COVID 19 Analysis

Tyler Kephart

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Required Packages

```
library(tidyverse)
library(lubridate)
library(usmap)
```

Part 1 - Basic Exploration of US Data

The New York Times (the Times) has aggregated reported COVID-19 data from state and local governments and health departments since 2020 and provides public access through a repository on GitHub. One of the data sets provided by the Times is county-level data for cumulative cases and deaths each day. This will be your primary data set for the first two parts of your analysis.

County-level COVID data from 2020, 2021, and 2022 has been imported below. Each row of data reports the cumulative number of cases and deaths for a specific county each day. A FIPS code, a standard geographic identifier, is also provided which you will use in Part 2 to construct a map visualization at the county level for a state.

Additionally, county-level population estimates reported by the US Census Bureau has been imported as well. You will use these estimates to calculate statistics per 100,000 people.

```
# Import New York Times COVID-19 data
# Import Population Estimates from US Census Bureau

us_counties_2020 <- read_csv(
    "https://raw.githubusercontent.com/nytimes/covid-19-data/master/us-counties-2020.csv")
us_counties_2021 <- read_csv(
    "https://raw.githubusercontent.com/nytimes/covid-19-data/master/us-counties-2021.csv")
us_counties_2022 <- read_csv(
    "https://raw.githubusercontent.com/nytimes/covid-19-data/master/us-counties-2022.csv")

us_population_estimates <- read_csv("fips_population_estimates.csv")
```

Question 1

Your first task is to combine and tidy the 2020, 2021, and 2022 COVID data sets and find the total deaths and cases for each day since March 15, 2020 (2020-03-15). The data sets provided from the NY Times also includes statistics from Puerto Rico, a US territory. You may remove these observations from the data as they will not be needed for your analysis. Once you have tidied the data, find the total COVID-19 cases and deaths since March 15, 2020. Write a sentence or two after the code block communicating your results. Use inline code to include the `max_date`, `us_total_cases`, and `us_total_deaths` variables. To write inline code use `r`.

```
# combine the 2020, 2021, and 2022 COVID data sets
us_counties <- rbind(
                    us_counties_2020,
```

```
                    us_counties_2021,
                    us_counties_2022,
                    deparse.level = 1) %>%
                # exclude Puerto Rico, idk why other territories get to stay
                filter(state != "Puerto Rico",
                       # filter from March 15, 2020 and after
                       date >= as.Date("2020-03-15"))
# summarize total cases and deaths by date
daily_totals <- us_counties %>%
                    group_by(date) %>%
                    summarise(total_deaths = sum(deaths),
                              total_cases = sum(cases))
daily_totals
```

```
## # A tibble: 1,022 x 3
##    date       total_deaths total_cases
##    <date>            <dbl>       <dbl>
##  1 2020-03-15           68        3595
##  2 2020-03-16           91        4502
##  3 2020-03-17          117        5901
##  4 2020-03-18          162        8345
##  5 2020-03-19          212       12387
##  6 2020-03-20          277       17998
##  7 2020-03-21          359       24507
##  8 2020-03-22          457       33050
##  9 2020-03-23          577       43474
## 10 2020-03-24          783       53899
## # i 1,012 more rows
```

```
# set variables for inline code usage
max_date <- max(daily_totals$date)
us_total_cases <- max(daily_totals$total_cases)
us_total_deaths <- max(daily_totals$total_deaths)
```

```
# Your output should look similar to the following tibble:
#
#   A tibble: 657 x 3
#       date          total_deaths   total_cases
#      <date>            <dbl>         <dbl>
#   1 2020-03-15           68          3595
#   2 2020-03-16           91          4502
#   3 2020-03-17          117          5901
#   4 2020-03-18          162          8345
#   5 2020-03-19          212         12387
#   6 2020-03-20          277         17998
#   7 2020-03-21          359         24507
#   8 2020-03-22          457         33050
#   9 2020-03-23          577         43474
#  10 2020-03-24          783         53899
# ... with 647 more rows
```

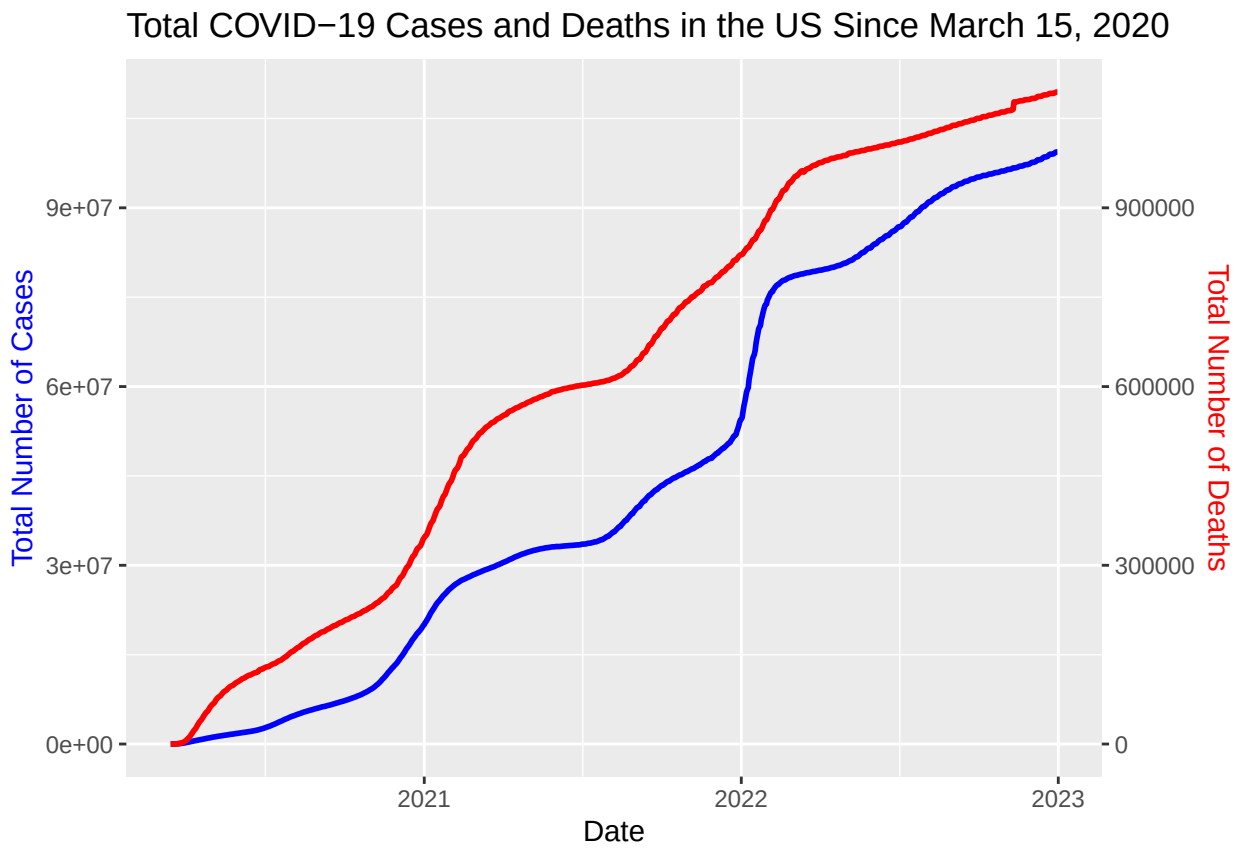
As of December 31, 2022, there was more than 99.37 million cases and 1.09 million deaths from COVID-19 in the United States (excluding Puerto Rico).

Question 2

Create a visualization for the total number of deaths and cases in the US since March 15, 2020. Before you create your visualization, review the types of plots you can create using the ggplot2 library and think about which plots would be

effective in communicating your results. After you have created your visualization, write a few sentences describing your visualization. How could the plot be interpreted? Could it be misleading?

```
# plot for the total number of US cases and deaths since March 15, 2020
ggplot(daily_totals, aes(x = date)) +
    geom_line(aes(y = total_cases, color = "Cases"), linewidth = 1) +
    # scaling deaths for visibility
    geom_line(aes(y = total_deaths * 100, color = "Deaths"), linewidth = 1) +
    # set up y axis for 2 variables
    scale_y_continuous(name = "Total Number of Cases",
                       # add second axis for deaths
                       sec.axis = sec_axis(~./100, name = "Total Number of Deaths")) +
    # color the y axis titles to match the plotted lines
    theme(axis.title.y.left = element_text(color = "blue"),
          axis.title.y.right = element_text(color = "red")) +
    labs(title = "Total COVID-19 Cases and Deaths in the US Since March 15, 2020",
        x = "Date") +
    # remove legend name
    theme(legend.position = "none") +
    scale_color_manual(values = c("Cases" = "blue", "Deaths" = "red"))
```



There seems to have been a spike in cases early 2022 that was possibly due to increased travel during the holiday season in the United States.

Question 3

While it is important to know the total deaths and cases throughout the COVID-19 pandemic, it is also important for local and state health officials to know the the number of new cases and deaths each day to understand how rapidly the virus is spreading. Using the table you created in Question 1, calculate the number of new deaths and cases each day and a seven-day average of new deaths and cases. Once you have organized your data, find the days that saw the largest number of new cases and deaths. Write a sentence or two after the code block communicating your results.

```r
# calculate number of new deaths and cases each day
daily_7day_avg <- daily_totals %>%
    mutate(
        delta_deaths_1 = total_deaths - lag(total_deaths),
        delta_cases_1 = total_cases - lag(total_cases))
# calculate rolling averages
calculate_rolling_average <- function(x, window_size) {
    sapply(seq_along(x), function(i) {
        if (i < window_size) return(NA)
        mean(x[(i - window_size + 1):i])
    })
}
# add 7-day rolling averages
daily_7day_avg <- daily_7day_avg %>%
    mutate(
        delta_deaths_7 = calculate_rolling_average(delta_deaths_1, 7),
        delta_cases_7 = calculate_rolling_average(delta_cases_1, 7)
    )
daily_7day_avg
```

```
## # A tibble: 1,022 x 7
##    date       total_deaths total_cases delta_deaths_1 delta_cases_1
##    <date>            <dbl>       <dbl>          <dbl>         <dbl>
##  1 2020-03-15           68        3595             NA            NA
##  2 2020-03-16           91        4502             23           907
##  3 2020-03-17          117        5901             26          1399
##  4 2020-03-18          162        8345             45          2444
##  5 2020-03-19          212       12387             50          4042
##  6 2020-03-20          277       17998             65          5611
##  7 2020-03-21          359       24507             82          6509
##  8 2020-03-22          457       33050             98          8543
##  9 2020-03-23          577       43474            120         10424
## 10 2020-03-24          783       53899            206         10425
## # i 1,012 more rows
## # i 2 more variables: delta_deaths_7 <dbl>, delta_cases_7 <dbl>
```

```r
# find the days with the largest number of new cases and deaths
max_new_cases_date <- daily_7day_avg %>%
    slice_max(order_by = delta_cases_1, n = 1)
max_new_deaths_date <- daily_7day_avg %>%
    slice_max(order_by = delta_deaths_1, n = 1)
```

```r
#  Your output should look similar to the following tibble:
#
#  date
#  total_deaths     >  the cumulative number of deaths up to and including the associated date
#  total_cases      >  the cumulative number of cases up to and including the associated date
#  delta_deaths_1   >  the number of new deaths since the previous day
#  delta_cases_1    >  the number of new cases since the previous day
#  delta_deaths_7   >  the average number of deaths in a seven-day period
#  delta_cases_7    >  the average number of cases in a seven-day period
#==
#  A tibble: 813 x 7
#    date          total_deaths   total_cases   delta_deaths_1    delta_cases_1  delta_deaths_7  delta_cases
#    <date>           <dbl>          <dbl>         <dbl>              <dbl>        <dbl>            <dbl>
#  1 2020-03-15          68          3600           0                    0         NA               NA
#  2 2020-03-16          91          4507          23                  907         NA               NA
#  3 2020-03-17         117          5906          26                 1399         NA               NA
```

```
#  4 2020-03-18          162          8350           45                2444        NA                NA
#  5 2020-03-19          212         12393           50                4043        NA                NA
#  6 2020-03-20          277         18012           65                5619        NA                NA
#  7 2020-03-21          360         24528           83                6516        NA                NA
#  8 2020-03-22          458         33073           98                8545      55.7              4210.
#  9 2020-03-23          579         43505          121               10432      69.7              5571.
# 10 2020-03-24          785         53938          206               10433      95.4              6862.
# ... with 803 more rows
```

As of December 31, 2022, the most amount of new cases in a single day happened on January 10, 2022 with 1.427097×10^6 cases. The most amount of new deaths in a single day happened on November 11, 2022 with 1.0037×10^4 deaths.

