A brief tutorial on runing Maxent in R

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Contents

1. setup the working environment

1.1 load packages

```
library(dismo)
library(raster)
library(knitr)
knitr::opts_knit$set(root.dir = 'd:/projects/2017_7_workshop_enm_R')
```

1.2 set up the Maxent path

```
# download maxent.jar 3.3.3k, and place the file in the desired folder
utils::download.file(url="https://raw.githubusercontent.com/mrmaxent/Maxent/master/ArchivedReleases/3.3
                     mode="wb") ## wb for binary file, otherwise maxent.jar can not execute
# also note that both R and Java need to be the same bit (either 32 or 64) to be compatible to run
```

2. prepare data input

2.1 load environmental layers

```
# load GIS layers
clim <- list.files("data/bioclim/",pattern=".bil$",full.names = T)
clim <- stack(clim) ## stacking the bioclim variables to process them at one go
```

2.2 occurrence data

2.2.1 download occurrence data

```
# download occurrence data from GBIF
if(file.exists("data/occ_raw")){
  #cat(1)
  load("data/occ_raw")

}else{
  #cat(2)
  occ_raw <- gbif("Dasypus novemcinctus")
  save(occ_raw,file = "data/occ_raw")
  write.csv("data/occ_raw.csv")
}

#head(occ_raw)
```

2.2.2 clean occurrence data

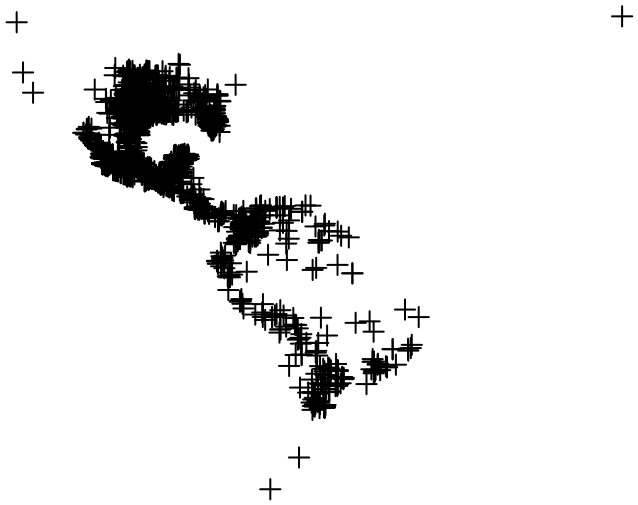
```
# remove bad coordinates, where either the lat or long coordinate is missing
occ_clean <- subset(occ_raw,(!is.na(lat))&(!is.na(lon)))
cat(nrow(occ_raw)-nrow(occ_clean), "records are removed")
```

```
## 2426 records are removed
```

```
# remove duplicated data based on latitude and longitude
dups <- duplicated(occ_clean[c("lat","lon")])
occ_unique <- occ_clean[!dups,]
cat(nrow(occ_clean)-nrow(occ_unique), "records are removed")
```

```
## 1506 records are removed
```

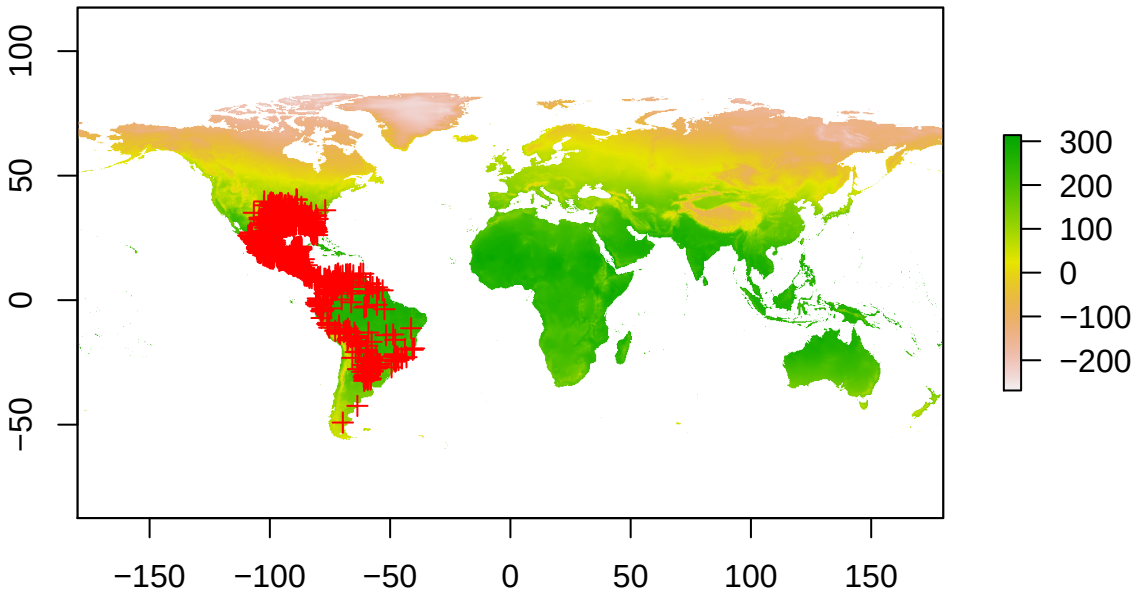
```
# make occ spatial
coordinates(occ_unique) <- ~ lon + lat
plot(occ_unique) ## we may notice an erroneous point
```



```
# remove some errors
occ_unique <- occ_unique[which(occ_unique$lon>-110 &
                                 occ_unique$lon < -40),]

# make occ sparse (keep one occ per cell)
cells <- cellFromXY(clim[[1]],occ_unique)
dups <- duplicated(cells)
occ_final <- occ_unique[!dups,]
cat(nrow(occ_unique)-nrow(occ_final), "records are removed")
```

```
## 1124 records are removed
```

```
plot(clim[[1]]) ## to draw the first layer (or replace [[1]] with any nth number of the layers with in t
plot(occ_final,add=T,col="red") ## the 'add=T' tells R to put the incoming data on the existing layer (t
```

