

Vaccination Rates LA County

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Step 1: Importing and Fixing the Data

Variable name on R vs. Variable name on Excel:

X12..with.1..Dose = 12+ with 1+ Dose

Population..12.. = Population (12+)

X12..Pop..Vaccinated.... = 12+ Pop. Vaccinated (%)

```
la_c <- read.csv("LA-County-COVID-19-Vaccine-Dashboard-Community-2021-10-24.csv")
head(la_c) # Looks messy, for R standards
```

```
##      City.Community X12..with.1..Dose Population..12..
## 1 City of Agoura Hills      15,212      18,920
## 2 City of Alhambra      64,216      76,362
## 3 City of Arcadia      45,160      53,504
## 4 City of Artesia      12,420      15,043
## 5 City of Avalon        760        3,266
## 6 City of Azusa      30,563      43,954
## X12..Pop..Vaccinated....
## 1      80.4%
## 2      84.1%
## 3      84.4%
## 4      82.6%
## 5      23.3%
## 6      69.5%
```

```
dim(la_c) # Dimeensions of our data frame
```

```
## [1] 345  4
```

```
la_c$City.Community <- as.character(la_c$City.Community)
# For the next 3 lines, we'll change the class of
# the last 3 variables to numeric to make things easier.
la_c$X12..with.1..Dose <- as.numeric(gsub("[\\,]", "", la_c$X12..with.1..Dose))
```

```
## Warning: NAs introduced by coercion
```

```
la_c$Population..12.. <- as.numeric(gsub("[\\,]", "", la_c$Population..12..))

## Warning: NAs introduced by coercion

la_c$X12..Pop..Vaccinated.... <- as.numeric(gsub("[\\%,]", "", la_c$X12..Pop..Vaccinated....))

## Warning: NAs introduced by coercion

head(la_c) # Looks much better now
```

```
##      City.Community X12..with.1..Dose Population..12..
## 1 City of Agoura Hills      15212      18920
## 2 City of Alhambra      64216      76362
## 3 City of Arcadia      45160      53504
## 4 City of Artesia      12420      15043
## 5 City of Avalon      760      3266
## 6 City of Azusa      30563      43954
## X12..Pop..Vaccinated....
## 1      80.4
## 2      84.1
## 3      84.4
## 4      82.6
## 5      23.3
## 6      69.5
```

Step 2: Cleaning the Data

```
summary(la_c)

## City.Community      X12..with.1..Dose Population..12.. X12..Pop..Vaccinated....
## Length:345      Min.      : 10      Min.      : 11      Min.      :17.60
## Class :character 1st Qu.: 2659      1st Qu.: 3233      1st Qu.:70.58
## Mode :character  Median : 12120      Median : 13422      Median :76.30
##      Mean      : 20641      Mean      : 25965      Mean      :74.32
##      3rd Qu.: 28727      3rd Qu.: 35430      3rd Qu.:81.40
##      Max.      :300966      Max.      :404580      Max.      :99.50
##      NA's      :21      NA's      :5      NA's      :21
```

```
# Looks about right considering this is LA County,
# however, those NA's need to be taken care of.
nr <- which(is.na(la_c$X12..with.1..Dose) == TRUE) # Checks index of NA's
nr
```

```
## [1] 36 82 100 115 152 175 177 219 227 238 241 250 265 268 298 308 314 325 330
## [20] 334 343
```

```
which(is.na(la_c$Population..12..) == TRUE)
```

```
## [1] 227 238 268 325 330
```

```
which(is.na(la_c$X12..Pop..Vaccinated....) == TRUE)
```

```
## [1] 36 82 100 115 152 175 177 219 227 238 241 250 265 268 298 308 314 325 330
## [20] 334 343
```

```
# Appears that all our NA's happen on the same observations...
```

```
la_c2 <- la_c[-nr, ]
```

```
summary(la_c2) # No NA's; success
```

```
## City.Community      X12..with.1..Dose Population..12.. X12..Pop..Vaccinated....
## Length:324          Min.      :    10      Min.      :    20      Min.      :17.60
## Class :character     1st Qu.: 2659      1st Qu.: 3649      1st Qu.:70.58
## Mode  :character     Median : 12120     Median : 15070     Median :76.30
##                      Mean      : 20641     Mean      : 26944     Mean      :74.32
##                      3rd Qu.: 28727     3rd Qu.: 36333     3rd Qu.:81.40
##                      Max.      :300966     Max.      :404580     Max.      :99.50
```

```
# Now we check for duplicate observations
```

```
which(duplicated(la_c2) == TRUE) # No duplicates
```

```
## integer(0)
```

```
# We are done with cleaning the data
```

