Problem set 4

2025-10-05

In the next problem set, we plan to explore the relationship between COVID-19 death rates and vaccination rates across US states by visually examining their correlation. This analysis will involve gathering COVID-19 related data from the CDC's API and then extensively processing it to merge the various datasets. Since the population sizes of states vary significantly, we will focus on comparing rates rather than absolute numbers. To facilitate this, we will also source population data from the US Census to accurately calculate these rates.

In this problem set we will learn how to extract and wrangle data from the data US Census and CDC APIs.

1. Get an API key from the US Census at https://api.census.gov/data/key_signup.html. You can't share this public key. But your code has to run on a TFs computer. Assume the TF will have a file in their working directory named `census-key.R` with the following one line of code:

```
census_key <- "A_CENSUS_KEY_THAT_WORKS"
```

Write a first line of code for your problem set that defines `census_key` by running the code in the file `census-key.R`.

```
source("census-key.R")
```

2. The US Census API User Guide provides details on how to leverage this valuable resource. We are interested in vintage population estimates for years 2021 and 2022. From the documentation we find that the *endpoint* is:

```
url <- "https://api.census.gov/data/2021/pep/population"
```

Use the **httr2** package to construct the following GET request.

```
https://api.census.gov/data/2021/pep/population?get=POP_2020,POP_2021,NAME&for=state:*&key=Y(
```

Create an object called `request` of class `httr2_request` with this URL as an endpoint. Hint: Print out `request` to check that the URL matches what we want.

```
library(httr2)
request <- request(url) |> req_url_query(get = "POP_2020,POP_2021,NAME",
 ↪  `for` = "state:*", key = census_key)
```

3. Make a request to the US Census API using the `request` object. Save the response to and object named `response`. Check the response status of your request and make sure it was successful. You can learn about *status codes* here.

```
response <- request |> req_perform()
```

4. Use a function from the **httr2** package to determine the content type of your response.

```
resp_content_type(response)
```

```
[1] "application/json"
```

5. Use just one line of code and one function to extract the data into a matrix. Hints: 1) Use the `resp_body_json` function. 2) The first row of the matrix will be the variable names and this OK as we will fix in the next exercise.

```
population <- resp_body_json(response, simplifyVector = TRUE)
```

6. Examine the `population` matrix you just created. Notice that 1) it is not tidy, 2) the column types are not what we want, and 3) the first row is a header. Convert `population` to a tidy dataset. Remove the state ID column and change the name of the column with state names to `state_name`. Add a column with state abbreviations called `state`. Make sure you assign the abbreviations for DC and PR correctly. Hint: Use the **janitor** package to make the first row the header.

```
library(tidyverse)
library(janitor)
population <- population |>
  row_to_names(row_number = 1) |>
  as_tibble() |>
  select(-state) |>
```

