Reproducible Report on COVID19 Data

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```
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 1.9.3     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
```

```
library(lubridate)
```

Introduction

COVID 19 data project, based heavily on examples provided in class.

Loading Data

Load global and US data.

```
global_deaths <- read_csv("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/refs/heads/master/
```

```
## 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 <- read_csv("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/refs/heads/master/csse_
```

```
## 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.
```

```
global_cases <- read_csv("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/refs/heads/master/cs
```

```
## 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_deaths <- read_csv("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/refs/heads/master/csse_
```

```
## 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.
```

```
#global_deaths <- read_csv("time_series_covid19_deaths_global.csv")
#us_cases <- read_csv("time_series_covid19_confirmed_US.csv")
#global_cases <- read_csv("time_series_covid19_confirmed_global.csv")
#us_deaths <- read_csv("time_series_covid19_deaths_US.csv")

uid <- read_csv("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/refs/heads/master/csse_covid_
```

```
## 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.
```

```
#uid <- read_csv("UID_ISO_FIPS_LookUp_Table.csv") %>% select(-c(Lat, Long_, Combined_Key, code3, iso2,
```

Tidying Data

Create tables of global and US cases and deaths.

```
global_cases_pivot <- global_cases %>% pivot_longer(cols = -c(`Province/State`, `Country/Region`, Lat, L
global_deaths_pivot <- global_deaths %>% pivot_longer(cols = -c(`Province/State`, `Country/Region`, Lat
```

```
us_cases_pivot <- us_cases %>% pivot_longer(cols = -(UID:Combined_Key), names_to = "date", values_to = "
us_deaths_pivot <- us_deaths %>% pivot_longer(cols = -(UID:Population), names_to = "date", values_to = "
us <- us_cases_pivot %>% full_join(us_deaths_pivot)
```

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

Merge Tables

Combine global deaths and cases counts with population of the area.

```
global <- global_cases_pivot %>% full_join(global_deaths_pivot) %>% rename(Country_Region = `Country/Reg
```

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

```
global <- global %>% unite("Combined_Key", c(Province_State, Country_Region), sep = ", ", na.rm = TRUE,
global <- global %>% left_join(uid, by = c("Province_State", "Country_Region")) %>% select(-c(UID, FIPS)
```

Combine US deaths and cases counts with population of the area.

```
us_by_state <- us %>% group_by(Province_State, Country_Region, date) %>% summarize(cases = sum(cases), d
```

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

