Final Covid 19

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Necessary Libraries

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.0.4
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(lubridate)
library(ggplot2)
```

Import the data

```
url_in <- "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covi
file_names <- c("time_series_covid19_confirmed_US.csv",  "time_series_covid19_confirmed_global.csv", "ti
urls <- str_c(url_in, file_names)
global_cases <- read_csv(urls[2])
```

```
## Rows: 289 Columns: 1147
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr    (2): Province/State, Country/Region
## dbl (1145): Lat, Long, 1/22/20, 1/23/20, 1/24/20, 1/25/20, 1/26/20, 1/27/20,...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

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

```
## Rows: 289 Columns: 1147
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr    (2): Province/State, Country/Region
## dbl (1145): Lat, Long, 1/22/20, 1/23/20, 1/24/20, 1/25/20, 1/26/20, 1/27/20,...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

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

```
## Rows: 3342 Columns: 1154
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr    (6): iso2, iso3, Admin2, Province_State, Country_Region, Combined_Key
## dbl (1148): UID, code3, FIPS, Lat, Long_, 1/22/20, 1/23/20, 1/24/20, 1/25/20...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

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

```
## Rows: 3342 Columns: 1155
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr    (6): iso2, iso3, Admin2, Province_State, Country_Region, Combined_Key
## dbl (1149): UID, code3, FIPS, Lat, Long_, Population, 1/22/20, 1/23/20, 1/24...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

Transform the data for visualization and analysis

```
# transform global data
global_cases <- global_cases %>% pivot_longer(cols = -c(`Province/State`, `Country/Region`, Lat, Long),
global_deaths <- global_deaths %>% pivot_longer(cols = -c(`Province/State`, `Country/Region`, Lat, Long
global <- global_cases %>% full_join(global_deaths) %>% rename(Country_Region = `Country/Region`, Provi
```

```
## Joining with `by = join_by(`Province/State`, `Country/Region`, date)`
```

```
global <- global %>% filter(cases > 0)
summary(global)
```

```
##  Province_State     Country_Region          date                cases
##  Length:306827      Length:306827      Min.   :2020-01-22   Min.   :       1
##  Class :character   Class :character   1st Qu.:2020-12-12   1st Qu.:    1316
##  Mode  :character   Mode  :character   Median :2021-09-16   Median :   20365
##                                        Mean   :2021-09-11   Mean   : 1032863
##                                        3rd Qu.:2022-06-15   3rd Qu.:  271281
```

```
##                                      Max.   :2023-03-09   Max.   :103802702
##      deaths
##  Min.   :      0
##  1st Qu.:      7
##  Median :    214
##  Mean   :  14405
##  3rd Qu.:   3665
##  Max.   :1123836
```

```
# Verify that the following isn't a single outlier
global %>% filter(cases>100000000)
```

```
## # A tibble: 80 x 5
##    Province_State Country_Region date       cases  deaths
##    <chr>          <chr>          <date>     <dbl>   <dbl>
##  1 <NA>           US             2022-12-20 100050937 1088341
##  2 <NA>           US             2022-12-21 100233060 1089383
##  3 <NA>           US             2022-12-22 100329204 1089979
##  4 <NA>           US             2022-12-23 100368433 1090186
##  5 <NA>           US             2022-12-24 100374955 1090208
##  6 <NA>           US             2022-12-25 100378169 1090223
##  7 <NA>           US             2022-12-26 100390601 1090252
##  8 <NA>           US             2022-12-27 100501536 1090608
##  9 <NA>           US             2022-12-28 100614880 1091598
## 10 <NA>           US             2022-12-29 100718983 1092522
## # i 70 more rows
```

```
# transform US data
US_cases <- US_cases %>% pivot_longer(cols = -(UID:Combined_Key), names_to = "date", values_to = "cases
US_deaths <- US_deaths %>% pivot_longer(cols = -(UID:Population), names_to = "date", values_to = "deaths
US <- US_cases %>% full_join(US_deaths)
```

