

```

#installing required libraries
library(terra)
library(sf)
library(dplyr)
library(ggplot2)
library(spatstat)

#Loading the shape file and reading
##This file contains all the mammals from the whole world
#-----
filename <-

"/Users/srijan/Documents/Academic_Stuffs/Projects/Himalayan_Biogeogra
phy/MAMMALS_TERRESTRIAL_ONLY/MAMMALS_TERRESTRIAL_ONLY.shp"

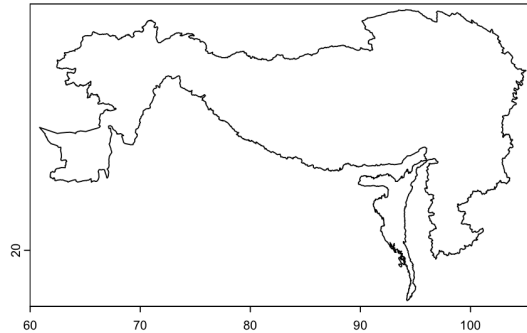
s <- vect(filename) #spat vector
s

class      : SpatRaster
dimensions : 119, 197, 1 (nrow, ncol, nlyr)
resolution : 25000, 25000 (x, y)
extent     : 6766643, 11691643, 1797832, 4772832 (xmin, xmax, ymin, ymax)
coord. ref.: +proj=merc +lon_0=0 +k=1 +x_0=0 +y_0=0 +R=6371000 +units=m +no_defs
source(s)  : memory
name       : lyr.1
min value  : 0
max value  : 1

h = df_world = as.data.frame(s) #copying s as data frame
newarea = expanse(s, unit = "km", transform = TRUE) / 10 ^ 10
#Finding the area of each species

#Loading the Boundary File
#-----
hindukush =
"/Users/srijan/Documents/Academic_Stuffs/Projects/Himalayan_Biogeogra
phy/Outline Boundary of Hindu Kush Himalayan (HKH)
Region/data/outline.shp"
hind <- vect(hindukush)
plot(hind)

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#Intersecting the himalaya part with the actual shape file
#-----
inter <-
  intersect(s, hind)      #intersecting the himalayan part with whole
plot(inter)

writeVector(
  int,
  "F:/Projects/Himalayan_Biogeography/Mamals Data/mam.shp",
  filetype = "ESRI Shapefile",
  #writing the intersection to a shape file
  #writing this as a shape file
  overwrite = TRUE
)

#Work only with the Clipped data
#-----
clipdat =
  "/Users/srijan/Documents/Academic_Stuffs/Projects/Himalayan_Biogeogra
phy/Mamals Data/mam.shp" #Reading the above written shape file
clip = vect(clipdat)    #spat vector

mamclip = as.data.frame(clip) #extracting clip as data frame
```

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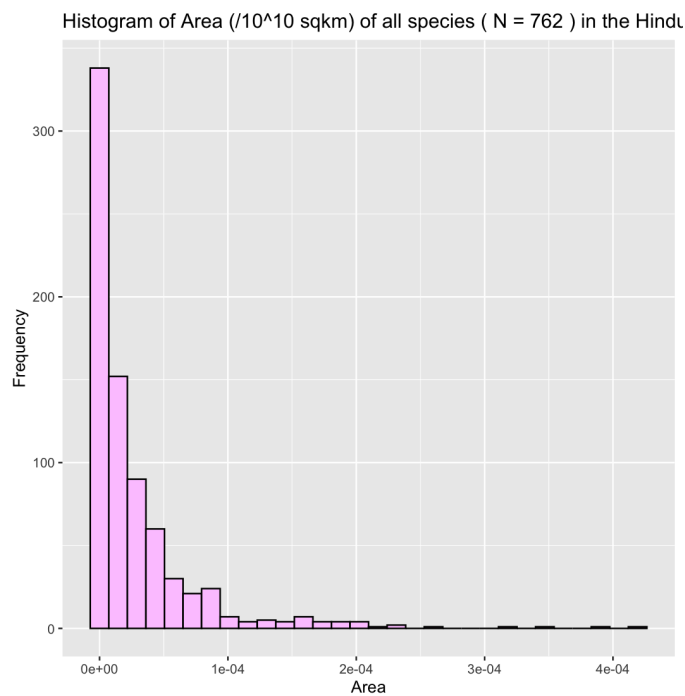
mamclip1 = mamclip[,-c(29, 30, 31)] #the last three columns are
extra, removing them

areahind = expance(clip, unit = "km", transform = TRUE) / 10 ^ 10
#put unit also

#Histogram for the area occupied in hindukush by the species
#-----
df1 = as.data.frame(cbind(c(1:length(areahind)), areahind))

