

Supplementary Data SD3. Script and plots used for estimate AUC, OR and AICc values with different feature classes and regularization multipliers in the models.

#Evaluating ecological niche of the genus Tympanoctomys and their species

#Line 8-118: Tympanoctomys

#Line 120-200: T. barrerae

#Line 230-330:T. kirchnerorum (current records)

#Genus Tympanoctomys

```
rm(list=ls())
```

```
library(sp)
```

```
library(raster)
```

```
library(dismo)# Needs maxent.jar in Java carpet
```

```
library(rJava)
```

```
library(rgdal)
```

```
library(maptools)
```

```
library(rgeos)
```

```
library(spam)
```

```
library(grid)
```

```
library(maps)
```

```
library(fields)
```

```
library(parallel)
```

```
library(ENMeval)
```

```
options(digits=5)
```

```
setwd("C:/Users/USUARIO/OneDrive/Spatial_ecology_RVR/PAPERS/JM/REVISION  
/Supplementary_files/Supplementary Data S3/Tympanoctomys")
```

#Configurating

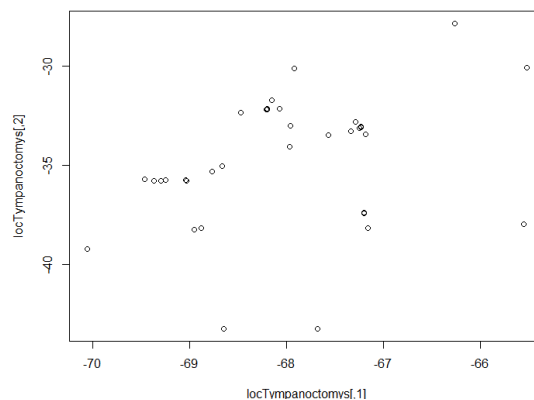
```
options(java.parameters = "-Xmx1g")
```

#Upload current ocurrences of the genus

```
Tympanoctomys <- read.csv("Tympanoctomys.csv",header=TRUE, sep=',',  
stringsAsFactors=F)
```

```
locTympanoctomys <- cbind(Tympanoctomys$x,Tympanoctomys$y)
```

```
plot(locTympanoctomys)
```



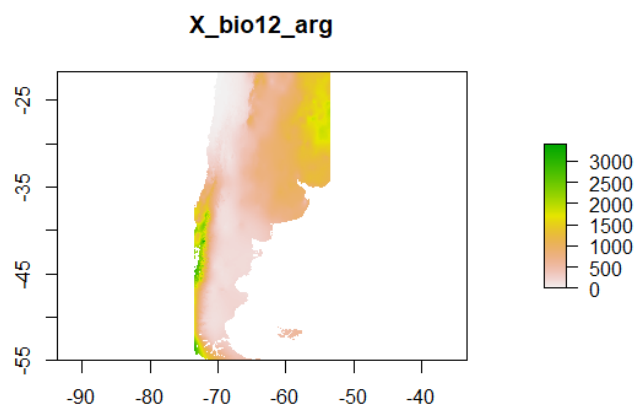
```
loc_Tympanoctomys <- list.files(pattern = "*.csv")
```

```
for (i in 1:length(loc_Tympanoctomys)) assign(loc_Tympanoctomys[i],
read.csv(loc_Tympanoctomys[i]))
```

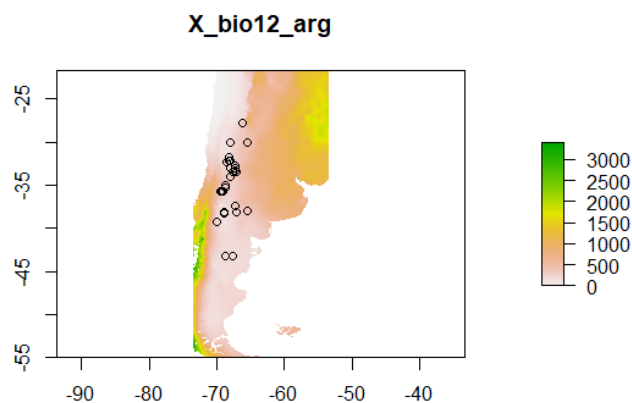
#Apply spatial thinning if exists GBIF data

#Import bioclimatic data (predictor variables)

```
env_layers <- list.files(pattern='asc', full.names=TRUE)
env_predictors <- stack(env_layers) # making a stack
projection(env_predictors) <- CRS('+proj=longlat +datum=WGS84 +no_defs
+ellps=WGS84 +towgs84=0,0,0')
env_predictors # resume
names(env_predictors) # names of vars
plot(env_predictors,1)
```



```
points(cbind(locTympanoctomys, pch=24,col='black',cex=0.7))
```



#Create a MCP

```
PolMC <- function (xy) {
  xy <- as.data.frame(coordinates(xy))
  coords.t <- chull(xy[, 1], xy[, 2]) #chull is from grDevices
  xy.bord <- xy[coords.t, ]
  xy.bord <- rbind(xy.bord[nrow(xy.bord), ], xy.bord)
  p <- SpatialPolygons(list(Polygons(list(Polygon(as.matrix(xy.bord))), 1)))
}
```

```
PMC_Tympanoctomys <- PolMC(locTympanoctomys) # Tympanoctomys barrerae
```

#Creating a buffer

```
Buff_PMC_Tympanoctomys <- gBuffer(PMC_Tympanoctomys, width = .9) # 0.9
degrees
```