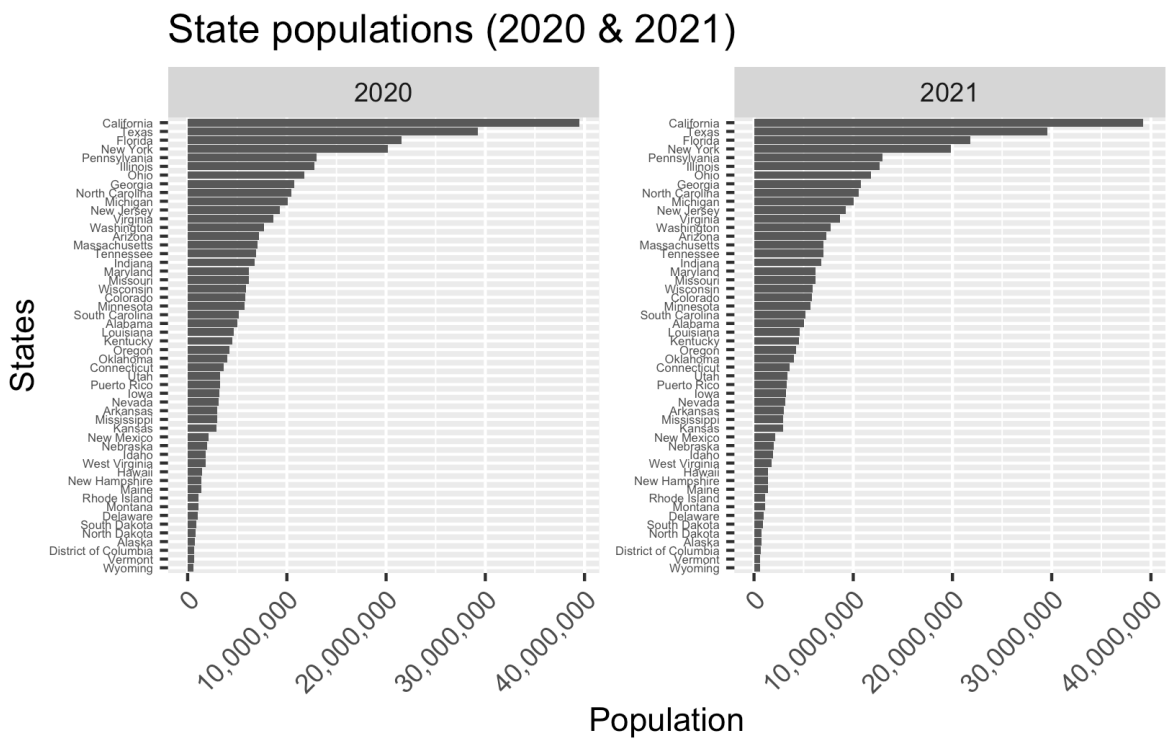
```
  rename(state_name = NAME) |>
  pivot_longer(
    cols = starts_with("POP_"),
    names_to = "year",
    values_to = "population"
  ) |>
  mutate(
    year = parse_number(year),
    population = parse_number(population),
    state = case_when(
      state_name == "District of Columbia" ~ "DC",
      state_name == "Puerto Rico" ~ "PR",
      TRUE ~ state.abb[match(state_name, state.name)]
    )
  ) |>
  relocate(state, .after = state_name)
population
```

```
# A tibble: 104 x 4
   state_name   state  year population
   <chr>        <chr> <dbl>      <dbl>
 1 Oklahoma     OK     2020    3962031
 2 Oklahoma     OK     2021    3986639
 3 Nebraska     NE     2020    1961455
 4 Nebraska     NE     2021    1963692
 5 Hawaii       HI     2020    1451911
 6 Hawaii       HI     2021    1441553
 7 South Dakota SD     2020     887099
 8 South Dakota SD     2021     895376
 9 Tennessee    TN     2020    6920119
10 Tennessee    TN     2021    6975218
# i 94 more rows
```

7. As a check, make a barplot of states' 2021 and 2022 populations. Show the state names in the y-axis ordered by population size. Hint: You will need to use `reorder` and use `facet_wrap`.

```
population |>
  filter(year %in% c(2020, 2021)) |>
  ggplot(aes(x = reorder(state_name, population), y = population)) +
  geom_col() +
```

```
  coord_flip() +
  facet_wrap(~ year, scales = "free_y") +
  scale_y_continuous(labels = \(x) format(x, big.mark = ",", scientific =
   ↪  FALSE)) +
  labs(x = "States", y = "Population", title = "State populations (2020 &
   ↪  2021)") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        axis.text.y = element_text(size = 4))
```



8. The following URL:

```
url <-
 ↪  "https://github.com/datasciencelabs/2025/raw/refs/heads/main/data/regions.json"
```

points to a JSON file that lists the states in the 10 Public Health Service (PHS) defined by CDC. We want to add these regions to the `population` dataset. To facilitate this create a data frame called `regions` that has two columns `state_name`, `region`, `region_name`. One of the regions has a long name. Change it to something shorter.

```r
library(jsonlite)
library(purrr)
regions <- fromJSON(url) |>
  unnest(states) |>
  transmute(
    state_name  = states,
    region = as.integer(region),
    region_name = region_name
  ) |>
  mutate(
    region_name = if_else(
      region_name == "New York and New Jersey, Puerto Rico, Virgin Islands",
      "NY/NJ & Territories",
      region_name
    )
  ) |>
  filter(state_name %in% c(state.name, "District of Columbia", "Puerto
   ↪  Rico"))
regions
```

```
# A tibble: 52 x 3
   state_name    region region_name
   <chr>          <int> <chr>
 1 Connecticut        1 New England
 2 Maine              1 New England
 3 Massachusetts      1 New England
 4 New Hampshire      1 New England
 5 Rhode Island       1 New England
 6 Vermont            1 New England
 7 New Jersey         2 NY/NJ & Territories
 8 New York           2 NY/NJ & Territories
 9 Puerto Rico        2 NY/NJ & Territories
10 Delaware           3 Mid-Atlantic
# i 42 more rows
```

