

COVID19_Data

2024-10-14

COVID-19 Data Analysis Project

This data analysis examines COVID-19 case and death data for US, and globally from January of 2020 to March of 2023. The original raw data sets include information about the US county where the case was recorded, population of the county, and the date of the case. This project aims to answer the question, what were the US COVID cases that resulted in death compared to the overall case, and how does Colorado compare to the other states overall?

Possible Bias

In any data science project, it is important to note the potential sources of bias and ensure they are identified to others consuming the information, as well as any appropriate mitigation steps are taken in analysis, if possible. Some possible sources of bias in this COVID-19 data set are;

1. Under-Reporting: At the height of the pandemic, many communities did not have the resources to support adequate testing. There were also periods where testing was either inaccessible or not free, which may have prevented some people from testing. This could cause the number of cases to be lower than reality.
2. Asymptomatic Cases: For some individuals, COVID-19 symptoms were lessened or not noticeable at all, so those individuals may have not gotten tested but still carried or had the potential to spread the virus. This could cause the number of cases to be lower than reality.
3. Healthcare Funding: During the pandemic, some hospital's resourcing and federal aid was dependent on the number of COVID-19 cases being treated at the hospital. This could cause an inflation in the number of reported COVID-19 deaths or cases in order for hospitals to get essential resources to support patients.

```
#Importing Data
library(tidyverse)
library(lubridate)
library(forecast)
library(mgcv)

url_in <- "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_cov

file_names <- c("time_series_covid19_confirmed_US.csv", "time_series_covid19_confirmed_global.csv", "t

urls <- str_c(url_in,file_names)

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

#Looking at Global Cases

```
global_cases <- global_cases[, !(names(global_cases) %in% c("Admin2", "Lat", "Long_", "UID", "iso2", "iso3", "code3", "FIPS10-4", "Country_Region", "Province_State", "Combined_Key", "date"))]
global_cases <- global_cases %>% rename(Country_Region = Country.Region, Province_State = Province.State)
global_deaths <- global_deaths %>% rename(Country_Region = Country.Region, Province_State = Province.State)

global_deaths <- global_deaths %>% pivot_longer(cols = -c('Province_State', 'Country_Region', 'Lat', 'Long_', 'UID', 'iso2', 'iso3', 'code3', 'FIPS10-4'), names_to = "date")
global_cases <- global_cases %>% pivot_longer(cols = -c('Province_State', 'Country_Region'), names_to = "date")

global_cases <- global_cases %>% mutate(date = gsub("^X", "", date)) %>% mutate(date = gsub("^((\\d){4})(\\d){2}(\\d){2}", "\\1-\\2-\\3", date))
global_deaths <- global_deaths %>% mutate(date = gsub("^X", "", date)) %>% mutate(date = gsub("^((\\d){4})(\\d){2}(\\d){2}", "\\1-\\2-\\3", date))
global <- global_cases %>% full_join(global_deaths) %>% mutate(date = mdy(date))
global <- global %>% filter(cases > 0)
```

#Examining US Cases

```
US_cases <- US_cases[, !(names(US_cases) %in% c("UID", "Lat", "Long_", "UID", "iso2", "iso3", "code3", "FIPS10-4", "Country_Region", "Province_State", "Combined_Key", "date"))]
US_cases <- US_cases %>% pivot_longer(cols = -c('Province_State', 'Country_Region', 'Combined_Key', 'Admin2', 'date'), names_to = "date")
US_cases <- US_cases %>% mutate(date = mdy(date))

US_deaths <- US_deaths[, !(names(US_deaths) %in% c("UID", "Lat", "Long_", "UID", "iso2", "iso3", "code3", "FIPS10-4", "Country_Region", "Province_State", "Combined_Key", "date"))]
US_deaths <- US_deaths %>% pivot_longer(cols = -c('Province_State', 'Country_Region', 'Combined_Key', 'Admin2', 'date'), names_to = "date")
US_deaths <- US_deaths %>% mutate(date = mdy(date))