Step 3: Visualizations and Analysis

```
la_c3 <- la_c2
```

```
# Let's compare the population to the percent of that
```

```
# population that vaccinated.
```

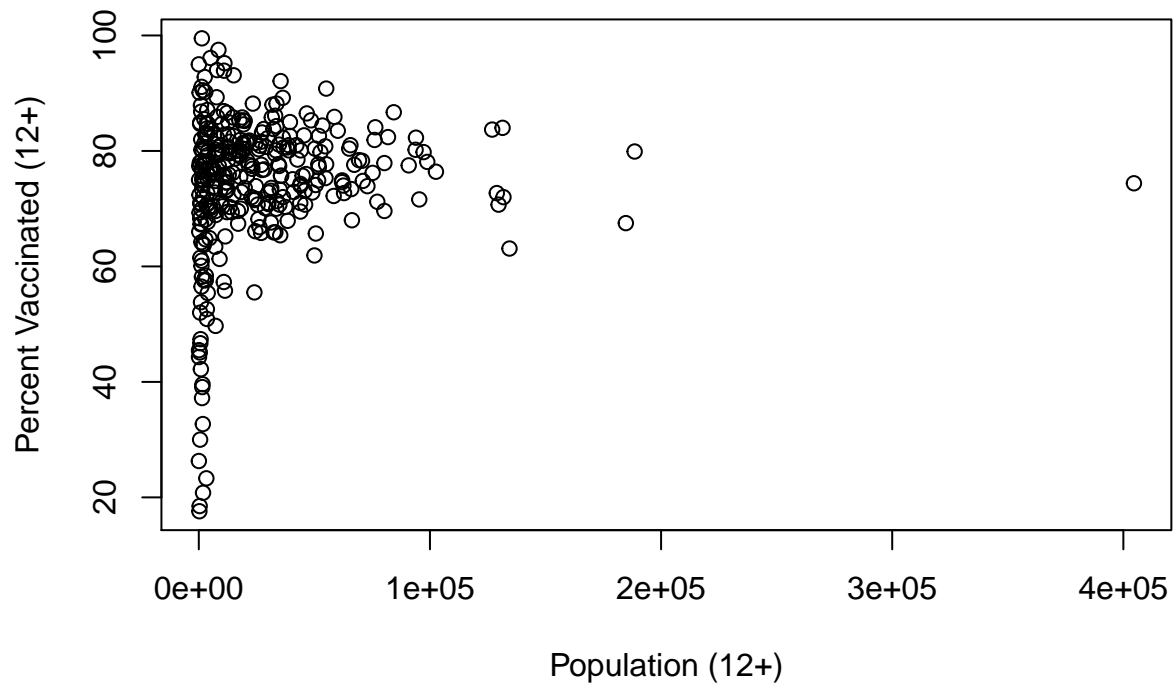
```
plot(la_c3$X12..Pop..Vaccinated.... ~ la_c3$Population..12..,
```

```
      xlab = "Population (12+)",
```

```
      ylab = "Percent Vaccinated (12+)",
```

```
      main = "Total Population vs Percent Vaccinated (Age 12+)" # Doesn't show a pattern...
```

Total Population vs Percent Vaccinated (Age 12+)

