

Final Report

due November 16, 2021 by 11:59 PM

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11/16/21

#Load Data

Your original .Renviron will be backed up and stored in your R HOME directory if needed.

Your API key has been stored in your .Renviron and can be accessed by Sys.getenv("CENSUS_API_KEY").

To use now, restart R or run `readRenviron("~/Renviron")`

[1] "abc8289fa2ba274ced76d97c7f8ee31666a2c931"

#v18 <- load_variables(2018, "acs5", cache = TRUE)

#View(v18)

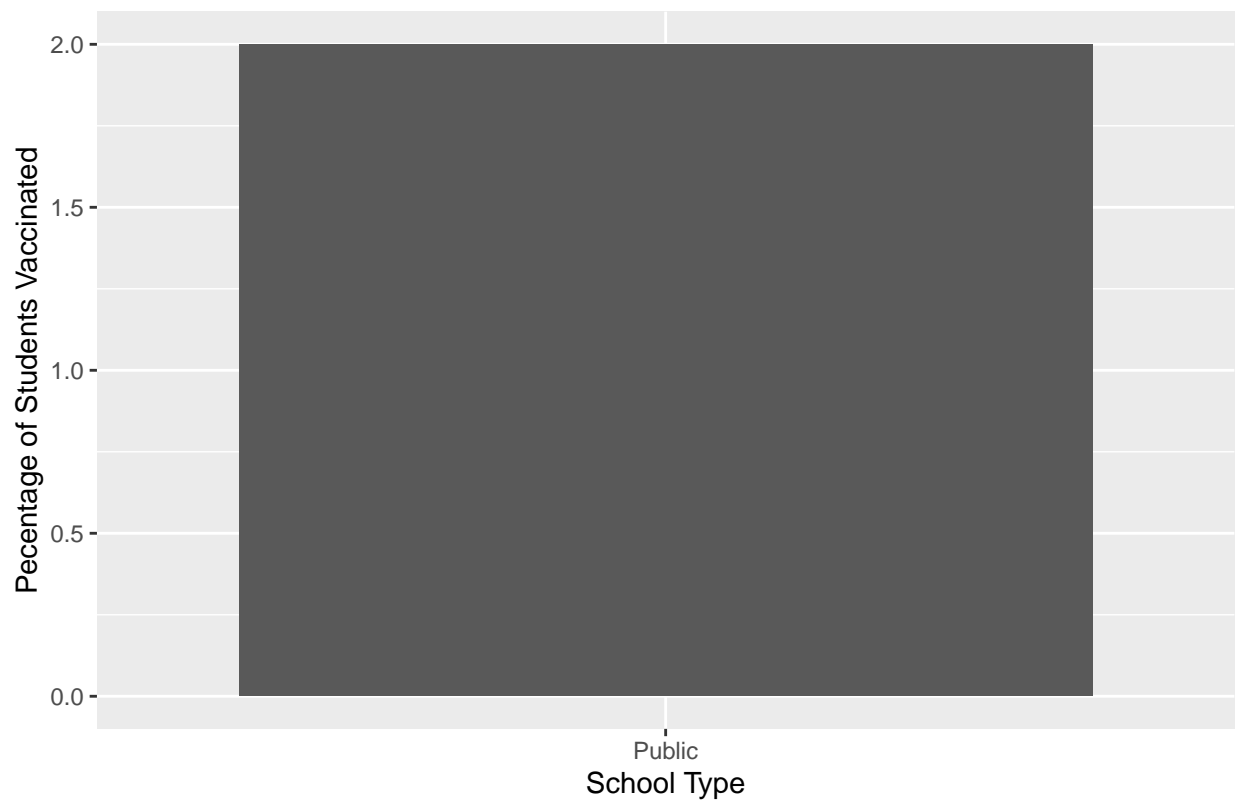
#Research Question

How do measles vaccination rates vary across the country and demographics in schools?

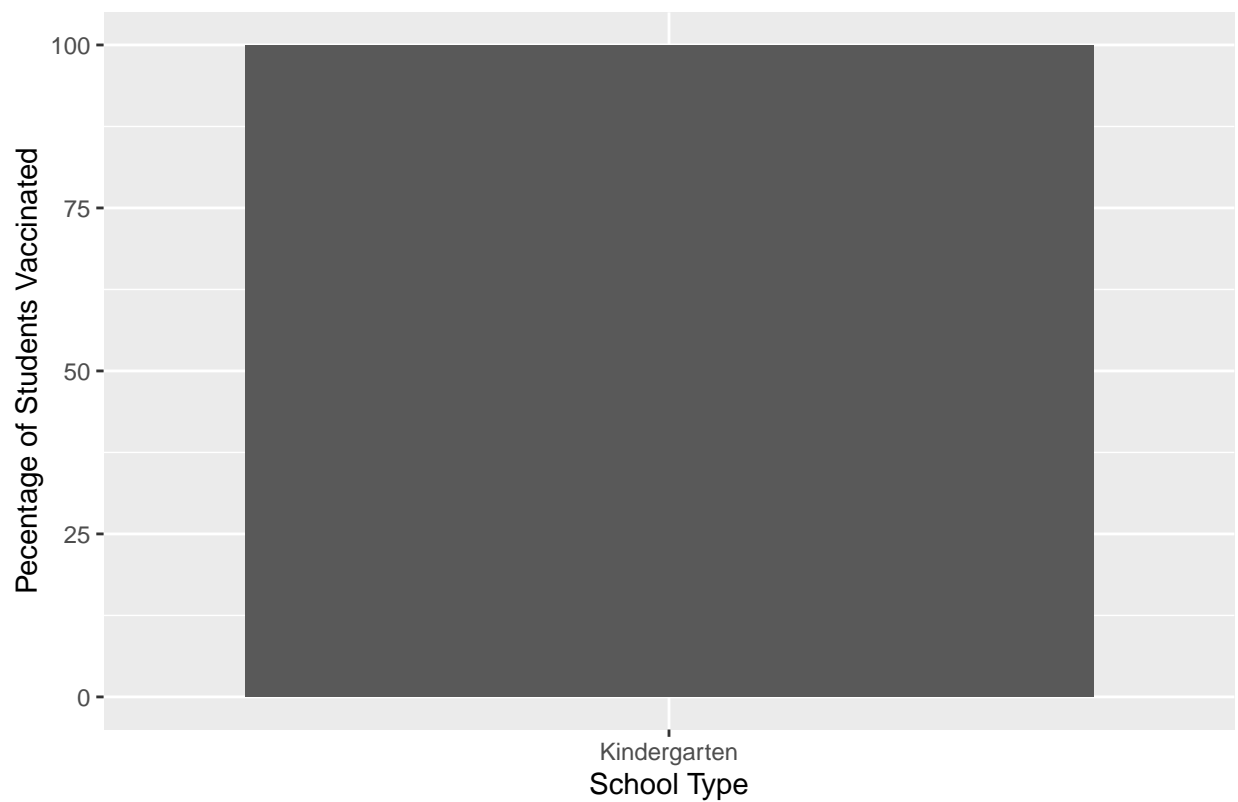
realrate vaccination status vs. state, realrate vaccination status vs. type of school, each type of exemption (personal, religious, and medical) vs. state exemption vs. type of school. To analyze vaccination and exemption rates by states, we will use spatial data to show the change in these rates across the country. Then, we can use two-sample t-tests to test for significance of vaccination and exemption rates between different types of schools. If there are significantly lower vaccination rates in private schools vs. other types of schools, this will support our main hypothesis.

Data Wrangling

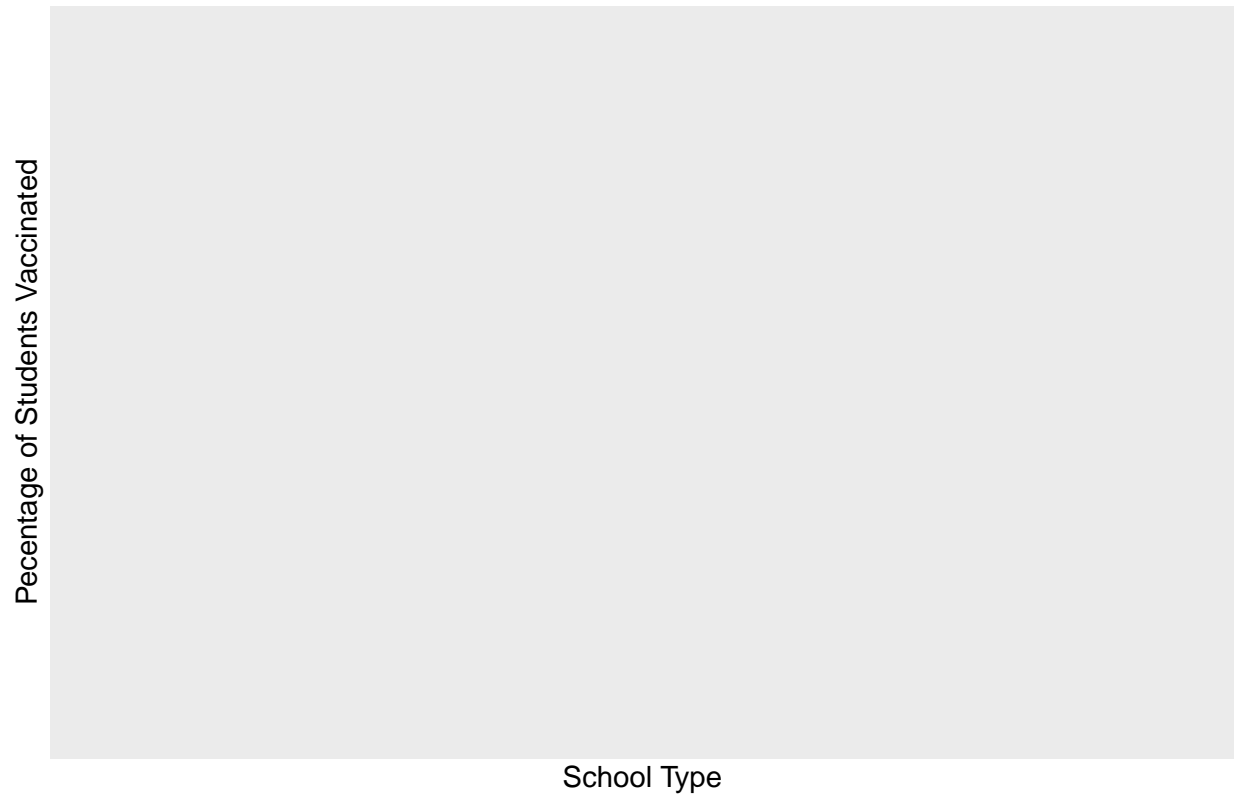
Vaccination Rates Across Different School Types



