Using geodiversity to improve SDMs for data poor species

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Project: Using geodiversity to improve SDMs for data poor species

Description: This code calculates geodiversity metrics. It calculates SD of CHELSA biodiversity variables at multiple radii (3, 9, 15, 21, 27, 33 km). It calculcates the SD of elevation over the same radii.

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Inputs: Uses SRTM elevation data, annual cloud cover, and 4 preselected CHELSA Bioclim variables to generation geodiversity measures at various radii.

Outputs: raster files for each variable with values calculated over 6 different radii.

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library(geodiv)  
library(raster)  
library(rnaturalearth)  
library(dplyr)  
library(rgeos)  
library(maps)  
library(sf)  
library(rgdal)

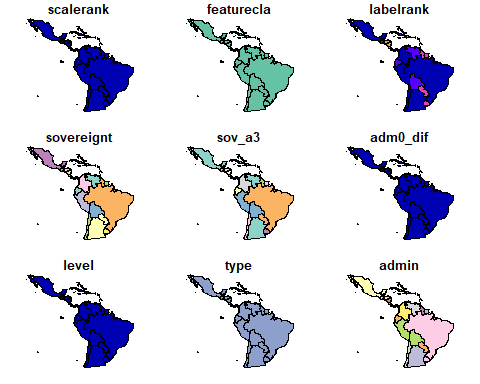
Process and prepare SRTM elevation data

srtm <- raster("D:/zarnetske\_lab/elevation/srtm\_1km.tif")  
  
# Pull in world map  
worldMap <- ne\_countries(scale = "medium", type = "countries", returnclass = "sf")  
  
# Subset world map to region of interest for future cropping.   
  
SA\_study\_region <- worldMap %>% filter(region\_wb == "Latin America & Caribbean")  
  
# Crop the study region to the bounding box of interest  
study\_region\_crop <-st\_crop(SA\_study\_region, xmin = -120, xmax = -30, ymin = -30, ymax = 40)

## Warning: attribute variables are assumed to be spatially constant throughout all  
## geometries

plot(study\_region\_crop)

## Warning: plotting the first 9 out of 63 attributes; use max.plot = 63 to plot  
## all



# Crop SRTM raster to that of the study region  
srtm\_sr <- crop(srtm, study\_region\_crop)

setwd(“D:/zarnetske\_lab/CHELSA\_4\_only”) writeRaster(srtm\_sr, filename=“srtm\_crop”, format=“GTiff”)

## SRTM

Calculate SD of SRTM at all radii mentioned above.

window <- matrix(1, nrow = 3, ncol = 3)  
sd <- focal\_metrics(srtm\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
#   
#setwd("D:/zarnetske\_lab/chelsa\_sd/3x")  
# writeRaster(sd$sd, filename="sd\_3km", format="GTiff")  
  
#set to a 9km window, which is appropriate given the home range of the species being tested (this may change in future iterations)  
window <- matrix(1, nrow = 9, ncol = 9)  
sd.9 <- focal\_metrics(srtm\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/9x")  
#writeRaster(sd.9$sd, filename="sd\_9km", format="GTiff")  
  
# set to a 15 km window  
 window <- matrix(1, nrow = 15, ncol = 15)  
 sd.15 <- focal\_metrics(srtm\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
# setwd("D:/zarnetske\_lab/chelsa\_sd/15x")  
# writeRaster(sd.15$sd, filename="sd\_15km", format="GTiff")  
  
  
#set to a 21 km window  
window <- matrix(1, nrow = 21, ncol = 21)  
sd.21 <- focal\_metrics(srtm\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/21x")  
#writeRaster(sd.21$sd, filename="sd\_21km", format="GTiff")  
  
  
#set to a 27 km window, which is appropriate given the home range of the species being tested (this may change in future iterations)  
window <- matrix(1, nrow = 27, ncol = 27)  
sd.27 <- focal\_metrics(srtm\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/27x")  
#writeRaster(sd.27$sd, filename="sd\_27km", format="GTiff")  
  
#set to a 33 km window, which is appropriate given the home range of the species being tested (this may change in future iterations)  
window <- matrix(1, nrow = 33 , ncol = 33)  
sd.33 <- focal\_metrics(srtm\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/33x")  
#writeRaster(sd.33$sd, filename="sd\_33km", format="GTiff")

