Modeling ecologically different species

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First, use the following commands to avoid Java errors:

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

Then load *dismo* and other necessary packages:

```
library(raster)
library(rgdal)
library(rgeos)
library(spocc)
library(spThin)
library(dismo)
library(ENMeval)
library(dplyr)
library(maps)
```

Now loading occurence data:

```
spp <- c('Cassia ferruginea','Myrcia silvatica', 'Scinax nebulosus','Sclerurus cearensis')
colors <- c('green','orange','purple','blue')
occs.xy <- list()
occs.xy[[1]] <- read.csv("data/occs/cassia_ferruginea.csv")
occs.xy[[2]] <- read.csv("data/occs/myrcia_silvatica.csv")
occs.xy[[3]] <- read.csv("data/occs/s_nebulosus.csv")
occs.xy[[4]] <- read.csv("data/occs/s_cearensis.csv")
enclaves_extent <- extent(-41, -34,-8,-2)
for (i in 1:length(occs.xy)) {
  colnames(occs.xy[[i]]) <- c('longitude','latitude')
  sp::coordinates(occs.xy[[i]]) <- ~ longitude + latitude
  occs.xy[[i]] <- crop(occs.xy[[i]],enclaves_extent)
}
```

Reading environmental data, BR shapefiles and setting other geographical boundaries:

```
br <- crop(readOGR(dsn = 'data/br/', layer = 'br'),enclaves_extent)
# Getting environmental data
env <- list()
periods.names <- c('Present','Late Holocene (0.3 - 4.2 ka)','Middle Holocene (4.2 - 8.326 ka) ',
             'Early Holocene (8.326 - 11.7 ka)','Younger Dryas Stadial (11.7 ka - 12.9 ka)',
```

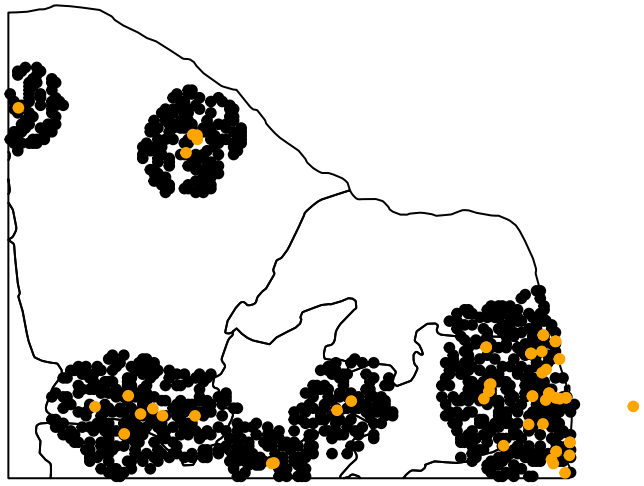
```
             'Bølling-Allerød (12.9 ka - 14.7 ka)','Heinrich Stadial 1 (14.7 ka - 17 ka)',
             'Last Glacial Maximum (ca. 21 ka)','Last Interglacial (ca. 130 ka)')
periods <- c('01_cur','02_LH','03_MH','04_EH','05_YDS','06_BA','07_HS','08_LGM','09_LIG')
folders <- list.dirs('data/bioclim')[-1]
for (i in 1:length(folders)) {
  env[[i]] <- crop(stack(list.files(path = paste0(folders[i]), pattern = ".tif$", full.names = T)),
                   enclaves_extent)
}
```

Getting background points through minimum convex polygon:

