Covid19

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Importing nessary library and download CSV data from the Github Data Repository by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (https://github.com/CSSEGISandData/COVID-19/tree/master/csse_covid_19_data/csse_covid_19_time_series).

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.1.2     v dplyr   1.0.6
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(lubridate)
```

```
##
## Attaching package: 'lubridate'

## The following objects are masked from 'package:base':
##
##     date, intersect, setdiff, union
```

```
uid_lookup_url <- "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/U
url_in <- "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covi

uid <- read_csv(uid_lookup_url) %>%
  select(-c(Lat, Long_, Combined_Key, code3, iso2, iso3, Admin2))
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   UID = col_double(),
```

```
##   iso2 = col_character(),
##   iso3 = col_character(),
##   code3 = col_double(),
##   FIPS = col_character(),
##   Admin2 = col_character(),
##   Province_State = col_character(),
##   Country_Region = col_character(),
##   Lat = col_double(),
##   Long_ = col_double(),
##   Combined_Key = col_character(),
##   Population = col_double()
## )
```

```
file_names <- c("time_series_covid19_confirmed_US.csv",
                "time_series_covid19_confirmed_global.csv",
                "time_series_covid19_deaths_US.csv",
                "time_series_covid19_deaths_global.csv",
                "time_series_covid19_recovered_global.csv")
urls <- str_c(url_in, file_names)

US_cases <- read_csv(urls[1])
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   .default = col_double(),
##   iso2 = col_character(),
##   iso3 = col_character(),
##   Admin2 = col_character(),
##   Province_State = col_character(),
##   Country_Region = col_character(),
##   Combined_Key = col_character()
## )
## i Use `spec()` for the full column specifications.
```

```
global_cases <- read_csv(urls[2])
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   .default = col_double(),
##   `Province/State` = col_character(),
##   `Country/Region` = col_character()
## )
## i Use `spec()` for the full column specifications.
```

```
US_deaths <- read_csv(urls[3])
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   .default = col_double(),
```

```
##   iso2 = col_character(),
##   iso3 = col_character(),
##   Admin2 = col_character(),
##   Province_State = col_character(),
##   Country_Region = col_character(),
##   Combined_Key = col_character()
## )
## i Use `spec()` for the full column specifications.
```

```
global_deaths <- read_csv(urls[4])
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   .default = col_double(),
##   `Province/State` = col_character(),
##   `Country/Region` = col_character()
## )
## i Use `spec()` for the full column specifications.
```

Create and tidy Dataframes with R frendly colum names and drop coloums not needed for this assignment. All the of the final dataframes are created in this code block, with required coloums and data points.

```
global_cases <- global_cases %>%
  pivot_longer(cols = -c('Province/State',
                         'Country/Region',
                         'Lat',
                         'Long'),
               names_to = "date",
               values_to = "cases") %>%
  select(-c(Lat, Long))

global_deaths <- global_deaths %>%
  pivot_longer(cols = -c('Province/State',
                         'Country/Region',
                         'Lat',
                         'Long'),
               names_to = "date",
               values_to = "deaths") %>%
  select(-c(Lat, Long))

global <- global_cases %>%
  full_join(global_deaths) %>%
  rename(Country_Region = 'Country/Region',
         Province_State = 'Province/State') %>%
  mutate(date = mdy(date)) %>%
  filter(cases > 0) %>%
  unite("Combined_Key",
        c(Province_State, Country_Region),
        sep = ", ",
```

```
        na.rm = TRUE,
        remove = FALSE) %>%
  left_join(uid, by = c("Province_State", "Country_Region")) %>%
  select(-c(UID, FIPS)) %>%
  select(Province_State, Country_Region, date, cases,
         deaths, Population, Combined_Key)
```

```
## Joining, by = c("Province/State", "Country/Region", "date")
```

```
US_cases <- US_cases %>%
  pivot_longer(cols = -(UID:Combined_Key),
               names_to = "date",
               values_to = "cases") %>%
  select(Admin2:cases) %>%
  mutate(date = mdy(date)) %>%
  select(-c(Lat, Long_))

US_deaths <- US_deaths %>%
  pivot_longer(cols = -(UID:Population),
               names_to = "date",
               values_to = "deaths") %>%
  select(Admin2:deaths) %>%
  mutate(date = mdy(date)) %>%
  select(-c(Lat, Long_))

US <- US_cases %>%
  full_join(US_deaths)
```

```
## Joining, by = c("Admin2", "Province_State", "Country_Region", "Combined_Key", "date")
```

```
US_by_state <- US %>%
  group_by(Province_State, Country_Region, date) %>%
  summarise(cases = sum(cases), deaths = sum(deaths),
            Population = sum(Population)) %>%
  mutate(deaths_per_mill = deaths *1000000 / Population) %>%
  select(Province_State, Country_Region, date,
         cases, deaths, deaths_per_mill, Population) %>%
  ungroup()
```

```
## `summarise()` has grouped output by 'Province_State', 'Country_Region'. You can override using the `
```

```
US_by_state <- US_by_state %>%
  mutate(new_cases = cases - lag(cases),
         new_deaths = deaths - lag(deaths))

