Frugivoria: Ecuadorian Birds & Mammals richness

Beth E. Gerstner

7/7/2020

```r
library(sf)
```

```
## Linking to GEOS 3.7.2, GDAL 2.4.2, PROJ 5.2.0
```

```r
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(ggplot2)
library(scico)
library(rnaturalearth)
library(purrr)
library(smoothr)
```

```
##
## Attaching package: 'smoothr'
```

```
## The following object is masked from 'package:stats':
##
##     smooth
```

```r
library(rgbif)
library(lwgeom)
```

```
## Linking to liblwgeom 3.0.0beta1 r16016, GEOS 3.7.2, PROJ 5.2.0
```

Load packages

```r
library(sf)
library(rgeos)
```

```
## Loading required package: sp
```

```
## rgeos version: 0.5-3, (SVN revision 634)
##  GEOS runtime version: 3.7.2-CAPI-1.11.2
##  Linking to sp version: 1.4-1
```

```
##  Polygon checking: TRUE
library(rgdal)

## rgdal: version: 1.4-8, (SVN revision 845)
##  Geospatial Data Abstraction Library extensions to R successfully loaded
##  Loaded GDAL runtime: GDAL 2.4.2, released 2019/06/28
##  Path to GDAL shared files: /Library/Frameworks/R.framework/Versions/4.0/Resources/library/rgdal/gda
##  GDAL binary built with GEOS: FALSE
##  Loaded PROJ.4 runtime: Rel. 5.2.0, September 15th, 2018, [PJ_VERSION: 520]
##  Path to PROJ.4 shared files: /Library/Frameworks/R.framework/Versions/4.0/Resources/library/rgdal/p
##  Linking to sp version: 1.4-1
```

Pull shapefiles for frugivorous species (only mammals at this point)

```
setwd("/Users/bethgerstner/Desktop/MSU/Zarnetske_Lab/Data/IUCN_Data/TERRESTRIAL_MAMMALS/TERRESTRIAL_MAM
IUCN_mam <-read_sf("/Users/bethgerstner/Desktop/MSU/Zarnetske_Lab/Data/IUCN_Data/TERRESTRIAL_MAMMALS_2/
mam_frug_ec <- read.csv("/Users/bethgerstner/Desktop/MSU/Zarnetske_Lab/Data/Elton_Traits_birds_mammals/
```

Subset IUCN mammal shapefile by: creating new column in the shapefile so that each shapefile has a unique identifier

```
IUCN_mam$new_id = 1:nrow(IUCN_mam)

# list of unique species names for frugivorous mammals in Ecuador made above

mam_frug_sn <-as.vector(unique(mam_frug_ec$IUCN_species_name))

# Subset the new IDs made above by those that have species names matching the frugivorous subset
shapes   = IUCN_mam$new_id[IUCN_mam$binomial %in% mam_frug_sn] # shapes = ID numbers for subset

# Subsets the IUCN shapefiles to those with IDs matching the frugivorous subset
IUCN_mam_df = IUCN_mam[IUCN_mam$new_id %in% shapes,] #268 shapefiles for species list (209 species)

#write the shapefile to a file
#setwd("/Users/bethgerstner/Desktop/MSU/Zarnetske_Lab/Data/Elton_Traits_birds_mammals/mx_species")
#st_write(IUCN_mam_df, "ec_mammals.shp")
```

