

An introduction to SpeciesAtlas

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1 - Introduction

Species Distributions Models (SDMs) are widely used to model species habitat using occurrences and environmental data. Recently, SMDs have been used to investigate the effect of climate change on species distribution. When used in this context, being able to quantify uncertainties becomes an important matter. To address this issue we propose a framework allowing to work easily with 5 different statistical models, as well as different climatic models, scenarios and species' dispersion capabilities. Changes in species' habitats are useful information for reserve managers but are, unfortunately, difficult to obtain without the required skills. This package aims to ease the access to such informations.

In this vignette we will showcase the use of the **speciesatlasR** package which allows to create synthetic sheet assessing species vulnerability to climate change. It also generates community level maps of climate refuge areas for biodiversity. SMDs are modelled using the **Biomod2** package in an ensemble modelling framework. The package takes advantage of multithreading to enhance performances.

Here we show an example of the use of **speciesatlas**, illustrating how to format the data prior to the analyses, how to view the outputs and how to get the resulting figures.

2 - Data-set

The data for lemurs presences have been extracted from Brown & Yoder (2015), we will use a subset of 355 observations points belonging to 4 differents species. Data points come from a wide range of sources and can be viewed in the original article. Points are kept in the World Geodetic System (epsg:4326)

Present climatic data come from WorldClim Fick & Hijmans (2017), predictions from ('CCAFS climate'). To simplify the process we will only use 4 differents variables :

- Annual mean temperature (MAT)
- Annual mean precipitation (MAP)
- Annual Temperature saisonality (TSeas)
- Annual Precipitation saisonality (TPres)

In order to reduce computing time for future data we will use only use :

- three climatic models : CCSM4 (CC), GISS-E2-R (GS) and HadGEM2-ES (HE) ;
- one scenarios : rcp 8.5 ;
- one time period : 2085

All the data have been downloaded at a 30' spatial resolution and projected in the desired projection system and resolution (here epsg:32738, 1-km²).



Figure 1: Babakoto (Indri indri), ref: Frank Vassen

2.1 - Formating climatic data

We first load the `raster` package in order to prepare the climatic data.

```
# Load libraries
library(raster)
library(speciesatlas)

path.data <- system.file("extdata", package = "speciesatlas")
```

The climatic data are available within the `speciesatlas` R package. For present data, it can be loaded as follow :

```
# Loading data from WorldClim
present <- brick(paste0(path.data, "/current.tif"))
# Renaming variables of interest
names(present) <- c(paste0("current", 1:36), "temp", paste0("current",
  38:39), "tseas", paste0("current", 41:47), "prec", "bioclim1",
  "bioclim2", "pseas", paste0("current", 52:67), "pet", "cwd",
  "ndm")
# Transform from RasterBrick to Rastertack
present <- stack(present)
```

Then we load the future climatic data :

```
# First we provide information about the model, scenarios et
# years we want to use
fut.var <- list(c("cc", "he", "gs"), c("85"), c("2085"))
# Empty vector to stock raster list
future <- vector("list")
i.mod <- 1

# And then we load each file Looping first through differents
# scenarios Then through the years
for (j in 1:length(fut.var[[2]])) {
  for (l in 1:length(fut.var[[3]])) {
    future[[i.mod]] <- vector("list")
    for (mc in 1:length(fut.var[[1]])) {
      # And finally for each years and scenarios, we load the 3
      # climatic predictions
      future[[i.mod]][[mc]] <- stack(paste0(path.data,
        "/", fut.var[[1]][mc], "_", fut.var[[2]][j],
        "_", fut.var[[3]][l], ".tif"))
      names(future[[i.mod]][[mc]]) <- c(paste0("current",
        1:36), "temp", paste0("current", 38:39), "tseas",
        paste0("current", 41:47), "prec", "bioclim1",
        "bioclim2", "pseas", paste0("current", 52:67),
        "pet", "cwd", "ndm")
      future[[i.mod]][[mc]] <- stack(future[[i.mod]][[mc]])
    }
    i.mod <- i.mod + 1
  }
}
```

There is no need to normalize the data as the package takes care of it.