```
## Joining with `by = join_by(Admin2, Province_State, Country_Region,
## Combined_Key, date)`
```

```
global <- global %>% unite("Combined_Key", c(Province_State, Country_Region), sep = ", ", na.rm = TRUE,
# add population statistics to global data
uid_lookup_url <- "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/
uid <- read_csv(uid_lookup_url) %>% select(-c(Lat,Long_, Combined_Key, code3, iso2, iso3, Admin2))
```

```
## Rows: 4321 Columns: 12
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (7): iso2, iso3, FIPS, Admin2, Province_State, Country_Region, Combined_Key
## dbl (5): UID, code3, Lat, Long_, Population
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
global <- global %>% left_join(uid, by = c("Province_State", "Country_Region")) %>% select(-c(UID, FIPS
# Final preparations for plotting and visualizing the data
US_by_state <- US %>% group_by(Province_State, Country_Region, date) %>% summarize(cases = sum(cases),
```

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

```
US_totals <- US_by_state %>% group_by(Country_Region, date) %>% summarize(cases = sum(cases), deaths = s
```

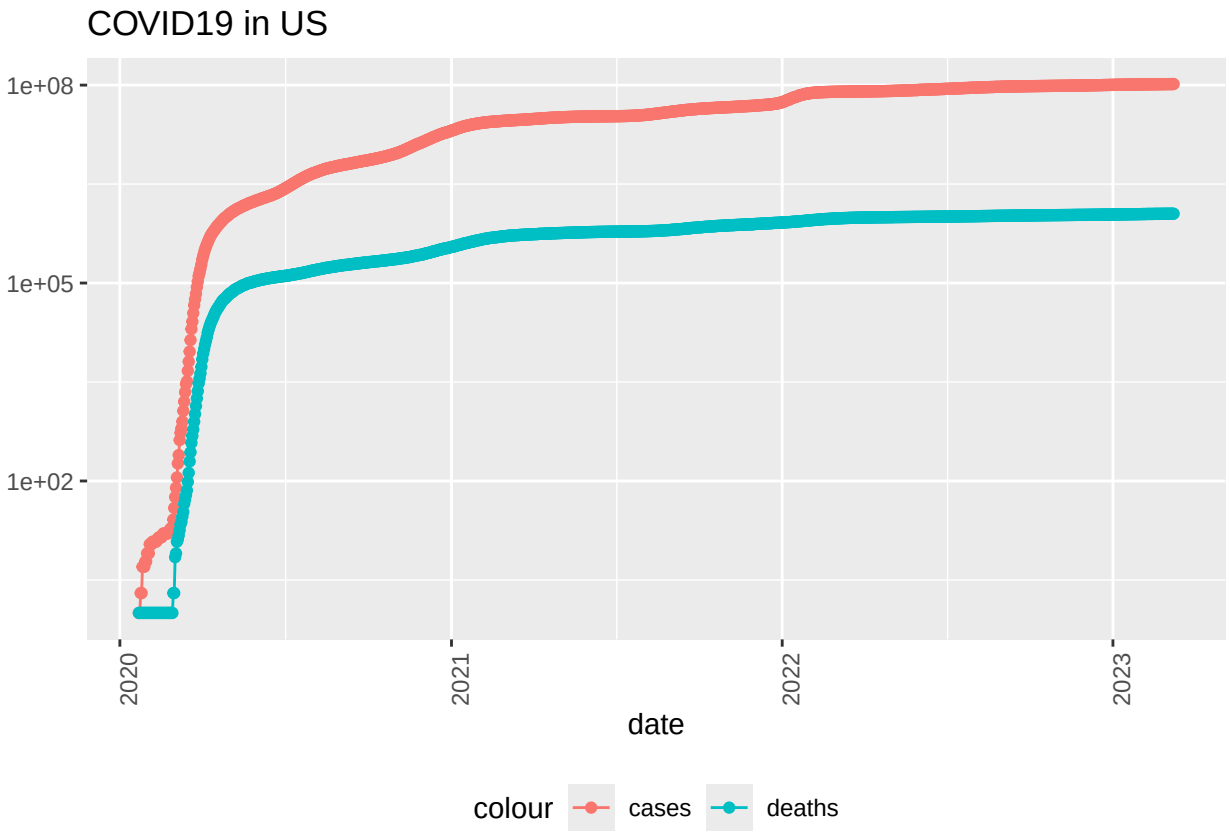
```
## `summarise()` has grouped output by 'Country_Region'. You can override using
## the `.groups` argument.
```

Visualizing US statistics

