

# Covid-19 Data

2022-11-18

## INTRO

I will be going through the Covid-19 data. The primary question I am interested in is what was the effect of the Covid-19 vaccine on Covid-19 cases and deaths. I will be going through the Covid-19 data that was looked in class and Vaccine data from the site Listed below.

My hypothesis is that the number of deaths\_per\_thou should be lower in the states with the highest vaccination rates.

In order to build this RMD file we the following packages: library(tidyverse) library(lubridate)

## Tidy the Data

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr  0.3.5
## v tibble  3.1.8      v dplyr  1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.3      v forcats 0.5.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(lubridate)
```

```
## Loading required package: timechange
##
## Attaching package: 'lubridate'
##
## The following objects are masked from 'package:base':
##
##     date, intersect, setdiff, union
```

```
# Just assign a name to a variable. (str)
url_in <- "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/csse_

# Same as above... create an array with 4 names.
file_names <- c("time_series_covid19_confirmed_US.csv", "time_series_covid19_deaths_US.csv" )

# concatenate each one with the url_in.
```

```
urls <- str_c(url_in,file_names)
```

```
urlvaccine <- "https://raw.githubusercontent.com/owid/covid-19-data/master/public/data/vaccinations,  
# read those and assign to variables.
```

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

```
## Rows: 3342 Columns: 1151  
## -- Column specification -----  
## Delimiter: ","  
## chr (6): iso2, iso3, Admin2, Province_State, Country_Region, Combined_Key  
## dbl (1145): UID, code3, FIPS, Lat, Long_, 1/22/20, 1/23/20, 1/24/20, 1/25/20...  
##  
## i Use 'spec()' to retrieve the full column specification for this data.  
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
us_deaths <- read_csv(urls[2])
```

```
## Rows: 3342 Columns: 1152  
## -- Column specification -----  
## Delimiter: ","  
## chr (6): iso2, iso3, Admin2, Province_State, Country_Region, Combined_Key  
## dbl (1146): UID, code3, FIPS, Lat, Long_, Population, 1/22/20, 1/23/20, 1/24...  
##  
## i Use 'spec()' to retrieve the full column specification for this data.  
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
Vaccine_data <- read_csv(urlvaccine)
```

```
## Rows: 50148 Columns: 16  
## -- Column specification -----  
## Delimiter: ","  
## chr (1): location  
## dbl (14): total_vaccinations, total_distributed, people_vaccinated, people...  
## date (1): date  
##  
## i Use 'spec()' to retrieve the full column specification for this data.  
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
uid <- "https://raw.githubusercontent.com/CSSEGISandData/COVID-19/master/csse_covid_19_data/UID_ISO,
```

```
popul <- read_csv(uid)
```

```
## Rows: 4321 Columns: 12  
## -- Column specification -----  
## Delimiter: ","  
## chr (7): iso2, iso3, FIPS, Admin2, Province_State, Country_Region, Combined_Key  
## dbl (5): UID, code3, Lat, Long_, Population  
##  
## i Use 'spec()' to retrieve the full column specification for this data.  
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```

# Now we are going to join the population in global.

# DO THE SAME THINGS WITH US CASES:
us_cases <- us_cases %>% pivot_longer(cols = -(UID:Combined_Key), names_to = "date", values_to = "cases")
us_cases <- us_cases %>% select(Admin2:cases)
us_cases <- us_cases %>% mutate(date = mdy(date))

# DO THE SAME WITH US DEATHS (INCLUDING POPULATION)

us_deaths <- us_deaths %>% pivot_longer(cols = -(UID:Population), names_to = "date", values_to = "deaths")
us_deaths <- us_deaths %>% select(Admin2:deaths)
us_deaths <- us_deaths %>% mutate(date = mdy(date))
us_deaths <- us_deaths %>% select(-c(Lat,Long_))

# Combine the two
US_by_state <- us_cases %>% full_join(us_deaths)

```

```

## Joining, by = c("Admin2", "Province_State", "Country_Region", "Combined_Key",
## "date")

```

## Transform

Lets add a few more columns and start to look at some things of interest.

```

# Started another one to now go through and visualize and analyze some of the data above

# Group the data by the following:
US_by_state <- US_by_state %>% group_by(Province_State, Country_Region, date)

# add the following:
US_by_state <- US_by_state %>% summarise(cases = sum(cases), deaths = sum(deaths), Population = sum(Population))

```

```

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

```

```

# Add another column
US_by_state <- US_by_state %>% mutate(deaths_per_mill = deaths * 1000000 / Population)
US_by_state <- US_by_state %>% mutate(cases_per_mill = cases * 1000000 / Population)
# Ungroup
US_by_state <- US_by_state %>% ungroup()

US_state_totals <- US_by_state %>% group_by(Province_State) %>% summarise(deaths=max(deaths), cases=max(cases))

# Lets add the Vaccine Data to the US_state_totals

VaccineTotals <- Vaccine_data %>% select(date,location, people_fully_vaccinated)

# Lets get the totals for each state

VaccineTotals <- VaccineTotals %>% group_by(location) %>% summarise(People_fully_vaccinated=max(people_fully_vaccinated))

```

```
# rename location to Province_State
VaccineTotals <- VaccineTotals %>% rename(Province_State = location)

# Lets combine this with the US_State_totals

US_state_totals <- US_state_totals %>% full_join(VaccineTotals)
```

```
## Joining, by = "Province_State"
```

```
# Lets add another column for percent

US_state_totals <- US_state_totals %>% mutate(VaccinePercent = People_fully_vaccinated/population )

# Lets Cleanup Vaccine data as well.

Vaccine_data <- Vaccine_data %>% select(date, location, people_fully_vaccinated )
Vaccine_data <- Vaccine_data %>% rename(Province_State = `location`)
```

## Interesting Charts

Now lets take a look at some interesting states.

```
# Here is a list of states with the most deaths.

US_state_totals %>% slice_max(deaths_per_thou, n=10)
```

```
## # A tibble: 10 x 8
##   Province_State deaths    cases population cases_per_~1 death~2 Peopl~3 Vacci~4
##   <chr>          <dbl>    <dbl>      <dbl>      <dbl>    <dbl>    <dbl>    <dbl>
## 1 Arizona        33076 2440294    7278717      335.    4.54 4809730    0.661
## 2 Oklahoma       17940 1287378    3956971      325.    4.53 2393713    0.605
## 3 Mississippi   13351 989282     2976149      332.    4.49 1597932    0.537
## 4 West Virginia  7960 642760    1792147      359.    4.44 1070043    0.597
## 5 New Mexico     9054 670301    2096829      320.    4.32 1577485    0.752
## 6 Arkansas       13001 1005930    3017804      333.    4.31 1716584    0.569
## 7 Alabama        21001 1642062    4903185      335.    4.28 2607186    0.532
## 8 Tennessee      29225 2510002    6829174      368.    4.28 3843967    0.563
## 9 Michigan       42096 3057222    9986857      306.    4.22 6225457    0.623
## 10 New Jersey    35995 3046838    8882190      343.    4.05 7031019    0.792
## # ... with abbreviated variable names 1: cases_per_thou, 2: deaths_per_thou,
## # 3: People_fully_vaccinated, 4: VaccinePercent
```

Let us take a look at some states with the lowest death rates:

```
US_state_totals %>% slice_min(deaths_per_thou, n=10)
```

```
## # A tibble: 10 x 8
##   Province_State deaths    cases popul~1 cases~2 death~3 Peopl~4 Vacci~5
##   <chr>          <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 American Samoa    34 8.32e3    55641     150.    0.611   42467     0.763
```

```
## 2 Northern Mariana Islan~    41 1.37e4  55144    248.    0.744  43953  0.797
## 3 Virgin Islands            130 2.48e4  107268    231.    1.21   58951  0.550
## 4 Hawaii                    1834 3.80e5 1415872    268.    1.30 1154399  0.815
## 5 Vermont                    910 1.51e5  623989    243.    1.46   535103  0.858
## 6 Puerto Rico               5810 1.10e6 3754939    293.    1.55 2685604  0.715
## 7 Utah                      5287 1.09e6 3205958    340.    1.65 2141235  0.668
## 8 Alaska                    1486 3.07e5  740995    414.    2.01   476567  0.643
## 9 District of Columbia      1430 1.78e5  705749    252.    2.03   638828  0.905
## 10 Washington               15683 1.93e6 7614893    253.    2.06 5795079  0.761
## # ... with abbreviated variable names 1: population, 2: cases_per_thou,
## #   3: deaths_per_thou, 4: People_fully_vaccinated, 5: VaccinePercent
```

Lets take a look at the Vaccination rates

```
US_state_totals %>% slice_max(VaccinePercent, n=10)
```

```
## # A tibble: 10 x 8
##   Province_State deaths cases popul~1 cases~2 death~3 Peopl~4 Vacci~5
##   <chr>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 District of Columbia    1430 1.78e5 705749    252.    2.03   638828  0.905
## 2 Guam                    420 6.10e4 164229    371.    2.56  144432  0.879
## 3 Rhode Island           3865 4.60e5 1059361    434.    3.65   929813  0.878
## 4 Vermont                    910 1.51e5  623989    243.    1.46   535103  0.858
## 5 Massachusetts          24249 2.22e6 6892503    322.    3.52 5810671  0.843
## 6 Maine                   2921 3.17e5 1344212    236.    2.17 1120822  0.834
## 7 Connecticut            12196 9.76e5 3565287    274.    3.42 2961528  0.831
## 8 Hawaii                  1834 3.80e5 1415872    268.    1.30 1154399  0.815
## 9 Maryland                16513 1.36e6 6045680    226.    2.73 4821895  0.798
## 10 Northern Mariana Islan~    41 1.37e4  55144    248.    0.744  43953  0.797
## # ... with abbreviated variable names 1: population, 2: cases_per_thou,
## #   3: deaths_per_thou, 4: People_fully_vaccinated, 5: VaccinePercent
```

Lets Take a look at the states with the minimum Vaccine Rates

```
US_state_totals %>% slice_min(VaccinePercent, n=10)
```

```
## # A tibble: 10 x 8
##   Province_State deaths cases population cases_per_~1 death~2 Peopl~3 Vacci~4
##   <chr>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Wyoming          2002 185159   578759    320.    3.46  306951  0.530
## 2 Alabama          21001 1642062  4903185    335.    4.28 2607186  0.532
## 3 Mississippi      13351 989282  2976149    332.    4.49 1597932  0.537
## 4 Missouri         22825 1773865  6626371    268.    3.44 3625649  0.547
## 5 Virgin Islands    130 24792   107268    231.    1.21   58951  0.550
## 6 Louisiana         18738 1570671  4648794    338.    4.03 2558088  0.550
## 7 Tennessee         29225 2510002  6829174    368.    4.28 3843967  0.563
## 8 Idaho              5399 519850  1787065    291.    3.02 1009286  0.565
## 9 Arkansas          13001 1005930  3017804    333.    4.31 1716584  0.569
## 10 Georgia          42427 3065390 10617423    289.    4.00 6086702  0.573
## # ... with abbreviated variable names 1: cases_per_thou, 2: deaths_per_thou,
## #   3: People_fully_vaccinated, 4: VaccinePercent
```

## ANALYSIS

From the above data let's take a look at the following states:

I picked Massachusetts as it was a state with a pretty large population.. compared to the rest of the states.

Massachusetts 24249 2220962 6892503 322.2287 3.5181704 5810671

I thought it was important to pick something that was quite a bit further away from the Northeast.

Hawaii 1834 380098 1415872 268.4551 1.2953148 1154399

I picked these as these were the two states with the lowest vaccination rates. They also had population over one Million.

Alabama 21001 1642062 4903185 334.8970 4.283134 2607186 Missouri 22825 1773682 6626371 267.6702

```
# Lets look at the us totals as well. This was done in class
```

```
us_totals <- US_by_state %>% group_by(Country_Region, date) %>% summarize(cases=sum(cases), deaths=
```

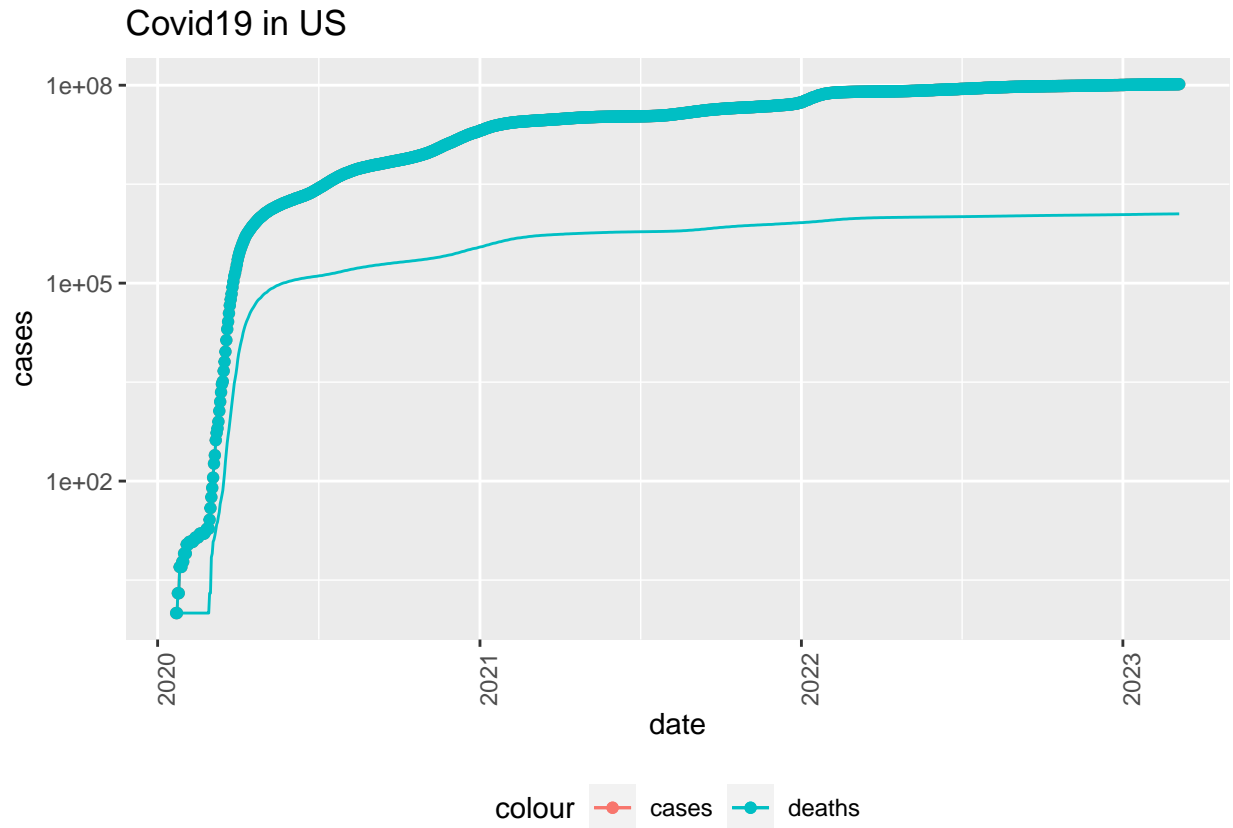
```
## 'summarise()' has grouped output by 'Country_Region'. You can override using  
## the '.groups' argument.
```