## Cloud Cover

Read in mean annual cloud cover raster from Jetz 2016 (generated from MODIS) and process raster

cloud <- raster("C:/Users/bgers/Desktop/MSU/Zarnetske\_Lab/Data/Cloud\_forest\_prediction\_Jetz\_2016/MODCF\_meanannual.tiff")  
  
  
# Crop cloud raster to that of the study region  
cloud\_sr <- crop(cloud, study\_region\_crop)  
#setwd("C:/Users/bgers/Desktop")  
#writeRaster(cloud\_sr, filename="cloud\_crop", format="GTiff")

Set to a 3km window same as above

window <- matrix(1, nrow = 3, ncol = 3)  
cloud.3 <- focal\_metrics(cloud\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
   
setwd("D:/zarnetske\_lab/chelsa\_sd/3x")  
writeRaster(cloud.3$sd, filename="cloud\_3km", format="GTiff")  
  
#set to a 9km window  
window <- matrix(1, nrow = 9, ncol = 9)  
cloud.9 <- focal\_metrics(cloud\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/9x")  
#writeRaster(cloud.9$sd, filename="cloud\_9km", format="GTiff")  
  
#set to a 15 km window  
window <- matrix(1, nrow = 15, ncol = 15)  
cloud.15 <- focal\_metrics(cloud\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
   
#setwd("D:/zarnetske\_lab/chelsa\_sd/15x")  
#writeRaster(cloud.15$sd, filename="cloud\_15km", format="GTiff")  
  
  
#set to a 21 km window  
window <- matrix(1, nrow = 21, ncol = 21)  
cloud.21 <- focal\_metrics(cloud\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/21x")  
#writeRaster(cloud.21$sd, filename="cloud\_21km", format="GTiff")  
  
  
#set to a 27 km window  
window <- matrix(1, nrow = 27, ncol = 27)  
cloud.27 <- focal\_metrics(cloud\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/27x")  
#writeRaster(cloud.27$sd, filename="cloud\_27km", format="GTiff")  
  
#set to a 33 km window, which is appropriate given the home range of the species being tested (this may change in future iterations)  
window <- matrix(1, nrow = 33 , ncol = 33)  
cloud.33 <- focal\_metrics(cloud\_sr, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/33x")  
#writeRaster(cloud.33$sd, filename="cloud\_33km", format="GTiff")

## BioClim variables

Process environmental variables to only be for the study region Set working directory to folder where environmental data is stored

setwd("D:/zarnetske\_lab/CHELSA\_full")  
  
  
# Making stack of all 19 bioclimatic variables  
env <- list.files(pattern='tif', full.names=TRUE)  
env <- stack(env)  
  
# Crop extent to a smaller region so it is easier to work with  
# Crop environmental variables by the larger extent  
  
env.clip <- crop(env, study\_region\_crop)  
  
#write cropped CHELSA data to file  
setwd("D:/zarnetske\_lab/CHELSA\_full/CHELSA\_crop")  
for (i in 1:19) {  
 writeRaster(env.clip[[i]], paste0(strsplit(names(env.clip[[i]]),"CHELSA\_1")[[1]][1],'.tif'))  
}  
  
#SD of CHELSA at 3 resolutions 3, 9, 15, 21, 27, 33  
# variables  
#Bio5: Max Temperature of Warmest Month  
#Bio6: Min Temperature of Coldest Month  
#Bio13: Precipitation of Wettest Month   
#Bio14: Precipitation of Driest Month

Generating the CHELSA geodiversity rasters

#Pull bio5 out of stack  
bio5 <- env.clip[[15]]  
  
# #SD of bio5 3km  
window <- matrix(1, nrow = 3 , ncol = 3)  
bio5\_sd\_3km <- focal\_metrics(bio5, window, metrics = list('sd'),  
 progress = TRUE)  
  
# setwd("D:/zarnetske\_lab/chelsa\_sd/3x")  
# writeRaster(bio5\_sd\_3km$sd, filename="bio5\_sd\_3km", format="GTiff")  
  
#SD of bio5 9km  
window <- matrix(1, nrow = 9 , ncol = 9)  
bio5\_sd\_9km <- focal\_metrics(bio5, window, metrics = list('sd'),  
 progress = TRUE)  
  