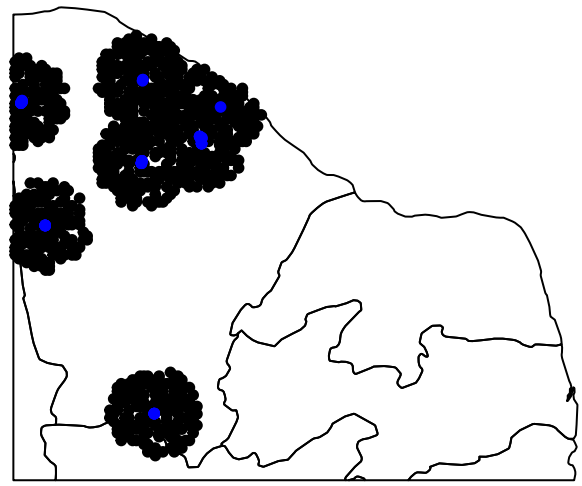
```
# Creating empty lists
bgExt <- list()
envsBgMsk <- list()
bg.xy <- list()

for (i in 1:length(occs.xy)) {
  bgExt[[i]] <- rgeos::gBuffer(occs.xy[[i]], width = 0.5)

  # mask the environmental rasters by the background extent shape
  envsBgMsk[[i]] <- raster::mask(env[[1]], bgExt[[i]])
  bg.xy[[i]] <- dismo::randomPoints(envsBgMsk[[i]], 1000)
  # convert matrix output to data frame
  bg.xy[[i]] <- as.data.frame(bg.xy[[i]])
  plot(br)
  points(bg.xy[[i]], col = 'black', pch = 20)
  points(occs.xy[[i]], col = colors[i], pch = 20)
  title(paste0(spp[i],' - Presence and Background'))
  dev.copy(tiff,filename=paste0('output/',spp[i],' - Presence and Background.tif'),
           width = 6, height = 5, units = "in", res = 500)
  dev.off()
}
```

Cassia ferruginea − Presence and Background

Myrcia silvatica − Presence and Background



Scinax nebulosus − Presence and Background



Running ENMeval to evaluate different Maxent models:

```
ev <- list()
best <- list()
# Creating optimize function
optimize <- function(res) {
  ###Remove any candidate model which has an AUC less than 0.51= models with no discrimination
  opt.auc <- res[res[,4] >= 0.5,]
  ###Remove any candidates which have no parameters
  no.param <- opt.auc[opt.auc[,13] > 1,]
  ###Remove any candidates where the AIC score was NA (too many parameters)
  noAICNA<- no.param[which(!is.na(no.param$AICc)),]
  ###Remove any models which have an OR of zero
  noOR0 <- noAICNA[noAICNA[,9] != 0,]
  ###Order the remaining list by lowest OR then highest AUC, sequentially
  ordered<-noOR0[with(noOR0, order(avg.test.or10pct, -avg.test.AUC)), ]
  ###Grab the settings of that first model (the optimal model)
  ordered[1,]
}

for (i in 1:length(occs.xy)) {
  ev[[i]]<-ENMevaluate(occ = occs.xy[[i]], env = env[[1]], bg.coords = bg.xy[[i]],
                       RMvalues = seq(1,5,0.5), fc = c("L","LQ","H","LQH"),
                       method = "checkerboard2", n.bg = 1000, rasterPreds = T, parallel = T,
                       numCores = 8, algorithm = 'maxent.jar')
  best[[i]]<-optimize(ev[[i]]@results)
```

```
}

##Creating a data frame with the best model for each species

best.models <- data.frame(species = spp,
                          betamultipliers = c('5','4','1','5'),
                          linear = c('true','false','true','true'),
                          quadratic = c('true','false','false','true'),
                          hinge = c('false','true','false','true'))
```

Running Maxent models:

```
##Calibrating model
dir.create('output/maxent_models/')
mod <- list()
for (i in 1:length(spp)) {
  dir.create(paste0('output/maxent_models/',spp[i]))
  mod[[i]] <- maxent(
    x=env[[1]], # bio stack
    p=occs.xy[[i]], # locality csv
    factors = NULL,
    path = paste0('output/maxent_models/',spp[i]),
    args=c(paste0('betamultiplier=',best.models[i,2]),
           paste0('linear=',best.models[i,3]),
           paste0('quadratic=',best.models[i,4]),
           paste0('hinge=',best.models[i,3]),
           'product=false',
           'threshold=false',
           'threads=8',
           'responsecurves=true',
           'jackknife=true',
           'askoverwrite=false',
           'autofeature=false')
    )
}

##Linear = false did not work
```

