An example of species distribution modeling with `biomod2`

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Contents

1 Introduction

This vignette illustrates how to build, evaluate and project a single species distribution model using biomod2 package. The three main modeling steps, described bellow, are the following :

1. formatting the data
2. computing the models
3. making the projections

The example is deliberately simple (few technicals explanations) to make sure it is easy to transpose to your own data relatively simply.

Here we are going to modeled the current and future (2050) distribution of Gulo Gulo.

NOTE 1:
Several other vignettes will be written soon to help you to go through biomod2 details and subtleties

2 Formatting the data

In this vignette, we will work (because it is a quite common case) with :

- presences/absences points data
- environmental raster layers (e.g. Worldclim)

Let's import our data.

R input

```
# load the library
library(biomod2)
# load our species data
DataSpecies <- read.csv(system.file("external/species/mammals_table.csv",
                                    package="biomod2"))
head(DataSpecies)
```

R output

```
  X X_WGS84 Y_WGS84 ConnochaetesGnou GuloGulo PantheraOnca
1 1   -94.5      82                0        0           0
2 2   -91.5      82                0        1           0
3 3   -88.5      82                0        1           0
4 4   -85.5      82                0        1           0
5 5   -82.5      82                0        1           0
6 6   -79.5      82                0        1           0
  PteropusGiganteus TenrecEcaudatus VulpesVulpes
1                 0               0           0
2                 0               0           0
3                 0               0           0
4                 0               0           0
5                 0               0           0
6                 0               0           0
```

R input

```
# the name of studied species
myRespName <- 'GuloGulo'
# the presence/absences data for our species
myResp <- as.numeric(DataSpecies[,myRespName])
# the XY coordinates of species data
myRespXY <- DataSpecies[,c("X_WGS84","Y_WGS84")]
# load the environmental raster layers (could be .img, ArcGIS
# rasters or any supported format by the raster package)

# Environmental variables extracted from Worldclim (bio_3, bio_4,
# bio_7, bio_11 & bio_12)
myExpl = stack( system.file( "external/bioclim/current/bio3.grd",
                             package="biomod2"),
                system.file( "external/bioclim/current/bio4.grd",
                             package="biomod2"),
                system.file( "external/bioclim/current/bio7.grd",
                             package="biomod2"),
                system.file( "external/bioclim/current/bio11.grd",
                             package="biomod2"),
                system.file( "external/bioclim/current/bio12.grd",
                             package="biomod2"))
```

NOTE 2:
You may not have absences data. As all models need both presences and absences to run, you may need to add some pseudo-absences (or background data) to your data. That is necessary in the case of presence-only, and may be useful in the case of insufficient absence data.
`biomod2` offers some tools to do it more or less automatically. 3 algorithms are now implemented to extract a range of pseudo-absence data: 'random', 'SRE' and 'disk'. A vignette will be written soon to explain how to do. Waiting for this, you can refer to `BIOMOD_FormatingData` help file

NOTE 3:
If your environmental data are in matrix (or data.frame) format, you have to give a species as vector having a length that match with the number of rows of your environmental dataset. That implies to add NA's in all points where you do not have information on species presence-absence.

When your data are correctly loaded, you have to transform them in an appropriate `biomod2` format. This is done using `BIOMOD_FormatingData`.

NOTE 4:
If you have both presence-absence data and a large number of presence (not the case here), it's strongly recommended to split your data.frame into two pieces and to keep a part for evaluating all your models on the same data.set (i.e. eval.xxx args)

R input

```
myBiomodData <- BIOMOD_FormatingData(resp.var = myResp,
                                     expl.var = myExpl,
                                     resp.xy = myRespXY,
                                     resp.name = myRespName)
```

R output

```
-=-=-=-=-=-=-=-= GuloGulo Data Formating -=-=-=-=-=-=-=-=

> No pseudo absences selection !
      ! No data has been set aside for modeling evaluation
-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
```

At this point, check whether the data are correctly formatted by printing and plotting the created object.