```
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) %>% summarize(cases = sum(cases), deaths = s
```

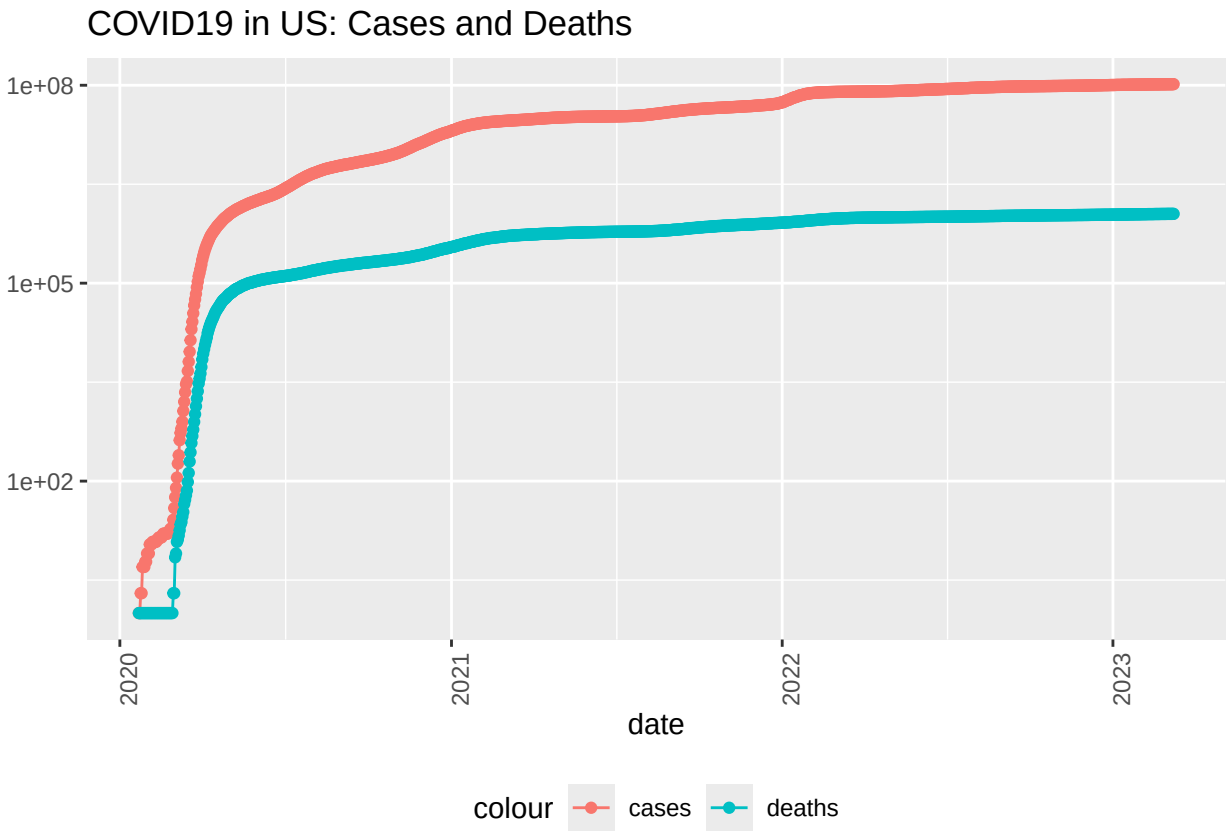
```
## `summarise()` has grouped output by 'Country_Region'. You can override using
## the `.groups` argument.
```

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

Visualization

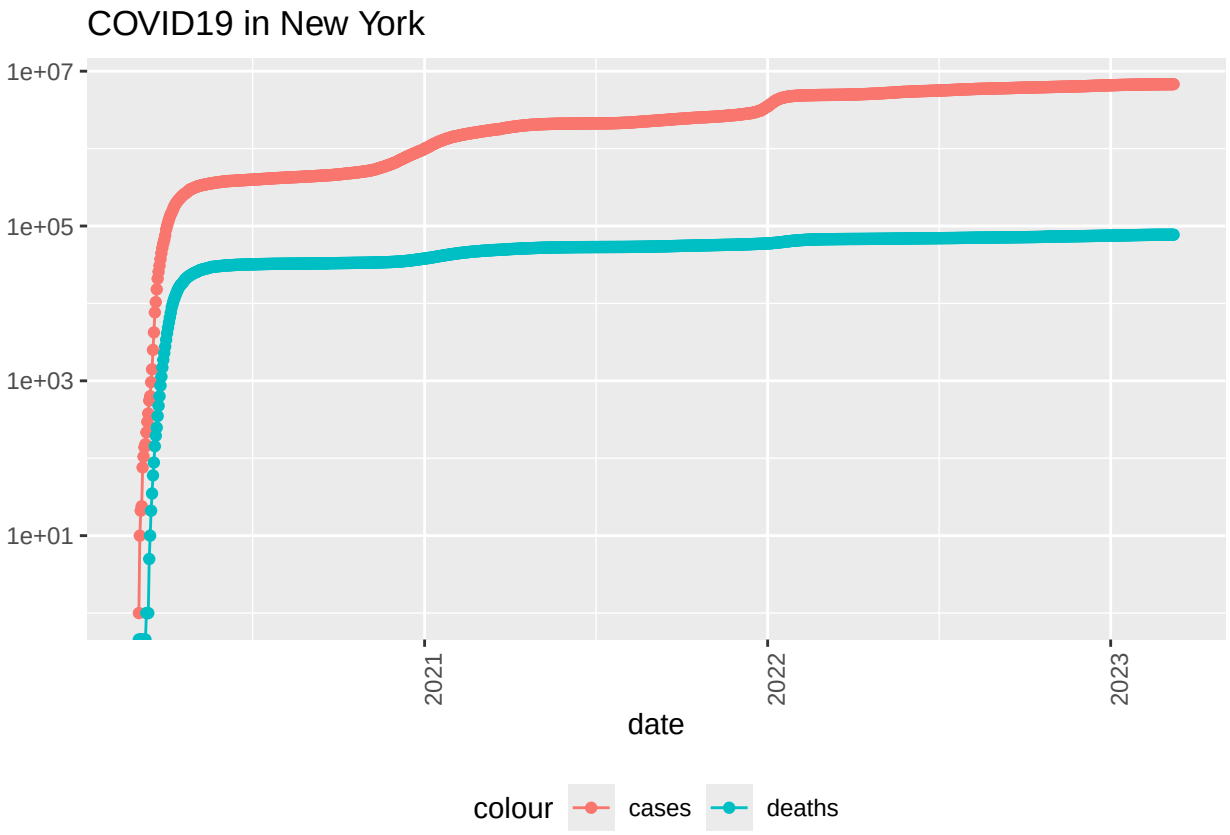
Plot cases and deaths over time, in US and in New York. Cumulative counts increase over time.

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




