Tracking COVID-19 Cases Across Different Settlement Types in New York State

https://github.com/sgm22/MiltonZouKhalsa___ENV872_EDA_FinalProject

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0.1.1 Rationale

Coronavirus disease (COVID-19) is an infectious disease caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus, n.d.). The virus is primarily spread from person to person through respiratory droplets and as such, population density plays a role in the transmission of the virus with many experts suggesting that physical distancing is an effective way to combat its spread (CDCMMWR, 2020; What Is Coronavirus?, 2022). Since COVID-19 was declared a global pandemic in March 2020 by the World Health Organization (WHO) in March 2020, there has been a resurgence in COVID-19 infections across the globe as a result of new strains of the virus (CDC, 2020). Policy decisions to protect human health leverages data that such as case numbers, hospitalizations, and death resulting from COVID-19 to project COVID-19 spread (Truelove et al., n.d.). Very few epidemiological COVID-19 models incorporate population density explicitly even though population density is thought to be an important factor(Hamidi et al., 2020; Wong & Li, 2020).

In New York State, since the beginning of the pandemic there has been over 6 million cases of COVID-19. In January 2022, the state recorded the highest number of cases while in April 2020, it recorded the highest record of death (Times, 2020). The density of people in New York State varies drastically across the state with 43% of the state's population living in the five boroughs of New York City (New York State Tracking Program | Tracking | NCEH | CDC, 2019). Of the 62 counties in the State, Kings County is the most populated with over 2 million residents, while Hamilton County is the least populated with about 4,485 residents (New York Population 2022 (Demographics, Maps, Graphs), n.d.). With physical distancing playing an important role in reducing the likelihood of infection, this paper explores how well absolute population and population density predict COVID-19 case numbers in the diversely sized New York State. Further, we explore whether the relationship between absolute population and population density changes among different settlement types.

Settlement types are defined as population centers of humans who have developed a long-term community in a specific area (Settlements Overview & Types | What Are Settlements?, n.d.). In this study, settlement types are classified as rural, micropolitan, and urban. We define rural settlements as counties with a population size of less than 25,000 people, micropolitans as counties with a population size of between 25,000 and 49,999 people, and an urban settlement as a county with more than 50,000 people (adapted from USDA ERS - What Is Rural?, n.d.). We hope that by better understanding the importance of population size and density on COVID-19 prevalence and how that varies across settlement type, we are able to better understand if population density and/or absolute population can be used as a proxy when formulating policy decisions around COVID-19.

0.1.2 Research Questions

1. What is the correlation between population density and absolute population and the number of COVID-19 cases across New York State?
2. What is the relationship between the predictor variable: settlement types and the response variable: cumulative COVID-19 cases?
3. What is the correlation between absolute population and population density and the number of COVID-19 tests does done? Does the stronger correlated relationship vary among settlement types?

Set-up Working Directory, Import and Merge Data sets

> In order to answer our research question, we imported data that contains information about New York (NY) state population size and density by county in 2022 from the U.S. Census Bureau. This information was then combined with data regarding number of positive COVID-19 cases, quantity of COVID-19 tests conducted and other relevant information collected by the New York Department of Health from March 1, 2020 to November 22, 2022.

```
################# Set working directory ################################

getwd() #Check working directory
```

```
## [1] "/Users/danleizou/MiltonZouKhalsa__ENV872_EDA_FinalProject3"
```

```
#Load packages

library(rvest)
library(tidyverse)
library(ggplot2)
library(ggpubr)
library (lubridate)
library (dplyr)
library(sf)
library (leaflet)
library(mapview)
library(AER)
library (corrplot)
library(RColorBrewer)
library(knitr)
library(MASS)
library(kableExtra)

#Set theme

my_theme <- theme_bw(base_size = 12) +
  theme(axis.text = element_text(color = "black"),
      legend.position = "top", legend.justification = "center") +
  theme(plot.title = element_text(hjust = 0.5))
theme_set(my_theme)


#Import NY State county level COVID data (March 1, 2020 to November 22, 2022) from NY
```

```r
ny_covid_dat <- read.csv("./Data/Raw_Data/NY_COVID_County_Level.csv")

ny_covid_dat #View Data
```

```
##              County sum_new_positives sum_cumulative_no_of_positive
## 1            Albany             75450                      31527049
## 2          Allegany             10396                       4540770
## 3             Bronx            480247                     214795050
## 4            Broome             56238                      23809846
## 5    Capital Region            273064                     109650058
## 6       Cattaraugus             18648                       7739886
## 7            Cayuga             19636                       8258733
## 8  Central New York            219659                      88806060
## 9        Chautauqua             28390                      11963811
## 10          Chemung             25750                      10781572
## 11         Chenango             11387                       4672090
## 12          Clinton             21495                       7897140
## 13         Columbia             13108                       5333242
## 14         Cortland             12837                       5327906
## 15         Delaware              9685                       3752771
## 16         Dutchess             79872                      34848939
## 17             Erie            259074                     110683234
## 18            Essex              7336                       2731432
## 19     Finger Lakes            291710                     125914355
## 20         Franklin             11662                       4435661
## 21           Fulton             15935                       6306546
## 22          Genesee             16033                       6962833
## 23           Greene             10413                       4408700
## 24         Hamilton              1054                        432991
## 25         Herkimer             16859                       7020942
## 26        Jefferson             25649                       9657042
## 27            Kings            860573                     362966136
## 28            Lewis              7069                       3184476
## 29       Livingston             13875                       5860772
## 30      Long Island           1047899                     463920471
## 31          Madison             16241                       6602449
## 32       Mid-Hudson            732389                     333323687
## 33    Mohawk Valley            132784                      55129169
## 34           Monroe            184340                      81266752
## 35       Montgomery             14485                       5881959
## 36           Nassau            515433                     225331004
## 37         New York            553801                     212308156
## 38    New York City           2908643                    1224453265
## 39          Niagara             57583                      24783016
```

```
## 40    North Country             99779                      38597015
## 41           Oneida             66461                      28508629
## 42         Onondaga            137709                      55993243
## 43          Ontario             25002                      10107862
## 44           Orange            131134                      58559762
## 45          Orleans             10149                       4331454
## 46           Oswego             33236                      12623729
## 47           Otsego             12728                       4951672
## 48           Putnam             29694                      12765002
## 49           Queens            813384                     345088691
## 50       Rensselaer             40127                      15928044
## 51         Richmond            200638                      89295232
## 52         Rockland            112172                      53675641
## 53         Saratoga             59019                      22929569
## 54      Schenectady             41888                      17263319
## 55        Schoharie              6316                       2459421
## 56         Schuyler              4209                       1680264
## 57           Seneca              7336                       2910342
## 58    Southern Tier            170688                      68994999
## 59        STATEWIDE           6250706                    2668499796
## 60          Steuben             24398                      10006178
## 61     St. Lawrence             25514                      10258273
## 62          Suffolk            532466                     238589467
## 63         Sullivan             23209                       9439839
## 64            Tioga             13520                       5420118
## 65         Tompkins             25501                       8872160
## 66           Ulster             40739                      17116464
## 67           Warren             18009                       6588480
## 68       Washington             15050                       5671655
## 69            Wayne             21009                       8496183
## 70      Westchester            315569                     146918040
## 71 Western New York            374091                     159710717
## 72          Wyoming              9682                       4267904
## 73            Yates              4284                       1710253
##    sum_total_number_of_tests sum_cumulative_no_of_tests median_test_positive
## 1                    1402792                  718954664                2.43%
## 2                     248725                  135187844                1.67%
## 3                    8847438                 4167554932                2.62%
## 4                    1183008                  600726726                2.85%
## 5                    5255122                 2645289344                2.42%
## 6                     307715                  159238111                2.01%
## 7                     395524                  199795061                2.05%
## 8                    4404505                 2280257150                2.70%
## 9                     529410                  284656873               17.24%
## 10                    482115                  240229506                2.80%
```

```
## 11         237180         120749908      2.41%
## 12         405091         204944024     16.67%
## 13         253036         134198616      1.94%
## 14         306593         162613835      2.11%
## 15         200498         101931557      2.24%
## 16        1482191         765609824      2.30%
## 17        4230697        2209228099      2.52%
## 18         165134          82082708      1.87%
## 19        5627645        2925577026      3.11%
## 20         217883         104817335     19.51%
## 21         230615         114053436      1.69%
## 22         274587         141618902     20.54%
## 23         181361          91910867      2.54%
## 24          20261          10356622      0.00%
## 25         325883         165269120      1.80%
## 26         407594         191971766      2.41%
## 27       18713833        8370878686      2.45%
## 28         104111          52934295     17.14%
## 29         285393         152289219     21.57%
## 30       16896935        8450017694      3.21%
## 31         372206         191580055      1.89%
## 32       13407104        6513198457      3.08%
## 33        2740911        1402887769      2.05%
## 34        3656142        1917145805      3.25%
## 35         223329         114646701     17.02%
## 36        8400598        4188172601      2.99%
## 37       14450368        6672796856      2.09%
## 38       60433651       27893288263      2.51%
## 39         904150         468974555     20.69%
## 40        1940611         970267992      2.58%
## 41        1527340         790655393      2.04%
## 42        2797843        1457537033      2.87%
## 43         480819         244314298      2.55%
## 44        1968284         904265527      3.72%
## 45         158360          79497423     19.67%
## 46         532339         268731166      1.81%
## 47         312369         158059656      2.10%
## 48         490627         243060578      2.59%
## 49       14735060        6902671989      2.49%
## 50         875724         447596670     21.30%
## 51        3686952        1779385800      3.25%
## 52        2358136        1029309794      3.01%
## 53        1076644         532008522      2.44%
## 54         837442         420680184     23.60%
## 55         121375          60203463     18.29%
```

```
## 56                  99602               47465529          1.82%
## 57                 139448               69545097         19.57%
## 58                5973213             3285431777          2.02%
## 59              122900394            59623500954          3.05%
## 60                 476678              233587858          2.50%
## 61                 620537              323161242          2.05%
## 62                8496337             4261845093          3.43%
## 63                 377092              162432097          3.13%
## 64                 234100              115425950          2.59%
## 65                3060032             1825314743         10.08%
## 66                 867586              439724686          2.64%
## 67                 339906              161155740          2.31%
## 68                 288217              138784081          2.00%
## 69                 383003              193346376          2.53%
## 70                5863188             2968795951          2.92%
## 71                6220697             3257285482          2.22%
## 72                 158197               82232070         18.97%
## 73                  91696               45587836         14.29%
```

```r
#Import NY population data (2022)

ny_pop_dat <- read.csv("./Data/Raw_Data/NY_County_Level_Population_Data.csv",stringsAsFa

ny_pop_dat
```

```
##            County pop2022 area_milessquared density_permilessquared
## 1           Kings 2782348           69.8126              39854.5289
## 2          Queens 2440412          108.7681              22436.8367
## 3   New York City 1715927           22.6558              75738.8946
## 4         Suffolk 1532434          911.7219               1680.8130
## 5           Bronx 1490164           42.0506              35437.3653
## 6          Nassau 1407022          284.8100               4940.2121
## 7     Westchester 1015525          430.5160               2358.8553
## 8            Erie  961276         1042.6977                921.9125
## 9          Monroe  762463          657.2105               1160.1504
## 10       Richmond  501151           58.1779               8614.1174
## 11       Onondaga  478414          778.4094                614.6046
## 12         Orange  407010          811.6988                501.4299
## 13       Rockland  343657          173.5039               1980.6877
## 14         Albany  316976          522.8113                606.2914
## 15       Dutchess  295595          795.6356                371.5206
## 16       Saratoga  238689          809.9962                294.6792
## 17         Oneida  231575         1212.4134                191.0033
## 18        Niagara  211906          522.3527                405.6761
```

```
## 19        Broome  198299         705.7655              280.9701
## 20        Ulster  181723        1124.2350              161.6415
## 21    Rensselaer  161470         652.4322              247.4893
## 22   Schenectady  158727         204.5787              775.8727
## 23    Chautauqua  126207        1060.2265              119.0378
## 24     Jefferson  116819        1268.6770               92.0794
## 25        Oswego  116609         951.6435              122.5343
## 26       Ontario  113364         644.0640              176.0136
## 27  St. Lawrence  107817        2680.3786               40.2245
## 28      Tompkins  106576         474.6493              224.5363
## 29        Putnam   97260         230.3116              422.2975
## 30       Steuben   92502        1390.5728               66.5208
## 31         Wayne   90785         603.8264              150.3495
## 32       Chemung   83212         407.3527              204.2751
## 33       Clinton   79387        1037.8526               76.4916
## 34      Sullivan   78840         968.1347               81.4349
## 35   Cattaraugus   76386        1308.3601               58.3830
## 36        Cayuga   75492         691.5917              109.1569
## 37       Madison   66930         654.8646              102.2043
## 38        Warren   65743         866.9581               75.8318
## 39      Columbia   61264         634.7275               96.5202
## 40    Livingston   61122         631.7622               96.7484
## 41    Washington   60920         831.1669               73.2945
## 42      Herkimer   59263        1411.5299               41.9849
## 43       Genesee   58050         492.9359              117.7638
## 44        Otsego   57776        1001.7094               57.6774
## 45        Fulton   52882         495.4601              106.7331
## 46    Montgomery   49394         403.1168              122.5302
## 47         Tioga   47921         518.6096               92.4028
## 48        Greene   47673         647.1615               73.6648
## 49      Franklin   46747        1629.0705               28.6955
## 50      Chenango   46568         893.5573               52.1153
## 51      Cortland   46303         498.7729               92.8338
## 52      Allegany   45958        1029.3002               44.6498
## 53      Delaware   43574        1442.4601               30.2081
## 54       Wyoming   40207         592.7513               67.8311
## 55       Orleans   39835         391.2631              101.8113
## 56         Essex   36983        1794.2666               20.6118
## 57        Seneca   33526         323.7095              103.5682
## 58     Schoharie   29106         621.8189               46.8078
## 59         Lewis   26482        1274.6433               20.7760
## 60         Yates   24660         338.1428               72.9278
## 61      Schuyler   17810         328.3332               54.2437
## 62      Hamilton    5161        1717.3817                3.0052
```

```r
#Merge data sets

combined_dat_ny_covid_pop <- ny_pop_dat %>%
  left_join(ny_covid_dat, by = "County")

## Add column for to classify counties into settlement types

combined_dat_ny_covid_pop <- combined_dat_ny_covid_pop %>%
  mutate(settlement_type = case_when(pop2022<=25000 ~ 'Rural',
                                     25000<=pop2022 & pop2022<50000 ~ 'Micropolitan',
                                     pop2022>= 50000 ~ 'Urban'))

summary(combined_dat_ny_covid_pop) # Check data for new columns
```

```
##     County             pop2022         area_milessquared density_permilessquared
##  Length:62          Min.   :   5161   Min.   :  22.66   Min.   :    3.01
##  Class :character   1st Qu.:  48289   1st Qu.: 441.55   1st Qu.:   73.02
##  Mode  :character   Median :  86998   Median : 653.65   Median :  113.46
##                     Mean   : 328482   Mean   : 760.09   Mean   : 3279.30
##                     3rd Qu.: 236910   3rd Qu.:1022.40   3rd Qu.:  418.14
##                     Max.   :2782348   Max.   :2680.38   Max.   :75738.89
##  sum_new_positives sum_cumulative_no_of_positive sum_total_number_of_tests
##  Min.   :   1054   Min.   :4.330e+05             Min.   :   20261
##  1st Qu.:  12905   1st Qu.:5.329e+06             1st Qu.:  240066
##  Median :  23804   Median :9.156e+06             Median :  406342
##  Mean   : 138799   Mean   :5.937e+07             Mean   : 2723930
##  3rd Qu.:  64600   3rd Qu.:2.758e+07             3rd Qu.: 1462341
##  Max.   :2908643   Max.   :1.224e+09             Max.   :60433651
##  sum_cumulative_no_of_tests median_test_positive settlement_type
##  Min.   :1.036e+07          Length:62            Length:62
##  1st Qu.:1.241e+08          Class :character     Class :character
##  Median :2.024e+08          Mode  :character     Mode  :character
##  Mean   :1.304e+09
##  3rd Qu.:7.539e+08
##  Max.   :2.789e+10
```