R input

```
myBiomodData
```

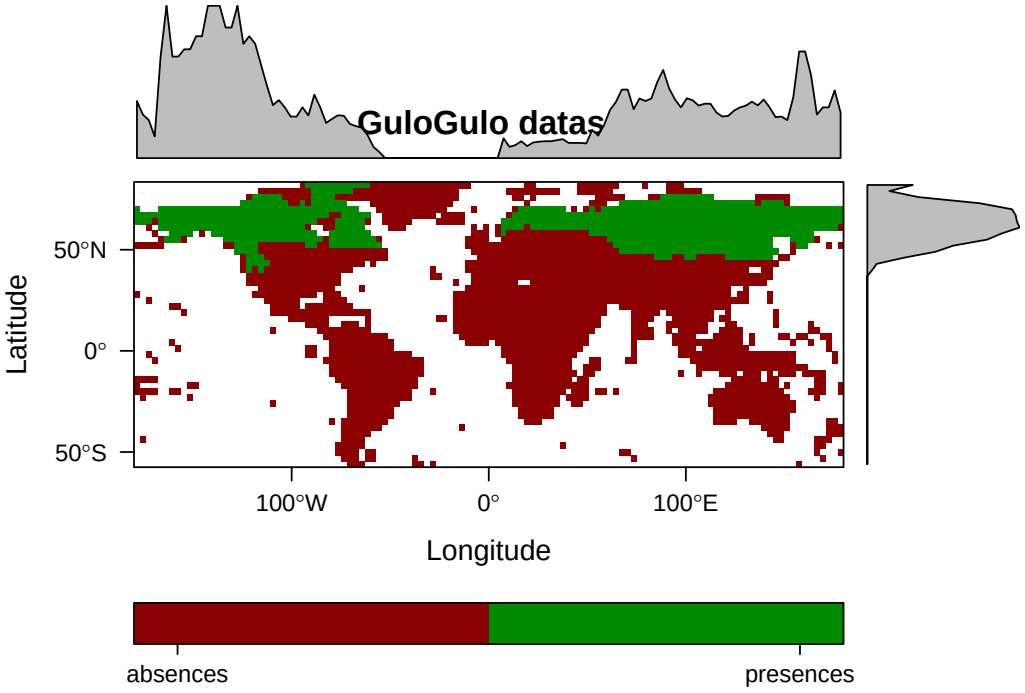
R output

```
-=-=-=-=-=-=-=-= 'BIOMOD.formated.data' -=-=-=-=-=-=-=-=

sp.name =  GuloGulo

         661 presences,  1827 true absences and  0
undifined points in dataset
```

```
        5 explanatory variables

      bio3           bio4            bio7
 Min.   :10.2   Min.   :   72   Min.   : 54.5
 1st Qu.:21.2   1st Qu.: 2641   1st Qu.:186.0
 Median :35.0   Median : 6682   Median :306.2
 Mean   :40.3   Mean   : 7358   Mean   :310.9
 3rd Qu.:56.4   3rd Qu.:11752   3rd Qu.:424.6
 Max.   :92.0   Max.   :22314   Max.   :718.0
     bio11           bio12
 Min.   :-447.7   Min.   :   0
 1st Qu.:-184.3   1st Qu.: 276
 Median :  24.2   Median : 563
 Mean   :  -2.6   Mean   : 854
 3rd Qu.: 196.3   3rd Qu.:1201
 Max.   : 283.0   Max.   :5431

-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

R input

```
plot(myBiomodData)
```



The colors for this plot match with...

- Presences
- Absences

3 Modeling

3.1 Building models

This step may be considered as the core of the modeling procedure within `biomod2`. Here you have to choose between 10 different algorithms ('GLM', 'GBM', 'GAM', 'CTA', 'ANN', 'SRE', 'FDA', 'MARS', 'RF', 'MAXENT').
Before running the models, you can customize their set of parameters and options using `BIOMOD_ModelingOptions`. The created object is then given to `BIOMOD_Modeling` in the next step. For the sake of simplicity, we keep all default options.

NOTE 5:
A vignette on models' parametrization will be available soon

R input

```
# 2. Defining Models Options using default options.
myBiomodOption <- BIOMOD_ModelingOptions()
```

We are now ready for running the set of models on our species. As we do not have evaluation data, we will make 3-fold cross-validation (number controlled by "NbRunEval" argument) of our models by randomly splitting our data set into 2 subsets : "DataSplit"

R input

```
# 3. Computing the models

myBiomodModelOut <- BIOMOD_Modeling(
                            myBiomodData,
                            models = c('SRE','CTA','RF','MARS','FDA'),
                            models.options = myBiomodOption,
                            NbRunEval=3,
                            DataSplit=80,
                            Prevalence=0.5,
                            VarImport=3,
                            models.eval.meth = c('TSS','ROC'),
                            SaveObj = TRUE,
                            rescal.all.models = TRUE,
                            do.full.models = FALSE,
                            modeling.id = paste(myRespName,"FirstModeling",sep=""))
```

R output

```
Loading required library...

Checking Models arguments...

Creating suitable Workdir...