```
state <- "New York"
  us_by_state %>% filter(Province_State == state) %>% filter(cases > 0) %>% ggplot(aes(x = date, y = cas
```

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



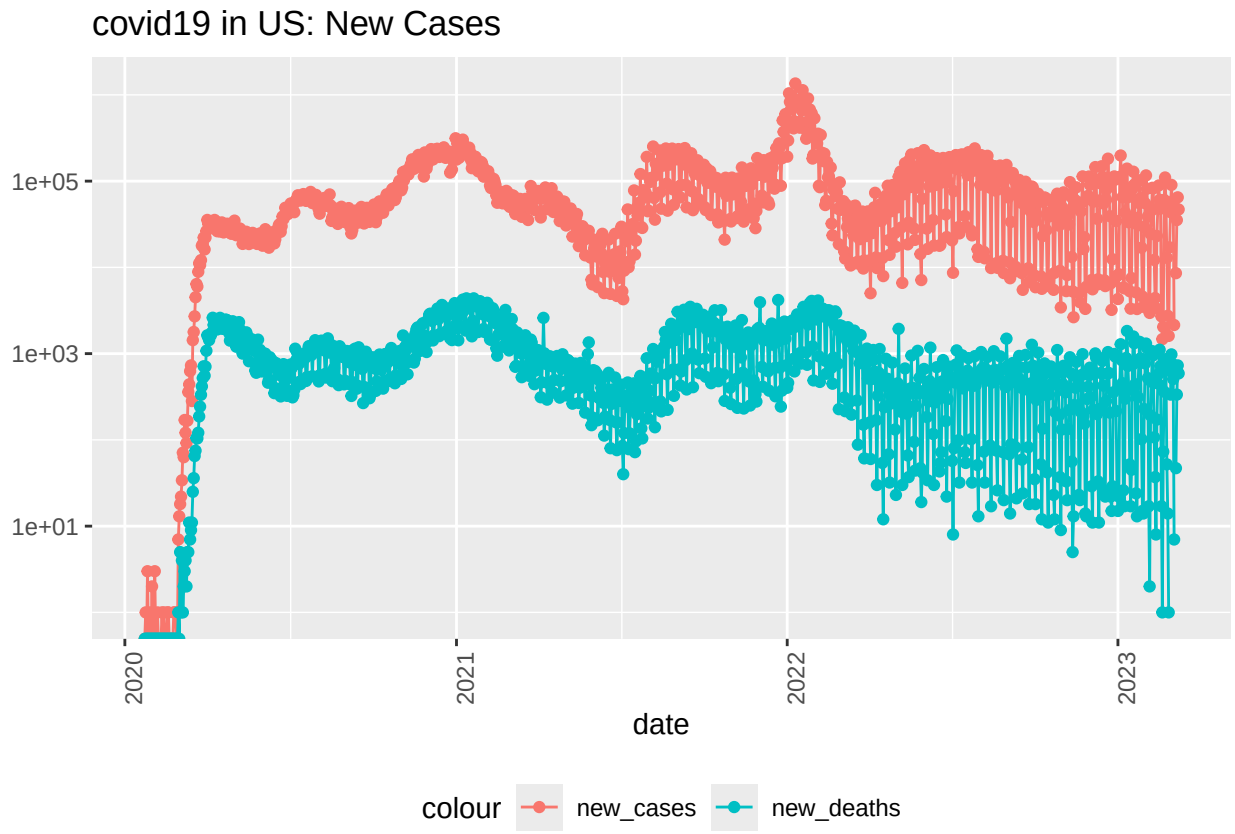
Delta

Plot new cases and new deaths, rather than cumulative total.