Load in a world map

```
worldMap <- ne_countries(scale = "medium", type = "countries", returnclass = "sf")

# country subset. In this case we are removing the Galapagos by defining the bounding box around the Ec
CRpoly <- worldMap %>% filter(sovereignt == "Ecuador")
ecuador_shp <-st_crop(CRpoly, c(xmin=-84, xmax=-75.24961, ymin=-4.990625, ymax=1.455371))

## although coordinates are longitude/latitude, st_intersection assumes that they are planar
```

```
## Warning: attribute variables are assumed to be spatially constant throughout all
## geometries
# trim the map to appropriate study area. This zooms out of Ecuador, which will be easier for visualiza
limsCR <- st_buffer(ecuador_shp, dist = 9) %>% st_bbox()

## Warning in st_buffer.sfc(st_geometry(x), dist, nQuadSegs, endCapStyle =
## endCapStyle, : st_buffer does not correctly buffer longitude/latitude data

## dist is assumed to be in decimal degrees (arc_degrees).
# neighboring countries (will include Colombia as well)
adjacentPolys <- st_touches(ecuador_shp, worldMap)

## although coordinates are longitude/latitude, st_touches assumes that they are planar
neighbours <- worldMap %>% slice(pluck(adjacentPolys, 1))

# countries
divpolPlot <-
  ggplot() +
  geom_sf(data = neighbours, color = "white") +
  geom_sf(data = ecuador_shp) +
  coord_sf(
    xlim = c(limsCR["xmin"], limsCR["xmax"]),
    ylim = c(limsCR["ymin"], limsCR["ymax"])
  ) +
  scale_x_continuous(breaks = c(-84)) +
  theme(
    plot.background = element_rect(fill = "#f1f2f3"),
    panel.background = element_rect(fill = "#2F4051"),
    panel.grid = element_blank(),
    line = element_blank(),
    rect = element_blank()
  )
divpolPlot
```

plot hulls

```r
hullsPlot <-
  ggplot() +
  geom_sf(data = neighbours, color = "white") +
  geom_sf(data = ecuador_shp) +
  geom_sf(data = IUCN_mam_df, aes(fill = binomial), alpha = 0.7) +
  scale_fill_scico_d(palette = "davos", direction = -1, end = 0.9, guide = FALSE) +
  coord_sf(
    xlim = c(limsCR["xmin"], limsCR["xmax"]),
    ylim = c(limsCR["ymin"], limsCR["ymax"])
  ) +
  scale_x_continuous(breaks = c(-84)) +
  theme(
    plot.background = element_rect(fill = "#f1f2f3"),
    panel.background = element_rect(fill = "#2F4051"),
    panel.grid = element_blank(),
    line = element_blank(),
    rect = element_blank()
  )
hullsPlot
```

4
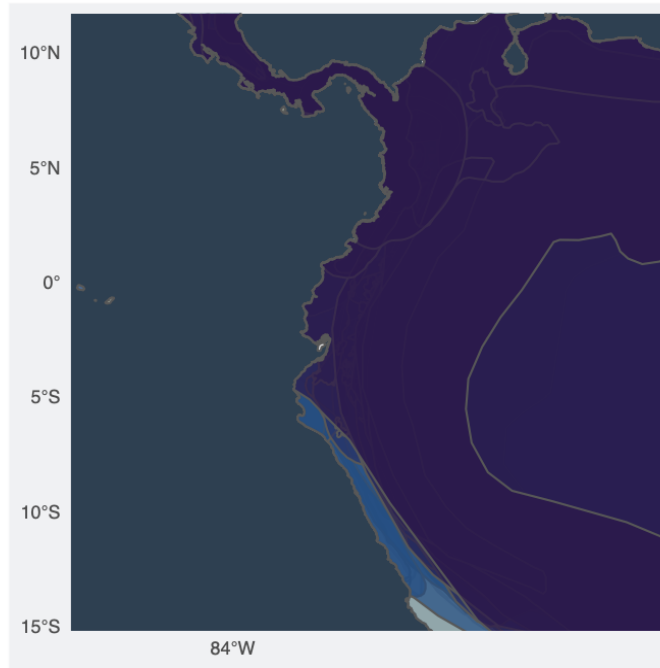
define a grid

```r
CRGrid <- ecuador_shp %>%
  st_make_grid(cellsize = 0.2) %>%
  st_intersection(ecuador_shp) %>%
  st_cast("MULTIPOLYGON") %>%
  st_sf() %>%
  mutate(cellid = row_number())
```

```
## although coordinates are longitude/latitude, st_relate_pattern assumes that they are planar
```

```
## although coordinates are longitude/latitude, st_intersection assumes that they are planar
```

