# Sok-1005 assignment 3

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```
rm (list = ls())
library(tidyverse)
```

```
Warning: package 'tidyverse' was built under R version 4.2.2

Warning: package 'ggplot2' was built under R version 4.2.2

Warning: package 'tidyr' was built under R version 4.2.2

Warning: package 'readr' was built under R version 4.2.2

Warning: package 'purrr' was built under R version 4.2.2

Warning: package 'dplyr' was built under R version 4.2.2

Warning: package 'stringr' was built under R version 4.2.2

Warning: package 'forcats' was built under R version 4.2.2

Warning: package 'lubridate' was built under R version 4.2.2

-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.0     v readr     2.1.4
v forcats   1.0.0     v stringr   1.5.0
v ggplot2   3.4.1     v tibble    3.1.8
v lubridate 1.9.2     v tidyr     1.3.0
v purrr     1.0.1
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becor
```

```
library(janitor)
```

```
Attaching package: 'janitor'

The following objects are masked from 'package:stats':

    chisq.test, fisher.test
```

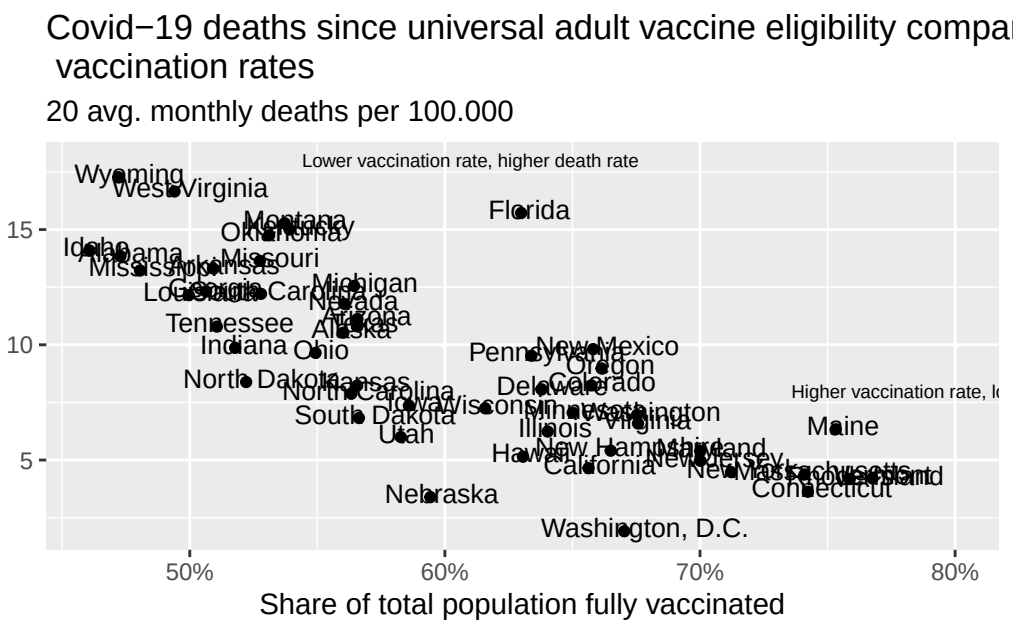
```
library(lubridate)
library(jsonlite)
```

```
Warning: package 'jsonlite' was built under R version 4.2.2
```

```
Attaching package: 'jsonlite'

The following object is masked from 'package:purrr':

    flatten
```

```
covid_deaths <-fromJSON("https://static01.nyt.com/newsgraphics/2021/12/20/us-coronavirus-d
```

```
covid_deaths %>%
  ggplot(aes(x=fully_vaccinated_pct_of_pop, y=deaths_per_100k, label = name)) +
  geom_point() +
  geom_text(hjust=.4, vjust=.3, size=3.4) +
  annotate("text", x = 0.61, y = 18, label = "Lower vaccination rate, higher death rate",
  annotate("text", x = 0.80, y = 8, label = "Higher vaccination rate, lower death ate", si
labs(title = "Covid-19 deaths since universal adult vaccine eligibility compared with\n va
subtitle = "20 avg. monthly deaths per 100.000",
y=" ",
x="Share of total population fully vaccinated",
caption = "") +
scale_x_continuous(labels = scales::percent)
```