```
# Ungroup them.
```

```
us_totals <- us_totals %>% ungroup()
```

```
# SHOW THE GRAPH OF DEATHS VS. CASES
```

```
us_totals %>% filter(cases > 0) %>% ggplot(aes(x=date, y=cases)) +geom_line(aes(color = "cases")) +g
```



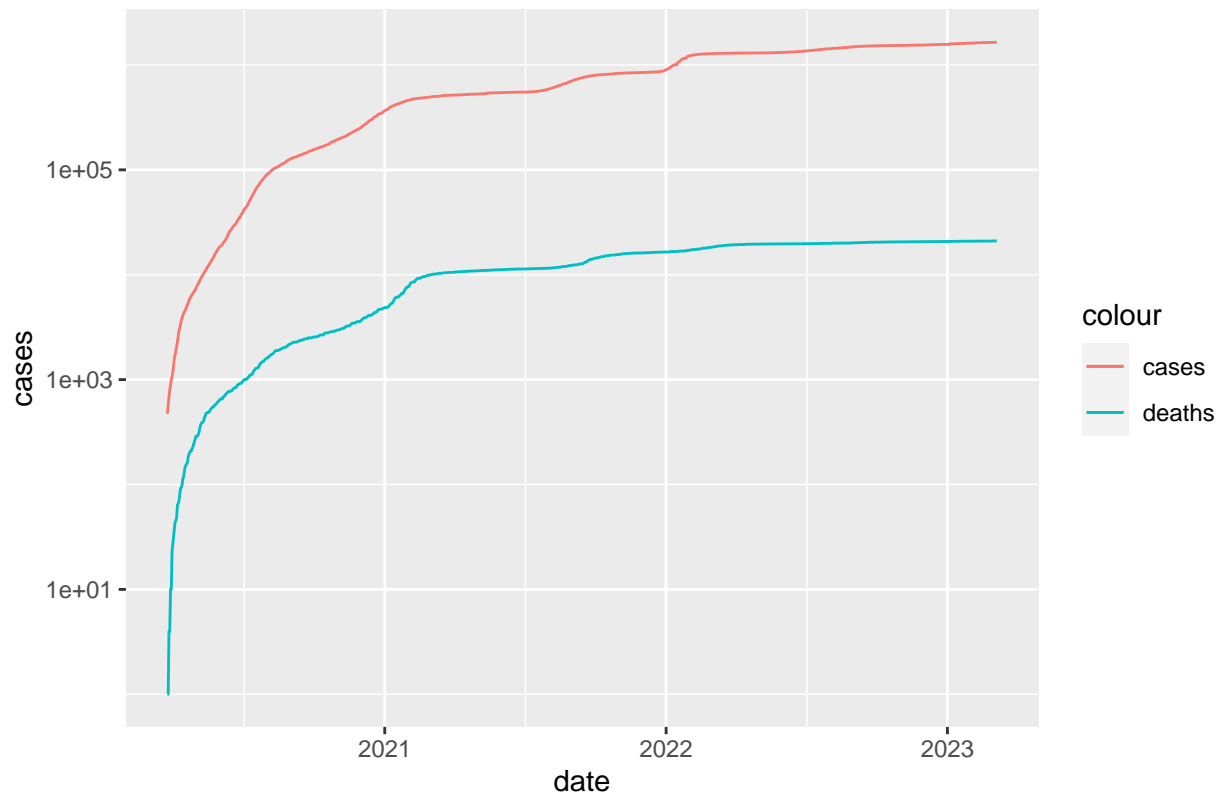
## Visualize

It looks like overall the cases and death rates are flat. This was what we would expect from looking at the US Data above.

*# Lets take a look at the 4 states we picked above. Two from the lowest catagory and two from the high*

```
US_by_state %>% filter(cases > 0, deaths > 0, Province_State == "Alabama") %>% ggplot(aes(x=date, y=
```

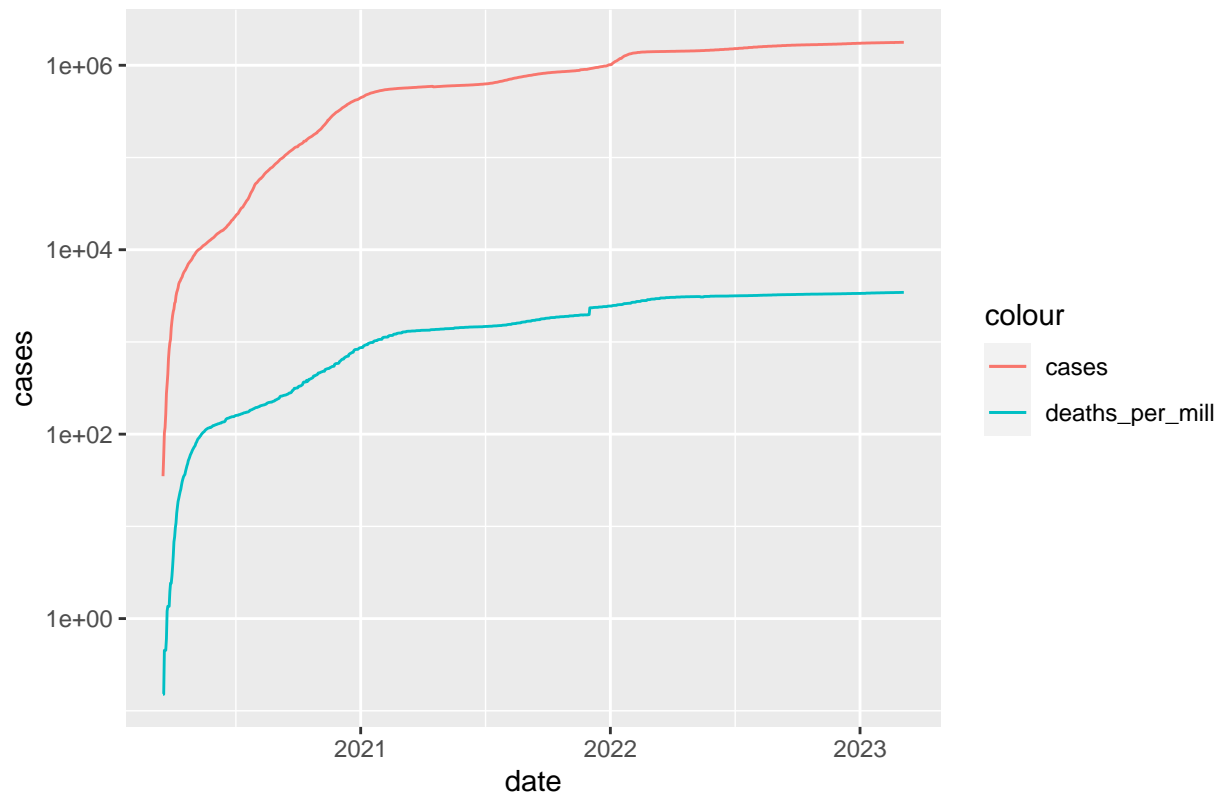
Covid19 in Alabama



