COVID19_steps

2024-04-16

Import 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   3.5.0     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- 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
```

Read in the data from the csv file.

```
## Get current data in the four files
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)
```

Read in the data to see what we have.

```
global_cases <- read_csv(urls[2])
global_deaths <- read_csv(urls[4])
US_cases <- read_csv(urls[1])
US_deaths <- read_csv(urls[3])
```

Merge date columns and case numbers for global_cases.

```
global_cases <- global_cases %>% pivot_longer(
  cols = matches("\\d{1,2}/\\d{1,2}/\\d{2}"),
  names_to = "date",
  values_to = "cases")
```

Remove unneeded columns for global_cases.

```
global_cases_clean <- global_cases %>%
  select(-c(Lat, Long))
```

Merge date columns and case numbers for global_deaths.

```
global_deaths <- global_deaths %>% pivot_longer(
  cols = matches("\\d{1,2}/\\d{1,2}/\\d{2}"),
  names_to = "date",
  values_to = "deaths"
)
```

Remove unneeded columns for global_deaths.

```
global_deaths_clean <- global_deaths %>%
  select(-c(Lat, Long))
```

Merge

```
global <- global_cases_clean %>% full_join(global_deaths_clean)
```

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

Fix Dates

```
global <- global %>% mutate(date = myd(date))
```

Process US_cases

```
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_))
```

Join them.

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

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

```r
global <- rename(global, Province_State = `Province/State`,
                 Country_Region = `Country/Region`)
```

```r
global <- global %>%
  unite("Combined_Key",
        c(Province_State, Country_Region),
        sep = ", ",
        na.rm = TRUE,
        remove = FALSE)
```

```r
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.
```

```r
global <- global %>%
  left_join(uid, by = c("Province_State", "Country_Region")) %>%
  select(-c(UID, FIPS)) %>%
  select(Province_State, Country_Region, date, cases, deaths, Population, Combined_Key)
```

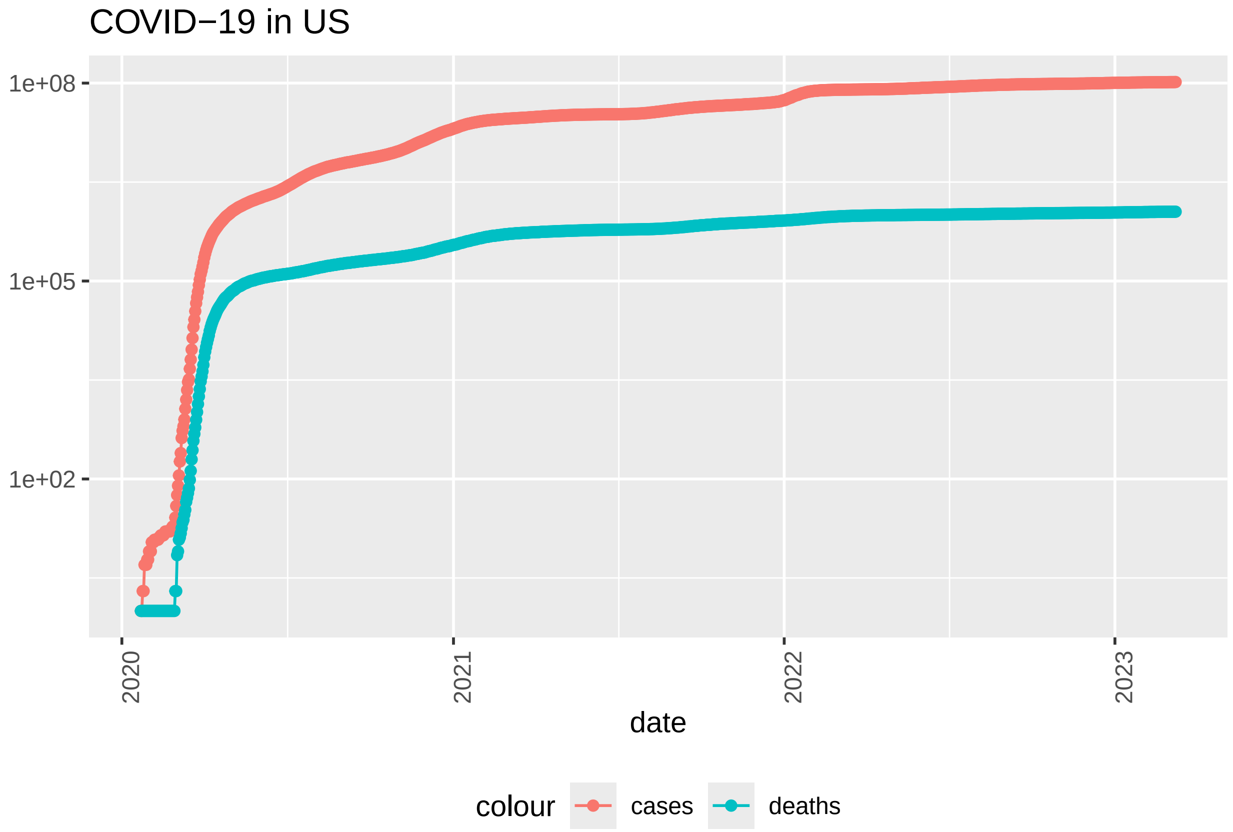
```r
US_by_state <- US %>% group_by(Province_State, Country_Region, date) %>%
  summarize(cases = sum(cases), deaths = sum(deaths),
            Population = sum(Population)) %>%
  mutate(deaths_per_mill = deaths *1000000 / Population) %>%
  select(Province_State, Country_Region, date, cases, deaths,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