0.2 Dataset Information

> We acquired our 2020 to 2022 COVID-19 data from the New York Department of Health and population data from the U.S. Census Bureau on November 24th, 2022. County names did not match between the census data and NY Department of Health data. We wrangled our data by removing the word "county" from each county in the census data. In addition to the 62 counties, the NY Health Department broke counties down into smaller sections resulting in more than 62 counties. Since we only want to work with the original counties, we left-merged the NY health data onto the county data on November 24th, 2022. We are using the merged version as our main data source. Additionally on November 24th, 2022, we uploaded the geospatial shape file that was incorporated in class for ENV872.Using the shape file, we selected for counties in New York State. Data types and variable types for the combined data were set on November 27th, 2022.

Data Information: https://www.census.gov/library/stories/state-by-state/new-york-population-change-between-census-decade.html COVID-19 Variant Data | Department of Health (ny.gov) – (March 1, 2020, to November 22, 2022) cb_2018_us_county_20m.shp state FIPS code 36

Keywords

ENV872, COVID-19, COVID, virus, virus spread, New York, New York State

```
##                           Variable
## 1                           County
## 2                          pop2022
## 3                area_milessquared
## 4             density_milessquared
## 5                sum_new_positives
## 6  sum_cumulative_no_of_positives
## 7        sum_total_number_of_tests
## 8      sum_cumulative_no_of_tests
## 9             median_test_positive
## 10                 settlement_type
##
## 1
## 2
## 3
## 4
## 5
## 6
## 7                                                                                                  The
## 8                                                                         Running total for the number
## 9  For the dates before 4/4/2022: The median percentage of all COVID tests reported t
## 10
```

```
##       Coding          Units Minimum.Value Maximum.Value Missing
## 1  character            N/A           N/A           N/A       0
## 2    integer            N/A          5161       2782348       0
## 3    numeric miles squared       22.6558      2680.379       0
## 4    numeric miles squared        3.0052      75738.89       0
## 5    integer            N/A          1054       2908643       0
## 6    integer            N/A        432991    1224453000       0
## 7    integer            N/A         20261      60433650       0
## 8    integer            N/A      10356620   27893290000       0
## 9  character            N/A           N/A           N/A       0
## 10 character            N/A           N/A           N/A       0
```

0.3 Exploratory Analysis and Data Visualization

The merged data set was exploring for missing values and abnormal values using the R functions, "head", "summary" and "dim". Further, to better understand the distribution of the variables that we use in our analysis, we plotted a series of histograms. The graphical exploration of the distribution of the variables showed that the variables, "sum_cumulative_no_of_positive", "sum_cumulative_no_of_tests", "pop2022" and "density_permilessquared" are right-skewed. That is, most of the data points were located on the left side of the histograms plotted for each variable. For improved visualization, we log transformed the variables to get their distributions closer to a normal distribution. After each log-transformation, we carried out Shapiro–Wilk tests to check the normality of the transformed distributions. The p-value of each log-transformed distribution was less than 0.05 indicating that the evidence supported the fact that log-transformed distributions were still not normally distributed. We also explored and visualized the distribution of the absolute population and population density across the various settlement types using box plots.

0.3.1 Tabular Exploration

```
head(combined_dat_ny_covid_pop)
```

```
##          County pop2022 area_milessquared density_permilessquared
## 1         Kings 2782348           69.8126               39854.529
## 2        Queens 2440412          108.7681               22436.837
## 3 New York City 1715927           22.6558               75738.895
## 4       Suffolk 1532434          911.7219                1680.813
## 5         Bronx 1490164           42.0506               35437.365
## 6        Nassau 1407022          284.8100                4940.212
##   sum_new_positives sum_cumulative_no_of_positive sum_total_number_of_tests
## 1            860573                     362966136                  18713833
## 2            813384                     345088691                  14735060
## 3           2908643                    1224453265                  60433651
## 4            532466                     238589467                   8496337
## 5            480247                     214795050                   8847438
## 6            515433                     225331004                   8400598
##   sum_cumulative_no_of_tests median_test_positive settlement_type
## 1                 8370878686                2.45%           Urban
## 2                 6902671989                2.49%           Urban
## 3                27893288263                2.51%           Urban
## 4                 4261845093                3.43%           Urban
## 5                 4167554932                2.62%           Urban
```

```
## 6                4188172601               2.99%           Urban
```

```r
summary(combined_dat_ny_covid_pop) #View Data
```

```
##     County             pop2022        area_milessquared density_permilessquared
##  Length:62          Min.   :   5161   Min.   :  22.66   Min.   :    3.01
##  Class :character   1st Qu.:  48289   1st Qu.: 441.55   1st Qu.:   73.02
##  Mode  :character   Median :  86998   Median : 653.65   Median :  113.46
##                     Mean   : 328482   Mean   : 760.09   Mean   : 3279.30
##                     3rd Qu.: 236910   3rd Qu.:1022.40   3rd Qu.:  418.14
##                     Max.   :2782348   Max.   :2680.38   Max.   :75738.89
##  sum_new_positives sum_cumulative_no_of_positive sum_total_number_of_tests
##  Min.   :   1054   Min.   :4.330e+05             Min.   :   20261
##  1st Qu.:  12905   1st Qu.:5.329e+06             1st Qu.:  240066
##  Median :  23804   Median :9.156e+06             Median :  406342
##  Mean   : 138799   Mean   :5.937e+07             Mean   : 2723930
##  3rd Qu.:  64600   3rd Qu.:2.758e+07             3rd Qu.: 1462341
##  Max.   :2908643   Max.   :1.224e+09             Max.   :60433651
##  sum_cumulative_no_of_tests median_test_positive settlement_type
##  Min.   :1.036e+07          Length:62            Length:62
##  1st Qu.:1.241e+08          Class :character     Class :character
##  Median :2.024e+08          Mode  :character     Mode  :character
##  Mean   :1.304e+09
##  3rd Qu.:7.539e+08
##  Max.   :2.789e+10
```

```r
dim(combined_dat_ny_covid_pop)
```

```
## [1] 62 10
```

```r
#View mean COVID cases and mean COVID test conducted by settlement types


collapsed_dat_settlement_types <- combined_dat_ny_covid_pop %>%
  group_by(settlement_type) %>%
  summarise(Mean_COVID_cases = mean(sum_cumulative_no_of_positive),
            Mean_Tests_Conducted = mean(sum_cumulative_no_of_tests),
            Mean_Absolute_Population = mean(pop2022),
            Mean_Settlement_Density = mean (density_permilessquared))

print(collapsed_dat_settlement_types) #View table
```

```
## # A tibble: 3 x 5
##   settlement_type Mean_COVID_cases Mean_Tests_Conducted Mean_Absolute_~1 Mean_~2
##   <chr>                      <dbl>                <dbl>            <dbl>   <dbl>
## 1 Micropolitan             4166072.             98127075.           41448.    64.2
## 2 Rural                    1274503.             34469996.           15877     43.4
## 3 Urban                   80411031.           1763706740.          438622.  4495.
## # ... with abbreviated variable names 1: Mean_Absolute_Population,
## #   2: Mean_Settlement_Density
```

