Species distribution modeling with three-step pseudo–absences

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November 14, 2014

Chapter 1

Introduction

This document provides an introduction to species distribution modeling (SDM) with three–step pseudo–absences.

Species distribution models (SDM) are statistical tools to predict the distribution of species in geographic space based on the relation of known species distribution to the environment. SDMs can be classified into *profile techniques* that only use distribution of presence data and *group discrimination techniques* that also require information of the environmental range where the species do not occur, that is, absence data. Due to the great effort involved in true absences sampling, most of the available datasets for predictive modeling are lacking in absence data (Zaniewski et al. (2002); Lobo et al. (2010)), thereby some authors apply profile techniques such as ecological niche factor analysis (ENFA; i.e. Cianfrani et al. (2010); McKinney et al. (2012)), Mahalanobis distance (MADIFA: i.e. Kuo (2010); Martin et al. (2012)) and environmental envelopes (BIOCLIM and DOMAIN: i.e. Giovanelli et al. (2010); Monk et al. (2010)). However, given that group discrimination techniques generally perform better (Elith and et al (2006); Engler et al. (2004); Chefaoui and Lobo (2008)), the most common methodological approach is to use group discrimination techniques relative to the available environment or background samples, also known as pseudo–absences, thus obtaining a representation of the environmental range in the region of study.

One of the most simple methods of generating pseudo–absences is to perform a random selection of the entire study area (Jiang et al. (2014); Carone et al. (2014); Sequeira et al. (2014)). However, it rises the risk of introducing false absences into the model from locations that are suitable for the species. Faced with this problem, several authors employ a presence–only algorithm as a preliminary step to move pseudo–absences away in the environmental space (Zaniewski et al. (2002); Engler et al. (2004); Barbet-Massin et al. (2012); Liu et al. (2013)).

The way of generating pseudo–absences strongly influences the results obtained (Lobo et al. (2010); Wisz and Guisan (2009); Barbet-Massin et al. (2012); Hirzel et al. (2001)), as well as the extent from which background is sampled, a constraint distribution of pseudo–absences around presence locations can lead to misleading models while the opposite, can inflate artificially test statistics and predictions, as well as potentially less informative response variables (VanDerWal and Shoo (2009)).

This document shows an example of a full Species distribution modeling process carried out with the `mopa` package in R. Pseudo–absences are generated in three-steps combining profiling techniques and background extent limitations.

If you want to know more about SDM in R, you could consult, for example, documentation from package `dismo` made by Robert J. Hijmans and Jane Elith.

Chapter 2

Getting started

2.1 Install mopa

The `mopa` is available from github repository.

```
> devtools::install_git("https://github.com/miturbide/mopa")
> library(mopa)
```

2.2 Species occurrence data

Regarding presence data, Hernandez et al. (2006) suggested that research in environmental niche modeling should focus in broad distribution subunits that are based on distinct genetic linages, in this connection Gonzalez et al. (2011) demostrated that omission error is reduced when biologically meaningful data is modeled. Thus, functions in the `mopa` package are prepared to run with more than one group of presences at the same time (could be a list of either distribution subunits of a single species or distribution of multiple species), anyway, functions also perform with a single group or species (data frame). In this example we use a data set (list) of two phylogenetic groups (H11 and H5) of *Quercus* sp in Europe. This is, R–object `Oak_phylo2`, available with the `mopa` package.

```
> data(eu)
> data(Oak_phylo2)
> plot(eu, col="grey")
> for (i in 1:length(Oak_phylo2)){
+   points(Oak_phylo2[[i]], pch="*", cex=0.5,
+         col = colors()[i*50])
+ }
```
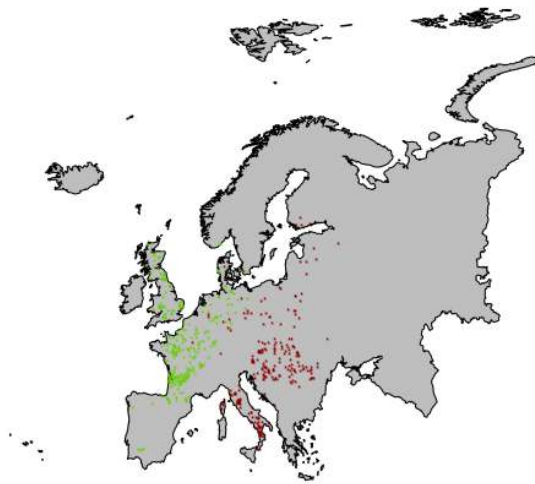
2.3 Environmental variables