ggplot(df1, aes(x = areahind)) +
  geom_histogram(
    fill = "#ffccff",
    col = "black") +
  labs(
    title = paste(
      "Histogram of Area (/10^10 sqkm) of all species ( N =",
      length(areahind),
      ") in the Hindukush"
    ),
    x = "Area",
    y = "Frequency"
  )

```



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# Histogram for the area occupied in the whole world by the species
living in Hindukush
#-----
-----

int = which(
  h$id_no %in% mamclip1$id_no &
  h$legend %in% mamclip1$legend &
  h$source %in% mamclip1$source &
  h$island %in% mamclip1$island &
  h$subspecies %in% mamclip1$subspecies &
  #extracting only the himalayan part
  h$dist_comm %in% mamclip1$dist_comm &
  h$compiler %in% mamclip1$compiler &
  h$yrcompiled %in% mamclip1$yrcompiled &
  h$SHAPE_Leng %in% mamclip1$SHAPE_Leng
)

newarea_world = newarea[int] #extracting area of those species only

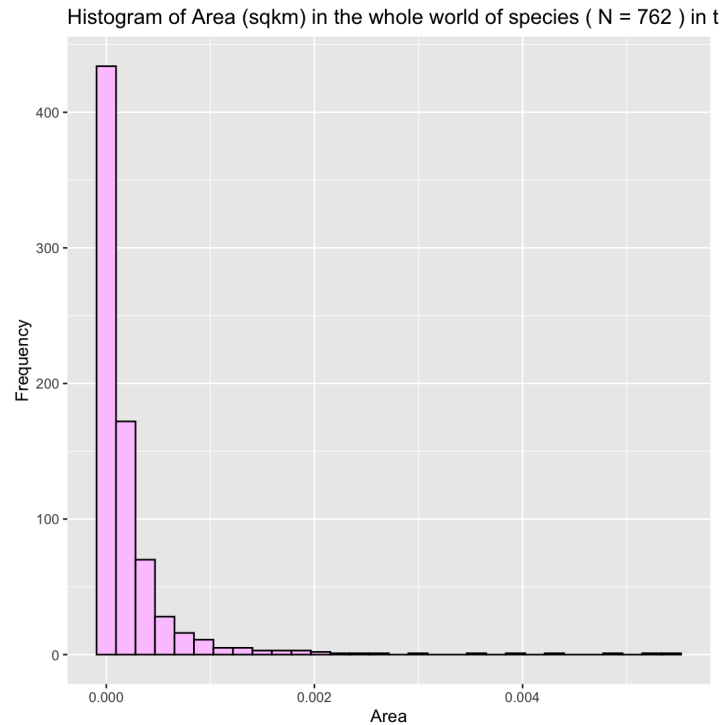
df2 = as.data.frame(cbind(c(1:length(newarea_world)), newarea_world))

ggplot(df2, aes(x = newarea_world)) +

  geom_histogram(
    fill = "#ffccff",
    col = "black") +

  labs(
    title = paste(
      "Histogram of Area (sqkm) in the whole world of species ( N =",
      length(areahind),
      ") in the Hindukush"
    ),
    x = "Area",
    y = "Frequency"
  )

