Mapping US Vaccination Data in R

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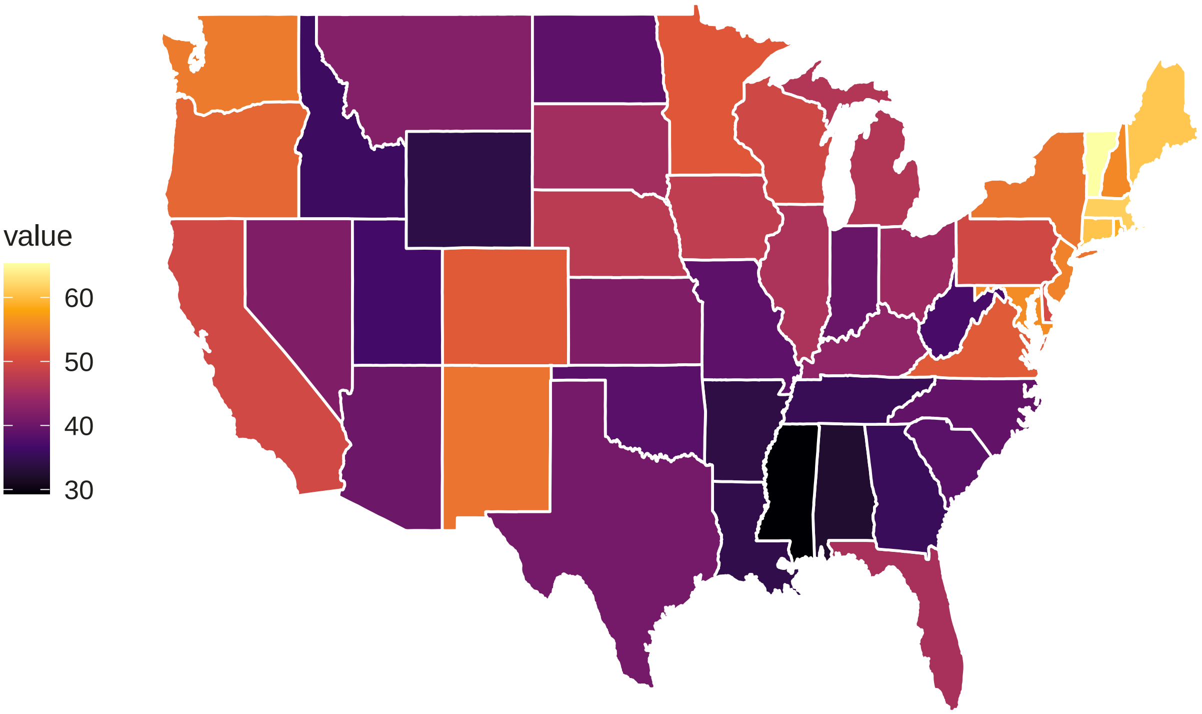
```
knitr::opts_chunk$set(echo = TRUE)
## load packages
library(tidyverse)
library(ggplot2)
library(readr)
library(maps)
library(viridis)
library(choroplethr)
library(choroplethrMaps)
```

Data Visualization using *ggplot2* package

```
### Data Visualization with ggplot2
### Map of confirmed COVID-19 cases

## read covid-19 dataset into R and assign it to an object
## source https://github.com/owid/covid-19-data
covid_raw <- read_csv("data/us_state_vaccinations.csv")
View(covid_raw)

# filter by date
today_covid <-
  covid_raw %>%
  filter(date=='2021-06-28') %>%
  select(location, people_fully_vaccinated_per_hundred)

# convert states to lowercase to match reference map
today_covid$location <- tolower(today_covid$location)

# rename column names and ny state to match reference map
colnames(today_covid) <- c('region','value')
today_covid$region <-
  plyr::revalue(today_covid$region, c("new york state" = "new york"))

# read map into R and assign it to an object
us_map <- map_data("state")

# merge vaccination data with map long/lat columns
today_covid_map <- merge(us_map, today_covid, by = "region")
```

```r
ggplot(today_covid_map, aes(long, lat, group = group)) +
  geom_polygon(aes(group=group, fill = value), color = "white") +
  scale_fill_viridis_c(option = "B") +
  theme_void() +
  guides(colour = guide_legend()) +
  labs(title = "People fully vaccinated per hundred in the United States",
       caption = "State-by-state data on United States COVID-19 vaccinations from the CDC") +
  theme(legend.text = element_text(size = 10), legend.position = "left",
    text = element_text(color = "#22211d"),
    panel.background = element_rect(fill = "#ffffff", color = NA),
    legend.background = element_rect(fill = "#ffffff", color = NA))
```