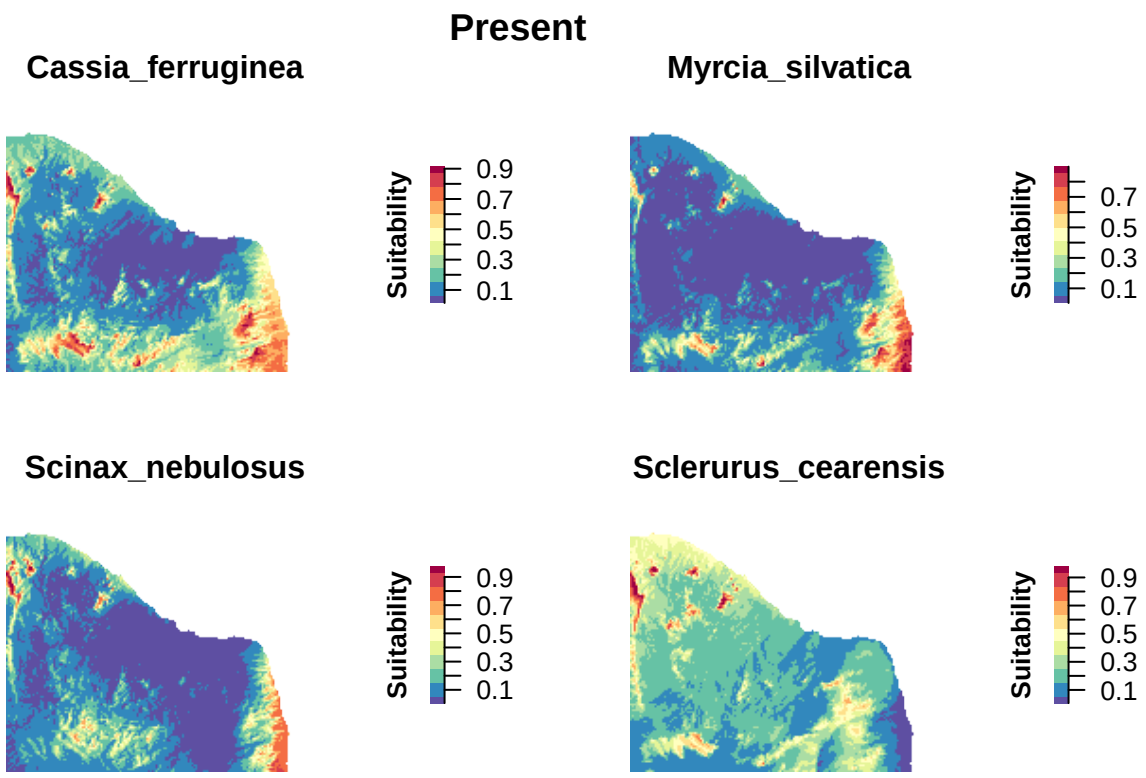
Now projecting into different periods

```
proj <- list()
for (j in 1:length(periods)) {
  dir.create(paste0('output/maxent_models/',periods[j]))
  proj[[j]] <- list()
  for (i in 1:length(spp)) {
    proj[[j]][[i]] <- predict(
      object = mod[[i]],
      x = env[[j]],
      filename = paste0('output/maxent_models/',periods[j],'/',spp[i],'.asc'),
      na.rm = T,
      format = 'ascii',#or GTiff
      overwrite = F,
      args = "logistic"
```

```
    )
  }
}
```