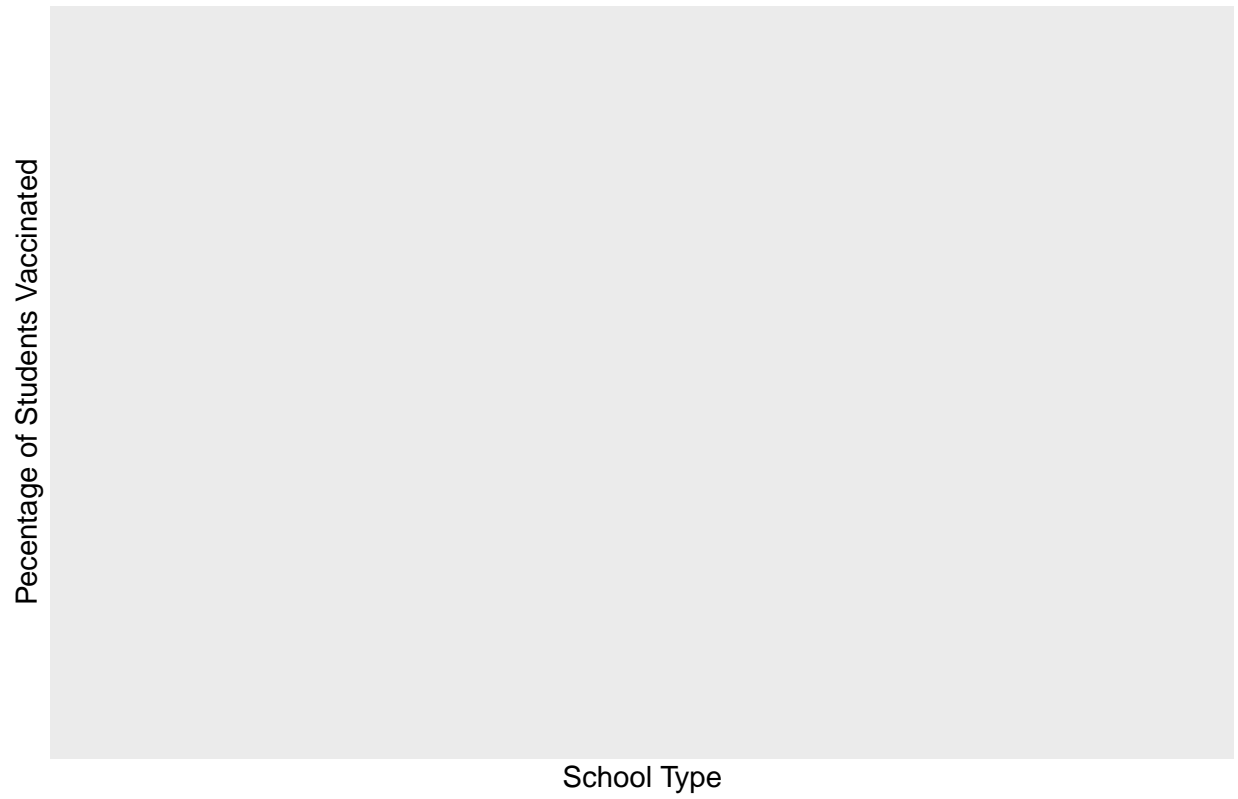
Vaccination Rates Across Different School Types



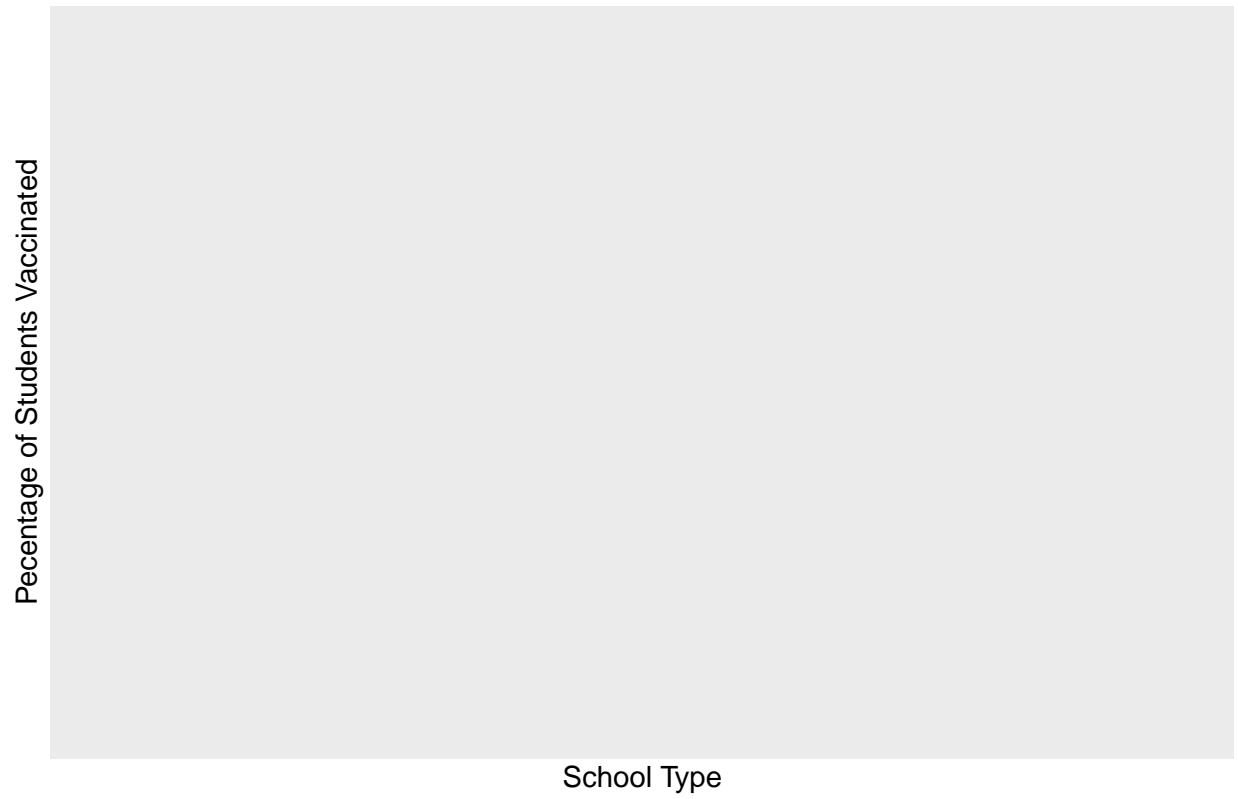
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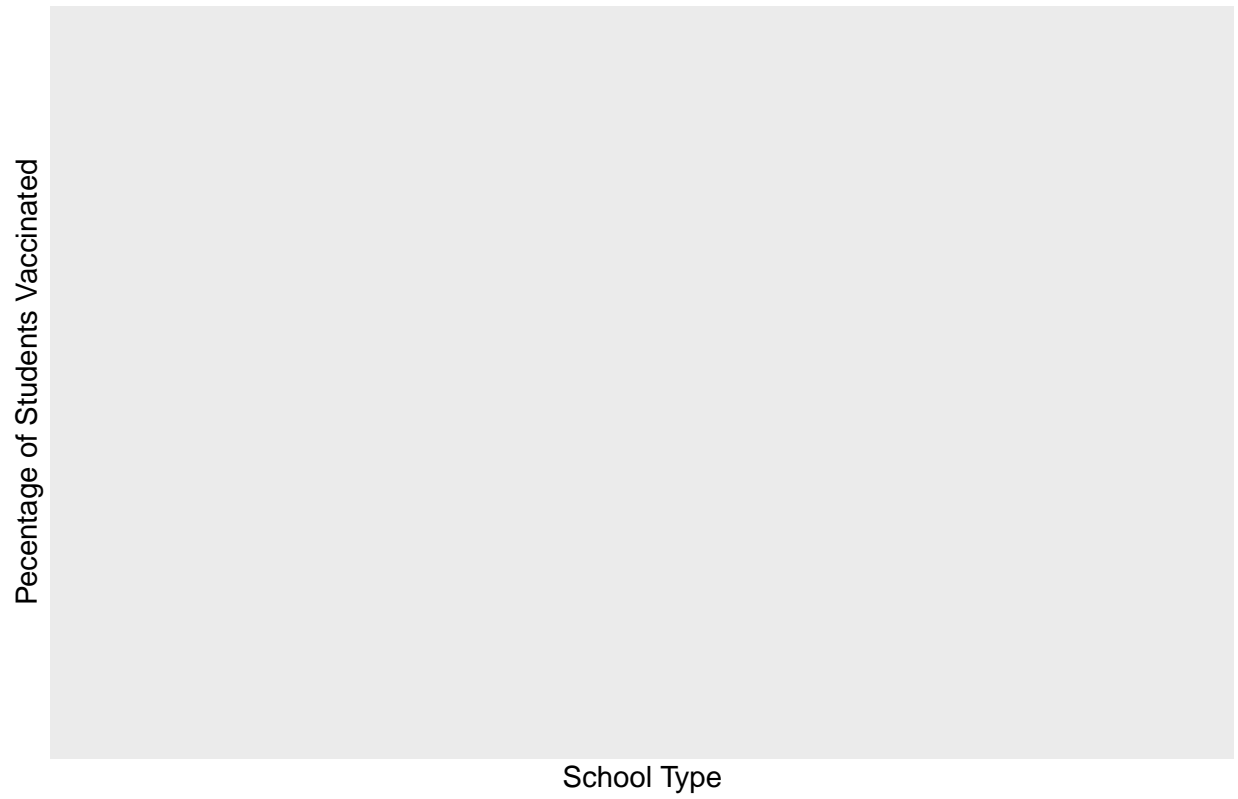
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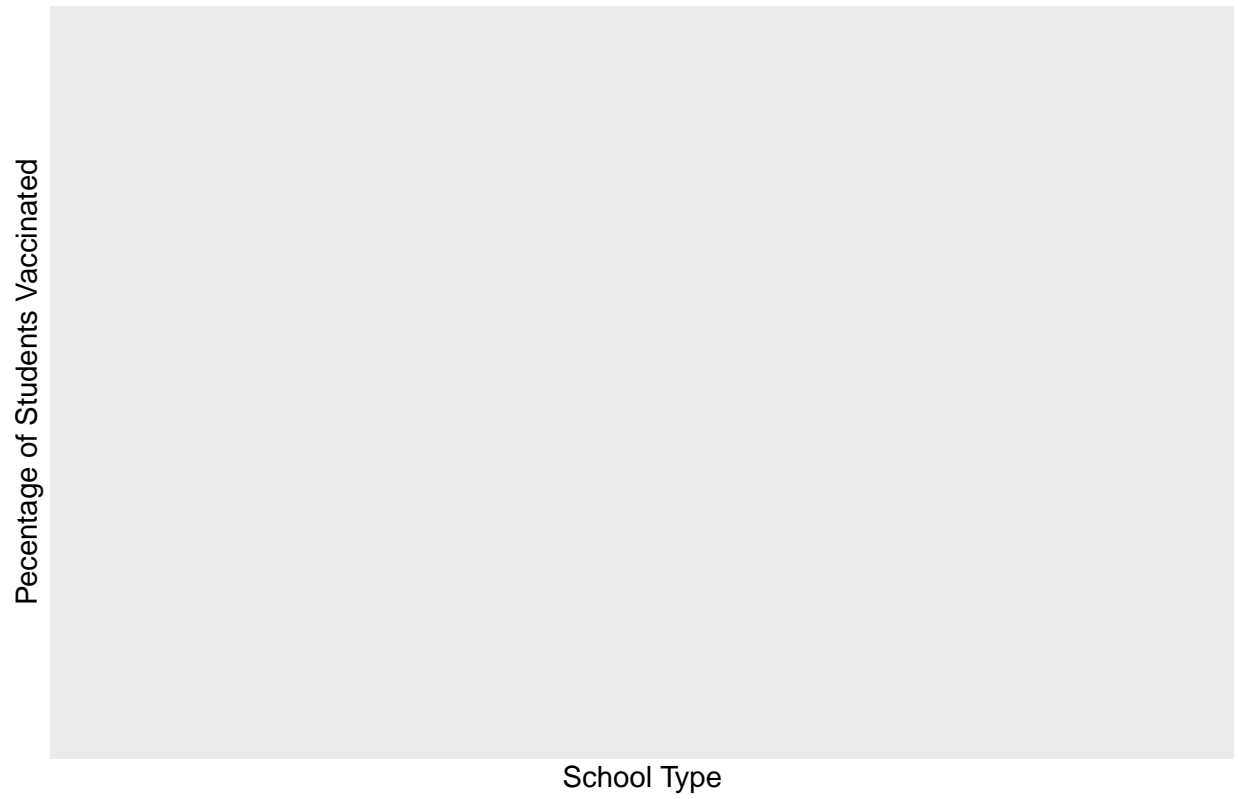
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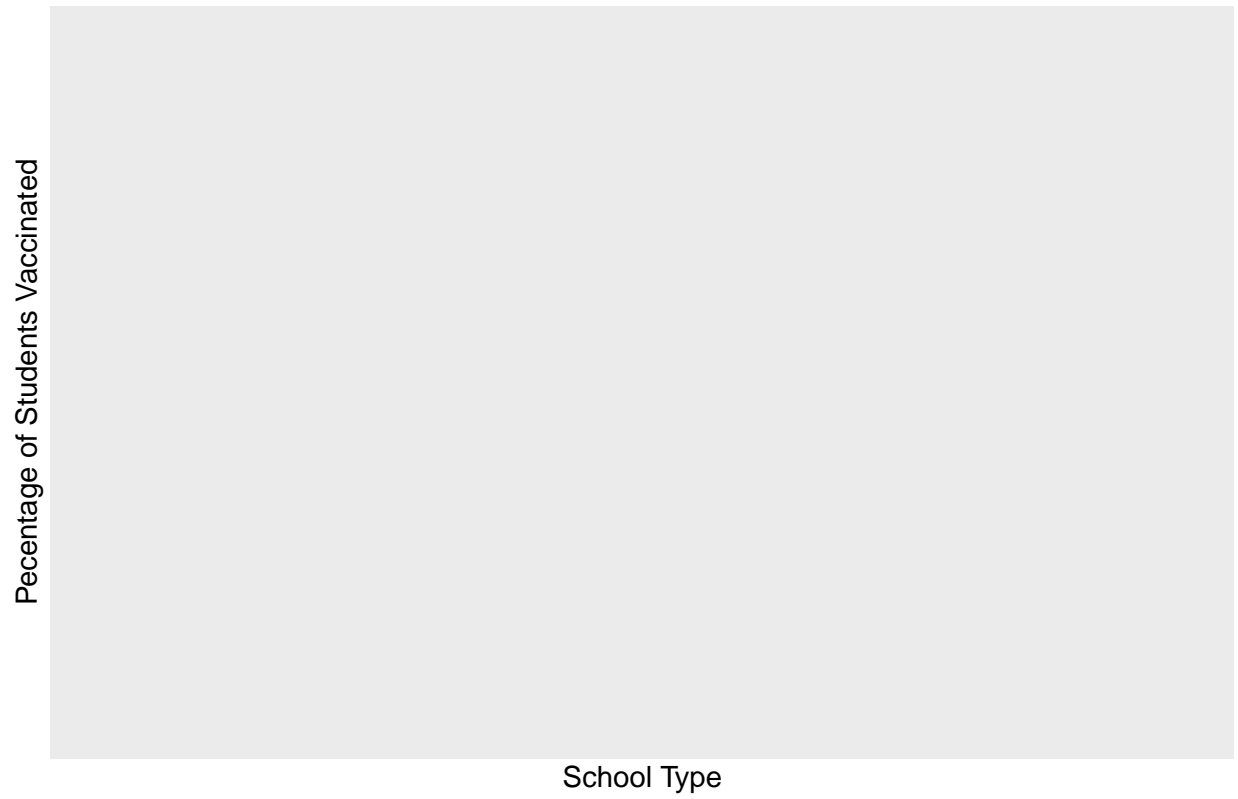
Vaccination Rates Across Different School Types