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

```r
US_totals <- US_by_state %>% group_by(Country_Region, date) %>%
  summarize(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()
```

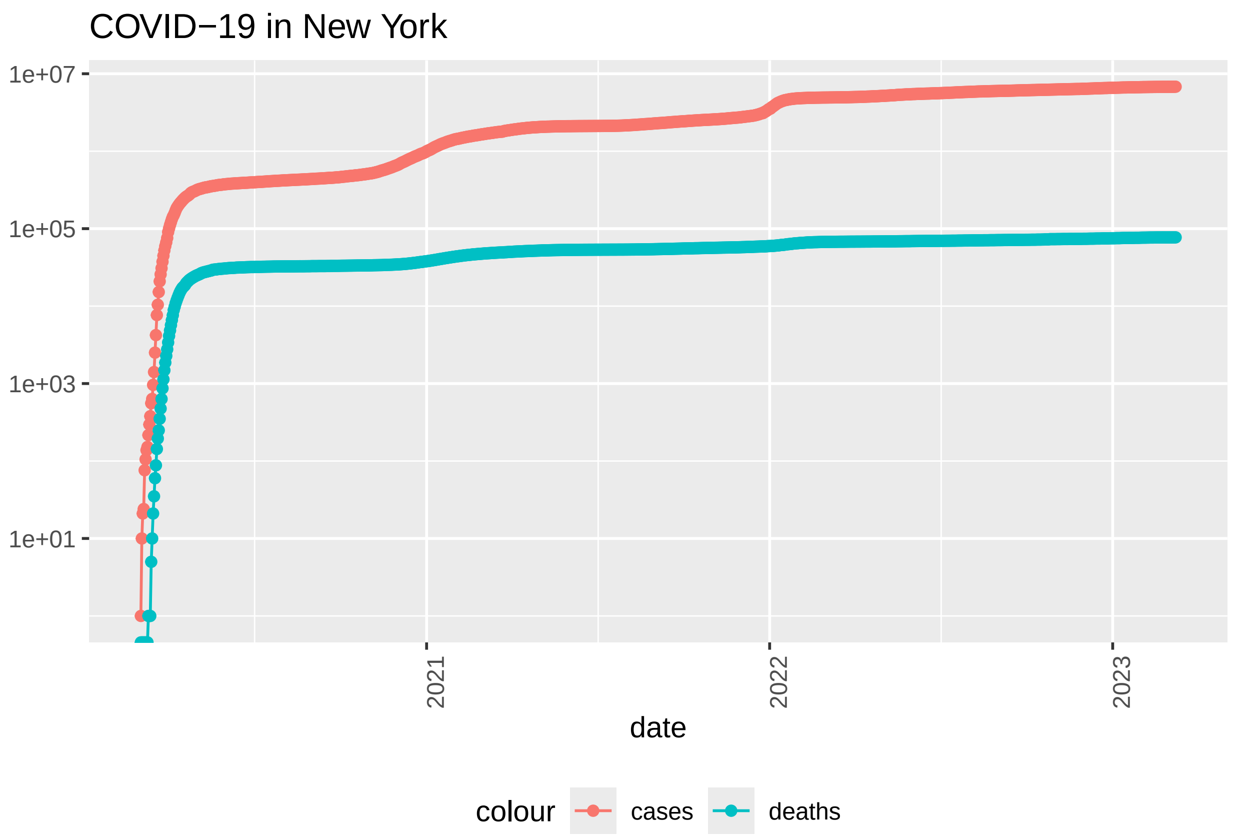
```
## ‘summarise()‘ has grouped output by ’Country_Region’. You can override using
## the ‘.groups‘ argument.
```

```r
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 = "COVID-19 in US", y= NULL)
```



```
state <- "New York"
US_by_state %>%
  filter(Province_State == state) %>%
  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 = str_c("COVID-19 in ", state), y= NULL)
```