Predictor variables are typically organized as raster (grid) type files. The set of predictor variables (rasters) can be used to make a 'RasterStack', which is a collection of 'RasterLayer' objects (see Raster-class in the raster package for more info).

```
> # RatserStack of envirinmental variables
> data(biostack)
> plot(biostack)
```
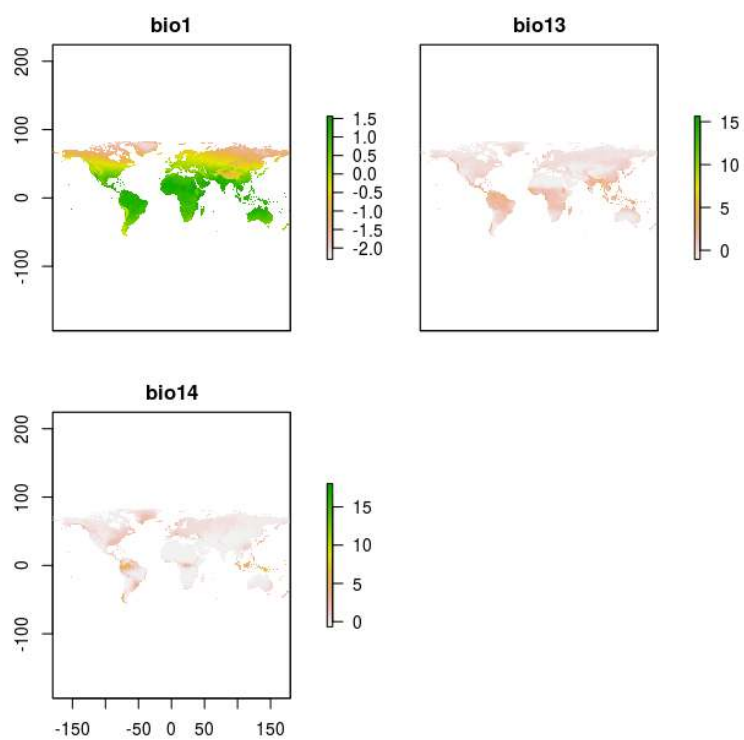
Chapter 3

Study area and background

3.1 Creation of the background grid

The regular point grid which covers the continental area can be created as follows:

```
> library(raster)
> ac<-xyFromCell(biostack[[1]], 1:ncell(biostack[[1]]))
> ex<-extract(biostack[[1]], ac)
> sp_grid<-SpatialPoints(ac[-which(is.na(ex)),])
> projection(sp_grid)<-CRS("+proj=longlat +init=epsg:4326")
```

Anyway, R–object `sp_grid` is available in `mopa`, covering the World at 10 km resolution.

3.2 Limit study area to the bounding boxes around presences

Function `boundingCoords` creates the matrix of bounding coordinates around point records (xy records). In this case, since `Oak_phylo2` object is a list of two groups of points, a list of two matrixes will be created.

```
> oak.extension<-boundingCoords(Oak_phylo2)
```

Function `delimit` creates polygon shapes from bounding coordinates and limits `SpatialPoints` data (`sp_grid`) to the defined boundaries, in other words, does the intersection of the background point grid with the bounding boxes. A list with two objects is obtained, (1)bbs: polygon shape of the bounding boxes and (2)bbs.grid: list of data frames of the background point grid limited by the bounding coordinates.

```
> box.grid<-delimit(oak.extension, sp_grid, names(Oak_phylo2))
> plot(box.grid[[1]])
> for (i in 1:length(Oak_phylo2)){
+   points(Oak_phylo2[[i]], col=colors()[i*50])
+ }
```
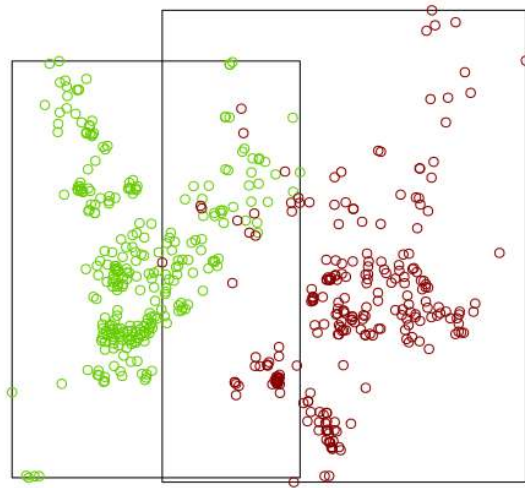
Chapter 4