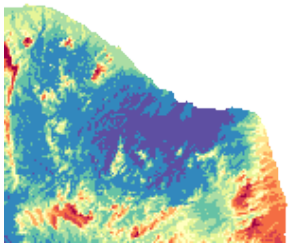
Reading output asc files and plotting results:

```
mxt <- list()
for (i in 1:length(periods)) {
  mxt[[i]] <- list()
  files <- list.files(path = paste0('output/maxent_models/',periods[i]), pattern = '.asc', full.names =
  mxt[[i]] <- stack(files)
}
library(RColorBrewer)
for (i in 1:length(mxt)) {
  par(bty='n', oma = c(0, 0, 2, 0))
  r.range <- c(min(na.omit(values(mxt[[i]]))),max(na.omit(values(mxt[[i]]))))
  plot(mxt[[i]], col = rev(brewer.pal(11, 'Spectral')), axes=FALSE,legend.width=1,
       axis.args=list(at=round(seq(r.range[1], r.range[2], 0.1),2),
                      labels=round(seq(r.range[1], r.range[2], 0.1),2)),
       legend.args=list(text='Suitability', side=4, font=2, line=-2, cex=0.8))
  title(periods.names[[i]], outer = TRUE, line = 0.2)
  dev.copy(tiff,filename=paste0('output/maxent_models/',periods[i],'.tif'),
           width = 10, height = 6, units = "in", res = 500)
  dev.off()
}
```

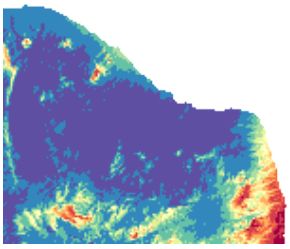


Late Holocene (0.3 − 4.2 ka)

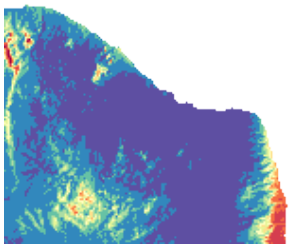
Cassia_ferruginea



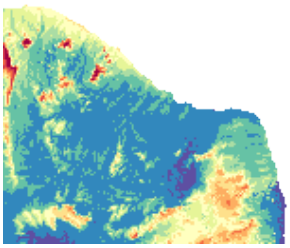
Myrcia_silvatica



Scinax_nebulosus

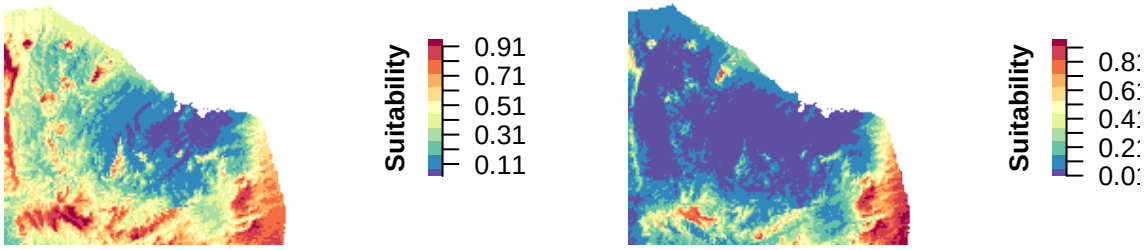


Sclerurus_cearensis



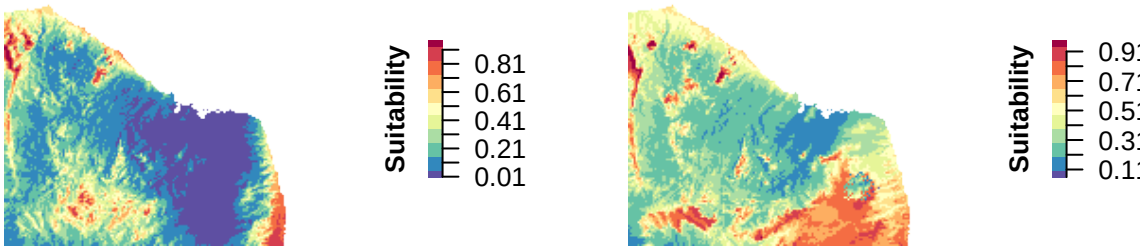
Middle Holocene (4.2 − 8.326 ka)

