

DTSA Final

October 14, 2023

1 I. Data Cleaning and EDA

```
[4]: library(lubridate)
      library(tidyverse)
```

```
Attaching core tidyverse packages      tidyverse
2.0.0
dplyr   1.1.2      readr   2.1.4
forcats 1.0.0      stringr 1.5.0
ggplot2 3.4.2      tibble  3.2.1
purrr   1.0.1      tidyr   1.3.0

Conflicts
tidyverse_conflicts()
dplyr::filter() masks stats::filter()
dplyr::lag()     masks stats::lag()
Use the conflicted package
(<http://conflicted.r-lib.org/>) to force all conflicts to
become errors
```

```
[6]: # Load data, change from wide to long format and get basic summary
url_in <- "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/
↪csse_covid_19_data/csse_covid_19_time_series/"
file_names <- c("time_series_covid19_confirmed_US.csv",
                "time_series_covid19_deaths_US.csv")
urls <- str_c(url_in, file_names)
US_cases <- read_csv(urls[1])
US_deaths <- read_csv(urls[2])
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)
summary(US)

```

Rows: 3342 Columns: 1154

Column specification

Delimiter: ","

chr (6): iso2, iso3, Admin2, Province_State, Country_Region, Combined_Key
dbl (1148): UID, code3, FIPS, Lat, Long_, 1/22/20, 1/23/20, 1/24/20, 1/25/20...

Use `spec()` to retrieve the full column specification for this data.

Specify the column types or set `show_col_types = FALSE` to quiet this message.

Rows: 3342 Columns: 1155

Column specification

Delimiter: ","

chr (6): iso2, iso3, Admin2, Province_State, Country_Region, Combined_Key
dbl (1149): UID, code3, FIPS, Lat, Long_, Population, 1/22/20, 1/23/20, 1/24...

Use `spec()` to retrieve the full column specification for this data.

Specify the column types or set `show_col_types = FALSE` to quiet this message.

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

Admin2	Province_State	Country_Region	Combined_Key
Length:3819906	Length:3819906	Length:3819906	Length:3819906
Class :character	Class :character	Class :character	Class :character
Mode :character	Mode :character	Mode :character	Mode :character

date	cases	Population	deaths
Min. :2020-01-22	Min. : -3073	Min. : 0	Min. : -82.0
1st Qu.:2020-11-02	1st Qu.: 330	1st Qu.: 9917	1st Qu.: 4.0
Median :2021-08-15	Median : 2272	Median : 24892	Median : 37.0
Mean :2021-08-15	Mean : 14088	Mean : 99604	Mean : 186.9
3rd Qu.:2022-05-28	3rd Qu.: 8159	3rd Qu.: 64979	3rd Qu.: 122.0
Max. :2023-03-09	Max. :3710586	Max. :10039107	Max. :35545.0

This would be useful for anyone looking to analyze the progression of COVID-19 in the US over

time. By fetching the data directly from a trusted source (Johns Hopkins University) and processing it into a usable format, researchers and analysts can gain insights into the trends and patterns of the pandemic in the US.

```
[7]: # The data is segmented by country so we can modify the data to get totals by
      ↪state and the whole USA
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 = "COVID19 in US", y = NULL)
```