US <- US_cases %>% full_join(US_deaths)
US <- US %>% filter(cases > 0)
```

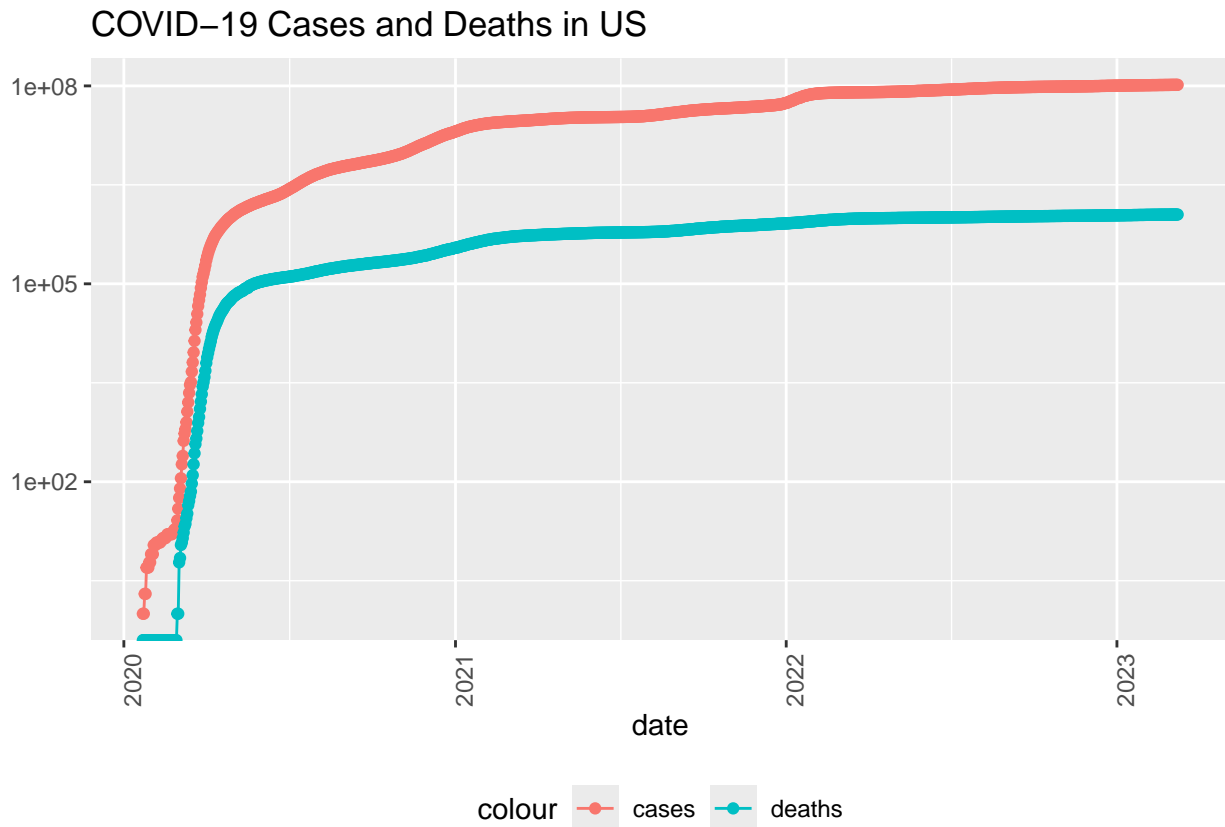
#Plotting US Data

```
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()

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()