0.3.2 Graphical Exploration

```
# Visualizing Distribution of Variables

###################### COVID-19 Cases ##############################

ggplot(data = combined_dat_ny_covid_pop, aes(sum_cumulative_no_of_positive))+
  geom_histogram() +
  xlab ("Cumulative Number of Positive COVID-19 Tests") +
  ggtitle("Histogram of Cumulative Number of Positive COVID-19 Tests")
```

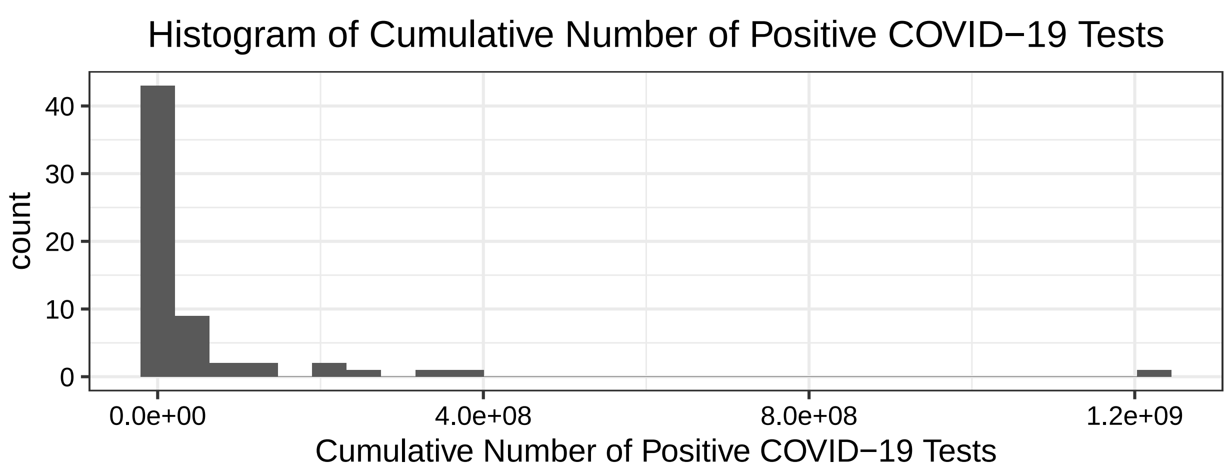


Figure 1: Cumulative Number of Positive COVID-19 Tests

```
## Log Transform

ggplot(data = combined_dat_ny_covid_pop, aes(log(sum_cumulative_no_of_positive))) +
  geom_histogram() +
  xlab ("Log of Cumulative Number of Positive COVID-19 Tests") +
  ggtitle("Histogram of Log of Cumulative Number of Positive COVID-19 Tests")
```

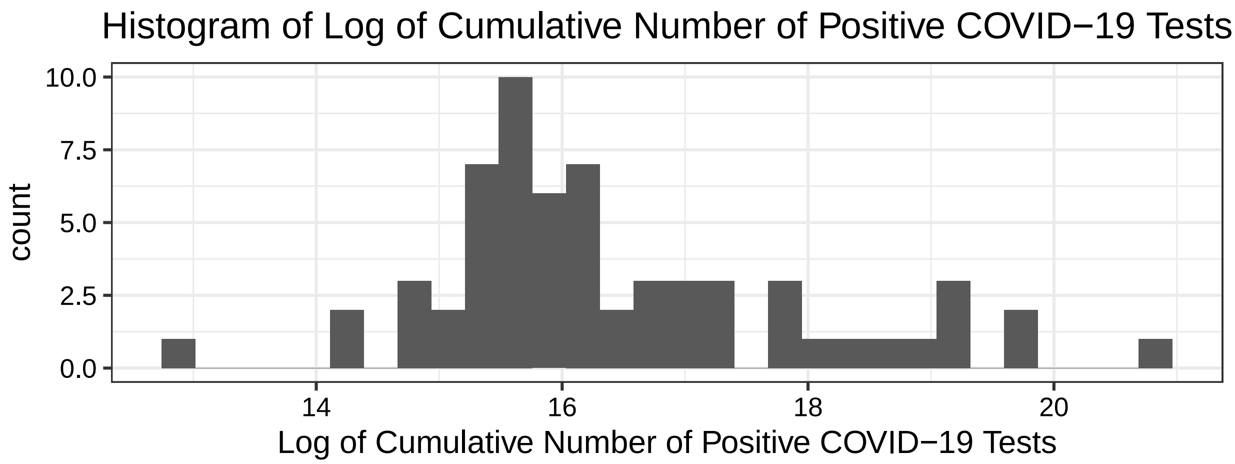


Figure 2: Log of Cumulative Number of Positive COVID-19 Tests

```
shapiro.test(log(combined_dat_ny_covid_pop$sum_cumulative_no_of_positive)) #Check normal
```

```
##
##  Shapiro-Wilk normality test
##
## data:  log(combined_dat_ny_covid_pop$sum_cumulative_no_of_positive)
## W = 0.92854, p-value = 0.001407
```

```
####################### Number of COVID Tests Conducted #######################

ggplot(data = combined_dat_ny_covid_pop, aes(sum_cumulative_no_of_tests))+
  geom_histogram() +
  xlab ("Cumulative Number of COVID-19 Tests Conducted") +
  ggtitle("Histogram of Cumulative Number of COVID-19 Tests Conducted")
```

```
## Log Transform

ggplot(data = combined_dat_ny_covid_pop, aes(log(sum_cumulative_no_of_tests))) +
  geom_histogram() +
  xlab ("Log of Cumulative Number of COVID-19 Tests Conducted") +
  ggtitle("Histogram of Log of Cumulative Number of COVID-19 Tests Conducted")
```

```
shapiro.test(log(combined_dat_ny_covid_pop$sum_cumulative_no_of_tests)) #Check normality
```

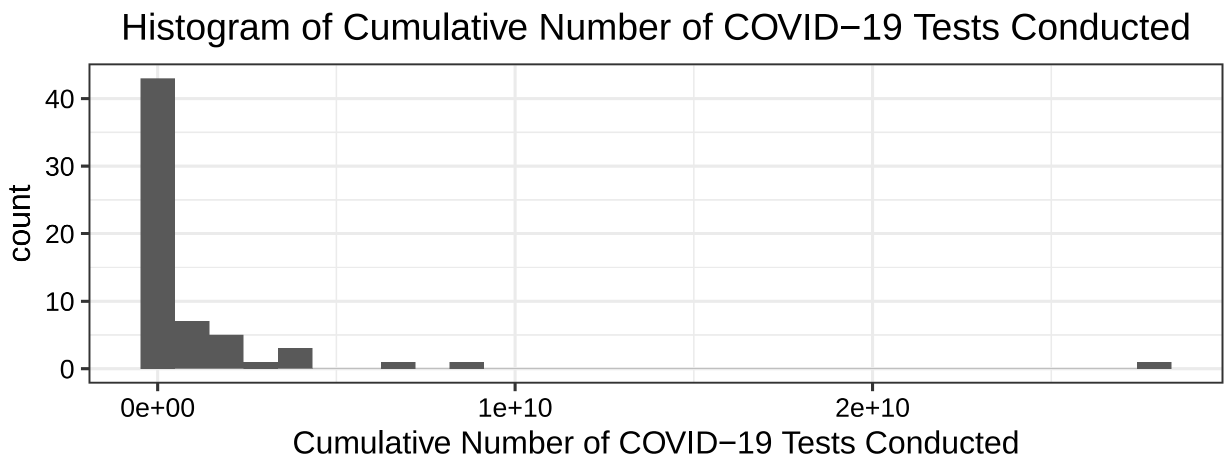


Figure 3: Cumulative Number of COVID-19 Tests Conducted

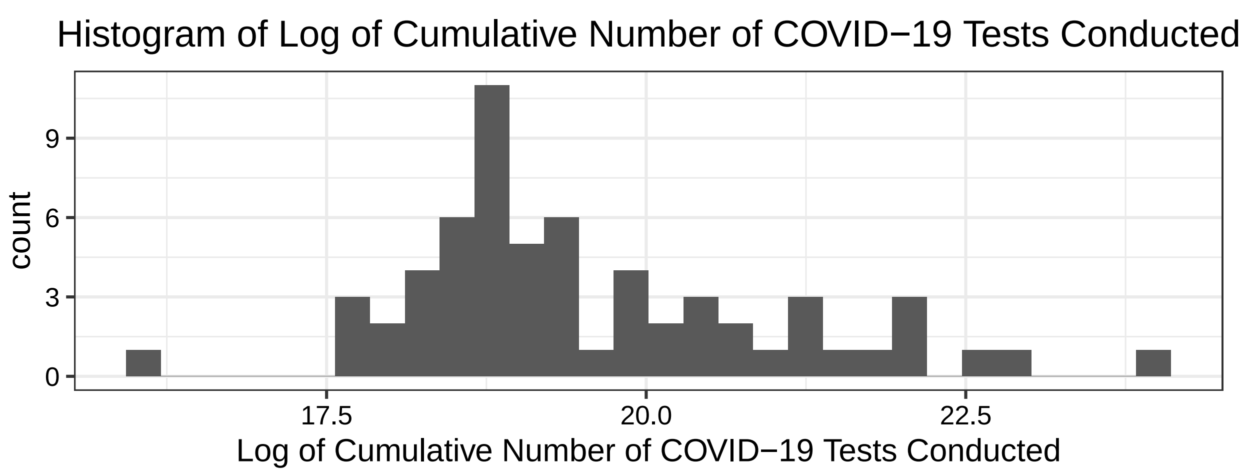


Figure 4: Log of Cumulative Number of Positive COVID-19 Tests Conducted

```
##
##  Shapiro-Wilk normality test
##
## data:  log(combined_dat_ny_covid_pop$sum_cumulative_no_of_tests)
## W = 0.94091, p-value = 0.004985
```

```
######################### County Population ##########################

ggplot(data = combined_dat_ny_covid_pop, aes(pop2022)) +
  geom_histogram() +
  xlab("Absolute Population Size of Counties Across New York State 2022") +
  ggtitle ("Histogram of Population of Counties Across New York State")
```