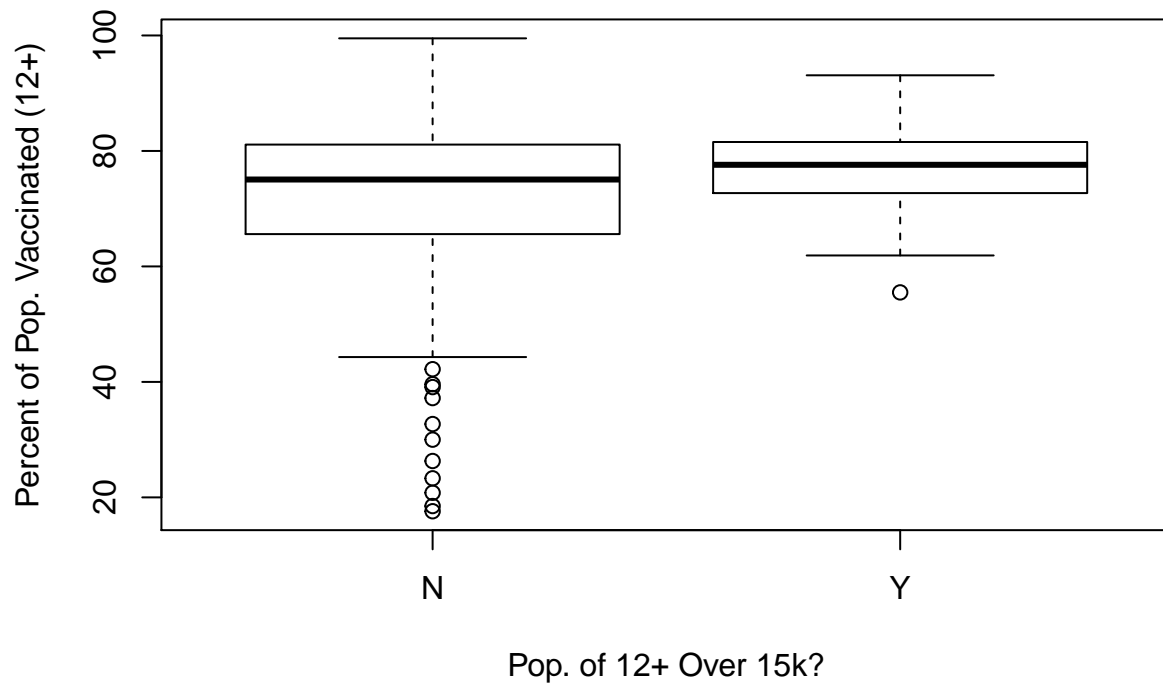


```
# Let's see if the more populated areas of
# LA County have a higher vaccination rate.
# We'll use a population of 15k as our arbitrary cutoff point
# between sparsely populated and highly populated.
tp <- which(la_c3$Population..12.. >= 15000)
over10k <- rep("N", 324)
over10k[tp] <- "Y"
la_c3 <- cbind(la_c3, over10k)
table(la_c3$over10k) # Amount of areas over/under pop. of 15k
```