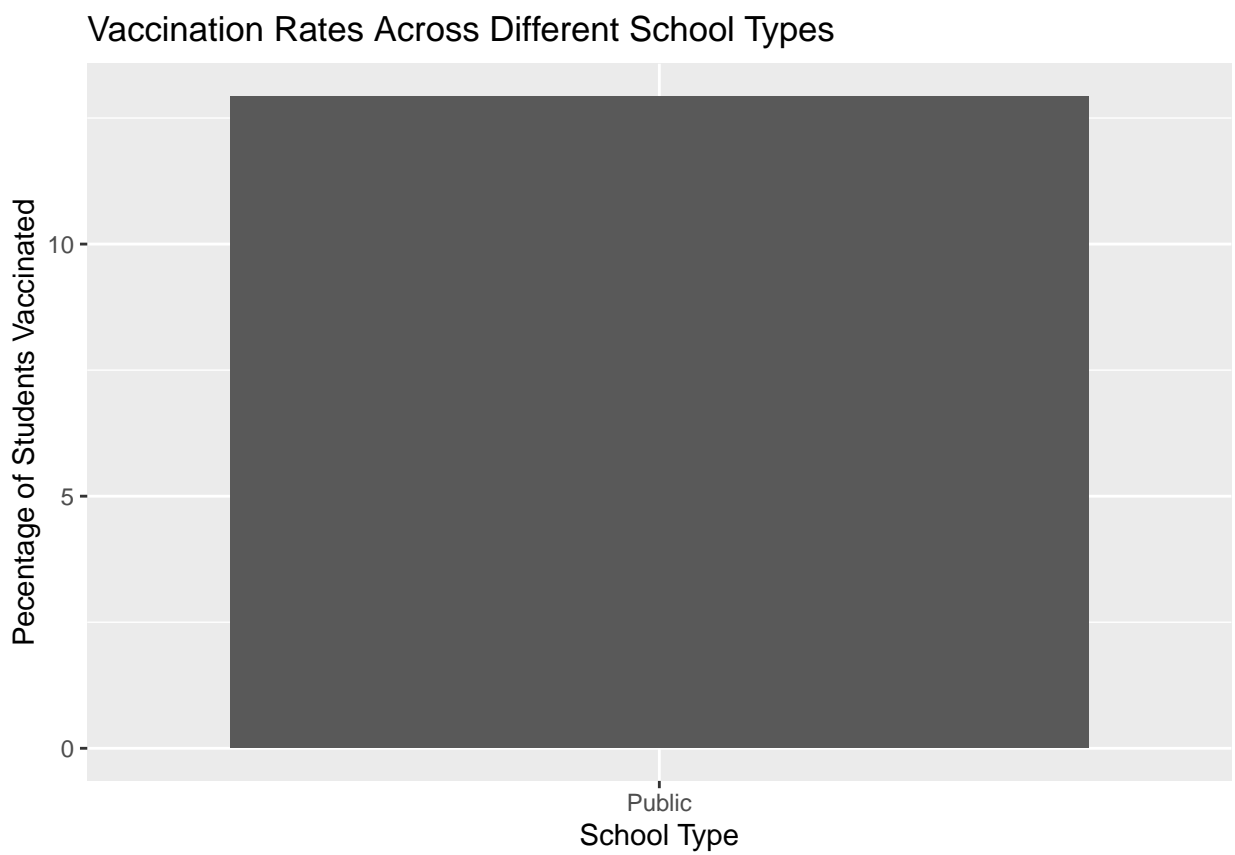


Vaccination Rates Across Different School Types

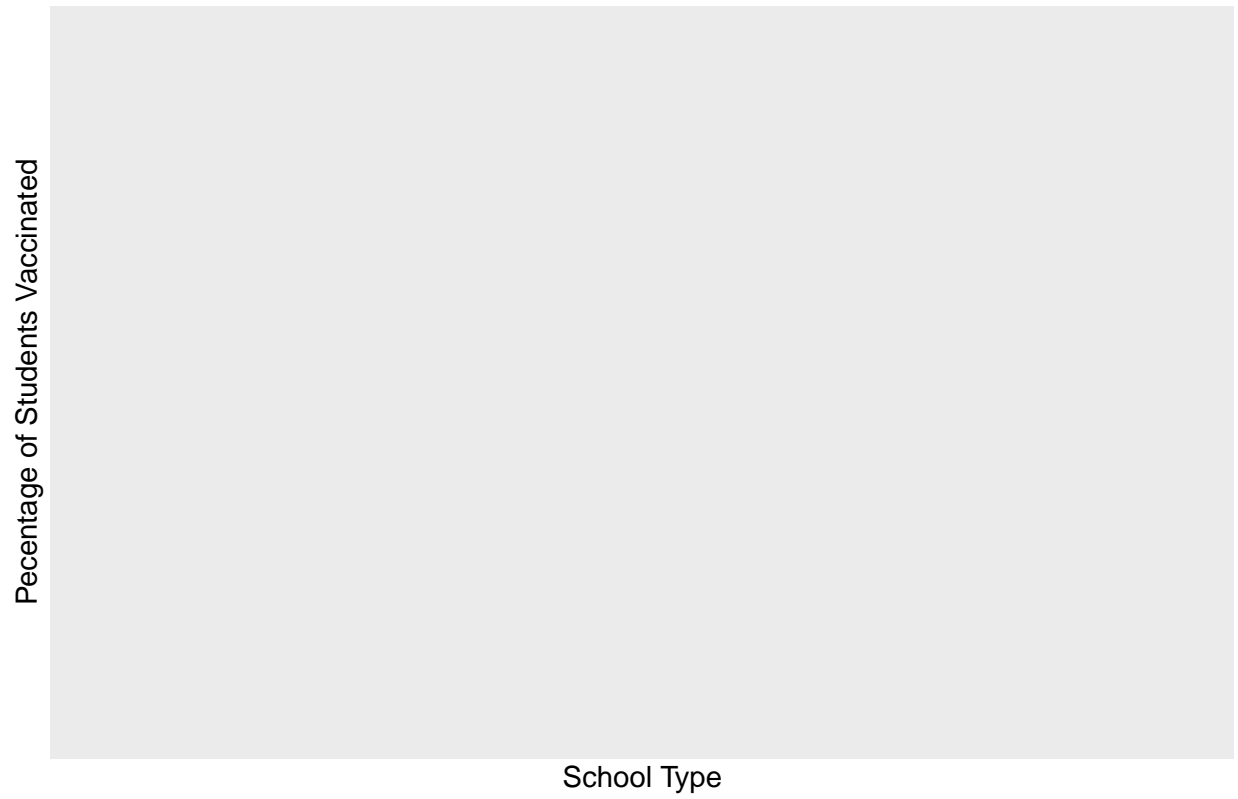


Vaccination Rates Across Different School Types

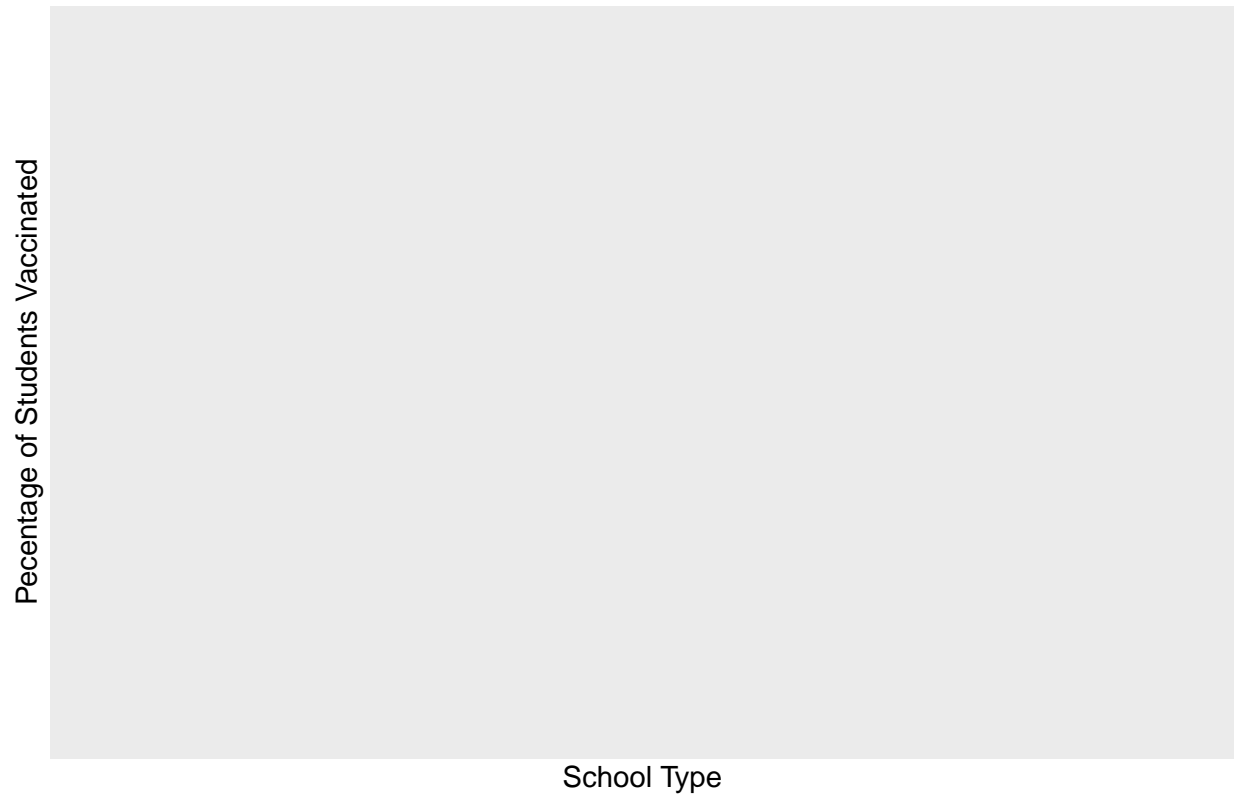




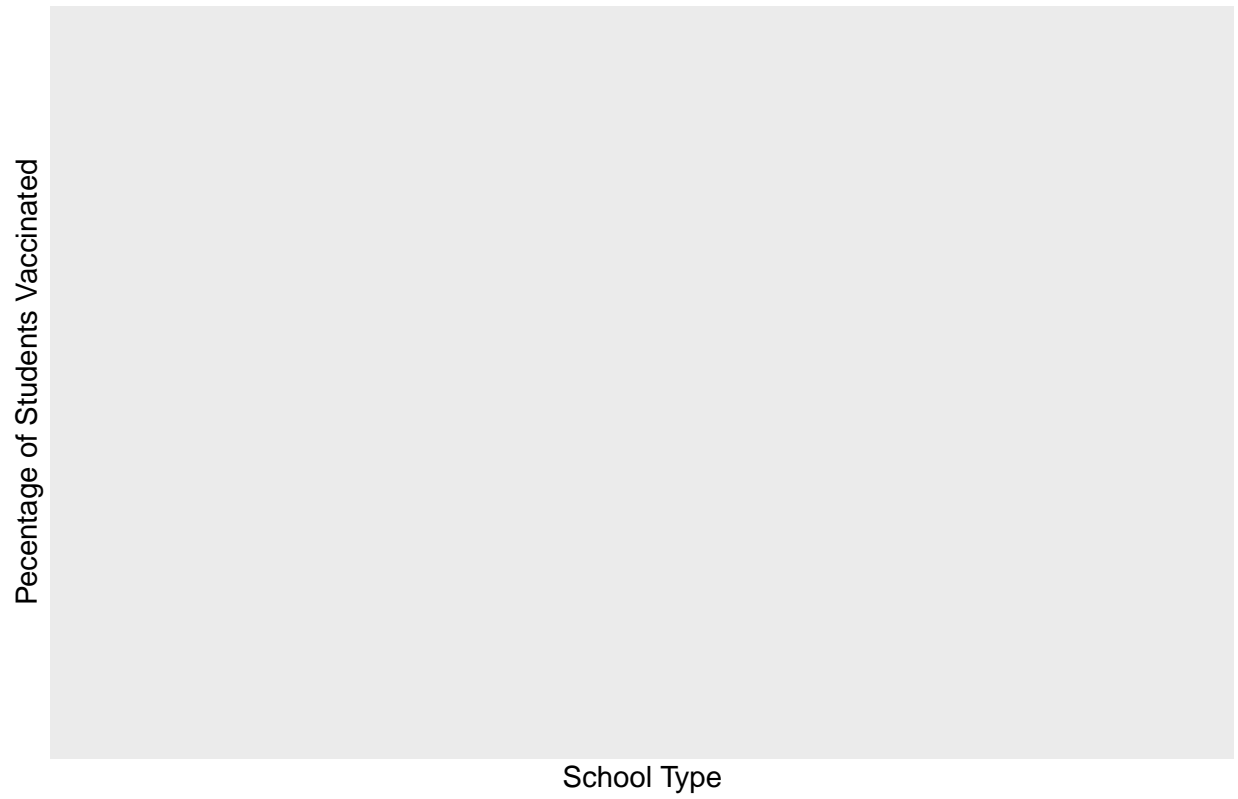