US_totals <- US_by_state %>%
  group_by(Country_Region, date) %>%
  summarise(cases = sum(cases), deaths = sum(deaths),
            Population = sum(Population)) %>%
  mutate(deaths_per_mill = deaths *1000000 / Population) %>%
  select(Country_Region, date,
         cases, deaths, deaths_per_mill, Population) %>%
  ungroup()
```

```
## `summarise()` has grouped output by 'Country_Region'. You can override using the `.groups` argument.
```

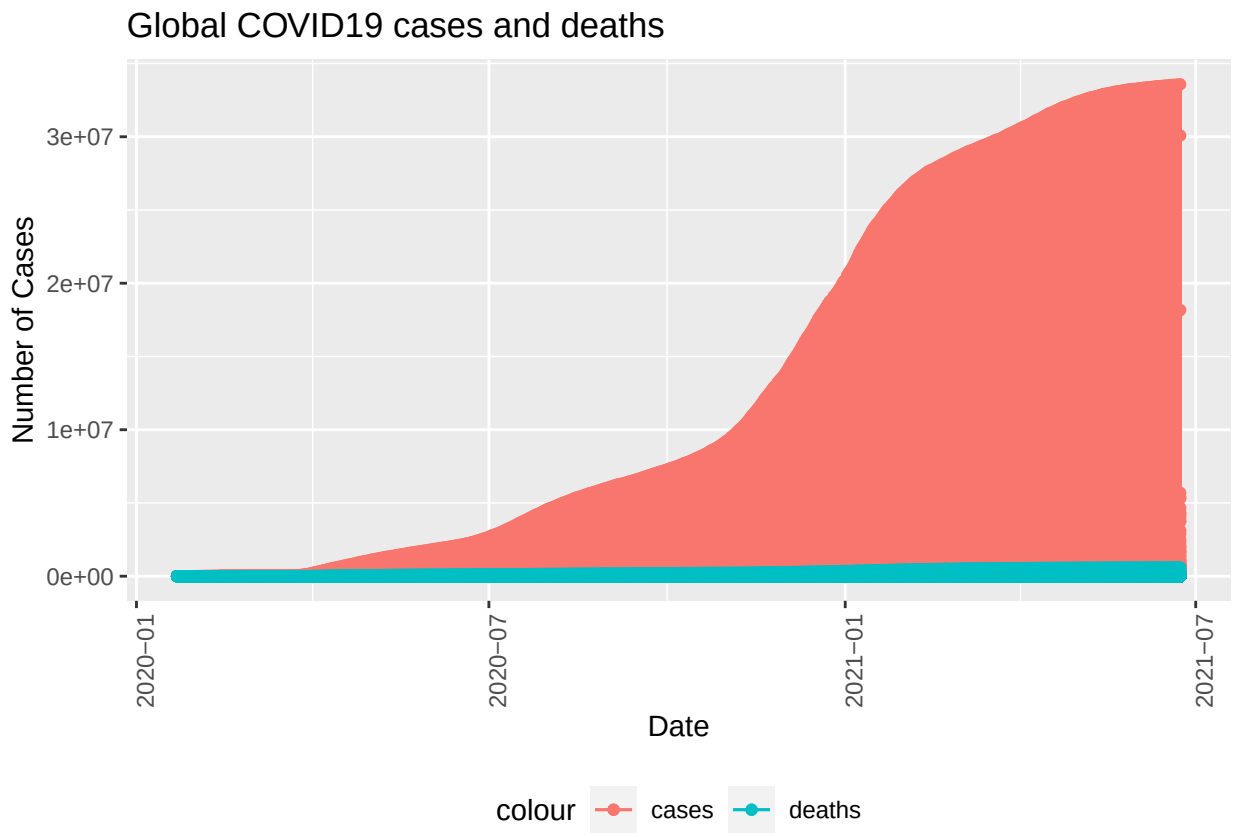
```
By_country <- global %>%
  group_by(Province_State, Country_Region, date) %>%
  summarise(cases = sum(cases), deaths = sum(deaths),
            Population = sum(Population)) %>%
  mutate(deaths_per_mill = deaths *1000000 / Population) %>%
  select(Province_State, Country_Region, date,
         cases, deaths, deaths_per_mill, Population) %>%
  ungroup()
```