Question 4

Create a new table, based on the table from Question 3, and calculate the number of new deaths and cases per 100,000 people each day and a seven day average of new deaths and cases per 100,000 people.

```
# aggregate US population by year
us_population_totals <- us_population_estimates %>%
    group_by(Year) %>%
    summarize(total_population = sum(Estimate))

# add year to daily_totals
daily_7day_avg_yr <- daily_7day_avg %>%
    mutate(year = year(date))

# join with population totals
daily_7day_avg_yr_pop <- daily_7day_avg_yr %>%
    left_join(us_population_totals, by = c("year" = "Year"))

# calculate metrics per 100,000 people
daily_7day_avg_per_100k <- daily_7day_avg_yr_pop %>%
    mutate(
        total_deaths = (total_deaths / total_population) * 100000,
        total_cases = (total_cases / total_population) * 100000,
        delta_deaths_1 = (delta_deaths_1 / total_population) * 100000,
        delta_cases_1 = (delta_cases_1 / total_population) * 100000,
        delta_deaths_7 = calculate_rolling_average(delta_deaths_1, 7),
        delta_cases_7 = calculate_rolling_average(delta_cases_1, 7)
    ) %>%
    select(date,
            total_deaths,
            total_cases,
            delta_deaths_1,
            delta_cases_1,
            delta_deaths_7,
            delta_cases_7)
daily_7day_avg_per_100k
```

```
## # A tibble: 1,022 x 7
##    date       total_deaths total_cases delta_deaths_1 delta_cases_1
##    <date>            <dbl>       <dbl>          <dbl>         <dbl>
##  1 2020-03-15       0.0205        1.08       NA              NA
##  2 2020-03-16       0.0275        1.36        0.00694         0.274
##  3 2020-03-17       0.0353        1.78        0.00784         0.422
##  4 2020-03-18       0.0489        2.52        0.0136          0.737
##  5 2020-03-19       0.0640        3.74        0.0151          1.22
```

```
##  6 2020-03-20       0.0836        5.43        0.0196          1.69
##  7 2020-03-21       0.108         7.39        0.0247          1.96
##  8 2020-03-22       0.138         9.97        0.0296          2.58
##  9 2020-03-23       0.174        13.1         0.0362          3.14
## 10 2020-03-24       0.236        16.3         0.0621          3.14
## # i 1,012 more rows
## # i 2 more variables: delta_deaths_7 <dbl>, delta_cases_7 <dbl>
```

```
#  Your output should look similar to the following tibble:
#
#  date
#  total_deaths     >  the cumulative number of deaths up to and including the associated date
#  total_cases      >  the cumulative number of cases up to and including the associated date
#  delta_deaths_1   >  the number of new deaths since the previous day
#  delta_cases_1    >  the number of new cases since the previous day
#  delta_deaths_7   >  the average number of deaths in a seven-day period
#  delta_cases_7    >  the average number of cases in a seven-day period
#==
#  A tibble: 657 x 7
#       date         total_deaths   total_cases   delta_deaths_1   delta_cases_1 delta_deaths_7 delta_cases_7
#      <date>            <dbl>         <dbl>          <dbl>           <dbl>           <dbl>          <dbl>
#   1 2020-03-15         0.0205        1.08                0               0              NA             NA
#   2 2020-03-16         0.0275        1.36          0.00694           0.274              NA             NA
#   3 2020-03-17         0.0353        1.78          0.00784           0.422              NA             NA
#   4 2020-03-18         0.0489        2.52           0.0136           0.737              NA             NA
#   5 2020-03-19         0.0640        3.74           0.0151            1.22              NA             NA
#   6 2020-03-20         0.0836        5.43           0.0196            1.69              NA             NA
#   7 2020-03-21         0.108         7.39           0.0247            1.96              NA             NA
#   8 2020-03-22         0.138         9.97           0.0296            2.58          0.0168           1.27
#   9 2020-03-23         0.174        13.1            0.0362            3.14          0.0209           1.68
#  10 2020-03-24         0.236        16.3            0.0621            3.14          0.0287           2.07
```

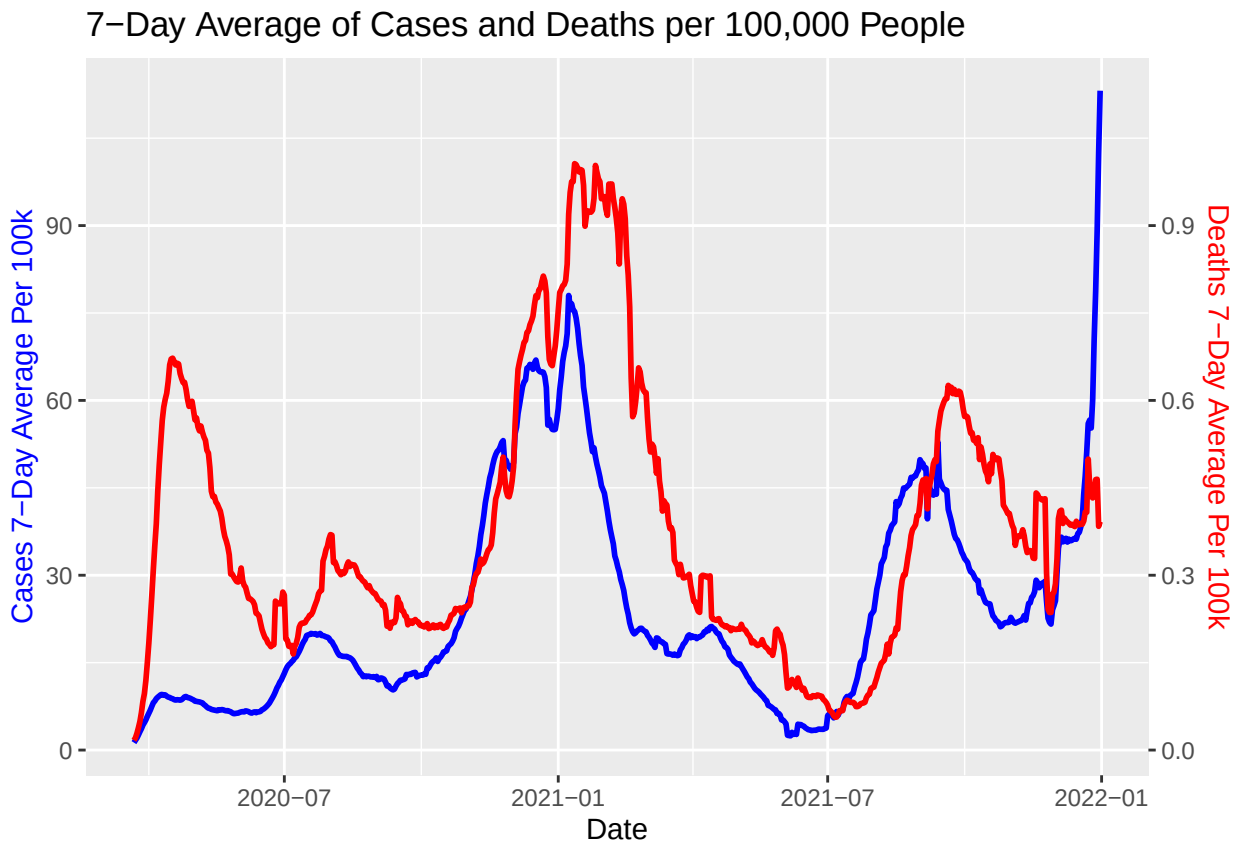
The increasing values for delta_deaths_1 and delta_cases_1 suggest a rising trend in both metrics, which is further confirmed by the increasing delta_deaths_7 and delta_cases_7. This type of data can be useful for understanding the progression of the pandemic and the effectiveness of interventions over time.

Question 5

Create a visualization to compare the seven-day average cases and deaths per 100,000 people.

```
# compare 7-day average cases and deaths per 100k people
daily_7day_avg_per_100k %>%
    filter(!is.na(delta_cases_7)) %>%
    ggplot(aes(x = date)) +
    geom_line(aes(y = delta_cases_7, color = "Cases"), linewidth = 1) +
    # scale for visibility
    geom_line(aes(y = delta_deaths_7 * 100, color = "Deaths"), linewidth = 1) +
    # set up y axis for 2 variables
    scale_y_continuous(name = "Cases 7-Day Average Per 100k",
                       # add second axis for deaths
                       sec.axis = sec_axis(~./100, name = "Deaths 7-Day Average Per 100k")) +
    # color the y axis titles to match the plotted lines
    theme(axis.title.y.left = element_text(color = "blue"),
          axis.title.y.right = element_text(color = "red")) +
    labs(title = "7-Day Average of Cases and Deaths per 100,000 People",
         x = "Date") +
    # remove legend name
```

```
    theme(legend.position = "none") +
    scale_color_manual(values = c("Cases" = "blue", "Deaths" = "red"))
```



The plot really highlights the increased rates of cases and deaths around January 2021.

Part 2 - US State Comparison

While understanding the trends on a national level can be helpful in understanding how COVID-19 impacted the United States, it is important to remember that the virus arrived in the United States at different times. For the next part of your analysis, you will begin to look at COVID related deaths and cases at the state and county-levels.

Question 1

Your first task in Part 2 is to determine the top 10 states in terms of total deaths and cases between March 15, 2020, and December 31, 2021.

Once you have both lists, briefly describe your methodology and your results.

```
# top 10 states for total deaths and cases between 2020-03-15 and 2021-12-31
state_totals_end2021 <- us_counties %>%
    # just need to filter to 2021-12-31 as totals are already as of that date
    filter(date == "2021-12-31") %>%
    group_by(state, date) %>%
    summarise(total_deaths = sum(deaths),
              total_cases = sum(cases)) %>%
    # sort totals
    arrange(desc(total_cases),
            desc(total_deaths))
```

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

```
state_totals_end2021
```

```
## # A tibble: 55 x 4
## # Groups:   state [55]
##    state          date       total_deaths total_cases
##    <chr>          <date>            <dbl>       <dbl>
##  1 California     2021-12-31        76709     5515613
##  2 Texas          2021-12-31        76062     4574881
##  3 Florida        2021-12-31        62504     4166392
##  4 New York       2021-12-31        58993     3473970
##  5 Illinois       2021-12-31        31017     2154058
##  6 Pennsylvania   2021-12-31        36705     2036424
##  7 Ohio           2021-12-31        29447     2016095
##  8 Georgia        2021-12-31        30283     1798497
##  9 Michigan       2021-12-31        28984     1706355
## 10 North Carolina 2021-12-31        19436     1685504
## # i 45 more rows
```

```
# Your transformed data should look similar to the following tibble:
#
# A tibble: 51 x 4
#    state                date       total_deaths  total_cases
#    <chr>               <date>          <dbl>       <dbl>
#  1 California          2021-12-31        76709      5515613
#  2 Texas               2021-12-31        76062      4574881
#  3 Florida             2021-12-31        62504      4166392
#  4 New York            2021-12-31        58993      3473970
#  5 Illinois            2021-12-31        31017      2154058
#  6 Pennsylvania        2021-12-31        36705      2036424
#  7 Ohio                2021-12-31        29447      2016095
#  8 Georgia             2021-12-31        30283      1798497
#  9 Michigan            2021-12-31        28984      1706355
# 10 North Carolina      2021-12-31        19436      1685504
# ... with 41 more rows
```

The three most populated states (California, Texas, and Florida) also had the most deaths and cases among the states.

Question 2

Determine the top 10 states in terms of deaths per 100,000 people and cases per 100,000 people between March 15, 2020, and December 31, 2021.

Once you have both lists, briefly describe your methodology and your results. Do you expect the lists to be different than the one produced in Question 1? Which method, total or per 100,000 people, is a better method for reporting the statistics?

```
# create population totals for the states
state_population_totals <- us_population_estimates %>%
    group_by(STNAME, Year) %>%
    summarize(total_population = sum(Estimate))
```

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

```
# join to state totals
state_totals_end2021 %>%
    # add year to join on
    mutate(year = year(date)) %>%
    left_join(
        # filter to just 2021
        filter(state_population_totals, Year == 2021),
        by = c("state" = "STNAME")) %>%
    # make _per_100k columns
    mutate(deaths_per_100k = (total_deaths / total_population) * 100000,
           cases_per_100k = (total_cases / total_population) * 100000) %>%
    # select the needed columns
    select(state, date, deaths_per_100k, cases_per_100k) %>%
    # sort totals per 100k
    arrange(desc(cases_per_100k), desc(deaths_per_100k))
```

```
## # A tibble: 55 x 4
## # Groups:   state [55]
##    state        date       deaths_per_100k cases_per_100k
##    <chr>        <date>               <dbl>          <dbl>
##  1 North Dakota 2021-12-31            265.          22482.
##  2 Alaska       2021-12-31            130.          21310.
##  3 Rhode Island 2021-12-31            280.          21093.
##  4 South Dakota 2021-12-31            278.          20014.
##  5 Wyoming      2021-12-31            264.          19979.
##  6 Tennessee    2021-12-31            296.          19783.
##  7 Kentucky     2021-12-31            269.          19173.
##  8 Florida      2021-12-31            287.          19128.
##  9 Utah         2021-12-31            113.          19088.
## 10 Wisconsin    2021-12-31            190.          19008.
## # i 45 more rows
```

```
# Your transformed data should look similar to the following tibble:
#
# A tibble: 51 x 4
#    state                 date           deaths_per_100k  cases_per_100k
#    <chr>                <date>               <dbl>          <dbl>
#  1 North Dakota         2021-12-31           265.           22482.
#  2 Alaska               2021-12-31           130.           21310.
#  3 Rhode Island         2021-12-31           280.           21093.
#  4 South Dakota         2021-12-31           278.           20014.
#  5 Wyoming              2021-12-31           264.           19979.
#  6 Tennessee            2021-12-31           296.           19783.
#  7 Kentucky             2021-12-31           269.           19173.
#  8 Florida              2021-12-31           287.           19128.
#  9 Utah                 2021-12-31           113.           19088.
# 10 Wisconsin            2021-12-31           190.           19008.
# ... with 41 more rows
```

North Dakota, Alaska, Rhode Island, South Dakota, and Wyoming are some of the least populated states in the United states and that could be why the cases per 100K people are high.