```
# Find out maximum date (how far the data goes)
max(US_totals$date)
```

```
## [1] "2023-03-09"
```

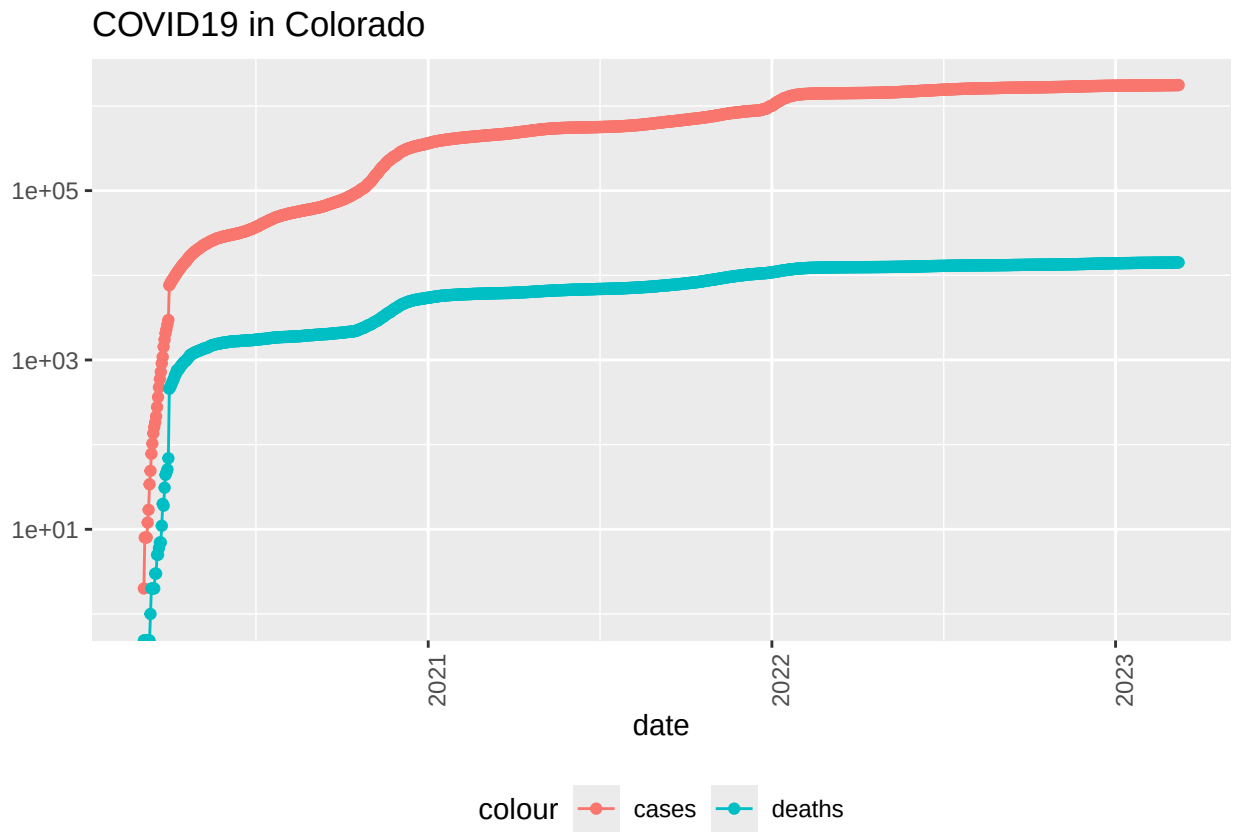
```
US_totals %>% filter(cases > 0) %>% ggplot(aes(x = date, y = cases)) + geom_line(aes(color = "cases")) +
```



Visualizing data for Colorado