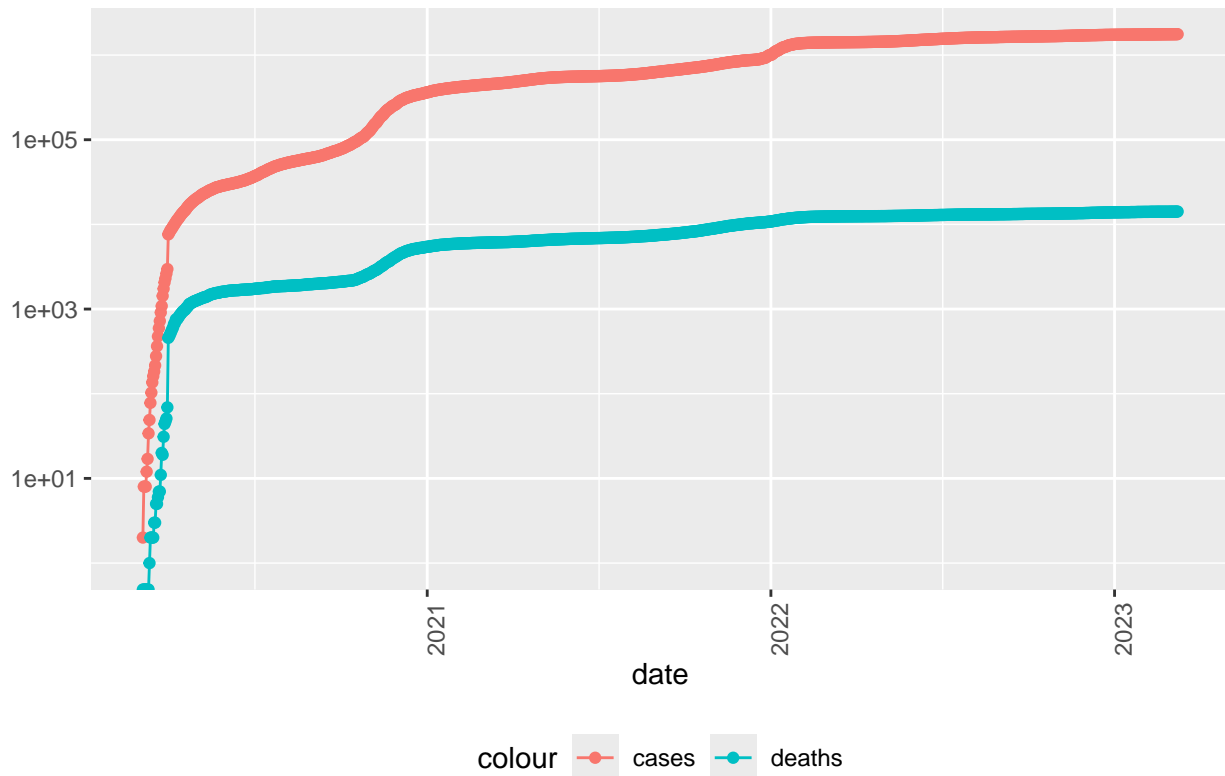
US_totals %>%
  filter(cases > 0) %>%
  ggplot (aes(x = date, y = cases)) +
  geom_line (aes (color = "cases")) +
  geom_point(aes(color = "cases")) +
  geom_line(aes (y = deaths, color = "deaths")) +
  geom_point (aes(y = deaths, color = "deaths")) +
  scale_y_log10() +
  theme(legend.position="bottom",
```

```
axis.text.x = element_text(angle = 90)) +
labs(title = "COVID-19 Cases and Deaths in US", y= NULL)
```



