

OCURRENCIA _ BROMELIAS

C.P.P.

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Ejercicio de clase en Sistemática, Biología. Univerdiad Industrial de Santander. Colombia

Guiones de práctica: Mapas

Inicialmente cargar paquetes y librerías

```
library(ggplot2) # ggplot() fortify()
library(dplyr) # %>% select() filter() bind_rows()
library(rgdal) # readOGR() spTransform()
library(raster) # intersect()
library(ggsn) # north2() scalebar()
library(rworldmap) # getMap()
library(ggmap)
```

Leer tablas de Ocurrencias de especies

```
B.ACUM<- read.csv("B.acum.csv", sep = ";")
E.ERECTI<- read.csv("E.erect.csv", sep = ";")
D.STRO<- read.csv("D.strob.csv", sep = ";")
```

#Visualizar

```
head(B.ACUM)
```

Llamada de columnas

Nombre_Científico - Longitud - Latitud

```
vars1 <- c("key", "scientificName", "decimalLongitude",
"decimalLatitude")
bacum_trim = B.ACUM %>% dplyr::select(one_of(vars1))
eerecti_trim =E.ERECTI%>% dplyr::select(one_of(vars1))
dstro_trim =D.STRO%>% dplyr::select(one_of(vars1))
```

Crear tablas

```
write.table(bacum_trim)
write.table(eerecti_trim)
write.table(dstro_trim)
```

Unificar tablas

```
BROM_trim <- bind_rows(bacum_trim, erecti_trim, dstro_trim)

str(BROM_trim)
```

Verificar que nombres de especies sean consistentes

```
unique(BROM_trim$scientificName)
```

Necesitas limpiarlos

```
BROM_trim$scientificName <- BROM_trim$scientificName %>%
  recode("Brocchinia acuminata L.B.Sm." = "Brocchinia acuminata",
        "Encholirium erectiflorum L.B.Sm." = "Encholirium erectiflorum",
        "Deuterocohnia strobilifera var. strobilifera" = "Deuterocohnia
strobilifera", "Deuterocohnia strobilifera var. inermis L.B.Sm." =
"Deuterocohnia strobilifera", "Deuterocohnia strobilifera Mez" =
"Deuterocohnia strobilifera")
```

De nuevo Verificación de Nombres de especies

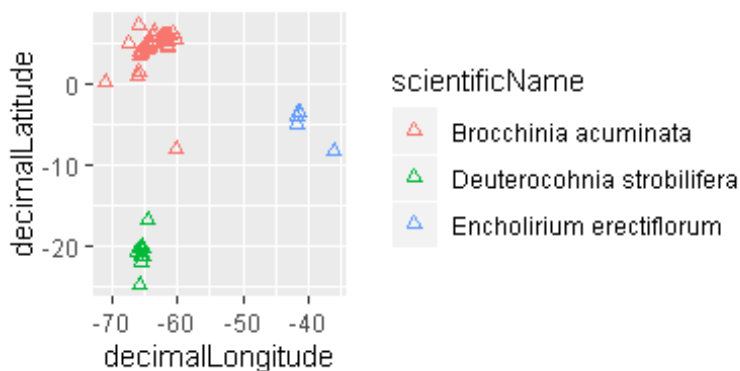
```
unique(BROM_trim$scientificName)
```

```
## [1] "Brocchinia acuminata"      "Encholirium erectiflorum"
## [3] "Deuterocohnia strobilifera"
```

Hecho.

Gráfico- preliminar

```
ggplot(BROM_trim, aes(x = decimalLongitude, y = decimalLatitude,
  colour = scientificName)) +
  geom_point(shape = 2)
```