2.2 - Formating presences points

Secondly, we need to load the presence points. `speciesatlas` works by aggregating each species results at a community level, corresponding to a given taxonomic group. Here we only work with lemurs, but more taxonomic group may be added on a same run. Although, be aware that doing so means the same climatic variables will be used for the differents taxonomic groups.

Presence data are stored in a list with the following structure :

```
[[1]]
[[1]]$`species`
[1] Eulemur fulvus      Allocebus trichotis Avahi laniger      Hapalemur griseus
Levels: Allocebus trichotis Avahi laniger Eulemur fulvus Hapalemur griseus

[[1]]$Lat
[1] -19.70000 -14.32861 -21.18300 -18.74623

[[1]]$Long
[1] 47.80000 48.58611 48.33400 48.75815

[[1]]$Taxo.group
[1] "lemurs"

[[2]]
[[2]]$`species`
[1] Adansonia digitata      Adansonia madagascariensis Adansonia grandidieri
[4] Adansonia rubrostipa
4 Levels: Adansonia digitata Adansonia grandidieri ... Adansonia rubrostipa

[[2]]$Lat
[1] -16.03030 -12.95461 -20.87564 -14.74680

[[2]]$Long
[1] 45.57406 49.12567 44.10619 47.37811

[[2]]$Taxo.group
[1] "baobabs"
```

Figure 2: Structure used for the presences points

The following code may help you build such a list. Here, each taxonomic group must be in a single text file, named after the group, with three columns (scientificname, decimalLat, decimalLong), separated with a semicolon.

```
# First we select the taxonomic groups we want to modele
taxon.names <- c("lemurs")
# We then create an empty list
df.orig <- vector("list", length = length(taxon.names))

# And we loop through the different file to gather the
# informations
for (sp in 1:length(taxon.names)) {
  taxon <- read.csv(file = paste0(path.data, "/", taxon.names[sp],
    ".txt"), header = TRUE, sep = ";")
  df.orig[[sp]]$Species <- taxon$scientificname
  df.orig[[sp]]$Lat <- taxon$decimalLat
  df.orig[[sp]]$Long <- taxon$decimalLong
  df.orig[[sp]]$Taxo.group <- taxon.names[sp]
}
```

3 - Filling in the rest of the informations & starting the package

`speciesatlas` allows for different parts of its algorithm to be run or not. This allows to rerun some parts without starting from scratch again. Please note that each part should be run at least once before being disabled.

```
# True by default
run.models <- T
run.plots <- T
run.taxo <- T
run.map <- T
```

Then we need to select which variables will be used for the modelisation :

```
model.var <- c("temp", "tseas", "prec", "pseas", "cwg", "foret")
```

By default, `speciesatlas` uses the maximum number of cores available minus one. You may overwrite this behaviour by setting `n.cores` to any values lesser than `parallel::detectCores()-1`:

```
# Here we only use two cores
n.core <- 2
```

Finally, we need to set the book title, authors and choose the output type between “pdf”, “html” or “both” :

```
out.type <- "both"
title.book <- "A Good Title"
author.book <- "John Doe & John Smith"
```

Once everything is set, it's time to start the package. This may take a while :

```
fun.main(df.orig, run.models, run.plots, run.taxo, run.map, model.var,
  environ, future, fut.var, maxent.path, n.core, out.type,
  title.book, author.book)
```

4 - Results

5 - Atlas Outputs

- References

Brown, J.L. & Yoder, A.D. (2015) Shifting ranges and conservation challenges for lemurs in the face of climate change. *Ecology and Evolution*, **5**, 1131–1142.

CCAFS climate. <http://www.ccafs-climate.org/>.

Fick, S.E. & Hijmans, R.J. (2017) WorldClim 2: New 1-km spatial resolution climate surfaces for global land areas. *International Journal of Climatology*, **37**, 4302–4315.