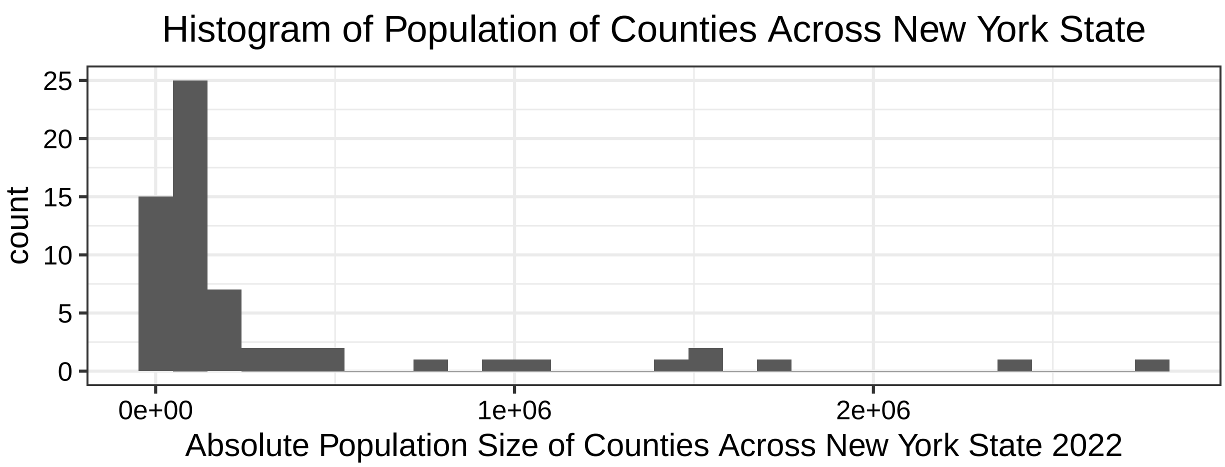


Figure 5: Population of Counties Across New York State

```
## Log Transform

ggplot(data = combined_dat_ny_covid_pop, aes(log(pop2022))) +
  geom_histogram() +
  xlab("Log of Absolute Population of Counties Across New York State 2022 ") +
  ggtitle ("Log of Histogram of Population of Counties Across New York State")
```

```
shapiro.test(log(combined_dat_ny_covid_pop$pop2022)) #Check normaliity
```

```
##
##  Shapiro-Wilk normality test
##
## data:  log(combined_dat_ny_covid_pop$pop2022)
## W = 0.93542, p-value = 0.002814
```

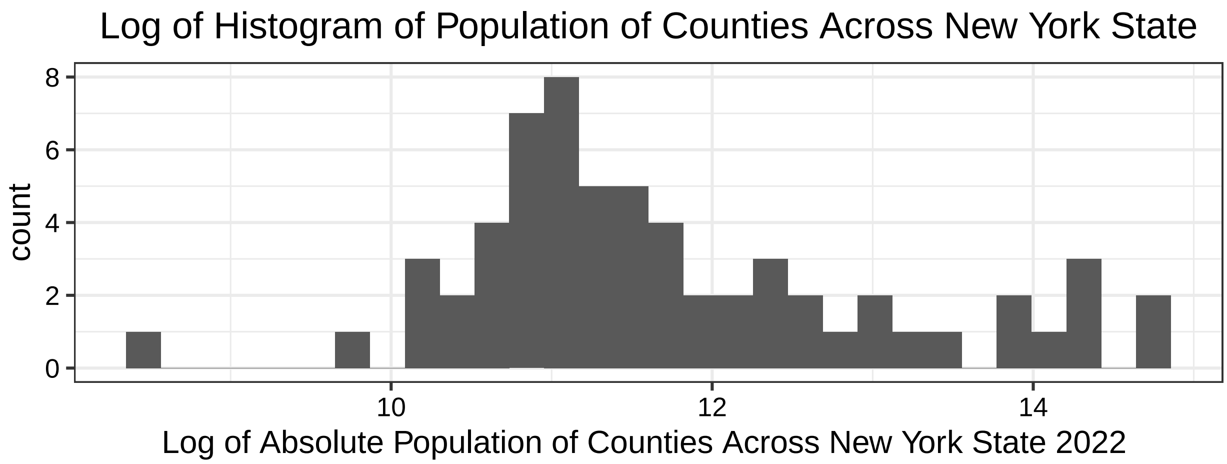


Figure 6: Log of Population of Counties Across New York State

```r
################################### County Density ############################

ggplot(data = combined_dat_ny_covid_pop, aes(density_permilessquared)) +
  geom_histogram() +
  xlab("Density of Counties Across New York State") +
  ggtitle (" Histogram of Density of Counties Across New York State")
```

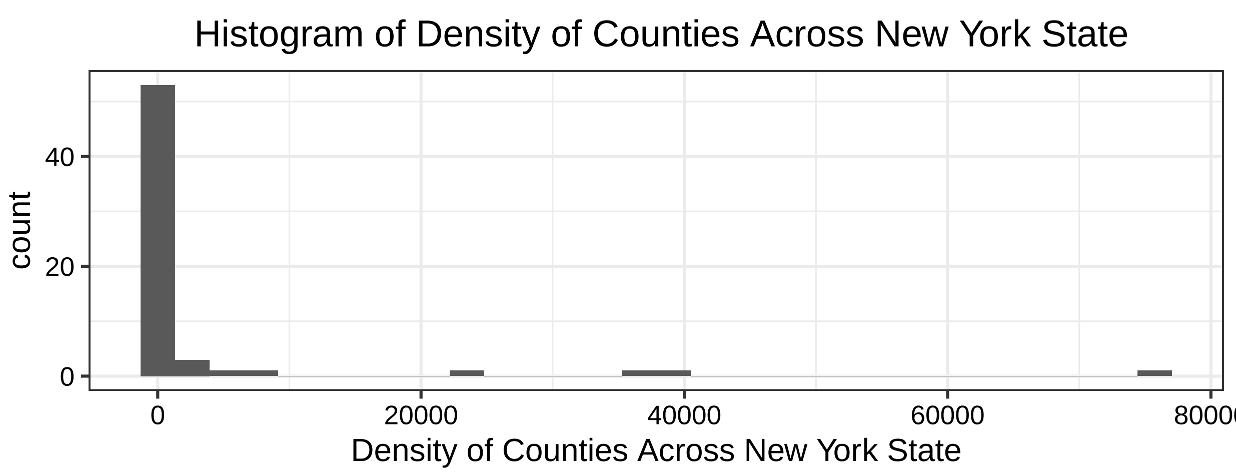


Figure 7: Density of Counties Across New York State

```r
## Log Transform

ggplot(data = combined_dat_ny_covid_pop, aes(log(density_permilessquared))) +
```

```
  geom_histogram() +
  xlab("Log of Density of Counties Across New York State") +
  ggtitle (" Log of Histogram of Density of Counties Across New York State")
```

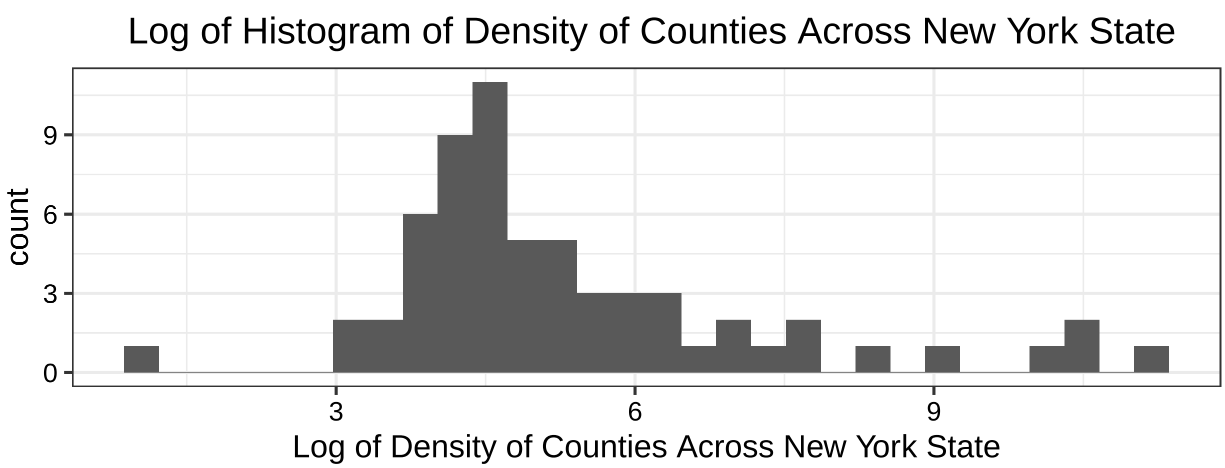


Figure 8: Log of Density of Counties Across New York State

```
shapiro.test(log(combined_dat_ny_covid_pop$density_permilessquared)) #Check normality
```

```
##
##  Shapiro-Wilk normality test
##
## data:  log(combined_dat_ny_covid_pop$density_permilessquared)
## W = 0.87808, p-value = 1.73e-05
```

```
########### Visualize Distribution of Predictor Variables by Settlement Type

ggplot(data = combined_dat_ny_covid_pop, aes(x= settlement_type, y= log(density_permiles
  geom_boxplot() +
  ggtitle ("Log of Absolute Population Size of Counties by Settlement Type") +
  xlab("Settlement Types") +
  ylab("Log of Absolute Population Size 2022")
```

```
ggplot(data = combined_dat_ny_covid_pop, aes(x= settlement_type, y= log(pop2022), fill =
  geom_boxplot() +
    ggtitle ("Log of Population Density of Counties by Settlement Type") +
  xlab("Settlement Types") +
  ylab("Log of Absolute Population Size 2022")
```