```
## `summarise()` has grouped output by 'Province_State', 'Country_Region'. You can override using the `
```

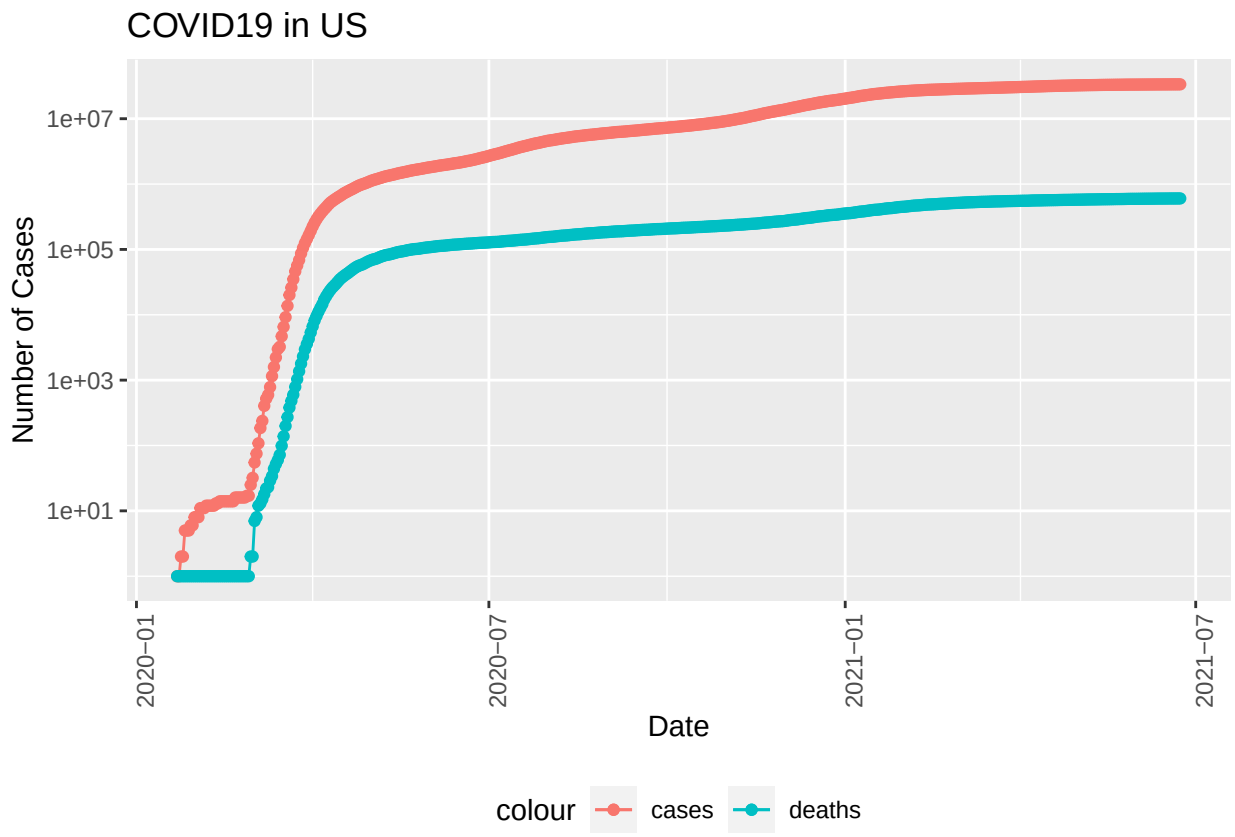
```
US_totals <- US_totals %>%
  mutate(new_cases = cases - lag(cases),
         new_deaths = deaths - lag(deaths))

US_date <- US_by_state %>%
  mutate(Month = str_sub(date,6,7), # Seperating the Month
         Day = str_sub(date,9,10), # Seperating the Day
         Year = str_sub(date,1,4)) # Seperating the year

global <- global %>%
  mutate(new_cases = cases - lag(cases),
         new_deaths = deaths - lag(deaths),
         Month = str_sub(date,6,7),
         Day = str_sub(date,9,10),
         Year = str_sub(date,1,4))
```

Ploting global and US COVID19 cases and deaths graphs. I made an effort to graph each indivual US states, however due to fixed graph size it's barly readable, breaking it down country wise (using global dataframe) is every worse (I am unable to fingure out how to scale the graph size). The facet_wrap() R fuction is not very useful here, since we have lot of indivual sub-graphs. This worked very nicely in NYPD shooting dataset where data was facet_wrap() with yearly sub-graphs.

```
global %>%
  filter(cases > 0) %>%
  ggplot(aes(x = date, y = cases)) +
  geom_line(aes(color = "cases")) +
  geom_point(aes(color = "cases")) +
  geom_line(aes(y = deaths, color = "deaths")) +
  geom_point(aes(y = deaths, color = "deaths")) +
  theme(legend.position="bottom",
        axis.text.x = element_text(angle = 90)) +
  labs(title = "Global COVID19 cases and deaths", x = "Date", y = "Number of Cases")
```




