Choropleth Map (COVID-19, Nepal)

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Introduction

We are going to make a choropleth map showing the total number of cases of Coronavirus in districts of Nepal.

Loading the required libraries

```
library(ggplot2)
library(rgdal)
library(readr)
library(dplyr)
```

Importing the dataset and mapfile

```
# Map file
Nepal_map = readOGR("https://github.com/sulovek/Data-Analysis-Projects/raw/master/Datasets/nepal_map.ge
```

```
## OGR data source with driver: GeoJSON
## Source: "https://github.com/sulovek/Data-Analysis-Projects/raw/master/Datasets/nepal_map.geojson", la
## with 77 features
## It has 3 fields
```

```
Nepal_map = Nepal_map[order(Nepal_map$DISTRICT, decreasing = F),]
plot(Nepal_map)
```

```
# Dataset containing confirmend cases (Districtwise)
coronadata <- read_csv("https://raw.githubusercontent.com/sulovek/Data-Analysis-Projects/master/Datasets
```

```
## Parsed with column specification:
## cols(
##   DISTRICT = col_character(),
##   CONFIRMED = col_double(),
##   DEATHS = col_double(),
##   RECOVERED = col_double()
## )
```

```
# NA in zero values
coronadata[coronadata == 0] <- NA
```

Merging

```
Nepal_map$CASES = coronadata$CONFIRMED
```

Fortifying

```
Nepal_df = fortify(Nepal_map, region = "DISTRICT")
```

```
## Warning in RGEOSUnaryPredFunc(spgeom, byid, "rgeos_isvalid"): Self-intersection
## at or near point 80.908712981182234 30.294248276334642
```

```
## Warning in RGEOSUnaryPredFunc(spgeom, byid, "rgeos_isvalid"): Self-intersection
## at or near point 83.925143511256692 27.542968981486169
```

```
## SpP is invalid
```

```
## Warning in rgeos::gUnaryUnion(spgeom = SpP, id = IDs): Invalid objects found;
## consider using set_RGEOS_CheckValidity(2L)
```

```
choro_dat <- data.frame(region=Nepal_map@data$DISTRICT,
                        value=Nepal_map@data$CASES,
                        stringsAsFactors=FALSE)
```

For Labelling

```
centroids = setNames(do.call("rbind.data.frame", by(Nepal_df, Nepal_df$group, function(x) {Polygon(x[c(
district = data.frame(choro_dat$region)
district = district[order(district$choro_dat.region),]
centroids$label = district
```

Plot

```
Nepal_df = rename(Nepal_df, region = id)
corona_map <- left_join(Nepal_df, choro_dat, by = "region")
ggplot(corona_map, aes(long, lat, group = group))+
  geom_polygon(aes(fill = value), color = "white")+
  scale_fill_continuous(name = "Cases", limits = c(0, 619), low="#ffeda0", high="#f03b20", guide="colorl
  theme_void()+
  labs(title = "COVID-19", subtitle = "June 14, 2020
Dr. Sulove Koirala", caption = "Data Source: MoHP Nepal")+
  with(centroids, annotate(geom="text", x = long, y = lat, label=label, size=2)) +
  theme(
    plot.title = element_text(color = "black", size = 16, face = "bold", hjust = 0.5),
    plot.subtitle = element_text(color = "grey", hjust = 0.5),
    plot.caption = element_text(face = "italic", hjust = 0.9, vjust = 1.5),
    legend.position = "bottom")
```

COVID−19

June 14, 2020

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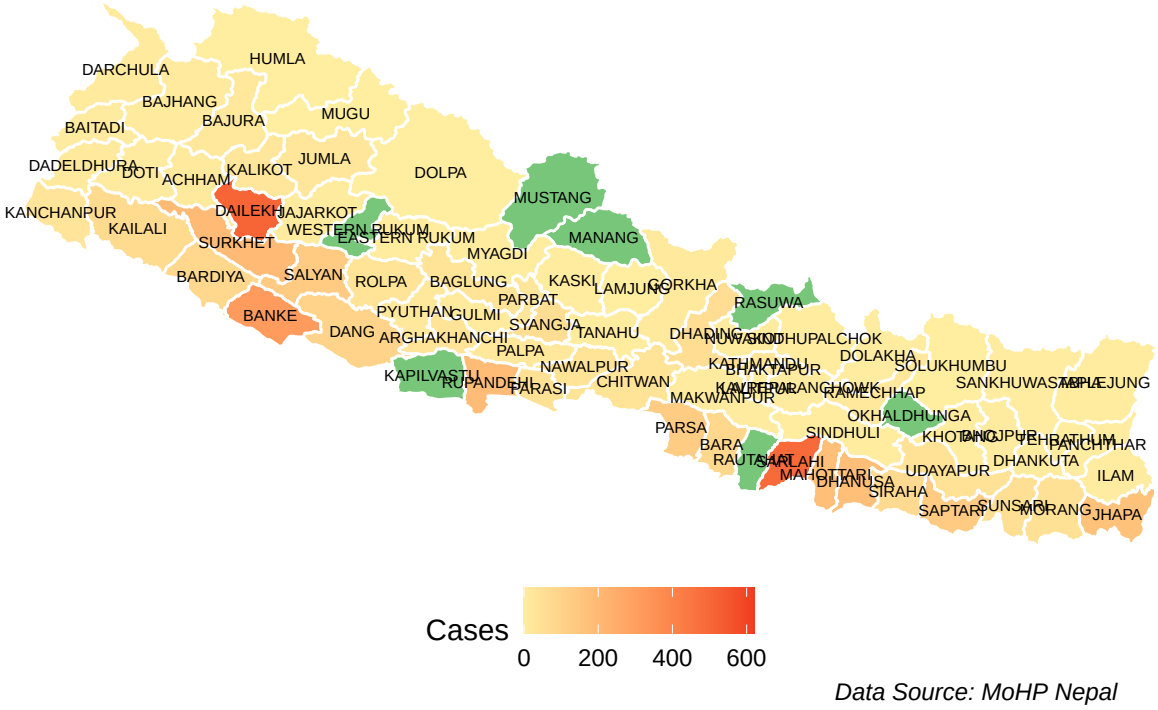

Data Source: MoHP Nepal

Bibiliography

COVID 19 - Active Cases, Deaths and Recovered. (n.d.). Retrieved June 14, 2020, from https://kathmandupost.com/covid19