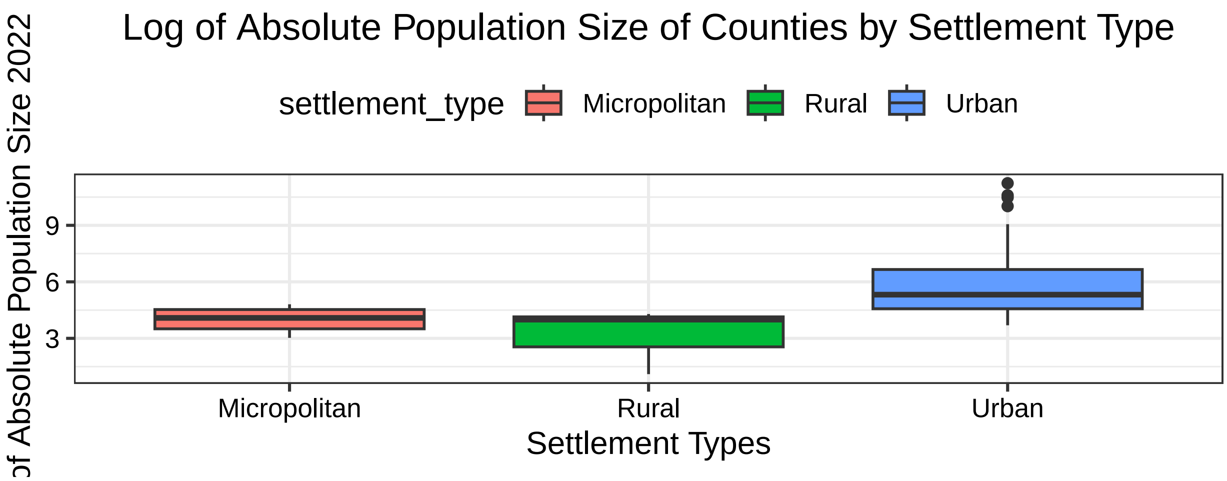


Figure 9: Log of Absolute Population Size of Counties by Settlement Type

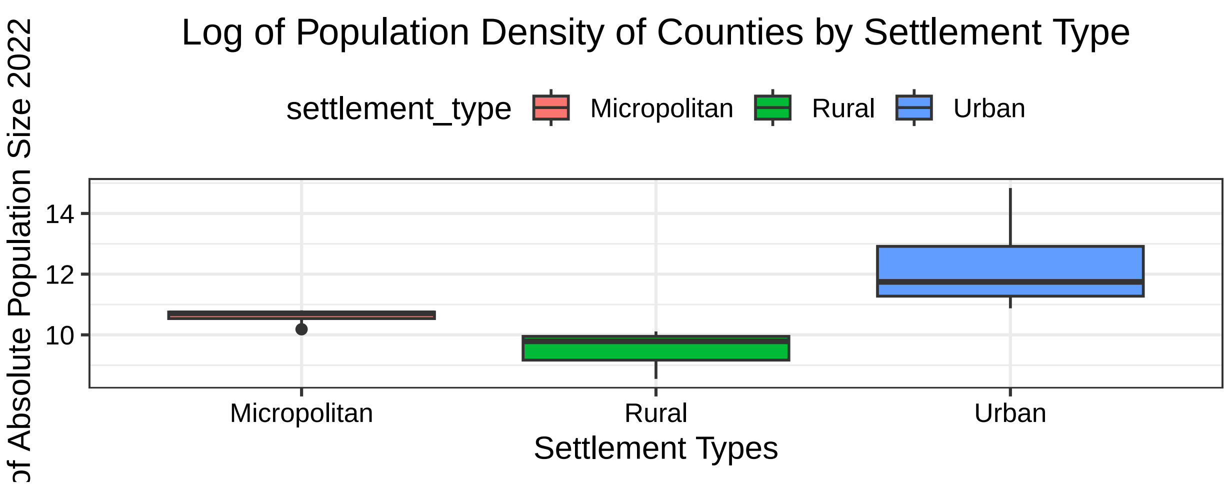


Figure 10: Log of Population Density of Counties by Settlement Type

0.3.3 Spatial Context of Data

```r
# Map of New York County Population Levels

# The EPSG code of the New York counties dataset is 4269. This is a geographic coordin

uscounty <- st_read('./Data/Spatial_Files/cb_2018_us_county_20m.shp', stringsAsFactors =
 filter(STATEFP == 36)
```

```
## Reading layer `cb_2018_us_county_20m' from data source
##   `/Users/danleizou/MiltonZouKhalsa__ENV872_EDA_FinalProject3/Data/Spatial_Files/cb_2
##   using driver `ESRI Shapefile'
## Simple feature collection with 3220 features and 9 fields
## Geometry type: MULTIPOLYGON
## Dimension:     XY
## Bounding box:  xmin: -179.1743 ymin: 17.91377 xmax: 179.7739 ymax: 71.35256
## Geodetic CRS:  NAD83
```

```r
# Reveal the names of the columns
colnames(combined_dat_ny_covid_pop)
```

```
##  [1] "County"                        "pop2022"
##  [3] "area_milessquared"             "density_permilessquared"
##  [5] "sum_new_positives"             "sum_cumulative_no_of_positive"
##  [7] "sum_total_number_of_tests"     "sum_cumulative_no_of_tests"
##  [9] "median_test_positive"          "settlement_type"
```

```r
# Join the flow data to our NWIS gage location spatial dataframe.
combined_dat_join <- merge(x = uscounty,
                           y = combined_dat_ny_covid_pop,
                           by.x = "NAME",
                           by.y = "County")

# Show the column names of the joined dataset.
colnames(combined_dat_join)
```

```
##  [1] "NAME"                          "STATEFP"
##  [3] "COUNTYFP"                      "COUNTYNS"
##  [5] "AFFGEOID"                      "GEOID"
##  [7] "LSAD"                          "ALAND"
##  [9] "AWATER"                        "pop2022"
## [11] "area_milessquared"             "density_permilessquared"
```

```
## [13] "sum_new_positives"             "sum_cumulative_no_of_positive"
## [15] "sum_total_number_of_tests"     "sum_cumulative_no_of_tests"
## [17] "median_test_positive"          "settlement_type"
## [19] "geometry"
```

```r
# Show the dimensions of this joined dataset.
dim(combined_dat_join)
```

```
## [1] 61 19
```

```r
# Map the population of each New York county in 2022.
ggplot() +
  geom_sf(data = combined_dat_join, aes(fill = log(pop2022))) +
  scale_fill_gradientn(colours = terrain.colors(10)) +
  ggtitle("COVID-19 in New York",
          subtitle = "Population by County in 2022") +
  labs(fill = 'Log of Variable')
```

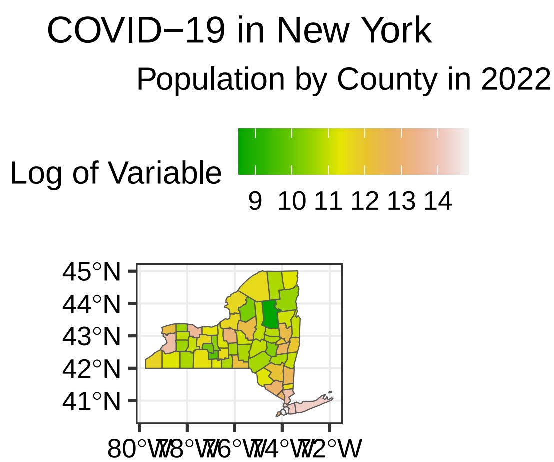


Figure 11: Population of New York Counties

```r
# Map the settlement types of each New York county in 2022.
ggplot() +
  geom_sf(data = combined_dat_join, aes(fill = settlement_type)) +
  ggtitle("COVID-19 in New York",
          subtitle = "Settlement Types by County in 2022") +
  labs(fill = 'Settlement Types')
```

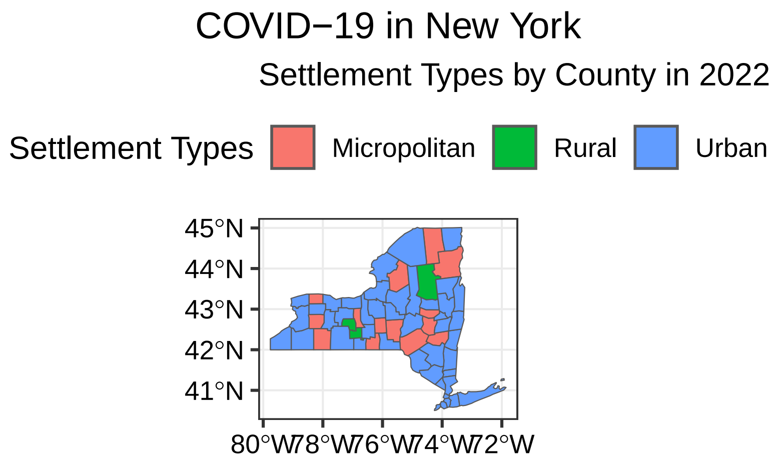


Figure 12: Settlement Types of New York Counties

```
# Map the sum of the cumulative number of tests administered in each New York county i
ggplot() +
  geom_sf(data = combined_dat_join, aes(fill = log(sum_cumulative_no_of_tests))) +
  scale_fill_gradientn(colours = terrain.colors(10)) +
  ggtitle("COVID-19 in New York",
          subtitle = "Cumulative Number of Tests Administered") +
  labs(fill = 'Log of Variable')
```

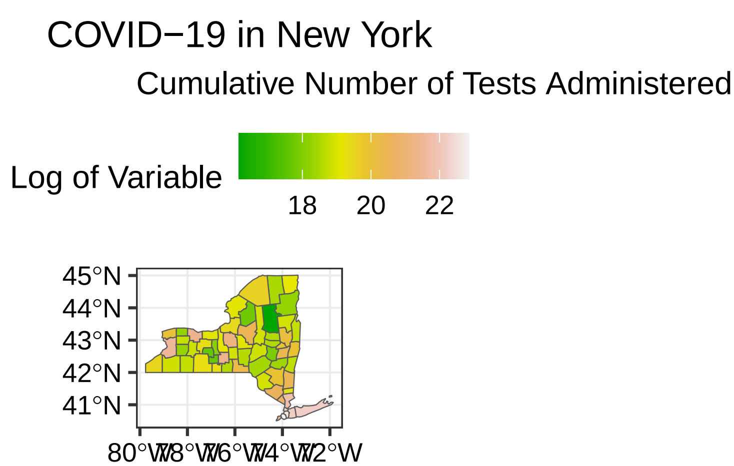


Figure 13: Cumulative Number of Tests Administered in Each New York County

```r
# Map the sum of the cumulative number of positive test results in each New York count
ggplot() +
  geom_sf(data = combined_dat_join, aes(fill = log(sum_cumulative_no_of_positive))) +
  scale_fill_gradientn(colours = terrain.colors(10)) +
  ggtitle("COVID-19 in New York",
          subtitle = "Cumulative Number of Positive Test Results in 2022") +
  labs(fill = 'Log of Variable')
```