Three–step pseudo–absences generation

4.1 STEP1: environmental profiling

The first step is the selection of the environmental unsuitable areas with a presence only algorithm (function `OCSVMprofiling`). We run One-class support vector machines (OCSVM) (Scholkopf and Smola (2001)) for each oak group.

```
> unsuitable.bg <-OCSVMprofiling(xy = Oak_phylo2,
+                     varstack = biostack,
+                     bbs.grid = box.grid$bbs.grid)
> plot(unsuitable.bg$absence$H11, pch="*")
> points(unsuitable.bg$presence$H11, pch="*", col= "pink2")
```
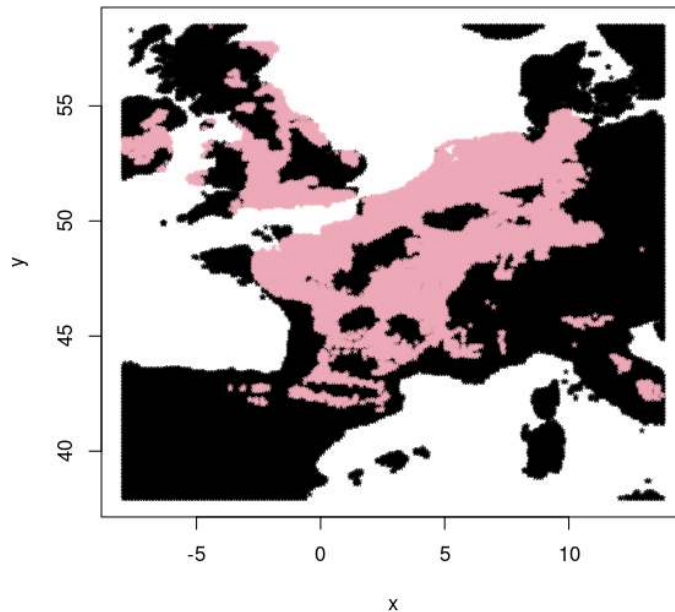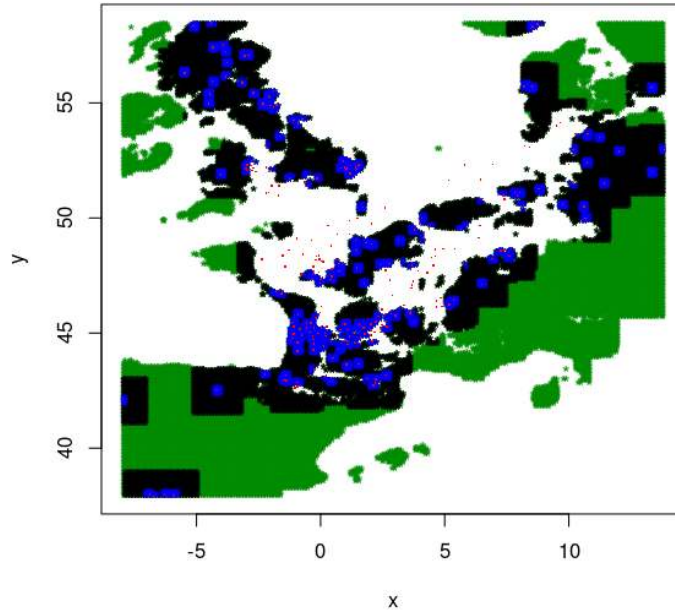
4.2 STEP2: background extents

The second step is the limitation of the background by the definition of a threshold distance. To do so, here we apply a criteria based in the performance of the SDM considering different extents in each study area. Thus, before modeling, backgrounds of different extent must be created with function `bgRadio`. In the example below, extents are created for a sequence of 100 km between distances, from 20 km to the length of the half diagonal of the bounding box.

```
> ext <-bgRadio(xy = Oak_phylo2, bounding.coords = oak.extension,
+        bg.absence = unsuitable.bg$absence, start = 0.166,
+   by = 0.83, unit = "decimal degrees")

[1] "creating background point-grids for species 1 out of 2"
[1] "creating background point-grids for species 2 out of 2"

> plot(ext$H11$km520, col="green4", pch="*")
> points(ext$H11$km120, pch="*")
> points(ext$H11$km20, pch="*", col="blue")
> points(Oak_phylo2$H11, col="red", pch= ".", cex=1.5)
```

Listed matrixes with xy coordinates are obtained, each matrix correspond to a different background extent.