Question 3

Now, select a state and calculate the seven-day averages for new cases and deaths per 100,000 people. Once you have calculated the averages, create a visualization using ggplot2 to represent the data.

```r
# Colorado case and death totals from 2020-03-15 to 2021-12-31 per 100k people
colorado_7day_avg <- us_counties %>%
    # filter dates
    filter(between(date, as.Date("2020-03-15"), as.Date("2021-12-31")),
           state == "Colorado") %>%
    group_by(state, date) %>%
    # sum up deaths and cases
    summarise(total_deaths = sum(deaths),
              total_cases = sum(cases)) %>%
    # add tear to join on
    mutate(year = year(date)) %>%
    left_join(
        # filter to just Colorado and join on year
        filter(state_population_totals, STNAME == "Colorado"),
        by = c("year" = "Year")) %>%
    mutate(
        # create 1-day deltas to create 7-day averages
        delta_deaths_1 = total_deaths - lag(total_deaths),
        delta_cases_1 = total_cases - lag(total_cases),
        # create the per 100k metrics
        deaths_per_100k = (total_deaths / total_population) * 100000,
        cases_per_100k = (total_cases / total_population) * 100000,
        # re-use function for 7-day rolling average
        deaths_7_day = calculate_rolling_average((delta_deaths_1 / total_population) * 100000, 7),
        cases_7_day = calculate_rolling_average((delta_cases_1 / total_population) * 100000, 7),
        # shorten name of column
        population = total_population) %>%
    # grab only the needed columns
    select(state,
           date,
           total_deaths,
           total_cases,
           population,
           deaths_per_100k,
           cases_per_100k,
           deaths_7_day,
           cases_7_day)
```

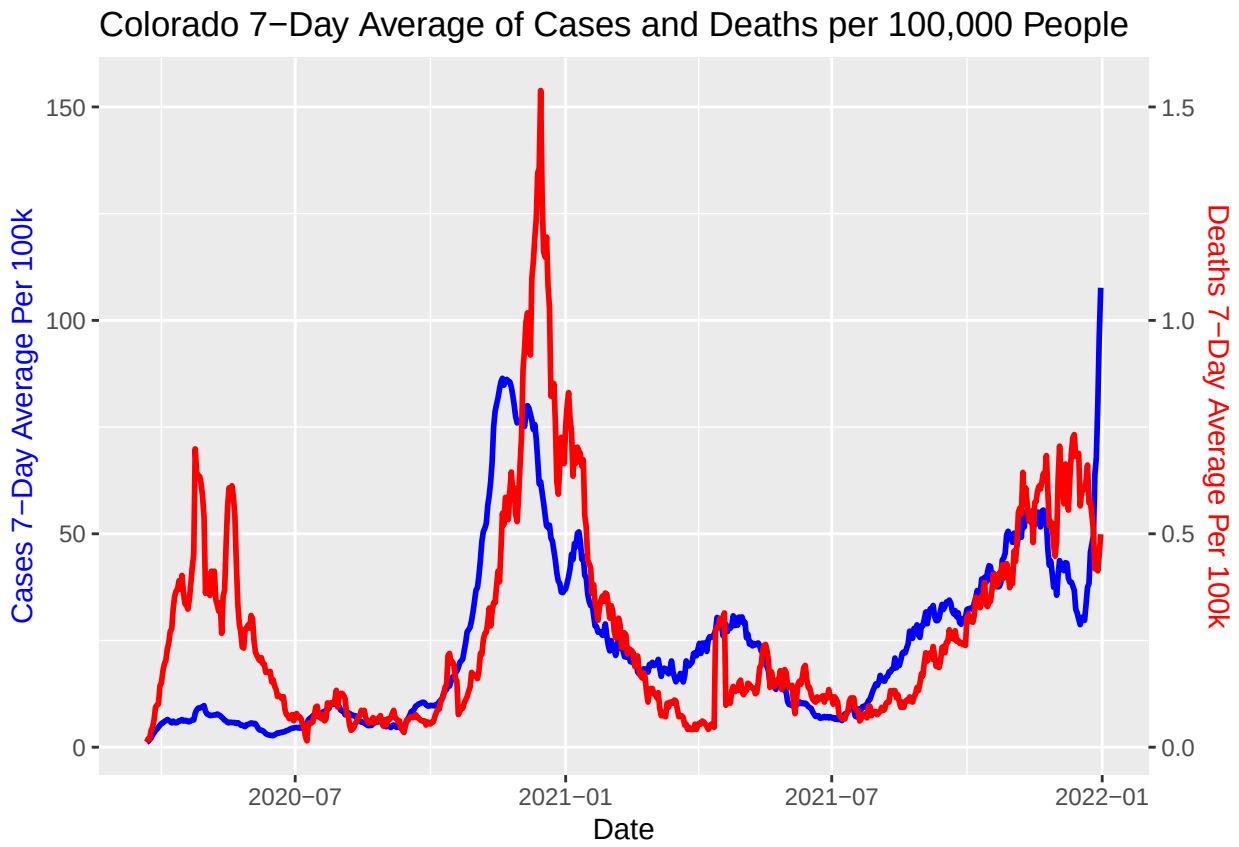
```
## `summarise()` has grouped output by 'state'. You can override using the
## `.groups` argument.
```

```r
colorado_7day_avg
```

```
## # A tibble: 657 x 9
## # Groups:   state [1]
##    state    date       total_deaths total_cases population deaths_per_100k
##    <chr>    <date>            <dbl>       <dbl>      <dbl>           <dbl>
##  1 Colorado 2020-03-15            2         136    5784308          0.0346
##  2 Colorado 2020-03-16            2         161    5784308          0.0346
##  3 Colorado 2020-03-17            3         183    5784308          0.0519
##  4 Colorado 2020-03-18            3         216    5784308          0.0519
##  5 Colorado 2020-03-19            5         278    5784308          0.0864
##  6 Colorado 2020-03-20            5         364    5784308          0.0864
##  7 Colorado 2020-03-21            6         475    5784308          0.104
##  8 Colorado 2020-03-22            7         591    5784308          0.121
##  9 Colorado 2020-03-23           10         721    5784308          0.173
## 10 Colorado 2020-03-24           11         912    5784308          0.190
## # i 647 more rows
```

```
## # i 3 more variables: cases_per_100k <dbl>, deaths_7_day <dbl>,
## #   cases_7_day <dbl>
```

```r
# plot the 7-day average
colorado_7day_avg %>%
    filter(!is.na(cases_7_day)) %>%
    ggplot(aes(x = date)) +
    geom_line(aes(y = cases_7_day, color = "Cases"), linewidth = 1) +
    # scale for visibility
    geom_line(aes(y = deaths_7_day * 100, color = "Deaths"), linewidth = 1) +
    # set up y axis for 2 variables
    scale_y_continuous(name = "Cases 7-Day Average Per 100k",
                       # add second axis for deaths
                       sec.axis = sec_axis(~./100, name = "Deaths 7-Day Average Per 100k")) +
    # color the y axis titles to match the plotted lines
    theme(axis.title.y.left = element_text(color = "blue"),
          axis.title.y.right = element_text(color = "red")) +
    labs(title = "Colorado 7-Day Average of Cases and Deaths per 100,000 People",
         x = "Date") +
    # remove legend name
    theme(legend.position = "none") +
    scale_color_manual(values = c("Cases" = "blue", "Deaths" = "red"))
```




```
# Your transformed data should look similar to the following tibble:
#
# A tibble: 656 × 9
#     state    date       total_deaths total_cases population deaths_per_100k cases_per_100k deaths_7_day  ca
#     <chr>    <date>            <dbl>       <dbl>      <dbl>           <dbl>          <dbl>        <dbl>
#  1 Colorado 2020-03-15            2         136    5784308          0.0346           2.35           NA
#  2 Colorado 2020-03-16            2         161    5784308          0.0346           2.78           NA
```

```
#  3 Colorado 2020-03-17          3      183      5784308        0.0519          3.16          NA
#  4 Colorado 2020-03-18          3      216      5784308        0.0519          3.73          NA
#  5 Colorado 2020-03-19          5      278      5784308        0.0864          4.81          NA
#  6 Colorado 2020-03-20          5      364      5784308        0.0864          6.29          NA
#  7 Colorado 2020-03-21          6      475      5784308        0.104           8.21          NA
#  8 Colorado 2020-03-22          7      591      5784308        0.121           10.2          0.0123
#  9 Colorado 2020-03-23         10      721      5784308        0.173           12.5          0.0198
# 10 Colorado 2020-03-24         11      912      5784308        0.190           15.8          0.0198
# ... with 646 more rows
```

Looks like a lot of cases and deaths around the winter holidays at the end of 2021 and 2022 in Colorado.

Question 4

Using the same state, identify the top 5 counties in terms of deaths and cases per 100,000 people.

```
# get totals for each Colorado county
colorado_county_totals <- us_counties %>%
    # filter dates (sample below has 2021-12-20 so I'm filtering to that)
    filter(date == as.Date("2021-12-20"),
           state == "Colorado") %>%
    # need fips in case of duplicate county names
    group_by(county, date, fips) %>%
    select(county, date, fips, deaths, cases)
# most deaths
colorado_county_totals %>% arrange(desc(deaths))
```

```
## # A tibble: 64 x 5
## # Groups:   county, date, fips [64]
##    county    date       fips  deaths  cases
##    <chr>     <date>     <chr>  <dbl>  <dbl>
##  1 El Paso   2021-12-20 08041   1355 119772
##  2 Denver    2021-12-20 08031   1065 106747
##  3 Jefferson 2021-12-20 08059   1061  76732
##  4 Adams     2021-12-20 08001   1057  90476
##  5 Arapahoe  2021-12-20 08005   1046  95769
##  6 Pueblo    2021-12-20 08101    643  30739
##  7 Weld      2021-12-20 08123    569  55599
##  8 Mesa      2021-12-20 08077    445  29542
##  9 Larimer   2021-12-20 08069    393  47444
## 10 Douglas   2021-12-20 08035    361  48740
## # i 54 more rows
```

```
# most cases
colorado_county_totals %>% arrange(desc(cases))
```

```
## # A tibble: 64 x 5
## # Groups:   county, date, fips [64]
##    county    date       fips  deaths  cases
##    <chr>     <date>     <chr>  <dbl>  <dbl>
##  1 El Paso   2021-12-20 08041   1355 119772
##  2 Denver    2021-12-20 08031   1065 106747
##  3 Arapahoe  2021-12-20 08005   1046  95769
##  4 Adams     2021-12-20 08001   1057  90476
##  5 Jefferson 2021-12-20 08059   1061  76732
##  6 Weld      2021-12-20 08123    569  55599
```

```
##  7 Douglas   2021-12-20 08035    361  48740
##  8 Larimer   2021-12-20 08069    393  47444
##  9 Boulder   2021-12-20 08013    323  36754
## 10 Pueblo    2021-12-20 08101    643  30739
## # i 54 more rows
```

```
# samples below don't account for per 100k people
# so I don't know why the question asks for it
# but here is how the data would look like per 100k people

# create Colorado counties population tibble
co_counties_population2021 <- us_population_estimates %>%
    filter(Year == 2021, STNAME == "Colorado") %>%
    mutate(CTYNAME = gsub(" County", "", CTYNAME))
# per 100k Colorado county totals
colorado_county_totals_per_100k <- colorado_county_totals %>%
    # join to population tibble on county names
    left_join(co_counties_population2021, by = c("county" = "CTYNAME")) %>%
    # get per 100k columns
    mutate(deaths_per_100k = (deaths / Estimate) * 100000,
           cases_per_100k = (cases / Estimate) * 100000,
           fips = fips.x) %>%
    # select columns we want
    select(county, date, fips, deaths_per_100k, cases_per_100k)
# most deaths per 100k
colorado_county_totals_per_100k %>% arrange(desc(deaths_per_100k))
```

```
## # A tibble: 64 x 5
## # Groups:   county, date [64]
##    county     date       fips  deaths_per_100k cases_per_100k
##    <chr>      <date>     <chr>           <dbl>          <dbl>
##  1 Bent       2021-12-20 08011            660.         33721.
##  2 Otero      2021-12-20 08089            613.         17801.
##  3 Conejos    2021-12-20 08021            578.         15449.
##  4 Washington 2021-12-20 08121            494.         15676.
##  5 Cheyenne   2021-12-20 08017            469.         14294.
##  6 Crowley    2021-12-20 08025            449.         41434.
##  7 Logan      2021-12-20 08075            442.         24354.
##  8 Morgan     2021-12-20 08087            421.         14365.
##  9 Pueblo     2021-12-20 08101            379.         18122.
## 10 Moffat     2021-12-20 08081            364.         17004.
## # i 54 more rows
```

```
# most cases per 100k
colorado_county_totals_per_100k %>% arrange(desc(cases_per_100k))
```

```
## # A tibble: 64 x 5
## # Groups:   county, date [64]
##    county     date       fips  deaths_per_100k cases_per_100k
##    <chr>      <date>     <chr>           <dbl>          <dbl>
##  1 Crowley    2021-12-20 08025           449.          41434.
##  2 Bent       2021-12-20 08011           660.          33721.
##  3 Lincoln    2021-12-20 08073           141.          24947.
##  4 Logan      2021-12-20 08075           442.          24354.
##  5 Fremont    2021-12-20 08043           306.          21065.
##  6 Pitkin     2021-12-20 08097            34.6         19593.
##  7 Rio Blanco 2021-12-20 08103           170.          19456.
##  8 Kiowa      2021-12-20 08061           275.          19146.
```

```
##  9 Mesa       2021-12-20 08077           283.          18776.
## 10 Alamosa    2021-12-20 08003           314.          18324.
## # i 54 more rows
```

