference regions, namely checklists and range maps. Includes functions to obtain data from the Global Biodiversity Information Facility <<https://www.gbif.org/>> and from the Global Inventory of Floras and Traits <<https://gift.uni-goettingen.de/home>>. Alternatively, the user can input their own data. Furthermore, provides easy visualisation of the data and the results through the plotting functions. Especially suited for large datasets. The reference for the methodology is: Arlé et al. (under review).

**Depends** R (>= 3.5.0)

**Imports** data.table, geojsonio, graphics, grDevices, jsonlite, maptools, methods, plotfunctions, raster, rgbif, rgeos, rworldmap, sp, stats

**License** GPL (>= 2)

**Encoding** UTF-8

**URL** <https://github.com/EduardoArle/bRacatus>

**BugReports** <https://github.com/EduardoArle/bRacatus/issues>

**LazyData** true

**RoxygenNote** 7.1.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-05-28 19:30:02 UTC

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|          |                 |
|----------|-----------------|
| accuracy | <i>accuracy</i> |
|----------|-----------------|

---

### Description

Estimates the Accuracy of Each Point Record.

### Usage

```
accuracy(signals)
```

### Arguments

|         |   |
|---------|---|
| signals | output of the function "signalCalculation". A data.frame including the original point data and the signals sent by the reference regions. |
|---------|---|

### Value

The data.frame with the species occurrence information and an extra column indicating the estimated accuracy of each point.

---

|                    |                           |
|--------------------|---------------------------|
| availableCountries | <i>availableCountries</i> |
|--------------------|---------------------------|

---

**Description**

List of countries and entities names for checklists

**Usage**

```
availableCountries()
```

**Value**

This function provides a list of countries and entities names available with rworldmaps for checklists

**Examples**

```
country_list <- availableCountries()
```

---

|              |                     |
|--------------|---------------------|
| biogeoStatus | <i>biogeoStatus</i> |
|--------------|---------------------|

---

**Description**

Estimates the biogeographic status of each point record.

**Usage**

```
biogeoStatus(signals)
```

**Arguments**

|         |  |
|---------|--|
| signals | output of the function signalCalculation. A dataFrame including the original point data and the signals sent by the reference regions. |
|---------|--|

**Value**

The dataFrame with the species occurrence information and an extra column indicating the estimated biogeographic status of each point.

---

|                  |                          |
|------------------|--------------------------|
| countryChecklist | <i>countryChecklists</i> |
|------------------|--------------------------|

---

**Description**

Prepares user provided reference regions on a country level

**Usage**

```
countryChecklist(countries, biogeo_status)
```

**Arguments**

`countries`        vector with one or more country names  
`biogeo_status`    vector informing the status of each country: alien, native or unknown

**Value**

This function provides shapefiles of countries with the correspondent biogeographic status of the species.

**Examples**

```
country_checklist <- countryChecklist(
  c("Brazil", "Argentina", "Uruguay", "Paraguay"),
  c("native", "alien", "unknown", "native"))
```

---

|        |               |
|--------|---------------|
| getOcc | <i>getOcc</i> |
|--------|---------------|

---

**Description**

Downloads GBIF records iterating when necessary to overcome the limitation of 200,000 records

**Usage**

```
getOcc(species)
```

**Arguments**

`species`        character, species binomial name

**Value**

This function downloads all records for a species from GBIF that have coordinates info. If necessary it loops several times to overcome the limit of 200,000 occurrences imposed by `occ_search` function. It returns a data table.

**Examples**

```
sps_occurrence <- get0cc("Hemitriccus mirandae")
```

---

|             |                    |
|-------------|--------------------|
| giftRegions | <i>giftRegions</i> |
|-------------|--------------------|

---

**Description**

Gets regions listed by GIFT for plant species

**Usage**

```
giftRegions(species, min_size = 1000, max_size = 1e+11)
```

**Arguments**

|          |  |
|----------|--|
| species  | character, species binomial name   |
| min_size | numeric, minimum size of checklists (in km2) to be included in the analysis. |
| max_size | numeric, maximum size of checklists (in km2) to be included in the analysis. |

**Value**

This function returns a list containing three shapefiles derived by information supplied by GIFT. "regs" includes all the features corresponding to regions where the species has been listed as present. "regs\_native" includes all the features corresponding to regions where the species has been listed as native. And "regs\_alien" includes all the features corresponding to regions where the species has been listed as alien.

**Examples**

```
gift_reference_regions <- giftRegions("Boreava aptera")
```

---

|         |                              |
|---------|------------------------------|
| give0cc | <i>Input occurrence data</i> |
|---------|------------------------------|

---

**Description**

Prepares user provided georeferenced biological data for the models

**Usage**

```
give0cc(
  occ_data,
  species = "species",
  longitude = "longitude",
  latitude = "latitude"
)
```

**Arguments**

|           |   |
|-----------|---|
| occ_data  | table containing latitude and longitude       |
| species   | col.name containing the species information   |
| longitude | col.name containing the longitude information |
| latitude  | col.name containing the latitude information  |

**Value**

This function standardises the user provided georeferenced biological data to be fed into the models.

