COVID-19 Data Analysis

Peter Tarara

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Data Source

I will be using data from the COVID-19 Data Repository by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University for my analysis. The repository contains data related to COVID cases and can be found here: https://github.com/CSSEGISandData/COVID-19

Data Summary and Tidying

```
url_in <-
  paste0("https://raw.githubusercontent.com/",
         "CSSEGISandData/COVID-19/master/",
         "csse_covid_19_data/csse_covid_19_time_series/")

file_names <-
  c("time_series_covid19_confirmed_global.csv",
    "time_series_covid19_deaths_global.csv",
    "time_series_covid19_confirmed_US.csv",
    "time_series_covid19_deaths_US.csv")

urls <- str_c(url_in, file_names)

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

```
## Rows: 289 Columns: 994
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr   (2): Province/State, Country/Region
## dbl (992): 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[2])
```

```
## Rows: 289 Columns: 994
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr   (2): Province/State, Country/Region
```

```
## dbl (992): 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(urls[3])
```

```
## Rows: 3342 Columns: 1001
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr   (6): iso2, iso3, Admin2, Province_State, Country_Region, Combined_Key
## dbl (995): 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[4])
```

```
## Rows: 3342 Columns: 1002
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr   (6): iso2, iso3, Admin2, Province_State, Country_Region, Combined_Key
## dbl (996): 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_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) %>%
  mutate(date = mdy(date))
```

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

```
global <- global %>% filter(cases > 0) #issue with this filter

summary(global)
```

```
##  Province/State     Country/Region          date                cases
##  Length:262916      Length:262916      Min.   :2020-01-22   Min.   :       1
##  Class :character   Class :character   1st Qu.:2020-11-02   1st Qu.:     959
##  Mode  :character   Mode  :character   Median :2021-06-29   Median :   14833
##                                        Mean   :2021-06-25   Mean   :  825013
##                                        3rd Qu.:2022-02-19   3rd Qu.:  214798
##                                        Max.   :2022-10-07   Max.   :96686904
##      deaths
##  Min.   :      0
##  1st Qu.:      6
##  Median :    168
##  Mean   :  12905
##  3rd Qu.:   3056
##  Max.   :1062513
```

```
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")
```

```
global <- global %>%
  unite("Combined_Key",
        c(`Province/State`, `Country/Region`),
        sep = ", ",
        na.rm = TRUE,
        remove = FALSE)

uid_lookup_url <-
  paste0("https://raw.githubusercontent.com/",
  "CSSEGISandData/COVID-19/master/csse_covid_",
  "19_data/UID_ISO_FIPS_LookUp_Table.csv")

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 %>% rename(`Country_Region` = `Country/Region`)
global <- global %>% rename(`Province_State` = `Province/State`)