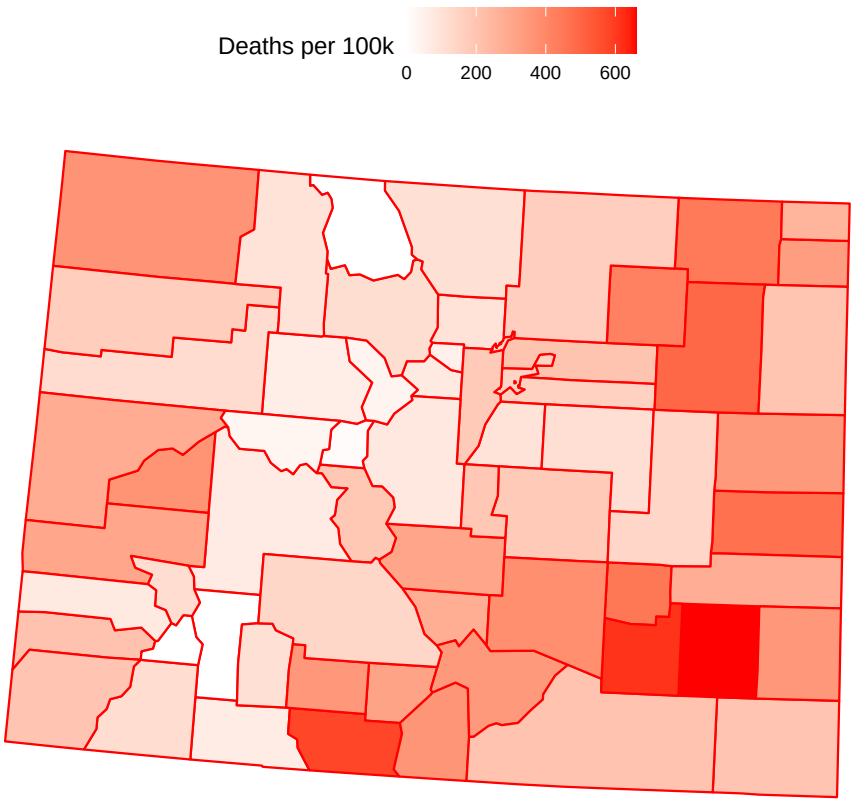
```
# Your transformed data should be similar to the following tibbles:
#
# Arranged by deaths:
# A tibble: 64 × 4
#    county       date       fips    total_deaths   total_cases
#    <chr>       <date>      <chr>       <dbl>         <dbl>
#  1 El Paso    2021-12-20    08041       1355         119772
#  2 Denver     2021-12-20    08031       1065         106747
#  3 Jefferson  2021-12-20    08059       1061          76732
#  4 Adams      2021-12-20    08001       1057          90476
#  5 Arapahoe   2021-12-20    08005       1046          95769
#  6 Pueblo     2021-12-20    08101        643          30739
#  7 Weld       2021-12-20    08123        569          55599
#  8 Mesa       2021-12-20    08077        445          29542
#  9 Larimer    2021-12-20    08069        393          47444
# 10 Douglas    2021-12-20    08035        361          48740
# ... with 54 more rows
#
#
# Arranged by cases:
# A tibble: 64 × 4
#    county       date       fips   total_deaths   total_cases
#    <chr>       <date>      <chr>     <dbl>         <dbl>
#  1 El Paso    2021-12-20    08041     1355         119772
#  2 Denver     2021-12-20    08031     1065         106747
#  3 Arapahoe   2021-12-20    08005     1046          95769
#  4 Adams      2021-12-20    08001     1057          90476
#  5 Jefferson  2021-12-20    08059     1061          76732
#  6 Weld       2021-12-20    08123      569          55599
#  7 Douglas    2021-12-20    08035      361          48740
#  8 Larimer    2021-12-20    08069      393          47444
#  9 Boulder    2021-12-20    08013      323          36754
# 10 Pueblo     2021-12-20    08101      643          30739
# ... with 54 more rows
```

Arapahoe county had more cases and less deaths than both Jefferson and Adams counties. However, when actually looking at the per 100k people data, we can see counties that are not in the sample lists.

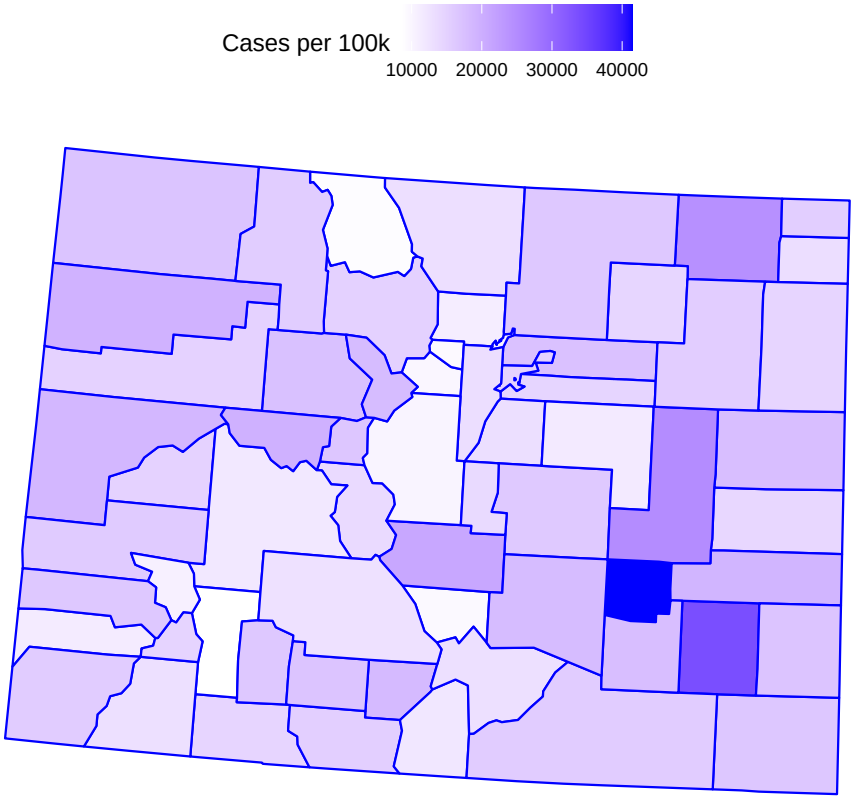
Question 5

Modify the code below for the map projection to plot county-level deaths and cases per 100,000 people for your state.

```
# plot deaths per 100k per county in Colorado
plot_usmap(regions = "county",
           include="CO",
           data = colorado_county_totals_per_100k,
           values = "deaths_per_100k",
           color = "red") +
    scale_fill_continuous(low = "white",
                          high = "red",
                          name = "Deaths per 100k") +
    theme(legend.position = "top")
```




```
# plot cases per 100k per county in Colorado
plot_usmap(regions = "county",
           include="CO",
           data = colorado_county_totals_per_100k,
           values = "cases_per_100k",
           color = "blue") +
    scale_fill_continuous(low = "white",
                          high = "blue",
                          name = "Cases per 100k") +
    theme(legend.position = "top")
```




```
# Copy and modify the code below for your state.
#
# plot_usmap arguments:
#   regions: can be one of ("states", "state", "counties", "county"). The default is "states"
#   include: The regions to include in the resulting map. If regions is "states"/"state", the value can be ei
#   data: values to plot on the map
#   values: the name of the column that contains the values to be associated with a given region.
#   color: the map outline color.
#
# Reference the plot_usmap documentation for further information using ?plot_usmap

# plot_usmap(regions = "county", include="CO", data = colorado_county, values = "total_deaths", color = "blue
#   scale_fill_continuous(low = "white", high = "blue", name = "Deaths per 100,000")
```

It can be seen that the deaths and cases per 100k people is high for counties that are not as populous as major metros like El Paso county.

Question 6

Finally, select three other states and calculate the seven-day averages for new deaths and cases per 100,000 people for between March 15, 2020, and December 31, 2021.

```
# create a function so that I'm not copy/pasting too much
state_7day_avg <- function(us_state) {
    us_counties %>%
    # filter dates
    filter(between(date, as.Date("2020-03-15"), as.Date("2021-12-31")),
           state == us_state) %>%
    group_by(state, date) %>%
```

```
    # sum up deaths and cases
    summarise(total_deaths = sum(deaths),
              total_cases = sum(cases)) %>%
    # add tear to join on
    mutate(year = year(date)) %>%
    left_join(
        # filter to just Colorado and join on year
        filter(state_population_totals, STNAME == us_state),
        by = c("year" = "Year")) %>%
    mutate(
        # create 1-day deltas to create 7-day averages
        delta_deaths_1 = total_deaths - lag(total_deaths),
        delta_cases_1 = total_cases - lag(total_cases),
        # create the per 100k metrics
        deaths_per_100k = (total_deaths / total_population) * 100000,
        cases_per_100k = (total_cases / total_population) * 100000,
        # re-use function for 7-day rolling average
        deaths_7_day = calculate_rolling_average((delta_deaths_1 / total_population) * 100000, 7),
        cases_7_day = calculate_rolling_average((delta_cases_1 / total_population) * 100000, 7),
        # shorten name of column
        population = total_population) %>%
    # grab only the needed columns
    select(state,
           date,
           total_deaths,
           total_cases,
           population,
           deaths_per_100k,
           cases_per_100k,
           deaths_7_day,
           cases_7_day)
}
# California 7-day average
state_7day_avg("California")
```

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

```
## # A tibble: 657 x 9
## # Groups:   state [1]
##    state      date       total_deaths total_cases population deaths_per_100k
##    <chr>      <date>            <dbl>       <dbl>      <dbl>           <dbl>
##  1 California 2020-03-15            6         478   39499738          0.0152
##  2 California 2020-03-16           11         588   39499738          0.0278
##  3 California 2020-03-17           14         732   39499738          0.0354
##  4 California 2020-03-18           17         893   39499738          0.0430
##  5 California 2020-03-19           19        1067   39499738          0.0481
##  6 California 2020-03-20           24        1283   39499738          0.0608
##  7 California 2020-03-21           28        1544   39499738          0.0709
##  8 California 2020-03-22           35        1851   39499738          0.0886
##  9 California 2020-03-23           39        2240   39499738          0.0987
## 10 California 2020-03-24           52        2644   39499738          0.132
## # i 647 more rows
## # i 3 more variables: cases_per_100k <dbl>, deaths_7_day <dbl>,
## #   cases_7_day <dbl>
```

```r
# Oregon 7-day average
state_7day_avg("Oregon")
```

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

```
## # A tibble: 657 x 9
## # Groups:   state [1]
##    state  date       total_deaths total_cases population deaths_per_100k
##    <chr>  <date>            <dbl>       <dbl>      <dbl>           <dbl>
##  1 Oregon 2020-03-15            1          39    4241544          0.0236
##  2 Oregon 2020-03-16            1          46    4241544          0.0236
##  3 Oregon 2020-03-17            2          66    4241544          0.0472
##  4 Oregon 2020-03-18            3          74    4241544          0.0707
##  5 Oregon 2020-03-19            3          87    4241544          0.0707
##  6 Oregon 2020-03-20            3         114    4241544          0.0707
##  7 Oregon 2020-03-21            4         137    4241544          0.0943
##  8 Oregon 2020-03-22            5         161    4241544          0.118
##  9 Oregon 2020-03-23            5         191    4241544          0.118
## 10 Oregon 2020-03-24            8         209    4241544          0.189
## # i 647 more rows
## # i 3 more variables: cases_per_100k <dbl>, deaths_7_day <dbl>,
## #   cases_7_day <dbl>
```

```r
# Washington 7-day average
state_7day_avg("Washington")
```