Cassia_ferruginea



Myrcia_silvatica

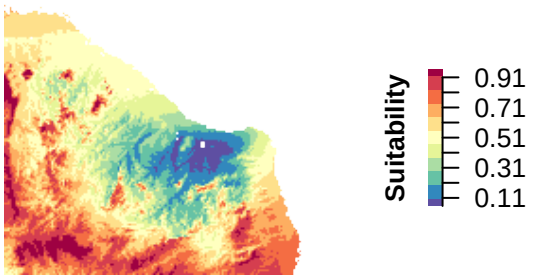
Scinax_nebulosus



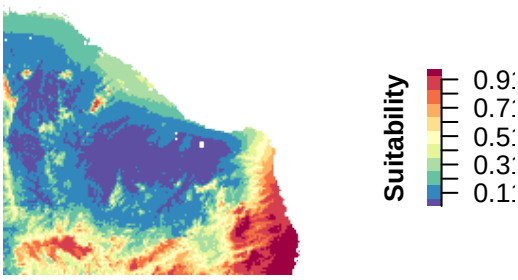
Sclerurus_cearensis

Early Holocene (8.326 − 11.7 ka)

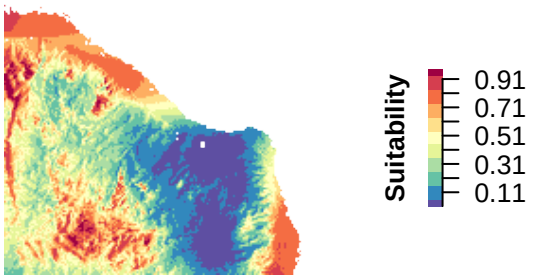
Cassia_ferruginea



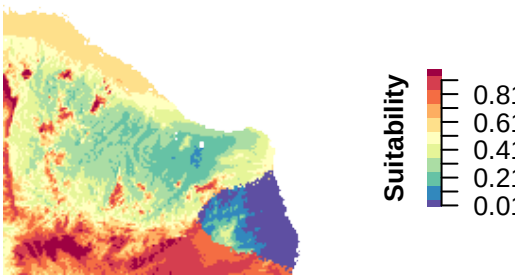
Myrcia_silvatica



Scinax_nebulosus

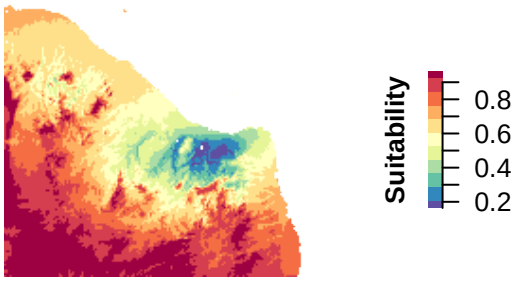


Sclerurus_cearensis

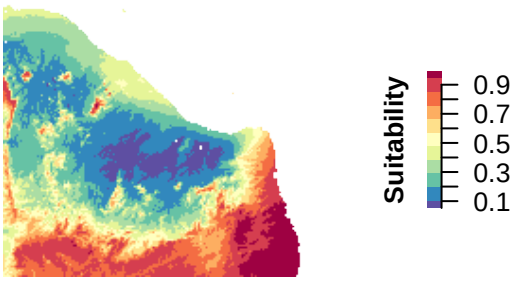


Younger Dryas Stadial (11.7 ka − 12.9 ka)