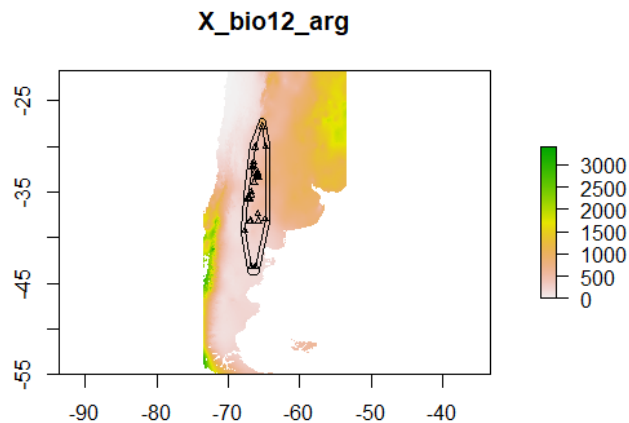
#All visualizations

```
plot(env_predictors,1)
```

```
plot(PMC_Tympanoctomys,add=T) # visualizar el PMC
```

```
plot(Buff_PMC_Tympanoctomys, add=T) # visualizar el PMC y su buffer
```

```
points(locTympanoctomys,pch=24,col='black',cex=0.5) # visualizar los puntos de
presencia de una especie
```



#Cutting environments from the buffer

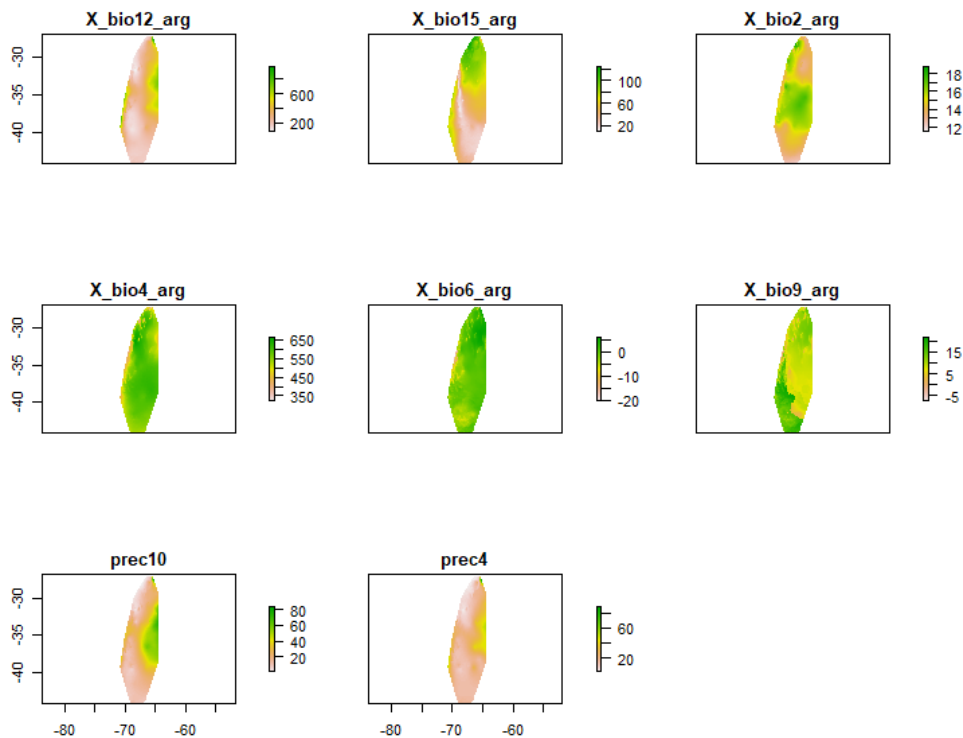
```
pred_Tympanoctomys_box <- crop(env_predictors,
```

```
extent(Buff_PMC_Tympanoctomys))
```

```
pred_Tympanoctomys <- mask(pred_Tympanoctomys_box,
```

```
Buff_PMC_Tympanoctomys)
```

```
plot(pred_Tympanoctomys) #visualize
```



#Saving

```
writeRaster(pred_Tympanoctomys,
"C:/Users/USUARIO/OneDrive/Spatial_ecology_RVR/PAPERS/JM/REVISION/Suppl
ementary_files/Supplementary Data SD3/Tympanoctomys/Tympanoctomys_vars",
bylayer=TRUE, format="ascii")
```

```
#Put maxent.jar file (from the downloaded software) in Rversion/dismo/java
```

```
#Creating range of settings, current environments
```

```
Tympanoctomys_test <- ENMevaluate(locTympanoctomys, pred_Tympanoctomys,
bg.coords = NULL,
RMvalues=seq(0.5, 4, 0.5), fc=c("L", "LQ", "LQH" ), method =
"block", overlap=F) # FC: (L)lineal, (Q)quadratic and (H)hinge
```

```
#### Running ENMevaluate using maxnet v.0.1.2 ####
```

```
## Doing evaluations using spatial blocks...
```

```
##|=====
=====| 100%
```

```
##ENMeval completed in 19 minutes 49.3 seconds.
```

```
metricsvalues_Tympanoctomys <- Tympanoctomys_test@results
metricsvalues_Tympanoctomys
```

```
#Write a table
```

```
write.table(metricsvalues_Tympanoctomys, file="metrics_Tympanoctomys.csv",
row.names=FALSE, col.names=TRUE)
metrics_Tympanoctomys <- read.csv("metrics_Tympanoctomys.csv",header=TRUE,
sep=',', stringsAsFactors=F)
```

```
#Checking results
```

```
Tympanoctomys_test@predictions #prediction proprieties
```

```
Tympanoctomys_test@occ.pts # presence points for the models
```

```
Tympanoctomys_test@bg.pts # background cells
```

```
# Which settings gave delta.AICc < 2?
```

```
aicmods <- which(Tympanoctomys_test@results$delta.AICc < 2)
```

```
Tympanoctomys_test@results[aicmods,]
```

```
##settings features rm train.AUC avg.test.AUC var.test.AUC avg.diff.AUC
var.diff.AUC
```

```
##3 LQH_0.5 LQH 0.5 0.9475394 0.626225 0.1072642 0.3206112
0.1280434
```

```
##avg.test.orMTP var.test.orMTP avg.test.or10pct var.test.or10pct AICc delta.AICc
w.AIC
```

