Mappeinnlevering2

Eov016

2 2 2022

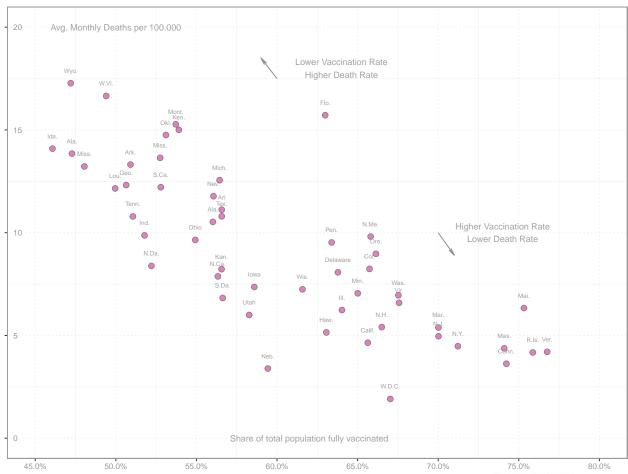
OPPGAVE1

```
#Etter å ha funnet json filen fra NY-times ved å lese gjennom sidekilden, lastet
#jeg opp linken. Deretter gjorde jeg den om til df slik jeg ville ha den.
url <- read_json("https://static01.nyt.com/newsgraphics/2021/12/20/us-coronavirus-deaths-2021/ff0adde21
cov_json_res <- url</pre>
str(cov_json_res)
## List of 51
## $ :List of 6
    ..$ name
                                     : chr "Alabama"
                                    : chr "USA-01"
##
     ..$ geoid
##
    ..$ deaths_before
                                    : int 10790
cov_json <- lapply(cov_json_res, function(x) {</pre>
 x[sapply(x, is.null)] <- NA
 unlist(x)
})
NYT_cov_data <-as.data.frame(do.call("rbind", cov_json))</pre>
str(NYT_cov_data)
## 'data.frame':
                    51 obs. of 6 variables:
## $ name
                                 : chr "Alabama" "Alaska" "Arizona" "Arkansas" ...
## $ geoid
                                 : chr "USA-01" "USA-02" "USA-04" "USA-05" ...
## $ deaths_before
                                 : chr "10790" "318" "17153" "5699" ...
                                 : chr "5590" "634" "6663" "3308" ...
## $ deaths
#Konverterer til numeric, som etter as_tibble() blir double (numeric)
as_tibble(NYT_cov_data)
## # A tibble: 51 x 6
##
                       geoid deaths_before deaths deaths_per_100k fully_vaccinate~
      name
      <chr>
                       <chr> <chr>
                                            <chr> <chr>
                       USA-01 10790
                                             5590
                                                    13.84706814898~ 0.4728
## 1 Alabama
## 2 Alaska
                       USA-02 318
                                            634
                                                    10.52622170652~ 0.5602
NYT_cov_data$fully_vaccinated_pct_of_pop <-</pre>
 as.numeric(as.character(NYT_cov_data$fully_vaccinated_pct_of_pop))
NYT_cov_data$deaths_per_100k <-
```

```
as.numeric(as.character(NYT_cov_data$deaths_per_100k))
NYT_cov_data$deaths_before <-</pre>
  as.numeric(as.character(NYT_cov_data$deaths_before))
NYT_cov_data$deaths <-
  as.numeric(as.character(NYT_cov_data$deaths))
str(NYT_cov_data)
## 'data.frame':
                     51 obs. of 6 variables:
                                          "Alabama" "Alaska" "Arizona" "Arkansas" ...
## $ name
                                   : chr
                                          "USA-01" "USA-02" "USA-04" "USA-05" ...
## $ geoid
                                   : chr
## $ deaths before
                                   : num 10790 318 17153 5699 61034 ...
## $ deaths
                                   : num 5590 634 6663 3308 15117 ...
as_tibble(NYT_cov_data)
## # A tibble: 51 x 6
##
                        geoid deaths_before deaths deaths_per_100k fully_vaccinate~
      name
##
      <chr>
                                        <dbl> <dbl>
                                                                 <dbl>
## 1 Alabama
                        USA-01
                                        10790
                                                 5590
                                                                 13.8
                                                                                   0.473
## 2 Alaska
                        USA-02
                                          318
                                                  634
                                                                 10.5
                                                                                   0.560
#Forsøkte å finne en måte å forkorte navnene på, men konkluderte med å bare endre
#på de en etter en før gaplot.
NYT_cov_data$name[NYT_cov_data$name == "Wyoming"] <- "Wyo."</pre>
NYT_cov_data$name[NYT_cov_data$name == "West Virginia"] <- "W.Vi."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Montana"] <- "Mont."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Idaho"] <- "Ida."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Alabama"] <- "Ala."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Mississippi"] <- "Miss."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Louisiana"] <- "Lou."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Tennessee"] <- "Tenn."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Indiana"] <- "Ind."</pre>
NYT_cov_data$name[NYT_cov_data$name == "North Dakota"] <- "N.Da."
NYT_cov_data$name[NYT_cov_data$name == "North Carolina"] <- "N.Ca."
NYT_cov_data$name[NYT_cov_data$name == "Kansas"] <- "Kan."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Hawaii"] <- "Haw."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Illinois"] <- "Ill."</pre>