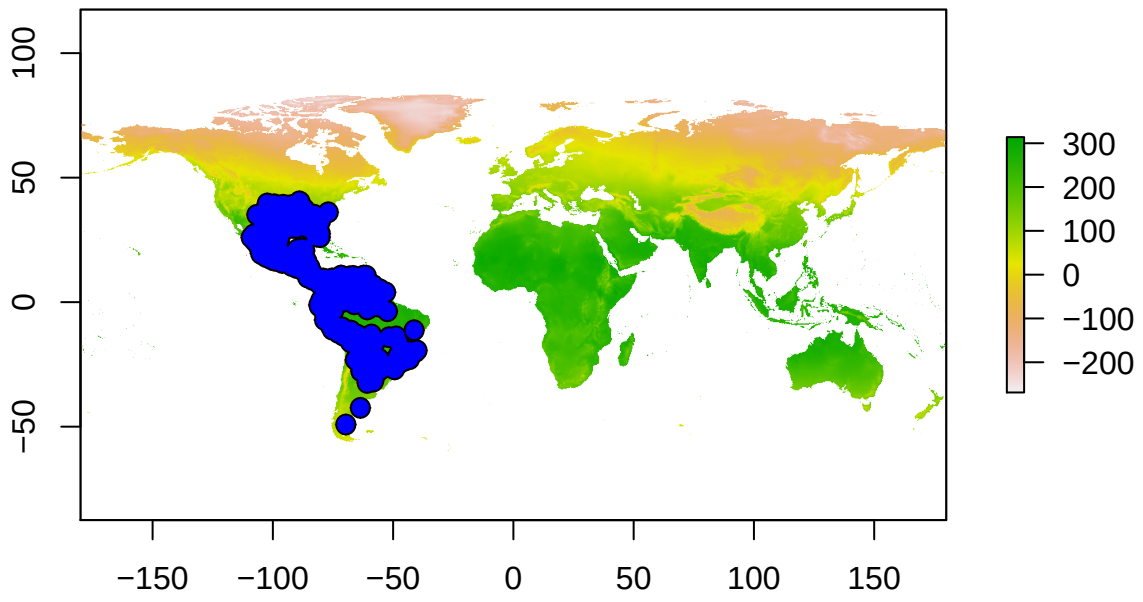


2.3 set up study area

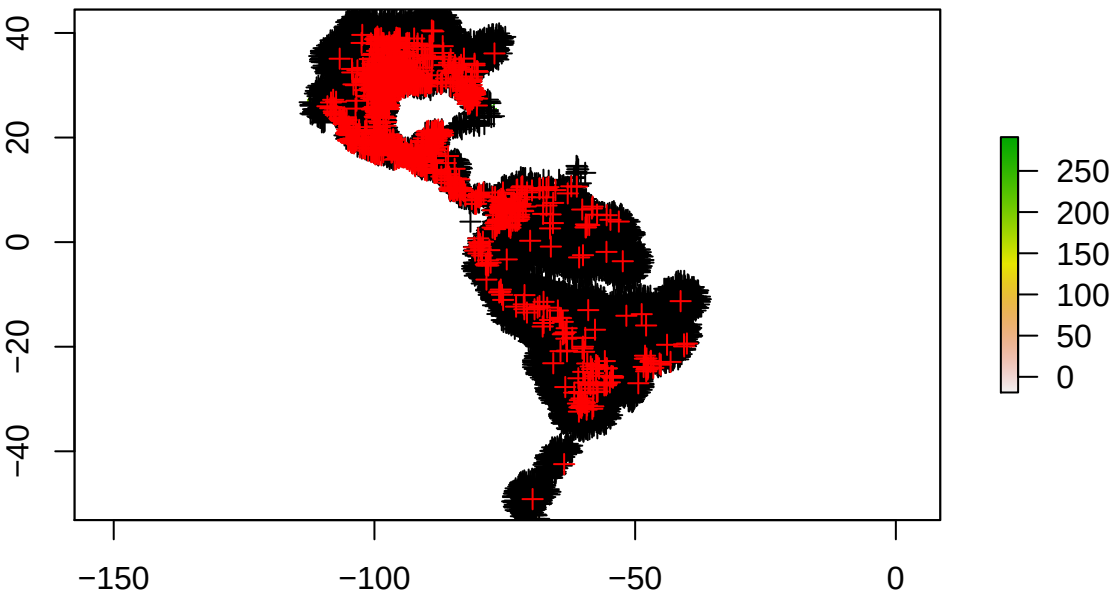
```
# this creates a buffer around the occurence data
occ_buff <- buffer(occ_final,4) ## 4 decimal degree
```

```
## Loading required namespace: rgeos
```

```
plot(clim[[1]]) ## this plots the first element ([[1]]) in the raster stack and adds the occurence data
plot(occ_final,add=T,col="red") ## this adds the occurrence data
plot(occ_buff,add=T,col="blue") ## this adds the buffer polygon
```




```
# if the area we will mask from is very large, use crop first; it will crop from a rectangle and then m
studyArea <- crop(clim,extent(occ_buff))  ## gives a coarser rectangle of the study area (a rectangle e

studyArea <- mask(studyArea,occ_buff) ## the 'study area' created by cropping and masking the raste sta

# save the buffer areas into raster files
writeRaster(studyArea,
            filename=paste0("data/studyarea/",names(studyArea),".asc"), ## a series of names for output
            format="ascii", ## the output format
            bylayer=TRUE, ## this will save a series of layers
            overwrite=T)

# select background points from this buffered area
set.seed(1) ## when the number provided to set.seed() function, the same random sample will be selected

bg <- sampleRandom(x=studyArea,
                   size=10000,
                   na.rm=T, ## na.rm is telling R to remove the 'Not Applicaple' points,
                   sp=T) ## sp is telling R to give us a spatially points
plot(studyArea[[1]])
plot(bg,add=T) ## add the background points to the plotted raster
plot(occ_final,add=T,col="red") ## add the occurrence data to the plottted raster
```