```
US_by_state %>% filter(cases > 0, deaths > 0, Province_State == "Missouri") %>% ggplot(aes(x=date
```

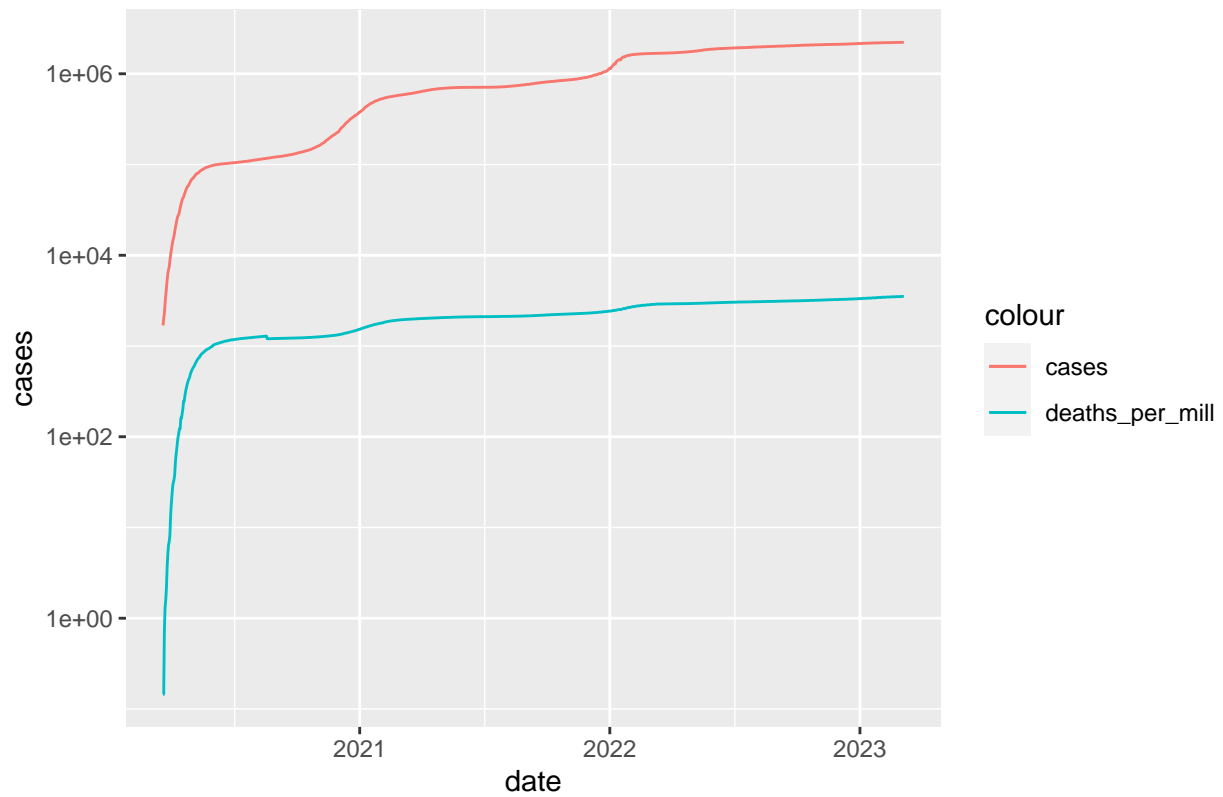


## Covid19 in Missouri



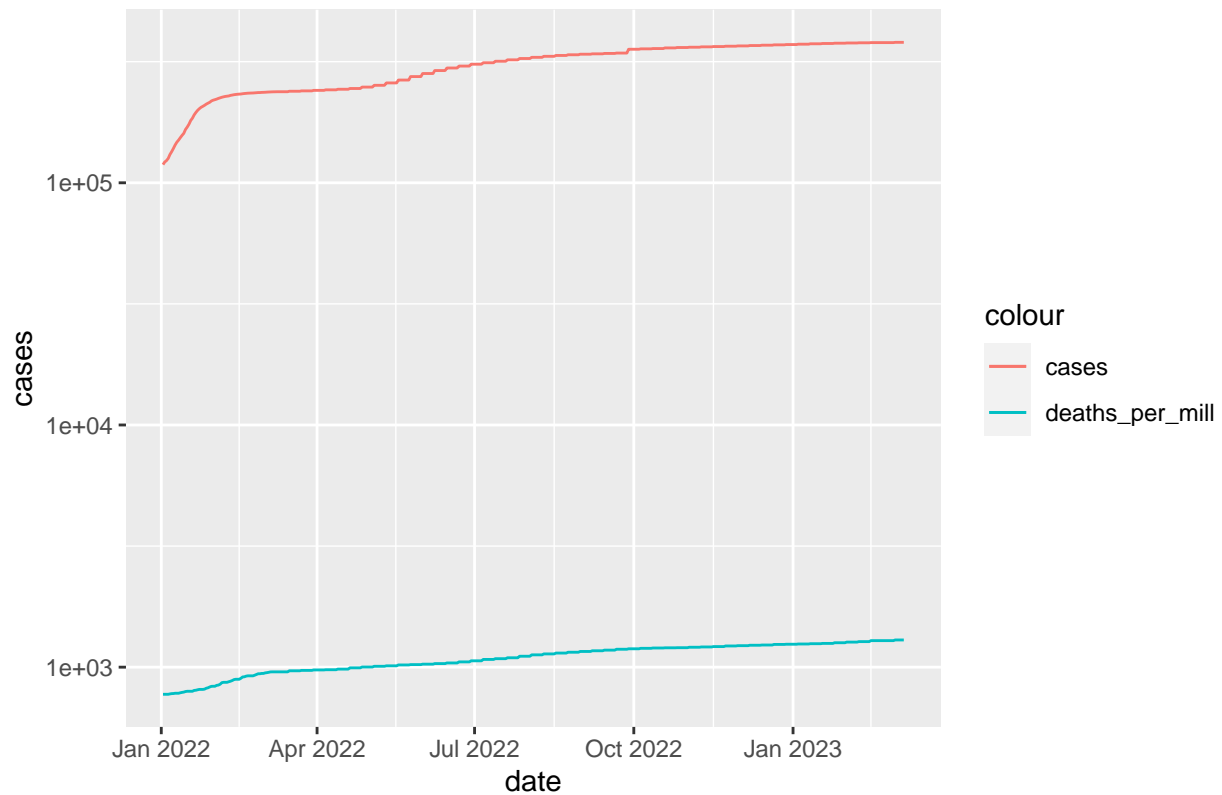
```
US_by_state %>% filter(cases > 0, deaths > 0, Province_State == "Massachusetts") %>% ggplot(aes
```

## Covid19 in Massachusetts



