Multi-species distribution modeling with `biomod2`

`biomod2` version : 1.0
R version 2.15.1 (2012-06-22)

Damien Georges & Wilfried Thuiller

July 6, 2012

Contents

1 Introduction

This vignette illustrates how to model several species all together with `biomod2`.
In `biomod2` almost all the functions are built to work on single species. This choice have been made to facilitate parallel computing on large dataframes and rasters.
The aim of this document is to show how to perform multi-species modeling with `biomod2`. This has many advantages and is not a difficult task.

In the next sections, we will provide examples on how to model a set of species and an introduction to parallel programming.

NOTE 1 :
We plan to develop in the near future additional functions to help users to deal with this multi-species modeling approach.

2 Multiple Species Computation

Functions allowing to model multiple species are not implemented yet. Thus, you will need to create a 'loop' around the functions related to the modeling steps in `biomod2` (e.g, initialisation, modeling, ensemble modeling, projection, ensemble forecasting) ... The best way for doing this task depends on the class of your input data. Let's start with with the `biomod2` data.

2.1 Loading the data

First, we need to load our species occurrence data. Here, species occurrences have been previously extracted and stored as a table (.csv format).

R input

```
# 1. loading species occurrences data
library(biomod2)
mySpeciesOcc <- read.csv( system.file(
                            "external/species/species_occ.csv",
                            package="biomod2"))
head(mySpeciesOcc)
```

R output

```
       x     y CapraIbex MelesMeles MyocastorCoypus
1 21.667 68.33        NA          1              NA
2 25.000 68.33        NA          1              NA
3 28.333 68.33        NA          1              NA
4 31.667 68.33        NA          1              NA
5  8.333 65.00        NA          1              NA
6 11.667 65.00        NA          1              NA
```

NOTE 2 :
The loaded table contains only 1 and NA's. Later, we will consider only the occurrences (i.e. 1) for selecting pseudo-absences from background data (RasterStack). You can find more details about input data supported by `biomod2` in the 'SupportedInputData' vignette.

In this example, our explanatory variables are stored in a RasterStack.

R input

```
# 2. loading environmental data

# Environmental variables extracted from Worldclim (bio_3, bio_4,
# bio_7, bio_11 & bio_12)
require(raster)
myExpl = stack( system.file( "external/climat/current/bio3.grd",
                             package="biomod2"),
                system.file( "external/climat/current/bio4.grd",
                             package="biomod2"),
```

```
                    system.file( "external/climat/current/bio7.grd",
                                 package="biomod2"),
                    system.file( "external/climat/current/bio11.grd",
                                 package="biomod2"),
                    system.file( "external/climat/current/bio12.grd",
                                 package="biomod2"))
```

We model the niches of 2 mammal species:

- MelesMeles
- MyocastorCoypus

2.2 Running the models with the for function

For each species, we will sequentially follow these steps:

1. Selecting data corresponding to a species
2. Putting this data in the `biomod2` format and selecting pseudo-absences (i.e. BIOMOD_FormatingData)
3. Building 'individual models' (i.e. BIOMOD_Modeling)
4. Building ensemble-models (i.e. BIOMOD_EnsembleModeling)
5. Making model projections (i.e. BIOMOD_Projection BIOMOD_EnsembleForecasting)

NOTE 3 :
The modeling steps applied to each species are the same as the one described in 'GettingStarted' vignette.

R input

```
# define the species of interest
sp.names <- c("MelesMeles", "MyocastorCoypus")
# loop on species == applying the same functions to each species
for(sp.n in sp.names){

  cat('\n',sp.n,'modeling...')
  ### definition of data
  ## i.e keep only the column of our species
  myResp <- as.numeric(mySpeciesOcc[,sp.n])
  # get NAs id
  na.id <- which(is.na(myResp))
  # remove NAs to force the pseudo-absence extraction from background data
  myResp <- myResp[-na.id]  ## presence-only data

  myRespCoord = mySpeciesOcc[-na.id,c('x','y')]  ## coordinates of the presence-only data
```

```
myRespName = sp.n

### Initialisation
myBiomodData <- BIOMOD_FormatingData(resp.var = myResp,
                                     expl.var = myExpl,
                                     resp.xy = myRespCoord,
                                     resp.name = myRespName,
                                     PA.nb.rep = 2,
                                     PA.nb.absences = 10*sum(myResp==1,
                                                             na.rm=TRUE),
                                     PA.strategy = 'random')


### Options definition
myBiomodOption <- BIOMOD_ModelingOptions()

### Modelling
myBiomodModelOut <- BIOMOD_Modeling(
                            myBiomodData,
                            models = c('SRE','CTA','RF','MARS','FDA'),
                            models.options = myBiomodOption,
                            NbRunEval=1,
                            DataSplit=80,
                            Yweights=NULL,
                            VarImport=3,
                            models.eval.meth = c('TSS','ROC'),
                            SaveObj = TRUE,
                            rescal.all.models = TRUE)

### Building ensemble-models
myBiomodEM <- BIOMOD_EnsembleModeling(
                        modeling.output = myBiomodModelOut,
                        chosen.models = 'all',
                        eval.metric = c('TSS'),
                        eval.metric.quality.threshold = c(0.85),
                        prob.mean = T,
                        prob.cv = T,
                        prob.ci = T,
                        prob.ci.alpha = 0.05,
                        prob.median = T,
                        committee.averaging = T,
                        prob.mean.weight = T,
                        prob.mean.weight.decay = 'proportional' )

### Do projections on current variable
myBiomomodProj <- BIOMOD_Projection(
                            modeling.output = myBiomodModelOut,
                            new.env = myExpl,
                            proj.name = 'current',
```

```
                              selected.models = 'all',
                              binary.meth= 'ROC',
                              compress = 'xz',
                              clamping.mask = F)

    ### Do ensemble-models projections on current variable
    myBiomodEF <- BIOMOD_EnsembleForecasting(
                            projection.output = myBiomomodProj,
                            EM.output = myBiomodEM,
                            binary.meth = 'TSS',
                            total.consensus = TRUE)
  }
```