4.3 STEP3: pseudo–absences sampling

In the third step, with function `PseudoAbsences`, you can create pseudo–absences either at random or with k–means clustering, by modifying argument `kmeans`. You can also set the prevalence (proportion of presences against pseudo–absences) and the exclusion buffer (minimum distance to be kept to presences without pseudo–absences).
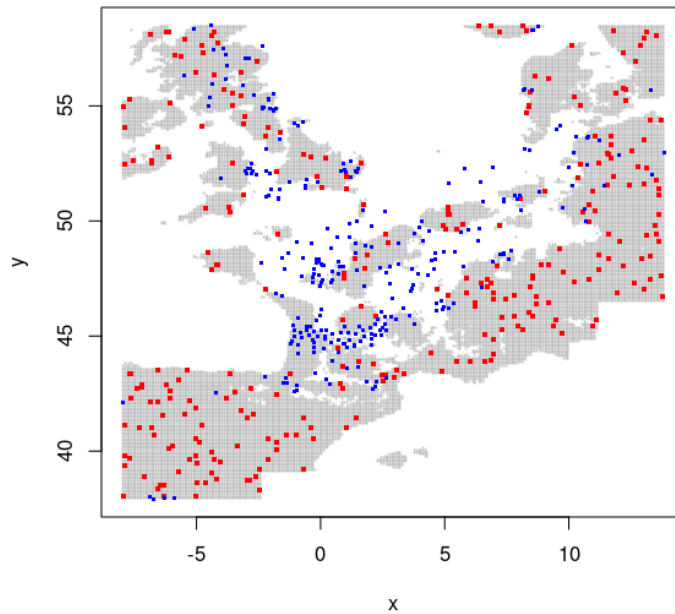
4.3.1 At random

In the example below, pseudo–absences are generated at random, in equal number to presences and keeping a 10 km distance to presences.

```
> pa_random <-PseudoAbsences(xy = Oak_phylo2, bg.grids = ext,
+       exclusion.buffer = 0.083, prevalence = 0.5,
+   kmeans = FALSE)

[1] "generating pseudo-absences for species 1 out of 2"
[1] "generating pseudo-absences for species 2 out of 2"

> plot(ext$H11[[5]], pch="*", col= "grey", cex=.5)
> points(pa_random$H11[[5]], col="red", pch=".", cex=4)
> points(Oak_phylo2$H11, col="blue", pch=".", cex=3)
```

4.3.2 With k–means clustering

In the example below, pseudo–absences are generated with k–means clustering, in equal number to presences and keeping a 10 km distance to presence.

```
> pa_kmeans <-PseudoAbsences(xy = Oak_phylo2, bg.grids = ext,
+         exclusion.buffer = 0.083, prevalence = 0.5,
+   kmeans = TRUE)

[1] "generating pseudo-absences for species 1 out of 2"
[1] "generating pseudo-absences for species 2 out of 2"

> plot(ext$H11[[5]], pch="*", col= "grey", cex=.5)
> points(pa_kmeans$H11[[5]], col="red", pch=".", cex=4)
> points(Oak_phylo2$H11, col="blue", pch=".", cex=3)
```
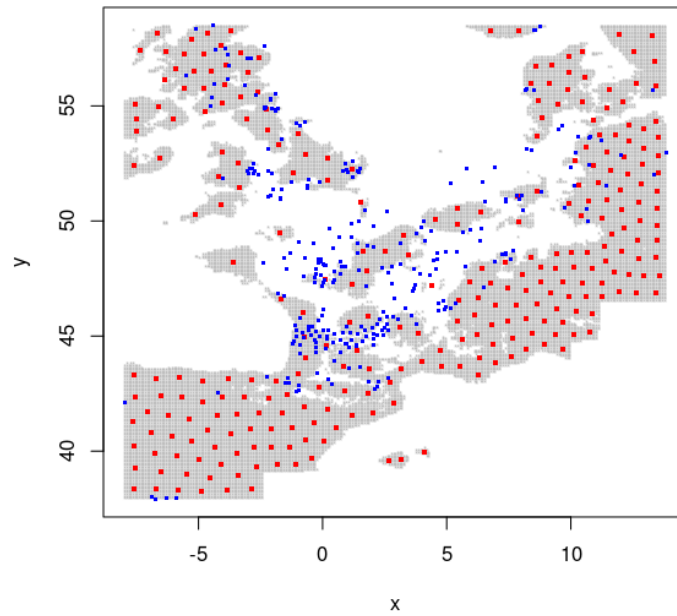
4.4   Put presences and pseudo–absences together

Function `bindPresAbs` binds presence and absence data for each background extension.

```
> presaus <-bindPresAbs(presences = Oak_phylo2,
+                       absences = pa_random)
```

Chapter 5

Species distribution modeling

The `allModeling` function does the species distribution modelling and k-fold cross validation for a set of presence/absence data per species corresponding to a different background extent. Algorithms supported are "glm", "svm", "maxent", "mars", "randomForest", "cart.rpart" and "cart.tree".