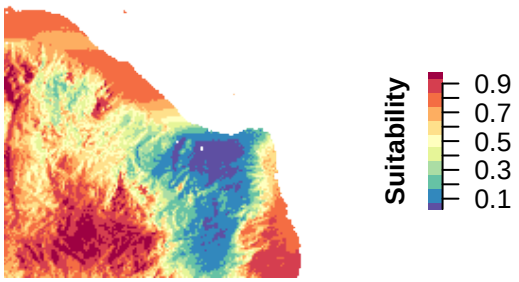
Cassia_ferruginea



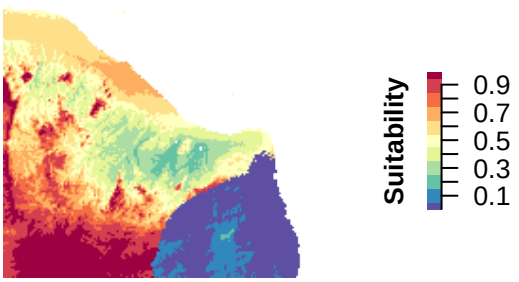
Myrcia_silvatica

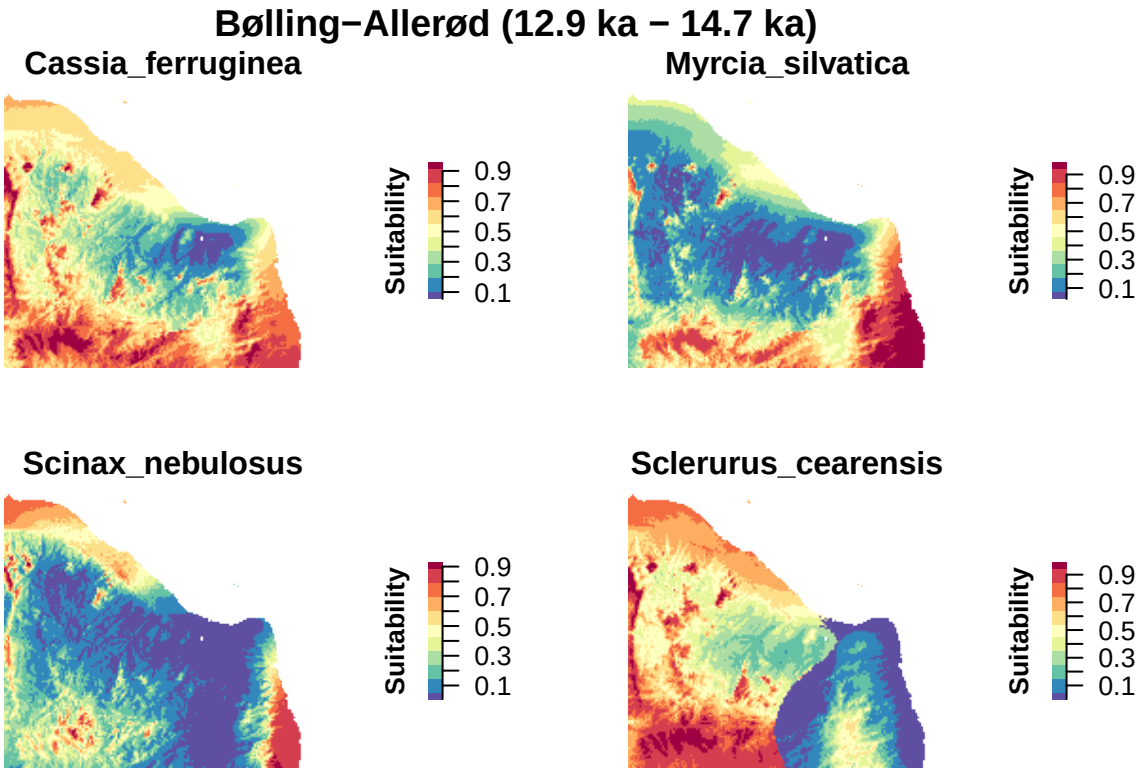


Scinax_nebulosus



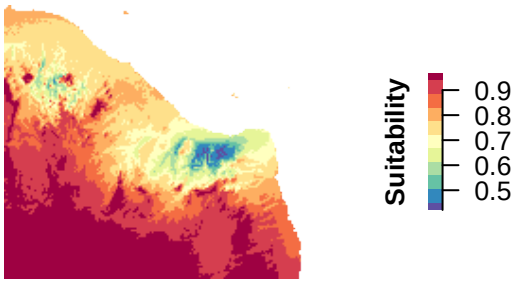
Sclerurus_cearensis



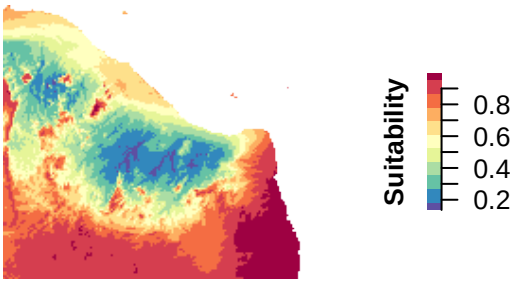

Bølling−Allerød (12.9 ka − 14.7 ka)
Cassia_ferruginea
Suitability
0.9
0.7
0.5
0.3
0.1
Myrcia_silvatica
Suitability
0.9
0.7
0.5
0.3
0.1