# setwd("D:/zarnetske\_lab/chelsa\_sd/9x")  
# writeRaster(bio5\_sd\_9km$sd, filename="bio5\_sd\_9km", format="GTiff")  
  
#SD of bio5 15km  
window <- matrix(1, nrow = 15 , ncol = 15)  
bio5\_sd\_15km <- focal\_metrics(bio5, window, metrics = list('sd'),  
 progress = TRUE)  
#   
# setwd("D:/zarnetske\_lab/chelsa\_sd/15x")  
# writeRaster(bio5\_sd\_15km$sd, filename="bio5\_sd\_15km", format="GTiff")  
  
#SD of bio5 21km  
window <- matrix(1, nrow = 21 , ncol = 21)  
bio5\_sd\_21km <- focal\_metrics(bio5, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/21x")  
#writeRaster(bio5\_sd\_21km$sd, filename="bio5\_sd\_21km", format="GTiff")  
  
#SD of bio5 27km  
window <- matrix(1, nrow = 27 , ncol = 27)  
bio5\_sd\_27km <- focal\_metrics(bio5, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/27x")  
#writeRaster(bio5\_sd\_27km$sd, filename="bio5\_sd\_27km", format="GTiff")  
  
#SD of bio5 33km  
window <- matrix(1, nrow = 33 , ncol = 33)  
bio5\_sd\_33km <- focal\_metrics(bio5, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/33x")  
#writeRaster(bio5\_sd\_33km$sd, filename="bio5\_sd\_33km", format="GTiff")  
#\_\_\_\_\_\_  
  
#Pull bio6 out of stack  
bio6 <- env.clip[[16]]  
  
# SD of bio6 3km  
window <- matrix(1, nrow = 3 , ncol = 3)  
bio6\_sd\_3km <- focal\_metrics(bio6, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/3x")  
#writeRaster(bio6\_sd\_3km$sd, filename="bio6\_sd\_3km", format="GTiff")  
  
#SD of bio6 9km  
window <- matrix(1, nrow = 9 , ncol = 9)  
bio6\_sd\_9km <- focal\_metrics(bio6, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/9x")  
#writeRaster(bio6\_sd\_9km$sd, filename="bio6\_sd\_9km", format="GTiff")  
  
# SD of bio6 15km  
window <- matrix(1, nrow = 15 , ncol = 15)  
bio6\_sd\_15km <- focal\_metrics(bio6, window, metrics = list('sd'),  
 progress = TRUE)  
#   
# setwd("D:/zarnetske\_lab/chelsa\_sd/15x")  
# writeRaster(bio6\_sd\_15km$sd, filename="bio6\_sd\_15km", format="GTiff")  
  
#SD of bio6 21km  
window <- matrix(1, nrow = 21 , ncol = 21)  
bio6\_sd\_21km <- focal\_metrics(bio6, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/21x")  
#writeRaster(bio6\_sd\_21km$sd, filename="bio6\_sd\_21km", format="GTiff")  
  
#SD of bio6 27km  
window <- matrix(1, nrow = 27 , ncol = 27)  
bio6\_sd\_27km <- focal\_metrics(bio6, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/27x")  
#writeRaster(bio6\_sd\_27km$sd, filename="bio6\_sd\_27km", format="GTiff")  
  
#SD of bio6 33km  
window <- matrix(1, nrow = 33 , ncol = 33)  
bio6\_sd\_33km <- focal\_metrics(bio6, window, metrics = list('sd'),  
 progress = TRUE)  
  
setwd("D:/zarnetske\_lab/chelsa\_sd/33x")  
writeRaster(bio6\_sd\_33km$sd, filename="bio6\_sd\_33km", format="GTiff")  
  
#\_\_\_\_\_\_  
  
#Pull bio13 out of stack  
bio13 <- env.clip[[5]]  
  
  
# #SD of bio13 3km  
window <- matrix(1, nrow = 3 , ncol = 3)  
bio13\_sd\_3km <- focal\_metrics(bio13, window, metrics = list('sd'),  
 progress = TRUE)  
#   
# setwd("D:/zarnetske\_lab/chelsa\_sd/3x")  
# writeRaster(bio13\_sd\_3km$sd, filename="bio13\_sd\_3km", format="GTiff")  
  