9. Add a region and region name columns to the `population` data frame.

```r
population <- left_join(population, regions, by = "state_name")
population
```

```
# A tibble: 104 x 6
```

```
   state_name   state  year population region region_name
   <chr>        <chr> <dbl>      <dbl>  <int> <chr>
 1 Oklahoma     OK     2020    3962031      6 South Central
 2 Oklahoma     OK     2021    3986639      6 South Central
 3 Nebraska     NE     2020    1961455      7 Central Plains
 4 Nebraska     NE     2021    1963692      7 Central Plains
 5 Hawaii       HI     2020    1451911      9 Pacific
 6 Hawaii       HI     2021    1441553      9 Pacific
 7 South Dakota SD     2020     887099      8 Mountain States
 8 South Dakota SD     2021     895376      8 Mountain States
 9 Tennessee    TN     2020    6920119      4 Southeast
10 Tennessee    TN     2021    6975218      4 Southeast
# i 94 more rows
```

10. From reading https://data.cdc.gov/ we learn the endpoint `https://data.cdc.gov/resource/pwn4-m3yp.` provides state level data from SARS-COV2 cases. Use the **httr2** tools you have learned to download this into a data frame. Is all the data there? If not, comment on why.

```
api <- "https://data.cdc.gov/resource/pwn4-m3yp.json"
cases_raw <- request(api) |>
  req_perform() |>
  resp_body_json(simplifyDataFrame = TRUE)
```

We see exactly 1,000 rows. We should be seeing over 52×3 rows per state.

The API defaults to only 1,000 records per request, so the response is truncated and doesn't include all data.

11. The reason you see exactly 1,000 rows is because CDC has a default limit. You can change this limit by adding `$limit=10000000000` to the request. Rewrite the previous request to ensure that you receive all the data. Then wrangle the resulting data frame to produce a data frame with columns `state`, `date` (should be the end date) and `cases`. Make sure the cases are numeric and the dates are in `Date` ISO-8601 format.

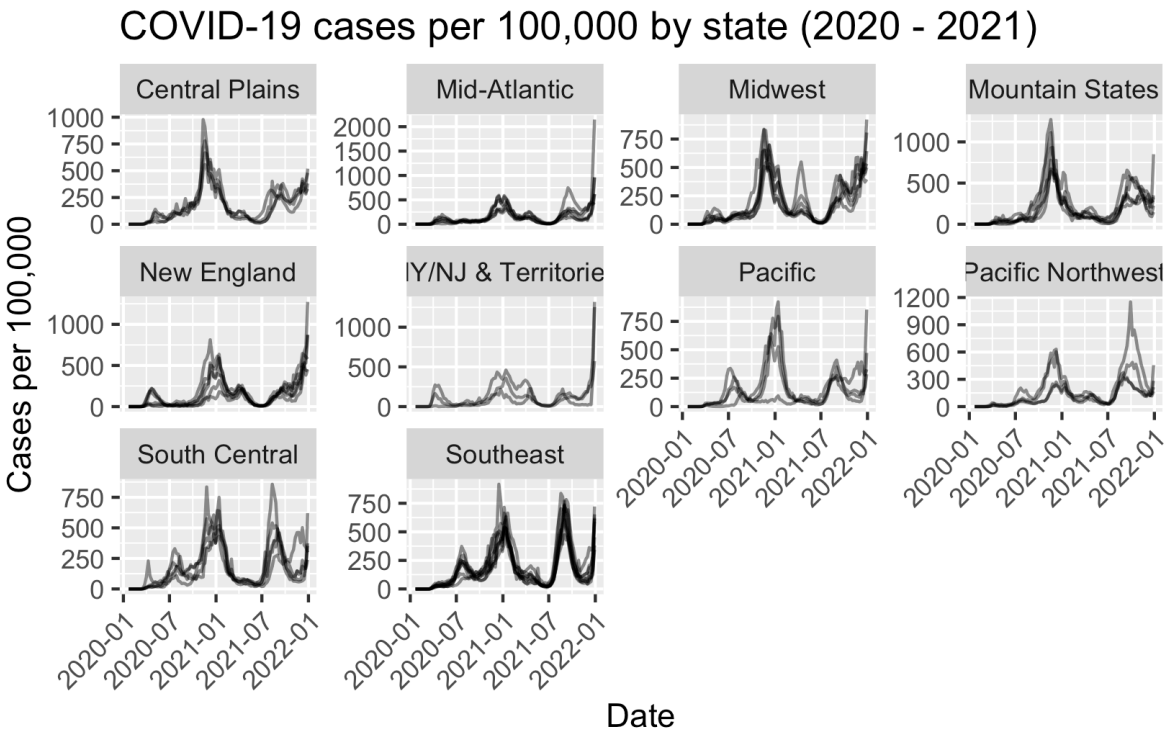
```
api <- "https://data.cdc.gov/resource/pwn4-m3yp.json"
cases_raw <- request(api) |>
  req_url_query("$limit" = 10000000000) |>
  req_perform() |>
  resp_body_json(simplifyDataFrame = TRUE)

cases <- cases_raw |>
  transmute(
    state = state,
```

```
    date  = ymd_hms(end_date, quiet = TRUE) |> as_date(),
    cases = parse_number(new_cases)
  ) |>
  filter(!is.na(state), !is.na(date), !is.na(cases))
```