```
us_totals %>% ggplot(aes(x = date, y = new_cases)) + geom_line(aes(color = "new_cases")) + geom_point(a
```

```
## 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()`).
```



Rates

Convert counts to rates, using available population data.

```
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
```

Model

Fit a linear model to the data to predict the number of deaths per thousand people, based on the number of cases per thousand people.

```
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(deaths_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
```

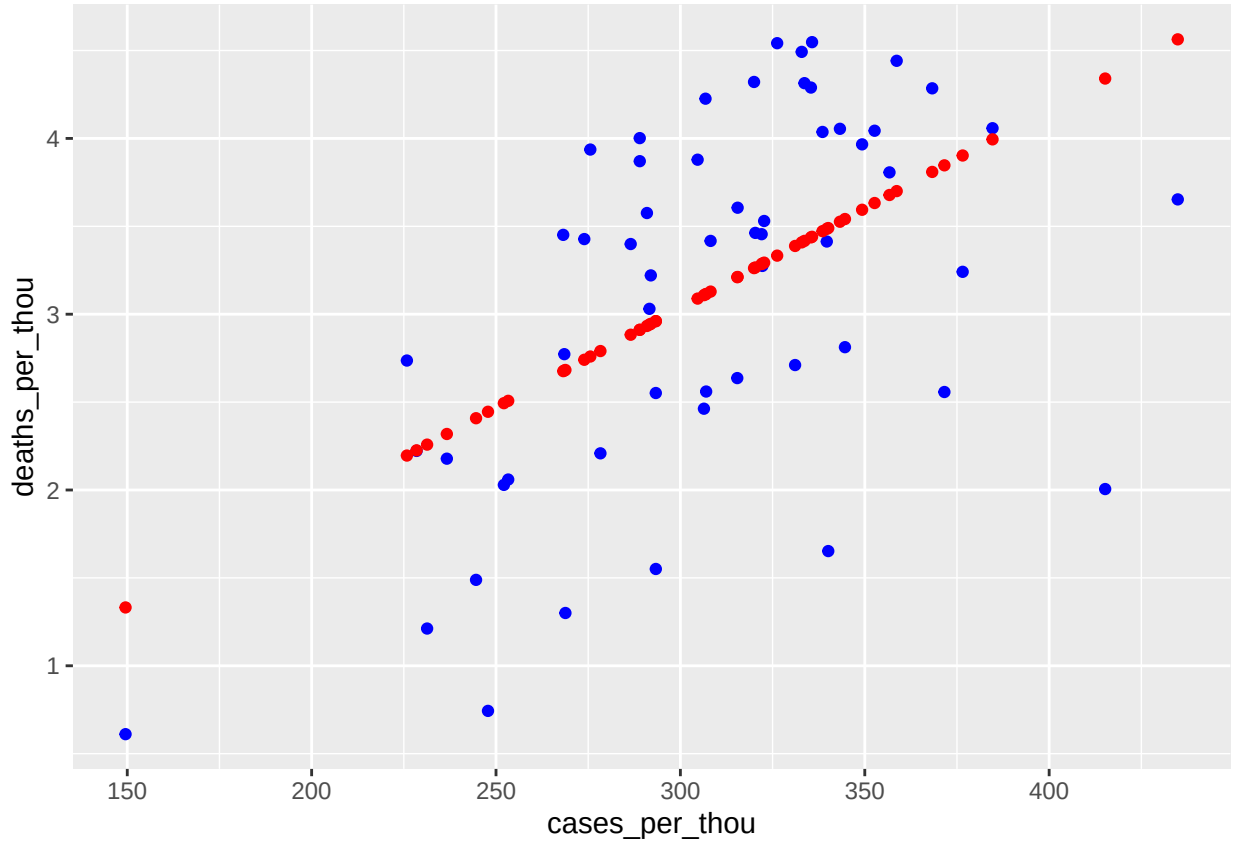
```
us_state_totals %>% slice_max(deaths_per_thou)
```

