

# Frugivoria: Ecuadorian Birds & Mammals richness

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```
library(sf)

## Linking to GEOS 3.7.2, GDAL 2.4.2, PROJ 5.2.0
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
library(ggplot2)
library(scico)
library(rnaturalearth)
library(purrr)
library(smoothr)

##
## Attaching package: 'smoothr'
## The following object is masked from 'package:stats':
##   smooth
library(rgbif)
library(lwgeom)

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

## Load packages

```
## 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

## 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/gdal
## 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/proj
## Linking to sp version: 1.4-1

```

## Pull shapefiles for frugivorous species (mammals and birds)

```

IUCN_mam <-read_sf("/Users/bethgerstner/Desktop/MSU/Zarnetske_Lab/Data/IUCN_Data/TERRESTRIAL_MAMMALS_2/"
IUCN_bird <-read_sf("/Users/bethgerstner/Desktop/MSU/Zarnetske_Lab/Data/IUCN_Data/BOTW/BOTW_shapefile/All_BOTW.shp"

# Pull in species/trait lists for Ecuador
mam_frug_ec <- read.csv("/Users/bethgerstner/Desktop/MSU/Zarnetske_Lab/Data/Elton_Traits_birds_mammals/mammals_ec.csv")
bird_frug_ec <- read.csv("/Users/bethgerstner/Desktop/MSU/Zarnetske_Lab/Data/Elton_Traits_birds_mammals/birds_ec.csv")

```

## 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")

```

## Same as above for birds

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

```

IUCN_bird$new_id = 1:nrow(IUCN_bird)

# list of unique species names for frugivorous mammals in Ecuador made above
bird_frug_sn <-as.vector(unique(bird_frug_ec$IUCN_species_name))

```

```

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

# Subsets the IUCN shapefiles to those with IDs matching the frugivorous subset
IUCN_bird_df = IUCN_bird[IUCN_bird$new_id %in% shapes,] #770 shapefiles for species list (463 species)

#combine both bird and mammal shapefile, but first remove columns that don't match between the two spat
IUCN_bird_df_short <- IUCN_bird_df[,c(2,16:19)]

#fix column names so that the two datasets match and can be appended to each other so we can plot richn
colnames(IUCN_bird_df_short)[which(names(IUCN_bird_df_short) == "SCINAME")] <- "IUCN_scientific_name"
IUCN_bird_df_short$new_id <- NULL

IUCN_mam_df_short <- IUCN_mam_df[,c(2,26:29)]
colnames(IUCN_mam_df_short)[which(names(IUCN_mam_df_short) == "binomial")] <- "IUCN_scientific_name"
colnames(IUCN_mam_df_short)[which(names(IUCN_mam_df_short) == "SHAPE_Leng")] <- "Shape_Leng"
colnames(IUCN_mam_df_short)[which(names(IUCN_mam_df_short) == "SHAPE_Area")] <- "Shape_Area"
IUCN_mam_df_short$new_id <- NULL

#bind two datasets together
all_frug_shp <- rbind(IUCN_mam_df_short, IUCN_bird_df_short)

#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(sovereignty == "Ecuador")
ecuador_shp <- st_crop(CRpoly, c(xmin=-84, xmax=-75.24961, ymin=-4.990625, ymax=1.455371))

# 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()

# neighboring countries (will include Colombia as well)
adjacentPolys <- st_touches(ecuador_shp, worldMap)
neighbours <- worldMap %>% slice(pluck(adjacentPolys, 1))