```
state <- "Colorado"
US_by_state %>% filter(Province_State == state) %>% filter(cases > 0) %>% ggplot(aes(x = date, y = cases
```

```
## Warning in scale_y_log10(): log-10 transformation introduced infinite values.
## log-10 transformation introduced infinite values.
```



Evaluate only new cases

In this case only new cases will be looked at to visualize if there is a trend for US data

```
## Transforming and looking at US new cases
US_by_state <- US_by_state %>% mutate(new_cases = cases - lag(cases), new_deaths = deaths - lag(deaths))
US_totals <- US_totals %>% mutate(new_cases = cases - lag(cases), new_deaths = deaths - lag(deaths))
US_totals %>% ggplot(aes(x = date, y = new_cases)) + geom_line(aes(color = "new_cases")) + geom_point(ae
```

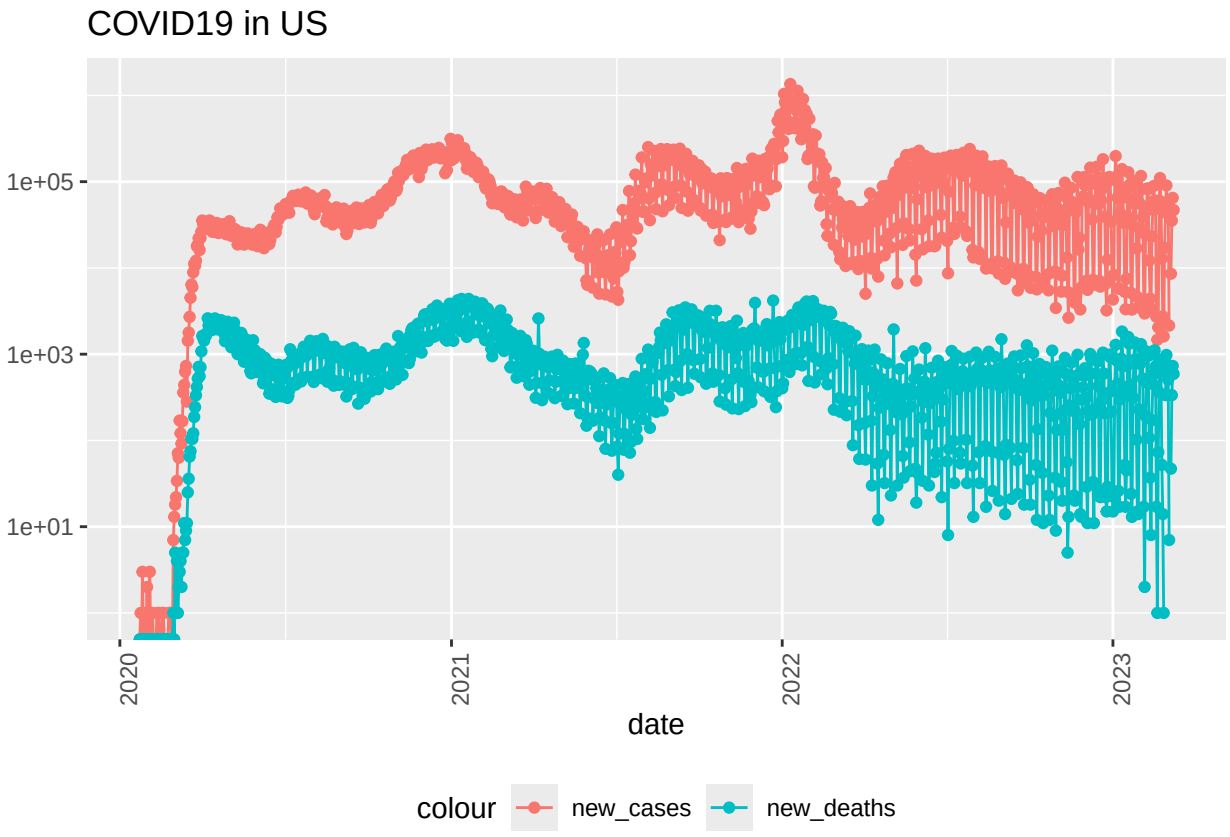
```
## Warning in transformation$transform(x): NaNs produced
```