2.4 split occurrence data into training & testing

```
# randomly select 50% for training
set.seed(1) ## get the same random sample for training and testing
selected <- sample(1:nrow(occ_final),nrow(occ_final)*0.5)
occ_train <- occ_final[selected,] ## this is the selection
occ_test <- occ_final[-selected,] ## this is the opposite of the selection
```

2.5 format data for Maxent

```
# extracting env conditions for training occ from the raster stack; a data frame is returned
p <- extract(clim,occ_train) ## env conditions for training occ this makes a dataframe since environmen
p_test <- extract(clim,occ_test) ## env conditions for testing occ
a <- extract(clim,bg)  ## env conditions for background
pa <- c(rep(1,nrow(p)), rep(0,nrow(a))) ## repeat the number 1 as many numbers as the number of raws in
## (rep(1,nrow(p)) creating the number of rows as the p data set to have the number one as the indicato
## rep(0,nrow(a)) creating the number of rows as the a data set to have the number zero as the indicato
## The c combines these ones and zeros into a new vector that can be added to the Maxent table
pder <- as.data.frame(rbind(p,a)) ## this makes a data frame with the environmental attributes of the p
```

3 Maxent models

3.1 simple implementation

```
mod <- maxent(x=pder, ## env conditions
              p=pa,   ## 1:presence or 0:absence
              path=paste0(getwd(),"/maxent_outputs"), ## folder to store maxent output; if we do not sp
              args=c("responsecurves") ## a lot of parameters can be specified here
              )
```

```
## Loading required namespace: rJava
```

```
## the maxent functions runs a model in the default settings..to change these parameters, you have to t

# view a maxent model in a html brower
mod
```

```
## class    : MaxEnt
## variables: bio1 bio10 bio11 bio12 bio13 bio14 bio15 bio16 bio17 bio18 bio19 bio2 bio3 bio4 bio5 bio6
```