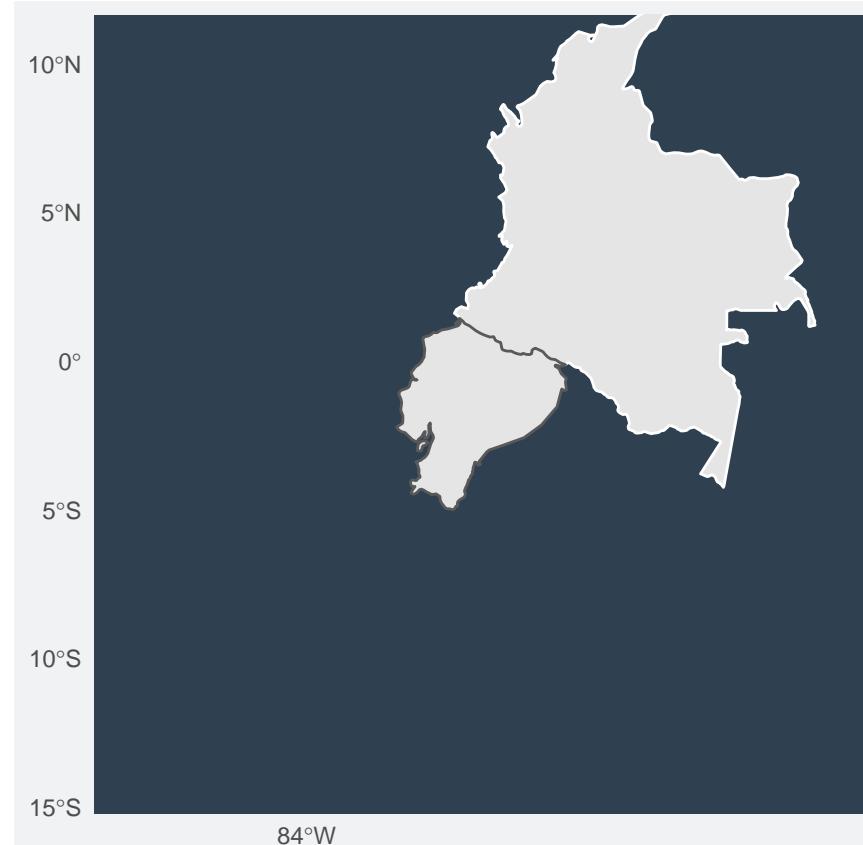
# countries
divpolPlot <-
  ggplot() +
  geom_sf(data = neighbours, color = "white") +
  geom_sf(data = ecuador_shp) +
  coord_sf(
    xlim = c(limsCR["xmin"], limsCR["xmax"]),
    ylim = c(limsCR["ymin"], limsCR["ymax"]))

```

```

) +
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

```



```

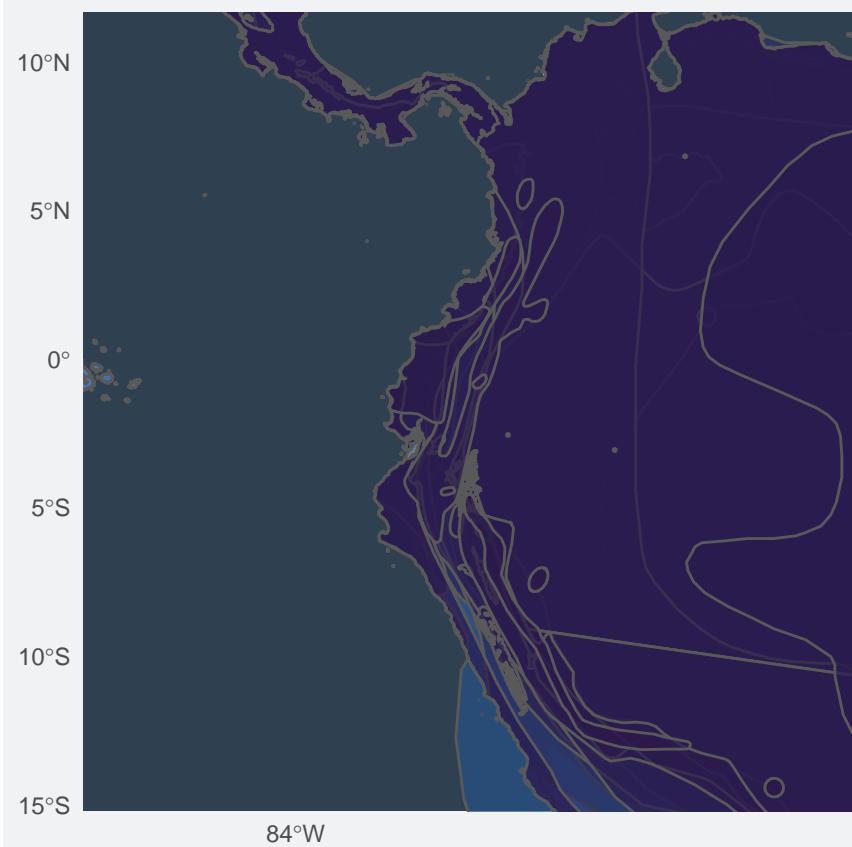
hullsPlot <-
ggplot() +
geom_sf(data = neighbours, color = "white") +
geom_sf(data = ecuador_shp) +
geom_sf(data = all_frug_shp, aes(fill = IUCN_scientific_name), alpha = 0.7) +
scale_fill_scico_d(palette = "davos", direction = -1, end = 0.9, guide = FALSE) +
coord_sf(
  xlim = c(limsCR["xmin"], limsCR["xmax"]),
  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

```



define a grid. Should I change the projection to utm so we can have a grid size in meters/km?