**Examples**

```
# Create a data.frame containing species names and coordinates

test_data <- data.frame(sps=rep("Equus acephalus",10),
  lon=c(-43.2, -58.4, -56, -44, -54.5, -57.4, -60.1, -68.5, -71.3, -47.5),
  lat=c(-22.9, -34.6, -34.8, -20, -25.5, -25.2, -3, -32.5, -41.1, -15.5),
  gender=rep("female",10), head_size=rep("headless individual"))

sps_occurrence <- giveOcc(test_data, "sps", "lon", "lat")
```

---

giveRegions

*giveRegions*

---

**Description**

Input checklist regions

**Usage**

```
giveRegions(regs, regs_native, regs_alien)
```

**Arguments**

|             |   |
|-------------|---|
| regs        | shapefile containing all regions of occurrence.           |
| regs_native | shapefile containing regions where the species is native. |
| regs_alien  | shapefile containing regions where the species is alien.  |

**Value**

This function returns a list containing three shapefiles derived by information supplied by GIFT. "regs" includes all the features corresponding to regions where the species has been listed as present. "regs\_native" includes all the features corresponding to regions where the species has been listed as native. And "regs\_alien" includes all the features corresponding to regions where the species has been listed as alien.

**Examples**

```
library(rworldmap)
world <- getMap()
regs <- world[c("Brazil", "Argentina", "Uruguay", "Paraguay"),]
regs_native <- world[c("Brazil", "Paraguay"),]
regs_alien <- world[c("Argentina"),]
regs_list <- giveRegions(regs, regs_native, regs_alien)
```

---

H\_mirandae\_sp

*Hemitriccus mirandae spatialPoints exemplary file*

---

**Description**

A SpatialPointsDataFrame containing the occurrences of *Hemitriccus mirandae* downloaded from GBIF

**Examples**

```
data("H_mirandae_sp")
```

---

ID\_raster

*Cell ID raster*

---

**Description**

A Raster half-degree raster of the world with unique IDs per cell

**Examples**

```
data("ID_raster")
```

---

Model\_accuracy

*Accuracy model*

---

**Description**

A glm accuracy model

**Examples**

```
data("Model_accuracy")
```

---

|              |                              |
|--------------|------------------------------|
| Model_biogeo | <i>Biogeographical model</i> |
|--------------|------------------------------|

---

**Description**

A glm biogeographical model

**Examples**

```
data("Model_biogeo")
```

---

|                  |                         |
|------------------|-------------------------|
| occSpatialPoints | <i>occSpatialPoints</i> |
|------------------|-------------------------|

---

**Description**

Downloads gbif records iterating when necessary to overcome the limitation of 200,000 records

**Usage**

```
occSpatialPoints(occ)
```

**Arguments**

|     |       |
|-----|-------|
| occ | table |
|-----|-------|

**Value**

This function creates spatialPoints from tables containing coordinates.

**Examples**

```
# Create a data.frame containing species names and coordinates  
sps_occurrence <- getOcc("Hemitriccus mirandae")  
sps_sp <- occSpatialPoints(sps_occurrence)
```

---

|              |                     |
|--------------|---------------------|
| plotAccuracy | <i>plotAccuracy</i> |
|--------------|---------------------|

---

### Description

Plot the species occurrences showing the estimated accuracy of points.

### Usage

```
plotAccuracy(  
  acc,  
  regional = TRUE,  
  reg.by = "country",  
  borders = TRUE,  
  col.features = "khaki",  
  col.bg = "azure2",  
  plot.range = FALSE,  
  range = NULL,  
  box = FALSE  
)
```

### Arguments

|              |  |
|--------------|--|
| acc          | dataTable of the species occurrence including a column with the estimated accuracy of points.  |
| regional     | logical, whether the whole world should be plotted as the background or only the region adjacent to the species countries of occurrence. |
| reg.by       | character, by countries where there are points or by area where the points are located.  |
| borders      | logical, whether country limits should be plotted.   |
| col.features | colour for plotting features.  |
| col.bg       | colour for plotting the background.  |
| plot.range   | logical, if TRUE, range maps should be provided as a shapefile in argument range.  |
| range        | shapefile, species range map.  |
| box          | logical, includes frame with coordinates locations.  |

### Value

This function plots the species occurrence with estimated accuracy of all points.

---

`plotBiogeoStatus`      *plotBiogeoStatus*

---

### Description

Plot the species occurrences showing the estimated biogeographical status of points.

### Usage

```
plotBiogeoStatus(  
  biogeo,  
  regional = TRUE,  
  reg.by = "country",  
  borders = TRUE,  
  col.features = "khaki",  
  col.bg = "azure2",  
  plot.range = FALSE,  
  range = NULL,  
  box = FALSE  
)
```

### Arguments

|                           |  |
|---------------------------|--|
| <code>biogeo</code>       | dataTable of the species occurrence including a column with the estimated biogeographical status of points.                              |
| <code>regional</code>     | logical, whether the whole world should be plotted as the background or only the region adjacent to the species countries of occurrence. |
| <code>reg.by</code>       | character, by countries where there are points or by area where the points are located.  |
| <code>borders</code>      | logical, whether country limits should be plotted.   |
| <code>col.features</code> | colour for plotting features.  |
| <code>col.bg</code>       | colour for plotting the background.  |
| <code>plot.range</code>   | logical, if TRUE, range maps should be provided as a shapefile in argument <code>range</code> .  |
| <code>range</code>        | shapefile, species range map.  |
| <code>box</code>          | logical, includes frame with coordinates locations.  |

### Value

This function plots the species occurrence with estimated biogeographical status of all points.