```
US_totals %>%
  filter(cases > 0) %>%
  ggplot(aes(x = date, y = cases)) +
  geom_line(aes(color = "cases")) +
  geom_point(aes(color = "cases")) +
  geom_line(aes(y = deaths, color = "deaths")) +
  geom_point(aes(y = deaths, color = "deaths")) +
  scale_y_log10() +
  theme(legend.position="bottom",
        axis.text.x = element_text(angle = 90)) +
  labs(title = "COVID19 in US", x = "Date", y = "Number of Cases")
```



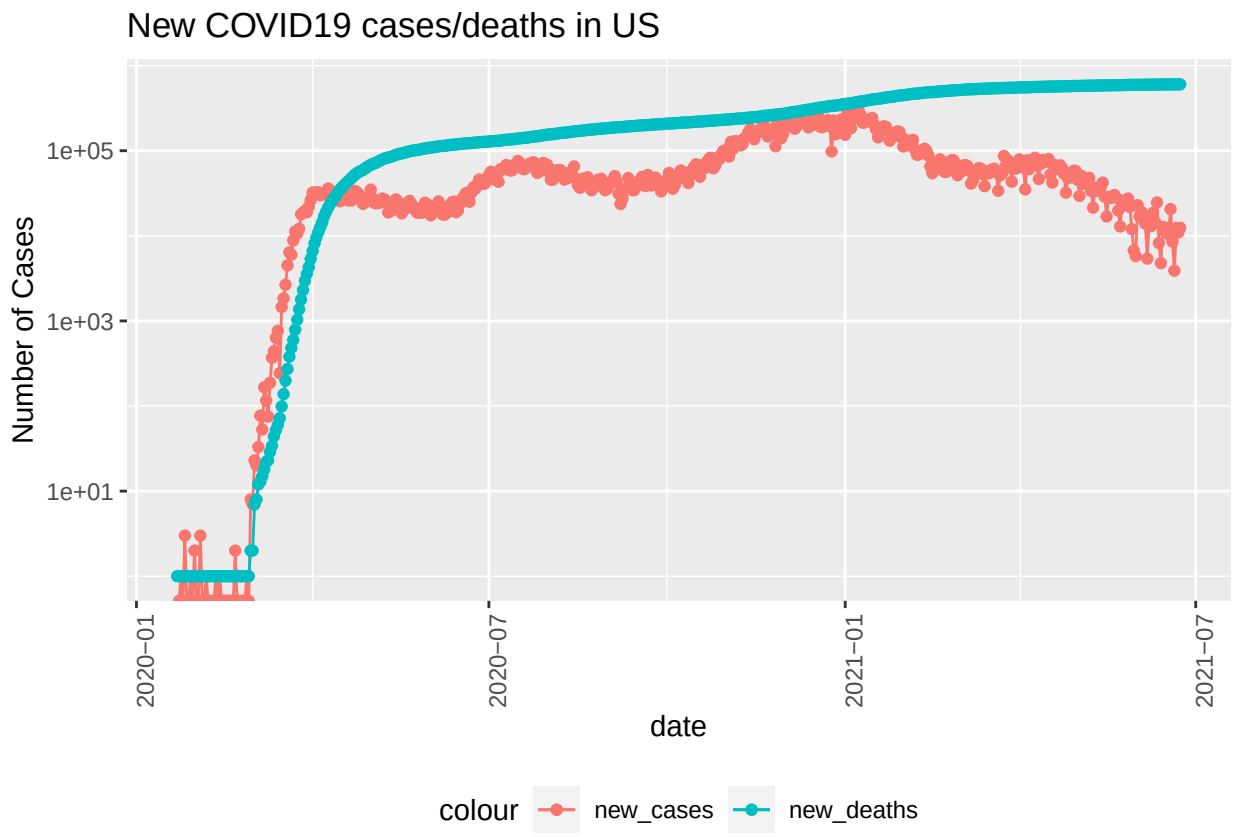

```
US_totals %>%
  ggplot(aes(x = date, y = new_cases)) +
  geom_line(aes(color = "new_cases")) +
  geom_point(aes(color = "new_cases")) +
  geom_line(aes(y = deaths, color = "new_deaths")) +
  geom_point(aes(y = deaths, color = "new_deaths")) +
  scale_y_log10() +
  theme(legend.position="bottom",
        axis.text.x = element_text(angle = 90)) +
  labs(title = "New COVID19 cases/deaths in US", y = "Number of Cases")
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Removed 1 row(s) containing missing values (geom_path).
```

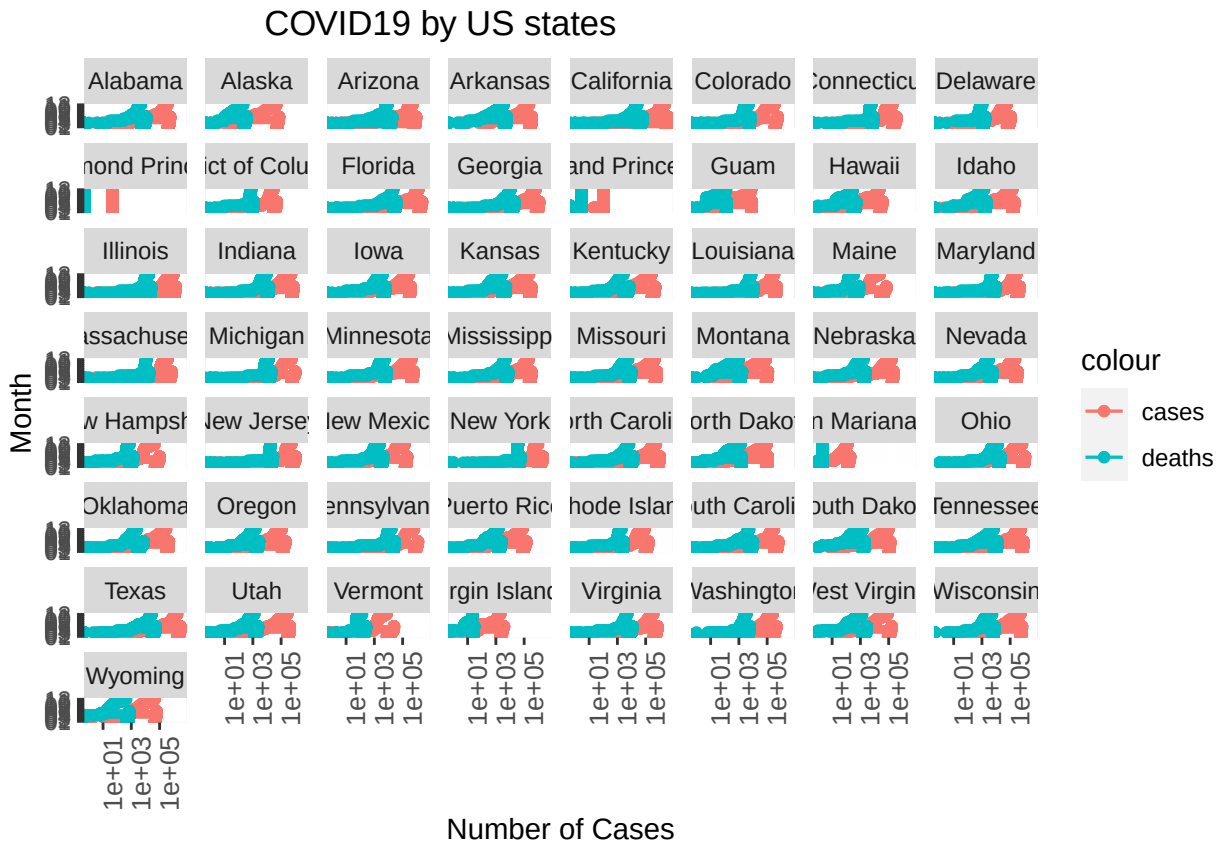
```
## Warning: Removed 1 rows containing missing values (geom_point).
```




