

How to make **biomod2** able to do MAXENT modeling

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

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1 Introduction

This vignette will show you how to configure your computer to be able to make MAXENT modelling in `biomod2`.

2 Java software

MAXENT is a java software so you need (if it's not done yet) to install a Java interpreter to be able to use this tools. You will the Java interpreter `java`. You should skip the following step if Java is already installed on your machine. We will consider the three most usual OS (i.e. Windows, Linux and Mac OS).

2.1 Windows

These instructions are specialized to Windows 7, but are similar for Windows XP and Windows Vista.

1. Download and install the latest version of the Java Platform, Standard Edition Development Kit (<http://www.oracle.com/technetwork/java/javase/downloads/index.html>).

NOTE 1 :

the installation directory for laterâprobably something like `C:\ProgramFiles\Java\jdkx.x.x_xx\bin`.

NOTE 2 :

Replace the `x.x.x_xx` by `jdk` version

2. Make sure that Windows can find the Java interpreter:

- Select Start → Computer → System Properties → Advanced system settings → Environment Variables → System variables → PATH.

NOTE 3 :

In Vista: select Start → My Computer → Properties → Advanced → Environment Variables → System variables → PATH

NOTE 4 :

In Windows XP: Select Start → Control Panel → System → Advanced → Environment Variables → System variables → PATH

- Prepends C:\ProgramFiles\Java\jdkx.x.x_xx\bin; to the beginning of the PATH variable.
- Click OK three times

3. make a test :

- Launch the command prompt via : All Programs → Accessories → Command Prompt. (If you already had a command prompt window open, close it and launch a new one.)
- Check that Java is installed, type the command prompt: `java -version`. If no error message returned, you can pass to next step.

2.2 Linux and Mac OS

In most of case, `java` is already install in your computer. To check it, open a terminal and simply type `java -version`. If no error message returned go to next step else follow instructions given to install Java Platform, Standard Edition Development Kit.

3 MAXENT software

To be be able to do MAXENT modelling you have to put a copy of `maxent.jar` file in your working directory.

1. download MAXENT software at <http://www.cs.princeton.edu/~schapire/maxent/>
2. uncompress the downloaded file
3. copy `maxent.jar` file and paste it in the directory where you will do your `biomod2` modelling.

4 A little test

If you have follow the previous sections, you should be able to use MAXENT as all other models in `biomod2`. Let's try it with `biomod2` data.

```
# load the library
library(biomod2)
# load our species raster
# we consider only the presences of Myocastor coypus species
myResp.ras <- raster( system.file(
                        "external/species/Myocastor_coypus.img",
                        package="biomod2") )
```

```

# extract the presences data

# the name
myRespName <- 'Myocastor'
# the XY coordinates of the presence
myRespXY <- xyFromCell(object=myResp.ras,
                        cell=which(myResp.ras[]>0))

# and the presence data
myResp <- extract(x=myResp.ras, y=myRespXY)
# 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/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"))

myBiomodData <- BIOMOD_FormatingData(resp.var = myResp,
                                    expl.var = myExpl,
                                    resp.xy = myRespXY,
                                    resp.name = myRespName,
                                    PA.nb.rep = 2,
                                    PA.nb.absences = 200,
                                    PA.strategy = 'random')

# 2. Defining Models Options using default options.
myBiomodOption <- BIOMOD_ModelingOptions()
# 3. Computing the models
myBiomodModelOut <- BIOMOD_Modeling(
  myBiomodData,
  models = c('SRE', 'RF', 'MAXENT'),
  models.options = myBiomodOption,
  NbRunEval=1,
  DataSplit=80,
  Yweights=NULL,
  VarImport=3,
  models.eval.meth = c('TSS', 'ROC'),
  SaveObj = TRUE,
  rescal.all.models = TRUE)

# let's have a look at different models scores
getModelsEvaluations(myBiomodModelOut)
# 4. Project our models over studied area
myBiomomodProj <- BIOMOD_Projection(modeling.output = myBiomodModelOut,

```

```
new.env = myExpl,  
proj.name = 'current',  
xy.new.env = myRespCoord,  
selected.models = 'all',  
binary.meth = 'ROC',  
filtered.meth = 'TSS',  
compress = 'xz',  
clamping.mask = T,  
do.stack=T)  
  
# make some plots sub-selected by str.grep argument  
plot(myBiomomodProj, str.grep = 'MAXENT')
```