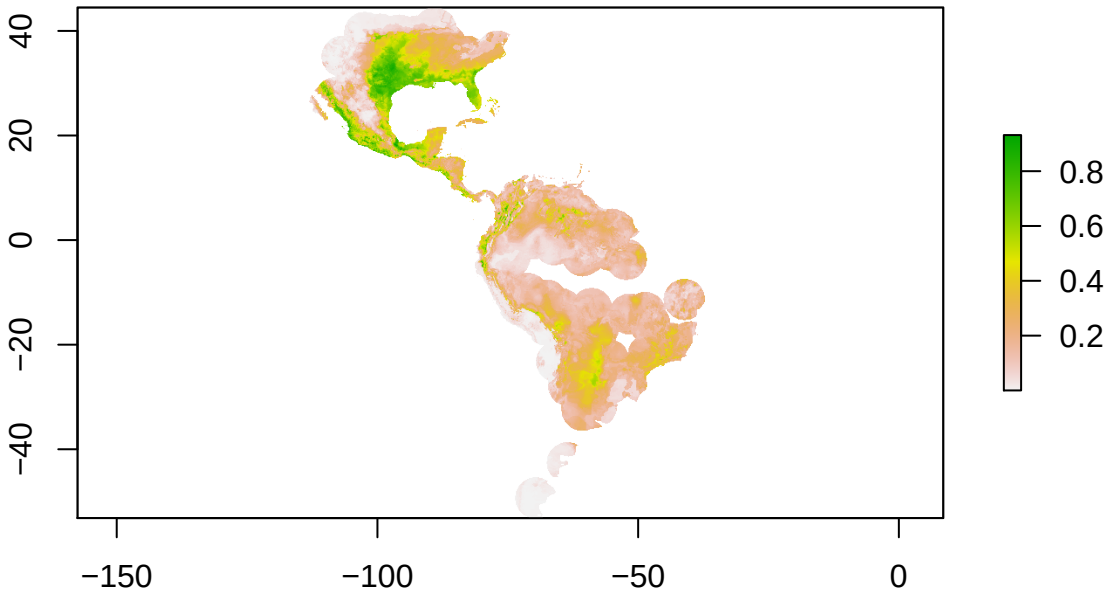
```
# view detailed results
mod@results
```

```
##                                                                 [,1]
## X.Training.samples                                          655.0000
## Regularized.training.gain                                     0.7265
## Unregularized.training.gain                                   0.9604
## Iterations                                                  500.0000
## Training.AUC                                                  0.8596
## X.Background.points                                       10575.0000
## bio1.contribution                                            17.1627
## bio10.contribution                                           20.4753
## bio11.contribution                                            8.7616
## bio12.contribution                                            8.4875
## bio13.contribution                                            1.8276
## bio14.contribution                                            0.7496
## bio15.contribution                                            9.2740
## bio16.contribution                                            0.6694
## bio17.contribution                                            0.6045
## bio18.contribution                                            0.9334
## bio19.contribution                                            0.9610
## bio2.contribution                                             1.0134
## bio3.contribution                                            15.1186
## bio4.contribution                                             1.3084
## bio5.contribution                                             8.2928
## bio6.contribution                                             3.3366
## bio7.contribution                                             0.3255
## bio8.contribution                                             0.1911
## bio9.contribution                                             0.5069
## bio1.permutation.importance                                  16.4025
## bio10.permutation.importance                                 10.6769
## bio11.permutation.importance                                  3.4186
## bio12.permutation.importance                                  7.1080
## bio13.permutation.importance                                  3.0867
## bio14.permutation.importance                                  3.9966
## bio15.permutation.importance                                 20.4166
```

```
## bio16.permutation.importance                                                    0.3416
## bio17.permutation.importance                                                    0.5438
## bio18.permutation.importance                                                    0.6744
## bio19.permutation.importance                                                    1.3227
## bio2.permutation.importance                                                     1.5541
## bio3.permutation.importance                                                     2.9937
## bio4.permutation.importance                                                    20.8722
## bio5.permutation.importance                                                     1.2303
## bio6.permutation.importance                                                     3.2102
## bio7.permutation.importance                                                     1.0008
## bio8.permutation.importance                                                     0.0737
## bio9.permutation.importance                                                     1.0766
## Entropy                                                                         8.5492
## Prevalence..average.of.logistic.output.over.background.sites.                   0.2410
## Fixed.cumulative.value.1.cumulative.threshold                                   1.0000
## Fixed.cumulative.value.1.logistic.threshold                                     0.0625
## Fixed.cumulative.value.1.area                                                   0.8119
## Fixed.cumulative.value.1.training.omission                                      0.0046
## Fixed.cumulative.value.5.cumulative.threshold                                   5.0000
## Fixed.cumulative.value.5.logistic.threshold                                     0.1355
## Fixed.cumulative.value.5.area                                                   0.6447
## Fixed.cumulative.value.5.training.omission                                      0.0229
## Fixed.cumulative.value.10.cumulative.threshold                                 10.0000
## Fixed.cumulative.value.10.logistic.threshold                                    0.1833
## Fixed.cumulative.value.10.area                                                  0.5157
## Fixed.cumulative.value.10.training.omission                                     0.0473
## Minimum.training.presence.cumulative.threshold                                  0.0200
## Minimum.training.presence.logistic.threshold                                    0.0054
## Minimum.training.presence.area                                                  0.9608
## Minimum.training.presence.training.omission                                     0.0000
## X10.percentile.training.presence.cumulative.threshold                          17.8502
## X10.percentile.training.presence.logistic.threshold                             0.2531
## X10.percentile.training.presence.area                                           0.3762
## X10.percentile.training.presence.training.omission                              0.0992
## Equal.training.sensitivity.and.specificity.cumulative.threshold                32.3187
## Equal.training.sensitivity.and.specificity.logistic.threshold                   0.3702
## Equal.training.sensitivity.and.specificity.area                                 0.2168
## Equal.training.sensitivity.and.specificity.training.omission                    0.2168
## Maximum.training.sensitivity.plus.specificity.cumulative.threshold             25.9220
## Maximum.training.sensitivity.plus.specificity.logistic.threshold                0.3177
## Maximum.training.sensitivity.plus.specificity.area                              0.2765
## Maximum.training.sensitivity.plus.specificity.training.omission                 0.1389
## Balance.training.omission..predicted.area.and.threshold.value.cumulative.threshold  2.0374
## Balance.training.omission..predicted.area.and.threshold.value.logistic.threshold    0.0965
## Balance.training.omission..predicted.area.and.threshold.value.area                  0.7536
## Balance.training.omission..predicted.area.and.threshold.value.training.omission     0.0076
## Equate.entropy.of.thresholded.and.original.distributions.cumulative.threshold  11.3240
## Equate.entropy.of.thresholded.and.original.distributions.logistic.threshold     0.1949
## Equate.entropy.of.thresholded.and.original.distributions.area                   0.4881
## Equate.entropy.of.thresholded.and.original.distributions.training.omission      0.0534
```