#SD of bio13 9km  
window <- matrix(1, nrow = 9 , ncol = 9)  
bio13\_sd\_9km <- focal\_metrics(bio13, window, metrics = list('sd'),  
 progress = TRUE)  
  
setwd("D:/zarnetske\_lab/chelsa\_sd/9x")  
writeRaster(bio13\_sd\_9km$sd, filename="bio13\_sd\_9km", format="GTiff")  
  
  
# #SD of bio13 15km  
window <- matrix(1, nrow = 15 , ncol = 15)  
bio13\_sd\_15km <- focal\_metrics(bio13, window, metrics = list('sd'),  
 progress = TRUE)  
#   
# setwd("D:/zarnetske\_lab/chelsa\_sd/15x")  
# writeRaster(bio13\_sd\_15km$sd, filename="bio13\_sd\_15km", format="GTiff")  
  
#SD of bio13 21km  
window <- matrix(1, nrow = 21 , ncol = 21)  
bio13\_sd\_21km <- focal\_metrics(bio13, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/21x")  
#writeRaster(bio13\_sd\_21km$sd, filename="bio13\_sd\_21km", format="GTiff")  
  
#SD of bio13 27km  
window <- matrix(1, nrow = 27 , ncol = 27)  
bio13\_sd\_27km <- focal\_metrics(bio13, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/27x")  
#writeRaster(bio13\_sd\_27km$sd, filename="bio13\_sd\_27km", format="GTiff")  
  
#SD of bio13 33km  
window <- matrix(1, nrow = 33 , ncol = 33)  
bio13\_sd\_33km <- focal\_metrics(bio13, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/33x")  
#writeRaster(bio13\_sd\_33km$sd, filename="bio13\_sd\_33km", format="GTiff")  
  
#\_\_\_\_\_\_  
  
#Pull bio14 out of stack  
bio14 <- env.clip[[6]]  
  
# #SD of bio13 3km  
window <- matrix(1, nrow = 3 , ncol = 3)  
bio14\_sd\_3km <- focal\_metrics(bio14, window, metrics = list('sd'),  
 progress = TRUE)  
#   
# setwd("D:/zarnetske\_lab/chelsa\_sd/3x")  
# writeRaster(bio14\_sd\_3km$sd, filename="bio14\_sd\_3km", format="GTiff")  
  
#SD of bio13 9km  
window <- matrix(1, nrow = 9 , ncol = 9)  
bio14\_sd\_9km <- focal\_metrics(bio14, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/9x")  
#writeRaster(bio14\_sd\_9km$sd, filename="bio14\_sd\_9km", format="GTiff")  
  
# #SD of bio14 15km  
window <- matrix(1, nrow = 15 , ncol = 15)  
bio14\_sd\_15km <- focal\_metrics(bio14, window, metrics = list('sd'),  
 progress = TRUE)  
#   
# setwd("D:/zarnetske\_lab/chelsa\_sd/15x")  
# writeRaster(bio14\_sd\_15km$sd, filename="bio14\_sd\_15km", format="GTiff")  
  
#SD of bio14 21km  
window <- matrix(1, nrow = 21 , ncol = 21)  
bio14\_sd\_21km <- focal\_metrics(bio14, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/21x")  
#writeRaster(bio14\_sd\_21km$sd, filename="bio14\_sd\_21km", format="GTiff")  
  
#SD of bio14 27km  
window <- matrix(1, nrow = 27 , ncol = 27)  
bio14\_sd\_27km <- focal\_metrics(bio14, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/27x")  
#writeRaster(bio14\_sd\_27km$sd, filename="bio14\_sd\_27km", format="GTiff")  
  
#SD of bio14 33km  
window <- matrix(1, nrow = 33 , ncol = 33)  
bio14\_sd\_33km <- focal\_metrics(bio14, window, metrics = list('sd'),  
 progress = TRUE)  
  
#setwd("D:/zarnetske\_lab/chelsa\_sd/33x")  
#writeRaster(bio14\_sd\_33km$sd, filename="bio14\_sd\_33km", format="GTiff")