```
US_date %>%
  filter(cases > 0) %>%
  ggplot(aes(x = Month, y = cases)) +
  geom_line(aes(color = "cases")) +
  geom_point(aes(color = "cases")) +
  geom_line(aes(y = deaths, color = "deaths")) +
  geom_point(aes(y = deaths, color = "deaths")) +
  facet_wrap( ~ Province_State) +
  coord_flip() +
  scale_y_log10() +
  theme(plot.title = element_text(hjust = 0.3),
  axis.text.x=element_text(angle=90, hjust=1, size=10),
  panel.spacing.x=unit(0.5, "lines")) +
  labs(x = "Month",
       y = "Number of Cases",
       title = "COVID19 by US states")
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

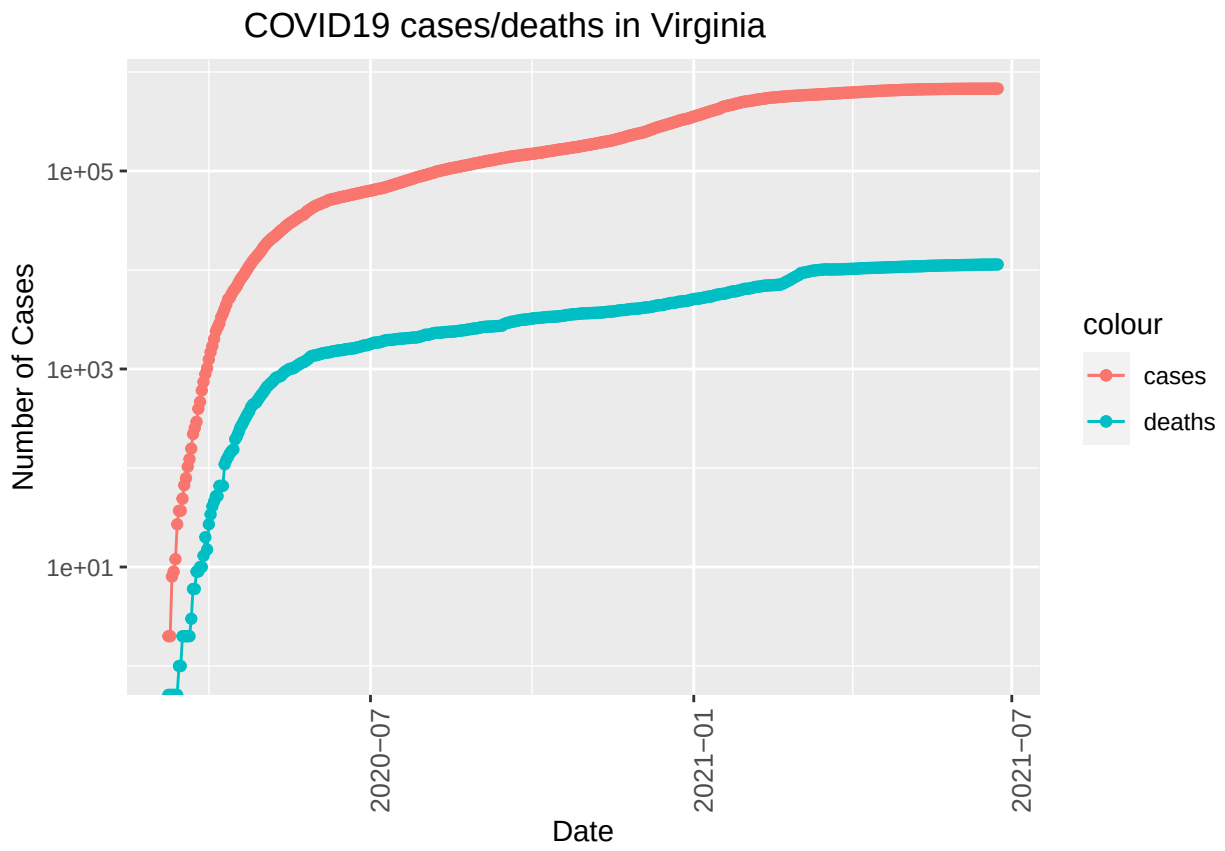
```