3.2 predict function

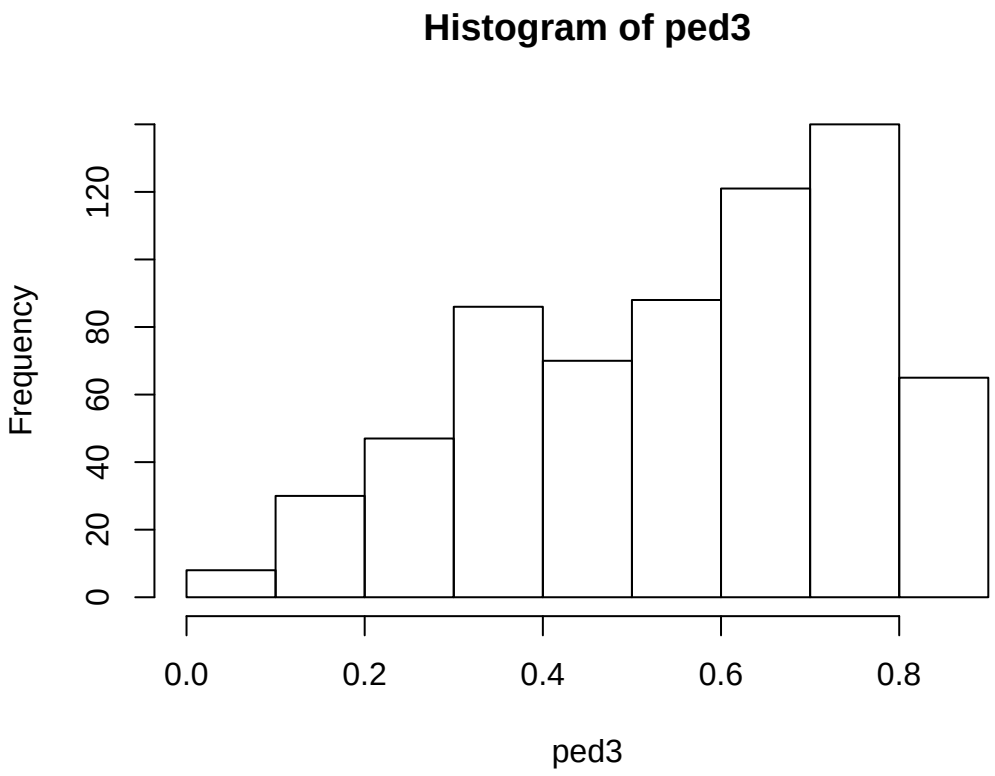
```
# maxent.R doesnt give us a prediction of training data/layers (unless you specify the projection layer
# a maxent model (in R) can be projected on raster layers or a dataframes

# example 1, project to out study area [raster]
ped1 <- predict(mod,studyArea)
plot(ped1)
```




```
# example 2, project to the world
#ped2 <- predict(mod,clim)
#plot(ped2)

# example 3, project training occurrences [dataframes]
ped3 <- predict(mod,p)
head(ped3)
```

```
## [1] 0.7553921 0.3420225 0.5019929 0.5993227 0.7655950 0.7684774
```

```
hist(ped3)
```



3.3 model evaluation

```
# using "training data" to evaluate
# "evaluate"" is an evaluation function from dismo package; p= presence and a=background
mod_eval_train <- dismo::evaluate(p=p,a=a,model=mod) #p & a are dataframes (the p and a are the trainin
print(mod_eval_train)
```

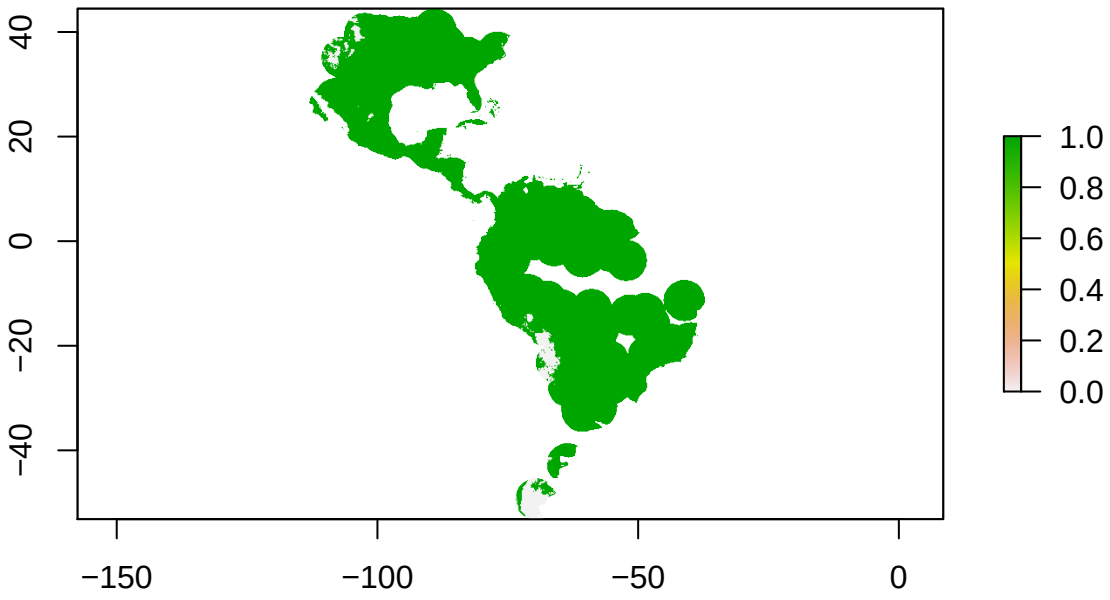
```
## class          : ModelEvaluation
## n presences    : 655
## n absences     : 10000
## AUC            : 0.8807075
## cor            : 0.4044683
## max TPR+TNR at : 0.3175671
```

```
# This is the test AUC
mod_eval_test <- dismo::evaluate(p=p_test,a=a,model=mod)
print(mod_eval_test) # training AUC may be higher than testing AUC
```

```
## class          : ModelEvaluation
## n presences    : 657
## n absences     : 10000
## AUC            : 0.8401474
## cor            : 0.3532565
## max TPR+TNR at : 0.3763733
```

```
# calculate thresholds of models
# threshold function is in dismo and based on the evaluation function
```

```r
thd1 <- threshold(mod_eval_train,"no_omission") # 0% omission rate [minimum training presence]
thd2 <- threshold(mod_eval_train,"spec_sens") # hiest TSS

# Only plot the predictions that are higher than the threshold....giving a binary output
plot(ped1>=thd1)  ## plotting points that are above the previously calculated tresholded value
```