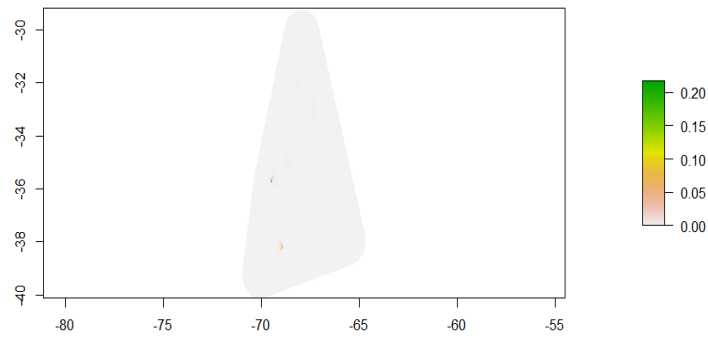
```
##3 0.4423077 0.1405325 0.625 0.09307199 1796.984 0 1
```

```
##parameters
```

```
##3 53
```

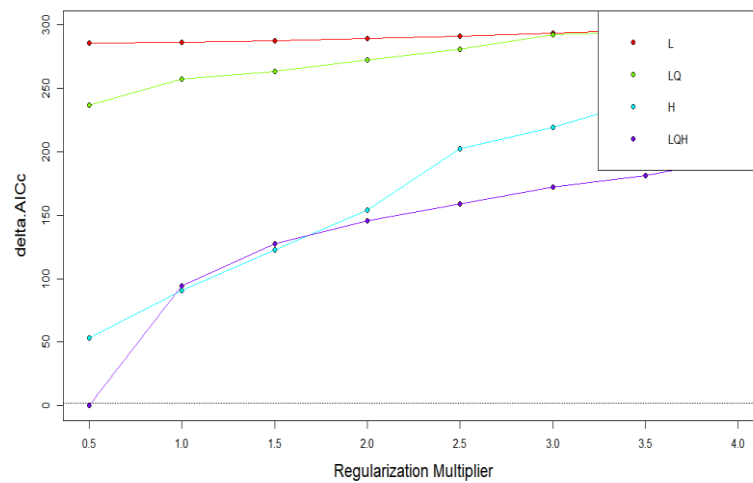
```
# View predictions in geographic space for these models
```

```
plot(Tympanoctomys_test@predictions[[aicmods]])
```



Plot delta.AICc Vs. RM's

eval.plot(Tympanoctomys_test@results)



#=====

#T. barrerae

rm(list=ls())

options(digits=5)

setwd("C:/Users/USUARIO/OneDrive/Spatial_ecology_RVR/PAPERS/JM/REVISION
/Supplementary_files/Supplementary Data S3/Tbarrerae")

library(sp)

library(raster)

library(dismo) # Needs maxent.jar in Java carpet

library(rJava)

library(rgdal)

library(maptools)

library(rgeos)

library(spam)

library(grid)

library(maps)

library(fields)

library(parallel)

library(ENMeval)

#Configurating

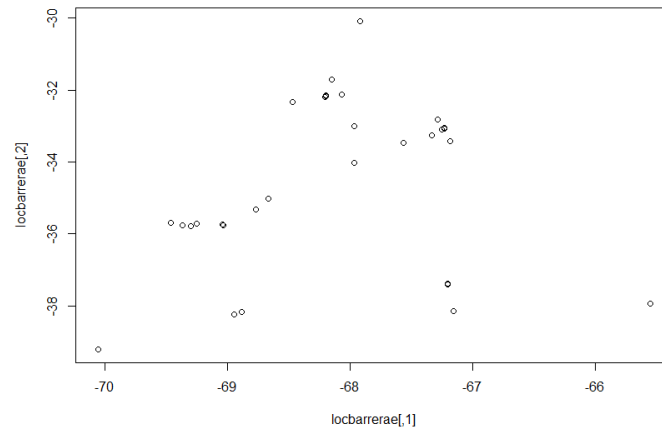
options(java.parameters = "-Xmx1g")

#Upload all occurrences of the species: T.barrerae

```
Tbarrerae <- read.csv("Tbarrerae.csv",header=TRUE, sep=',', stringsAsFactors=F)
```

```
locbarrerae <- cbind(Tbarrerae$x,Tbarrerae$y)
```

```
plot(locbarrerae)
```



```
loc_barrerae <- list.files(pattern = "*.csv")
```

```
for (i in 1:length(loc_barrerae)) assign(loc_barrerae[i], read.csv(loc_barrerae[i]))
```

