

How to set up MAXENT to be run within **biomod2**

biomod2 version : 1.2.0
R version 2.15.2 (2012-10-26)

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November 5, 2012

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1 Introduction

This vignette explain how to configure your computer to run MAXENT within biomod2.

2 Java software

Given MAXENT is a java software, a Java interpreter needs to be installed on your computer. Skip the following step if Java is already installed on your machine. We consider here the three most usual OS (i.e. Windows, Linux and Mac OS).

2.1 Windows

These instructions concern Windows 7, but should work with former XP and 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 later is probably 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 on 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 run MAXENT you need a copy of the `maxent.jar` file in your working directory (where R and biomod2 will be run).

1. download MAXENT software at <http://www.cs.princeton.edu/~schapire/maxent/>
2. uncompress the downloaded file
3. put a copy `maxent.jar` file somewhere on your hard drive (in your working directory by default).

NOTE 5 :

If you don't put `maxent.jar` file in your working directory, you will have to fill the `path_to_maxent.jar` MAXENT options argument with the link to this file.

4 A little test

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

```

R input
# 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 MAXENT Mododelling options
myBiomodOption <- BIOMOD_ModelingOptions(
  MAXENT = list( path_to_maxent.jar = getwd(),
                 maximumiterations = 200,
                 visible = FALSE,
                 linear = TRUE,

```

```
        quadratic = TRUE,
        product = TRUE,
        threshold = TRUE,
        hinge = TRUE,
        lq2lqptthreshold = 80,
        l2lqthreshold = 10,
        hingethreshold = 15,
        beta_threshold = -1,
        beta_categorical = -1,
        beta_lqp = -1,
        beta_hinge = -1,
        defaultprevalence = 0.5))

# 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')
```