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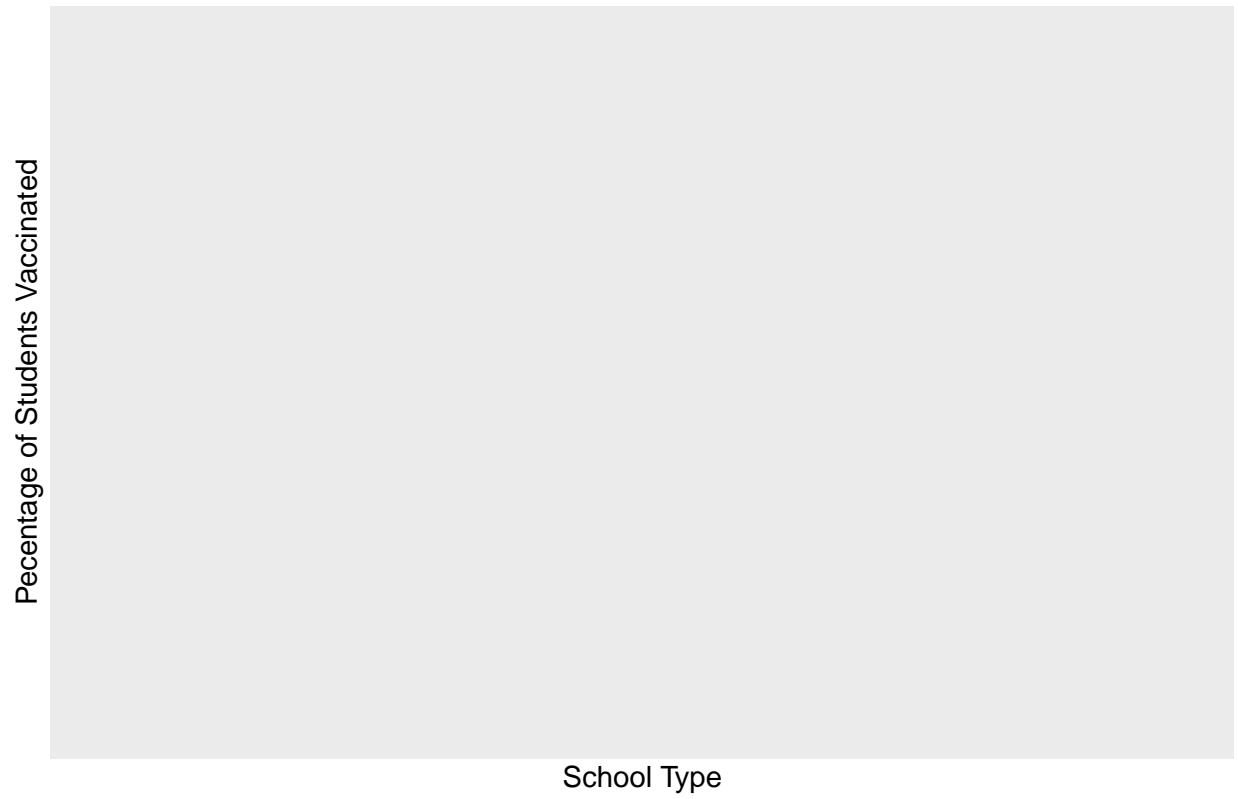
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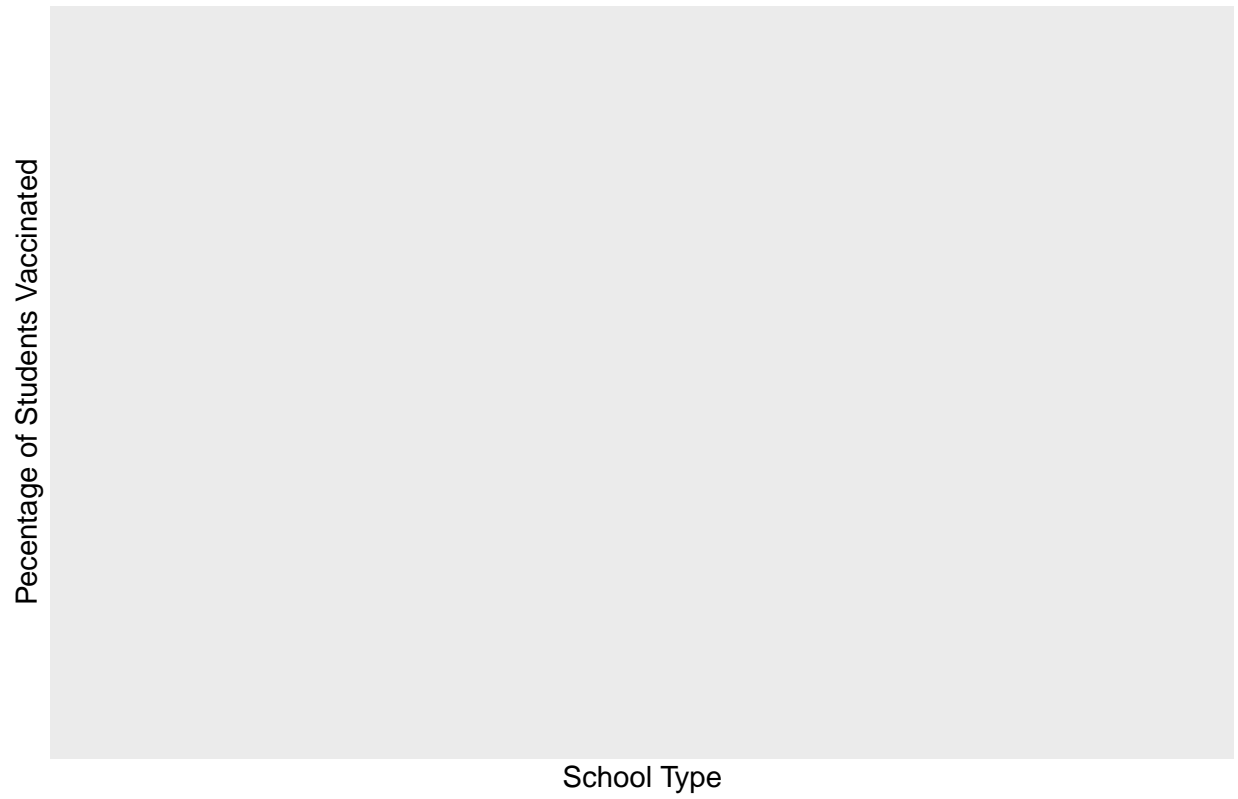
Vaccination Rates Across Different School Types