```
## Warning in scale_y_log10(): log-10 transformation introduced infinite values.
```

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

```
## Warning in scale_y_log10(): log-10 transformation introduced infinite values.
```

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

## Warning in scale_y_log10(): log-10 transformation introduced infinite values.

## Warning in transformation$transform(x): NaNs produced

## Warning in scale_y_log10(): log-10 transformation introduced infinite values.

## Warning: Removed 1 row containing missing values or values outside the scale range
## (`geom_line()`).

## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_point()`).

## Warning: Removed 1 row containing missing values or values outside the scale range
## (`geom_line()`).

## Warning: Removed 4 rows containing missing values or values outside the scale range
## (`geom_point()`).
```




```
US_state_totals <- US_by_state %>% group_by(Province_State) %>% summarize(deaths = max(deaths), cases =
US_state_totals %>% slice_min(deaths_per_thou, n = 10)
```

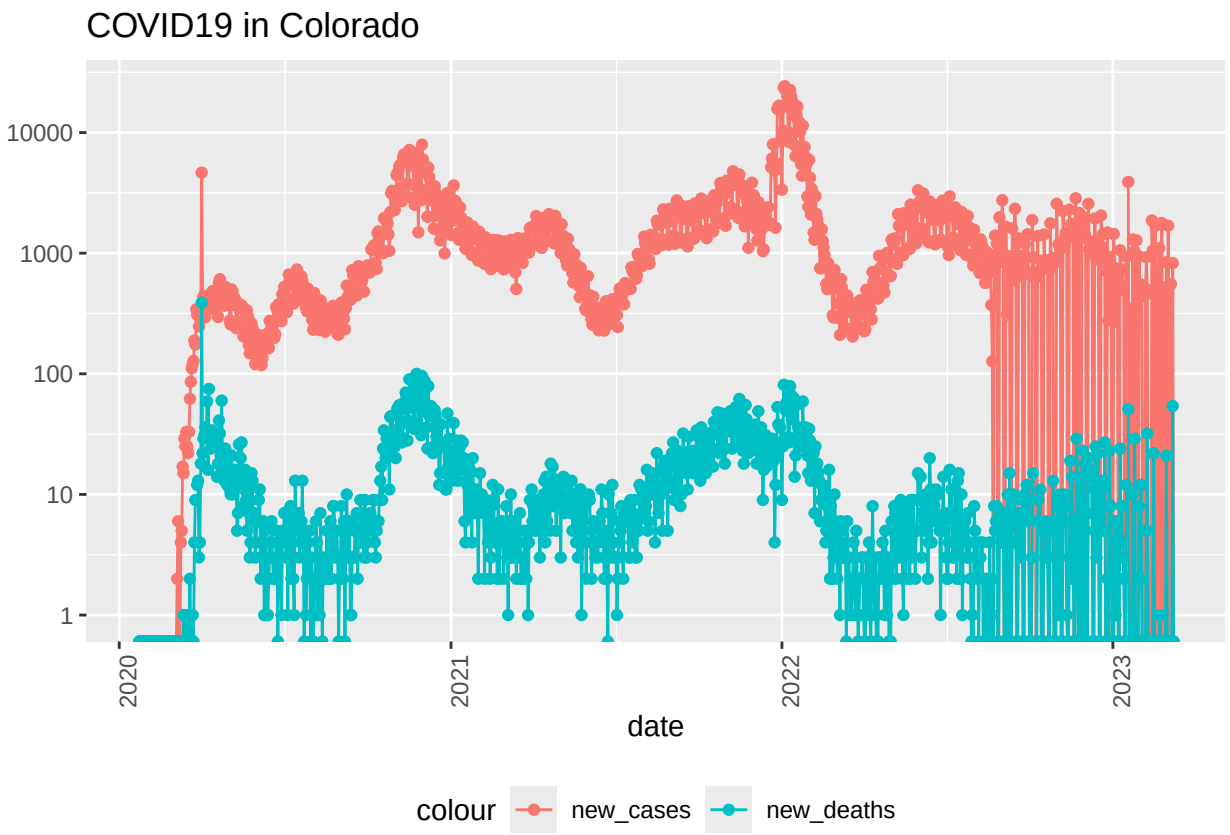
```
## # A tibble: 10 x 6
##    Province_State        deaths  cases population cases_per_thou deaths_per_thou
##    <chr>                  <dbl>  <dbl>      <dbl>          <dbl>           <dbl>
##  1 American Samoa            34 8.32e3      55641           150.           0.611
##  2 Northern Mariana Isl~     41 1.37e4      55144           248.           0.744
##  3 Virgin Islands           130 2.48e4     107268           231.           1.21
##  4 Hawaii                  1841 3.81e5    1415872           269.           1.30
##  5 Vermont                  929 1.53e5     623989           245.           1.49
##  6 Puerto Rico             5823 1.10e6    3754939           293.           1.55
##  7 Utah                    5298 1.09e6    3205958           340.           1.65
##  8 Alaska                  1486 3.08e5     740995           415.           2.01
##  9 District of Columbia    1432 1.78e5     705749           252.           2.03
## 10 Washington             15683 1.93e6    7614893           253.           2.06
```