        > Automatic weights creation to rise a 0.5 prevalence


-=-=-=-=-=-=-=-= GuloGulo Modeling Summary -=-=-=-=-=-=-=-=

 5  environmental variables ( bio3 bio4 bio7 bio11 bio12 )
Number of evaluation repetitions : 3
Models selected : SRE CTA RF MARS FDA

Total number of model runs : 15

-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=


-=-=-=- Run :  GuloGulo_AllData


-=-=-=-=-=-=- GuloGulo_AllData_RUN1

Model=Surface Range Envelop
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...
```

```
Model=Classification tree
         5 Fold Cross-Validation
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Breiman and Cutler's random forests for classification and regression
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Multiple Adaptive Regression Splines
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Flexible Discriminant Analysis
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...


-=-=-=-=-=-=- GuloGulo_AllData_RUN2

Model=Surface Range Envelop
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Classification tree
         5 Fold Cross-Validation
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Breiman and Cutler's random forests for classification and regression
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Multiple Adaptive Regression Splines
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Flexible Discriminant Analysis
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...


-=-=-=-=-=-=- GuloGulo_AllData_RUN3

Model=Surface Range Envelop
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...
```

```
Model=Classification tree
         5 Fold Cross-Validation
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Breiman and Cutler's random forests for classification and regression
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Multiple Adaptive Regression Splines
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

Model=Flexible Discriminant Analysis
        Model scaling...
        Evaluating Model stuff...
                        Evaluating Predictor Contributions...

-=-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

R input

When this step is over, have a look at some outputs :

- modeling summary

R input

```
myBiomodModelOut
```

R output

```
-=-=-=-=-=-=-=-=-=-=-= BIOMOD.models.out -=-=-=-=-=-=-=-=-=-=-=

Modeling id : GuloGuloFirstModeling

Species modeled : GuloGulo

Considered variables : bio3 bio4 bio7 bio11 bio12


Computed Models :  GuloGulo_AllData_RUN1_SRE
GuloGulo_AllData_RUN1_CTA GuloGulo_AllData_RUN1_RF
GuloGulo_AllData_RUN1_MARS GuloGulo_AllData_RUN1_FDA
GuloGulo_AllData_RUN2_SRE GuloGulo_AllData_RUN2_CTA
GuloGulo_AllData_RUN2_RF GuloGulo_AllData_RUN2_MARS
GuloGulo_AllData_RUN2_FDA GuloGulo_AllData_RUN3_SRE
GuloGulo_AllData_RUN3_CTA GuloGulo_AllData_RUN3_RF
GuloGulo_AllData_RUN3_MARS GuloGulo_AllData_RUN3_FDA


Failed Models :  none

-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

- models evaluations

R input
```
# get all models evaluation
myBiomodModelEval <- get_evaluations(myBiomodModelOut)
# print the dimnames of this object
dimnames(myBiomodModelEval)
```

R output
```
[[1]]
[1] "TSS" "ROC"

[[2]]
[1] "Testing.data" "Cutoff"       "Sensitivity"
[4] "Specificity"

[[3]]
[1] "SRE"  "CTA"  "RF"   "MARS" "FDA"

[[4]]
[1] "RUN1" "RUN2" "RUN3"

[[5]]
GuloGulo_AllData
       "AllData"
```

R input
```
# let's print the TSS scores of Random Forest
myBiomodModelEval["TSS","Testing.data","RF",,]
```

R output
```
 RUN1  RUN2  RUN3
0.916 0.907 0.879
```

R input
```
# let's print the ROC scores of all selected models
myBiomodModelEval["ROC","Testing.data",,,]
```

R output
```
      RUN1  RUN2  RUN3
SRE   0.866 0.858 0.856
CTA   0.942 0.954 0.917
RF    0.988 0.989 0.979
MARS  0.974 0.979 0.970
FDA   0.958 0.975 0.963
```

R input
```

```

- Relative importance of the explanatory variables

R input
```
# print variable importances
get_variables_importance(myBiomodModelOut)
```

R output
```
, , RUN1, AllData
```

```
       SRE   CTA    RF  MARS   FDA
Var1 0.388 0.285 0.165 0.358 0.257
Var2 0.380 0.285 0.164 0.356 0.252
Var3 0.370 0.285 0.167 0.360 0.256

, , RUN2, AllData

       SRE   CTA    RF  MARS   FDA
Var1 0.383 0.331 0.170 0.351 0.268
Var2 0.375 0.331 0.166 0.349 0.273
Var3 0.378 0.331 0.171 0.341 0.269

, , RUN3, AllData

       SRE   CTA    RF  MARS   FDA
Var1 0.364 0.317 0.159 0.384 0.275
Var2 0.372 0.317 0.159 0.405 0.270
Var3 0.378 0.317 0.165 0.390 0.276
```

NOTE 6:
Relative importance of variable returned are raw data. It may be usefull to normalise them to make them comparable one to another

3.2 Ensemble modeling

Here comes one of the most interesting features of `biomod2`. `BIOMOD_EnsembleModeling` combines individual models to build some kind of meta-model. In the following example, we decide to exclude all models having a TSS score lower than 0.7.

NOTE 7:
You can controle the way formal models are combined with em.by argument. The vignette "EnsembleModelingAssembly" illustrate the offered possibilities

R input