NYT cov data$name[NYT cov data$name == "Wisconsin"] <- "Wis."
NYT_cov_data$name[NYT_cov_data$name == "California"] <- "Calif."</pre>
NYT_cov_data$name[NYT_cov_data$name == "New Hampshire"] <- "N.H."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Maryland"] <- "Mar."</pre>
NYT_cov_data$name[NYT_cov_data$name == "South Dakota"] <- "S.Da."
NYT_cov_data$name[NYT_cov_data$name == "Colerado"] <- "Col."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Oregon"] <- "Ore."</pre>
NYT_cov_data$name[NYT_cov_data$name == "New Mexico"] <- "N.Me."
NYT_cov_data$name[NYT_cov_data$name == "Virginia"] <- "Vir."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Maine"] <- "Mai."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Florida"] <- "Flo."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Oklahoma"] <- "Okl."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Kentucky"] <- "Ken."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Missouri"] <- "Miss."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Michigan"] <- "Mich."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Nevada"] <- "Nev."</pre>
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```
NYT_cov_data$name[NYT_cov_data$name == "Arizona"] <- "Ari"</pre>
NYT_cov_data$name[NYT_cov_data$name == "Texas"] <- "Tex."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Alaska"] <- "Ala."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Minnesota"] <- "Min."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Colorado"] <- "Col."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Pennsylvania"] <- "Pen."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Georgia"] <- "Geo."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Arkansas"] <- "Ark."</pre>
NYT_cov_data$name[NYT_cov_data$name == "South Carolina"] <- "S.Ca."
NYT_cov_data$name[NYT_cov_data$name == "Washington"] <- "Was."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Nebraska"] <- "Neb."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Washington, D.C."] <- "W.D.C."
NYT_cov_data$name[NYT_cov_data$name == "New Jersey"] <- "N.J."</pre>
NYT_cov_data$name[NYT_cov_data$name == "New York"] <- "N.Y."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Massachusetts"] <- "Mas."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Connecticut"] <- "Conn."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Rhode Island"] <- "R.Is."</pre>
NYT_cov_data$name[NYT_cov_data$name == "Vermont"] <- "Ver."</pre>
#Fulgte NY-times sin graf, forsøkte å replisere den. Fikk med alt og tok meg noen friheter.
p <- ggplot(NYT_cov_data, aes(x=fully_vaccinated_pct_of_pop,</pre>
                               y = deaths_per_100k, label = name))
p + geom_point(position = "identity", fill = "mediumvioletred", alpha= 0.60, color = "black", size = 2.
  geom_text(vjust = 0, nudge_y = 0.5, size = 2.5, color = "gray60")+
  scale_x_{continuous}(labels = scales::percent, breaks=seq(0.45, 1.00, 0.05), limits = c(0.45, 0.80))+
  scale_y_continuous(name = "",limits = c(0, 20, 4))+
  labs(title = "Covid-19 deaths since universal adult vaccine eligibility compared with\n vaccineration
       x = "Share of total population fully vaccinated",
       v = "") +
  annotate(geom="text", x=0.50, y=20, label="Avg. Monthly Deaths per 100.000",
           color="gray60", size = 3.5)+
  annotate(geom = "segment", x = 0.60, xend = 0.59, y = 17.5, yend = 18.5, color = "gray50",
           arrow = arrow(angle = 10, length = unit(.3, "cm")))+
  annotate(geom="text", x=0.64, y=18, label="Lower Vaccination Rate\nHigher Death Rate",
           color="gray60", size = 3.5)+
  annotate(geom = "segment", x = 0.70, xend = 0.71, y = 10, yend = 8.9, color = "gray50",
           arrow = arrow(angle = 10, length = unit(.3, "cm")))+
  annotate(geom="text", x=0.74, y=10, label="Higher Vaccination Rate\nLower Death Rate",
           color="gray60", size = 3.5)+
  annotate(geom="text", x=0.62, y=-0.0, label="Share of total population fully vaccinated",
           color="gray60", size = 3.5)+
  theme(plot.title = element_text(face = "bold",hjust = 0.5),
        axis.title.x = element_text(hjust = 0.9, size = 5, color = "gray98"),
        axis.text = element_text(colour = "gray60"),
        axis.text.y = element_text(hjust = 0, margin = margin(0, -0.7, 0, 0, 'cm')),
        panel.background = element_rect(fill = "white", colour = "grey85"),
        panel.grid.major = element_line(colour = "gray92", linetype = "dotted"),
        panel.grid.minor = element_line(colour = "gray94", linetype = NULL),
        panel.border = element_rect(fill = alpha("white", 0.10),color = "gray60", size = 1))
```