Pedir ayuda de las funciones de paquetes

?ggplot

?geom_point

```
BROM_trim_us = BROM_trim %>% filter(decimalLongitude > 0)
```

Gráficar de nuevo

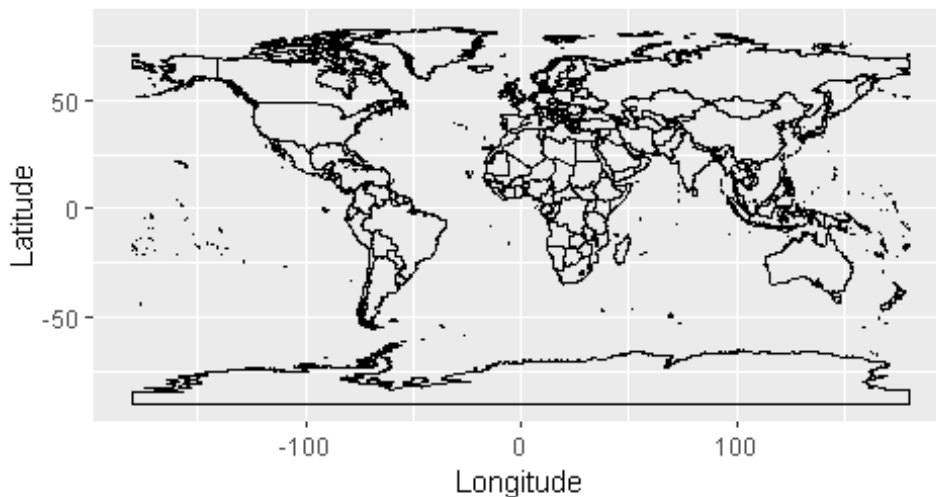
```
ggplot(BROM_trim_us, aes(x = decimalLongitude, y = decimalLatitude,  
  colour = scientificName)) +  
  geom_point(shape = 1)
```

Obtener Mapamundi con getMap

```
world <- getMap(resolution = "low")
```

Graficar datos espaciales con el mapa usando ggplot

```
ggplot() +  
  geom_polygon(data = world,  
    aes(x = long, y = lat, group = group),  
    fill = NA, colour = "black") +  
  geom_point(data = BROM_trim_us, # Add and plot species data  
    aes(x = decimalLongitude, y = decimalLatitude,  
    colour = scientificName)) +  
  coord_quickmap() + # Prevents stretching when resizing  
  theme_gray() + # Remove ugly grey background  
  xlab("Longitude") +  
  ylab("Latitude") +  
  guides(colour=guide_legend(title="Species"))
```



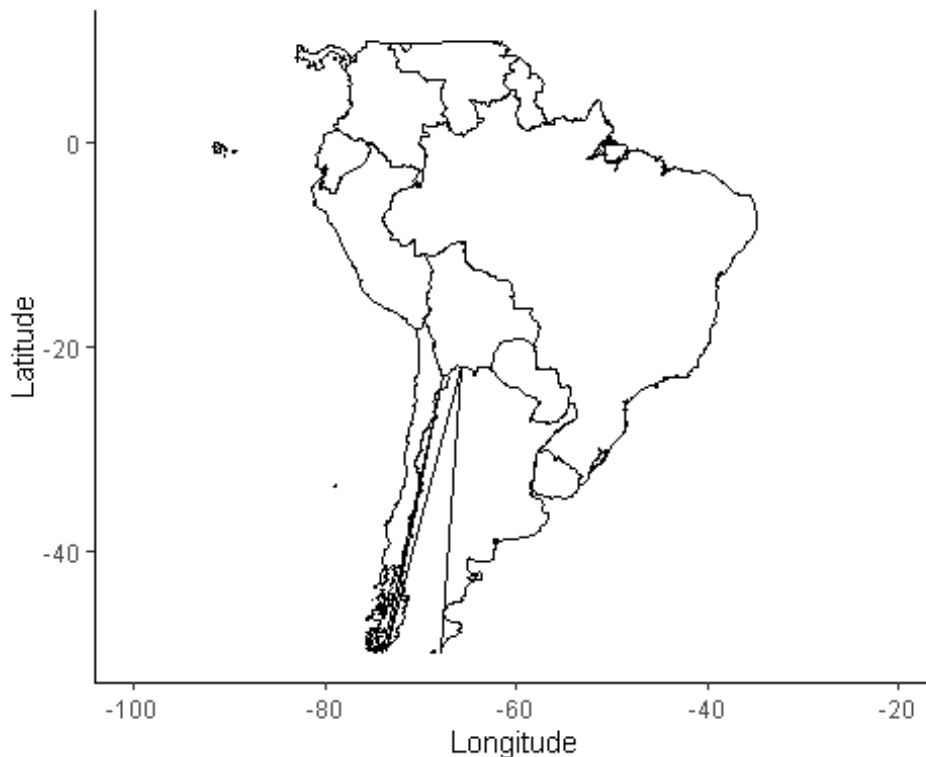
Crear un vector de: Nombres de países

```
saf_countries1 <- c("Brazil", "Bolivia", "Argentina", "Peru", "Colombia",  
"Ecuador", "Venezuela", "Paraguay", "Uruguay", "Guyana", "Chile",  
"Panama")
```

```
world_saf1 <- world[world@data$ADMIN %in% saf_countries1, ]
```