#Apply spatial thinning if exists GBIF data

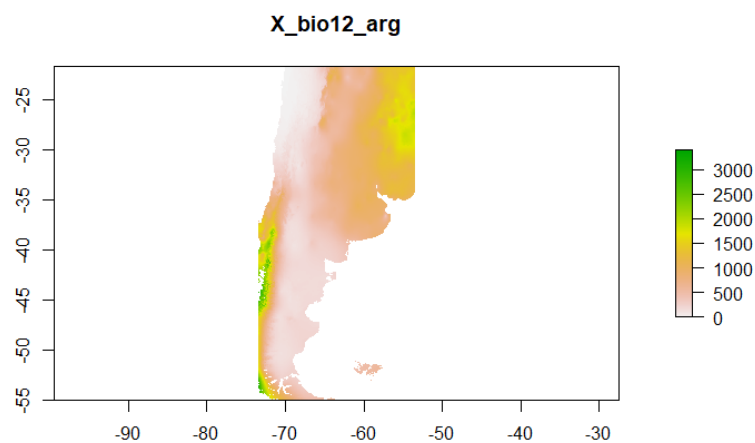
#Import bioclimatic data (predictor variables)

```
env_layers <- list.files(pattern='asc', full.names=TRUE)
```

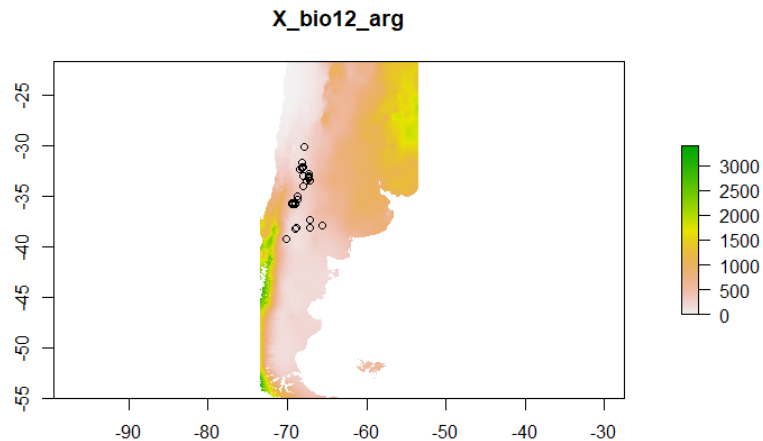
```
env_predictors <- stack(env_layers) # making a stack
```

```
projection(env_predictors) <- CRS('+proj=longlat +datum=WGS84 +no_defs  
+ellps=WGS84 +towgs84=0,0,0')
```

```
plot(env_predictors,1) # see that stack
```



```
points(cbind(locbarrerae, pch=24,col='black',cex=0.7))
```



#Create a MCP

```
PolMC <- function (xy) {
  xy <- as.data.frame(coordinates(xy))
  coords.t <- chull(xy[, 1], xy[, 2]) #chull is from grDevices
  xy.bord <- xy[coords.t, ]
  xy.bord <- rbind(xy.bord[nrow(xy.bord), ], xy.bord)
  p <- SpatialPolygons(list(Polygons(list(Polygon(as.matrix(xy.bord))), 1)))
}
```

```
PMC_barrerae <- PolMC(locbarrerae) # Tympanoctomys barrerae
```

#Creating a buffer

```
Buff_PMC_barrerae <- gBuffer(PMC_barrerae, width = .9) # 0.9 degrees
```

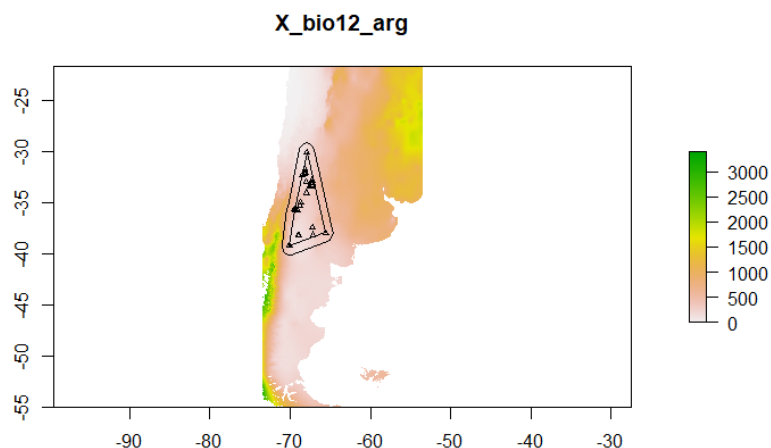
#All visualizations

```
plot(env_predictors,1)
```

```
plot(PMC_barrerae,add=T) # visualizar el PMC
```

```
plot(Buff_PMC_barrerae, add=T) # visualizar el PMC y su buffer
```

```
points(locbarrerae,pch=24,col='black',cex=0.5) # visualizar los puntos de presenica de una especie
```