Covid–19 deaths since universal adult vaccine eligibility compared with vaccineration rates



OPPGAVE2

Jeg tolker dette som at ca. 63.34% av befolkningen er full-vaksinert, altså er -36.66% ikke full-vaksinert. Det er veldig tydelig at med høyere vaksinasjons rate er det lavere dødstall pr. 100K. Basert på disse data, tolker jeg det som at tallene "31.15" er antall døde pr 100K statene samlet. Altså, er tallet på antall døde i dette tilfelle ca. 31.150 per 100K den perioden.

```
scale_x_continuous(labels = scales::percent, breaks=seq(0.45,1.00,0.05), limits = c(0.45, 0.80))+
scale_y_continuous(name = "",limits = c(0, 20, 4))+
labs(title = "Covid-19 deaths since universal adult vaccine eligibility compared with\n vaccineration
    x = "Share of total population fully vaccinated",
     v = "") +
annotate(geom="text", x=0.50, y=20, label="Avg. Monthly Deaths per 100.000",
         color="gray60", size = 3.5)+
annotate(geom = "segment", x = 0.60, xend = 0.59, y = 17.5, yend = 18.5, color = "gray50",
        arrow = arrow(angle = 10, length = unit(.3, "cm")))+
annotate(geom="text", x=0.64, y=18, label="Lower Vaccination Rate\nHigher Death Rate",
         color="gray60", size = 3.5)+
annotate(geom = "segment", x = 0.70, xend = 0.71, y = 10, yend = 8.9, color = "gray 50",
         arrow = arrow(angle = 10, length = unit(.3, "cm")))+
annotate(geom="text", x=0.74, y=10, label="Higher Vaccination Rate\nLower Death Rate",
         color="gray60", size = 3.5)+
annotate(geom="text", x=0.62, y=-0.0, label="Share of total population fully vaccinated",
         color="gray60", size = 3.5)+
theme(plot.title = element_text(face = "bold",hjust = 0.5),
     axis.title.x = element_text(hjust = 0.9, size =5, color = "gray98"),
      axis.text = element_text(colour = "gray60"),
      axis.text.y = element_text(hjust = 0, margin = margin(0, -0.7, 0, 0, 'cm')),
      panel.background = element_rect(fill = "white", colour = "grey85"),
     panel.grid.major = element_line(colour = "gray92", linetype = "dotted"),
     panel.grid.minor = element_line(colour = "gray94", linetype = NULL),
     panel.border = element rect(fill = alpha("white", 0.10),color = "gray60", size = 1))
```

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

Covid-19 deaths since universal adult vaccine eligibility compared with vaccineration rates