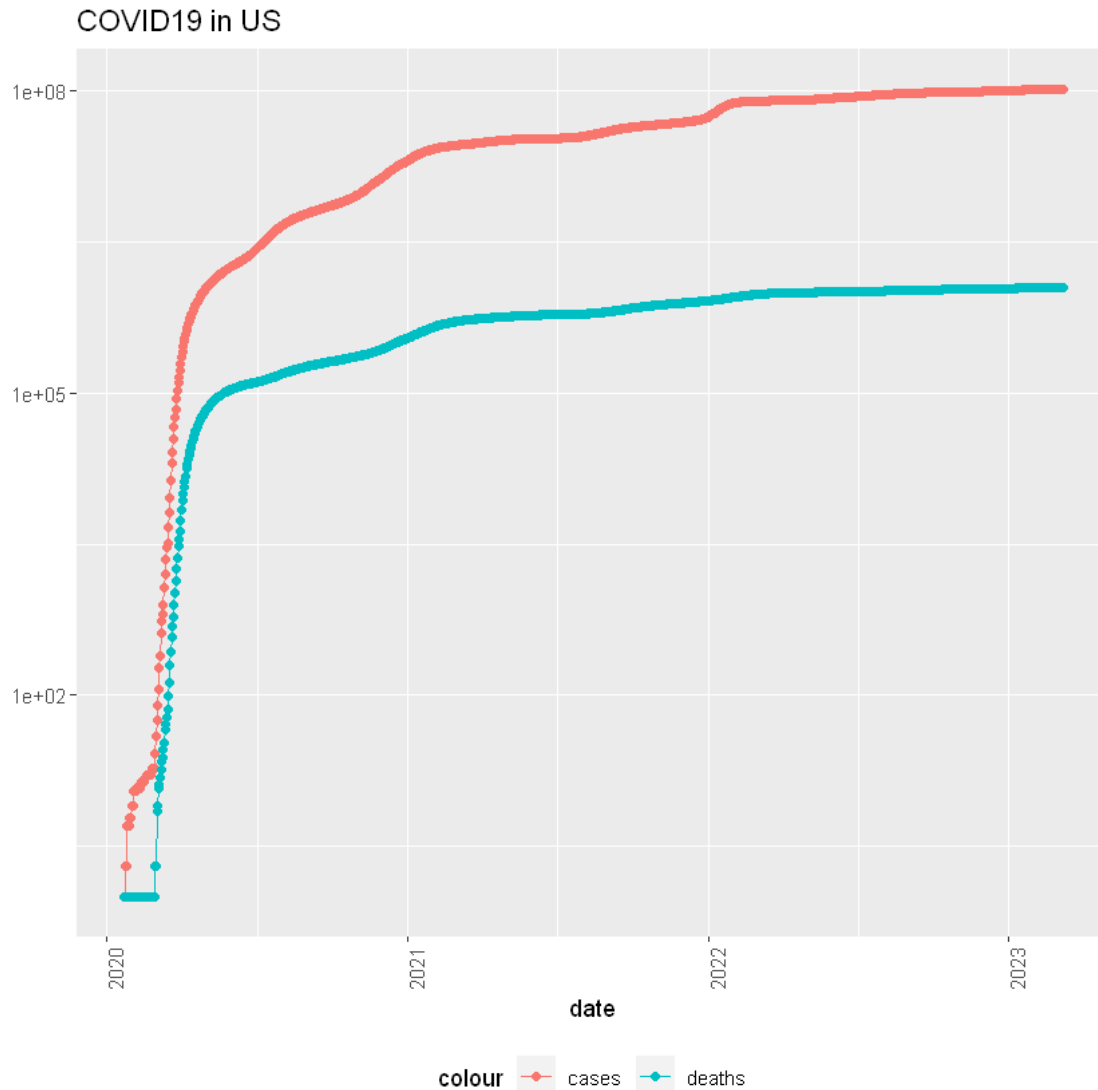
``summarise()`` has grouped output by 'Province_State', 'Country_Region'.

You can

override using the `` .groups `` argument.

``summarise()`` has grouped output by 'Country_Region'. You can override using

the `` .groups `` argument.



This provides an aggregated view of the COVID-19 situation in the USA, both at the state and national levels. By visualizing the data, stakeholders can make informed decisions, assess the efficacy of interventions, and track the progress of the pandemic.

```
[10]: 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 %>%
```