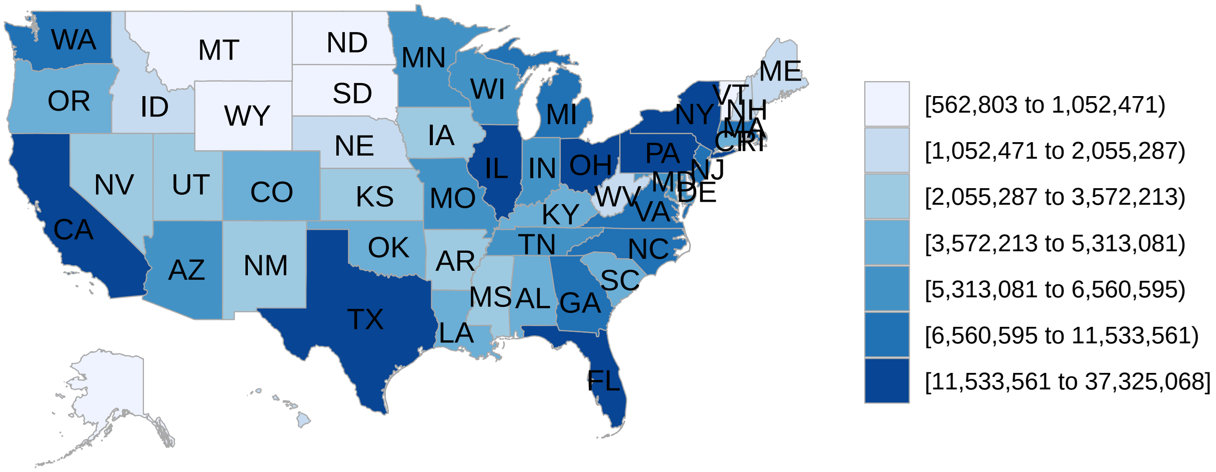
People fully vaccinated per hundred in the United States



State−by−state data on United States COVID−19 vaccinations from the CDC

Data Visualization using *choroplethr* package

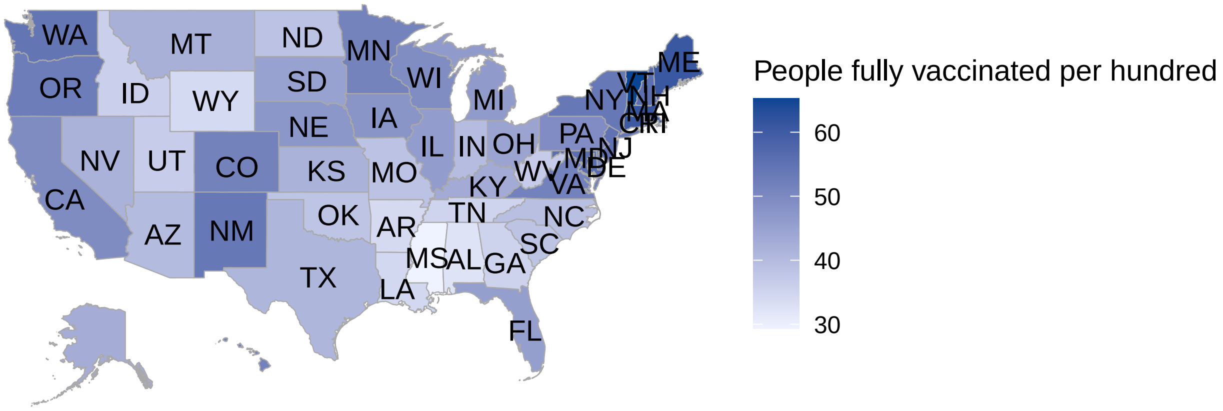
```r
## Data Visualization using choroplethr

# reference
data(df_pop_state)
state_choropleth(df_pop_state)
```



```
# us vaccination
state_choropleth(today_covid,
                 title = "State-by-state vaccination across the United States",
                 legend = "People fully vaccinated per hundred",
                 num_colors = 1)
```

```
## Warning in super$initialize(map.df, user.df): Your data.frame contains the
## following regions which are not mappable: american samoa, bureau of prisons,
## dept of defense, federated states of micronesia, guam, indian health svc, long
## term care, marshall islands, northern mariana islands, puerto rico, republic of
## palau, united states, veterans health, virgin islands
```

