Class17: Mini Project

Colin Mach (A16673100)

```
vax <- read.csv("covid19vaccinesbyzipcode_test.csv")
head(vax)
```

```
  as_of_date zip_code_tabulation_area local_health_jurisdiction    county
1 2021-01-05                   95446                    Sonoma    Sonoma
2 2021-01-05                   96014                  Siskiyou  Siskiyou
3 2021-01-05                   96087                    Shasta    Shasta
4 2021-01-05                   96008                    Shasta    Shasta
5 2021-01-05                   95410                 Mendocino Mendocino
6 2021-01-05                   95527                   Trinity   Trinity
  vaccine_equity_metric_quartile                vem_source
1                              2 Healthy Places Index Score
2                              2    CDPH-Derived ZCTA Score
3                              2    CDPH-Derived ZCTA Score
4                             NA            No VEM Assigned
5                              3    CDPH-Derived ZCTA Score
6                              2    CDPH-Derived ZCTA Score
  age12_plus_population age5_plus_population tot_population
1                4840.7                 5057           5168
2                 135.0                  135            135
3                 513.9                  544            544
4                1125.3                 1164             NA
5                 926.3                  988            997
6                 476.6                  485            499
  persons_fully_vaccinated persons_partially_vaccinated
1                       NA                           NA
2                       NA                           NA
3                       NA                           NA
4                       NA                           NA
5                       NA                           NA
6                       NA                           NA
```

```
  percent_of_population_fully_vaccinated
1                                     NA
2                                     NA
3                                     NA
4                                     NA
5                                     NA
6                                     NA
  percent_of_population_partially_vaccinated
1                                         NA
2                                         NA
3                                         NA
4                                         NA
5                                         NA
6                                         NA
  percent_of_population_with_1_plus_dose booster_recip_count
1                                     NA                  NA
2                                     NA                  NA
3                                     NA                  NA
4                                     NA                  NA
5                                     NA                  NA
6                                     NA                  NA
  bivalent_dose_recip_count eligible_recipient_count
1                        NA                       0
2                        NA                       0
3                        NA                       2
4                        NA                       2
5                        NA                       0
6                        NA                       0
                                                                redacted
1 Information redacted in accordance with CA state privacy requirements
2 Information redacted in accordance with CA state privacy requirements
3 Information redacted in accordance with CA state privacy requirements
4 Information redacted in accordance with CA state privacy requirements
5 Information redacted in accordance with CA state privacy requirements
6 Information redacted in accordance with CA state privacy requirements
```

Q1

percent_of_population_fully vaccinated details the total number of people fully vaccinated

Q2

zip_code_tabulation_area details the Zip code tabulation area

Q3

The earliest date is 1/5/2021

Q4

The latest date is 2/28/2023

Using the skim() function for a quick overview of a new data set

```
skimr::skim(vax)
```

Table 1: Data summary

Name	vax
Number of rows	199332
Number of columns	18
_____	
Column type frequency:	
character	5
numeric	13
_____	
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
as_of_date	0	1	10	10	0	113	0
local_health_jurisdiction	0	1	0	15	565	62	0
county	0	1	0	15	565	59	0
vem_source	0	1	15	26	0	3	0
redacted	0	1	2	69	0	2	0

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
zip_code_tabulation_area	0	1.00	93665.11	1817.38	90001	92257.75	93658.50	95380.50	97635.0	
vaccine_equity_metric_quartile	9831	0.95	2.44	1.11	1	1.00	2.00	3.00	4.0	
age12_plus_population	0	1.00	18895.01	8993.87	0	13469.50	13685.00	21756.00	28556.7	
age5_plus_population	0	1.00	20875.22	11105.97	0	14605.00	15364.00	24877.00	101902.0	
tot_population	9718	0.95	23372.72	12628.51	12	21260.00	18714.00	28168.00	111165.0	
persons_fully_vaccinated	16525	0.92	13962.38	5054.09	11	9300.00	8566.00	23302.00	37566.0	
persons_partially_vaccinated	16525	0.92	1701.64	2030.18	11	1650.00	1196.00	2535.00	39913.0	
percent_of_population_fully_vaccinated	20825	0.90	0.57	0.25	0	0.42	0.60	0.74	1.0	
percent_of_population_partially_vaccinated	20825	0.90	0.08	0.09	0	0.05	0.06	0.08	1.0	
percent_of_population_with_1_plus_dose	21859	0.89	0.63	0.24	0	0.49	0.67	0.81	1.0	
booster_recip_count	72872	0.63	5837.31	7165.81	11	297.00	2748.00	9438.25	59553.0	
bivalent_dose_recip_count	158664	0.20	2924.93	3583.45	11	190.00	1418.00	4626.25	27458.0	
eligible_recipient_count	0	1.00	12801.84	4908.33	0	504.00	6338.00	21973.00	37234.0	