4 Maxent parameters

4.1 select features

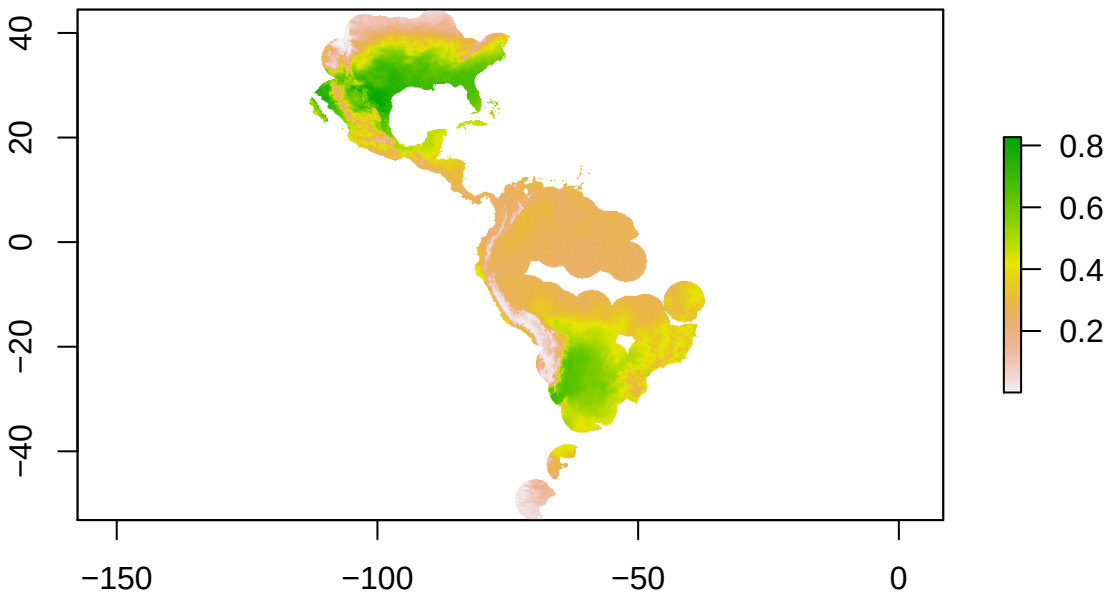
```r
# load the function that prepares parameters for maxent
source("code/Appendix2_prepPara.R")

mod1_autofeature <- maxent(x=pder[c("bio1","bio4","bio11")], ## env conditions, here we selected only 3
               p=pa, ## 1:presence or 0:absence
              path=paste0(getwd(),"/maxent_outputs1_auto"), ## path of maxent output, this is the folde
              args=prepPara(para_userfeatures=NULL) )  ## default is autofeature

# or select Linear& Quadratic features
mod1_lq <- maxent(x=pder[c("bio1","bio4","bio11")], ## env conditions, here we selected only 3 predicto
               p=pa, ## 1:presence or 0:absence
              path=paste0(getwd(),"/maxent_outputs1_lq"), ## path of maxent output, this is the folder
              args=prepPara(para_userfeatures="LQ") )  ## default is autofeature, here LQ represents Li
```

4.2 change beta-multiplier

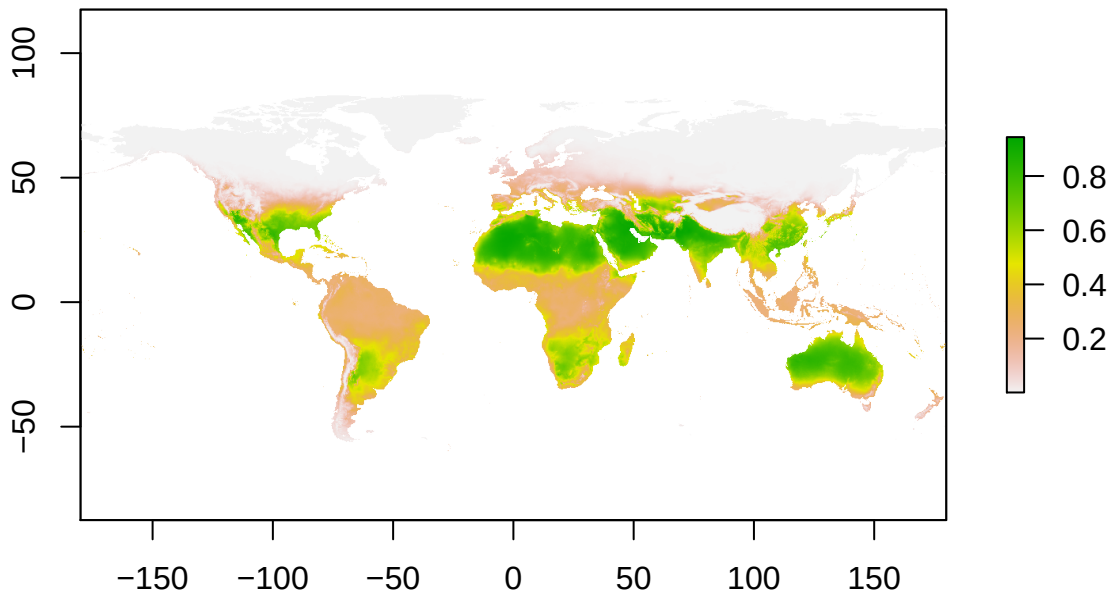
```
#change betamultiplier for all features
mod2 <- maxent(x=pder[c("bio1","bio4","bio11")],
               p=pa,
              path=paste0(getwd(),"/maxent_outputs2_o.5"),
              args=prepPara(para_userfeatures="LQ",
                            para_betamultiplier=0.5) )

mod2 <- maxent(x=pder[c("bio1","bio4","bio11")],
               p=pa,
              path=paste0(getwd(),"/maxent_outputs2_complex"),
              args=prepPara(para_userfeatures="LQH", ## include L, Q, H features
                            beta_lqp=1.5, ## use different betamultiplier for different features
                            beta_hinge=0.5 ) )
```

