#####################

### BIOMOD2 SCRIPT###

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library(reshape)

library(biomod2)

library(gam)

library(rgdal)

library(raster)

library(sp)

DataSpecies<-read.csv("Presence.data.csv")

myRespName<-"Species"

myResp<-as.numeric(DataSpecies[,"Species"])

myRespXY<-DataSpecies[,c('Longitude','Latitude')]

layers<-list.files(path='path/Current Env Layers',pattern='tif$',full.names=TRUE)

layers

myExpl=raster::stack(layers)

myBiomodData<-BIOMOD\_FormatingData(resp.var=myResp,expl.var=myExpl,resp.xy=myRespXY,resp.name=myRespName)

myBiomodData

Print\_Default\_ModelingOptions()

myBiomodOption<-BIOMOD\_ModelingOptions(GLM = list( ),

GAM = list( ),

GBM = list( ),

CTA = list( ),

ANN = list( ),

SRE = list( ),

FDA = list( ),

MARS = list( ),

RF = list( ),

MAXENT.Phillips= list(path\_to\_MAXENT.Phillips.jar = 'path/maxent.jar',

memory\_allocated = 512))

myBiomodOption

myBiomodModelOut<-BIOMOD\_Modeling(

myBiomodData,

models=c('GLM','GBM','GAM','CTA','ANN','SRE','FDA','MARS','RF','MAXENT.Phillips'),

models.options = myBiomodOption,

NbRunEval = 3,

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=''))

myBiomodModelOut

myBiomodModelEval<-get\_evaluations(myBiomodModelOut)

dimnames(myBiomodModelEval)

myBiomodModelEval['ROC',"Testing.data",,,]

myBiomodModelEval['TSS',"Testing.data",,,]

modelscores <- models\_scores\_graph( myBiomodModelOut,

by = 'models',

metrics = c('ROC','TSS') )

get\_variables\_importance(myBiomodModelOut)

##Ensemble modeling - chose evaluation metric

myBiomodEM<-BIOMOD\_EnsembleModeling(

modeling.output = myBiomodModelOut,

chosen.models = 'all',

em.by = 'all',

eval.metric = c('ROC'),

eval.metric.quality.threshold =c(0.81),

prob.mean=T,

prob.cv=T,

prob.ci=T,

prob.ci.alpha=0.05,

prob.median=T,

committee.averaging = T,

prob.mean.weight = T,

prob.mean.weight.decay = 'proportional')

myBiomodEM

get\_evaluations(myBiomodEM)

##PROJECTION - choose binary/filtered method - can add "filtered.meth='TSS',"

myBiomodProj<-BIOMOD\_Projection(

modeling.output=myBiomodModelOut,

new.env = myExpl,

proj.name='current',

selected.models = 'all',

binary.meth = 'ROC',

compress='TRUE',

build.clamping.mask=FALSE)

myBiomodProj

myCurrentProj<-get\_predictions(myBiomodProj)

myCurrentProj

##Can then do future projections

FutureLayers<-list.files(path='LGM',pattern='tif',full.names=TRUE)

FutureLayers

myExplFuture=stack(FutureLayers)

myBiomodModelOut

myBiomodProjFuture<-BIOMOD\_Projection(modeling.output = myBiomodModelOut,

new.env = myExplFuture,

proj.name = 'future',

selected.models = 'all',

binary.meth = 'ROC',

compress = 'xz',

clamping.mask=TRUE,

output.format='.grd')

myFutureProj<-get\_predictions(myBiomodProjFuture)

myFutureProj

##Ensemble Forcasting Current

myBiomodEF <- BIOMOD\_EnsembleForecasting(EM.output = myBiomodEM,

projection.output = myBiomodProj)

myBiomodEF

myBiomodEFgraph<-get\_predictions(myBiomodEF)

names(myBiomodEFgraph)

plot(yBiomodEFgraph)

##Ensemble Forcasting (2070 RCP2.6)

FutureLayers26<-list.files(path='2.6',pattern='tif',full.names=TRUE)

FutureLayers26

myExplFuture26=stack(FutureLayers26)

myBiomodModelOut

myBiomodProjFuture26<-BIOMOD\_Projection(modeling.output = myBiomodModelOut,

new.env = myExplFuture26,

proj.name = 'future2',

selected.models = 'all',

binary.meth = 'ROC',

compress = 'xz',

clamping.mask=TRUE,

output.format='.grd')

myFutureProj26<-get\_predictions(myBiomodProjFuture26)

myFutureProj26

myBiomodEFfuture26<- BIOMOD\_EnsembleForecasting(EM.output = myBiomodEM,

projection.output = myBiomodProjFuture26)

myBiomodEFfuture26

myBiomodEFfuturegraph26<-get\_predictions(myBiomodEFfuture26)

names(myBiomodEFfuturegraph26)

plot(myBiomodEFfuturegraph26)