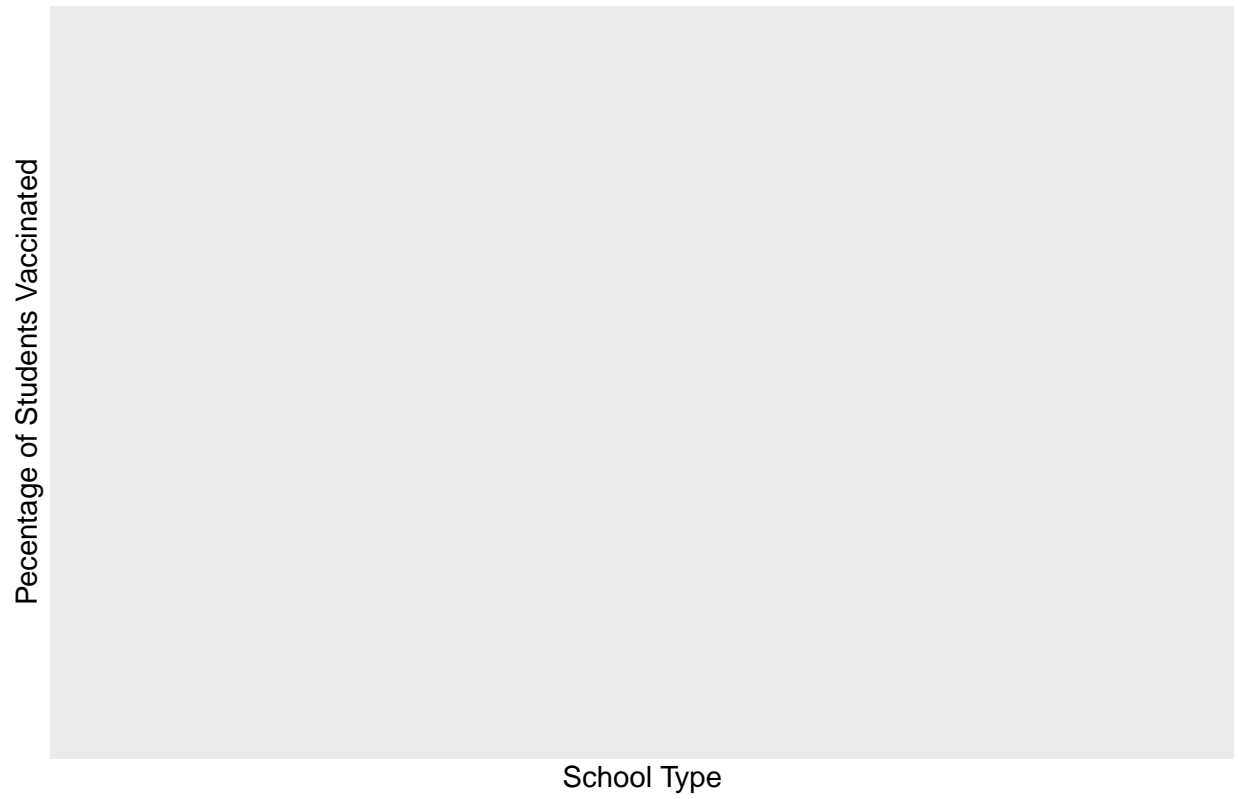
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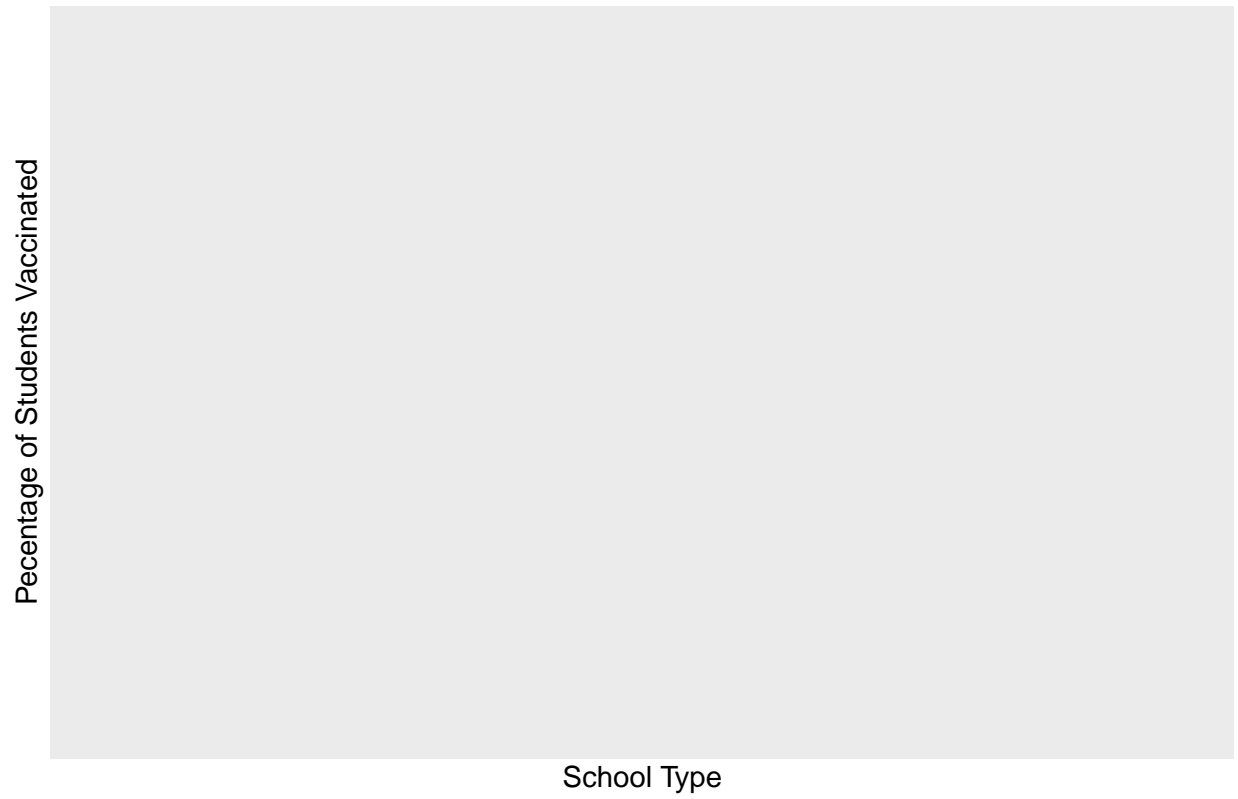
Vaccination Rates Across Different School Types



