

# Code description

## Contents

About . . . . .	1
Packages instalation . . . . .	1
Occurrence data . . . . .	1

## About

This document describes the R code used in Wallace.

## Packages instalation

Before start, install the following packages:

```
install.packages(devtools)
install.packages(rgbif)
install.packages(maptools)
install.packages(spThin)
install.packages(ENMeval)
install.packages(dismo)
install.packages(rgeos)
install.packages(repmis)
```

Now load them:

```
library(devtools)
library(rgbif)
library(maptools)
library(spThin)
library(ENMeval)
library(dismo)
library(rgeos)
library(repmis)
```

Load the functions necessary to run the analysis:

```
source('functions.R')
```

## Occurrence data

The analysis will be done for the following species:

```
gbifName <- 'tremarctos ornatus'
```

The search of occurrences will be limited to:

```
occurrences <- 20
```

Apply the function to obtain the gbif records for the selected species:

```
results <- occ_search(scientificName = gbifName, limit = occurrences, hasCoordinate = TRUE)
```

Rename the results:

```
gbifOrig <- results
```

Occurrence table changes:

```
cols <- c("name", "decimalLongitude", "decimalLatitude", "country", "stateProvince", "locality", "elevation")
locs.in <- results$data[!is.na(results$data[, 3]), ][, cols]
locs <- remDups(locs.in)
names(locs)[2:3] <- c("lon", "lat")
locs$origID <- row.names(locs)
```

Create the null object:

```
gbifoccs <- NULL
```

Adjusting table values:

```
gbifoccs <- rbind(gbifoccs, locs)
gbifoccs <- remDups(gbifoccs)
df <- gbifoccs
```

Selected points with the polygon:

```
ptseln <- c(1, 3, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18)
```

Subset with selected points:

```
ptsSel <- gbifoccs[ptseln, ]
df <- ptsSel
```