Scinax_nebulosus
Suitability
0.9
0.7
0.5
0.3
0.1
Sclerurus_cearensis
Suitability
0.9
0.7
0.5
0.3
0.1

Heinrich Stadial 1 (14.7 ka − 17 ka)

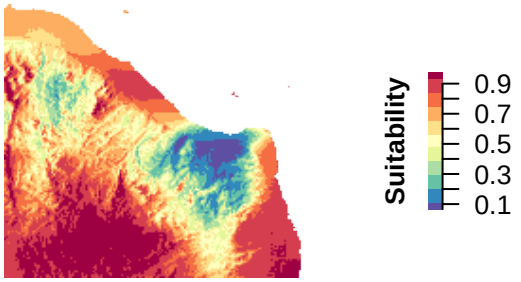
Cassia_ferruginea



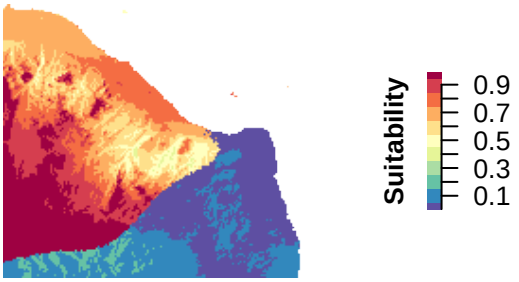
Myrcia_silvatica



Scinax_nebulosus

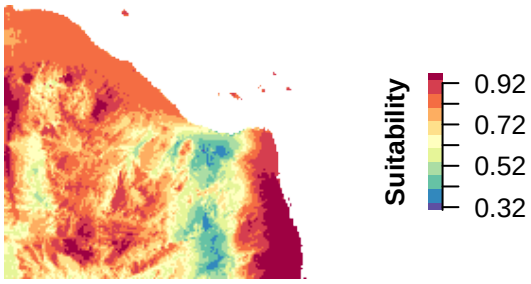


Sclerurus_cearensis

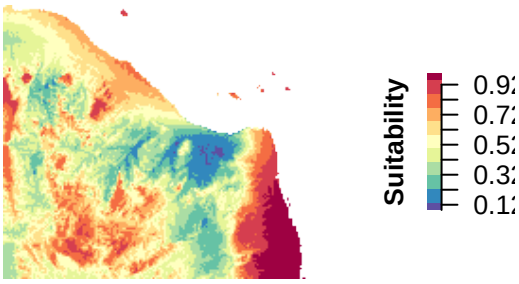


Last Glacial Maximum (ca. 21 ka)