Vaccination Rates Across Different School Types



Vaccination Rates Across Different School Types



Vaccination Rates Across Different School Types

Percentage of Students Vaccinated

School Type

Exploratory Data Analysis

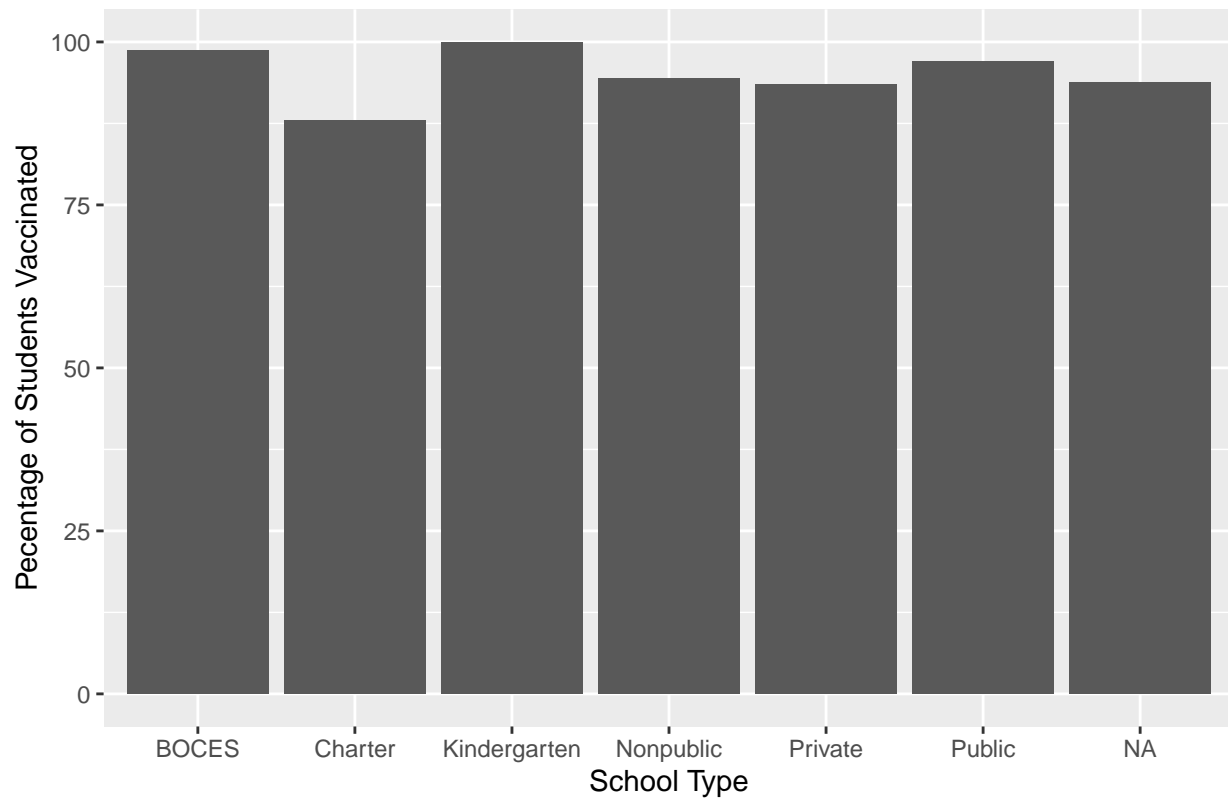
```
## # A tibble: 5,736 x 3
## # Groups:   mmr [3,901]
##   state      mmr      n
##   <chr>    <dbl> <int>
## 1 Arizona  15.4      3
## 2 Arizona  22.9      1
## 3 Arizona  37.9      1
## 4 Arizona  41.7      1
## 5 Arizona  42.9      1
## 6 Arizona  46.2      1
## 7 Arizona  47.4      1
## 8 Arizona  47.8      1
## 9 Arizona  48.0      1
## 10 Arizona 54.2      1
## # ... with 5,726 more rows

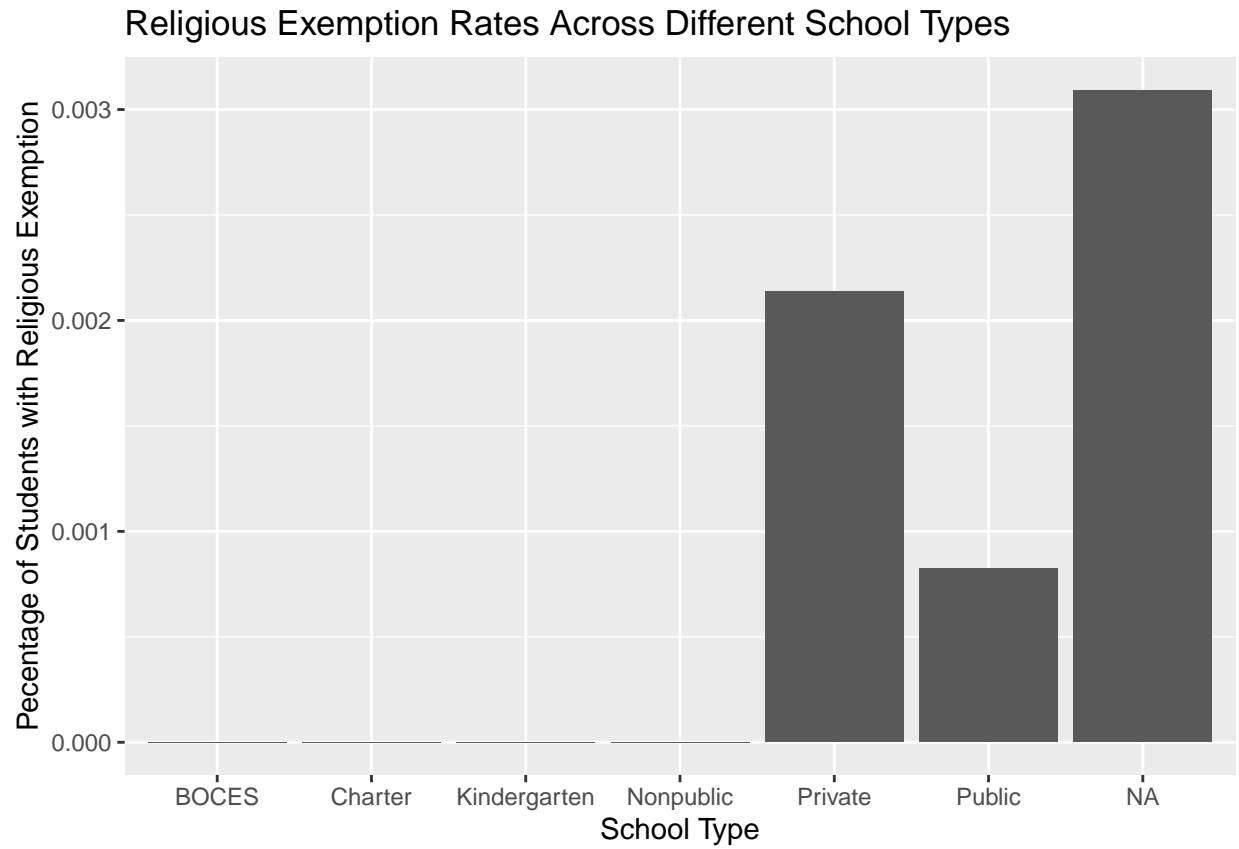
## # A tibble: 29 x 2
## # Groups:   state [29]
##   state      n
##   <chr>    <int>
## 1 Arizona  1171
## 2 Arkansas   567
## 3 California    1
## 4 Colorado     2
```

```
## 5 Connecticut 589
## 6 Florida 2672
## 7 Idaho 467
## 8 Illinois 7686
## 9 Iowa 1163
## 10 Maine 357
## # ... with 19 more rows

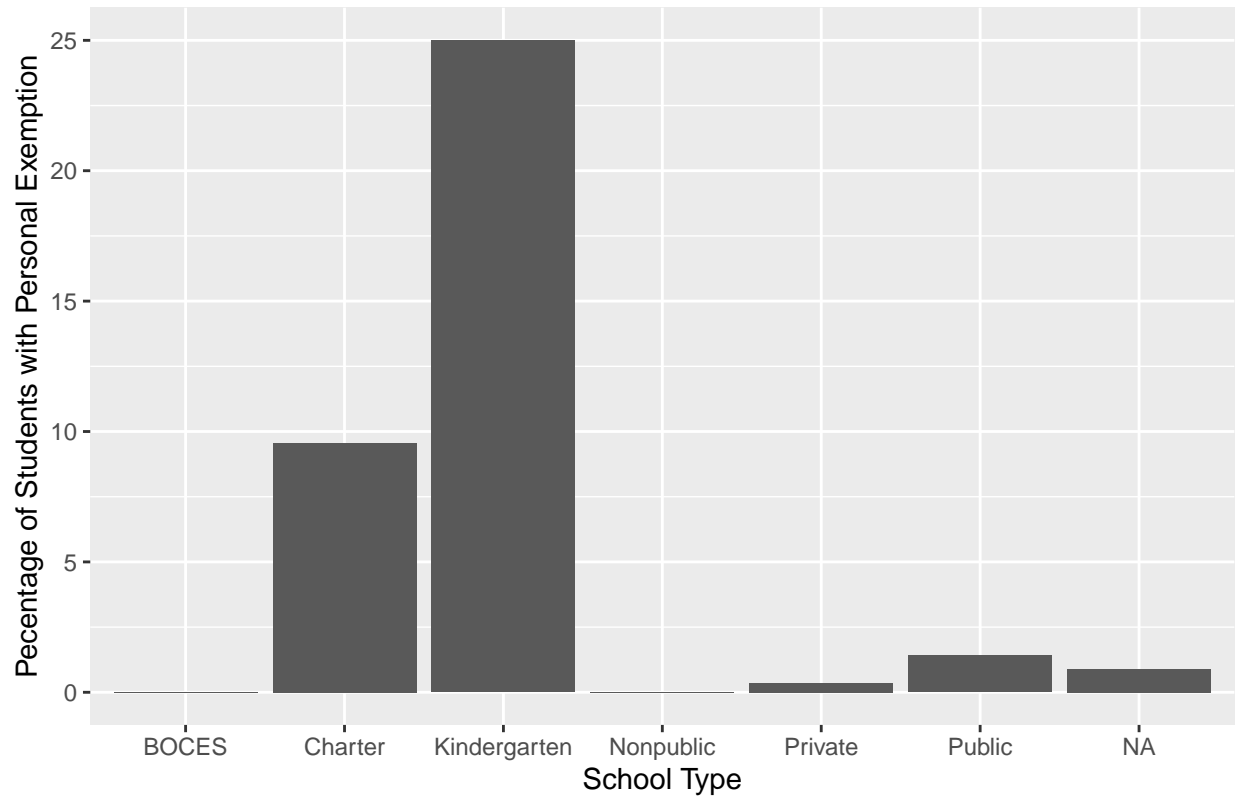
## # A tibble: 36 x 3
## # Groups:   type [7]
##   state      type      n
##   <chr>    <chr>  <int>
## 1 Arizona Charter   217
## 2 Arizona Private    74
## 3 Arizona Public   880
## 4 Arkansas <NA>    567
## 5 California Public     1
## 6 Colorado Kindergarten 2
## 7 Connecticut Nonpublic 18
## 8 Connecticut Public   571
## 9 Florida <NA>   2672
## 10 Idaho <NA>   467
## # ... with 26 more rows
```