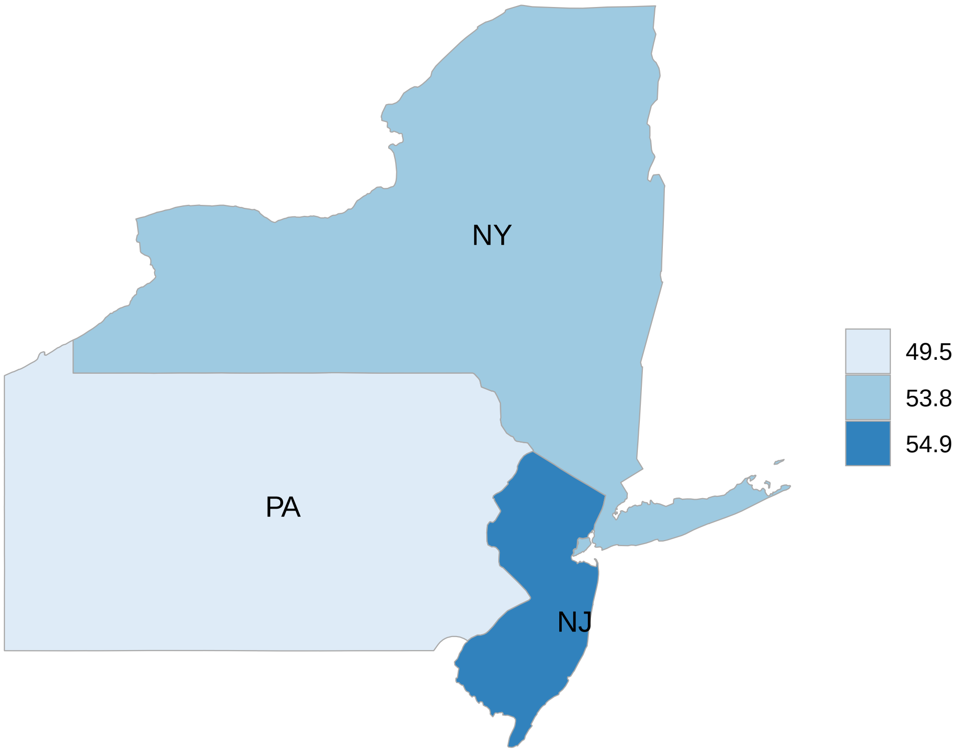
State−by−state vaccination across the United States



```r
# 5 quantiles, zoom in on vector of states
state_choropleth(today_covid, num_colors = 5,
                 zoom = c("new york", "pennsylvania", "new jersey"))
```

```
## Warning in super$initialize(map.df, user.df): Your data.frame contains the
## following regions which are not mappable: american samoa, bureau of prisons,
## dept of defense, federated states of micronesia, guam, indian health svc, long
## term care, marshall islands, northern mariana islands, puerto rico, republic of
## palau, united states, veterans health, virgin islands
```

```
## Warning in min(xx[xx > upper]): no non-missing arguments to min; returning Inf
```


NY
PA
NJ
49.5
53.8
54.9