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



```
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(aes(color = "new_cases")) +
  geom_line(aes(y = new_deaths, color = "new_deaths")) +
  geom_point(aes(y = new_deaths, color = "new_deaths")) +
  scale_y_log10() +
  theme(legend.position="bottom",
        axis.text.x = element_text(angle = 90)) +
    labs(title = "COVID-19 in US", y= NULL)
```

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

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

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## 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()‘).
```
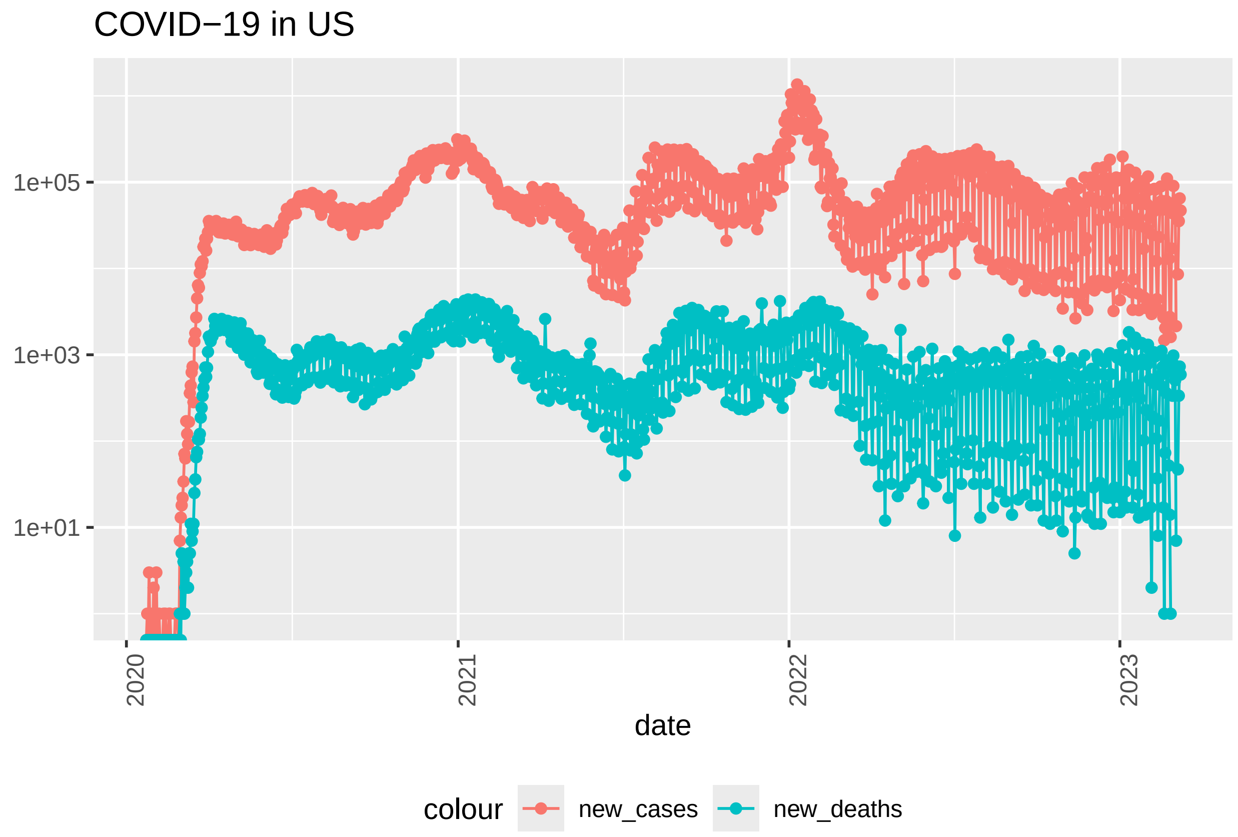



```
US_state_totals <- US_by_state %>%
  group_by(Province_State) %>%
  summarize(deaths = max(deaths), cases = max(cases),
            population = max(Population),
            cases_per_thou = 1000* cases / population,
            deaths_per_thou = 1000* deaths / population) %>%
  filter(cases > 0,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

```
US_state_totals %>%
  slice_min(deaths_per_thou, n=10) %>%
  select(deaths_per_thou, cases_per_thou, everything())
```

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

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

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

```
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)
```