12. For 2020 and 2021, make a time series plot of cases per 100,000 versus time for each state. Stratify the plot by region name. Make sure to label you graph appropriately.

```
cases |>
  transmute(
    state = state,
    date  = as.Date(date),
    cases = cases
  ) |>
  filter(state %in% c(state.abb, "DC", "PR")) |>
  left_join(
    population |>
      filter(year == 2021) |>
      select(state, region_name, population),
    by = "state"
  ) |>
  filter(!is.na(population)) |>
  mutate(cases_per_100k = 1e5 * cases / population) |>
  filter(format(date, "%Y") %in% c("2020", "2021")) |>
  ggplot(aes(x = date, y = cases_per_100k, group = state)) +
  geom_line(alpha = 0.5) +
  facet_wrap(~ region_name, scales = "free_y") +
  labs(
    x = "Date",
    y = "Cases per 100,000",
    title = "COVID-19 cases per 100,000 by state (2020 - 2021)"
  ) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



13. The dates in the `cases` dataset are stored as character strings. Use the **lubridate** package to properly parse the `date` column, then create a summary table showing the total COVID-19 cases by month and year for 2020 and 2021. The table should have columns for year, month (as month name), and total cases across all states. Order by year and month. Use the **knitr** package and `kable()` function to display the results as a formatted table.

```
library(lubridate)
library(knitr)
cases |>
  mutate(
    year  = year(date),
    month = month(date, label = TRUE, abbr = FALSE)
  ) |>
  filter(year %in% c(2020, 2021)) |>
  group_by(year, month) |>
  summarise(total_cases = sum(cases, na.rm = TRUE), .groups = "drop") |>
  arrange(year, month) |>
  kable(caption = "Total COVID-19 Cases by Month and Year (2020 - 2021)")
```

Table 1: Total COVID-19 Cases by Month and Year (2020 - 2021)

year	month	total_cases
2020	January	11
2020	February	68
2020	March	68245
2020	April	974032
2020	May	650943
2020	June	654904
2020	July	1989512
2020	August	1461283
2020	September	1415438
2020	October	1628598
2020	November	3932646
2020	December	7027128
2021	January	5808063
2021	February	2667511
2021	March	2068441
2021	April	1773591
2021	May	972915
2021	June	493635
2021	July	1137440
2021	August	3572562
2021	September	5027537
2021	October	2356302
2021	November	2322814
2021	December	5615644

14. The following URL provides additional COVID-19 data from the CDC in JSON format:

```
deaths_url <- "https://data.cdc.gov/resource/9bhg-hcku.json"
```

Use **httr2** to download COVID-19 death data from this endpoint. Make sure to remove the default limit to get all available data. Create a clean dataset called `deaths` with columns `state`, `date`, and `deaths` (renamed from the original column name). Ensure dates are in proper Date format and deaths are numeric.

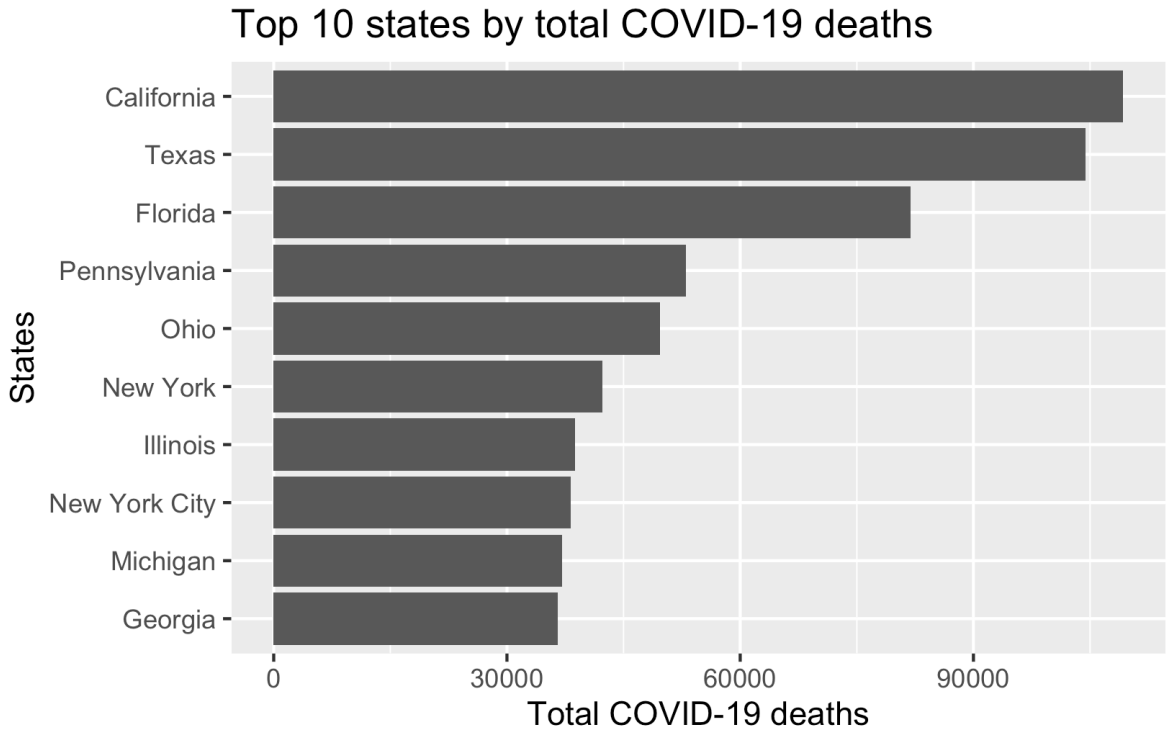
```
deaths_raw <- request(deaths_url) |>
  req_url_query("$limit" = 10000000000) |>
  req_perform() |>
  resp_body_json(simplifyDataFrame = TRUE)
```

```r
deaths <- as_tibble(deaths_raw) |>
  filter(group == "By Year", sex == "All Sexes", age_group == "All Ages",
   ↪  state != "United States") |>
  transmute(
    state  = state,
    date   = ymd_hms(end_date) |> as_date(),
    deaths = parse_number(covid_19_deaths)
  ) |>
  filter(!is.na(state), !is.na(date), !is.na(deaths))
deaths
```

```
# A tibble: 212 x 3
   state   date       deaths
   <chr>   <date>      <dbl>
 1 Alabama 2020-12-31   6706
 2 Alabama 2021-12-31   9719
 3 Alabama 2022-12-31   4226
 4 Alabama 2023-09-23    869
 5 Alaska  2020-12-31    254
 6 Alaska  2021-12-31    839
 7 Alaska  2022-12-31    330
 8 Alaska  2023-09-23     69
 9 Arizona 2020-12-31   9321
10 Arizona 2021-12-31  14060
# i 202 more rows
```

15. Using the `deaths` dataset you created, make a bar plot showing the total COVID-19 deaths by state. Show only the top 10 states with the highest death counts. Order the bars from highest to lowest and use appropriate labels and title.

```r
deaths |>
  group_by(state) |>
  summarise(total_deaths = sum(deaths, na.rm = TRUE), .groups = "drop") |>
  slice_max(total_deaths, n = 10, with_ties = FALSE) |>
  ggplot(aes(x = reorder(state, total_deaths), y = total_deaths)) +
  geom_col() +
  coord_flip() +
  labs(
    x = "States",
    y = "Total COVID-19 deaths",
    title = "Top 10 states by total COVID-19 deaths"
  )
```


Top 10 states by total COVID-19 deaths
California
Texas
Florida
Pennsylvania
Ohio
New York
Illinois
New York City
Michigan
Georgia
States
0
30000
60000
90000
Total COVID-19 deaths