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)
```

Visuals

```
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()
```

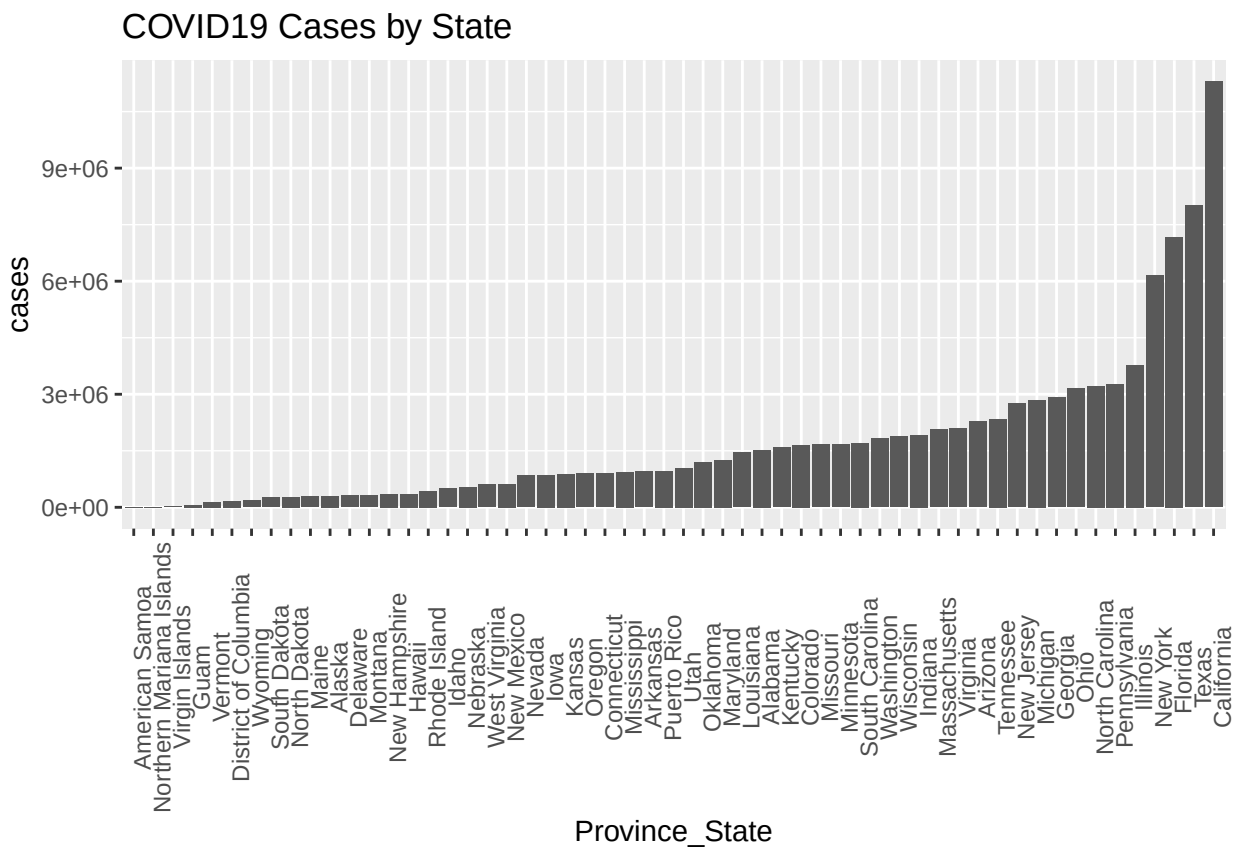
```
## `summarise()` has grouped output by 'Province_State', 'Country_Region'. You can
## override using the `.groups` argument.
```