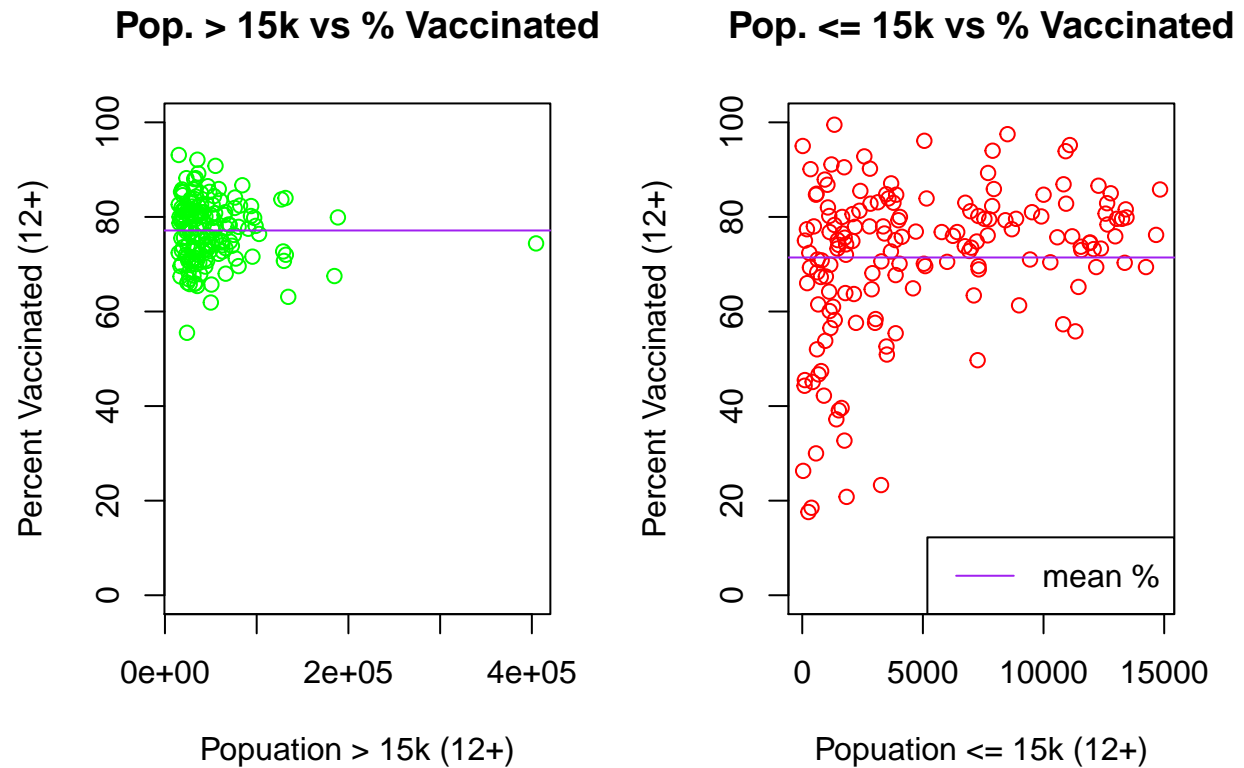
```
##
##    N    Y
## 160 164
```

```
plot(la_c3$over10k, la_c3$X12..Pop..Vaccinated....,
     xlab = "Pop. of 12+ Over 15k?",
     ylab = "Percent of Pop. Vaccinated (12+)",
     main = "Higher Population vs Lower Population Vax Rates")
```

Higher Population vs Lower Population Vax Rates



```
par(mfrow = c(1, 2))
plot(la_c3$X12..Pop..Vaccinated....[tp] ~ la_c3$Population..12..[tp],
     ylim = c(0, 100), xlab = "Popuation > 15k (12+)",
     ylab = "Percent Vaccinated (12+)", col = "green",
     main = "Pop. > 15k vs % Vaccinated")
abline(h = mean(la_c3$X12..Pop..Vaccinated....[tp]), col = "purple")
plot(la_c3$X12..Pop..Vaccinated....[-tp] ~ la_c3$Population..12..[-tp],
     ylim = c(0, 100), xlab = "Popuation <= 15k (12+)",
     ylab = "Percent Vaccinated (12+)", col = "red",
     main = "Pop. <= 15k vs % Vaccinated")
abline(h = mean(la_c3$X12..Pop..Vaccinated....[-tp]), col = "purple")
legend("bottomright", legend = c("mean %"), col = c("purple"), lty = 1)
```