```
US_by_state %>% filter(cases > 0, deaths > 0, Province_State == "Hawaii", date > "2022-01-01") %>% g
```

## Covid19 in Hawaii



# VISUALIZE

Now lets look at the Vaccine data and new Deaths and New cases.

*# Since all we care about is people who have been fully\_vaccinated.*

```
#Vaccine_data <- Vaccine_data %>% select(date, location, people_fully_vaccinated )
#Vaccine_data <- Vaccine_data %>% rename(Province_State = `location`)
```

*# Now lets go ahead and combine this with the states total.*

```
US_by_state_vaccine <- US_by_state %>% full_join(Vaccine_data,by=c("Province_State","date"))
```

*# Now lets just look at the new cases*

```
US_by_state_vaccine <- US_by_state_vaccine %>% mutate(new_cases = cases - lag(cases), new_deaths=new_deaths - lag(new_deaths))
```

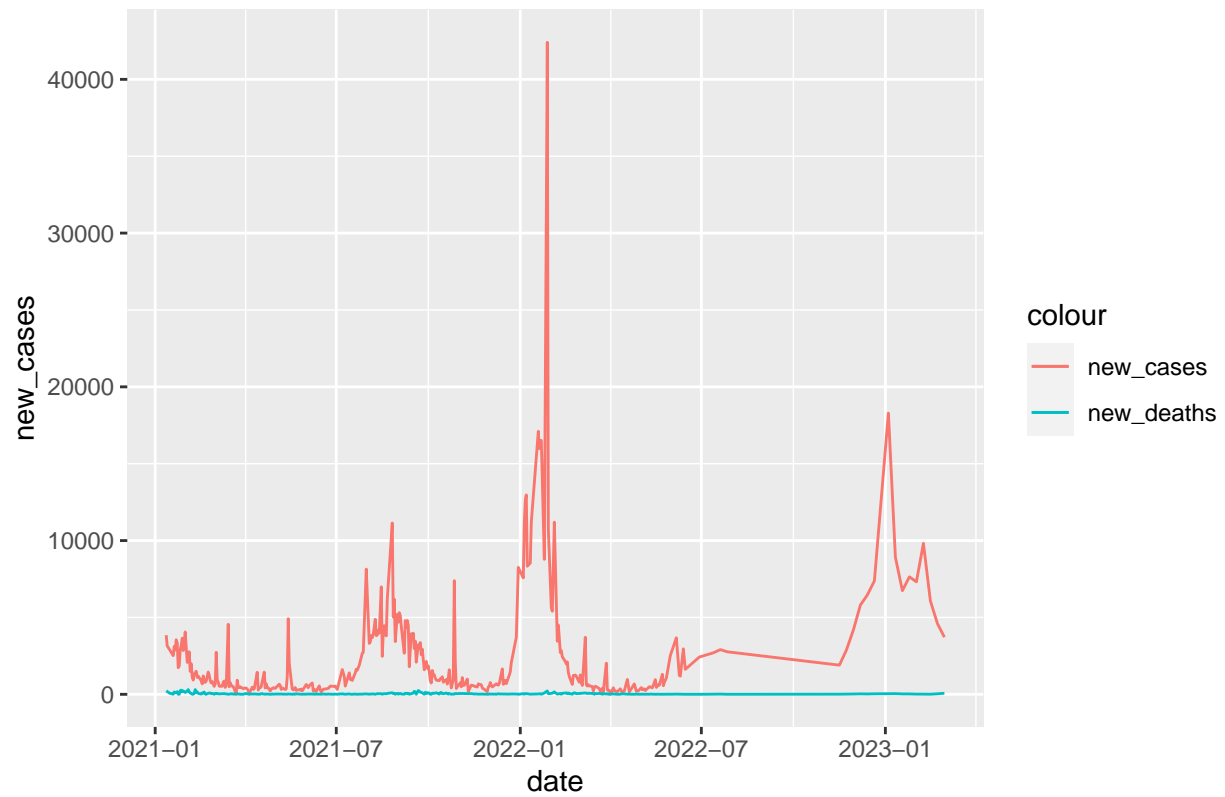
```
US_by_state_vaccine <- US_by_state_vaccine %>% mutate(Percent_deaths = new_deaths/new_cases *100)
```

```
US_by_state_vaccine <- US_by_state_vaccine %>% mutate(vaccine_per_hundred = 1000 * people_fully_vaccinated/Population)
```