Grafica con ggplot los países del vector

```
ggplot() +  
  geom_polygon(data = world_saf1,  
    aes(x = long, y = lat, group = group),  
    fill = NA, colour = "black") +  
  geom_point(data = BROM_trim_us, # Add and plot speices data  
    aes(x = decimalLongitude, y = decimalLatitude,  
      colour = scientificName)) +  
  coord_quickmap() +  
  xlim(-100, -20) # Set x axis Limits, xlim(min, max)  
  ylim(-50, 10) # Set y axis Limits  
  theme_classic() # Remove ugly grey background  
  xlab("Longitude") +  
  ylab("Latitude") +  
  guides(colour=guide_legend(title="Species"))
```

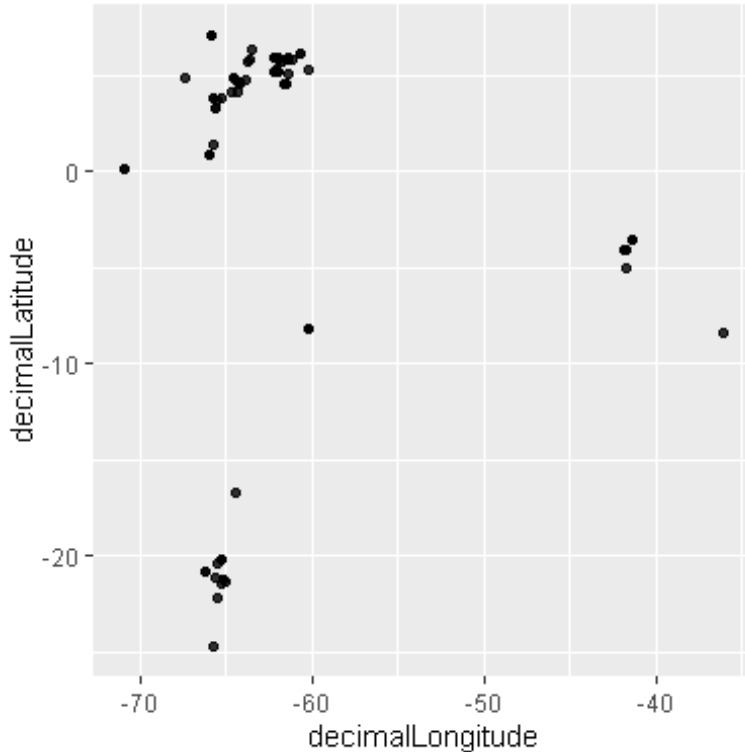


Leer datos unificados de las especies

```
Foste_rella = BROM_trim
```

Gráfico Preliminar

```
ggplot(Foste_rella, mapping = aes(x = decimalLongitude , y = decimalLatitude)) +  
  geom_point(alpha = 0.8)
```



```
library(raster)
```