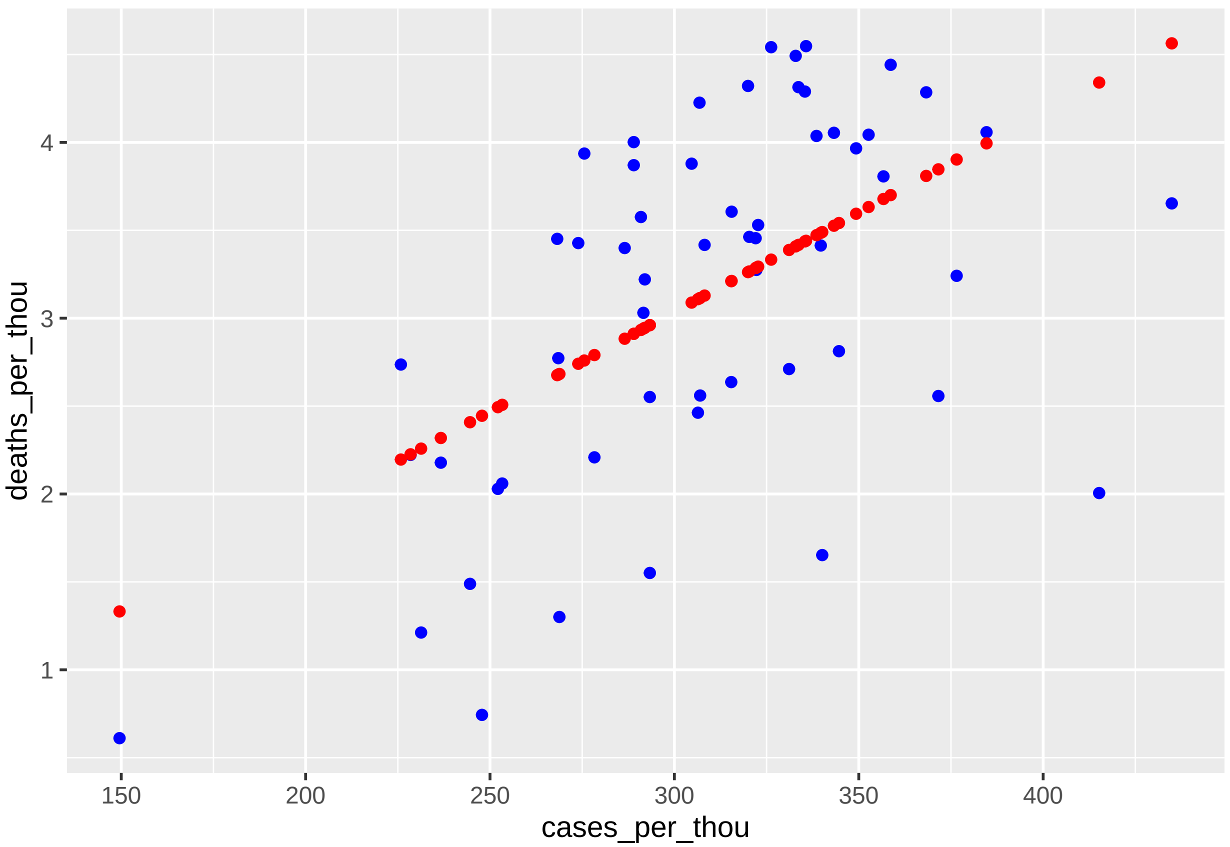
```
## # A tibble: 1 x 6
##   Province_State deaths  cases population cases_per_thou deaths_per_thou
##   <chr>           <dbl>  <dbl>      <dbl>          <dbl>           <dbl>
## 1 Rhode Island     3870 460697    1059361           435.            3.65
```

```
US_state_totals %>% mutate(pred = predict(mod))
```

```
## # A tibble: 56 x 7
##    Province_State  deaths  cases population cases_per_thou deaths_per_thou  pred
##    <chr>            <dbl>  <dbl>      <dbl>          <dbl>           <dbl> <dbl>
##  1 Alabama          21032 1.64e6    4903185           335.            4.29  3.44
##  2 Alaska            1486 3.08e5     740995           415.            2.01  4.34
##  3 American Samoa      34 8.32e3      55641           150.            0.611  1.33
##  4 Arizona          33102 2.44e6    7278717           336.            4.55  3.44
##  5 Arkansas         13020 1.01e6    3017804           334.            4.31  3.42
##  6 California      101159 1.21e7   39512223           307.            2.56  3.12
##  7 Colorado         14181 1.76e6    5758736           306.            2.46  3.11
##  8 Connecticut      12220 9.77e5    3565287           274.            3.43  2.74
##  9 Delaware          3324 3.31e5     973764           340.            3.41  3.49
## 10 District of Co~   1432 1.78e5     705749           252.            2.03  2.49
## # i 46 more rows
```

```
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") +
  geom_point(aes(x = cases_per_thou, y = pred), color = "red")
```



Biases: I could read into this data more than I am, but I've grounded myself in it because there are underlying factors that this visualization doesn't account for and all I can say conclusively is that case numbers and deaths positively correlate.