Q5

There are 13 numeric columns in this dataset.

Q6

```
sum(is.na(vax$persons_fully_vaccinated))
```

```
[1] 16525
```

There are 16525 NA values in the fully vaccinated column

Q7

```
round(sum(is.na(vax$persons_fully_vaccinated))/nrow(vax), digits = 3)*100
```

```
[1] 8.3
```

8.3% of the column for fully vaccinated data is missing

Q8

The data is missing probably because it wasn't reported in these specific zip codes for these dates or was redacted due to privacy laws due to being federal land or not state territory

```
library(lubridate)
```

```
Attaching package: 'lubridate'

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

    date, intersect, setdiff, union
```

```
today()
```

```
[1] "2023-03-07"
```

```
vax$as_of_date <- ymd(vax$as_of_date)
today() - vax$as_of_date[1]
```

```
Time difference of 791 days
```

Q9

7 days have passed since the last update of the dataset

```
today() - vax$as_of_date[nrow(vax)]
```

```
Time difference of 7 days
```

Q10

```
length(unique(vax$as_of_date))
```

```
[1] 113
```

There are 113 unique dates

```
library(zipcodeR)
geocode_zip('92037')
```

```
# A tibble: 1 x 3
  zipcode   lat   lng
  <chr>   <dbl> <dbl>
1 92037    32.8 -117.
```

```
zip_distance('92037','91108')
```

```
  zipcode_a zipcode_b distance
1     92037     91108   105.36
```

```
reverse_zipcode(c('92037', "92019"))
```

```
# A tibble: 2 x 24
  zipcode zipcode_~1 major~2 post_~3 common_c~4 county state   lat   lng timez~5
  <chr>   <chr>      <chr>   <chr>       <blob> <chr>  <chr> <dbl> <dbl> <chr>
1 92019   Standard   El Caj~ El Caj~ <raw 20 B> San D~ CA     32.8 -117. Pacific
2 92037   Standard   La Jol~ La Jol~ <raw 20 B> San D~ CA     32.8 -117. Pacific
# ... with 14 more variables: radius_in_miles <dbl>, area_code_list <blob>,
#   population <int>, population_density <dbl>, land_area_in_sqmi <dbl>,
#   water_area_in_sqmi <dbl>, housing_units <int>,
#   occupied_housing_units <int>, median_home_value <int>,
#   median_household_income <int>, bounds_west <dbl>, bounds_east <dbl>,
#   bounds_north <dbl>, bounds_south <dbl>, and abbreviated variable names
#   1: zipcode_type, 2: major_city, 3: post_office_city, ...
```

```
sd <- vax[vax$county =="San Diego",]
```

```
library(dplyr)
```

```
Attaching package: 'dplyr'

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

    filter, lag

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

    intersect, setdiff, setequal, union
```

```
sd <- filter(vax, county == "San Diego")
nrow(sd)
```

```
[1] 12091
```

```
sd.10 <- filter(vax, county =="San Diego" & age5_plus_population > 10000)
```

Q11

```
length(unique(sd))
```

```
[1] 18
```

There are 18 unique zip codes for San Diego

Q12

```
sd$zip_code_tabulation_area[which.max(sd$age12_plus_population)]
```

```
[1] 92154
```