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

```
## # A tibble: 657 x 9
## # Groups:   state [1]
##    state      date       total_deaths total_cases population deaths_per_100k
##    <chr>      <date>            <dbl>       <dbl>      <dbl>           <dbl>
##  1 Washington 2020-03-15           42         675    7718785           0.544
##  2 Washington 2020-03-16           48         794    7718785           0.622
##  3 Washington 2020-03-17           54         908    7718785           0.700
##  4 Washington 2020-03-18           68        1026    7718785           0.881
##  5 Washington 2020-03-19           75        1228    7718785           0.972
##  6 Washington 2020-03-20           83        1404    7718785           1.08
##  7 Washington 2020-03-21           95        1655    7718785           1.23
##  8 Washington 2020-03-22           97        1844    7718785           1.26
##  9 Washington 2020-03-23          110        2101    7718785           1.43
## 10 Washington 2020-03-24          123        2469    7718785           1.59
## # i 647 more rows
## # i 3 more variables: cases_per_100k <dbl>, deaths_7_day <dbl>,
## #   cases_7_day <dbl>
```

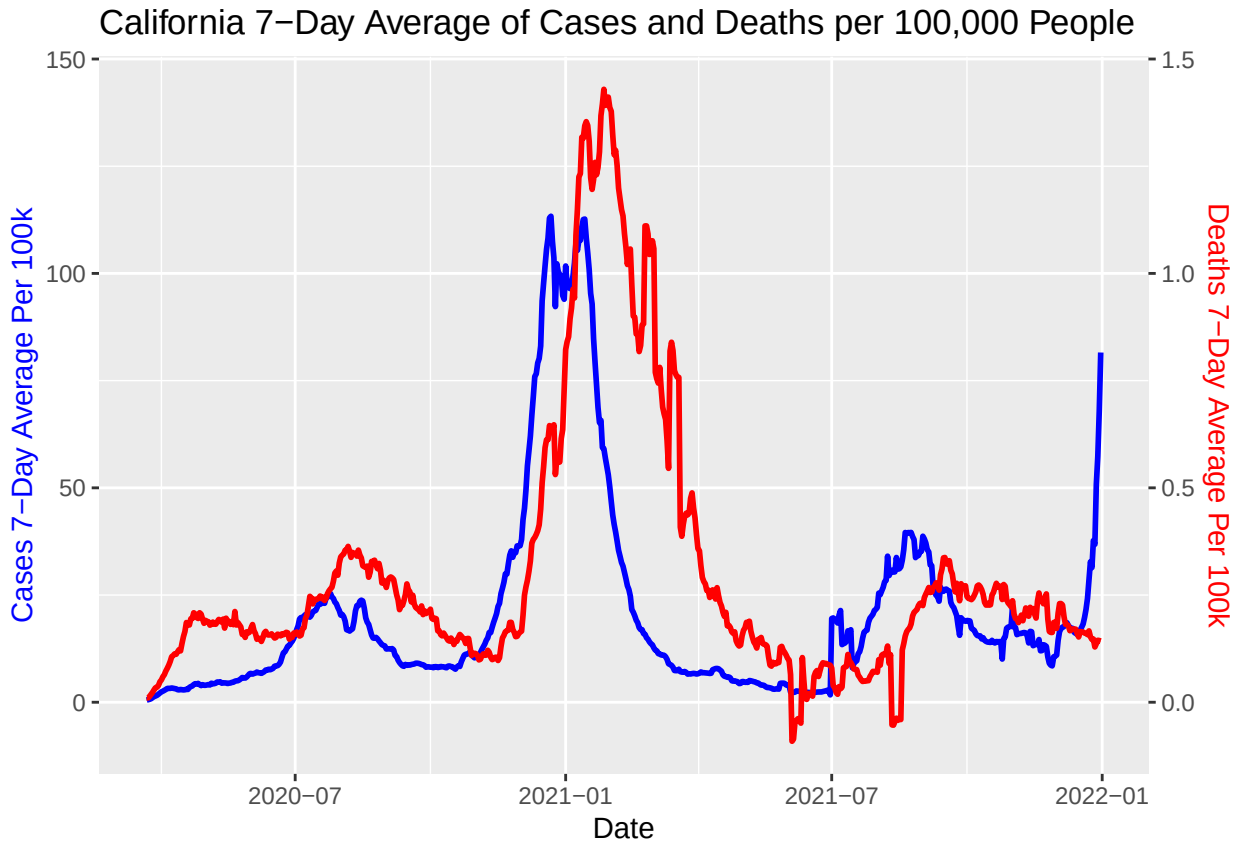
Creating a function from the code I used originally for Colorado (refer to Question 3) made things quick and easy.

Question 7

Create a visualization comparing the seven-day averages for new deaths and cases per 100,000 people for the four states you selected.

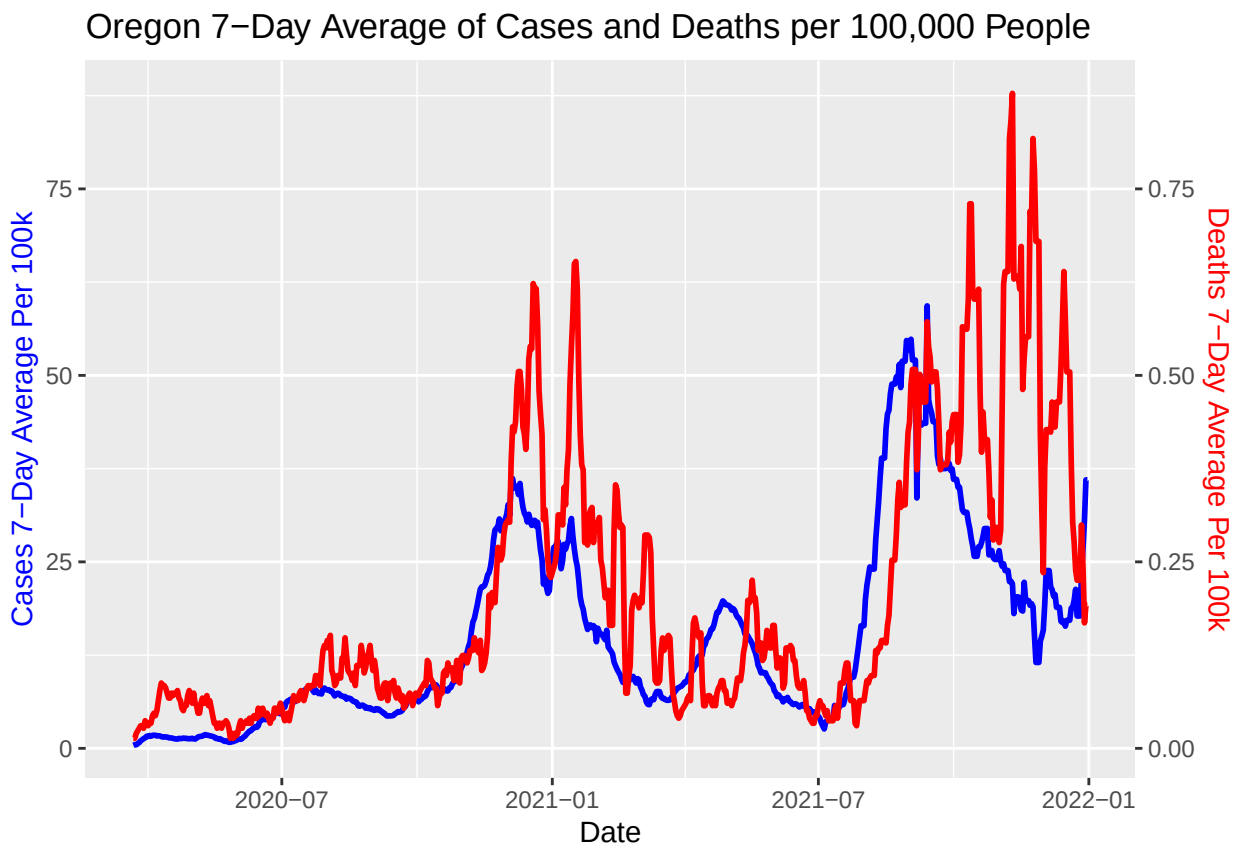
```r
# functions for the win
plot_state_7day_avg <- function(us_state) {
    # reusing function from Question 6
    state_7day_avg(us_state) %>%
    filter(!is.na(cases_7_day)) %>%
    ggplot(aes(x = date)) +
    geom_line(aes(y = cases_7_day, color = "Cases"), linewidth = 1) +
    # scale for visibility
    geom_line(aes(y = deaths_7_day * 100, color = "Deaths"), linewidth = 1) +
    # set up y axis for 2 variables
    scale_y_continuous(name = "Cases 7-Day Average Per 100k",
                       # add second axis for deaths
                       sec.axis = sec_axis(~./100, name = "Deaths 7-Day Average Per 100k")) +
    # color the y axis titles to match the plotted lines
    theme(axis.title.y.left = element_text(color = "blue"),
          axis.title.y.right = element_text(color = "red")) +
    labs(title = paste(us_state, "7-Day Average of Cases and Deaths per 100,000 People"),
         x = "Date") +
    # remove legend name
    theme(legend.position = "none") +
    scale_color_manual(values = c("Cases" = "blue", "Deaths" = "red"))
}
# it says four states even though Question 6 said 3,
# so I'll add another state besides Colorado as it was done in Question 3
# California
plot_state_7day_avg("California")
```

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



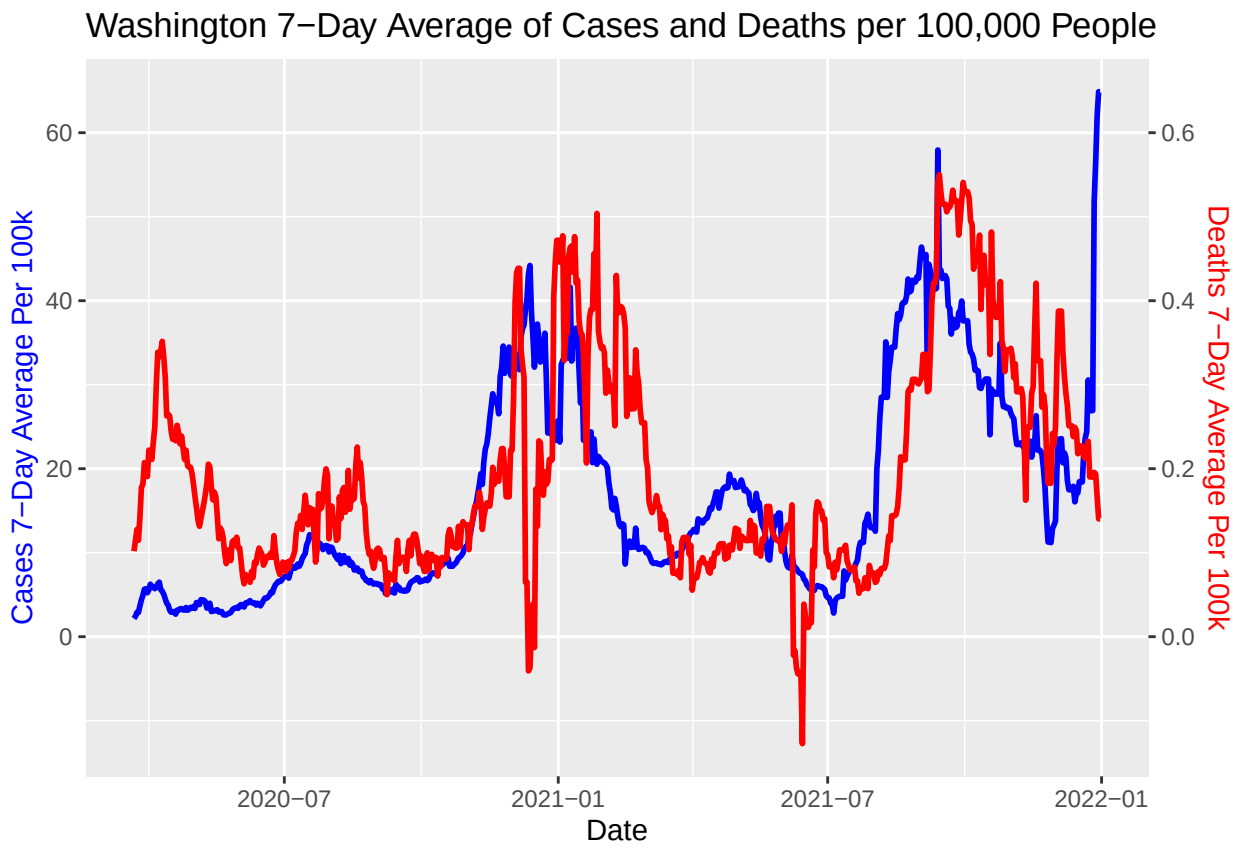
```
# Oregon
plot_state_7day_avg("Oregon")
```

