Assignment 3

Index No:- AS2017419

Dear Madam,

I am sorry to say about my issue in assignment of preparing report. My Rmarkdown file stucked, when I'm doing assignment last part. Then, I restarted my laptop. After restarting, I couldn't open my file in Rmarkdown. All codes that I have typed have fully deleted. Unfortunatly, I only knited first part of my outputs. I couldn't recover my file before the deadline of the project. Therefore, I re-wrote my all codes manually. That written file are attached into this pdf. Further, I attached the html file which has been knited into the lms with my written pdf.

I surely upload my html and Rmd files after solving my technical issue. I definetly try to send that as soon as possible.

Thank you!

W.H. Shashmi Kaushalya.

Title : Covid-19 Pandamic in Guinea.

W. H. Shashini Kaushalya - 2017419

** 1. Introduction **

Introduction details are included in attached html file.

1.1. Location of Guinea.
1.2 Climate condition of Guinea
1.3 Lock-down status of Guinea
} Information are included in attached html file.

1.4 Action taken by the government of Guinea.

 Guinea is a country that imposing some rules for their public. They informed some of prevention action from this corona virus. And they gave guidance to protect for the people of their country. Further, they have imposed few lockdown conditions in their country. Now, they vaccinated their people to improve the imunity of system of their public. In addition to that, they have given so many rules and regulation for the workplaces in their country.

code for getting location.

```
map_guinea <- leaflet() %>% addTiles() %>%
              setView(lng = -9.6966, lat = 9.9456,
                      zoom = 16) %>%
              addMarkers(lng = -9.6966, lat = 9.9456)

map_guinea
```

Packages.

```
library (sta 3262)
library (tidyverse)
library (maggrittr)
library (coronavirus)
library (ggplot2)
library (leaflet)
```

Getting country dataset

```
```{r, echo = FALSE}
get_individual_project_country ("AS20174419")
data("coronavirus")
head (coronavirus)
unique (coronavirus$country)
guinea_corona <- coronavirus %>% filter (country == "Guinea")
guinea_corona
summary (guinea_corona)
```

```{r, echo = FALSE, eval = FALSE, warning = FALSE}
Convert to a tibble
as.tibble (guinea_corona)
```

```{r, echo = FALSE, eval = FALSE}
#removing the province variable
guinea_corona1 <- select (guinea_corona, -c (province))
```

~~guinea_corona1~~

```{r, echo = FALSE, eval = FALSE}
#Identifying missing values in type of recovered.
tail (guinea_corona1, 46)
```
```

```{r, echo = FALSE}
# omitting missing values
guinea_corona_wider <- guinea_corona1 %>%
  pivot_wider(names_from = type, value_from = cases) %>%
  drop_na()
```
~~guinea_corona_wider~~
```{r, echo = FALSE}
# converting the long format
guinea_corona_new <- guinea_corona_wider %>%
  pivot_longer(3:7, names_to = "type", values_to = "cases")
```
~~guinea_corona_new~~
```{r, echo = FALSE, comment = NA}
head(guinea_corona_new)
summary(guinea_corona_new)
glimpse(guinea_corona_new)
```

2.1 Visualization of COVID-19 cases in Guinea

Visualization of COVID-19 confirmed, death, recovered cases in guinea

```{r, echo = FALSE}
P1 <- ggplot(guinea_corona_new, aes(date, cases)) +
  geom_line(color = "blue") +
  facet_wrap(.~type)
P1
```
```{r, echo = FALSE}
P2 <- ggplot(guinea_corona_new, aes(cases, type)) +
  geom_jitter()
P2
```

considering the active cases.

```{r, echo = FALSE}
active_cases_guinea <- guinea_corona_wider %>%
  mutate(total_active = cumsum(confirmed) - cumsum(recovered)
                        - cumsum(death))

P3 <- ggplot(active_cases_guinea, aes(date, total_active)) +
  geom_line(color = "green")

P3
```

Comparison with other countries

Here, this analysis are considered the neighbour countries of Guinea. This try to show how the other countries vary with coronavirus cases. Mainly, we consider main four countries, such as Mali, Liberia, Sierra Leone and Senegal.

```{r, echo = FALSE}
guinea_corona <- coronavirus %>% filter(country = "Guinea")
confirmed_cases_guinea <- guinea_corona %>% filter(type =
                                                   "confirmed")

mali_corona <- coronavirus %>% filter(country = "Mali")
confirmed_cases_mali <- mali_corona %>% filter(
                                        type = "confirmed")

liberia_corona <- coronavirus %>% filter(country = "Liberia")
confirmed_cases_liberia <- liberia_corona %>% filter(
                                        type = "confirmed")

Sengal_corona <- coronavirus %>% filter(country = "confirmed")
confirmed_cases_sengal <- sengal_corona %>% filter(type =
                                                   "confirmed")
```

sierra_Leone_corona <- coronaviruses %>% filter (country = "confirmed")

confirmed_sierra_Leone <- sierra_leone_corona %>% filter (type = "confirmed")

neighbour_confirmed_cases <- rbind (confirmed_cases_guinea, confirmed_cases_mali, confirmed_cases_liberia, confirmed_cases_senegal, confirmed_cases_sierra_Leone)

g1 <- ggplot (neighbour_confirmed_cases, aes (x = date, y = cases, col = country)) + geom_line () + ggtitle (" confirmed cases in Guinea's neighbour countries)

ggplotly (g1)

"""

```{r, echo = FALSE}

g2 <- ggplot ( neighbour_confirmed_cases aes ( x = country, y = cases, fill = country)) + geom_col ( ) + ggtitle (" confirmed cases of Guinea's neighbours by column char")

ggplotly (g2)

```

* After that, I can get death and recovered cases of neighbour countries of guinea using above ~~grap~~ codes. Here, we edit above codes to visualize that plots. From that plots, we can interprete how the covid-19 cases (death / recovered) change between ~~them~~ guinea and other countries.

* After getting all plots and tables, we can conclude my analysis in conclusion part.

* Then, I can discuss about my analysis in ~~the~~ discussion part using my interpretations and conclusion as well as my limitations.

* Then, I ~~not~~ include my reference part.