Q13

```
recentsd <- filter(vax, as_of_date == "2023-02-28")
mean(recentsd$percent_of_population_fully_vaccinated, na.rm = TRUE)*100
```

```
[1] 69.15199
```

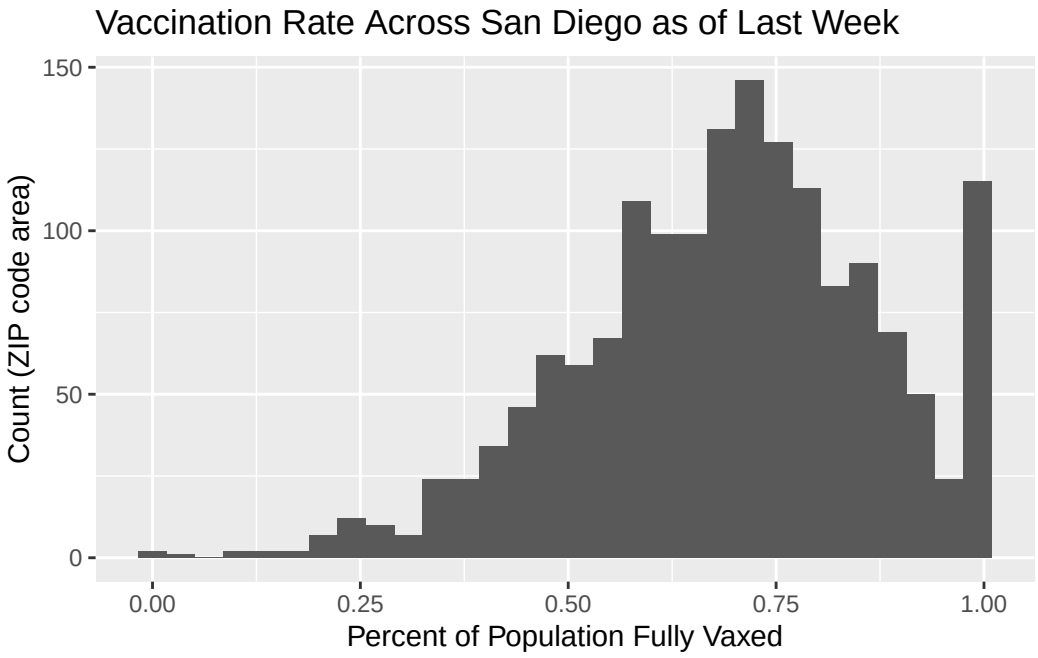
69% is the overall average of the percent of population fully vaccinated based on data we currently have in SD county as of 2023-02-28

Q14

```
library(ggplot2)
ggplot(recentsd, aes(x=percent_of_population_fully_vaccinated)) + geom_histogram() + labs
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
Warning: Removed 148 rows containing non-finite values (`stat_bin()`).
```



Focus on UCSD/La Jolla

```
ucsd <- filter(sd, zip_code_tabulation_area=="92037")
ucsd[1,]$age5_plus_population
```