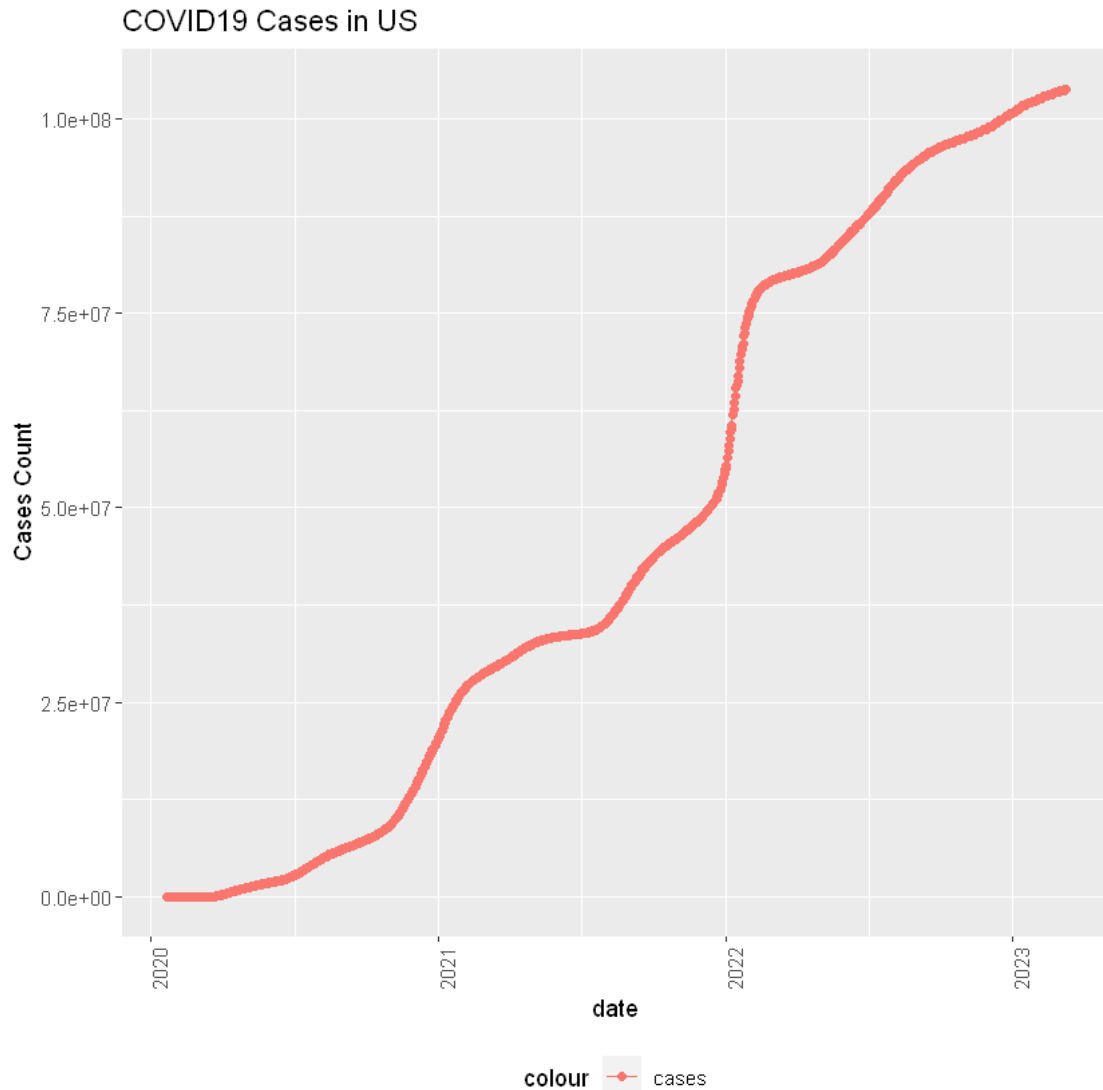
```

      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")) +
  theme(legend.position = "bottom", axis.text.x = element_text(angle = 90)) +
  labs(title = "COVID19 Cases in US", y = "Cases Count")

```

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



This provides a focused visualization of the cumulative confirmed cases of COVID-19 in the United States over time. By isolating and displaying only the cases metric, we gain a singular focus on simply cases. This facilitates a clearer interpretation of the data, enabling stakeholders, ranging from policymakers to the general public, to better gauge the situation in a narrower view.

```
[8]: US_by_state <- US_by_state %>%  
  mutate(  
    new_cases = cases - lag(cases),  
    new_deaths = deaths - lag(deaths),  
    cases_per_thou = cases * 1000 / Population,  
    deaths_per_thou = deaths * 1000 / Population  
  ) %>%  
  filter(cases > 0, Population > 0)
```

```

mod <- lm(deaths_per_thou ~ cases_per_thou, data = US_by_state)
summary(mod)

US_w_pred <- US_by_state %>% mutate(pred = predict(mod))
US_w_pred %>% ggplot() +
  geom_point(aes(x = cases_per_thou, y = deaths_per_thou), color = "blue") +
  geom_point(aes(x = cases_per_thou, y = pred), color = "red")