```
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()
```

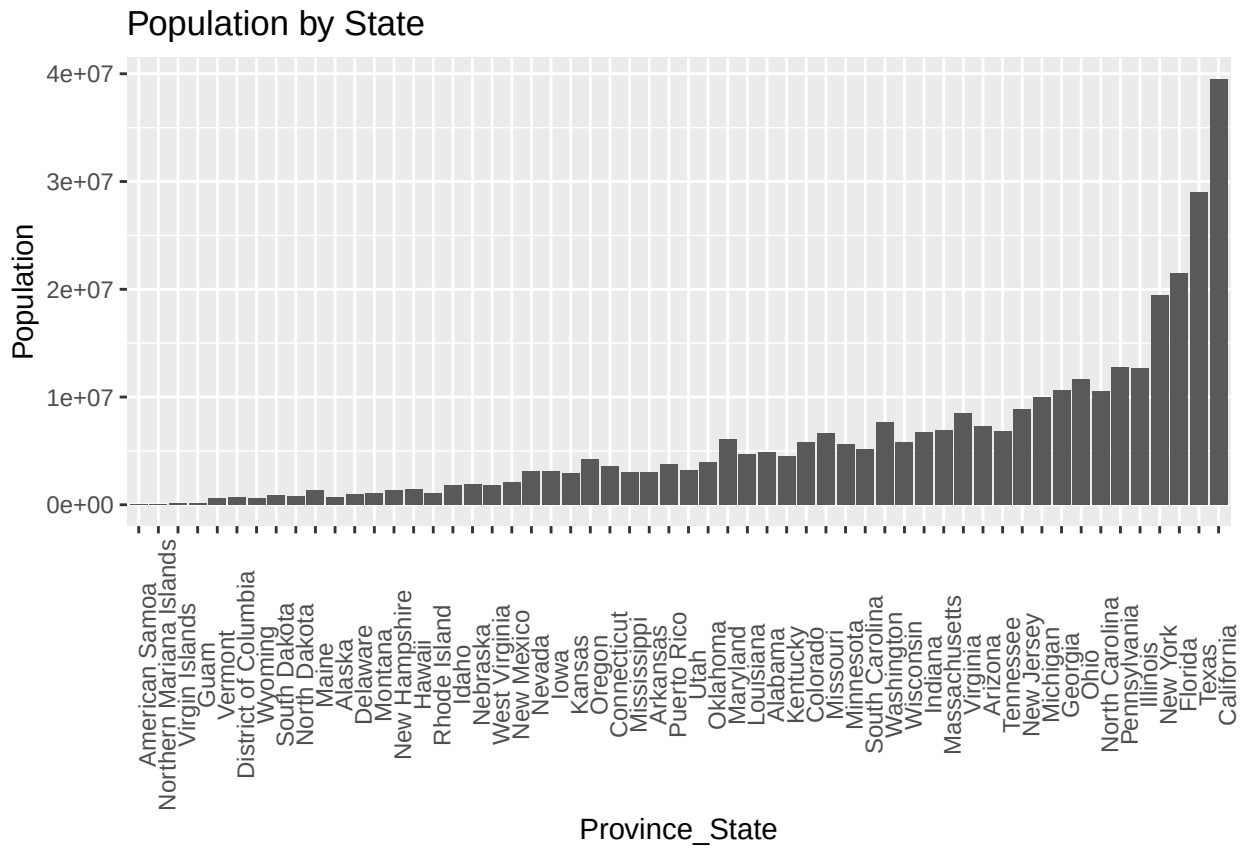
```
## `summarise()` has grouped output by 'Country_Region'. You can override using
## the `.groups` argument.
```

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


US_state_totals %>%
  mutate(Province_State = fct_reorder(Province_State, cases)) %>%
  filter(cases > 0) %>%
  ggplot(aes(x=Province_State, y=cases)) +
  geom_bar(stat="identity") +
```

```
  theme(legend.position = "bottom",
        axis.text.x = element_text(angle = 90)) +
  labs(title = "COVID19 Cases by State")
```




```
US_state_totals %>%
  mutate(Province_State = fct_reorder(Province_State, cases)) %>%
  filter(cases > 0) %>%
  ggplot(aes(x=Province_State, y=Population)) +
  geom_bar(stat="identity") +
  theme(legend.position = "bottom",
        axis.text.x = element_text(angle = 90)) +
  labs(title = "Population by State")
```



Anaylsis

When comparing the above two charts, it appears that the population count of a state is useful for predicting the total number of COVID cases. Although this is an obvious observation, I was curious to see if any outliers could raise more questions, such as a clear difference between states with various approaches to virus containment. To test this theory, I used a linear model to visualize the relationship between population and the number of COVID cases.