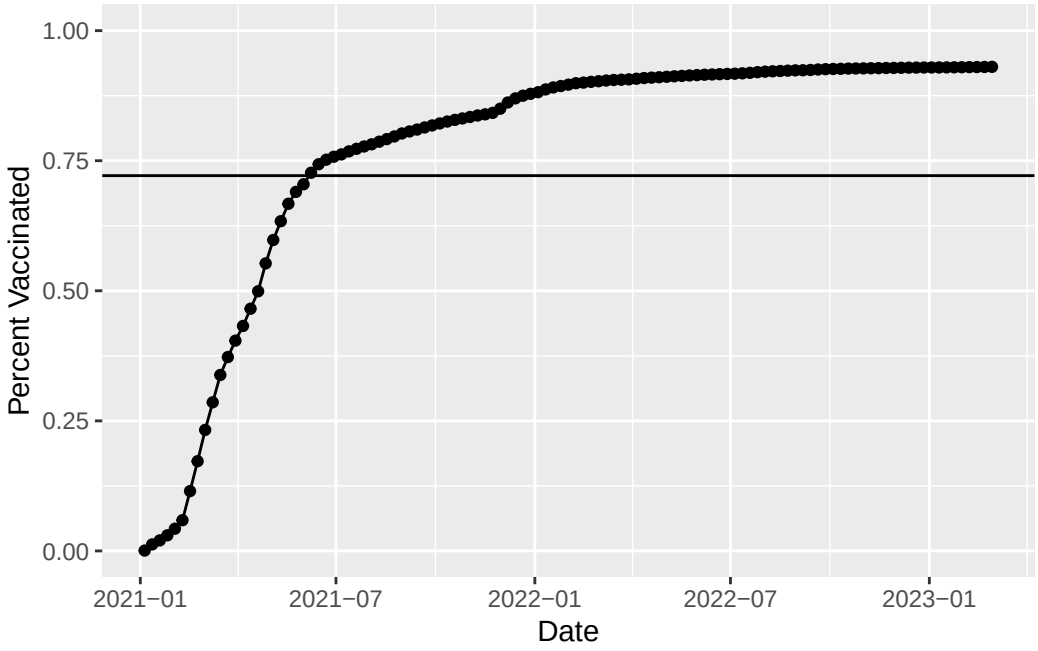
```
[1] 36144
```

Q15

```
ucsdgraph <- ggplot(ucsd) + aes(x = as_of_date, y = percent_of_population_fully_vaccinated
```

Q16

```
vax.36 <- filter(vax, age5_plus_population > 36144 & as_of_date == "2023-02-28")
meanline <- mean(vax.36$percent_of_population_fully_vaccinated)
ucsdgraph + geom_hline(aes(yintercept=meanline))
```



Q17

```
summary(vax.36$percent_of_population_fully_vaccinated)
```

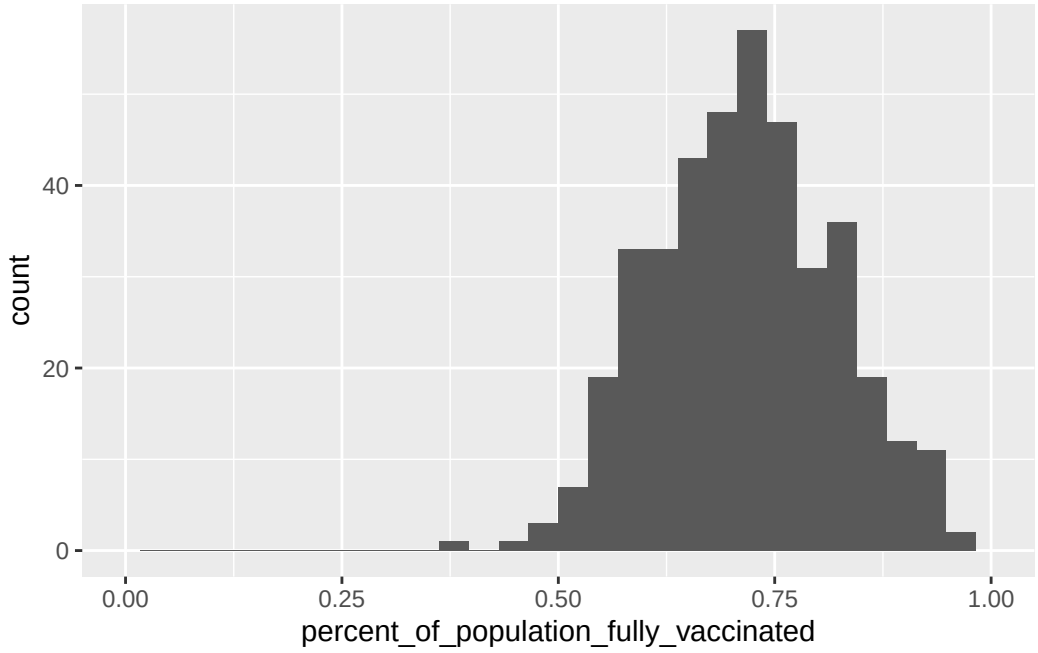
```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
 0.3804  0.6457  0.7181  0.7213  0.7907  1.0000 
```