##Ensemble Forcasting (2070 RCP8.5)

FutureLayers85<-list.files(path='8.5',pattern='tif',full.names=TRUE)

FutureLayers85

myExplFuture85=stack(FutureLayers85)

myBiomodModelOut

myBiomodProjFuture85<-BIOMOD\_Projection(modeling.output = myBiomodModelOut,

new.env = myExplFuture85,

proj.name = 'future5',

selected.models = 'all',

binary.meth = 'ROC',

compress = 'xz',

clamping.mask=TRUE,

output.format='.grd')

myFutureProj85<-get\_predictions(myBiomodProjFuture85)

myFutureProj85

myBiomodEFfuture85<- BIOMOD\_EnsembleForecasting(EM.output = myBiomodEM,

projection.output = myBiomodProjFuture85)

myBiomodEFfuture85

myBiomodEFfuturegraph5<-get\_predictions(myBiomodEFfuture85)

names(myBiomodEFfuturegraph85)

plot(myBiomodEFfuturegraph85)

##Estimate change in range

currentPred<-raster("Species/Species/proj\_current/proj\_current\_Species\_ROCbin.grd")

future2Pred <- raster("Species/Species/proj\_future2/proj\_future2\_Species\_ROCbin.grd")

future5Pred<-raster("Species/Species/proj\_future5/proj\_future5\_Species\_ROCbin.grd")

breaks=c(-0,1)

cols=rep("grey87",1)

cols[2]="steelblue4"

plot(currentPred,c(7),xlim=c(165,180),ylim=c(-48,-34),col=cols)

myBiomodRangeSize26 <- BIOMOD\_RangeSize(

CurrentPred=currentPred,

FutureProj=future26Pred)

myBiomodRangeSize26$Compt.By.Models

plot(myBiomodRangeSize26$Diff.By.Pixel,col=cols)

myBiomodRangeSize85 <- BIOMOD\_RangeSize(

CurrentPred=currentPred,

FutureProj=future85Pred)

myBiomodRangeSize85$Compt.By.Models

plot(myBiomodRangeSize85$Diff.By.Pixel,col=cols)

##PATCHSTATS

library(SDMTools)

library(igraph)

library(raster)

library(xlsx)

library(openxlsx)

currentPred2<-raster("Species/Species/proj\_current/proj\_current\_Species\_ROCbin.grd")

one<-clump(currentPred2,directions=8,gaps=FALSE)

f<-freq(one)

f<-as.data.frame(f)

str(which(f$count<=100))

str(f$value[which(f$count<=100)])

excludeID<-f$value[which(f$count<=100)]

formaskSieve<-one

formaskSieve[one %in% excludeID]<-NA

maskfreq<- freq(formaskSieve)

hist(maskfreq)

values(formaskSieve)[values(formaskSieve)>0]<-1

summary(formaskSieve)

formaskSieve

one<-clump(formaskSieve,directions=8,gaps=FALSE)

cl.data1=ClassStat(formaskSieve,bkgd=NA)

cl.data1

write.xlsx(cl.data1, "Species Current classstat.xlsx")

future2Pred <- raster("Species/Species/proj\_future2/proj\_future2\_Species\_ROCbin.grd")

one<-clump(future2Pred,directions=8,gaps=FALSE)

f<-freq(one)

f<-as.data.frame(f)

str(which(f$count<=100))

str(f$value[which(f$count<=100)])

excludeID<-f$value[which(f$count<=100)]

formaskSieve<-one

formaskSieve[one %in% excludeID]<-NA

maskfreq<- freq(formaskSieve)

hist(maskfreq)

values(formaskSieve)[values(formaskSieve)>0]<-1

summary(formaskSieve)

formaskSieve

one<-clump(formaskSieve,directions=8,gaps=FALSE)

cl.data1=ClassStat(formaskSieve,bkgd=NA)

cl.data1

write.xlsx(cl.data1, "Species rcp26 classstat.xlsx")

future5Pred <- raster("Species/Species/proj\_future5/proj\_future5\_Species\_ROCbin.grd")

one<-clump(future5Pred,directions=8,gaps=FALSE)

f<-freq(one)

f<-as.data.frame(f)

str(which(f$count<=100))

str(f$value[which(f$count<=100)])

excludeID<-f$value[which(f$count<=100)]

formaskSieve<-one

formaskSieve[one %in% excludeID]<-NA

maskfreq<- freq(formaskSieve)

hist(maskfreq)

values(formaskSieve)[values(formaskSieve)>0]<-1

summary(formaskSieve)

formaskSieve

one<-clump(formaskSieve,directions=8,gaps=FALSE)

cl.data1=ClassStat(formaskSieve,bkgd=NA)

cl.data1

write.xlsx(cl.data1, "Species rcp85 classstat.xlsx")