covid tree analysis

Cross sectional Analysis of Covid-19 Spread in US Counties

Introduction

Covid-19 or corona virus started its spread from China at the end of Year 2020. By February 2020, cases start to appear in the United States and spread rapidly across all the states. The growth in the number of cases has been exponential like any other case of infectious disease. Scientists and researchers around the world are actively looking at the data to understand this virus. In uncertain times like these, it is important to know the factors that affect the spread of this virus to make plausible predictions about the future.

Since the first case of covid-19 was discovered in the US in Snohomish county in the Washington State, the virus has now spread to other places and in some cities like New York and Chicago, the spread has been faster, making them new hotspots for the virus even though cities like Seattle & Los Angeles reported their first cases before these cities. A simple line graphs for some counties that saw their first case of infection around the same time shows the difference in the rate of virus spread.

This poses a question that; what are the different factors that are leading to differences in the pace of covid-19 spread across US counties? Can a cross sectional comparison of these counties help us identify any socio-economic or geographical feature that has any effect on virus spread and can we use these features to predict the number of infections for other counties that are behind in trend. We carry out a cross sectional analysis of counties and their features in comparison to the number of covid-19 cases reported by using statistical and data mining tools. The purpose of the report is to identify any trend or characteristics of counties that are connected to the pace of virus spread.

Data

- **Cases & Deaths:** We collect the data of total number of covid-19 infection cases and deaths at county level as on April 30, 2010. The data has been obtained from NYTimes Github repository. We selected 1462 counties which had non-zero number of deaths reported. This was done because ACS data was only available for counties that have any death reported for covid-19.We divided the total number of cases by population to have cases per hundred thousand of population. This gives a good comparison of cases across counties with different population size. From now on we will refer to cases as cases per hundred thousand of population. The density graph shows that a lot of counties have lower number of cases and a very skewed distribution of cases.
- **Days since first Case:** We calculated the total number of days since 1st infection for all counties as on April 30, 2020. This variable measures the time period for spread of virus. A scatter plot of days since first infection and number of cases per 100 thousand people shows that there is a general exponential trend but some counties have been able to keep their number of cases down even though the got the virus before other counties.

```
ggplot(covid, mapping = aes(days_since_first_infection1,cases1))+geom_point()+labs(title= "Scatter Plot
```