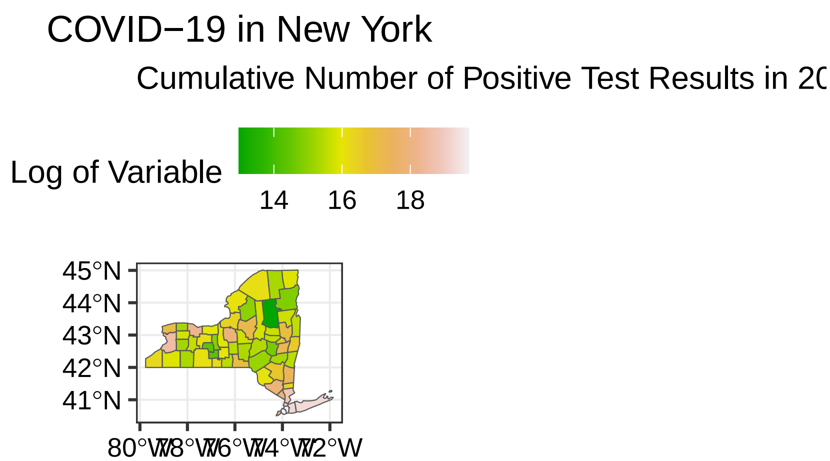


Figure 14: Cumulative Number of Positive Test Results in Each New York County

Export Processed data

```r
getwd() #Check working directory
```

```
## [1] "/Users/danleizou/MiltonZouKhalsa__ENV872_EDA_FinalProject3"
```

```r
#Full processed data set

write.csv2(combined_dat_ny_covid_pop,"./Data/Processed_Data/Combined_NY_COVID_Pop.csv")

#Collapsed data set

write.csv2(collapsed_dat_settlement_types,"./Data/Processed_Data/collapsed_dat_settlemen
```

0.4 Analysis

As a central question of this study is "How well does population density and absolute population predict COVID-19 cases?", the predictor variables are population density per miles squared and absolute population while the outcome variable is sum cumulative positive number of positive COVID-19 tests which is being used as a proxy for COVID-19 cases. Our unit of analysis is counties and settlement types depending on the primary objective of each sub-question. Settlement types are classified based on our definitions of rural, micropolitan, and urban settlement types. Our hypotheses for each study question is indicated below.

Question 1: What is the correlation between population density and absolute population and the number of COVID-19 cases (cumulative number of positive tests) across New York State?

Prior to the correlation analysis, the normality of absolute population, population density, and COVID-19 cases were examined and were determined to not be normally distributed (see exploratory analysis). The variables were log-transformed but were showed to still not be normally distributed after a Shapiro-Wilk test of normality was performed. As such, a Spearman correlation analysis for non-parametric data was carried out. The classification of the strength of the relationship was determined based on the value of r which ranges from 0 to 1 where r = 0 indicates no association and r = -1 or +1.

0.4.0.1 Absolute Population and COVID-19 Cases *Hypotheses*

Null Hypothesis: As the ranks of absolute population change, the ranks of the number of COVID-19 cases do not change.

Alternative Hypothesis: As the ranks of absolute population change, the ranks of the number of COVID-19 cases change.

Assumptions:

1. The relationship between both variables is monotonic.

```
# Spearman rank correlation test as distributions are skewed


correlation_results_absol_pop <- cor.test(x= log(combined_dat_ny_covid_pop$pop2022),
                                          y = log(combined_dat_ny_covid_pop$sum_cumulati
correlation_results_absol_pop
```

```
##
##  Spearman's rank correlation rho
##
## data:  log(combined_dat_ny_covid_pop$pop2022) and log(combined_dat_ny_covid_pop$sum_c
## S = 428, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.9892221
```

```
# Visualize plot (Log-transformed for better visualization)

ggplot(combined_dat_ny_covid_pop, aes(x = log(pop2022), y = log(sum_cumulative_no_of_pos
  geom_point() +
  ylab ("Log of COVID-19 Cases") +
  xlab ("Log of Absolute Population Across Counties") +
  ggtitle ("The Correlation Between Absolute Population
           Across Counties and COVID-19 Cases") +
  stat_smooth (method = 'lm') +
  annotate("text",x=9,y=20, label=(paste0("R=0.99")))
```

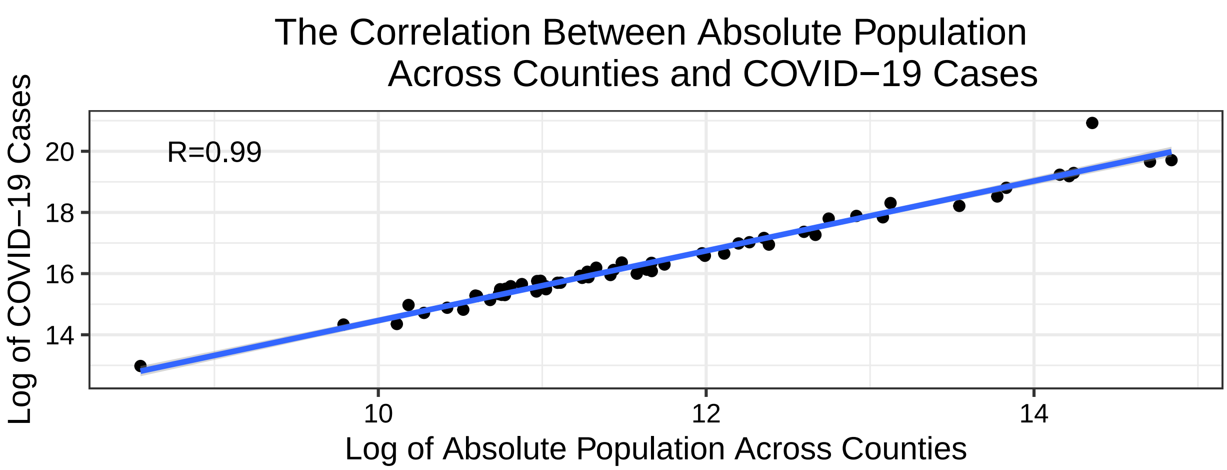


Figure 15: Correlation Between Absolute Population Across Counties and COVID-19 Cases

0.4.1 Population Density and COVID-19 Cases

Hypotheses:

Null Hypothesis: As the ranks of population density change, the ranks of the number of COVID-19 cases do not change.

Alternative Hypothesis: As the ranks of population density change, the ranks of the number of COVID-19 cases change.

Assumptions:

1. The relationship between both variables is monotonic.

```
# Spearman rank correlation test as distributions are skewed


correlation_results_pop_density <- cor.test(x= log(combined_dat_ny_covid_pop$density_per
                                             y = log(combined_dat_ny_covid_pop$sum_cumulati
correlation_results_pop_density
```

```
##
##  Spearman's rank correlation rho
##
## data:  log(combined_dat_ny_covid_pop$density_permilessquared) and log(combined_dat_ny
## S = 4522, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.8861273
```

```
# Visualize plot (Log-transformed for better visualization)

ggplot(combined_dat_ny_covid_pop, aes(x = log(density_permilessquared), y = log(sum_cumu
  geom_point() +
  xlab (" Log of Population Density (per miles squared)") +
  ylab ("Log of COVID-19 Cases") +
  ggtitle ("The Correlation Between Population Densities
           Across Counties and COVID-19 Cases") +
  geom_smooth (method = 'lm')+
  annotate("text",x=3,y=20, label=(paste0("R=0.89")))
```

Question 2: What is the relationship between the predictor variable: settlement types and the response variable: cumulative COVID-19 cases?

0.4.1.1 Negative Binomial Regression

In addition to the correlation analysis, we carried out a negative binomial regression to further understand the relationship between settlements types (determined by levels of absolute population) and cumulative COVID-19

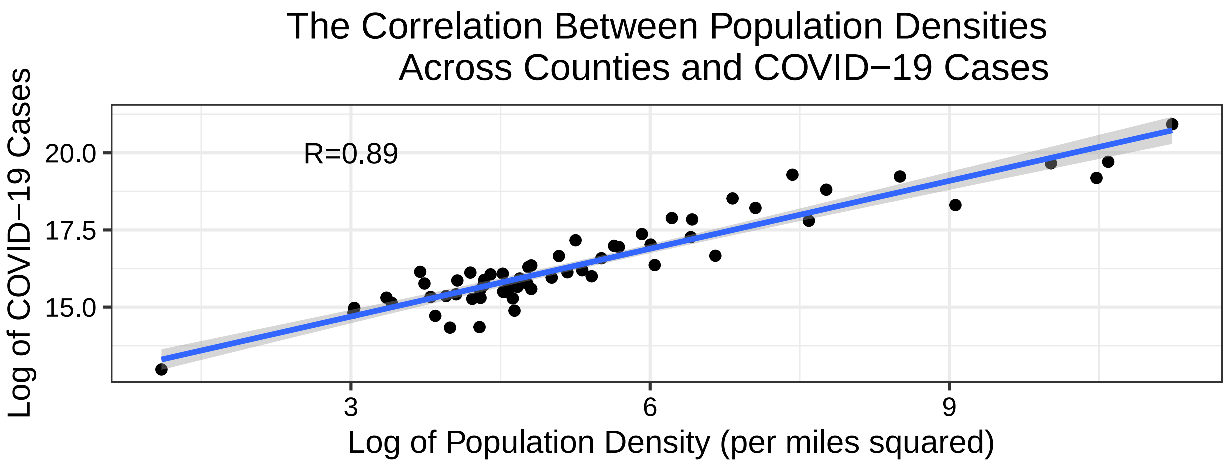


Figure 16: Correlation Between Population Densities Across Counties and COVID-19 Cases

cases. We used a negative binomial regression as based on the exploratory plots, we believed that the outcome variable can be classified as over-dispersed count data. We check our assumption that the outcome variable,“sum_cumulative_no_of_positive”, was overdispersed by carrying out a Poisson regression and found that the negative binomial regression was a better fit for the data. Further, we carried out a Chi-Square Goodness of Fit test for our negative binomial regression model with residual deviance of 75.355 on 59 degrees of freedom and the p-value obtained was 0.07. This means that the evidence is more supportive of the fact that the model is a good fit.