```
## # A tibble: 1 x 6
##   Province_State deaths   cases population cases_per_thou deaths_per_thou
##   <chr>           <dbl>   <dbl>      <dbl>          <dbl>           <dbl>
## 1 Arizona         33102 2443514    7278717           336.            4.55
```

```
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") +
```



Bias

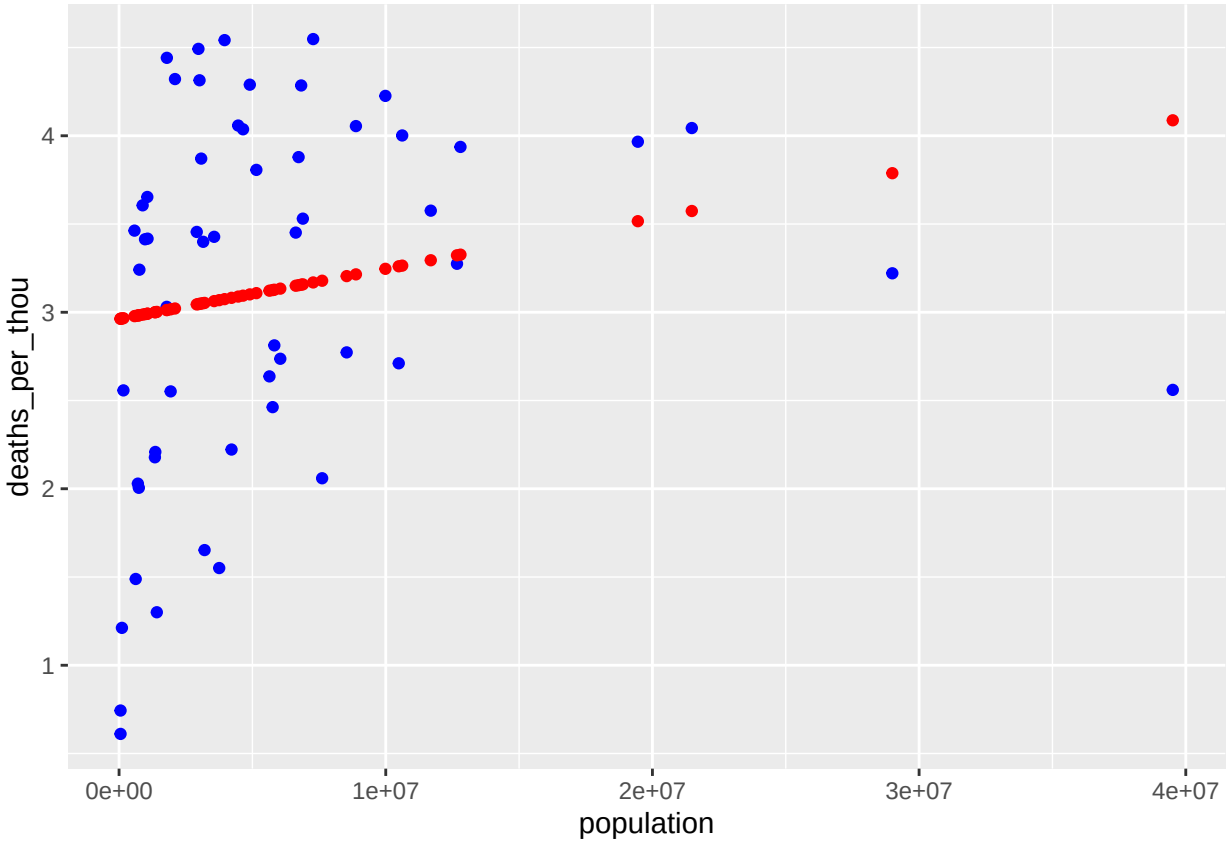
Differences in reporting processes and infrastructure in the different states could have caused case and death rates to be skewed. Different state resources may have resulted in more or less accurate identification of COVID as well, which could again affect rates. One proxy for the amount of resources in a state might be the population of that state.