```
#Plotting Colorado Data
US_by_state %>%
  filter(Province_State == "Colorado") %>%
  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 Cases and Deaths in Colorado", y= NULL)
```

COVID-19 Cases and Deaths in Colorado



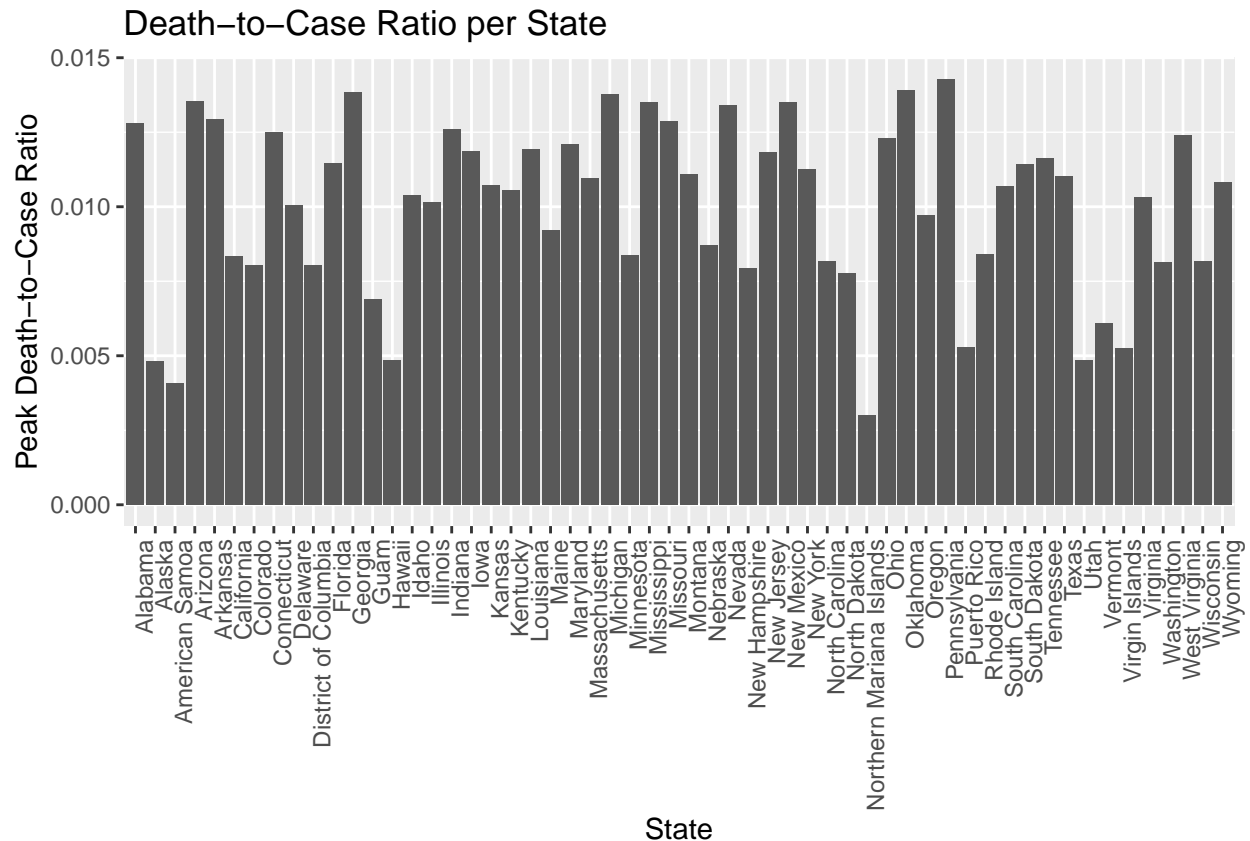
Cases and Deaths Over Time

The trends in the national cases and deaths over the collection period are reflected in the Colorado trends as well. This makes sense, because largely when there were spikes in cases, those trends would quickly be reflected nationally.

```
#Examining Peak Ratios for Death to Case variables
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)

#Plotting the Peak Death to Case Ratio Per State
US_state_totals <- US_state_totals %>% mutate(death_case_ratio = deaths_per_thou / cases_per_thou)

ggplot(US_state_totals, aes(x = Province_State, y = death_case_ratio)) + geom_col() +
  labs(title = "Death-to-Case Ratio per State", x = "State", y = "Peak Death-to-Case Ratio") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
```



#Examining Colorado Data

```
colorado_data <- US_cases %>% filter(Province_State == "Colorado")
colorado_data_clean <- colorado_data %>% group_by(date) %>% summarize(cases = sum(cases))
colorado_data_clean$date <- as.Date(colorado_data_clean$date)
US_state_totals %>% slice_min(deaths_per_thou, n = 15)
```