Hypotheses:

Null Hypothesis: There is no trend between the predictor variable (settlement types) and outcome variable (cumulative COVID-19 cases).

Alternative Hypothesis: There is a trend between the response (settlement types) and outcome variables (cumulative COVID-19 cases).

Assumptions:

1. The response variable (COVID cases) is a count variable.
2. Each observation of data is independent of each other.
3. The mean and variance are not equal.

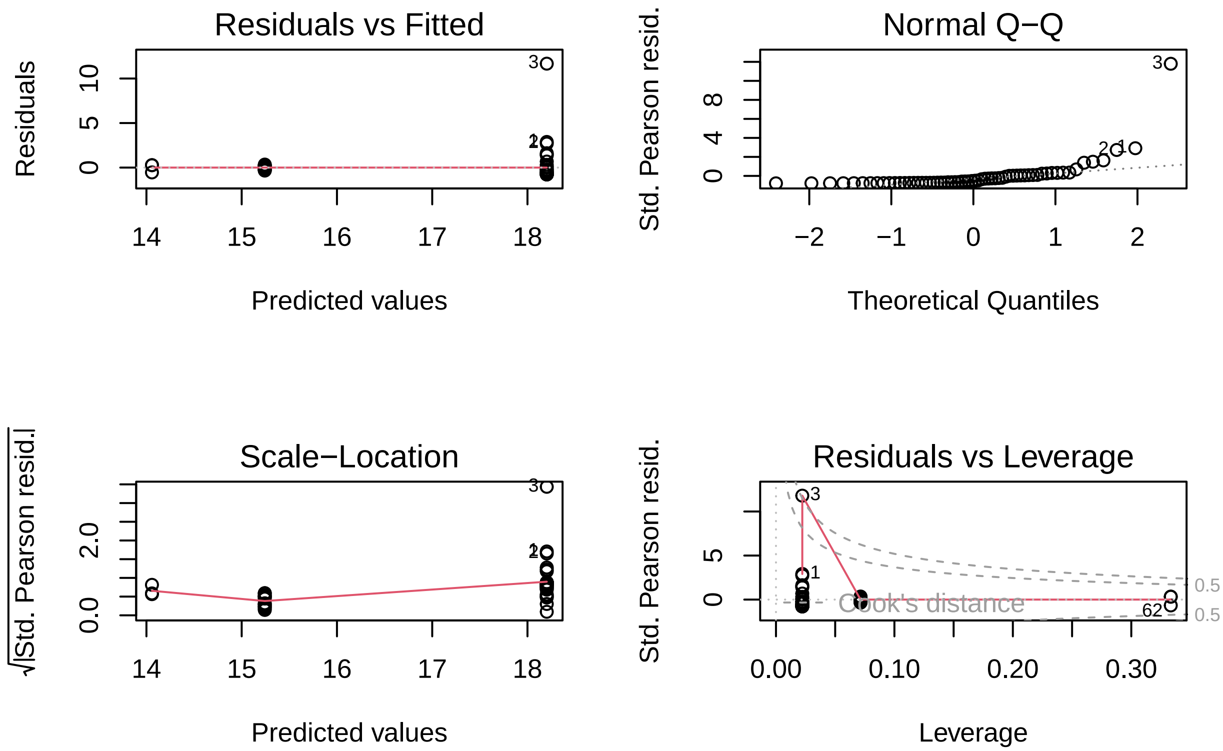
```
## Negative Binomial Regression

summary (modelnb <- glm.nb(sum_cumulative_no_of_positive ~ factor(settlement_type), data
```

```
##
```

```
## Call:
## glm.nb(formula = sum_cumulative_no_of_positive ~ factor(settlement_type),
##     data = combined_dat_ny_covid_pop, init.theta = 0.6722916249,
##     link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5768  -1.2869  -0.6950   0.0667   3.9330
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                   15.2425     0.3260  46.763  < 2e-16 ***
## factor(settlement_type)Rural  -1.1844     0.7759  -1.526    0.127
## factor(settlement_type)Urban   2.9602     0.3732   7.931 2.17e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.6723) family taken to be 1)
##
##     Null deviance: 122.511  on 61  degrees of freedom
## Residual deviance:  75.366  on 59  degrees of freedom
## AIC: 2273.8
##
## Number of Fisher Scoring iterations: 3
##
##
##               Theta:  0.672
##           Std. Err.:  0.102
##
##  2 x log-likelihood:  -2265.783
```

```
par (mfrow = c(2,2))
plot(modelnb) #Check fit
```




```
# Test of Fitness

pchisq(q=modelnb$deviance, df=modelnb$df.residual,
lower.tail=FALSE)  #Check model fit
```

```
## [1] 0.0740414
```

```
## Check our assumption that a negative binomial is a better model than the poisson mo

summary (modelpoisson <- glm(sum_cumulative_no_of_positive ~ factor(settlement_type), fa
```

```
##
## Call:
## glm(formula = sum_cumulative_no_of_positive ~ factor(settlement_type),
##     family = "poisson", data = combined_dat_ny_covid_pop)
##
## Deviance Residuals:
##    Min       1Q  Median       3Q      Max
## -11105  -10010   -5977      168    66186
##
```

```
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  15.2424841  0.0001309  116408   <2e-16 ***
## factor(settlement_type)Rural -1.1844175  0.0005279   -2244   <2e-16 ***
## factor(settlement_type)Urban  2.9601778  0.0001320   22427   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 1.0813e+10  on 61  degrees of freedom
## Residual deviance: 8.9559e+09  on 59  degrees of freedom
## AIC: 8955869537
##
## Number of Fisher Scoring iterations: 6
```

```
## Summary inference: Residual deviance is much larger than degrees of freedom (DF). N
```

Question 3: What is the correlation between absolute population and population density and the number of COVID-19 tests done?

> Similar to question 1, prior to the correlation analysis, the normality of absolute population, population density, and COVID-19 cases were examined and were determined to not be normally distributed (see exploratory analysis). The variables were log-transformed but were showed to still not be normally distributed after a Shapiro-Wilk test of normality was performed. As such, a Spearman correlation analysis for non-parametric data was carried out. The classification of the strength of the relationship was determined based on the value of r which ranges from 0 to 1 where r = 0 indicates no association and r = -1 or +1.

0.4.1.2 Absolute Population and COVID-19 Cases *Hypotheses:*

Null Hypothesis: As the ranks of absolute population change, the ranks of the number of COVID-19 tests conducted do not change.

Alternative Hypothesis: As the ranks of absolute population change, the ranks of the number of COVID-19 tests conducted change.

Assumptions

1. The relationship between both variables is monotonic.

```r
# Spearman rank correlation test as distributions are skewed


correlation_results_absol_pop <- cor.test(x= log(combined_dat_ny_covid_pop$pop2022),
                                          y = log(combined_dat_ny_covid_pop$sum_cumulati
correlation_results_absol_pop
```

```
##
##  Spearman's rank correlation rho
##
## data:  log(combined_dat_ny_covid_pop$pop2022) and log(combined_dat_ny_covid_pop$sum_c
## S = 996, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.9749188
```

```r
# Visualize plot (Log-transformed for better visualization)

ggplot(combined_dat_ny_covid_pop, aes(x = log(pop2022), y = log(sum_cumulative_no_of_tes
  geom_point() +
  ylab ("Log of COVID-19 Tests Conducted") +
  xlab ("Log of Absolute Population Across Counties") +
  ggtitle ("The Correlation Between Absolute Population
           Across Counties and COVID-19 Tests Conducted") +
  stat_smooth (method = 'lm') +
  annotate("text",x=9,y=22, label=(paste0("R=0.97")))
```

0.4.1.3 Population Density and COVID-19 Cases

Hypotheses:

Null Hypothesis: As the ranks of population density change, the ranks of the number of COVID-19 tests conducted do not change.

Alternative Hypothesis: As the ranks of population density change, the ranks of the number of COVID-19 tests conducted change.

Assumptions:

1. The relationship between both variables is monotonic.

```r
# Spearman rank correlation test as distributions are skewed

```

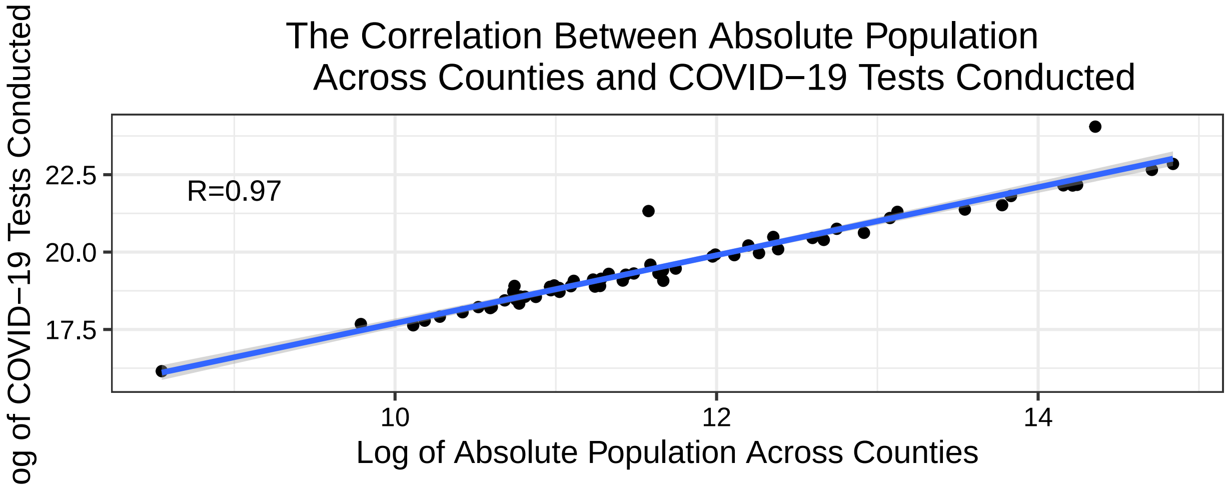


Figure 17: Correlation Between Absolute Population Across Counties and COVID-19 Tests Conducted

```
correlation_results_pop_density <- cor.test(x= log(combined_dat_ny_covid_pop$density_per
                                             y = log(combined_dat_ny_covid_pop$sum_cumulati
correlation_results_pop_density
```

```
##
##  Spearman's rank correlation rho
##
## data:  log(combined_dat_ny_covid_pop$density_permilessquared) and log(combined_dat_ny
## S = 5602, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.8589308
```

```
# Visualize plot (Log-transformed for better visualization)

ggplot(combined_dat_ny_covid_pop, aes(x = log(density_permilessquared), y = log(sum_cumu
  geom_point() +
  xlab (" Log of Population Density (per miles squared)") +
  ylab ("Log of COVID-19 Tests Conducted") +
  ggtitle ("The Correlation Between Population Densities
           Across Counties and COVID-19 Tests Conducted") +
  geom_smooth (method = 'lm')+
  annotate("text",x=3,y=23, label=(paste0("R=0.86")))
```

Question 3b: Does the stronger correlated relationship vary among settlement types?