```

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

```

## richness for convex hulls

```

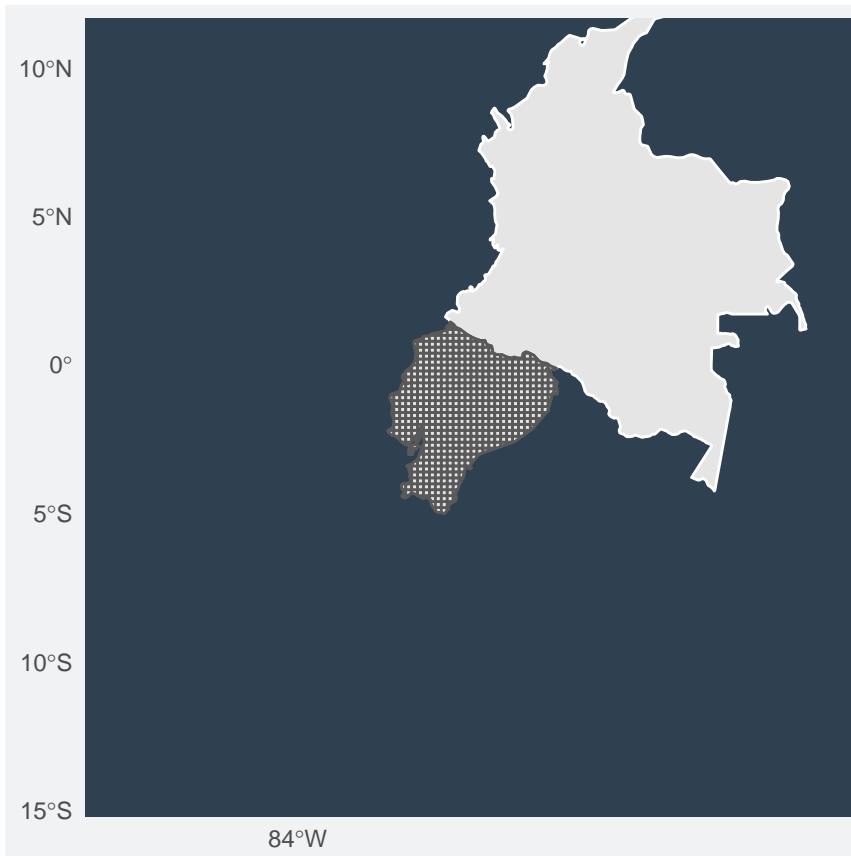
richness_gridE00 <- CRGrid %>%
  st_join(all_frug_shp) %>%
  mutate(overlap = ifelse(!is.na(id), 1, 0)) %>%

```

```
group_by(cellid) %>%
  summarize(num_species = sum(overlap))
```

## 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

```
gridRichCR_eoo <-  
  ggplot(richness_gridE00) +  
  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
```