Evaluate only new cases (state)

In this case only new cases will be looked at to visualize if there is a trend for CO data

```
## Transforming and looking at Colorado new cases
US_by_state %>% filter(Province_State == state) %>% ggplot(aes(x = date, y = new_cases)) + geom_line(aes
```

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

## Warning in scale_y_log10(): log-10 transformation introduced infinite values.

## Warning in transformation$transform(x): NaNs produced

## Warning in scale_y_log10(): log-10 transformation introduced infinite values.

## Warning in transformation$transform(x): NaNs produced

## Warning in scale_y_log10(): log-10 transformation introduced infinite values.

## Warning in transformation$transform(x): NaNs produced

## Warning in scale_y_log10(): log-10 transformation introduced infinite values.

## Warning: Removed 1 row containing missing values or values outside the scale range
## (`geom_line()`).

## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_point()`).

## Warning: Removed 1 row containing missing values or values outside the scale range
## (`geom_line()`).

## Warning: Removed 5 rows containing missing values or values outside the scale range
## (`geom_point()`).
```




```
US_state_totals <- US_by_state %>% group_by(Province_State) %>% summarize(deaths = max(deaths), cases =
US_state_totals %>% slice_min(deaths_per_thou, n = 10)
```

```
## # A tibble: 10 x 6
##    Province_State        deaths  cases population cases_per_thou deaths_per_thou
##    <chr>                  <dbl>  <dbl>      <dbl>          <dbl>           <dbl>
##  1 American Samoa            34 8.32e3      55641           150.           0.611
##  2 Northern Mariana Isl~     41 1.37e4      55144           248.           0.744
##  3 Virgin Islands           130 2.48e4     107268           231.           1.21
##  4 Hawaii                  1841 3.81e5    1415872           269.           1.30
##  5 Vermont                  929 1.53e5     623989           245.           1.49
##  6 Puerto Rico             5823 1.10e6    3754939           293.           1.55
##  7 Utah                    5298 1.09e6    3205958           340.           1.65
##  8 Alaska                  1486 3.08e5     740995           415.           2.01
##  9 District of Columbia    1432 1.78e5     705749           252.           2.03
## 10 Washington             15683 1.93e6    7614893           253.           2.06
```

Worst and Least impacted

What if the goal is to see which states suffered the least deaths, the most?