`biomod2` creates a folder for each modelled species. You can find all outputs in your working directory. You are now able to work on the outputs and combine them as you want.
To illustrate it let's create an α-diversity map (in this example, this is simply the sum of the binary outputs). We chose to consider only the binary files of 'total consensus ensemble-models projections' and focus our attention on the 'mean of probability' ensemble-model.

R input

```
# load the first species binary maps which will define the mask
alphaMap <- get(load(paste(sp.names[1],"/proj_current/",
                           sp.names[1],"_TotalConsensus.bin.TSS",
                           sep="")))[[1]]
# free up the workspace to avoid memory saturation.
rm(list=paste(sp.names[1],"_TotalConsensus.bin.TSS", sep=""))
# # add all other species map
for(sp.n in sp.names[-1]){
   # add layer
   alphaMap <- alphaMap + get(load(paste(sp.n,"/proj_current/",
                                         sp.n,"_TotalConsensus.bin.TSS",
                                         sep="")))[[1]]
   # free space
   rm(list=paste(sp.n,"_TotalConsensus.bin.TSS", sep=""))
 }
# summary of created raster
alphaMap
```

R output

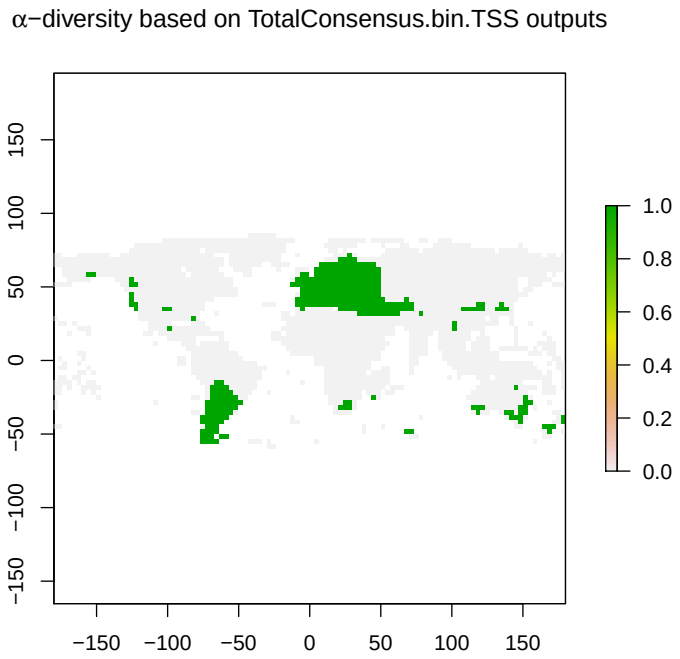
```
class       : RasterLayer
dimensions  : 45, 108, 4860  (nrow, ncol, ncell)
resolution  : 3.333, 3.333  (x, y)
extent      : -180, 180, -60, 90  (xmin, xmax, ymin, ymax)
coord. ref. : +proj=longlat +ellps=WGS84 +datum=WGS84 +no_defs +towgs84=0,0,0
values      : in memory
```

```
min value   : 0
max value   : 1
```

R input

Let's visualise our α-diversity map.

R input
```
plot(alphaMap, main = expression( paste(alpha, "-diversity based on",
                                        " TotalConsensus.bin.TSS outputs")))
```



NOTE 4 :
Here, our two species never co-occur, which explains why the α-diversity is never higher than 1.

NOTE 5 :
This example is presented with a loop. A more efficient way of programming is to use the lapply function, an inner R function for looping over objects.

2.3 Running the models with the lapply function

lapply is a very easy function to use. It only requires a vector with the species names and a function to run. Here, we just integrate the loop into MyBiomodSF function.