```
US_by_state_vaccine <- US_by_state_vaccine %>% mutate(cases_per_hundred = 1000 * cases/Population)
```

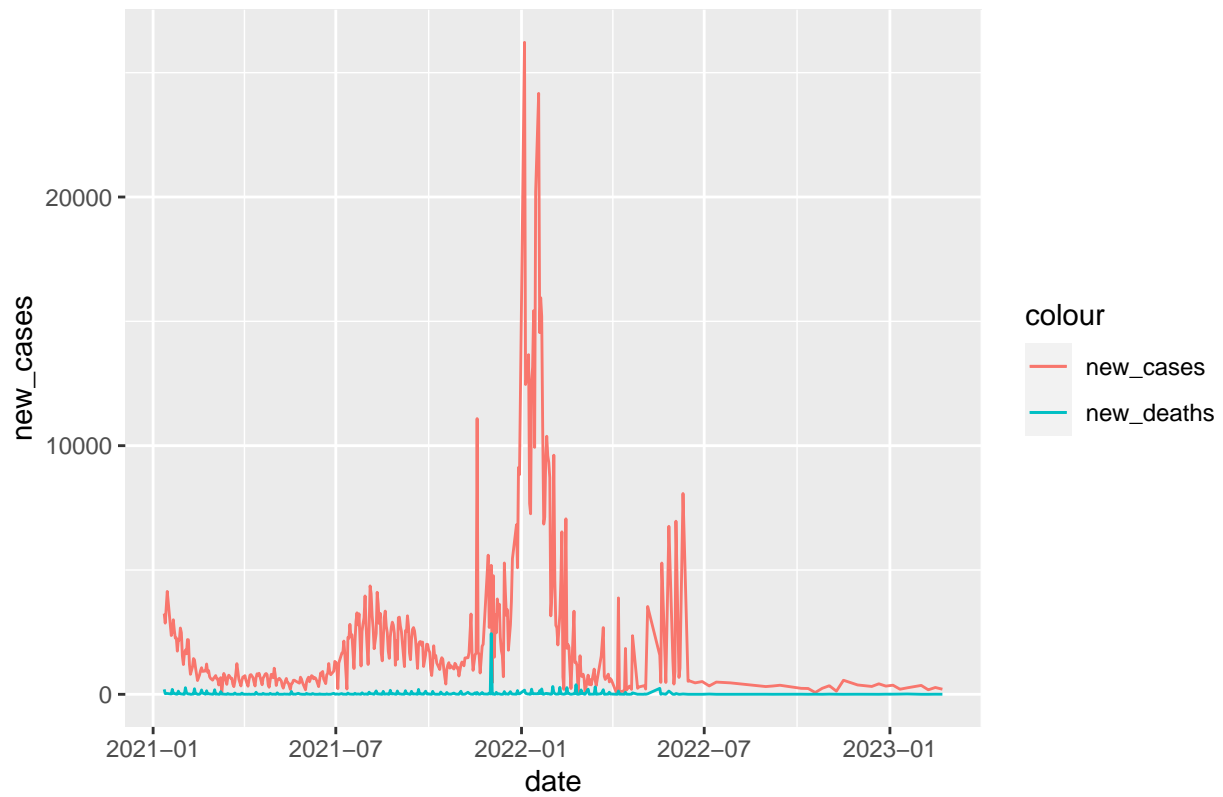
```
US_by_state_vaccine %>% filter(new_deaths > 0, people_fully_vaccinated > 0, new_cases > 0, Province_State != "US")
```

New Cases vs. Deaths in Alabama



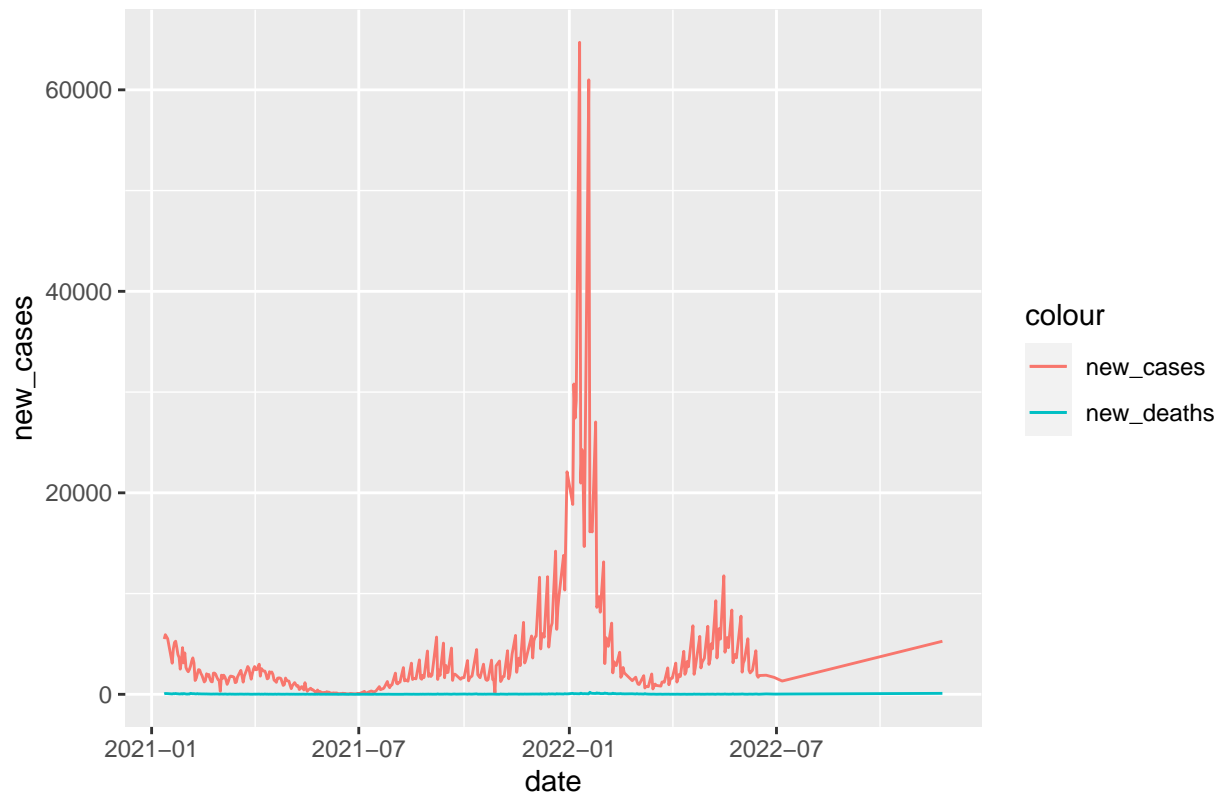
```
US_by_state_vaccine %>% filter(new_deaths > 0, people_fully_vaccinated > 0, new_cases > 0, Province.
```

New Cases vs. Deaths in Missouri



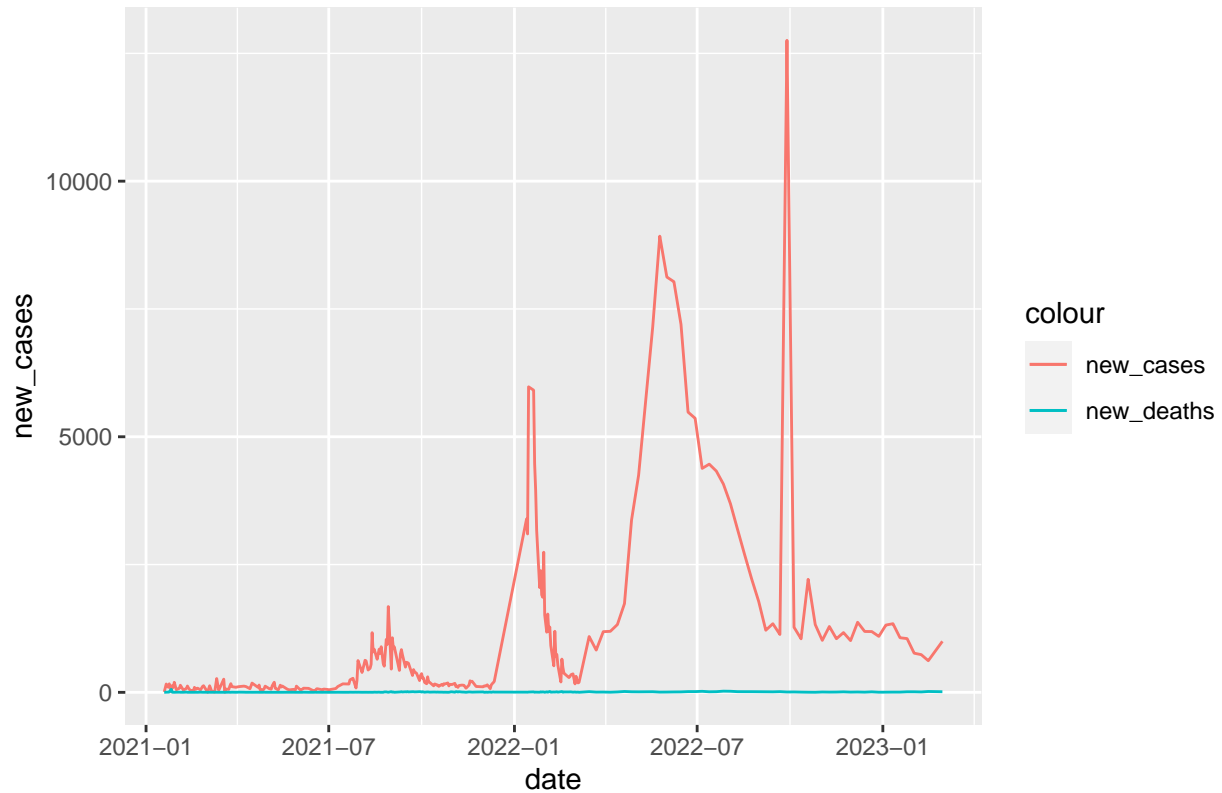
```
US_by_state_vaccine %>% filter(new_deaths > 0, people_fully_vaccinated > 0, new_cases > 0, Province
```

New Cases vs. Deaths in Massachusetts