```
## Who faired the best, the worst?
US_state_totals <- US_by_state %>% group_by(Province_State) %>% summarize(deaths = max(deaths), cases =
US_state_totals %>% slice_min(deaths_per_thou, n = 10)
```

```
## # A tibble: 10 x 6
##    Province_State        deaths  cases population cases_per_thou deaths_per_thou
##    <chr>                  <dbl>  <dbl>      <dbl>          <dbl>           <dbl>
##  1 American Samoa            34 8.32e3      55641           150.           0.611
##  2 Northern Mariana Isl~     41 1.37e4      55144           248.           0.744
##  3 Virgin Islands           130 2.48e4     107268           231.           1.21
##  4 Hawaii                  1841 3.81e5    1415872           269.           1.30
##  5 Vermont                  929 1.53e5     623989           245.           1.49
##  6 Puerto Rico             5823 1.10e6    3754939           293.           1.55
##  7 Utah                    5298 1.09e6    3205958           340.           1.65
##  8 Alaska                  1486 3.08e5     740995           415.           2.01
##  9 District of Columbia    1432 1.78e5     705749           252.           2.03
## 10 Washington             15683 1.93e6    7614893           253.           2.06
```

```
US_state_totals %>% slice_max(deaths_per_thou, n = 10)
```

```
## # A tibble: 10 x 6
##    Province_State deaths   cases population cases_per_thou deaths_per_thou
##    <chr>           <dbl>   <dbl>      <dbl>          <dbl>           <dbl>
##  1 Arizona         33102 2443514    7278717           336.            4.55
##  2 Oklahoma        17972 1290929    3956971           326.            4.54
##  3 Mississippi     13370  990756    2976149           333.            4.49
##  4 West Virginia    7960  642760    1792147           359.            4.44
##  5 New Mexico       9061  670929    2096829           320.            4.32
##  6 Arkansas        13020 1006883    3017804           334.            4.31
##  7 Alabama         21032 1644533    4903185           335.            4.29
##  8 Tennessee       29263 2515130    6829174           368.            4.28
##  9 Michigan        42205 3064125    9986857           307.            4.23
## 10 Kentucky        18130 1718471    4467673           385.            4.06
```

Modeling the data

Below the data will be plotted to determine a relation between cases per thousand and deaths per thousand, and also visualize to see which points faired better than expected and which did worse.

```
mod <- lm(deaths_per_thou ~ cases_per_thou, data = US_state_totals)
summary(mod)
```