```



```
#Histogram for ratio
#-----

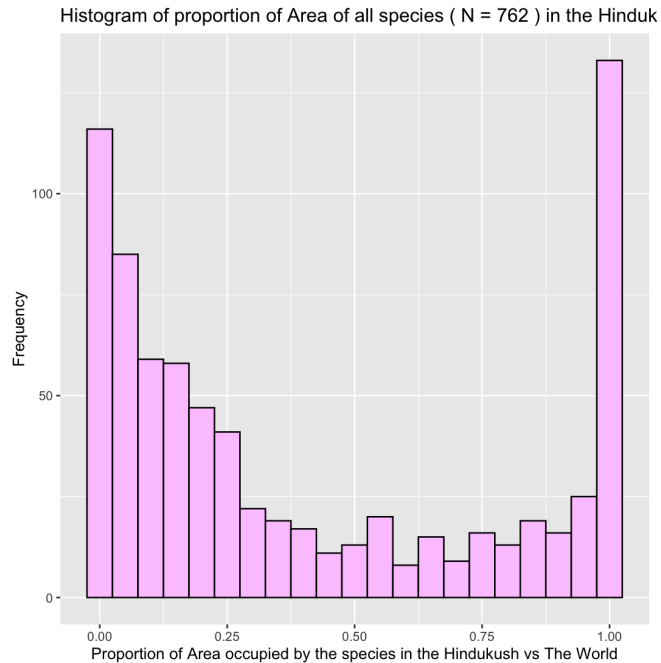
#ratio of area in the Hindukush to that of the world
mamratio = areahind / newarea_world

df3 = as.data.frame(cbind(c(1:length(mamratio)), mamratio))

ggplot(df3, aes(x = mamratio)) +

  geom_histogram(binwidth = 0.05,
                 fill = "#ffccff",
                 col = "black") +

  labs(
    title = paste(
      "Histogram of proportion of Area of all species ( N =",
      length(areahind),
      ") in the Hindukush"
    ),
    x = "Proportion of Area occupied by the species in the Hindukush
vs The World",
    y = "Frequency"
  )
```



```

maxhind = which(mamratio > 0.75) #Inspecting the species living
solely in hindukush
length(maxhind)

maxhind_ratio = mamratio[maxhind]

interval = table(cut(maxhind_ratio, seq(0.5, 1, 0.01))) #inspecting
the distribution

onlyhind = which(mamratio > 0.99) #Inspecting the species only living
in hindukush
onlyhind_ratio = mamratio[onlyhind]

df_onlyhind = df_world[onlyhind, ]

#Histogram for species only living in Hindukush
df4 = as.data.frame(cbind(c(1:length(maxhind)), y =
mamclip$presence[maxhind], z = maxhind_ratio))

ggplot(df4, aes(x = z)) +

  geom_histogram(binwidth = 0.05,
                 fill = "#ffccff",
                 col = "black") +

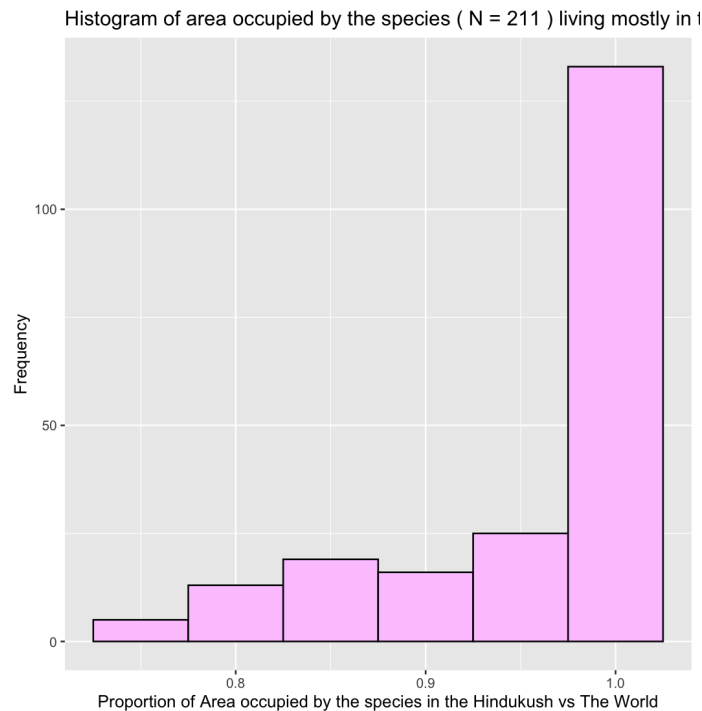
  labs(
    title = paste(

```

```

    "Histogram of area occupied by the species ( N =",
    length(maxhind),
    ") living mostly in the Hindukush"
  ),
  x = "Proportion of Area occupied by the species in the Hindukush
vs The World",
  y = "Frequency"
)

```



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#Changing the co-ord ref system
#-----