```
myBiomodEM <- BIOMOD_EnsembleModeling(
                      modeling.output = myBiomodModelOut,
                      chosen.models = 'all',
                      em.by='all',
                      eval.metric = c('TSS'),
                      eval.metric.quality.threshold = c(0.7),
                      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' )
```

R output

```
-=-=-=-=-=-=-=-=-= Build Ensemble Models -=-=-=-=-=-=-=-=-=

  ! all models available will be included in ensemble.modeling
  > Evaluation & Weighting methods summary :
     TSS over 0.7


 > TotalConsensus ensemble modeling
  ! Models projections for whole zonation required...
       > Projecting GuloGulo_AllData_RUN1_SRE ...
       > Projecting GuloGulo_AllData_RUN1_CTA ...
       > Projecting GuloGulo_AllData_RUN1_RF ...
       > Projecting GuloGulo_AllData_RUN1_MARS ...
       > Projecting GuloGulo_AllData_RUN1_FDA ...
       > Projecting GuloGulo_AllData_RUN2_SRE ...
       > Projecting GuloGulo_AllData_RUN2_CTA ...
       > Projecting GuloGulo_AllData_RUN2_RF ...
       > Projecting GuloGulo_AllData_RUN2_MARS ...
       > Projecting GuloGulo_AllData_RUN2_FDA ...
       > Projecting GuloGulo_AllData_RUN3_SRE ...
       > Projecting GuloGulo_AllData_RUN3_CTA ...
       > Projecting GuloGulo_AllData_RUN3_RF ...
       > Projecting GuloGulo_AllData_RUN3_MARS ...
       > Projecting GuloGulo_AllData_RUN3_FDA ...

  > Mean of probabilities...
                       Evaluating Model stuff...
  > Coef of variation of probabilities...
                       Evaluating Model stuff...
  > Confidence Interval...
                       Evaluating Model stuff...
                       Evaluating Model stuff...
  > Median of ptobabilities...
                       Evaluating Model stuff...
  >  Comittee averaging...
                       Evaluating Model stuff...
  > Prababilities wegthing mean...
                       Evaluating Model stuff...
-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
```

You can easily access to the data and outputs of `BIOMOD_Modeling` using some specific functions to make your life easier.
Let's see the meta-models evaluation scores.

NOTE 8:
We decide to evaluate all meta-models produced even the CV (Coefficient of Variation) one which is quite hard to interpret. You may consider it as: higher my score is, more the variation is localised where my species is forecasted as present.

R input

```
# print summary
myBiomodEM
```

R output

```
-=-=-=-=-=-=-= 'BIOMOD.EnsembleModeling.out' -=-=-=-=-=-=-=

sp.name : GuloGulo

expl.var.names : bio3 bio4 bio7 bio11 bio12


models computed:
GuloGulo_TotalConsensus_TSS_EMmean, GuloGulo_TotalConsensus_TSS_EMcv, GuloGulo_TotalConsensus_TSS_EMciI

-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

R input

```
# get evaluation scores
get_evaluations(myBiomodEM)
```

R output

```
$GuloGulo_TotalConsensus_TSS_EMmean
    Testing.data Cutoff Sensitivity Specificity
TSS        0.912    594        94.1        97.1

$GuloGulo_TotalConsensus_TSS_EMcv
    Testing.data Cutoff Sensitivity Specificity
TSS       -0.065    145       0.151       93.21

$GuloGulo_TotalConsensus_TSS_EMciInf
    Testing.data Cutoff Sensitivity Specificity
TSS        0.914    383        94.4       96.99

$GuloGulo_TotalConsensus_TSS_EMciSup
    Testing.data Cutoff Sensitivity Specificity
TSS        0.911    776        94.4       96.66

$GuloGulo_TotalConsensus_TSS_EMmedian
    Testing.data Cutoff Sensitivity Specificity
TSS        0.911    717        94.1       96.99

$GuloGulo_TotalConsensus_TSS_EMca
    Testing.data Cutoff Sensitivity Specificity
TSS        0.895    631        94.7       94.75

$GuloGulo_TotalConsensus_TSS_EMwmean
    Testing.data Cutoff Sensitivity Specificity
TSS        0.915    607        94.1       97.37
```

4 Projection

Once the models are calibrated and evaluated, we might want to project the potential distribution of the species over space and time. This is made using `BIOMOD_Projection`

NOTE 9:
All projections are stored directly on your hard drive

First let's project the individual models on our current conditions (the globe) to visualize them.