```
lm(deaths_per_100k ~ fully_vaccinated_pct_of_pop, data=covid_deaths)
```

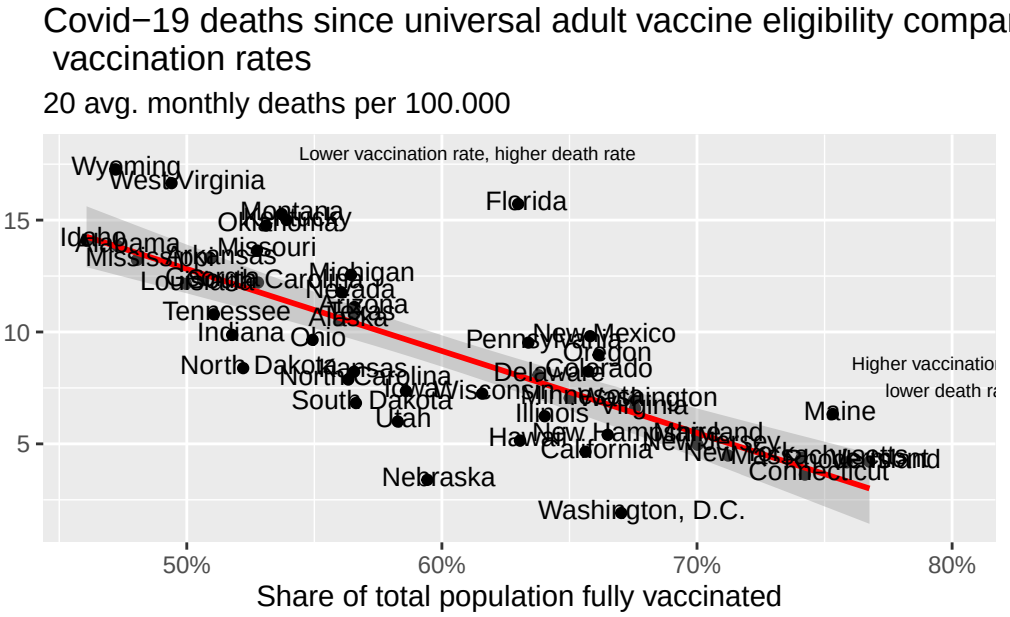
```
Call:
lm(formula = deaths_per_100k ~ fully_vaccinated_pct_of_pop, data = covid_deaths)

Coefficients:
                (Intercept)  fully_vaccinated_pct_of_pop
                      31.15                       -36.66
```

```
covid_deaths %>%
  ggplot(aes(x=fully_vaccinated_pct_of_pop, y=deaths_per_100k, label = name)) +
  geom_point() +
  geom_smooth(method = lm, colour='red') +
  geom_text(hjust=.4, vjust=.3, size=3.4) +
  annotate("text", x = 0.61, y = 18, label = "Lower vaccination rate, higher death rate",
  annotate("text", x = 0.80, y = 8, label = "Higher vaccination rate, \nlower death rate",
labs(title = "Covid-19 deaths since universal adult vaccine eligibility compared with\n va
subtitle = "20 avg. monthly deaths per 100.000",
y=" ",
x="Share of total population fully vaccinated",
```

```
  caption = "") +
  scale_x_continuous(labels = scales::percent)
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: The following aesthetics were dropped during statistical transformation: label
i This can happen when ggplot fails to infer the correct grouping structure in
  the data.
i Did you forget to specify a `group` aesthetic or to convert a numerical
  variable into a factor?
```




```
Coefficients:
                (Intercept)  fully_vaccinated_pct_of_pop
                      31.15                       -36.66
```

#the coefficient at -36.66 tells us that for every 1% increase in vaccine coverage there would be -36.66/100 = -0,3666 percent less people who would die from covid.

#the intercept tells us how many people would die if the percentage of people vaccinated were to drop by one percent. 31.15/100 = 0,3115%