## Warning: Transformation introduced infinite values in continuous y-axis
```




```
US_by_state %>%
  filter(Province_State == "Virginia") %>%
  filter(cases > 0) %>%
  ggplot(aes(x = date, y = cases)) +
  geom_line(aes(color = "cases")) +
  geom_point(aes(color = "cases")) +
  geom_line(aes(y = deaths, color = "deaths")) +
  geom_point(aes(y = deaths, color = "deaths")) +
  scale_y_log10() +
  theme(plot.title = element_text(hjust = 0.3),
  axis.text.x=element_text(angle=90, hjust=1, size=10),
  panel.spacing.x=unit(0.5, "lines")) +
  labs(title = "COVID19 cases/deaths in Virginia", x = "Date", y = "Number of Cases")
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

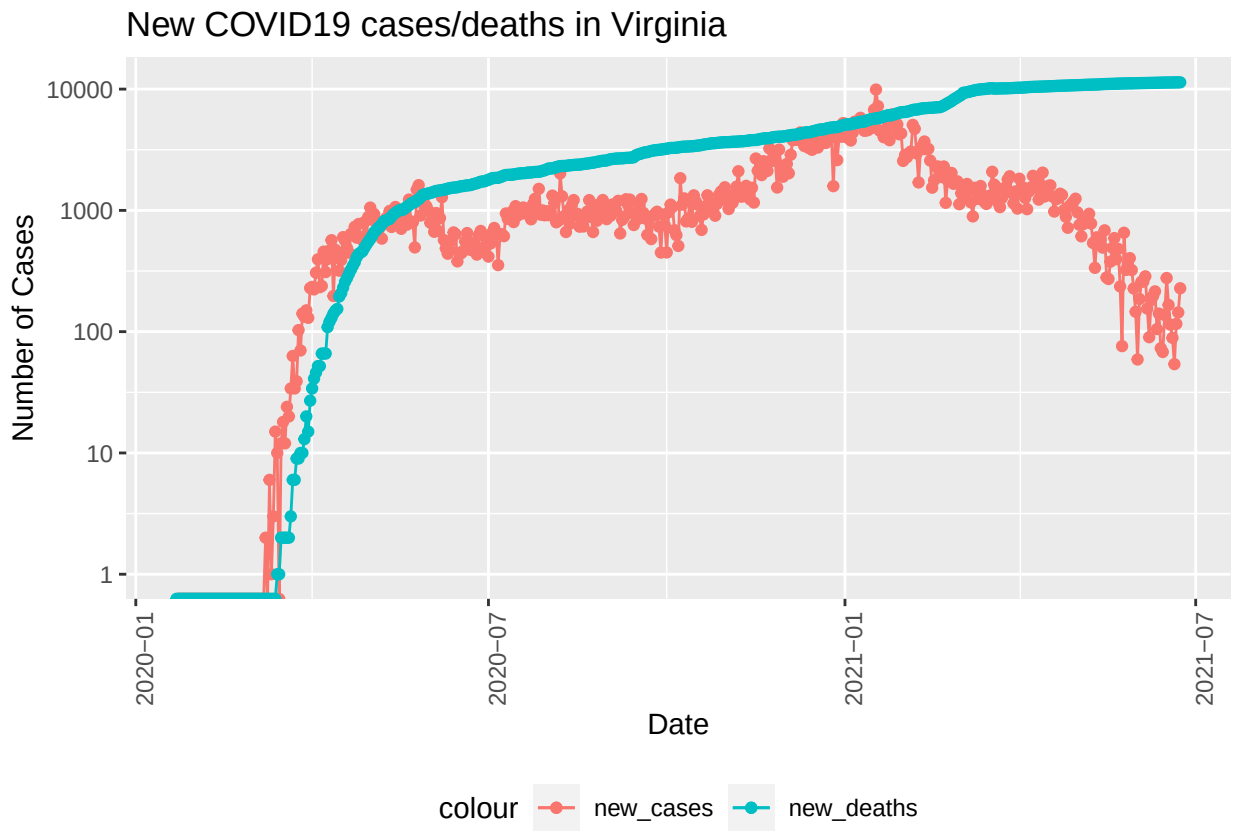