```
US_by_state_vaccine %>% filter(new_deaths > 0, people_fully_vaccinated > 0, new_cases > 0, Province.
```

## New Cases vs. Deaths in Hawaii



## MORE VISUALS

Lets see if the percent of deaths vs. new cases in each of the above states.

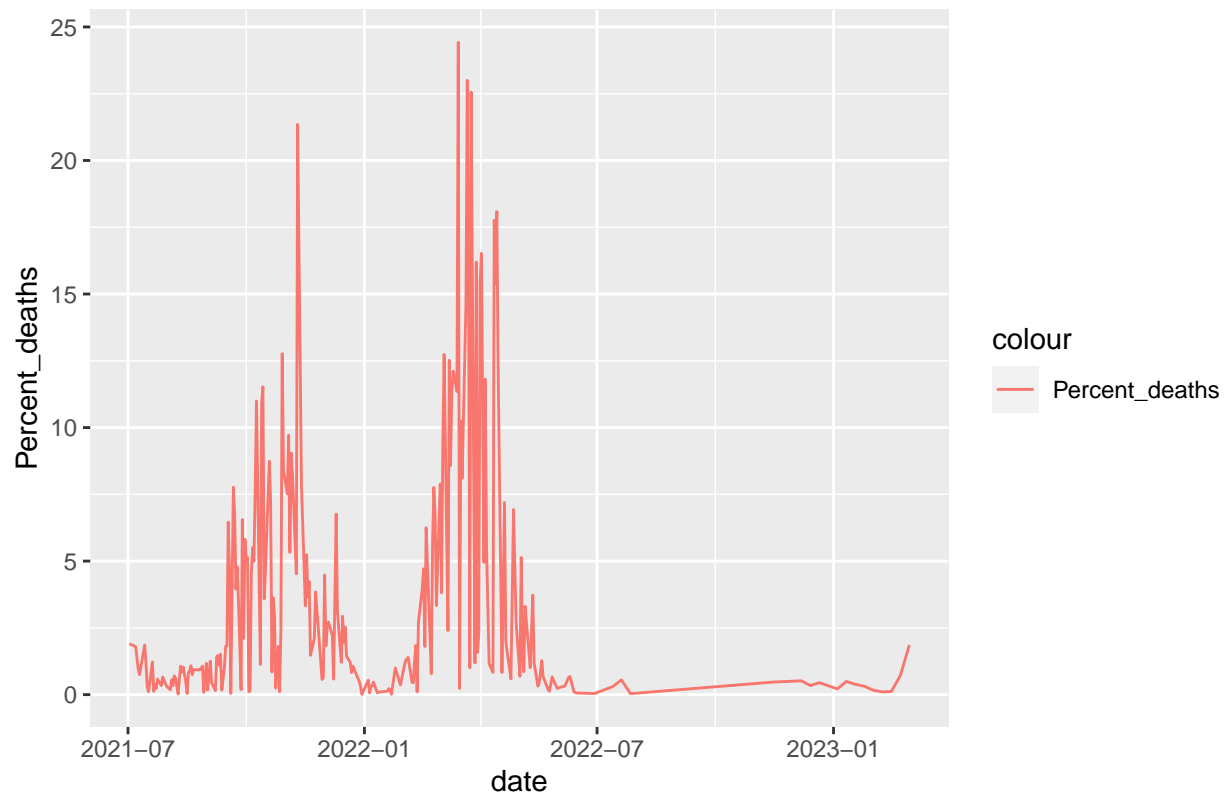
So our hypothesis was that states with the greater number of vaccinated residents should have lesser number of residents dying. So we are going to take a look at each of the states and see if that's true.

*# Some things to note. I took a look at all numbers after 2021-07-01. Mostly because we started vacci*

*# Lets take a look at Alabama First.*

```
US_by_state_vaccine %>% filter(new_deaths > 0, people_fully_vaccinated > 0, new_cases > 0, Province_Sta
```

Percent of People dying vs. Cases in Alabama

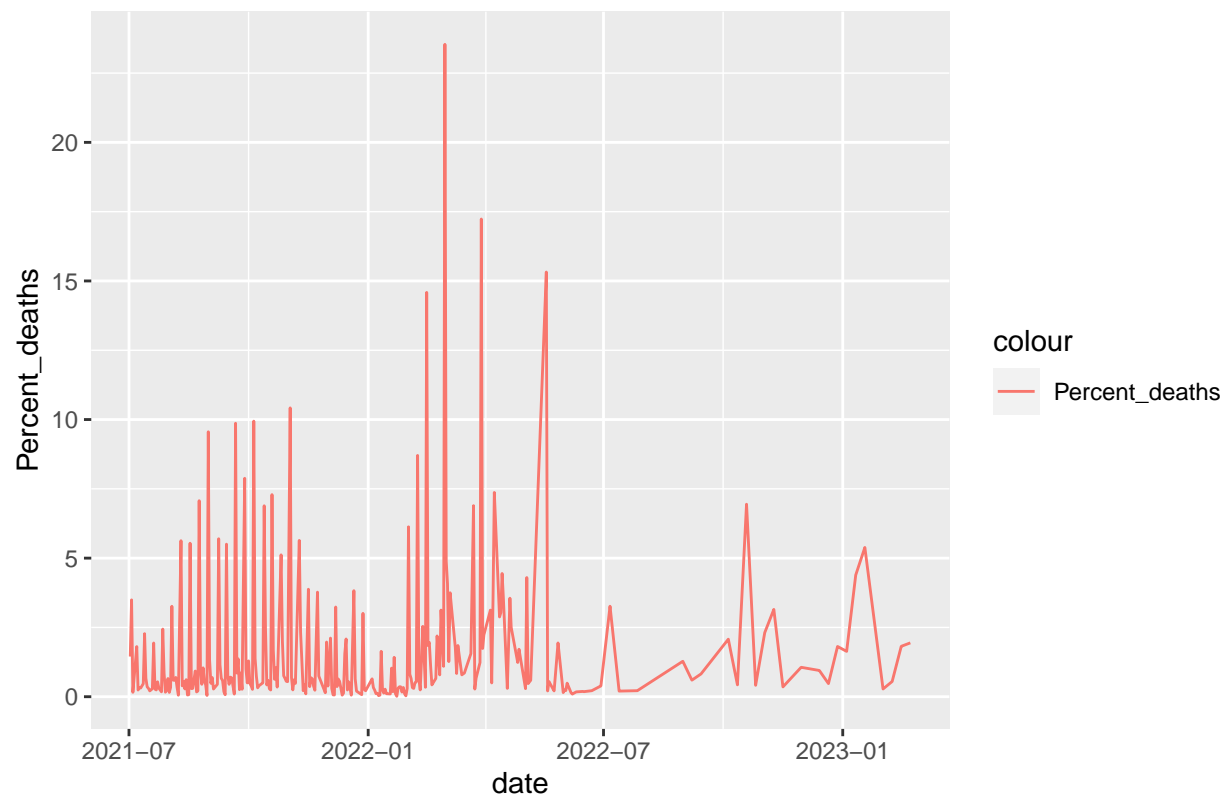