R input

```
# projection over the globe under current conditions
myBiomodProj <- BIOMOD_Projection(
                          modeling.output = myBiomodModelOut,
                          new.env = myExpl,
                          proj.name = 'current',
                          selected.models = 'all',
                          binary.meth = 'TSS',
                          compress = 'xz',
                          clamping.mask = F,
                          output.format = '.grd')
```

R output

```
-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=

        > Building clamping mask

        > Projecting GuloGulo_AllData_RUN1_SRE ...
        > Projecting GuloGulo_AllData_RUN1_CTA ...
        > Projecting GuloGulo_AllData_RUN1_RF ...
        > Projecting GuloGulo_AllData_RUN1_MARS ...
        > Projecting GuloGulo_AllData_RUN1_FDA ...
        > Projecting GuloGulo_AllData_RUN2_SRE ...
        > Projecting GuloGulo_AllData_RUN2_CTA ...
        > Projecting GuloGulo_AllData_RUN2_RF ...
        > Projecting GuloGulo_AllData_RUN2_MARS ...
        > Projecting GuloGulo_AllData_RUN2_FDA ...
        > Projecting GuloGulo_AllData_RUN3_SRE ...
        > Projecting GuloGulo_AllData_RUN3_CTA ...
        > Projecting GuloGulo_AllData_RUN3_RF ...
        > Projecting GuloGulo_AllData_RUN3_MARS ...
        > Projecting GuloGulo_AllData_RUN3_FDA ...

        > Building TSS binaries
-=-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

R input

```
# summary of crated oject
myBiomodProj
```

R output

```
-=-=-=-=-=-=-=-= 'BIOMOD.projection.out' -=-=-=-=-=-=-=-=-=

Projection directory : GuloGulo/current


sp.name : GuloGulo
```

```
expl.var.names : bio3 bio4 bio7 bio11 bio12


modeling id : GuloGuloFirstModeling (
GuloGulo/GuloGulo.GuloGuloFirstModeling.models.out )

models projected :
GuloGulo_AllData_RUN1_SRE, GuloGulo_AllData_RUN1_CTA, GuloGulo_AllData_RUN1_RF, GuloGulo_AllData_RUN1_M

-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

R input

```
# files created on hard drive
list.files("GuloGulo/proj_current/")
```

R output

```
 [1] "GuloGulo.current.projection.out"
 [2] "proj_current_ClampingMask.grd"
 [3] "proj_current_ClampingMask.gri"
 [4] "proj_current_GuloGulo.grd"
 [5] "proj_current_GuloGulo.gri"
 [6] "proj_current_GuloGulo_TotalConsensus_EMbyTSS.grd"
 [7] "proj_current_GuloGulo_TotalConsensus_EMbyTSS.gri"
 [8] "proj_current_GuloGulo_TotalConsensus_EMbyTSS_TSSbin.grd"
 [9] "proj_current_GuloGulo_TotalConsensus_EMbyTSS_TSSbin.gri"
[10] "proj_current_GuloGulo_TSSbin.grd"
[11] "proj_current_GuloGulo_TSSbin.gri"
```