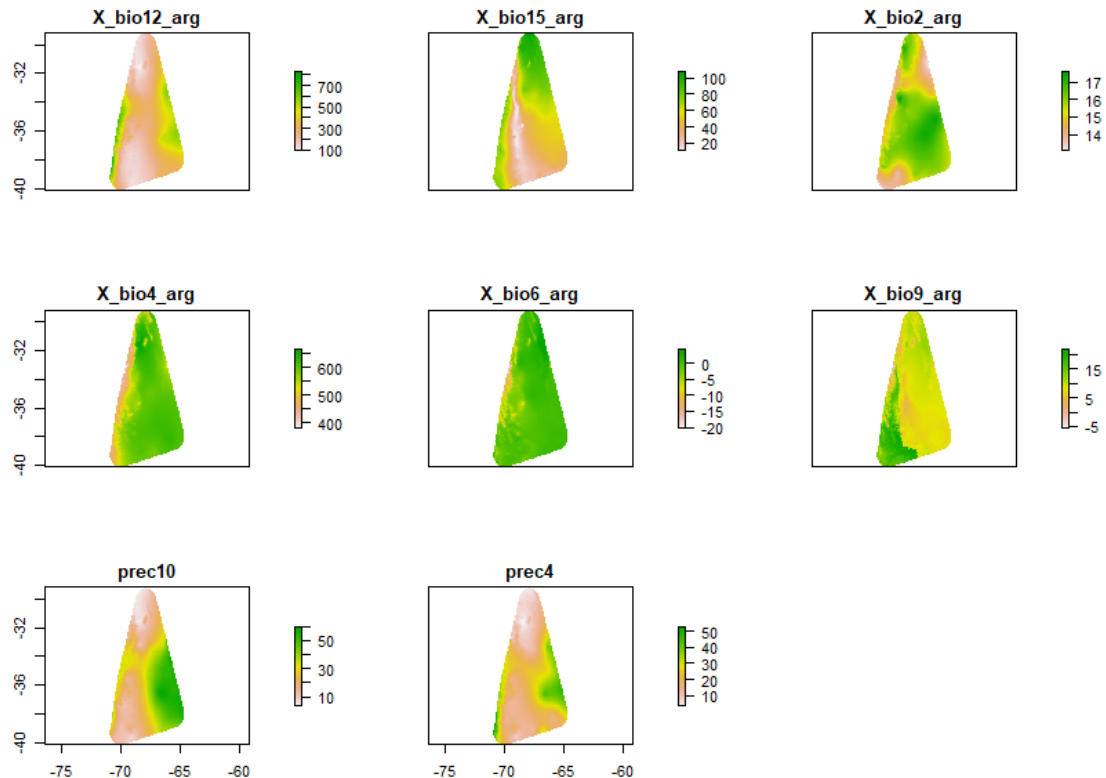


#Cutting environments from the buffer

```
pred_barrerae_box <- crop(env_predictors, extent(Buff_PMC_barrerae))
```

```
pred_barrerae <- mask(pred_barrerae_box, Buff_PMC_barrerae)
```

```
plot(pred_barrerae) # visualize
```



#Saving

```
writeRaster(pred_barrerae,
"C:/Users/USUARIO/OneDrive/Spatial_ecology_RVR/PAPERS/JM/REVISION/Suppl
ementary_files/Supplementary Data SD3/Tbarrerae/barrerae_vars", bylayer=TRUE,
format="ascii")
```

#Put maxent.jar file (from the downloaded software) in Rversion/dismo/java

#Creating range of settings

```
barrerae_test <- ENMevaluate(locbarrerae, pred_barrerae, bg.coords = NULL,
RMvalues=seq(0.5, 4, 0.5), fc=c("L", "LQ", "H", "LQH"), method =
"block", overlap=F) # FC: lineal, quadratic and hinge
```

*** Running ENMevaluate using maxnet v.0.1.2 ***

Doing evaluations using spatial blocks...

##|=====

| 100%

#ENMeval completed in 23 minutes 1.5 seconds.

```
metricsvalues_barrerae <- barrerae_test@results
```

```
metricsvalues_barrerae
```

#Write a table

```
write.table(metricsvalues_barrerae, file="metrics_barrerae.csv", row.names=FALSE,
col.names=TRUE)
```

```
metrics_barrerae <- read.csv("metrics_barrerae.csv",header=TRUE, sep=',',
stringsAsFactors=F)
```

```
View(metrics_barrerae)
```


#Checking results

barrerae_test@predictions #predicition proprieties

barrerae_test@occ.pts # presence points for the models

barrerae_test@bg.pts # background cells

Which settings gave delta.AICc < 2?

aicmods <- which(barrerae_test@results\$delta.AICc < 2)

barrerae_test@results[aicmods,]

##settings features rm train.AUC avg.test.AUC var.test.AUC avg.diff.AUC
var.diff.AUC

##4 LQH_0.5 LQH 0.5 0.9662 0.5378 0.030967 0.42826 0.030938

##avg.test.orMTP var.test.orMTP avg.test.or10pct var.test.or10pct AICc delta.AICc
w.AIC

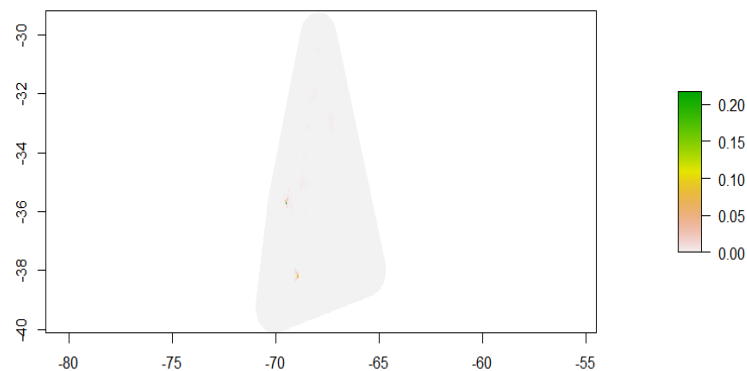
##4 0.53084 0.044381 0.80465 0.07307 1322.5 0 1