```
## # A tibble: 15 x 7
##   Province_State    deaths    cases population cases_per_thou deaths_per_thou
##   <chr>          <int>    <int>    <int>         <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   2785478        391.         1.90
## 8 District of Columbia 1432  1.78e5    705749        252.         2.03
## 9 Alaska            1486  3.08e5    728809        422.         2.04
## 10 Washington       15683  1.93e6   7614893        253.         2.06
## 11 Maine             2928  3.18e5   1344212        237.         2.18
## 12 New Hampshire     3003  3.78e5   1359711        278.         2.21
## 13 Oregon            9373  9.64e5   4217737        228.         2.22
## 14 Colorado         14181  1.76e6   5758736        306.         2.46
## 15 Nebraska          4936  5.67e5   1934408        293.         2.55
## # i 1 more variable: death_case_ratio <dbl>
```

Peak Colorado COVID-19 Cases Compared to US Overall

As we can see in the peak death-to-case ratio plot, Colorado ranked amongst the lower states in terms of death-to-case ratio over the course of the pandemic. Colorado had the 14th lowest peak death-to-case ratio out of the US states and territories. Also of note, only one state (Washington) had a larger population but lower death-to-case ratio.

```
#Modeling US Data
```

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

```
US_state_totals %>% slice_max(cases_per_thou, n = 5)
```

```
## # A tibble: 5 x 7
##   Province_State deaths   cases population cases_per_thou deaths_per_thou
##   <chr>          <int>   <int>    <int>         <dbl>         <dbl>
## 1 Rhode Island    3870  460697  1059361         435.          3.65
## 2 Alaska          1486  307655   728809         422.          2.04
## 3 Utah            5298 1090346  2785478         391.          1.90
## 4 Kentucky       18130 1718471  4467673         385.          4.06
## 5 North Dakota   2232  286950   762062         377.          2.93
## # i 1 more variable: death_case_ratio <dbl>
```