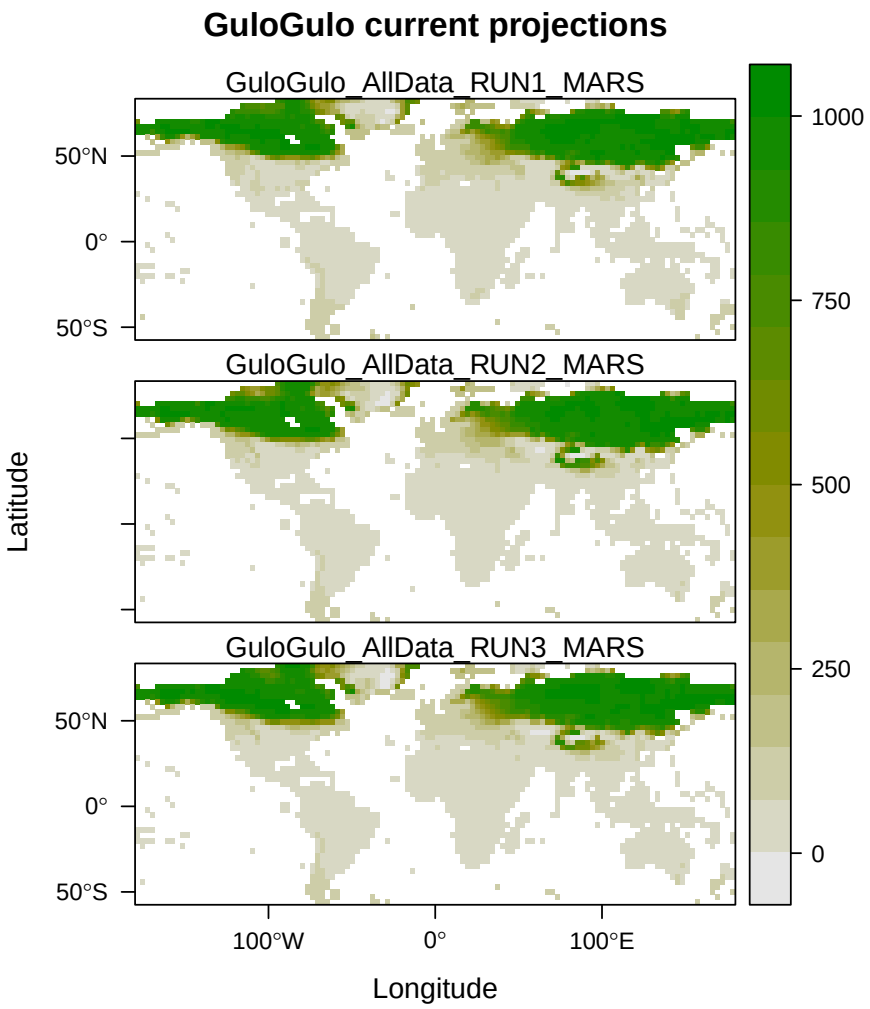
R input

R input

```
# make some plots sub-selected by str.grep argument
plot(myBiomodProj, str.grep = 'MARS')
```

R output

```
*** models_selected =  GuloGulo_AllData_RUN1_MARS GuloGulo_AllData_RUN2_MARS GuloGulo_AllData_RUN3_MARS
```



R input

```
# if you want to make custom plots, you can also get the projected map
myCurrentProj <- get_predictions(myBiomodProj)
```

R output

```
*** models_selected =  GuloGulo_AllData_RUN1_SRE GuloGulo_AllData_RUN1_CTA GuloGulo_AllData_RUN1_RF Gul
```

R input

```
myCurrentProj
```

R output

```
class       : RasterStack
dimensions  : 47, 120, 5640, 15  (nrow, ncol, ncell, nlayers)
resolution  : 3, 3  (x, y)
extent      : -180, 180, -57.5, 83.5  (xmin, xmax, ymin, ymax)
coord. ref. : +proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0
names       : GuloGulo_AllData_RUN1_SRE, GuloGulo_AllData_RUN1_CTA, GuloGulo_AllData_RUN1_RF, GuloGulo_
min values  :                         0,                        18,                         3,
max values  :                      1000,                       946,                      1000,
```

Then we can project the potential distribution of the species over time, i.e. into the future.

R input

```
# load environmental variables for the future.
myExplFuture = stack( system.file( "external/bioclim/future/bio3.grd",
                                   package="biomod2"),
                      system.file( "external/bioclim/future/bio4.grd",
                                   package="biomod2"),
                      system.file( "external/bioclim/future/bio7.grd",
                                   package="biomod2"),
                      system.file( "external/bioclim/future/bio11.grd",
                                   package="biomod2"),
                      system.file( "external/bioclim/future/bio12.grd",
                                   package="biomod2"))
myBiomodProjFuture <- BIOMOD_Projection(
                                  modeling.output = myBiomodModelOut,
                                  new.env = myExplFuture,
                                  proj.name = 'future',
                                  selected.models = 'all',
                                  binary.meth = 'TSS',
                                  compress = 'xz',
                                  clamping.mask = T,
                                  output.format = '.grd')
```