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newcrs = "+proj=merc +lon_0=0 +k=1 +x_0=0 +y_0=0 +a=6371000
+b=6371000 +units=m +no_defs "
newclip <-
  terra::project(clip, newcrs)
newhind <-
  terra::project(hind, newcrs)

```

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#Making a binary grid for each of the species
#-----

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newclip_1 = aggregate(newclip, by = "sci_name") #First dissolving the
rows with same scientific name

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#Making a grid
r <- rast(newhind) #raster of the new projected boundary
res(r) <- 25000 #setting resolution = 25 km
values(r) <-
  1:ncell(r) #Assigning some unique value to each cell for
  identifiability
rpoly <-
  as.polygons(r) #Changing spatraster to spatvector(polygons), as we
  will be cropping and cropping requires both of same format

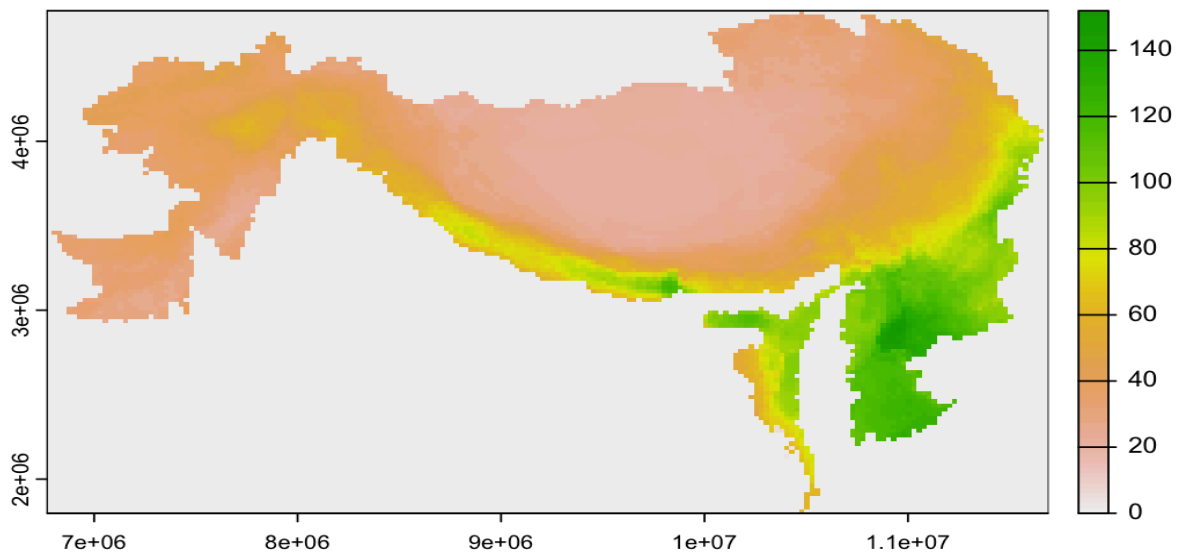
#Doing for the first species in the dissolved spatvector
sp1 = newclip_1[1] #the first species
int1 <- crop(rpoly, sp1) #cropping the raster
r1 = r #making a new raster
values(r1) <- 0 #assigning all to 0
r1[int1] = 1 #Now changing all locations of first species to 1
rast_sp = r1 #now creating a grand raster with all species of which
first layer will be the first species

#Now doing this for all species and then adjoin one by one
for (i in 2:nrow(newclip_1)) {
  sp = newclip_1[i]
  int <- crop(rpoly, sp)
  r_copy = r
  values(r_copy) <- 0
  r_copy[int] <- 1
  rast_sp = c(rast_sp, r_copy) #new layer added with whatever is
}

#Now summing up cellwise to see the density of species in each of the
cell
rast_sum = sum(rast_sp)

#Plotting the sum of the rasters
plot(rast_sum, col = terrain.colors(100, rev = T))

```

```
#Importing libraries for the world map
library(sf)
library(rnaturalearth)
library(rnaturalearthdata)

#Overlaying the country borders
#-----
world <-
  ne_countries(scale = "medium", returnclass = "sf") #Map of the
whole world
world_vect = vect(world) #as spat vector

hind_countries <-
  crop(world_vect, hind) #Then cropping with the himalayan part

newborder <-
  terra::project(hind_countries, newcrs) #Changing to our required
co-ordinate system

#Importing libraries for the world map
library(sf)
library(rnaturalearth)
library(rnaturalearthdata)

#Overlaying the country borders
#-----
world <-
```

```

    ne_countries(scale = "medium", returnclass = "sf") #Map of the
whole world
world_vect = vect(world) #as spat vector

plot(world_vect) #Plotting

hind_countries <-
  crop(world_vect, hind) #Then cropping with the himalayan part
plot(hind_countries)

newborder <-
  terra::project(hind_countries, newcrs) #Changing to our required
co-ordinate system

#Saving the images in a pdf file
#-----
pdf(file =
"/Users/srijan/Documents/Academic_Stuffs/Projects/Himalayan_Biogeogra
phy/Mammals.pdf",
  #creating the directory
  width = 6,
  height = 4)

for (i in 1:592) {
  plot(rast_sp[[i]], main = paste(newclip_1$sci_name[i]))
  lines(newclip_1[i], col = "red", lwd = 0.8) #Plot
the images
  lines(newborder, col = "blue", lwd = 0.5)
}

plot(rast_sum, col = terrain.colors(100, rev = T), main = "Density
Wise Plots of Species in the Hindukush")
lines(newborder, col = "blue", lwd = 0.5)

dev.off() #make the pdf ready

```

Density Wise Plots of Species in the Hindukush

