

rMyCoPortal Example application

Franz-Sebastian Krah

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```
setwd("~")
setwd("Documents/PhD/proj/high_priority/rMyCoPortal_paper/R/")
setwd("PATH/TO/FOLDER WITH THIS SCRIPT")
```

```
## Run first time to install R package
```

```
# install.packages("devtools")
# devtools::install_github("FranzKrah/rMyCoPortal")
```

Then, make sure you have Docker installed (<https://www.docker.com>)

```
## Load libraries
library("rMyCoPortal")
library("biomod2") # make sure maxent.jar is in the same folder if you want
# MaxEnt can be downloaded here https://biodiversityinformatics.amnh.org/open\_source/maxent/
library("sf")
library("raster")
```

```
## Let's download some data for the famous fly agaric
am.rec <- mycoportal(taxon = "Amanita muscaria") # please run again if server doesn't respond immediate
am.rec
```

Plot species distribution

```
# plot_distmap(x = x, mapdatabase = "world") # interactive version
p.dist <- plot_distmap(x = am.rec, mapdatabase = "state", interactive = FALSE) # the default is interactive
p.dist
```

Plot species heatmap for USA

```
p.heat <- plot_datamap(x = am.rec, mapdatabase = "state")
```

Climate suitability modelling

```
rec <- am.rec@records
rec <- rec[!(is.na(rec$lat) | is.na(rec$lon)), ]

rec <- st_as_sf(x = rec,
               coords = c("lon", "lat"),
               crs = "+proj=longlat +datum=WGS84")
```

```

## crop to USA
area = list(min_long = -130, max_long = -60, min_lat = 25, max_lat = 52)
rec <- st_crop(rec,
               xmin = area$min_long,
               ymin = area$min_lat,
               xmax = area$max_long,
               ymax = area$max_lat
)

rec <- SpatialPointsDataFrame(coords = st_coordinates(rec),
                             data = as.data.frame(rec))
rec <- as.data.frame(rec)

## Retrieve WorldClim data for current climatic data
clim <- raster::getData(name = "worldclim", res = "2.5", var = "bio")
clim <- crop(clim, extent(area$min_long, area$max_long, area$min_lat, area$max_lat))
clim <- stack(clim)

# the name of studied species
myRespName <- 'Amanita_muscaria'

# the XY coordinates of species data
myRespXY <- rec[,c("X","Y")]
myRespXY[] <- apply(myRespXY, 2, function(x) as.numeric(as.character(x)))

clim.coord <- coordinates(clim)
colnames(clim.coord) <- colnames(myRespXY)

# some pseudo absence data
samp <- sample(nrow(clim.coord), 1000)
myRespXY <- rbind(data.frame(myRespXY), clim.coord[samp,])

# the presence/absences data for our species
myResp <- c(rep(1, nrow(rec)), rep(0, length(samp)))

d <- duplicated(paste(myRespXY$X, myRespXY$Y))
myRespXY <- myRespXY[!d,]
myResp <- myResp[!d]

```

Create BIOMOD data and model

```

myBiomodData <- BIOMOD_FormatingData(resp.var = myResp,
                                     expl.var = clim,
                                     resp.xy = as.matrix(myRespXY),
                                     resp.name = myRespName,
                                     na.rm = TRUE)

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

## Computing the models
myBiomodModelOut <- BIOMOD_Modeling(

```

```

myBiomodData,
models = c("MAXENT.Phillips"),
models.options = myBiomodOption, NbRunEval=1,
DataSplit=80,
Prevalence=0.5,
VarImport=3,
models.eval.meth = c('ROC', "TSS"),
SaveObj = TRUE,
rescal.all.models = TRUE,
do.full.models = FALSE,
modeling.id = paste(myRespName,"FirstModeling",sep=""))

# get all models evaluation
myBiomodModelEval <- get_evaluations(myBiomodModelOut)

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

# print variable importances
barplot(get_variables_importance(myBiomodModelOut)[,,,], beside = TRUE, las = 2)

## Projection on current environmental conditions
myBiomodProj <- BIOMOD_Projection(
  modeling.output = myBiomodModelOut,
  new.env = clim,
  proj.name = 'current',
  selected.models = 'all',
  binary.meth = 'TSS',
  compress = 'xz',
  clamping.mask = F,
  output.format = '.grd')

plot(myBiomodProj)

```

Projection on future environmental conditions

```

cc85 <- raster::getData('CMIP5', var='bio', res=2.5, rcp=85, model='CC', year=70)
cc85 <- crop(cc85, extent(area$min_long, area$max_long, area$min_lat, area$max_lat))
cc85 <- stack(cc85)

names(cc85) <- names(clim)

myBiomodProjectionFuture <- BIOMOD_Projection(
  modeling.output = myBiomodModelOut,
  new.env = cc85,
  proj.name = 'future',
  selected.models = 'all',
  binary.meth = 'TSS',
  compress = 'xz',
  clamping.mask = F,
  output.format = '.grd')

```

```
plot(myBiomodProjectionFuture)
```