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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Contents

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')
```