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



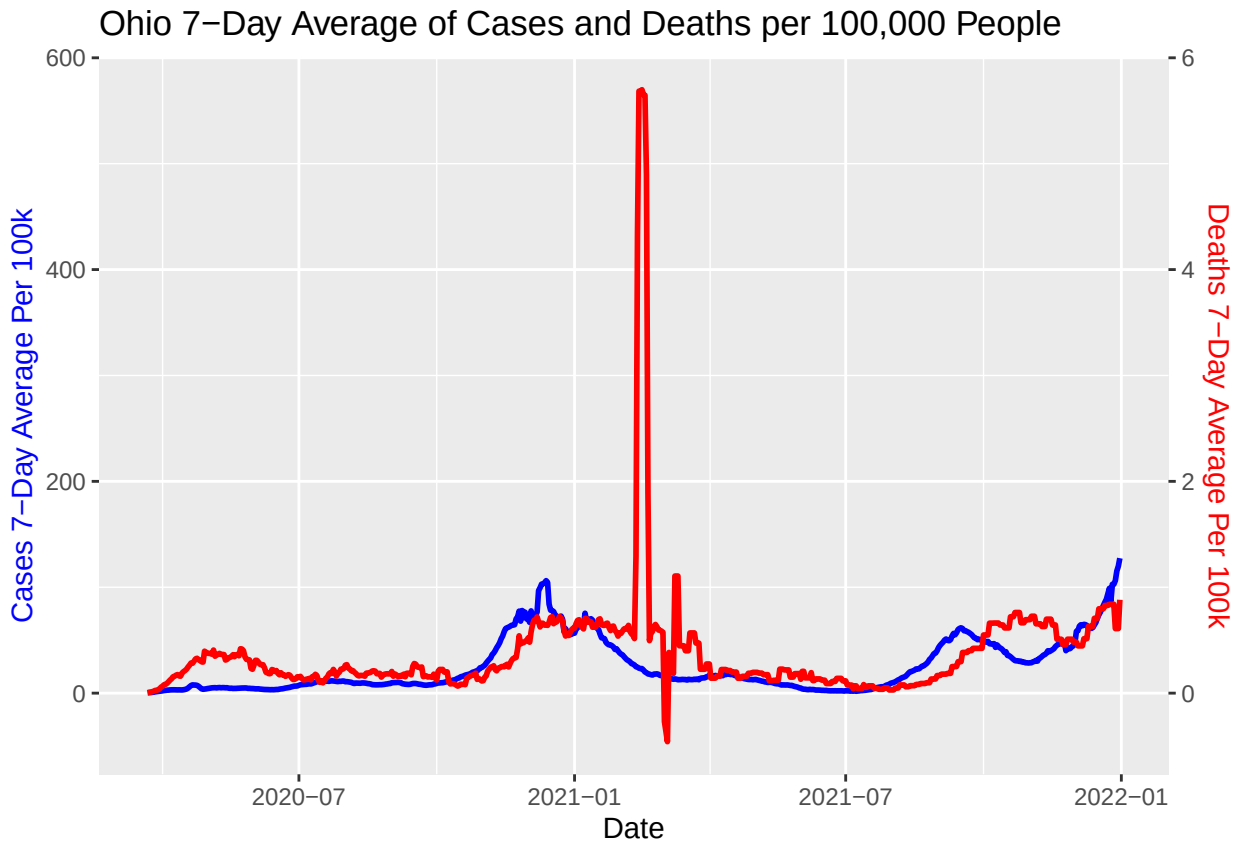

```
# Washington
plot_state_7day_avg("Washington")
```

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




```
# Ohio
plot_state_7day_avg("Ohio")
```

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



Functions really help a lot and the plots give a good visual to see the differences in cases and deaths for each of the states.

Part 3 - Global Comparison

```
# Import global COVID-19 statistics aggregated by the Center for Systems Science and Engineering (CSSE) at Jo
# Import global population estimates from the World Bank.

csse_global_deaths <- read_csv(
    "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covid_19_time_s
csse_global_cases <- read_csv(
    "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covid_19_time_s
csse_us_deaths <- read_csv(
    "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covid_19_time_s
csse_us_cases <- read_csv(
    "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_covid_19_time_s

global_population_estimates <- read_csv("global_population_estimates.csv")
```

Question 1

Using the state you selected in Part 2 Question 3 compare the daily number of cases and deaths reported from the CSSE and NY Times.

```
# Colorado NY Times data
nyt_colorado <- us_counties %>%
    # filter dates
    filter(between(date, as.Date("2020-03-15"), as.Date("2021-12-31")),
           state == "Colorado") %>%
```

```
    arrange(county) %>%
    select(fips, county, state, date, cases, deaths)
# US CSSE cases data
csse_us_c <- csse_us_cases %>%
    # remove unused columns
    select(-(UID:code3), -(Country_Region:Combined_Key)) %>%
    # pivot data for a column of dates and column of case numbers
    pivot_longer(contains('/'), names_to = "date", values_to = "cases") %>%
    # rename for readability
    rename(fips = FIPS, county = Admin2, state = Province_State)
# US CSSE death data
csse_us_d <- csse_us_deaths %>%
    # remove unused columns
    select(-(UID:code3), -(Country_Region:Population)) %>%
    # pivot data for a column of dates and column of death numbers
    pivot_longer(contains('/'), names_to = "date", values_to = "deaths") %>%
    # rename for readability
    rename(fips = FIPS, county = Admin2, state = Province_State)
# Colorado CSSE death and cases data
csse_colorado <- full_join(
    csse_us_c,
    csse_us_d,
    by = join_by(fips, county, state, date)) %>%
    # make date a date type
    mutate(date = as.Date(date, "%m/%d/%y")) %>%
    # just need Colorado data from 2020-03-15 and 2021-12-31
    filter(state == "Colorado",
           between(date, as.Date("2020-03-15"), as.Date("2021-12-31")))
csse_colorado
```

```
## # A tibble: 43,362 x 6
##     fips county state    date       cases deaths
##    <dbl> <chr>  <chr>    <date>     <dbl>  <dbl>
##  1  8001 Adams  Colorado 2020-03-15     6      0
##  2  8001 Adams  Colorado 2020-03-16     8      0
##  3  8001 Adams  Colorado 2020-03-17    10      0
##  4  8001 Adams  Colorado 2020-03-18    10      0
##  5  8001 Adams  Colorado 2020-03-19    10      0
##  6  8001 Adams  Colorado 2020-03-20    12      0
##  7  8001 Adams  Colorado 2020-03-21    14      0
##  8  8001 Adams  Colorado 2020-03-22    18      0
##  9  8001 Adams  Colorado 2020-03-23    25      0
## 10  8001 Adams  Colorado 2020-03-24    27      0
## # i 43,352 more rows
```

```
# get NY Times Colorado daily totals
nyt_colorado_totals <- nyt_colorado %>%
    group_by(state, date) %>%
    # sum up deaths and cases
    summarise(total_deaths = sum(deaths),
              total_cases = sum(cases))
```

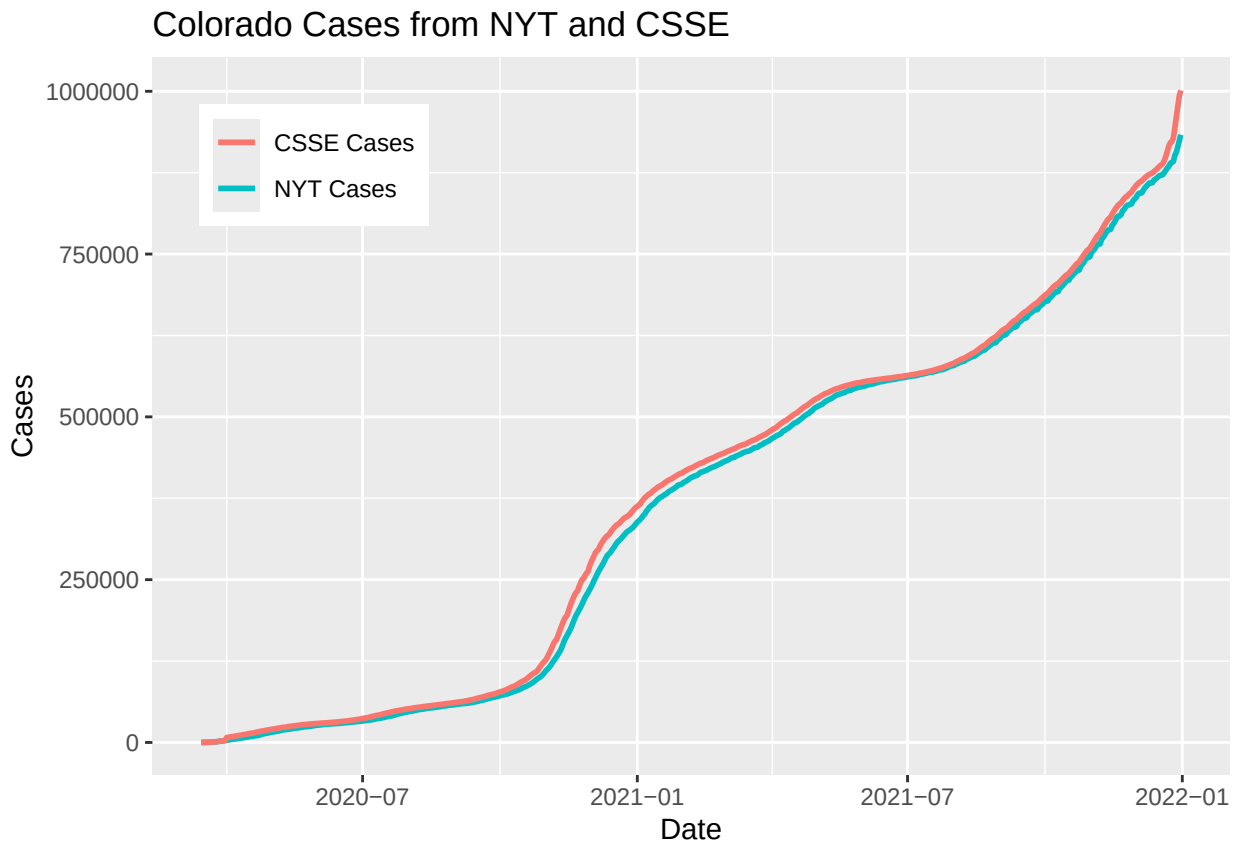
```
## `summarise()` has grouped output by 'state'. You can override using the
## `.groups` argument.
```

```
# get CSSE Colorado daily totals
csse_colorado_totals <- csse_colorado %>%
```

```
    group_by(state, date) %>%
    # sum up deaths and cases
    summarise(total_deaths = sum(deaths),
              total_cases = sum(cases))
```