4.3 specify projection layers

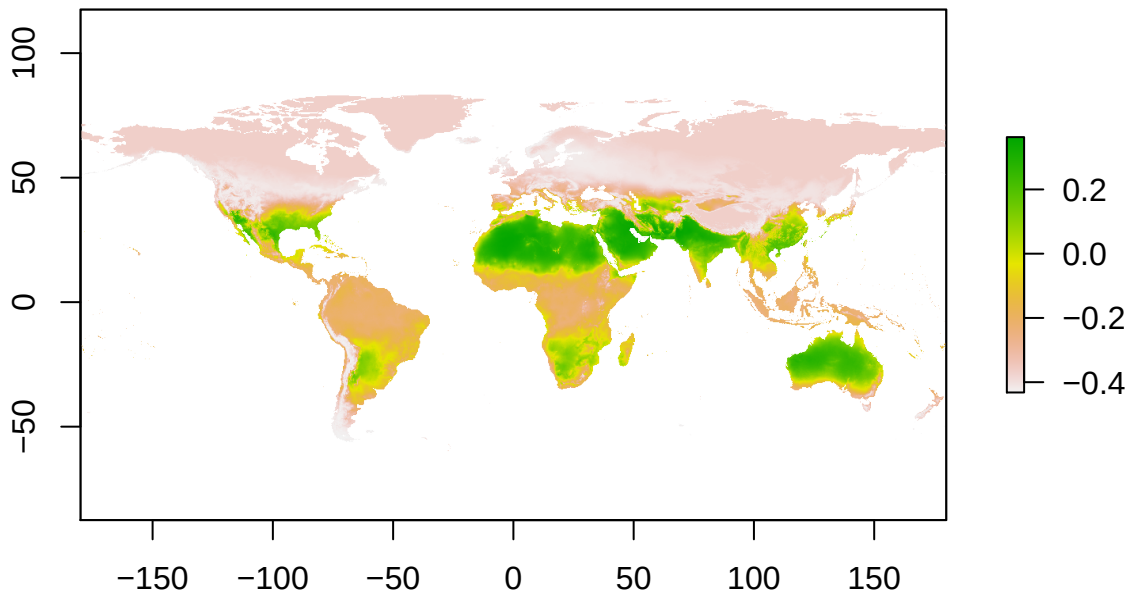
```
# note: 1)the projection layers must exist in the hard disk (as relative to computer RAM); (2) the name
mod3 <- maxent(x=pder[c("bio1","bio11")],
               p=pa,
              path=paste0(getwd(),"/maxent_outputs3_prj1"),
              args=prepPara(para_userfeatures="LQ",
                            para_betamultiplier=1,                      para_projectionlayers="D:/proje

# load the projected map
ped <- raster(paste0(getwd(),"/maxent_outputs3_prj1/species_studyarea.asc"))
plot(ped)
```




```
# we can also project on a broader map, but please caustion about the inaccuracy associated with model
mod3 <- maxent(x=pder[c("bio1","bio11")],
               p=pa,
              path=paste0(getwd(),"/maxent_outputs3_prj2"),
              args=prepPara(para_userfeatures="LQ",
                            para_betamultiplier=1,                    para_projectionlayers="D:/proje
# plot the map
ped <- raster(paste0(getwd(),"/maxent_outputs3_prj2/species_bioclim.asc"))
plot(ped)
```

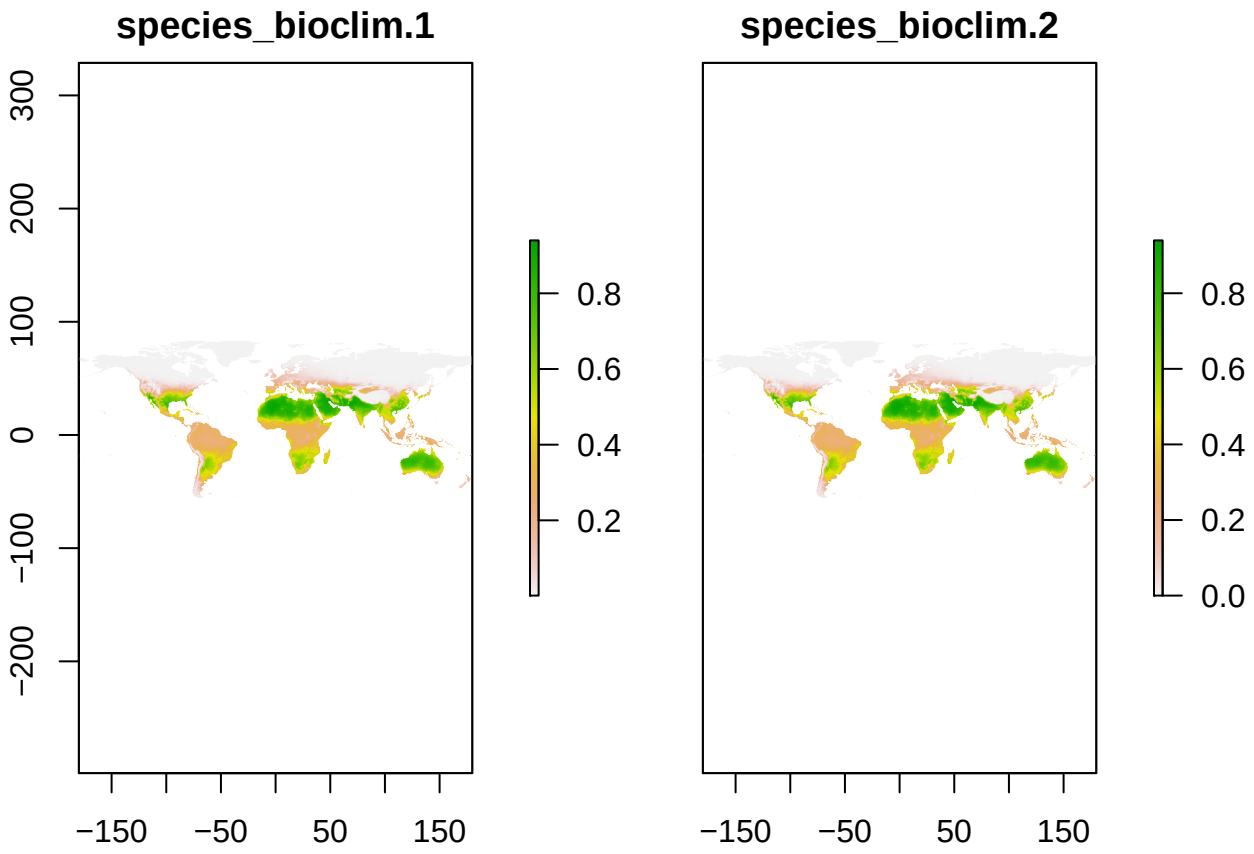



```
# simply check the difference if we used a different betamultiplier
mod3_beta1 <- maxent(x=pder[c("bio1","bio11")],
                p=pa,
               path=paste0(getwd(),"/maxent_outputs3_prj3"),
               args=prepPara(para_userfeatures="LQ",
                             para_betamultiplier=100, ## for an extreme example, set beta as 100
                             para_projectionlayers="D:/projects/2017_7_workshop_enm_R/data/bioclim") )
ped3 <- raster(paste0(getwd(),"/maxent_outputs3_prj3/species_bioclim.asc"))
plot(ped-ped3) ## quickly check the difference between the two predictions
```