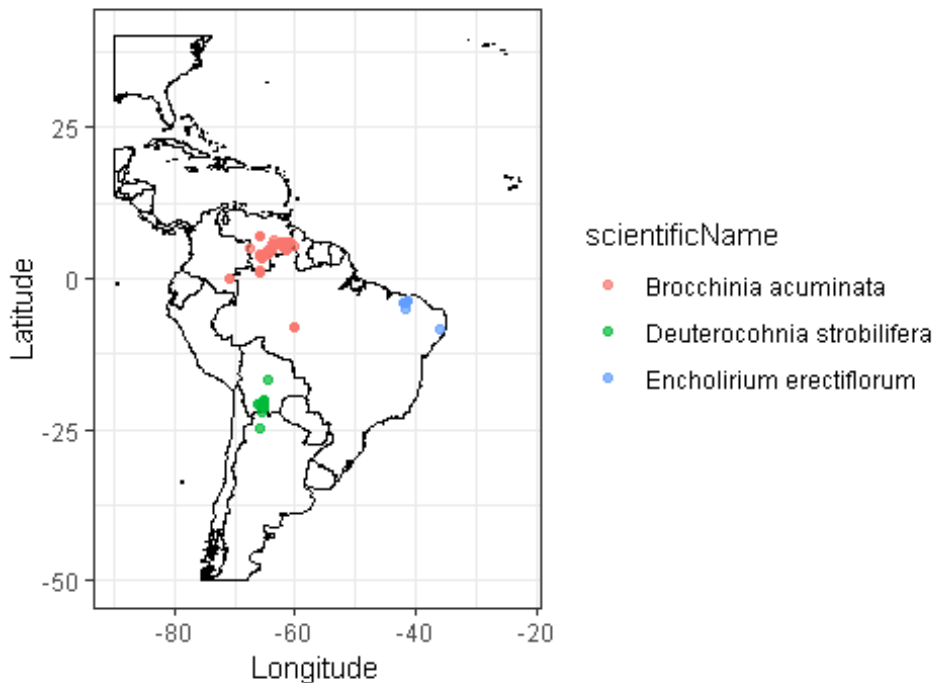
* Ajustar mi mapa con las coordenadas del sistema geográfico

```
Clip_BROM <- as(extent(-90, -20, -50, 40), "SpatialPolygons")  
proj4string(Clip_BROM) <- CRS(proj4string(world))  
world_clip <- raster::intersect(world, Clip_BROM)  
world_clip_f <- fortify(world_clip)
```

GRAFICAR MAPA CON PAÍSES Y DISTRIBUCIÓN DE ESPECIES

```
ggplot(Foste_rella, aes(x = decimalLongitude, y = decimalLatitude,  
  colour = scientificName)) +  
  geom_polygon(data = world_clip_f,  
    aes(x = long, y = lat, group = group),  
    fill = NA, colour = "black") +  
  geom_point(alpha = 0.7,  
    aes(x = decimalLongitude, y = decimalLatitude, colour = scientificName),  
    data = Foste_rella) +  
  theme_bw() +  
  xlab("Longitude") +
```

```
ylab("Latitude") +
coord_quickmap()
```



Grafica con archivo raster Regiones del neotrópico

Leer shapefile

```
SHP_dataaBRO <- readOGR(dsn = "Lowenberg_Neto_2014_shapefile", layer =
"Lowenberg_Neto_2014")

## OGR data source with driver: ESRI Shapefile
## Source: "D:\USUARIO\Desktop\TRABAJOS R
erre\Lab_SISTE_practica_conR\ProyecSISTE\Lowenberg_Neto_2014_shapefile",
layer: "Lowenberg_Neto_2014"
## with 55 features
## It has 9 fields
```

Verificar el ajuste

```
proj4string(SHP_dataaBRO)

## [1] "+proj=longlat +datum=NAD27 +no_defs +ellps=clrk66
+nadgrids=@conus,@alaska,@ntv2_0.gsb,@ntv1_can.dat"
```

Transformar con sistema WGS84

```
SHP_dataaBRO <- spTransform(SHP_dataaBRO, CRS("+proj=longlat  
+datum=WGS84"))
```

Sujetar polígonos espaciales

```
s_clip <- raster::intersect(SHP_dataaBRO, Clip_BROM)
```

Prueba de gráfica

```
plot(s_clip)
```



Ver estuctura de archivo raster Regiones

```
str(s_clip)
```

Ver nombres de archivo Raster Regiones

```
names(s_clip)
```

```
## [1] "NUMB"      "REGION"    "SOURCE"    "Province_1" "Dominions"  
## [6] "Subregio_1" "DOI"       "PaperURL"  "CITATION_1"
```