Measles Vaccination Rates Across Different School Types

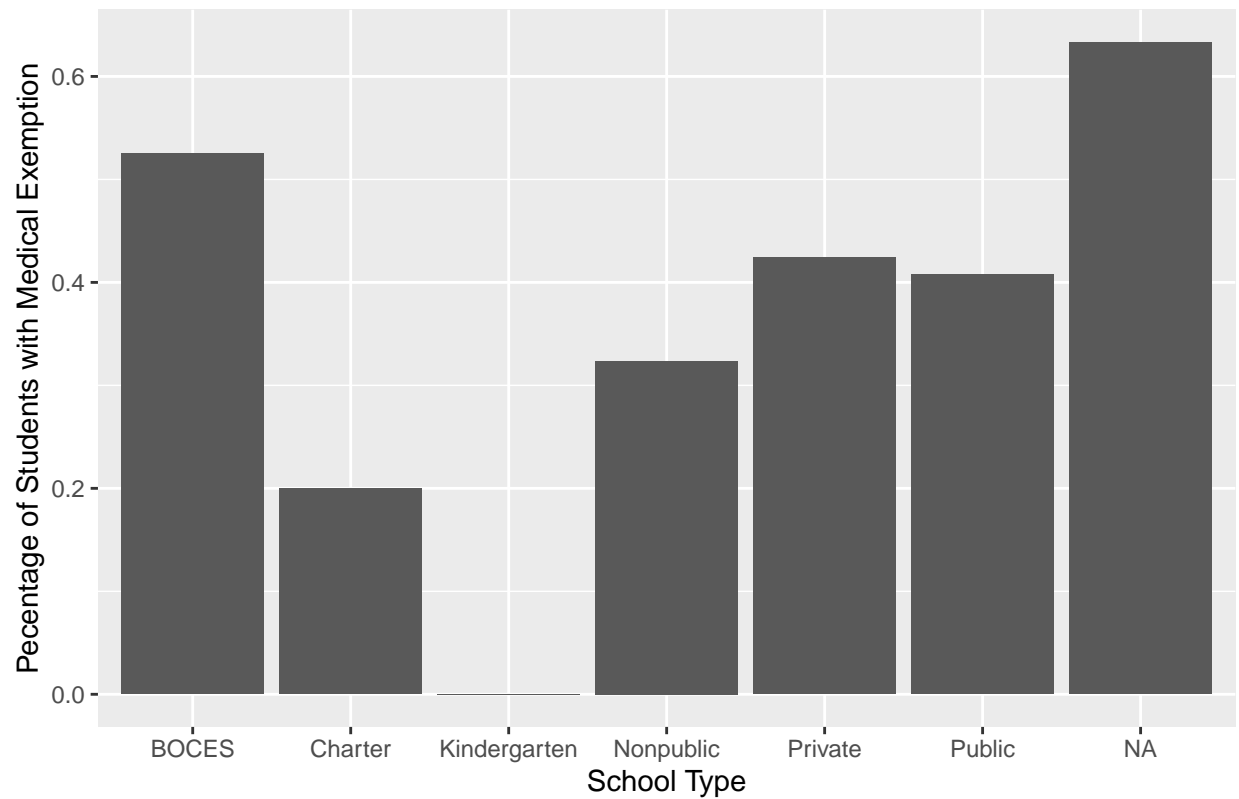




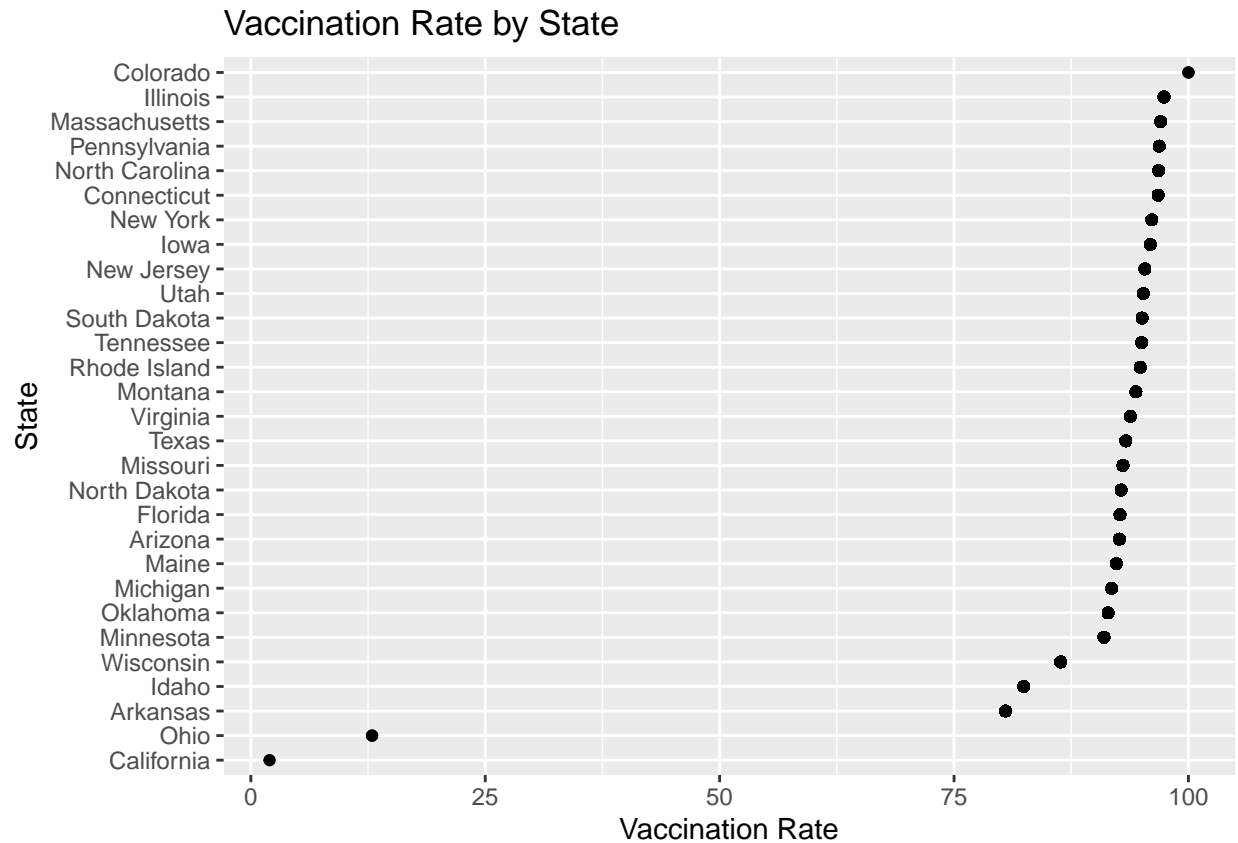
Personal Exemption Rates Across Different School Types



Medical Exemption Rates Across Different School Types



```
measles %>%
  ggplot(aes(x = statemean, y = reorder(state, statemean))) +
  geom_point() +
  labs(x = "Vaccination Rate", y = "State", title = "Vaccination Rate by State")
```