##parameters

##4 45

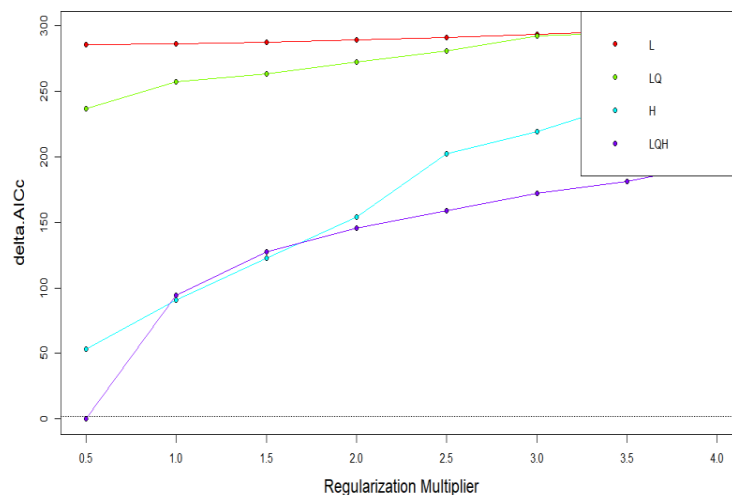
View predictions in geographic space for these models

plot(barrerae_test@predictions[[aicmods]])



Plot delta.AICc Vs. RM's

eval.plot(barrerae_test@results)

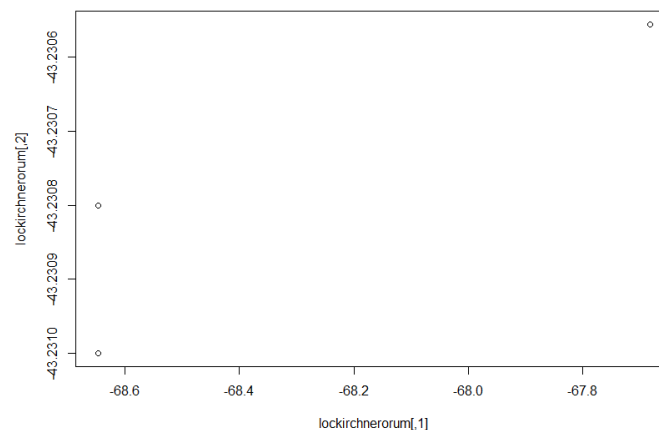


```

#=====
=====
#Species T. kirchnerorum with current records
rm(list=ls())
setwd("C:/Users/USUARIO/OneDrive/Spatial_ecology_RVR/PAPERS/JM/REVISION
/Supplementary_files/Supplementary Data S3/Tkirchnerorum")
library(sp)
library(raster)
library(dismo)# Needs maxent.jar in Java carpet
library(rJava)
library(rgdal)
library(maptools)
library(rgeos)
library(spam)
library(grid)
library(maps)
library(fields)
library(parallel)
library(ENMeval)
#Configurating
options(java.parameters = "-Xmx1g")

#Upload all ocurrences of the species: T.kirchnerorum
Tkirchnerorum <- read.csv("Tkirchnerorum.csv",header=TRUE, sep=',',
stringsAsFactors=F)
lockkirchnerorum <- cbind(Tkirchnerorum$x,Tkirchnerorum$y)
plot(lockkirchnerorum)

```



```

loc_kirchnerorum <- list.files(pattern = "*.csv")

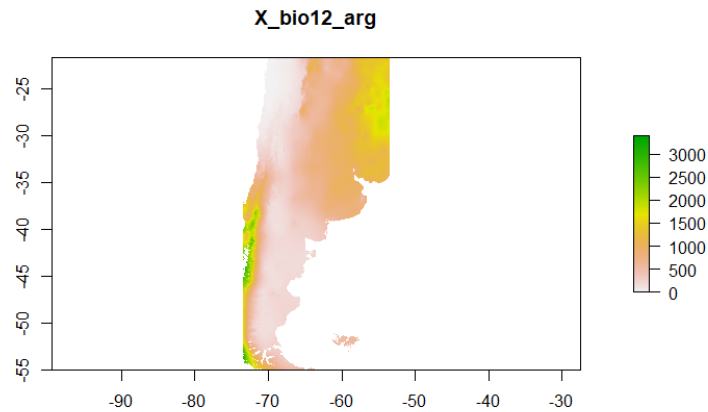
for (i in 1:length(loc_kirchnerorum)) assign(loc_kirchnerorum[i],
read.csv(loc_kirchnerorum[i]))

#Apply spatial thinning if exists GBIF data

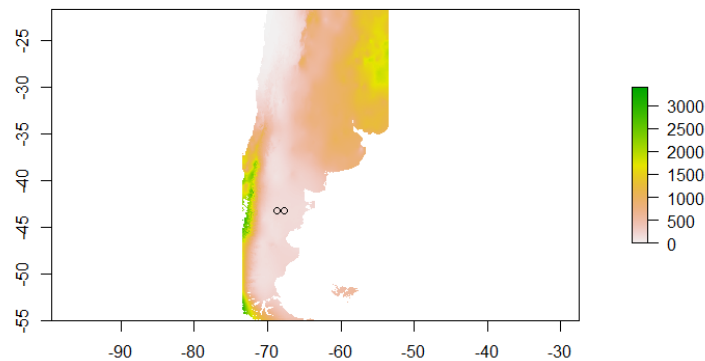
#Import bioclimatic data (predictor variables)
env_layers <- list.files(pattern='asc', full.names=TRUE)
env_predictors <- stack(env_layers) # making a stack