```
US_by_state %>%
  filter(Province_State == "Virginia") %>%
  ggplot(aes(x = date, y = new_cases)) +
  geom_line(aes(color = "new_cases")) +
  geom_point(aes(color = "new_cases")) +
  geom_line(aes(y = deaths, color = "new_deaths")) +
  geom_point(aes(y = deaths, color = "new_deaths")) +
  scale_y_log10() +
  theme(legend.position="bottom",
        axis.text.x = element_text(angle = 90)) +
  labs(title = "New COVID19 cases/deaths in Virginia", x = "Date", y = "Number of Cases")
```

```
## Warning in self$trans$transform(x): NaNs produced

## Warning in self$trans$transform(x): Transformation introduced infinite values in
## continuous y-axis

## Warning in self$trans$transform(x): NaNs produced

## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Removed 1 row(s) containing missing values (geom_path).
```

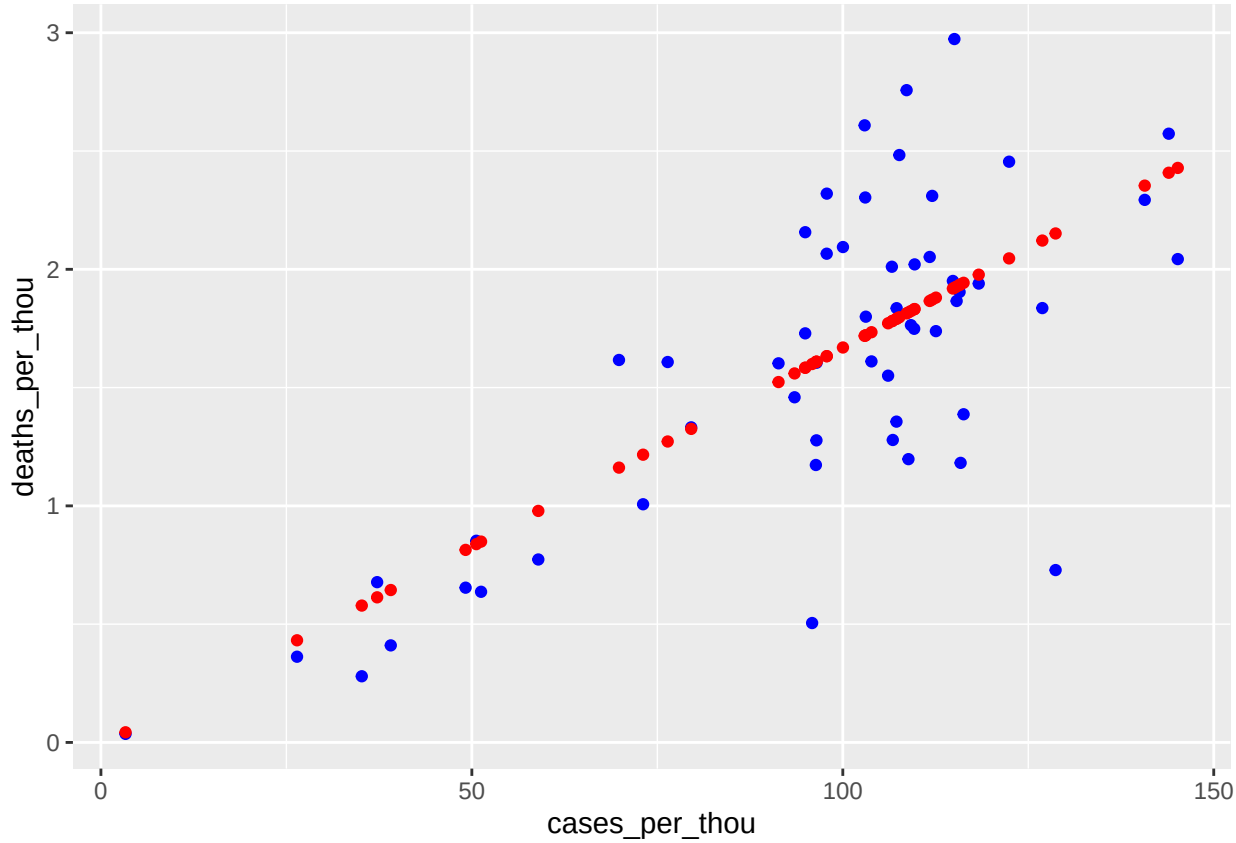
```
## Warning: Removed 1 rows containing missing values (geom_point).
```



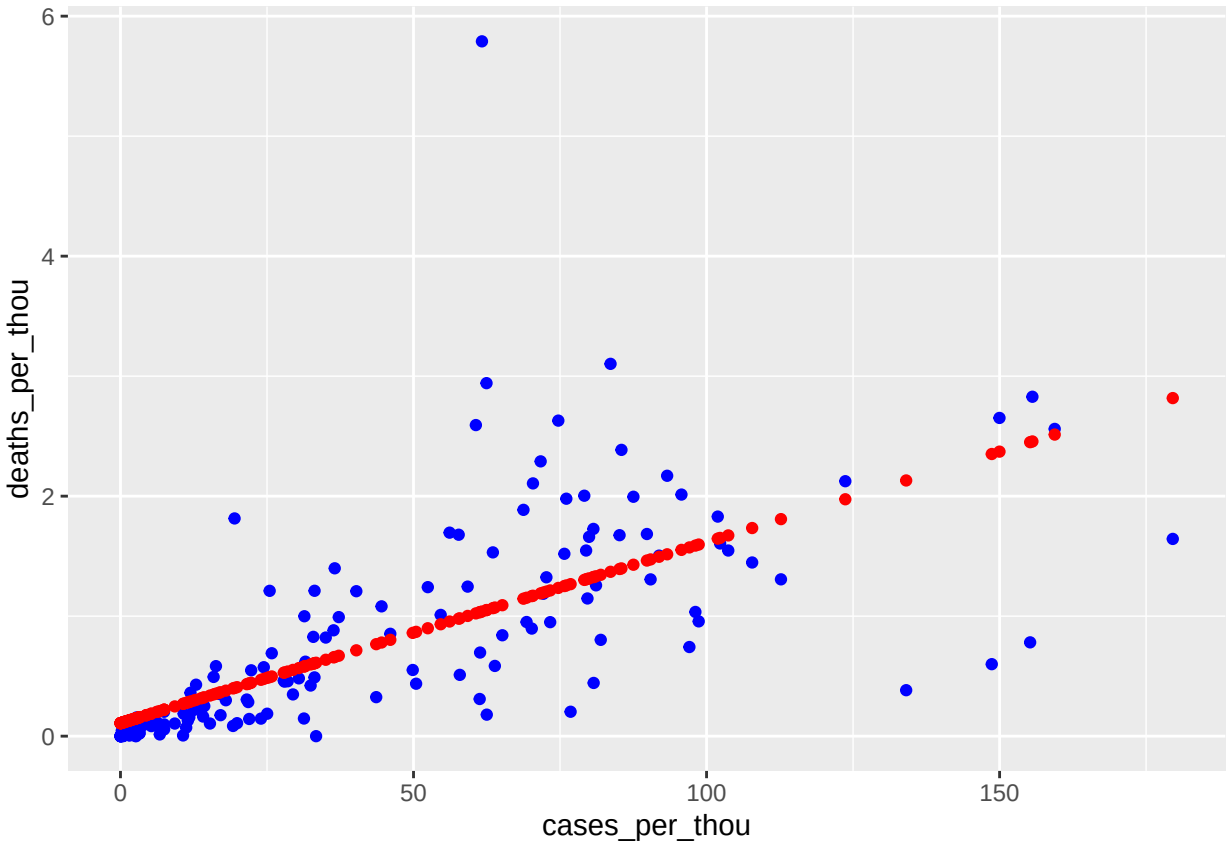
Using a linear model to predict the cases per thousand as a function of deaths per thousand. The same model is applied for global dataset as well. This is a very simple model to fit linear models. We can see there are many outliers that are very far from the prediction line.