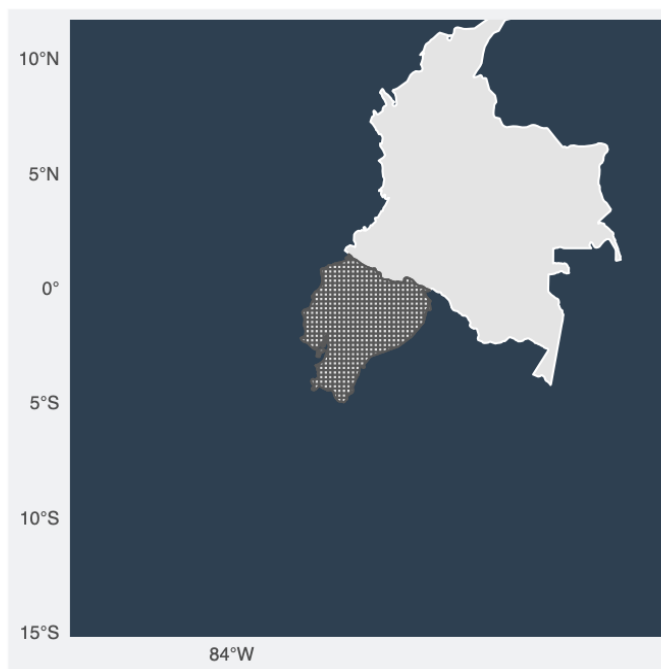## richness for convex hulls

```r
richness_gridEOO <- CRGrid %>%
  st_join(IUCN_mam_df) %>%
  mutate(overlap = ifelse(!is.na(id), 1, 0)) %>%
  group_by(cellid) %>%
  summarize(num_species = sum(overlap))
```

```
## although coordinates are longitude/latitude, st_intersects assumes that they are planar
```

```
## Warning in is.na(id): is.na() applied to non-(list or vector) of type 'closure'

## `summarise()` ungrouping output (override with `.groups` argument)
```

empty grid, more detailed in nature

```
gridPlot <-
  ggplot() +
  geom_sf(data = neighbours, color = "white") +
  geom_sf(data =ecuador_shp) +
  geom_sf(data = CRGrid) +
  coord_sf(
    xlim = c(limsCR["xmin"], limsCR["xmax"]),
    ylim = c(limsCR["ymin"], limsCR["ymax"])
  ) +
  scale_x_continuous(breaks = c(-84)) +
  theme(
    plot.background = element_rect(fill = "#f1f2f3"),
    panel.background = element_rect(fill = "#2F4051"),
    panel.grid = element_blank(),
    line = element_blank(),
    rect = element_blank()
  )
gridPlot
```

richness for convex hulls, more detailed

```r
gridRichCR_eoo <-
  ggplot(richness_gridEOO) +
  geom_sf(data = neighbours, color = "white") +
  geom_sf(data = ecuador_shp, fill = "grey", size = 0.1) +
  geom_sf(aes(fill = num_species), color = NA) +
  scale_fill_scico(palette = "davos", direction = -1, end = 0.9) +
  coord_sf(
    xlim = c(limsCR["xmin"], limsCR["xmax"]),
    ylim = c(limsCR["ymin"], limsCR["ymax"])
  ) +
  scale_x_continuous(breaks = c(-84)) +
  theme(
    plot.background = element_rect(fill = "#f1f2f3"),
    panel.background = element_rect(fill = "#2F4051"),
    panel.grid = element_blank(),
    line = element_blank(),
    rect = element_blank()
  ) + labs(fill = "richness")
gridRichCR_eoo
```