```

```
projection(env_predictors) <- CRS('+proj=longlat +datum=WGS84 +no_defs
+ellps=WGS84 +towgs84=0,0,0') # Características del stack
plot(env_predictors,1) # see that stack
```



```
points(cbind(lockkirchnerorum, pch=24,col='black',cex=0.7))
X_bio12_arg
```



#Create a MCP

```
PolMC <- function (xy) {
  xy <- as.data.frame(coordinates(xy))
  coords.t <- chull(xy[, 1], xy[, 2]) #chull is from grDevices
  xy.bord <- xy[coords.t, ]
  xy.bord <- rbind(xy.bord[nrow(xy.bord), ], xy.bord)
  p <- SpatialPolygons(list(Polygons(list(Polygon(as.matrix(xy.bord))), 1)))
}
```

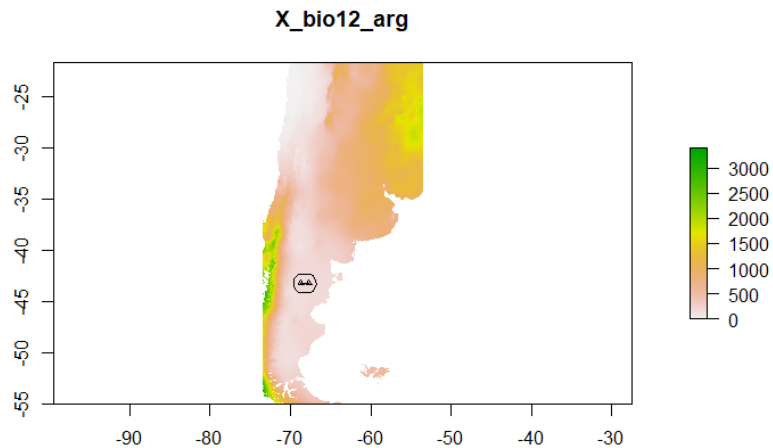
```
PMC_kirchnerorum <- PolMC(lockkirchnerorum) # Tympanoctomys kirchnerorum
```

#Creating a buffer

```
Buff_PMC_kirchnerorum <- gBuffer(PMC_kirchnerorum, width = .9) # 0.9 degrees
```

#All visualizations

```
plot(env_predictors,1)
plot(PMC_kirchnerorum,add=T) # visualizar el PMC
plot(Buff_PMC_kirchnerorum, add=T) # visualizar el PMC y su buffer
points(lockkirchnerorum,pch=24,col='black',cex=0.5) # visualizar los puntos de
presencia de una especie
```

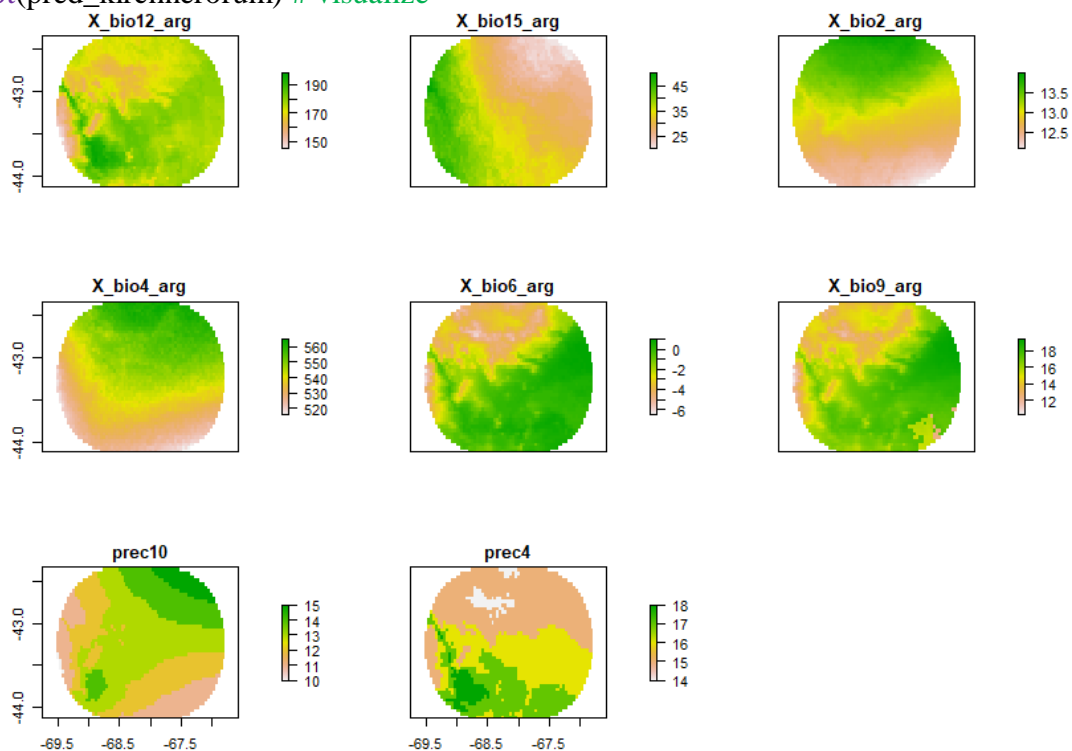


#Cutting environments from the buffer

```
pred_kirchnerorum_box <- crop(env_predictors, extent(Buff_PMC_kirchnerorum))
```

```
pred_kirchnerorum <- mask(pred_kirchnerorum_box, Buff_PMC_kirchnerorum)
```

```
plot(pred_kirchnerorum) # visualize
```



