

# Package ‘bRacatus’

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

**Version** 2.0.0

**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, methods, plotfunctions, raster, rgbif, rnaturalearth, sf, sp, stats

**License** GPL (>= 2)

**Encoding** UTF-8

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

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

**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.
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**Value**

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

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availableCountries	<i>availableCountries</i>
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**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>
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---

**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.

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countryChecklist	<i>countryChecklists</i>
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**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>
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---

**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 <- getOcc("Babiana tubulosa")
```

---

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("Babiana tubulosa")
```

---

giveOcc	<i>Input occurrence data</i>
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---

**Description**

Prepares user provided georeferenced biological data for the models

**Usage**

```
giveOcc(
  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(rnaturalearth)
world <- ne_countries(returnclass = "sf")
reg_names <- c("Brazil", "Argentina", "Uruguay", "Paraguay")
reg_native <- c("Brazil", "Paraguay")
reg_alien <- c("Argentina")
regs <- world[which(world$name_sort %in% reg_names),]
regs_native <- world[which(world$name_sort %in% reg_native),]
regs_alien <- world[which(world$name_sort %in% reg_alien),]
regs_list <- giveRegions(regs, regs_native, regs_alien)

```

---

glonafRegions

*glonafRegions*


---

**Description**

Gets regions listed by GloNAF for plant species

**Usage**

```
glonafRegions(species, native = "gift", nat_ref_reg = NULL)
```

**Arguments**

species	character, species binomial name
native	character, source for the native reference regions. Options are "gift", "range map", or "checklist". If "gift" is chosen, the function will automatically download native regions listed by GIFT for the species. If "range map" or "checklist" is chosen, the user must provide a shapefile with either the species range map, or the features representing regions where it has been listed as native. Default is "gift".
nat_ref_reg	shapefile containing either the species native range map or checklist. The user must inform which reference region data type is being provided in the parameter "native".

**Value**

This function returns a list containing three shapefiles derived by information supplied by GloNAF for the alien reference regions, and the chosen source for the native reference regions. "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**

```
glonaf_reference_regions <- glonafRegions("Ambrosia grayi")
```

---

H_mirandae_sp	<i>Hemitriccus mirandae spatialPoints exemplary file</i>
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---

**Description**

A SpatialPointsDataFrame containing the occurrences of Hemitriccus mirandae downloaded from GBIF

**Examples**

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

---

ID_raster	<i>Cell ID raster</i>
-----------	-----------------------

---

**Description**

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

**Examples**

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

---

Model_accuracy	<i>Accuracy model</i>
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---

**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

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")

sps_sp <- occSpatialPoints(sps_occurrence)
```

---

 plotAccuracy

*plotAccuracy*


---

### 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

biogeo	dataTable of the species occurrence including a column with the estimated biogeographical status 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 biogeographical status of all points.

---

`plotOcc`*plotOcc*

---

**Description**

Plot the species occurrences with map background for visualisation

**Usage**

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

**Arguments**

<code>occ</code>	dataTable of the species occurrence.
<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.

**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.

---

`pts`*pts example 1*

---

**Description**

A DataFrame pts example 1

**Examples**

```
data("pts")
```

---

 pts2
 

---

*pts example 2*


---

**Description**

A DataFrame pts example 2

**Examples**

```
data("pts2")
```

---

 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`*signals example 1*

---

**Description**

A SpatialPolygonsDataFrame signals example 1

**Examples**

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

---

`signals_2`*signals example 2*

---

**Description**

A SpatialPolygonsDataFrame signals example 2

**Examples**

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

---

`signals_3`*signals example 3*

---

**Description**

A SpatialPolygonsDataFrame signals example 3

**Examples**

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



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