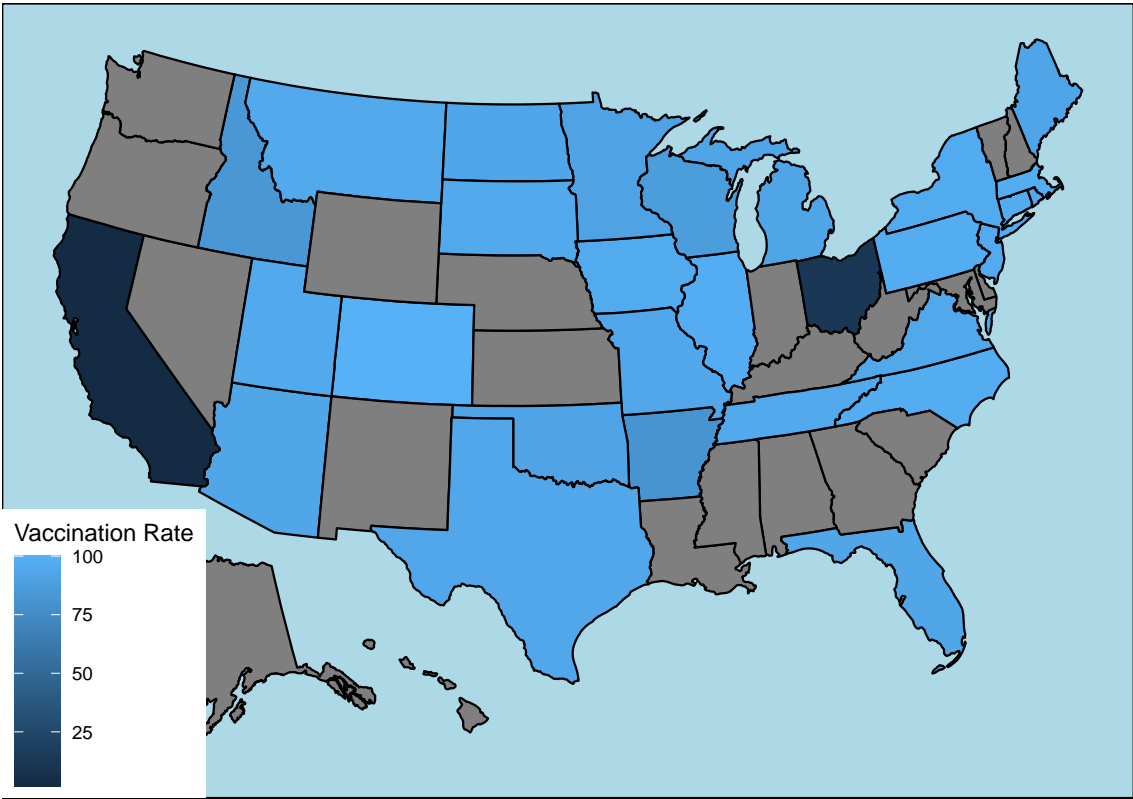


```

plotdata <- measles %>%
filter(realrate != (-1)) %>%
group_by(state) %>%
summarise(statemean = mean(realrate))
plot_usmap(data=plotdata, values = "statemean") +
  labs(title = "Vaccination Rate by State", fill = "Vaccination Rate") +
  theme(panel.background = element_rect(color = "black", fill = "lightblue"))

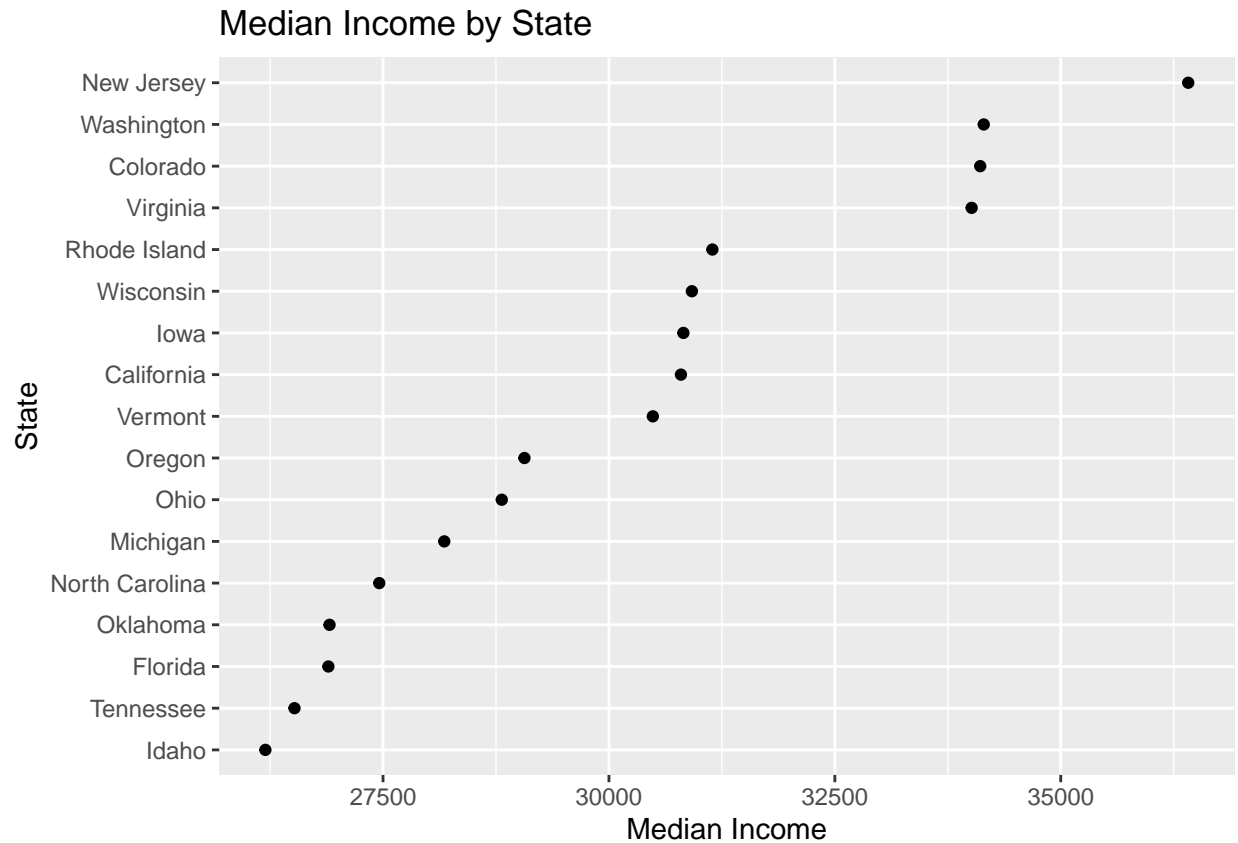
```

Vaccination Rate by State



```
## Getting data from the 2014-2018 5-year ACS

## # A tibble: 6 x 5
##   GEOID NAME      variable estimate moe
##   <chr> <chr>      <chr>      <dbl> <dbl>
## 1 01   Alabama B07011_001  25375  132
## 2 02   Alaska B07011_001  33413  428
## 3 04   Arizona B07011_001  28815  147
## 4 05   Arkansas B07011_001  24977  139
## 5 06   California B07011_001  30797   65
## 6 08   Colorado B07011_001  34109  231
```



```
## Getting data from the 2014-2018 5-year ACS
```

```
## # A tibble: 6 x 5
```

```
##   GEOID NAME      variable  estimate  moe
##   <chr> <chr>      <chr>      <dbl> <dbl>
## 1 01   Alabama    B02001_002  3317453 3345
## 2 02   Alaska     B02001_002  478834 1368
## 3 04   Arizona     B02001_002  5364141 9871
## 4 05   Arkansas    B02001_002  2302874 2783
## 5 06   California  B02001_002  23529068 26419
## 6 08   Colorado    B02001_002  4655584 5852
```

```
## Getting data from the 2014-2018 5-year ACS
```

```
## # A tibble: 6 x 5
```

```
##   GEOID NAME      variable  estimate  moe
##   <chr> <chr>      <chr>      <dbl> <dbl>
## 1 01   Alabama    B01003_001  4864680  NA
## 2 02   Alaska     B01003_001   738516  NA
## 3 04   Arizona     B01003_001  6946685  NA
## 4 05   Arkansas    B01003_001  2990671  NA
## 5 06   California  B01003_001  39148760  NA
## 6 08   Colorado    B01003_001  5531141  NA
```

```
#racerates <- left_join(race, population, by="GEOID") %>%
#pivot_wider(names_from = "variable", values_from = "estimate")
```



```
#incomerates <- left_join(income, measles, by = "statemean")

#summary(aov(state~statemean, data = measles))

measles3 <- measles %>%
  filter(type %in% c("Public", "Private")) %>%
  filter(realrate != (-1))

t.test(measles3$realrate~measles3$type)

##
## Welch Two Sample t-test
##
## data: measles3$realrate by measles3$type
## t = -11.461, df = 2665.4, p-value < 2.2e-16
## alternative hypothesis: true difference in means between group Private and group Public is not equal
## 95 percent confidence interval:
## -4.075441 -2.884605
## sample estimates:
## mean in group Private mean in group Public
## 93.47576 96.95578
```

Regression Analysis

```
measlerreg <- glm(cbind(numvaxx, unvaxx) ~ statefac, data=measles, family = binomial)
measlerreg

##
## Call: glm(formula = cbind(numvaxx, unvaxx) ~ statefac, family = binomial,
## data = measles)
##
## Coefficients:
## (Intercept) statefacArkansas statefacCalifornia
## 2.619172 -1.214998 -6.838680
## statefacColorado statefacFlorida statefacIllinois
## 7.890725 0.002825 1.122926
## statefacIowa statefacMaine statefacMichigan
## 0.587924 0.091579 -0.047001
## statefacMinnesota statefacMontana statefacNew Jersey
## -0.002653 -0.259731 0.670881
## statefacNorth Carolina statefacNorth Dakota statefacOhio
## 0.716962 0.062234 -4.680595
## statefacPennsylvania statefacRhode Island statefacSouth Dakota
## 0.900324 0.511840 0.790630
## statefacTennessee statefacUtah statefacVirginia
## 0.304427 0.476347 0.024633
##
## Degrees of Freedom: 28131 Total (i.e. Null); 28111 Residual
## (11347 observations deleted due to missingness)
## Null Deviance: 316800
## Residual Deviance: 177000 AIC: 255100

summary(measlerreg)
```

```
##
## Call:
## glm(formula = cbind(numvaxx, unvaxx) ~ statefac, family = binomial,
##      data = measles)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -154.356   -0.709    0.554    1.628   12.531
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.619172   0.013599  192.594 < 2e-16 ***
## statefacArkansas -1.214998   0.014364  -84.584 < 2e-16 ***
## statefacCalifornia -6.838680   1.007418  -6.788 1.13e-11 ***
## statefacColorado   7.890725  36.733652   0.215  0.82992
## statefacFlorida    0.002825   0.015823   0.179  0.85828
## statefacIllinois    1.122926   0.014195  79.107 < 2e-16 ***
## statefacIowa        0.587924   0.015962  36.833 < 2e-16 ***
## statefacMaine       0.091579   0.029166   3.140  0.00169 **
## statefacMichigan    -0.047001   0.017099  -2.749  0.00598 **
## statefacMinnesota   -0.002653   0.018816  -0.141  0.88786
## statefacMontana     -0.259731   0.016949 -15.324 < 2e-16 ***
## statefacNew Jersey   0.670881   0.021321  31.466 < 2e-16 ***
## statefacNorth Carolina 0.716962   0.020219  35.460 < 2e-16 ***
## statefacNorth Dakota  0.062234   0.036011   1.728  0.08395 .
## statefacOhio        -4.680595   0.401527 -11.657 < 2e-16 ***
## statefacPennsylvania  0.900324   0.021047  42.776 < 2e-16 ***
## statefacRhode Island  0.511840   0.049686  10.302 < 2e-16 ***
## statefacSouth Dakota  0.790630   0.052304  15.116 < 2e-16 ***
## statefacTennessee    0.304427   0.020575  14.796 < 2e-16 ***
## statefacUtah         0.476347   0.016331  29.169 < 2e-16 ***
## statefacVirginia     0.024633   0.018849   1.307  0.19125
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 316820  on 28131  degrees of freedom
## Residual deviance: 177046  on 28111  degrees of freedom
## (11347 observations deleted due to missingness)
## AIC: 255119
##
## Number of Fisher Scoring iterations: 8
# linear_reg() %>%
# set_engine("lm") %>%
# fit(statemean ~ estimate, data = measleincome) %>%
# tidy()
```