```
US_state_totals %>% slice_max(deaths_per_thou, n = 5)
```

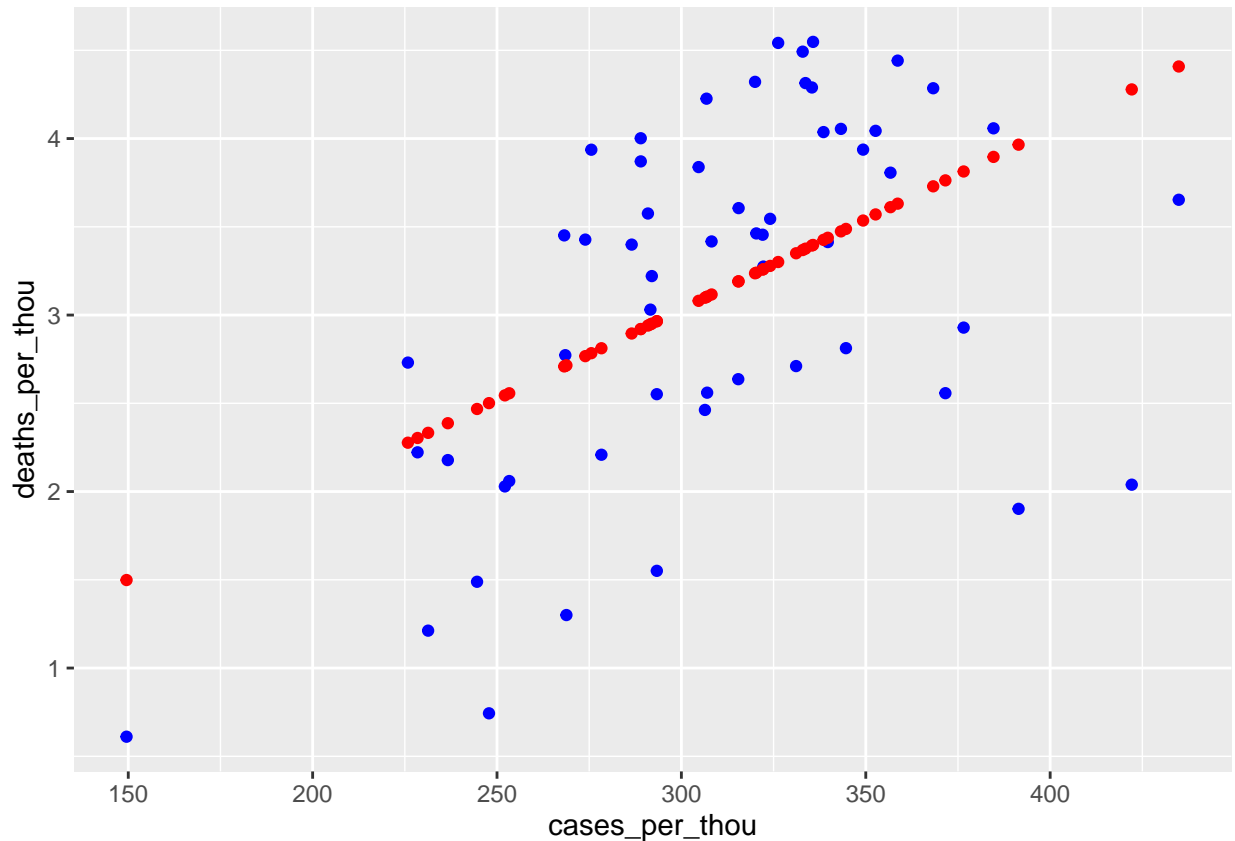
```
## # A tibble: 5 x 7
##   Province_State deaths   cases population cases_per_thou deaths_per_thou
##   <chr>          <int>   <int>    <int>         <dbl>         <dbl>
## 1 Arizona       33102 2443514   7278717         336.          4.55
## 2 Oklahoma      17972 1290929   3956971         326.          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
## # i 1 more variable: death_case_ratio <dbl>
```

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

```
## # A tibble: 56 x 8
##   Province_State deaths   cases population cases_per_thou deaths_per_thou
##   <chr>          <int>   <int>    <int>         <dbl>         <dbl>
## 1 Alabama       21032 1.64e6  4903185         335.          4.29
## 2 Alaska         1486 3.08e5   728809         422.          2.04
## 3 American Samoa    34 8.32e3   55641         150.          0.611
## 4 Arizona       33102 2.44e6  7278717         336.          4.55
## 5 Arkansas       13020 1.01e6  3017804         334.          4.31
## 6 California     101159 1.21e7  39512223         307.          2.56
## 7 Colorado       14181 1.76e6  5758736         306.          2.46
## 8 Connecticut     12220 9.77e5  3565287         274.          3.43
## 9 Delaware        3324 3.31e5   973764         340.          3.41
## 10 District of Columbia 1432 1.78e5   705749         252.          2.03
## # i 46 more rows
## # i 2 more variables: death_case_ratio <dbl>, pred <dbl>
```

```
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") +
```



Linear Model

As we can see in the model prediction above, the deaths per thousand and the cases per thousand don't show a strong linear relationship overall with respect to US data, but given the small range in deaths per thousand, there is a decent accuracy overall. The fact that this relationship isn't perfectly linear makes sense, because one would assume the number of deaths would decrease over time, as prevention methods and vaccines were more widely accessible and understood. While this graph isn't time series, it does include data from the entire time span (2020-2023), so one could draw the conclusion that because the deaths per case average went down over time, there may not be a noticeable trend of death/case ratio when looking over the entire duration of the pandemic.

Conclusion

In conclusion, I was able to analyze the COVID-19 dataset to understand the trends in cases, deaths, and the ratio of the two on a global scale, as well as a comparison between the US as a whole, and Colorado as an individual state.