R output

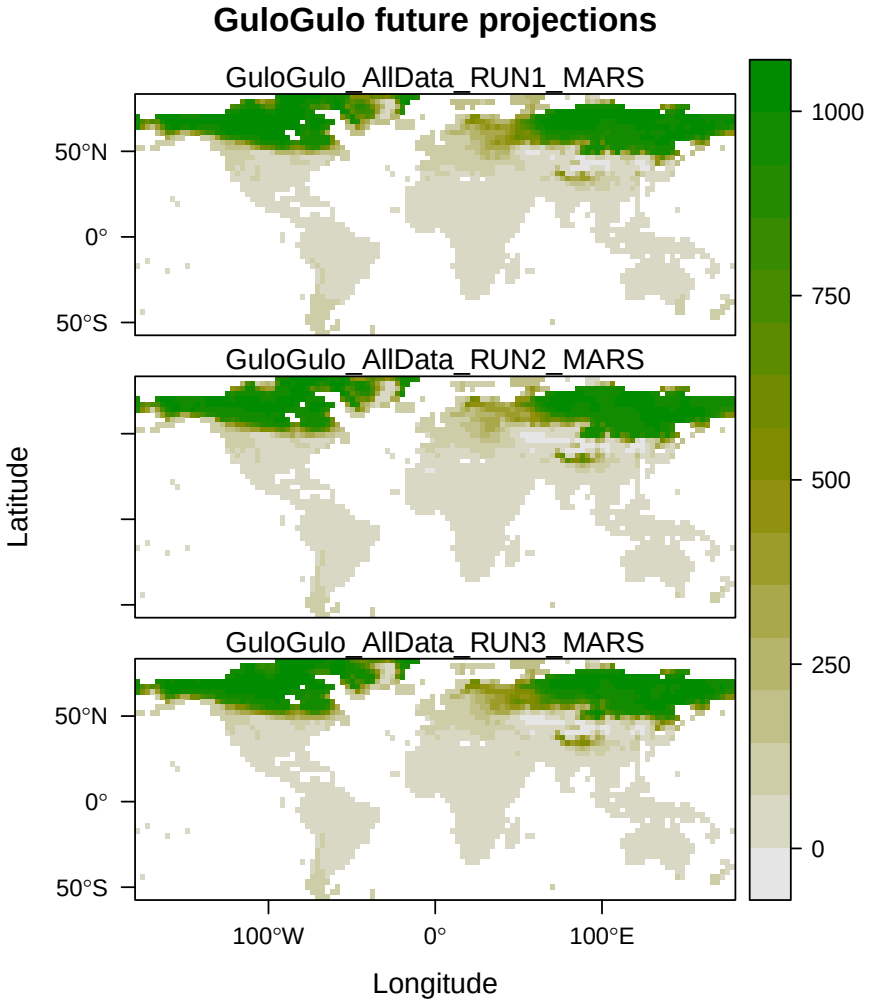
```
-=-=-=-=-=-=-=-=-= Do Models Projections -=-=-=-=-=-=-=-=-=

        > Building clamping mask

        > Projecting GuloGulo_AllData_RUN1_SRE ...
        > Projecting GuloGulo_AllData_RUN1_CTA ...
        > Projecting GuloGulo_AllData_RUN1_RF ...
        > Projecting GuloGulo_AllData_RUN1_MARS ...
        > Projecting GuloGulo_AllData_RUN1_FDA ...
        > Projecting GuloGulo_AllData_RUN2_SRE ...
        > Projecting GuloGulo_AllData_RUN2_CTA ...
        > Projecting GuloGulo_AllData_RUN2_RF ...
        > Projecting GuloGulo_AllData_RUN2_MARS ...
        > Projecting GuloGulo_AllData_RUN2_FDA ...
        > Projecting GuloGulo_AllData_RUN3_SRE ...
        > Projecting GuloGulo_AllData_RUN3_CTA ...
        > Projecting GuloGulo_AllData_RUN3_RF ...
        > Projecting GuloGulo_AllData_RUN3_MARS ...
        > Projecting GuloGulo_AllData_RUN3_FDA ...

        > Building TSS binaries
-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
```

R input

R input

```
# make some plots, sub-selected by str.grep argument
plot(myBiomodProjFuture, str.grep = 'MARS')
```

R output
```
*** models_selected =  GuloGulo_AllData_RUN1_MARS GuloGulo_AllData_RUN2_MARS GuloGulo_AllData_RUN3_MARS
```



The last step of this vignette is to make Ensemble Forcasting, that means to project the meta-models you have created with `BIOMOD_EnsembleModeling`. `BIOMOD_EnsembleForecasting` required the output of `BIOMOD_EnsembleModeling` and `BIOMOD_Projection`. It will combine the projections made according to models ensemble rules defined at the ensemble modelling step.

R input
```
myBiomodEF <- BIOMOD_EnsembleForecasting(
                        EM.output = myBiomodEM,
                        projection.output = myBiomodProj)
```

R output
```
-=-=-=-=-=-=-= Do Ensemble Models Projections -=-=-=-=-=-=-=

*** models_selected =  GuloGulo_AllData_RUN1_SRE GuloGulo_AllData_RUN1_CTA GuloGulo_AllData_RUN1_RF Gul

        > Projecting GuloGulo_TotalConsensus_TSS_EMmean ...

        > Projecting GuloGulo_TotalConsensus_TSS_EMcv ...

        > Projecting GuloGulo_TotalConsensus_TSS_EMciInf ...
```

```
> Projecting GuloGulo_TotalConsensus_TSS_EMciSup ...

> Projecting GuloGulo_TotalConsensus_TSS_EMmedian ...

> Projecting GuloGulo_TotalConsensus_TSS_EMca ...

> Projecting GuloGulo_TotalConsensus_TSS_EMwmean ...

-=-=-=-=-=-=-=-=-=-=-=-=-= Done -=-=-=-=-=-=-=-=-=-=-=-=-=
```

Object return has the same type than ones returned by `BIOMOD_Projection`. Moreover some additional files have been created in your projection folder ("`RasterStack`" or "`array`" depending on your projection type). This file contains your meta-models projections.