---

|         |                |
|---------|----------------|
| plotOcc | <i>plotOcc</i> |
|---------|----------------|

---

## Description

Plot the species occurrences with map background for visualisation

## Usage

```
plotOcc(occ, regional = TRUE)
```

## Arguments

|          |  |
|----------|--|
| occ      | dataTable of the species occurrence.   |
| regional | logical, whether the whole world should be plotted as the background or only the region adjacent to the species countries of occurrence. |

## Value

This function plots the species occurrence

## Examples

```
occ <- getOcc("Hemitriccus mirandae")

plotOcc(occ)

test_data <- data.frame(sps=rep("Equus acephalus",10),
  lon=c(-43.2, -58.4, -56, -44, -54.5, -57.4, -60.1, -68.5, -71.3, -47.5),
  lat=c(-22.9, -34.6, -34.8, -20, -25.5, -25.2, -3, -32.5, -41.1, -15.5),
  gender=rep("female",10), head_size=rep("headless individual"))

occ <- giveOcc(test_data, "sps", "lon", "lat")

plotOcc(occ)
# Plot occurrences with the whole world as background

plotOcc(occ, regional=FALSE)
```

---

plotRefReg

*plotRefReg*

---

### Description

Plot the species reference regions with map background for visualisation

### Usage

```
plotRefReg(ref_reg)
```

### Arguments

|         |  |
|---------|--|
| ref_reg | list containing three shapefiles derived by information supplied by GIFT. "regs" includes all the features corresponding to regions where the species has been listed as present. "regs_native" includes all the features corresponding to regions where the species has been listed as native. And "regs_alien" includes all the features corresponding to regions where the species has been listed as alien.. |
|---------|--|

### Value

This function plots three maps of the species occurrence, showing the regions where it is present, native and alien.

---

rangeMaps

*rangeMaps*

---

### Description

Prepares range maps input by the user to be used as reference regions

### Usage

```
rangeMaps(
  range,
  biogeo = "legend",
  native = "Extant (resident)",
  alien = "Introduced"
)
```

### Arguments

|        |  |
|--------|--|
| range  | SpatialPolygonsDataFrame   |
| biogeo | character, name of the column containing information on biogeographic status of features |
| native | character, entries in biogeo column representing the native range of the species         |
| alien  | character, entries in biogeo column representing the alien range of the species          |

**Value**

This function returns a list containing three shapefiles derived from information supplied by the species range map in a shapefile format. "regs" includes all the features corresponding to regions where the species has been listed as present. "regs\_native" includes all the features corresponding to regions where the species has been listed as native. And "regs\_alien" includes all the features corresponding to regions where the species has been listed as alien.

**Examples**

```
range_map_reference_regions <- rangeMaps(Range_Phalanger_orientalis)
```

---

```
Range_Phalanger_orientalis
  Range Phalanger orientalis
```

---

**Description**

A SpatialPolygonsDataFrame Range Phalanger orientalis

**Examples**

```
data("Range_Phalanger_orientalis")
```

---

```
signalCalculation    signalCalculation
```

---

**Description**

Calculates signals sent from reference regions to point records.

**Usage**

```
signalCalculation(ref_reg, pts, biogeo = TRUE)
```

**Arguments**

|         |   |
|---------|---|
| ref_reg | a list of shapefiles containing checklist regions as "presence", "native", and "alien" categories. These can be original checklists, or checklists derived from range maps.   |
| pts     | data.frame containing the point records and their coordinates.  |
| biogeo  | logical, whether the biogeographical status indices should be calculated or not. Default is true, however at least the native reference regions must be included in the data. |

**Value**

The data.frame of species occurrences with extra columns containing the location ID and presence signals for each point. If biogeo=TRUE, the data.frame also includes the nativeness and alienness indices.

---

|         |                          |
|---------|--------------------------|
| signals | <i>signals example 1</i> |
|---------|--------------------------|

---

**Description**

A SpatialPolygonsDataFrame signals example 1

**Examples**

```
data("signals")
```

---

|           |                          |
|-----------|--------------------------|
| signals_2 | <i>signals example 2</i> |
|-----------|--------------------------|

---

**Description**

A SpatialPolygonsDataFrame signals example 2

**Examples**

```
data("signals_2")
```

---

|           |                          |
|-----------|--------------------------|
| signals_3 | <i>signals example 3</i> |
|-----------|--------------------------|

---

**Description**

A SpatialPolygonsDataFrame signals example 3

**Examples**

```
data("signals_3")
```

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