```
mod <- lm(deaths_per_thou ~ population, data = us_state_totals)
summary(mod)
```

```
##
## Call:
## lm(formula = deaths_per_thou ~ population, data = us_state_totals)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.3521 -0.6953  0.3244  0.7287  1.4675
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.962e+00  1.761e-01  16.821   <2e-16 ***
## population  2.850e-08  1.894e-08   1.505    0.138
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 1.013 on 54 degrees of freedom
## Multiple R-squared:  0.04026,    Adjusted R-squared:  0.02249
## F-statistic: 2.265 on 1 and 54 DF,  p-value: 0.1381
```

```
us_tot_w_pred <- us_state_totals %>% mutate(pred = predict(mod))
us_tot_w_pred %>% ggplot() + geom_point(aes(x = population, y = deaths_per_thou), color = "blue") + geo
```



Conclusion

A linear model of death rate based on total population is not particularly reasonable. Population does not appear to be linearly related to the death rate. Very high population states appear to have relatively low death rates compared to moderately-sized states. Lower population states appear to have greatly varying death rates.

The same bias could apply here: differences in identification and recording of the cases and deaths may be affecting the perceived rates.

```
sessionInfo()
```

```
## R version 4.4.1 (2024-06-14 ucrt)
## Platform: x86_64-w64-mingw32/x64
## Running under: Windows 10 x64 (build 19045)
##
```

```
## Matrix products: default
##
##
## locale:
## [1] LC_COLLATE=English_United States.utf8
## [2] LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] lubridate_1.9.3 forcats_1.0.0   stringr_1.5.1   dplyr_1.1.4
##  [5] purrr_1.0.2     readr_2.1.5     tidyr_1.3.1     tibble_3.2.1
##  [9] ggplot2_3.5.1   tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##  [1] bit_4.5.0         gtable_0.3.5      highr_0.11        crayon_1.5.3
##  [5] compiler_4.4.1    tidyselect_1.2.1  tinytex_0.55      parallel_4.4.1
##  [9] scales_1.3.0      yaml_2.3.10       fastmap_1.2.0     R6_2.5.1
## [13] labeling_0.4.3    generics_0.1.3    curl_5.2.3        knitr_1.48
## [17] munsell_0.5.1     pillar_1.9.0      tzdb_0.4.0        rlang_1.1.4
## [21] utf8_1.2.4        stringi_1.8.4     xfun_0.48         bit64_4.5.2
## [25] timechange_0.3.0  cli_3.6.3         withr_3.0.1       magrittr_2.0.3
## [29] digest_0.6.37     grid_4.4.1        vroom_1.6.5       rstudioapi_0.17.0
## [33] hms_1.1.3         lifecycle_1.0.4   vctrs_0.6.5       evaluate_1.0.1
## [37] glue_1.8.0        farver_2.1.2      fansi_1.0.6       colorspace_2.1-1
## [41] rmarkdown_2.28    tools_4.4.1       pkgconfig_2.0.3   htmltools_0.5.8.1
```