```
# Lets take a look at Missouri.
```

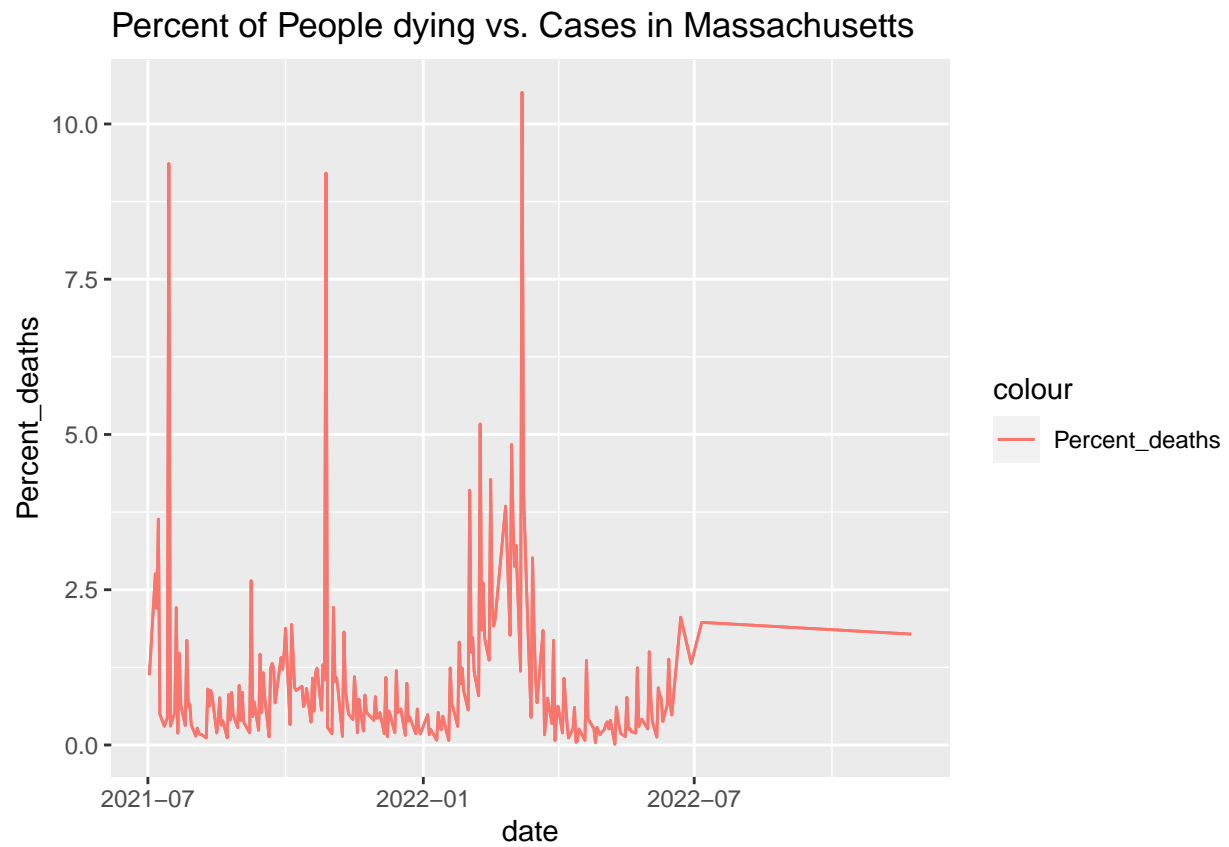
```
US_by_state_vaccine %>% filter(new_deaths > 0, people_fully_vaccinated > 0, new_cases > 0, Province_State
```



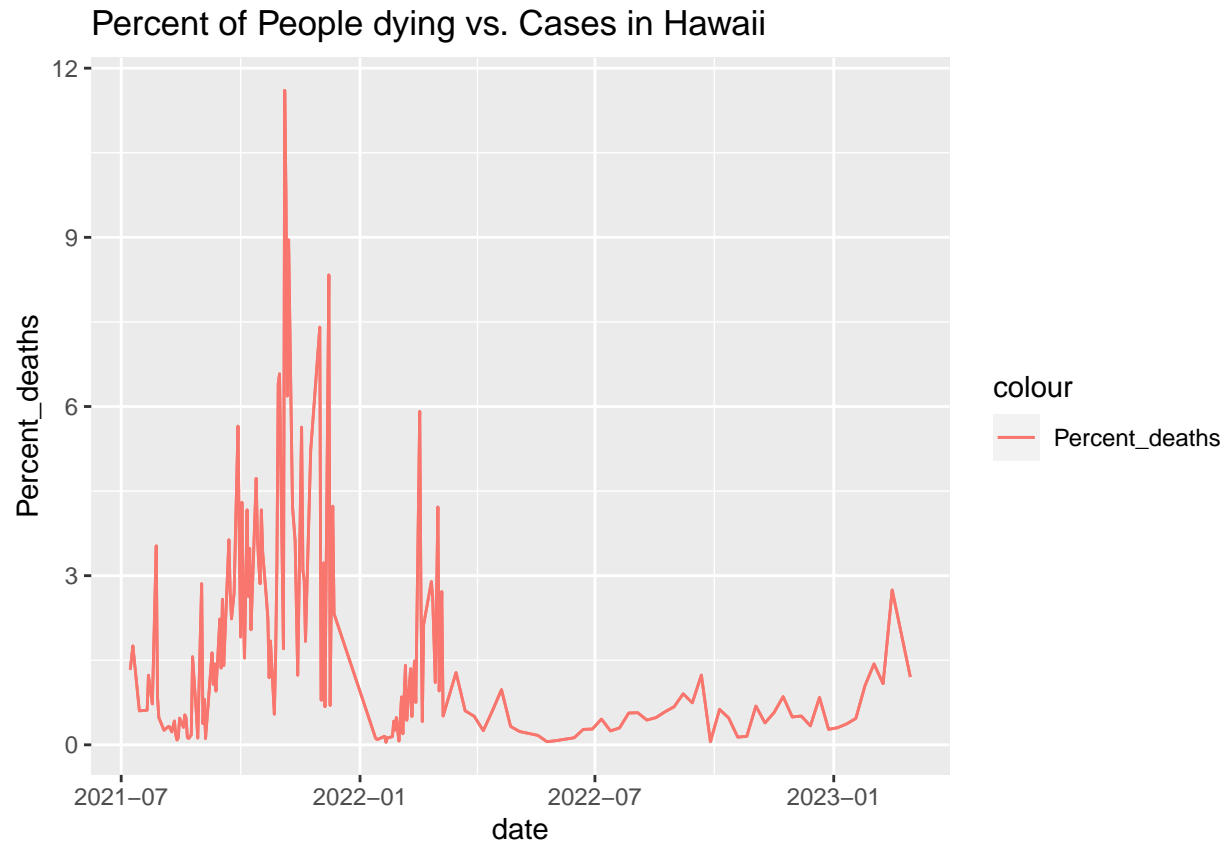
Percent of People dying vs. Cases in Missouri



```
US_by_state_vaccine %>% filter(new_deaths > 0, people_fully_vaccinated > 0, new_cases > 0, Province_State
```



```
US_by_state_vaccine %>% filter(new_deaths > 0, people_fully_vaccinated > 0, new_cases > 0, Province_State == "Massachusetts")
```



#### # ANALYSIS

As we can clearly see the death rate in states with high vaccination is quite a bit. Lets just take a look at Alabama and Massachusetts and you can see the chances of you dying from Covid-19 goes down dramatically.

#### BIAS

Personal Bias I think I picked Massachusetts as I have ties to that state.

Now sure how each state are collecting there data.

Demographics can also play a big role.