Q18

```
ggplot(vax.36,aes(percent_of_population_fully_vaccinated)) + geom_histogram() + xlim(0,1)
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
Warning: Removed 2 rows containing missing values (`geom_bar()`).
```



Q19

```
vax %>% filter(as_of_date == "2023-02-28") %>% filter(zip_code_tabulation_area=="92109") %
```

```
  percent_of_population_fully_vaccinated
1                               0.694572
```

```
vax %>% filter(as_of_date == "2023-02-28") %>% filter(zip_code_tabulation_area=="92040") %
```

```
  percent_of_population_fully_vaccinated
1                               0.550296
```

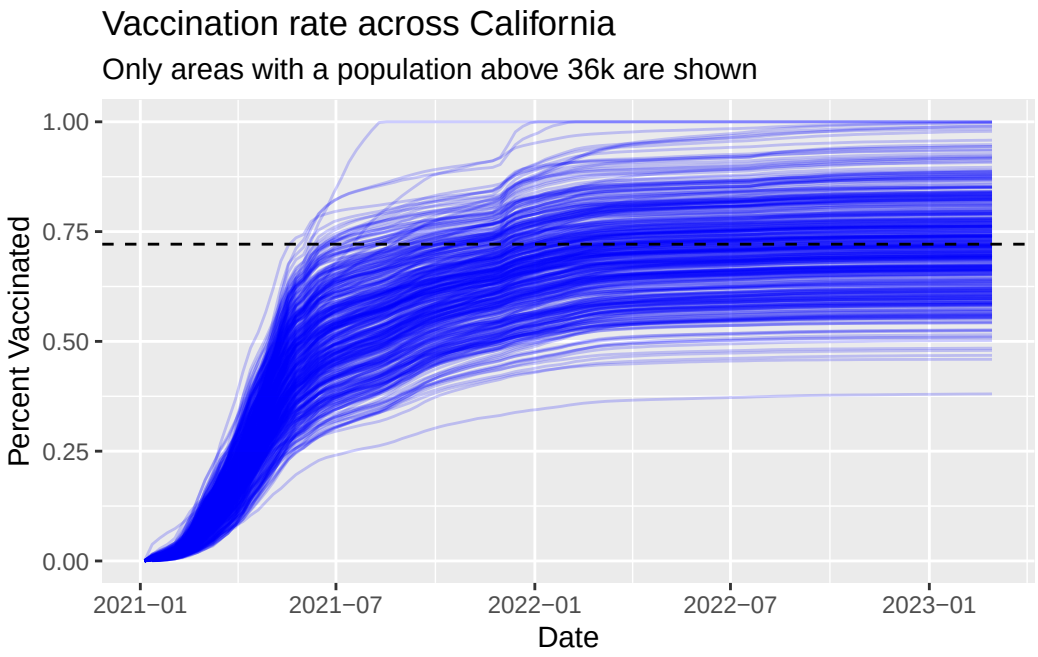
Both 92109 and 92040 ZIP code areas are below the average value I calculated for La Jolla vaccination rate.

Q20

```
vax.36.all <- filter(vax, age5_plus_population > 36144)


ggplot(vax.36.all) +
  aes(x = as_of_date, y = percent_of_population_fully_vaccinated,
      percent_of_population_fully_vaccinated,
      group=zip_code_tabulation_area) +
  geom_line(alpha=0.2, color="blue") +
  ylim(0,1) +
  labs(x="Date", y="Percent Vaccinated",
       title="Vaccination rate across California",
       subtitle="Only areas with a population above 36k are shown") +
  geom_hline(yintercept = meanline, linetype=2)
```

```
Warning: Removed 183 rows containing missing values (`geom_line()`).
```


Vaccination rate across California
Only areas with a population above 36k are shown
Percent Vaccinated
1.00
0.75
0.50
0.25
0.00
2021−01
2021−07
2022−01
2022−07
2023−01
Date