```

Call:

```
lm(formula = deaths_per_thou ~ cases_per_thou, data = US_by_state)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-2.40763	-0.35462	-0.04173	0.45783	1.49623

Coefficients:

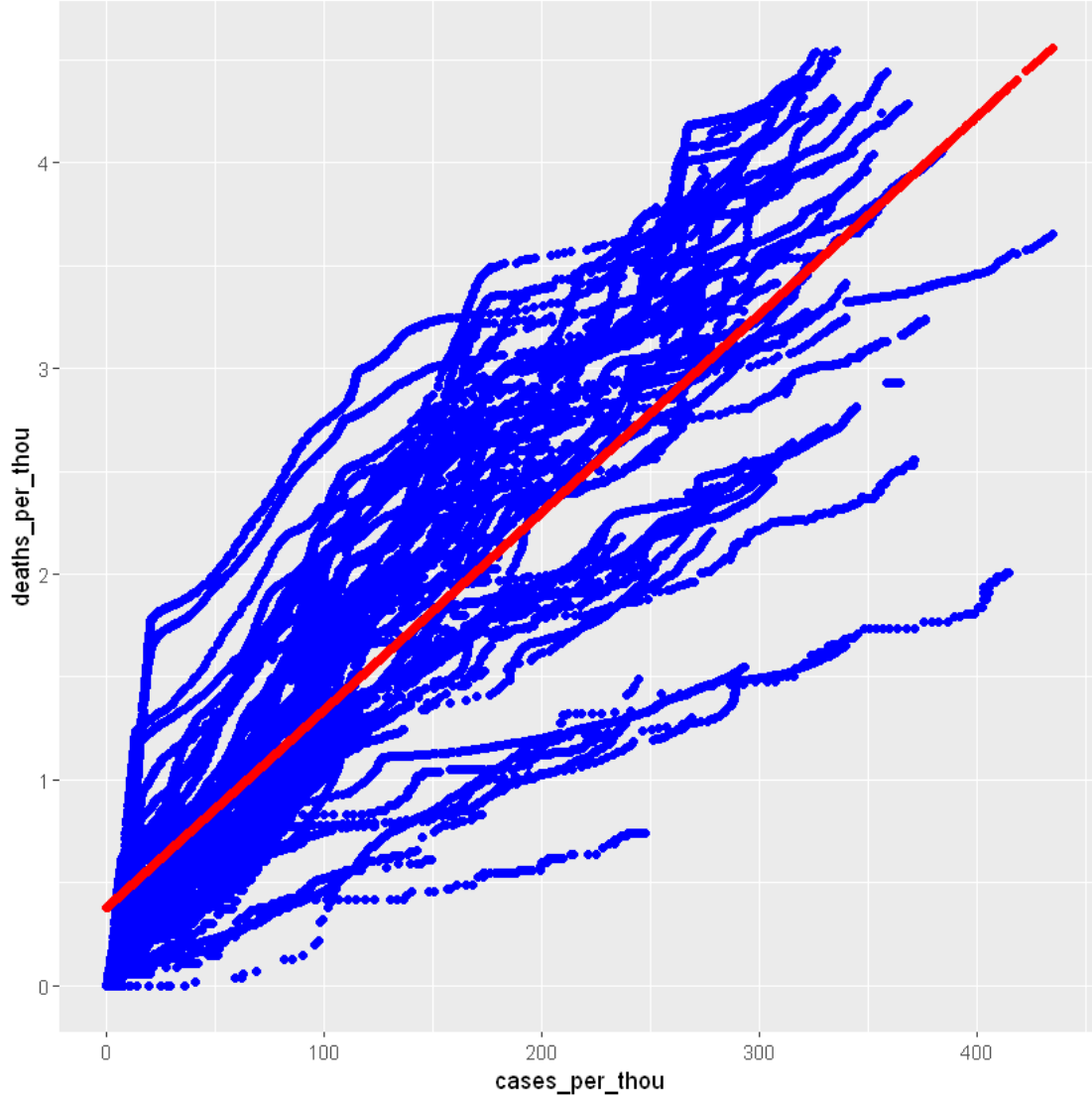
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.793e-01	4.159e-03	91.19	<2e-16 ***
cases_per_thou	9.611e-03	2.257e-05	425.77	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6349 on 61037 degrees of freedom

Multiple R-squared: 0.7481, Adjusted R-squared: 0.7481

F-statistic: 1.813e+05 on 1 and 61037 DF, p-value: < 2.2e-16



Here we aim to understand the relationship between the number of confirmed cases and deaths due to COVID-19. By creating a regression model, we can quantify how the number of cases (or the case rate) is related to the death rate. This might provide insights into the severity of the disease, the quality of medical care, or other factors affecting mortality. The visualization helps in comparing the actual death rates with the predicted ones, which can be useful for validation or to spot any anomalies or trends.

2 II. Conclusion

In our analysis of COVID-19's progression in the US, we employed data aggregation and visualization to highlight trends at state and national levels. By examining the relationship between confirmed cases and deaths, we gained insights into disease severity over time.