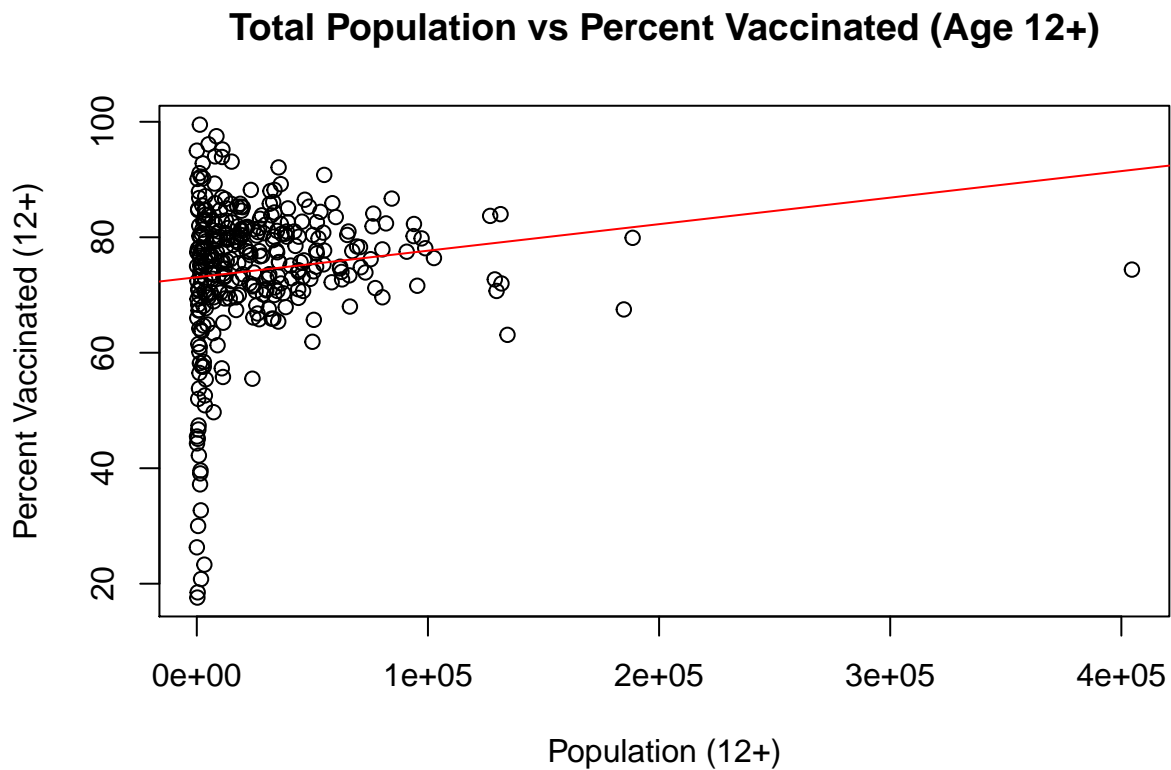
We do see that the more populated areas have a higher vaccination rate on average as we can see from the scatterplot where the higher pop. areas have a high concentration between 60% and 90%, whereas the lower pop. areas seems to show a more varied spread of the percentage vaccinated and a slightly lower average in general.

```
# Now let's a try a linear regression model
la_m <- lm(la_c3$X12..Pop..Vaccinated.... ~ la_c3$Population..12..)
summary(la_m)
```

```
##
## Call:
## lm(formula = la_c3$X12..Pop..Vaccinated.... ~ la_c3$Population..12..)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -55.490  -3.839   2.033   7.132  26.360
##
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      7.308e+01  8.511e-01  85.867   <2e-16 ***
## la_c3$Population..12.. 4.595e-05  1.870e-05   2.457   0.0146 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.35 on 322 degrees of freedom
## Multiple R-squared:  0.0184, Adjusted R-squared:  0.01535
## F-statistic: 6.035 on 1 and 322 DF,  p-value: 0.01455
```

```
plot(la_c3$X12..Pop..Vaccinated.... ~ la_c3$Population..12..,
     xlab = "Population (12+)",
     ylab = "Percent Vaccinated (12+)",
     main = "Total Population vs Percent Vaccinated (Age 12+)")
abline(la_m, col = "red")
```



While the summary of the model seems to be promising with how it shows a positive trend in vax rate as pop. increases, adding a regression line to the first scatterplot doesn't really work, although it could probably be useful to predict the vaccination rates of other districts not listed here. Unfortunately, this data set is fairly barebones, so we can't really do much else.

I'd love to try and add political alignments for each districts, but unfortunately, there is no current data set with such info and if it does, it groups all unincorporated regions into one.

For now, we do see that higher population areas do make a difference in vaccination rates, at least in the LA County.