```
US_state_totals <- US_by_state %>%
  group_by(Province_State) %>%
  summarize(deaths = max(deaths), cases = max(cases),
            Population = max(Population),
            cases_per_thou = 1000* cases / Population,
            deaths_per_thou = 1000* deaths / Population) %>%
  filter(cases > 0, Population > 0)


global_totals <- global %>%
  group_by(Country_Region) %>%
  summarize(deaths = max(deaths), cases = max(cases),
            Population = max(Population),
            cases_per_thou = 1000* cases / Population,
            deaths_per_thou = 1000* deaths / Population) %>%
```

```
  filter(cases > 0, Population > 0)

mod <- lm(deaths_per_thou ~ cases_per_thou, data = US_state_totals)
US_pred <- US_state_totals %>%
  mutate(pred = predict(mod))

US_pred %>%
  ggplot() +
  geom_point(aes(x = cases_per_thou, y = deaths_per_thou), color = "blue") +
  geom_point(aes(x = cases_per_thou, y = pred), color = "red")
```




```
global_mod <- lm(deaths_per_thou ~ cases_per_thou, data = global_totals)
global_pred <- global_totals %>%
  mutate(pred = predict(global_mod))

global_pred %>%
  ggplot() +
  geom_point(aes(x = cases_per_thou, y = deaths_per_thou), color = "blue") +
  geom_point(aes(x = cases_per_thou, y = pred), color = "red")
```



In conclusion, we downloaded the raw data from Systems Science and Engineering (CSSE) at Johns Hopkins University Github repository. The dataframe was then cleaned and tidy to do further data analysis. Plotting the data from dataframe, we see the total cases vs deaths and new cases and deaths for both US and global datasets. An attempt was made to do with facet_wrap() function to create sub-plots of US states, however it's not very readable since the plot size does not scale. Finally, linear model was used to predict the cases per thousand as a function of deaths per thousand. Since this is a linear model, it's will not be very use to for prediction for this kind of datasets. As we know the real world is not linear and virus behave in a differnt manner, there are lot of factors at play, from indiviual immunity to factors such as lockdown, public behavior and sensivity to the pendamic, etc. The model does not account of any of this, it just does liner calcualtion based on the dataset. We can clearly see there is lot of outliers that are significent distance away from the prediction line.