R input

```
myBiomodEF
```

R output

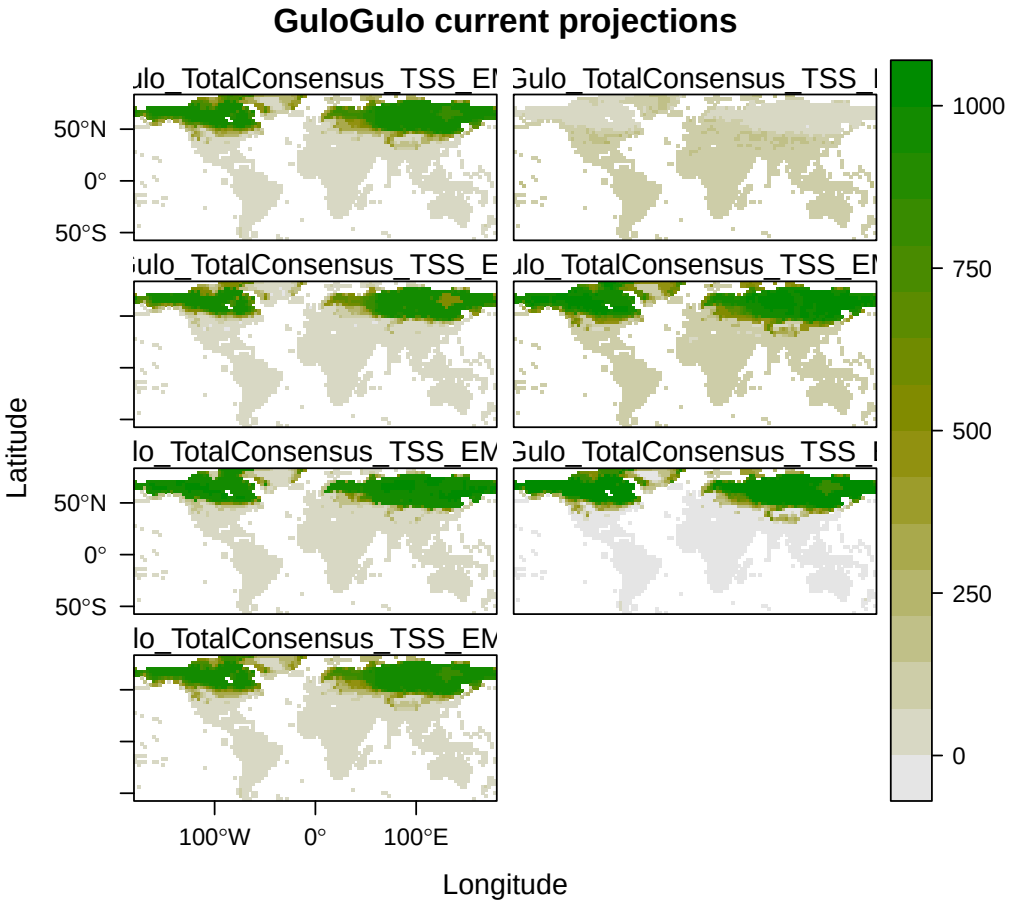
```
-=-=-=-=-=-=-=-=-= 'BIOMOD.projection.out' -=-=-=-=-=-=-=-=-=

Projection directory : GuloGulo/current


sp.name : GuloGulo

expl.var.names : bio3 bio4 bio7 bio11 bio12


modeling id : GuloGuloFirstModeling (
GuloGulo/GuloGulo.GuloGuloFirstModeling.models.out )

models projected :
GuloGulo_TotalConsensus_TSS_EMmean, GuloGulo_TotalConsensus_TSS_EMcv, GuloGulo_TotalConsensus_TSS_EMciI

-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=-=
```

R input

```
# reduce layer names for plotting convegences
plot(myBiomodEF)
```

R output

```
*** models_selected =  GuloGulo_TotalConsensus_TSS_EMmean GuloGulo_TotalConsensus_TSS_EMcv GuloGulo_Tot
```



5 Conclusion

This vignette describes how to build and test a range of models within `biomod2` but also how to build ensemble projections under current and future conditions. With few modifications, you should be able to apply the default functions onto your own dataset.