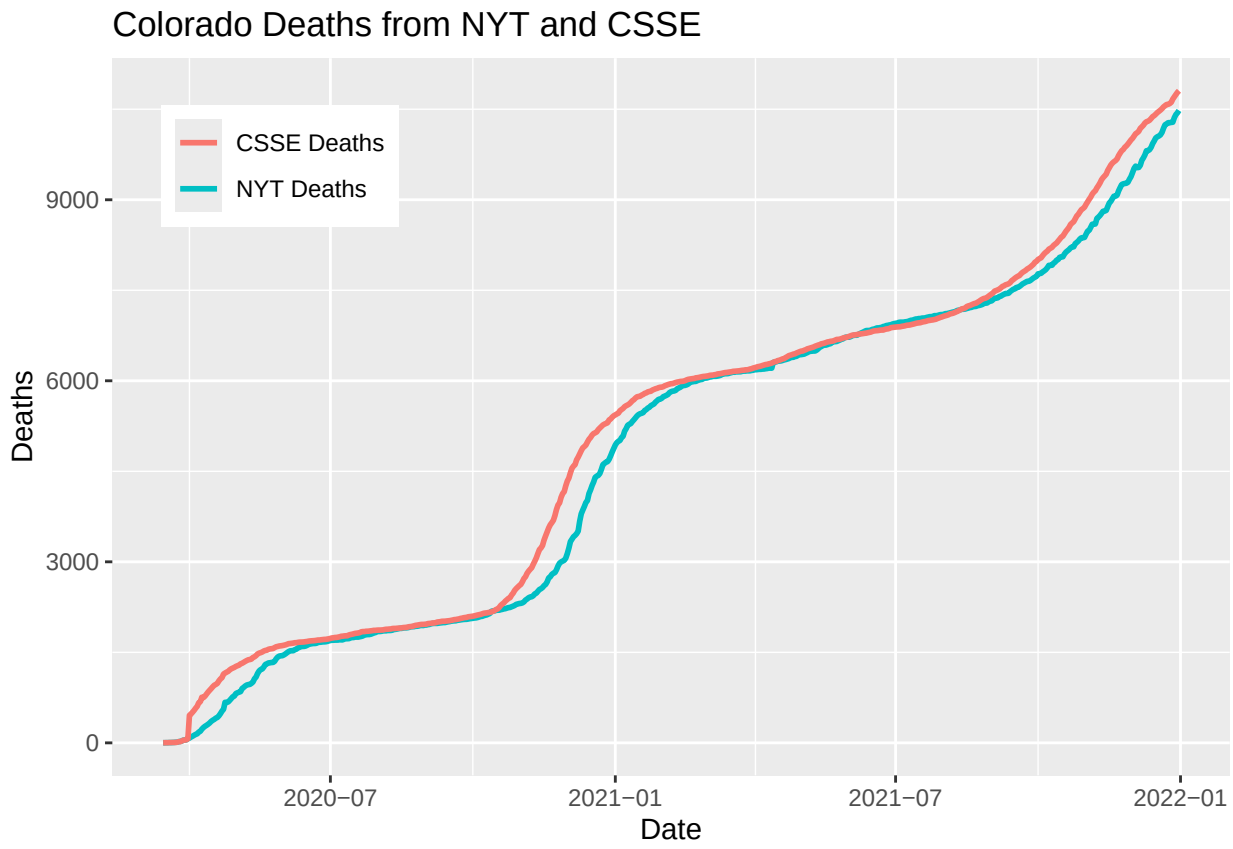
```
## `summarise()` has grouped output by 'state'. You can override using the
## `.groups` argument.
```

```
# full join to keep all observations from each to compare
colorado_totals <- full_join(nyt_colorado_totals,
                             csse_colorado_totals,
                             by = join_by(state, date),
                             suffix = c("_nyt", "_csse"))
# compare cases
colorado_totals %>%
    ggplot(aes(x = date)) +
    geom_line(aes(y = total_cases_nyt, color = "NYT Cases"), linewidth = 1) +
    geom_line(aes(y = total_cases_csse, color = "CSSE Cases"), linewidth = 1) +
    labs(title = "Colorado Cases from NYT and CSSE",
         x = "Date",
         y = "Cases") +
    theme(legend.title = element_blank(),
          legend.position = "inside",
          legend.position.inside = c(.15, .85))
```




```
# compare deaths
colorado_totals %>%
    ggplot(aes(x = date)) +
    geom_line(aes(y = total_deaths_nyt, color = "NYT Deaths"), linewidth = 1) +
```

```
    geom_line(aes(y = total_deaths_csse, color = "CSSE Deaths"), linewidth = 1) +
    labs(title = "Colorado Deaths from NYT and CSSE",
         x = "Date",
         y = "Deaths") +
    theme(legend.title = element_blank(),
          legend.position = "inside",
          legend.position.inside = c(.15, .85))
```




```
# Your tidied CSSE data for your selected state should look similar to the following tibble:
#
# A tibble: 43,362 × 6
#     fips  county  state       date       cases  deaths
#     <dbl> <chr>   <chr>       <date>     <dbl>  <dbl>
#  1  8001  Adams  Colorado   2020-03-15     6      0
#  2  8001  Adams  Colorado   2020-03-16     8      0
#  3  8001  Adams  Colorado   2020-03-17    10      0
#  4  8001  Adams  Colorado   2020-03-18    10      0
#  5  8001  Adams  Colorado   2020-03-19    10      0
#  6  8001  Adams  Colorado   2020-03-20    12      0
#  7  8001  Adams  Colorado   2020-03-21    14      0
#  8  8001  Adams  Colorado   2020-03-22    18      0
#  9  8001  Adams  Colorado   2020-03-23    25      0
# 10  8001  Adams  Colorado   2020-03-24    27      0
# ... with 43,352 more rows
```

There seems to be some variation in the data for cases and deaths in Colorado from NY Times and CSSE but look to be very similar.

Question 2

Now that you have verified the data reported from the CSSE and NY Times are similar, combine the global and US CSSE data sets and identify the top 10 countries in terms of deaths and cases per 100,000 people between March 15, 2020, and December 31, 2021.

```
# global daily cases
csse_global_daily_cases <- csse_global_cases %>%
    # remove unused columns
    select(-(Lat:Long)) %>%
    # rename to make pivot easier
    rename(province_state = `Province/State`, country_region = `Country/Region`) %>%
    # pivot data for a column of dates and column of case numbers
    pivot_longer(contains('/'), names_to = "date", values_to = "cases") %>%
    # make date a date type
    mutate(date = as.Date(date, "%m/%d/%y")) %>%
    # get country totals by grouping and summing up province/states
    group_by(country_region, date) %>%
    summarise(daily_cases = sum(cases)) %>%
    # filter date like the others 2020-03-15 to 2021-12-31
    filter(between(date, as.Date("2020-03-15"), as.Date("2021-12-31")))
# global daily deaths
csse_global_daily_deaths <- csse_global_deaths %>%
    # remove unused columns
    select(-(Lat:Long)) %>%
    # rename to make pivot easier
    rename(province_state = `Province/State`, country_region = `Country/Region`) %>%
    # pivot data for a column of dates and column of death numbers
    pivot_longer(contains('/'), names_to = "date", values_to = "deaths") %>%
    # make date a date type
    mutate(date = as.Date(date, "%m/%d/%y")) %>%
    # get country totals by grouping and summing up province/states
    group_by(country_region, date) %>%
    summarise(daily_deaths = sum(deaths)) %>%
    # filter date like the others 2020-03-15 to 2021-12-31
    filter(between(date, as.Date("2020-03-15"), as.Date("2021-12-31")))
# join together
csse_global_totals <- full_join(csse_global_daily_cases,
                                csse_global_daily_deaths,
                                by = join_by("country_region", "date")) %>%
    mutate(year = year(date)) %>%
    group_by(country_region, year) %>%
    summarise(total_cases = max(daily_cases),
              total_deaths = max(daily_deaths))
# csse global already has US cases so I don't need to join them with csse_us
# pivot the years and population
global_pop_est <- global_population_estimates %>%
    # rename to make pivot easier
    rename(country = `Country Name`, `2020` = `2020 [YR2020]`, `2021` = `2021 [YR2021]`) %>%
    pivot_longer(starts_with("2"),
                 names_to = "year",
                 values_to = "population") %>%
    # make year numeric
    mutate(year = as.numeric(year),
           population = as.numeric(population)) %>%
    # get what we need
    select(country, year, population)
# global totals per 100k
csse_global_totals_per_100k <- csse_global_totals %>%
```

```
    # group on country
    group_by(country_region) %>%
    # get totals for each country
    summarise(total_cases = sum(total_cases),
              total_deaths = sum(total_deaths)) %>%
    # inner join to only get countries that have data in both datasets
    inner_join(
        select(
            filter(global_pop_est, year == 2021), -year),
                  by = c("country_region" = "country")) %>%
    # calculate per 100k
    mutate(cases_per_100k = (total_cases / population) * 100000,
           deaths_per_100k = (total_deaths / population) * 100000)
# top 10 countries for deaths per 100k
csse_global_totals_per_100k %>%
    arrange(desc(deaths_per_100k)) %>%
    select(country_region, cases_per_100k, deaths_per_100k) %>%
    head(10)
```

```
## # A tibble: 10 x 3
##    country_region         cases_per_100k deaths_per_100k
##    <chr>                           <dbl>           <dbl>
##  1 Peru                            9928.            887.
##  2 Bulgaria                       13795.            560.
##  3 Bosnia and Herzegovina         12329.            536.
##  4 Moldova                        19930.            507.
##  5 North Macedonia                14883.            505.
##  6 Hungary                        16242.            501.
##  7 Montenegro                     35150.            498.
##  8 San Marino                     30985.            468.
##  9 Georgia                        31308.            439.
## 10 Belgium                        23766.            413.
```

```
# top 10 countries for cases per 100k
csse_global_totals_per_100k %>%
    arrange(desc(cases_per_100k)) %>%
    select(country_region, cases_per_100k, deaths_per_100k) %>%
    head(10)
```

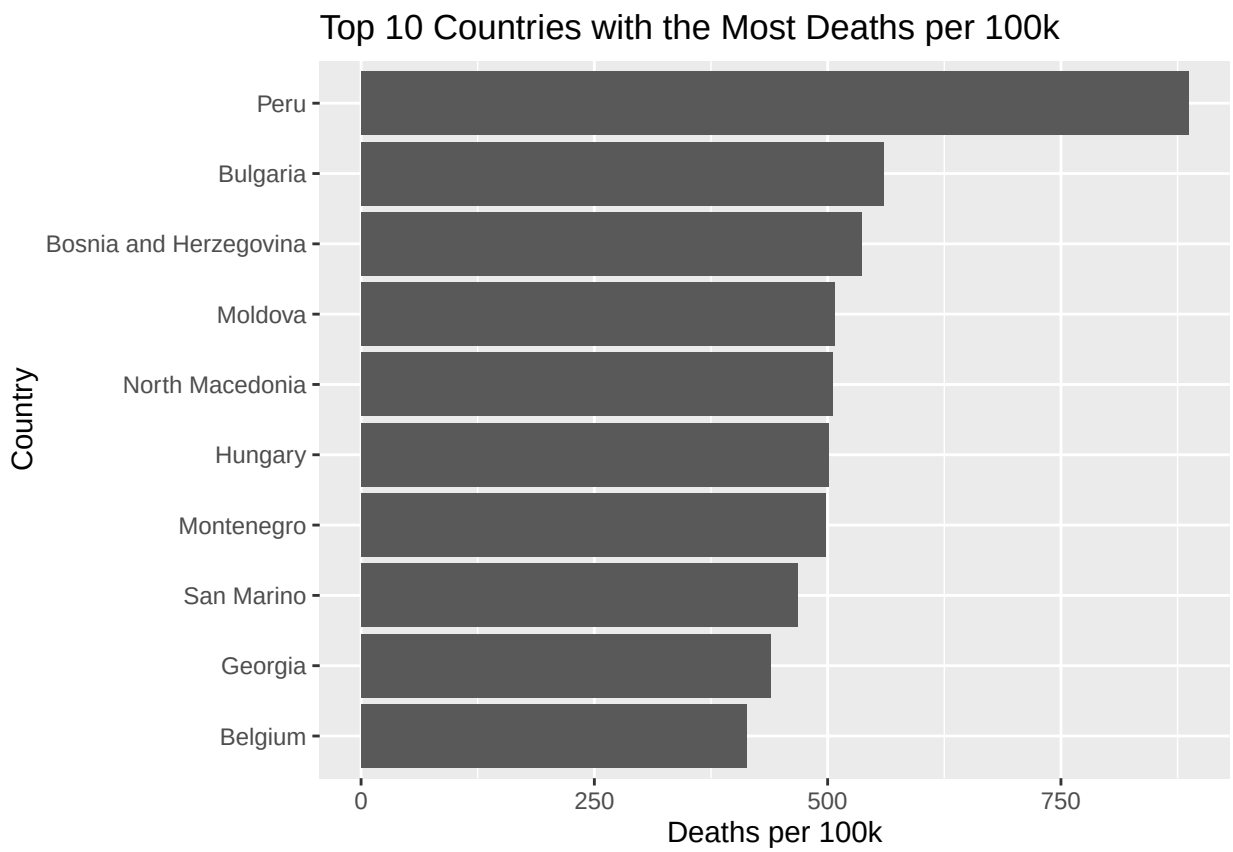
```
## # A tibble: 10 x 3
##    country_region cases_per_100k deaths_per_100k
##    <chr>                   <dbl>           <dbl>
##  1 Andorra                41284.            291.
##  2 Montenegro             35150.            498.
##  3 Georgia                31308.            439.
##  4 San Marino             30985.            468.
##  5 Slovenia               27901.            394.
##  6 Seychelles             25267.            135.
##  7 Lithuania              24204.            333.
##  8 Serbia                 23856.            232.
##  9 Belgium                23766.            413.
## 10 Luxembourg             23539.            221.
```

I used an inner join so that I only list the countries the I have data on.