```
##
## Call:
## lm(formula = deaths_per_thou ~ cases_per_thou, data = US_state_totals)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.3352 -0.5978  0.1491  0.6535  1.2086
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.36167    0.72480  -0.499     0.62
## cases_per_thou  0.01133    0.00232   4.881 9.76e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.8615 on 54 degrees of freedom
## Multiple R-squared:  0.3061, Adjusted R-squared:  0.2933
## F-statistic: 23.82 on 1 and 54 DF,  p-value: 9.763e-06
```

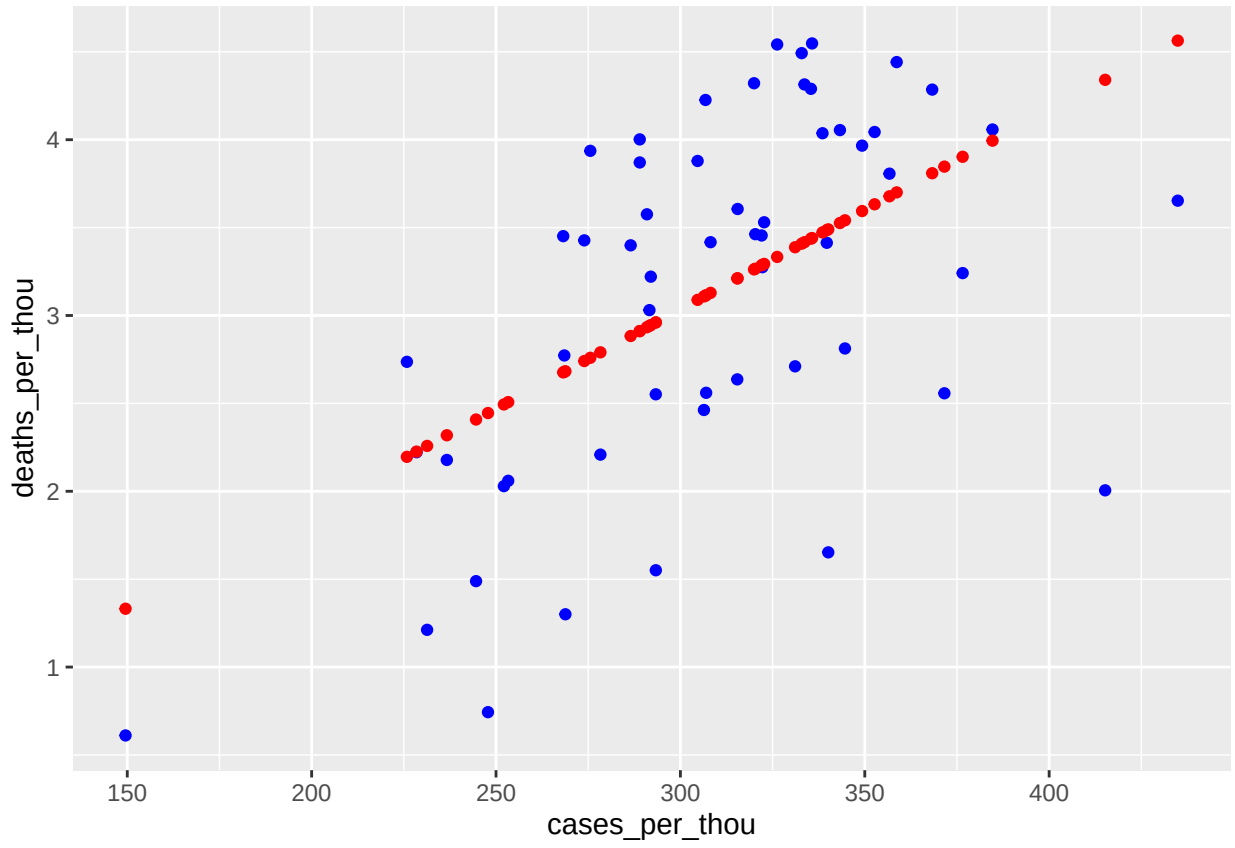
```
US_state_totals %>% slice_min(cases_per_thou)
```

```
## # A tibble: 1 x 6
##   Province_State deaths cases population cases_per_thou deaths_per_thou
##   <chr>           <dbl> <dbl>      <dbl>          <dbl>           <dbl>
## 1 American Samoa     34  8320      55641           150.           0.611
```

```
US_state_totals %>% slice_max(cases_per_thou)
```

```
## # A tibble: 1 x 6
##   Province_State deaths  cases population cases_per_thou deaths_per_thou
##   <chr>           <dbl>  <dbl>      <dbl>          <dbl>           <dbl>
## 1 Rhode Island     3870 460697    1059361           435.            3.65
```

```
x_grid <- seq(150, 450)
US_tot_w_pred <- US_state_totals %>% mutate(pred = predict(mod))
US_tot_w_pred %>% ggplot() + geom_point(aes(x = cases_per_thou, y = deaths_per_thou), color = "blue") +
```



Potential Biases

The biggest source of bias in this case would be reporting or rather under reporting in some parts of the world, especially in the early days of covid, most notably due to lack of funding, insufficient numbers of tests and potential for remote areas. The same can be said for deaths as one factor not put into consideration is a country or region's wealth, meaning a more accurate comparison would be between 2 regions of comparable wealth (i.e. GDP per capita) as opposed to already striggling countries being labeled as handling the epidemic worse than regions with higher fund availability.