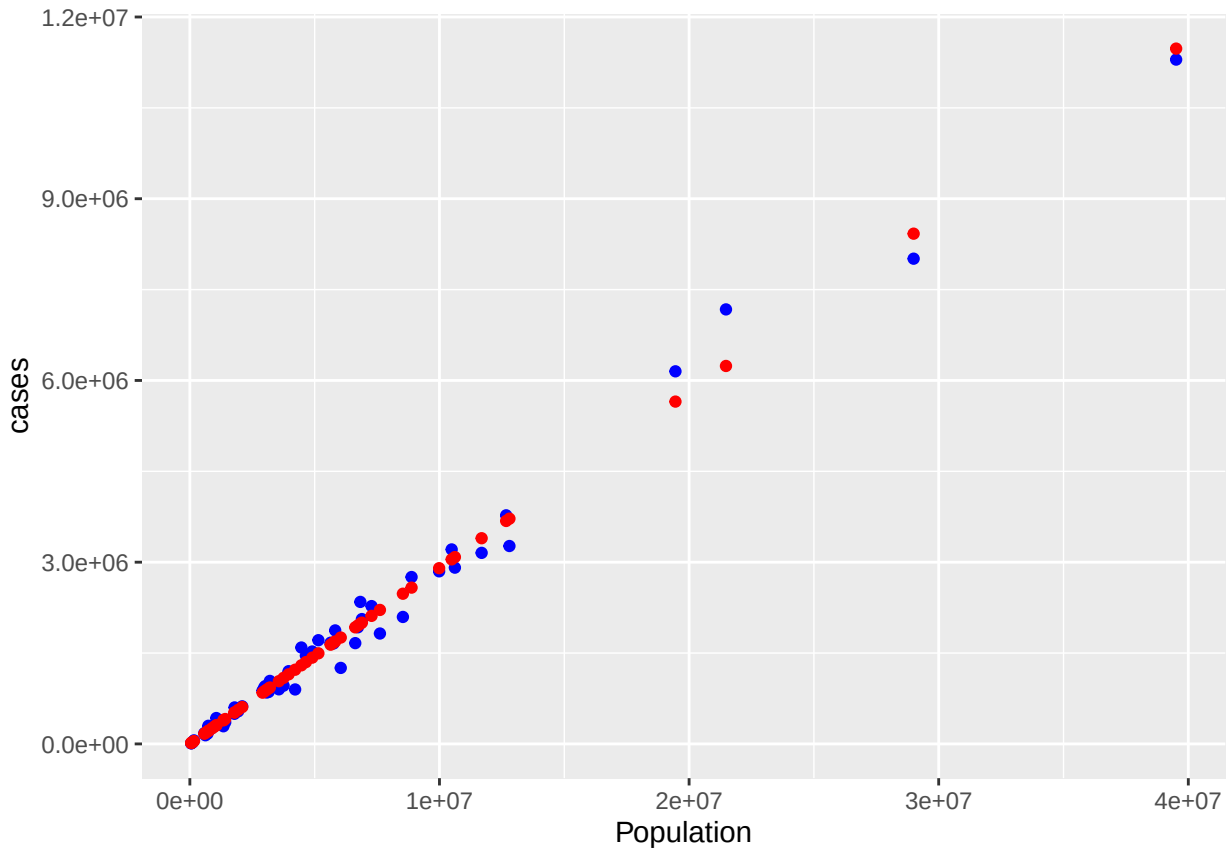
Model

```
mod <- lm(cases ~ Population, data = US_state_totals)

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

```
## # A tibble: 56 x 5
##    Province_State       deaths    cases Population      pred
##    <chr>                 <dbl>    <dbl>      <dbl>     <dbl>
##  1 Alabama               20473  1525724    4903185  1424132.
##  2 Alaska                 1393   298869     740995   215003.
##  3 American Samoa           34     8250      55641    15906.
##  4 Arizona               31406  2275235    7278717  2114231.
##  5 Arkansas              12276   953681    3017804   876423.
##  6 California            96217 11296777   39512223 11478160.
```

```
##  7 Colorado              13334  1658928    5758736  1672672.
##  8 Connecticut           11385   901180    3565287  1035468.
##  9 Delaware               3112   309804     973764   282623.
## 10 District of Columbia   1392   168678     705749   204764.
## # ... with 46 more rows
```

```
US_state_totals_w_pred <- US_state_totals %>% mutate(pred = predict(mod))

US_state_totals_w_pred %>% ggplot() +
geom_point(aes(x= Population, y = cases), color = "blue") +
 geom_point(aes(x= Population, y = pred), color = "red")
```



Conclusion and Bias

In the above chart, the red dots are the predictions, and the blue dots are the actual values. Based on this model, I believe it is fair to conclude that population is a valuable predictor of the total number of COVID cases per state.

My bias for this analysis would be my expectation that a greater population would lead to a higher number of COVID cases.