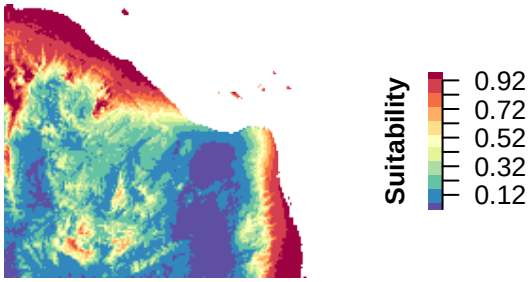
Cassia_ferruginea



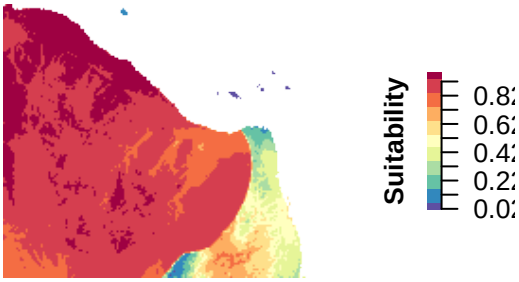
Myrcia_silvatica

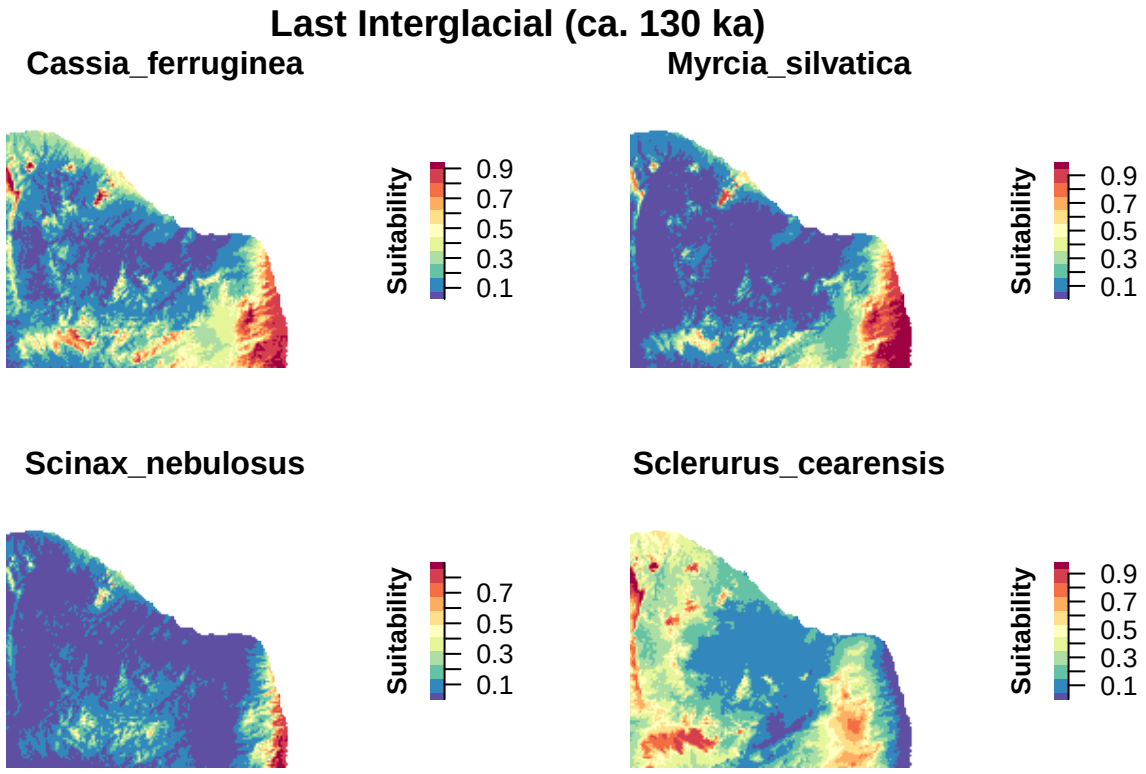


Scinax_nebulosus



Sclerurus_cearensis





Part two: testing niche equivalency