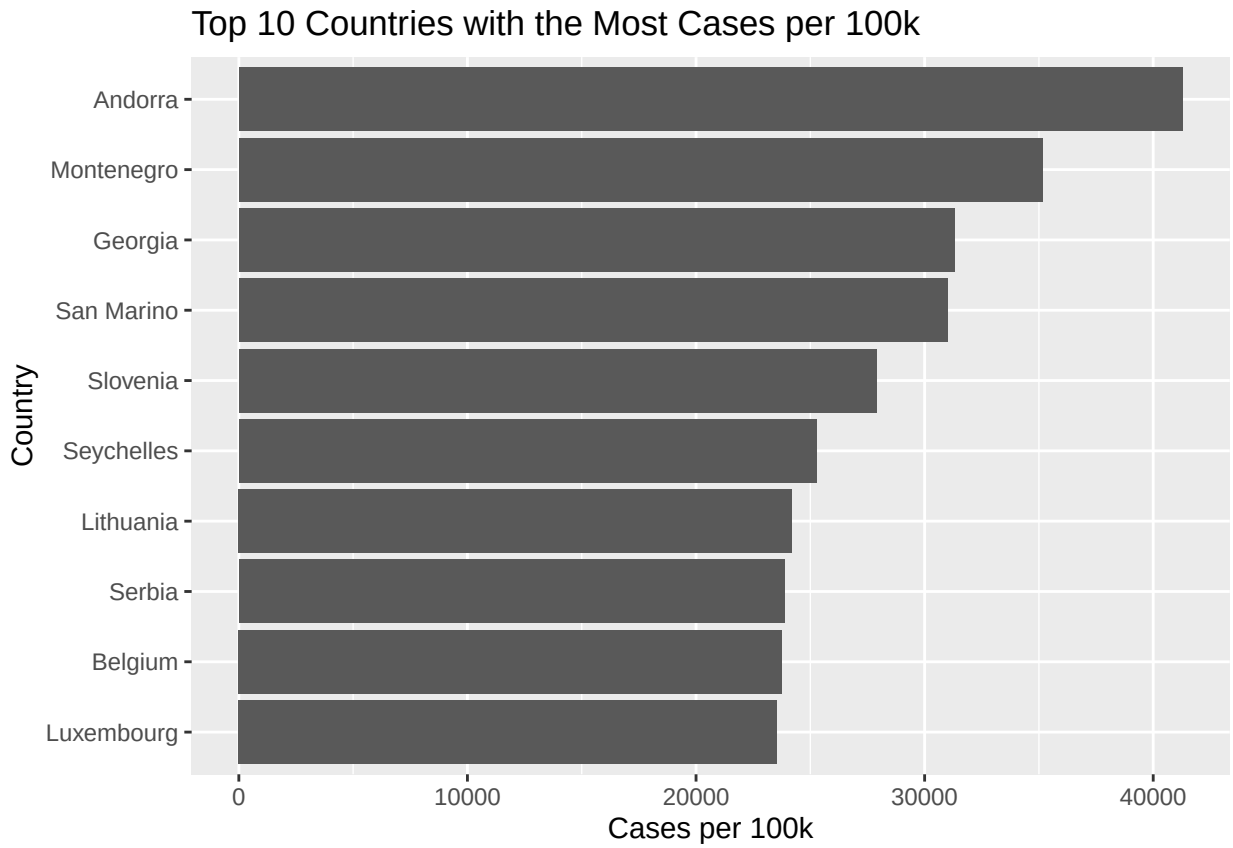
Question 3

Construct a visualization plotting the 10 countries in terms of deaths and cases per 100,000 people between March 15, 2020, and December 31, 2021. In designing your visualization keep the number of data you will be plotting in mind. You may wish to create two separate visualizations, one for deaths and another for cases.

```
# top 10 countries for deaths per 100k
csse_global_totals_per_100k %>%
    # get top 10
    arrange(desc(deaths_per_100k)) %>%
    head(10) %>%
    # plot deaths per 100k top 10
    ggplot(aes(x = deaths_per_100k, y = fct_reorder(country_region, deaths_per_100k))) +
    geom_col() +
    labs(title = "Top 10 Countries with the Most Deaths per 100k",
         x = "Deaths per 100k",
         y = "Country")
```




```
# top 10 countries for cases per 100k
csse_global_totals_per_100k %>%
    # get top 10
    arrange(desc(cases_per_100k)) %>%
    head(10) %>%
    # plot cases per 100k top 10
    ggplot(aes(x = cases_per_100k, y = fct_reorder(country_region, cases_per_100k))) +
    geom_col() +
    labs(title = "Top 10 Countries with the Most Cases per 100k",
         x = "Cases per 100k",
         y = "Country")
```



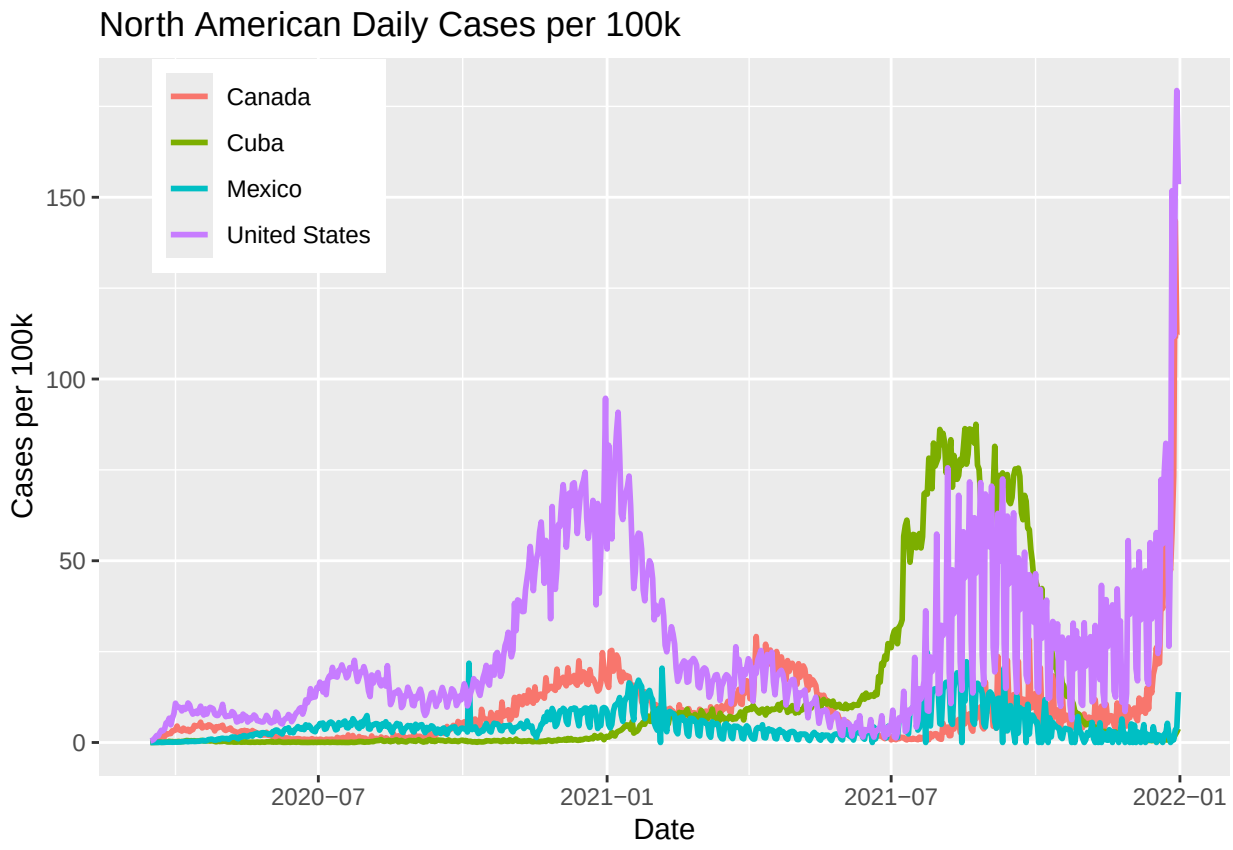
I used fct_reorder so that the countries would be ordered from most to least when they were plotted.

Question 4

Finally, select four countries from one continent and create visualizations for the daily number of confirmed cases per 100,000 and the daily number of deaths per 100,000 people between March 15, 2020, and December 31, 2021.

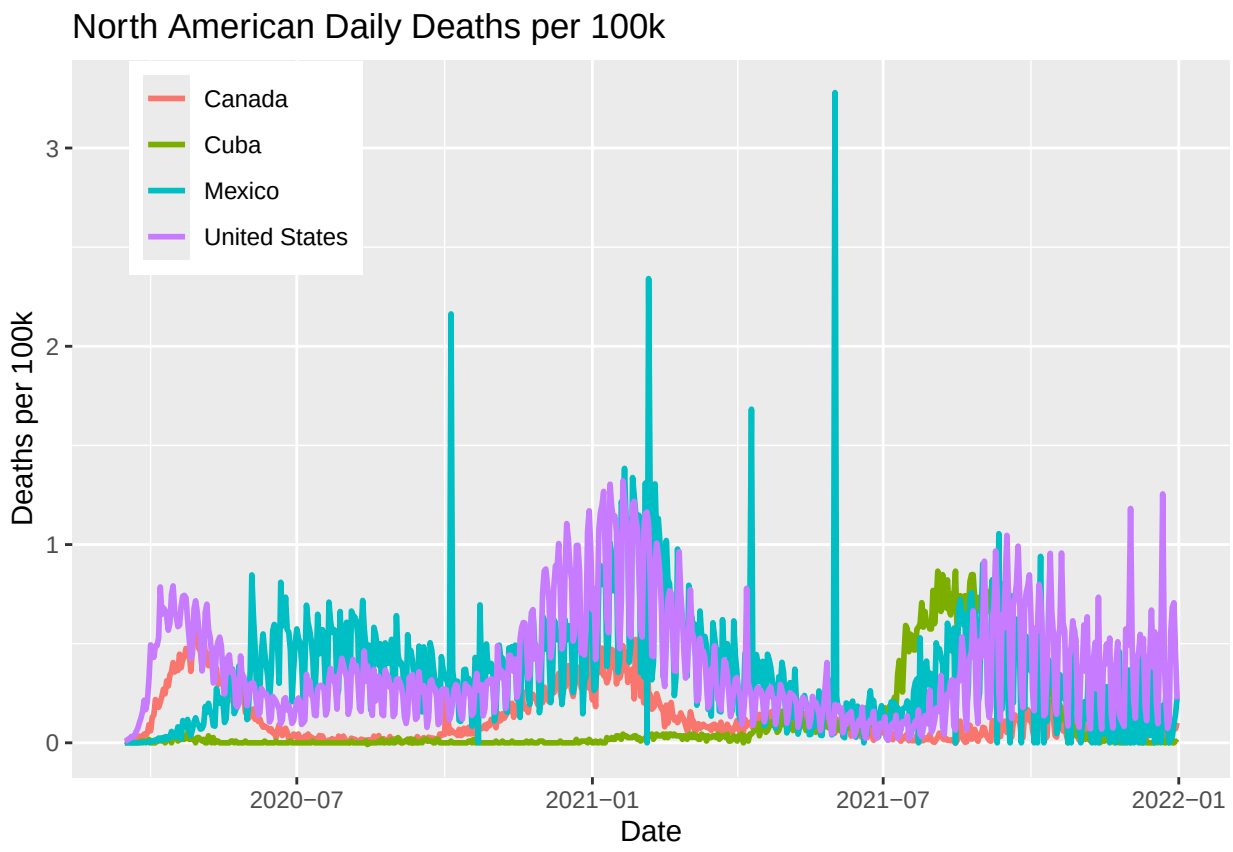
```
# csse global daily
csse_global_daily <- full_join(csse_global_daily_cases,
                               csse_global_daily_deaths,
                               by = join_by("country_region", "date"))
# replace US with United States
csse_global_daily$country_region <- replace(
    csse_global_daily$country_region,
    csse_global_daily$country_region == "US",
    "United States")
# get daily numbers for 4 north american countries
csse_n_america_daily <- csse_global_daily %>%
    # filter to 4 north american countries
    filter(country_region %in% c("Canada", "United States", "Mexico", "Cuba")) %>%
    # add year for joining
    mutate(year = year(date)) %>%
    # inner join to have data from both
    inner_join(global_pop_est,
               by = join_by("country_region" == "country", "year")) %>%
    # get per 100k
    # create 1-day deltas for new daily cases/deaths
    mutate(new_cases = daily_cases - lag(daily_cases),
           new_deaths = daily_deaths - lag(daily_deaths),
           cases_per_100k = (new_cases / population) * 100000,
```

```
            deaths_per_100k = (new_deaths / population) * 100000) %>%
    # get columns we need
    select(country_region, date, cases_per_100k, deaths_per_100k)
# plot daily cases
csse_n_america_daily %>%
    # remove na
    filter(!is.na(cases_per_100k)) %>%
    # set date as x
    ggplot(aes(x = date)) +
    # plot cases, color on country
    geom_line(aes(y = cases_per_100k, color = country_region), linewidth = 1) +
    labs(title = "North American Daily Cases per 100k",
         x = "Date",
         y = "Cases per 100k") +
    # move legend and remove legend title
    theme(legend.title = element_blank(),
          legend.position = "inside",
          legend.position.inside = c(.15, .85))
```




```
# plot daily deaths
csse_n_america_daily %>%
    # remove na
    filter(!is.na(deaths_per_100k)) %>%
    # set date as x
    ggplot(aes(x = date)) +
    # plot deaths, color on country
    geom_line(aes(y = deaths_per_100k, color = country_region), linewidth = 1) +
    labs(title = "North American Daily Deaths per 100k",
         x = "Date",
         y = "Deaths per 100k") +
```

```
    # move legend and remove legend title
    theme(legend.title = element_blank(),
          legend.position = "inside",
          legend.position.inside = c(.15, .85))
```



A rolling 7-day average would probably work better for these visuals but the question asked for daily cases and deaths. Unless the question was asking for total cases and deaths as time went on, then the question could have been worded better.