In the example below, we do a 10–fold cross validation of the "mars" modelling algorithm.

```
> modirs <-allModeling(data = presaus, varstack = biostack,
+              k = 10, algorithm = "mars", destdir = getwd(),
+              projection = CRS("+proj=longlat +init=epsg:4326"))
```

Named Rdata objects are stored in the specified path. Each Object is given a name indicating the algorithm, background extent, and species in this order (if a single species is provided no name is given for de species). Character object with listed files is returned. Each Rdata consists of a list with six components:

(1)allmod: fitted model with all data for training, (2)auc: AUC statistic in the cross validation, (3)kappa: kappa statistic in the cross validation, (4)tss: true skill statistic in the cross validation, (5)mod: fitted model with partitioned data, (6)p: cross model prediction.

To select the model corresponding to the geographical extent beyond which the AUC scored by the model does not increase we need to load the generated data and extract auc values with function `loadTestValues`.

```
> auc_mars <-loadTestValues(data = presaus, test = "auc",
+                         algorithm = "mars")

[1] "loading values for species 1"
[1] "loading values for species 2"

> library(lattice)
> levelplot(auc_mars ,aspect=5 ,at =seq(0.5,1,0.01),
+          col.regions=bpy.colors, xlab="Haplogroups",
+          ylab="Background extent (km)", main = "AUC")
```
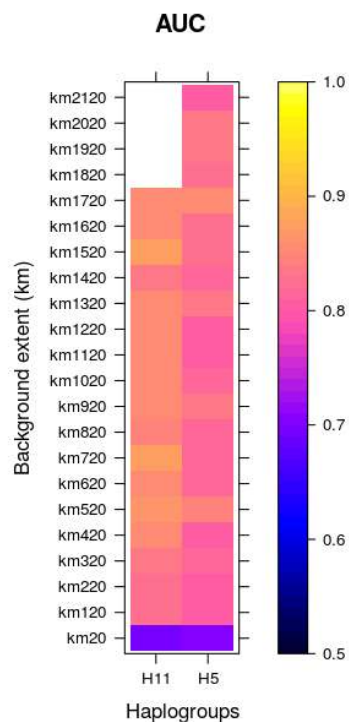
To extract the extent at which maximum AUC value is scored, we use function `indextent`.

```
> ind<-indextent(auc_mars)
> ind

 km820 km1820
     9     19
```

Thus, the `ind` object in this example gives the index of the background extent to be considered for each group/species and is going to be used to extract definitive model components and data with function `loadDefinitiveModel` as follows.

```
> def <-loadDefinitiveModel(presaus, ind, "allmod", "mars")
> #example of prediction
> projectionland <-biomat(cbind(box.grid[[2]][[1]],
+                   rep(1,nrow(box.grid[[2]][[1]]))),
+                   biostack)
> p <-predict(def[[1]], projectionland[,-1])->p
> spp<-SpatialPixelsDataFrame(box.grid[[2]][[1]],
+                        as.data.frame(p))
> ras<-raster(spp)
> plot(ras)
```
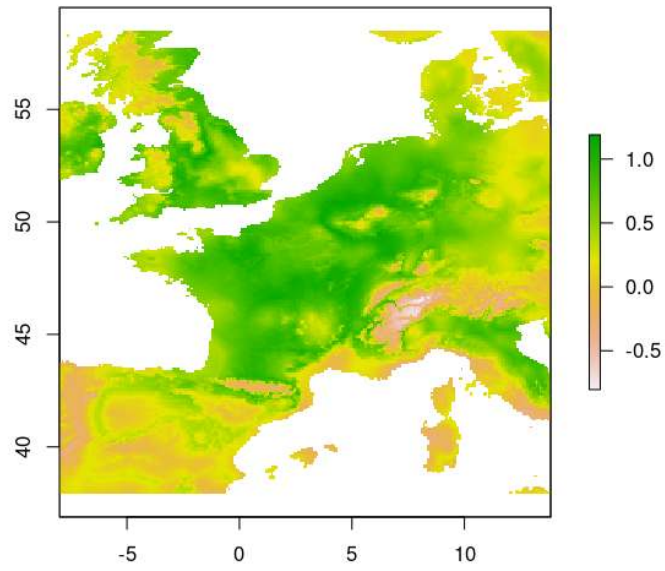
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