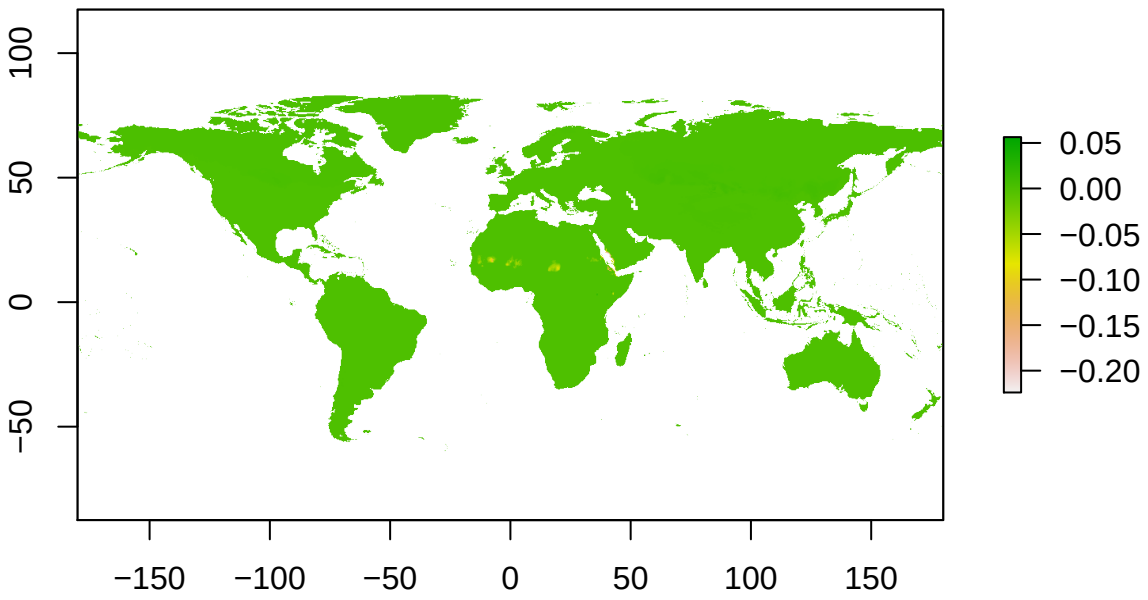


4.4 clamping function

```
# enable or disable clamping function; note clamping function is involved when projecting
mod4_clamp <- maxent(x=pder[c("bio1","bio11")],
                p=pa,
               path=paste0(getwd(),"/maxent_outputs4_clamp"),
               args=prepPara(para_userfeatures="LQ",
                             para_betamultiplier=1,
                             para_doclamp = TRUE,
                             para_projectionlayers="D:/projects/2017_7_workshop_enm_R/data/bioclim") )

mod4_noclamp <- maxent(x=pder[c("bio1","bio11")],
                p=pa,
               path=paste0(getwd(),"/maxent_outputs4_noclamp"),
               args=prepPara(para_userfeatures="LQ",
                             para_betamultiplier=1,
                             para_doclamp = FALSE,
                             para_projectionlayers="D:/projects/2017_7_workshop_enm_R/data/bioclim") )

ped_clamp <- raster(paste0(getwd(),"/maxent_outputs4_clamp/species_bioclim.asc") )
ped_noclamp <- raster(paste0(getwd(),"/maxent_outputs4_noclamp/species_bioclim.asc") )
plot(stack(ped_clamp,ped_noclamp))
```




```
plot(ped_clamp - ped_noclamp) ## we may notice small difference, especially clamp shows higher predicti
```


100
50
0
−50
−150
−100
−50
0
50
100
150
0.05
0.00
−0.05
−0.10
−0.15
−0.20