Fortify for ggplot2

```
s_clip_fo <- fortify(s_clip, region = "NUMB")
```

EXTRA LIBRERÍAS PARA GRAFICAR MAPA

```
library(RColorBrewer)
library("viridis")
library("ggsci")
library("ggplot2")
library("gridExtra")
```

ggplot de ecoregiones

```
map_BROM <- ggplot(Foste_rella, aes(x = decimalLongitude, y =
decimalLatitude)) +
  geom_point(shape = 1)+
  geom_polygon(data = s_clip_fo, aes(x = long, y = lat, group = group,
fill = id), color = "black", size = 0.5)+ theme_bw()+
  geom_point(alpha = 0.9, size = 3,
  aes(x = decimalLongitude, y = decimalLatitude, colour = scientificName,
size = 2),
  data = Foste_rella,)+
  theme_bw()+
  theme(legend.position="right") +
  theme(legend.title=element_blank()) +
  xlab("Longitud") +
  ylab("Latitud") +
  coord_quickmap()
```

Añadir Colores de relleno

```
map_BROM_col1 = map_BROM + scale_color_ucscgb()+
scale_fill_viridis(discrete = TRUE, alpha = 0.8)
```

Añadir comentarios

```
map_BROM_annot <- map_BROM_col1 + annotate("rect", xmin = -88 , xmax = -
35, ymin = -25, ymax = 10, fill="firebrick2", alpha=0.35) +
  annotate("text", x = -53.8, y = 19, size = 6.7, label = "Area Ocurrencia
  Bromeliaceae")
```

Añadir barra de escala

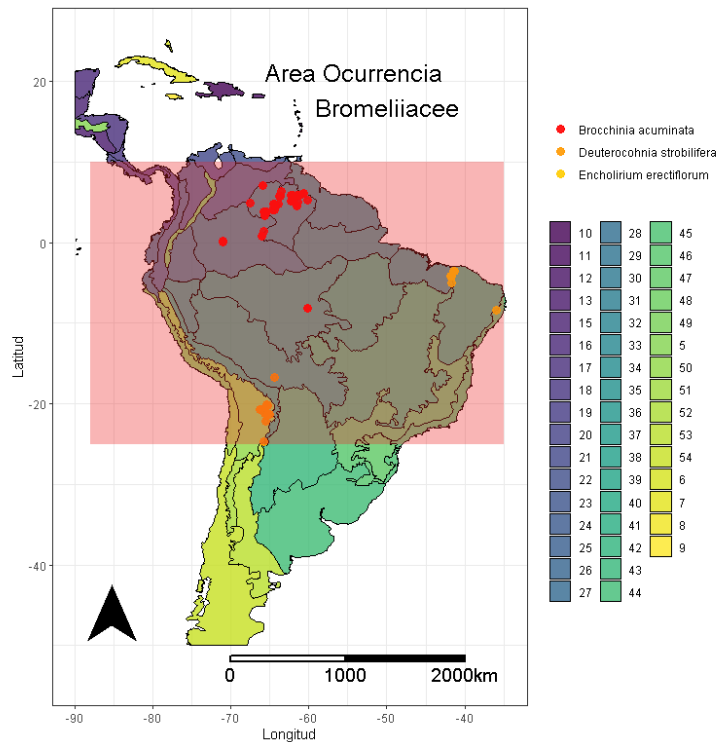
```
map_BROM_scale <- map_BROM_annot +
  scalebar(data = s_clip_fo,
  transform = TRUE, dist = 1000, dist_unit = "km", model='WGS84',
  height = 0.01,
  location = "bottomleft", anchor = c(x = -70, y = -52))
```

Añadir la flecha del Norte

Resultado

* Grafico de ocurrencia de especies en mapa de bioregiones.


```
north2(map_BROM_scale, x = 0.27, y = 0.18, scale = 0.1, symbol = 12)
```



Referencias

https://ourcodingclub.github.io/2016/12/11/maps_tutorial.html

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.