R input

```
MyBiomodSF <- function(sp.n){

    cat('\n',sp.n,'modeling...')
    ### definition of data for this run
    ## i.e keep only the column of our species
    myResp <- as.numeric(mySpeciesOcc[,sp.n])
    # get NAs id
    na.id <- which(is.na(myResp))
    # remove NAs to enforce PA sampling to be done on explanatory rasters
    myResp <- myResp[-na.id]

    myRespCoord = mySpeciesOcc[-na.id,c('x','y')]

    myRespName = sp.n

    ### Initialisation
    myBiomodData <- BIOMOD_FormatingData(resp.var = myResp,
                                         expl.var = myExpl,
                                         resp.xy = myRespCoord,
                                         resp.name = myRespName,
                                         PA.nb.rep = 2,
                                         PA.nb.absences = 10*sum(myResp==1,
                                                                 na.rm=TRUE),
                                         PA.strategy = 'random')


    ### Options definition
    myBiomodOption <- BIOMOD_ModelingOptions()

    ### Modelling
    myBiomodModelOut <- BIOMOD_Modeling(
                                myBiomodData,
                                models = c('SRE','CTA','RF','MARS','FDA'),
                                models.options = myBiomodOption,
                                NbRunEval=1,
                                DataSplit=80,
                                Yweights=NULL,
                                VarImport=3,
                                models.eval.meth = c('TSS','ROC'),
                                SaveObj = TRUE,
                                rescal.all.models = TRUE)

    ### Building ensemble-models
```

```
    myBiomodEM <- BIOMOD_EnsembleModeling(
                          modeling.output = myBiomodModelOut,
                          chosen.models = 'all',
                          eval.metric = c('TSS'),
                          eval.metric.quality.threshold = c(0.85),
                          prob.mean = T,
                          prob.cv = T,
                          prob.ci = T,
                          prob.ci.alpha = 0.05,
                          prob.median = T,
                          committee.averaging = T,
                          prob.mean.weight = T,
                          prob.mean.weight.decay = 'proportional' )

    ### Do projections on current varaiable
    myBiomomodProj <- BIOMOD_Projection(
                               modeling.output = myBiomodModelOut,
                               new.env = myExpl,
                               proj.name = 'current',
                               selected.models = 'all',
                               binary.meth= 'ROC',
                               compress = 'xz',
                               clamping.mask = F)

    ### Do ensemble-models projections on current varaiable
    myBiomodEF <- BIOMOD_EnsembleForecasting(
                            projection.output = myBiomomodProj,
                            EM.output = myBiomodEM,
                            binary.meth = 'TSS',
                            total.consensus = TRUE)

  }
```

Then, simply call the lapply function and give the vector of species names

```
R input
myLapply_SFModelsOut <- lapply( sp.names, MyBiomodSF)
```

3 Parallel computing

If you have a large range of species or/and if your data are extremely large , computation time may rapidly expand and become too long to be done within a loop.
The best way to deal with such cases is to do parallel programming. It means modeling species in different CPUs. At the end you will need to re-assemble together the outputs created especially if you aim at doing 'community' analyses such as calculating turnover or species richness.

In the best case you have an access to a cluster of computers. If not, you can have several computers and split your species into groups by hand. But you can also just have a single computer with several CPUs. In such case, you can easily parallelize on your multi-CPU single computer. The snowfall package will help you doing this.

NOTE 6 :
Parallel computing tools are developing fast in R, so whatever the type of parallel programming you want to do, tools may exist to help you! (look at packages snow, snowfall, xgrid, parallel)

4 Introduction to snowfall library

The snowfall package is useful to perform parallel computing with R jobs. The syntax is quite similar to the "lapply()" function we just presented above. The first thing to do is to download the snowfall library.

R input
```
install.packages('snowfall', dependencies=TRUE)
```

R input
```
library(snowfall)
```

The second thing to do is to create the function to parallelize (let's take the same as in the previous section). Here, we used the MyBiomodSF function created in the lapply presentation.

Then you have to give to snowfall all the variables and libraries that are used in the function.

R input
```
## Init snowfall
library(snowfall)
sfInit(parallel=TRUE, cpus=2 )  ## we select 2 CPUs. If you have 8 CPUs, put 8.
## Export packages
sfLibrary('biomod2', character.only=TRUE)
## Export variables
sfExport('mySpeciesOcc')
sfExport('myExpl')
sfExport('sp.names')
# you may also use sfExportAll() to export all your workspace variables

## Do the run
mySFModelsOut <- sfLapply( sp.names, MyBiomodSF)
## stop snowfall
sfStop( nostop=FALSE )
```

You will obtain exactly the same folder structure than if you worked in serial so you can compute your 'community' analyses exactly as previously.
NOTE 7 :
In case of computation on several computers, you have to merge all your species folders in a single folder, then you will get the same files as in a serial computation case.