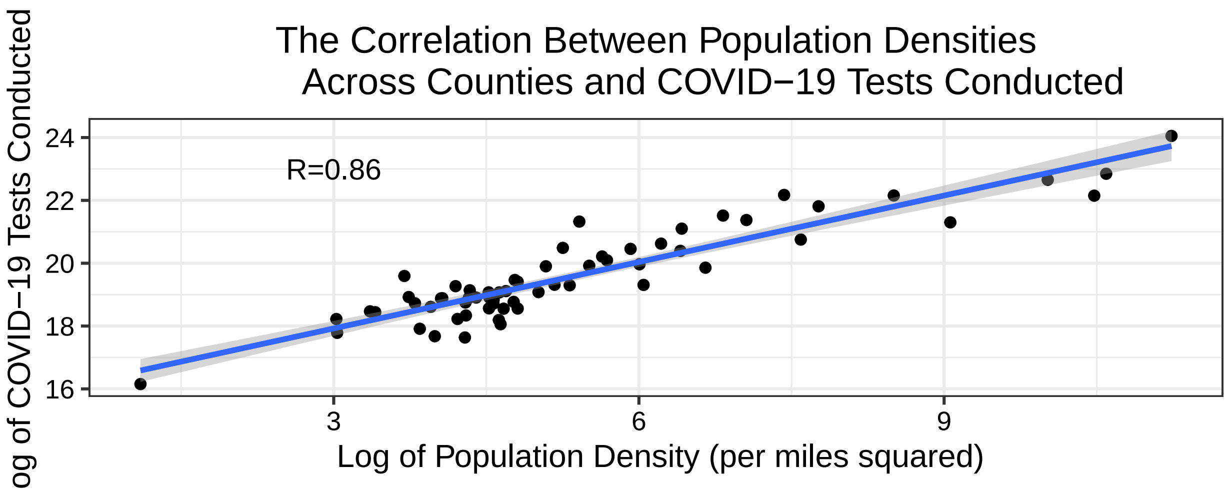


Figure 18: Correlation Between Absolute Population Densities Across Counties and COVID-19 Tests Conducted

```
### Correlation Plots by Settlement Type

##Urban

Urban_dat <- combined_dat_ny_covid_pop %>%
  filter(settlement_type=="Urban")


correlation_results_absolute_pop_urban <- cor.test(x= log(Urban_dat$pop2022),
                                                   y = log(Urban_dat$sum_cumulative_no_of_tests),

correlation_results_absolute_pop_urban
```

0.4.1.4 Absolute Population and Settlement Types

```
##
##  Spearman's rank correlation rho
##
## data:  log(Urban_dat$pop2022) and log(Urban_dat$sum_cumulative_no_of_tests)
## S = 632, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.9583663
```

```r
## Micropolitan

Micropolitan_dat <- combined_dat_ny_covid_pop %>%
  filter(settlement_type=="Micropolitan")


correlation_results_absolute_pop_microp <- cor.test(x= log(Micropolitan_dat$pop2022),
                                                    y = log(Micropolitan_dat$sum_cumulative_no_of_

correlation_results_absolute_pop_microp
```

```
##
##  Spearman's rank correlation rho
##
## data:  log(Micropolitan_dat$pop2022) and log(Micropolitan_dat$sum_cumulative_no_of_te
## S = 106, p-value = 0.002105
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.767033
```

```r
##Rural

Rural_dat <- combined_dat_ny_covid_pop %>%
  filter(settlement_type=="Rural")


correlation_results_absolute_pop_rural <- cor.test(x= log(Rural_dat$pop2022),
                                                   y = log(Rural_dat$sum_cumulative_no_of_tests),

correlation_results_absolute_pop_rural
```

```
##
##  Spearman's rank correlation rho
##
## data:  log(Rural_dat$pop2022) and log(Rural_dat$sum_cumulative_no_of_tests)
## S = 2, p-value = 1
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.5
```

```
ggplot(combined_dat_ny_covid_pop, aes(x = log(pop2022), y = log(sum_cumulative_no_of_pos
  geom_point() +
  ylab ("Log of Cumulative Number of COVID-19 Cases") +
  xlab ("Absolute Population (2022)")+
  facet_wrap(vars(settlement_type))
```

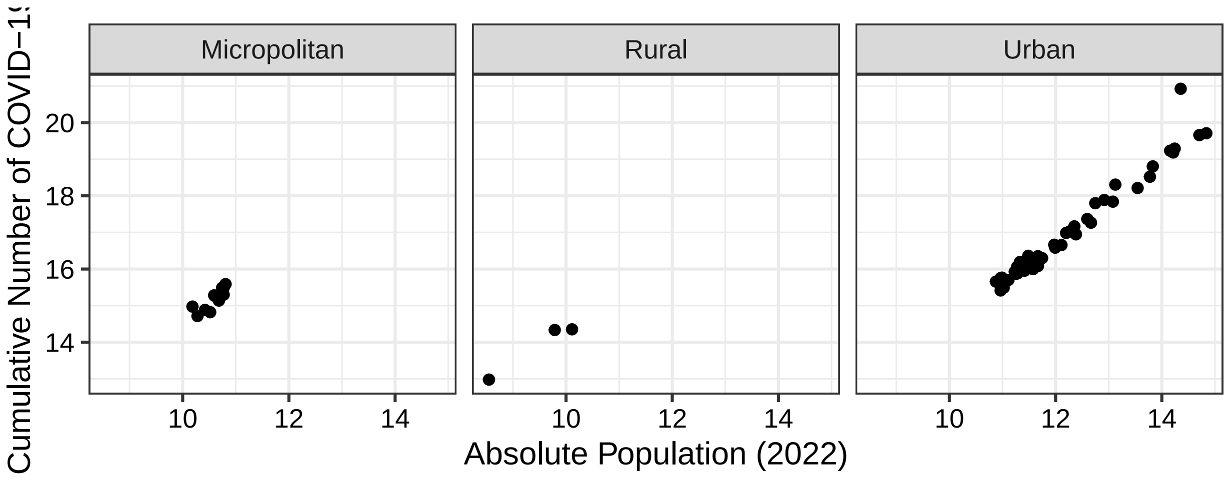


Figure 19: Log of Cumulative COVID-19 Cases Across Settlement Types

0.4.1.5 Visualization of 3b

0.5 Summary and Conclusions

0.5.0.1 General Overview of Data

The most populous county in New York State according to the information we obtained from the US Census Bureau is Kings County which has a population of over 2.7 million people. Meanwhile, the least populous county was Hamilton county with a little over 5000 residents. Despite Kings County have the most residents in the state, New York City was the most densely populated county - with 75,739 residents per squared miles. In addition to being the least populated county, Hamilton was the least dense of the 62 counties in New York State.

0.5.0.2 Correlation between Absolute Population and Population Density with COVID-19 Cases

We set out to answer our central question, "How well absolute population and population density predict COVID-19 case numbers in the diversely sized New York State?" by first examining the correlation between population density and absolute population and the number of COVID-19 cases across New York. In both cases of population density and absolute population, after performing a Spearman correlation for both variables we had a p-value of 2.2e-16, which suggests that the correlated relationship was statistically significant. This means we have sufficient evidence to reject our null hypothesis that as the ranks of absolute populationand population density change, the ranks of the number of COVID-19 cases do not change and instead accept our alternative hypothesis that as the ranks of absolute population and population density change, the ranks of the number of COVID-19 cases does change. It is also demonstrated in the visualized plots that there is indeed a positive correlation between the variables as the R-squared value for the population density plot was 0.89 and 0.99 for the absolute population plot. Both show a strong correlation, but it is stronger with absolute population.

0.5.0.3 Association between COVID-19 Cases and Settlement Types

In the second question, we examined the relationship between our predictor variable (settlement types) and response variable (cumulative COVID-19 cases). We did not control for potential confounding factors which limits the strength of the conclusions we are able to draw from this analysis. After performing a negative binomial regression, we observed that the variable level, rural, has a coefficient of -1.1844 which is associated with a p-value of 0.127. This means that when compared to the reference settlement level, micropolitan, the difference in the logs of the expected counts is expected to be 1.1844 lower for rural when compared to micropolitan. However, with a p-value of 0.127, the evidence is more supportive of the fact that this relationship is not significant. Meanwhile, we observed that when compared to the reference level, micropolitan, the difference in the logs of expected counts is expected to be 7.931 higher for urban settlements. The p-value obtained for this association is less than 0.05 indicating that the evidence is more supportive of the fact that this association is statistically significant.

0.5.0.4 Correlation between Absolute Population and Population Density with Number of COVID-19 Tests Conducted

In our last question, we examined the correlation between absolute population and population density and the number of COVID-19 tests conducted in New York. Similar to the results of our first question, after performing a Spearman rank correlation test with both absolute population and population density we found that both had a p-value of 2.2e-16, indicating that the correlated relationship was statistically significant.Therefore, we have sufficient evidence to reject both null hypotheses that as ranks of absolute populationand population density change, the the ranks of the number of COVID-19 tests conducted do not change. Instead, we accept our alternative hypotheses that as ranks of absolute population and population density change, the ranks of the number of COVID-19 tests conducted does change. This is also shown in our visualized plots, with the absolute population plot having an R-squared value of 0.97 and the population density plot having an R-squared value of 0.86. Both show a strong correlation, but it is stronger with absolute population.

After determining that the correlation between absolute population and number of COVID-19 tests conducted is stronger, we examined within those parameters to see if this correlation varies among settlement types. We performed the Spearman rank correlation test on all three settlement types. Urban settlements had a p-value of 2.2e-16 and an R-squared value of 0.96, micropolitan settlements had a p-value of 0.002 and an R-squared value of 0.77, and rural settlements had a p-value of 1 and an R-squared value of 0.5. Two of the p-values show that the correlated relationships are significant, and rural didn't have a significant correlated relationship. The correlation is strongest with urban settlements. However, we do acknowledge that the rural settlements only had 3 data points, which is much fewer than the amount of data of micropolitan and urban settlements.

0.6 Conclusion

In conclusion, we do see a strong correlation between both absolute population and population density and the number of COVID-19 cases in New York, as well as the relationship between both absolute population and population density and the number of COVID-19 tests conducted in New York. The absolute population correlation to the number of COVID-19 tests conducted was the stronger relationship. It is important for us to know the correlation between COVID-19 cases and settlement type so we can be better informed about what factors influence the spread of infectious diseases for the future.

0.7 References

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