#Saving

```
writeRaster(pred_kirchnerorum,
"C:/Users/USUARIO/OneDrive/Spatial_ecology_RVR/PAPERS/JM/REVISION/Suppl
ementary_files/Supplementary Data SD3/Tkirchnerorum/kirchnerorum_vars",
bylayer=TRUE, format="ascii")
```

#Put maxent.jar file (from the downloaded software) in Rversion/dismo/java

#Creating range of settings

```
kirchnerorum_test <- ENMevaluate(lockkirchnerorum, pred_kirchnerorum, bg.coords =
NULL,
```

```
RMvalues=seq(0.5, 4, 0.5), fc=c("L","LQ" ), method = "block",
overlap=F) # FC: lineal, quadratic and hinge
```

##*** Running ENMevaluate using maxnet v.0.1.2 ***

```
## Doing evaluations using spatial blocks...
##|=====
=====| 100%
##ENMeval completed in 2 minutes 45.6 seconds.
```

```
metricsvalues_kirchnerorum <- kirchnerorum_test@results
metricsvalues_kirchnerorum
```

```
#Write a table
```

```
write.table(metricsvalues_kirchnerorum, file="metrics_kirchnerorum_jackknife.csv",
row.names=FALSE, col.names=TRUE)
```

```
#Checking results
```

```
kirchnerorum_test@predictions #predicition proprieties
kirchnerorum_test@occ.pts # presence points for the models
kirchnerorum_test@bg.pts # background cells
```

```
# Which settings gave delta.AICc < 2?
```

```
aicmods <- which(kirchnerorum_test@results$delta.AICc < 2)
```

```
kirchnerorum_test@results[aicmods,]
```

```
##settings features rm train.AUC avg.test.AUC var.test.AUC avg.diff.AUC
var.diff.AUC
```

```
##16 LQ_4 LQ 4 0.9688296 0.8861396 0.07161257 0.08234086
0.06102016
```

```
##avg.test.orMTP var.test.orMTP avg.test.or10pct var.test.or10pct AICc delta.AICc
```

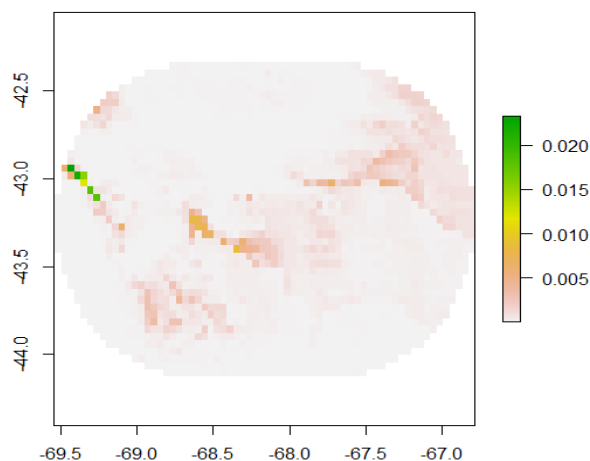
```
##16 0.125 0.0625 0.125 0.0625 127.6252 0
```

```
##w.AIC parameters
```

```
##16 0.8776257 5
```

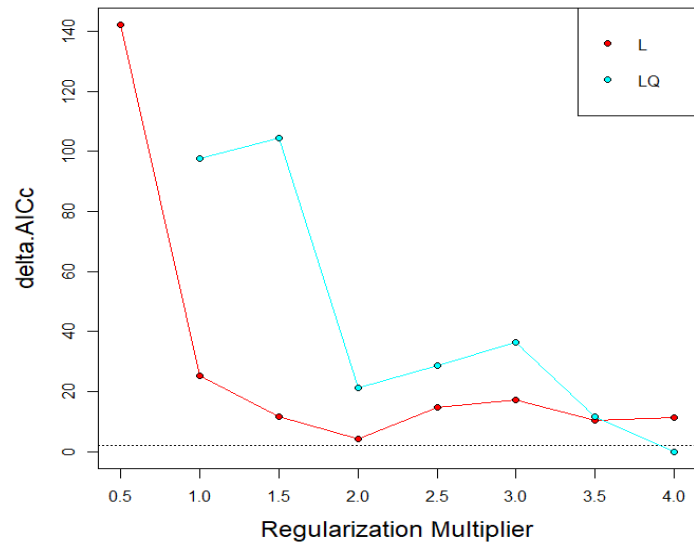
```
# View predictions in geographic space for these models
```

```
plot(kirchnerorum_test@predictions[[aicmods]])
```



```
# Plot delta.AICc Vs. RM's
```

```
eval.plot(kirchnerorum_test@results)
```



#=====