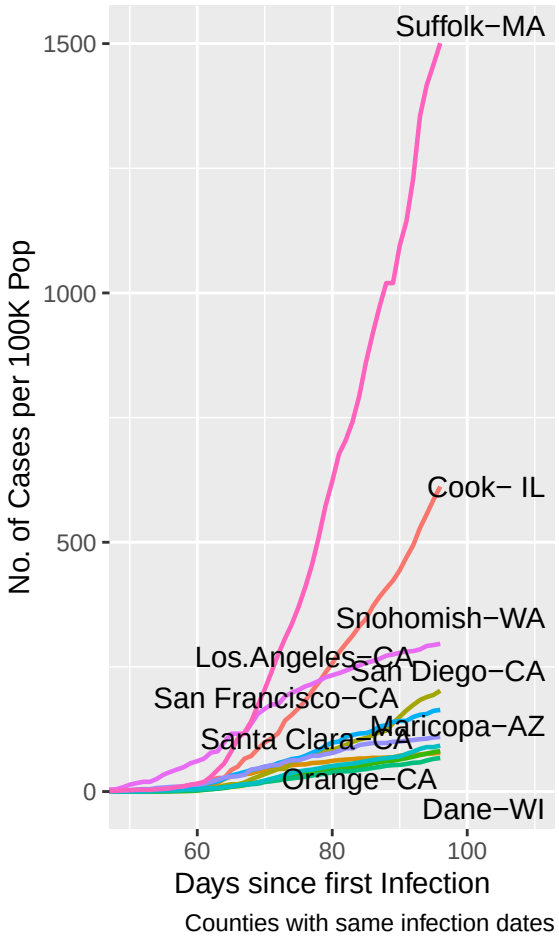


Figure 1: Trend Line Graph for Counties

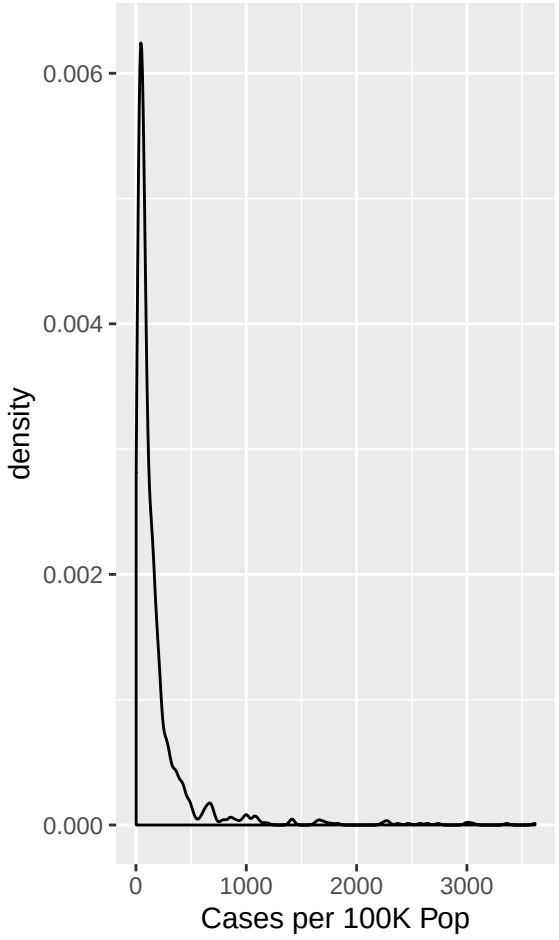
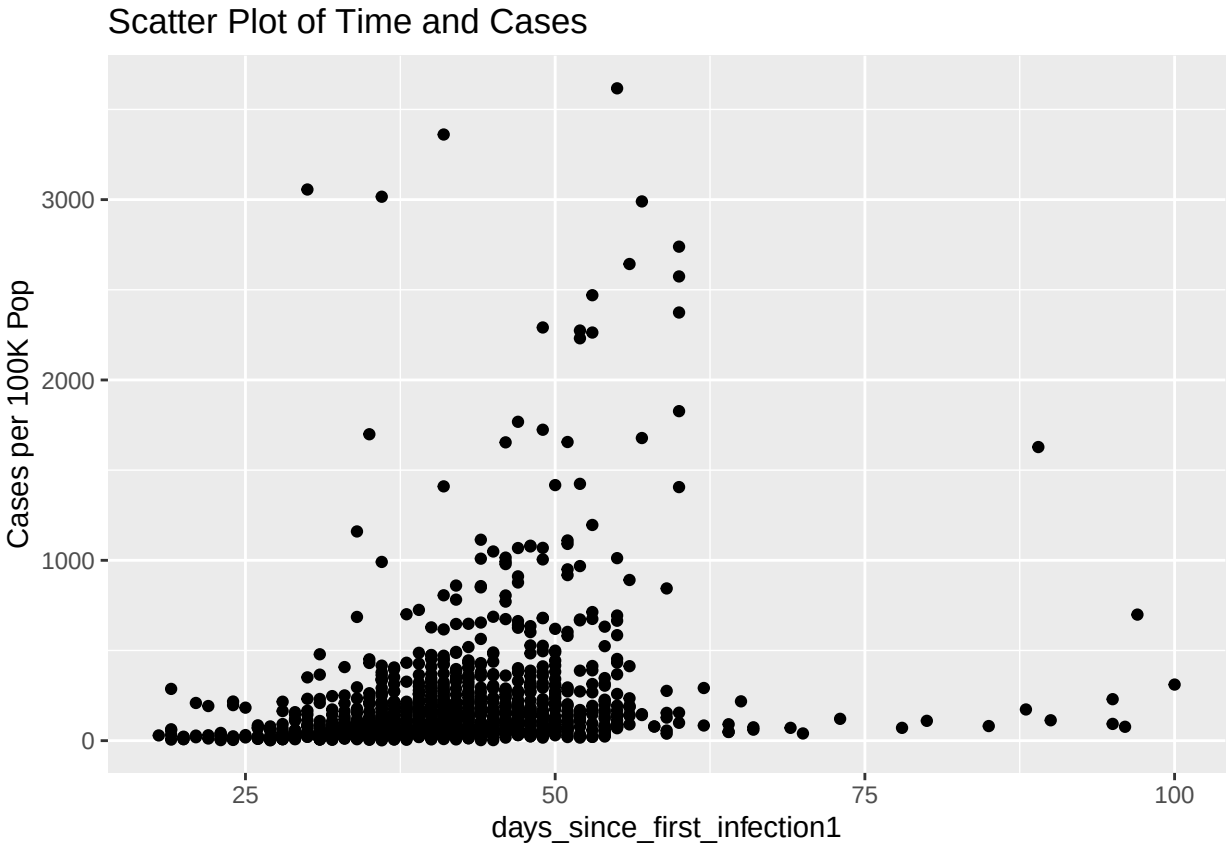


Figure 2: Density Graph for Number of Cases



- **Days since Stay at home orders:** Similarly, we calculated number of days since stay at home orders were issued by State and County authorities as on April 30, 2020. This gives us the time period for interventions taken by authorities. Along with this we also obtained Google's movement analytics for each county which gives a percentage decline in people's movement from the baseline average.
- **Socio-Economic Variables:** We obtained socio economic variables on the population of counties from American Community Survey reports. Main variables include: Unemployment rate, % of White, % of Households in Poverty, % of population employed in different industries, median income and % of population with a bachelor's degree.

- **Demographic Variables:** % of male, % of age between 18 and 64, % of White, Median age, % of total households as family etc. The complete list is attached in the appendix.
- **Geographical variables:** We obtained variables like population density, average of last 8 years highest summer temperature and humidity rate. We wanted to obtain the recent monthly averages for counties but could not find the latest data, so we used these variables.

There were many socio-economic variables that were very highly correlated, so we dropped some variables and finalized 30 variables for this analysis. The complete list of these variables is provided in the appendix.

Note :Before we start with our analysis, it is important that we acknowledge that number of cases reported depends heavily on the number of tests conducted. Unfortunately, testing policy has not been uniformed across US and that can lead to a measurement error in cases. Secondly, there are reports that the given time frame for start of covid-19 is not accurate and it is presumed that covid-19 reached many major cities of the US way before the first case was reported.

However, due to data limitation, we must assume that the official reporting of cases represents somewhat actual position for the start of virus infection. For testing, we tried to get data on total tests conducted on county level but only find the data at state level. So, we calculated total tests conducted per hundred thousand people for each state and then use it for each county in respective state. This is not perfect, but we

are assuming that the rate of testing is uniform across counties in each state and will help in differentiating counties of different states based on testing rates.

Methods

Principal Component Analysis

We use principal component analysis to see if we can look at the variations in the counties and evaluate if those variations are related to number of cases in these counties. After scaling the data, we see that 90% of variation in 30 explanatory variables can be explained by 16 principal components, pointing towards correlation between these variables.

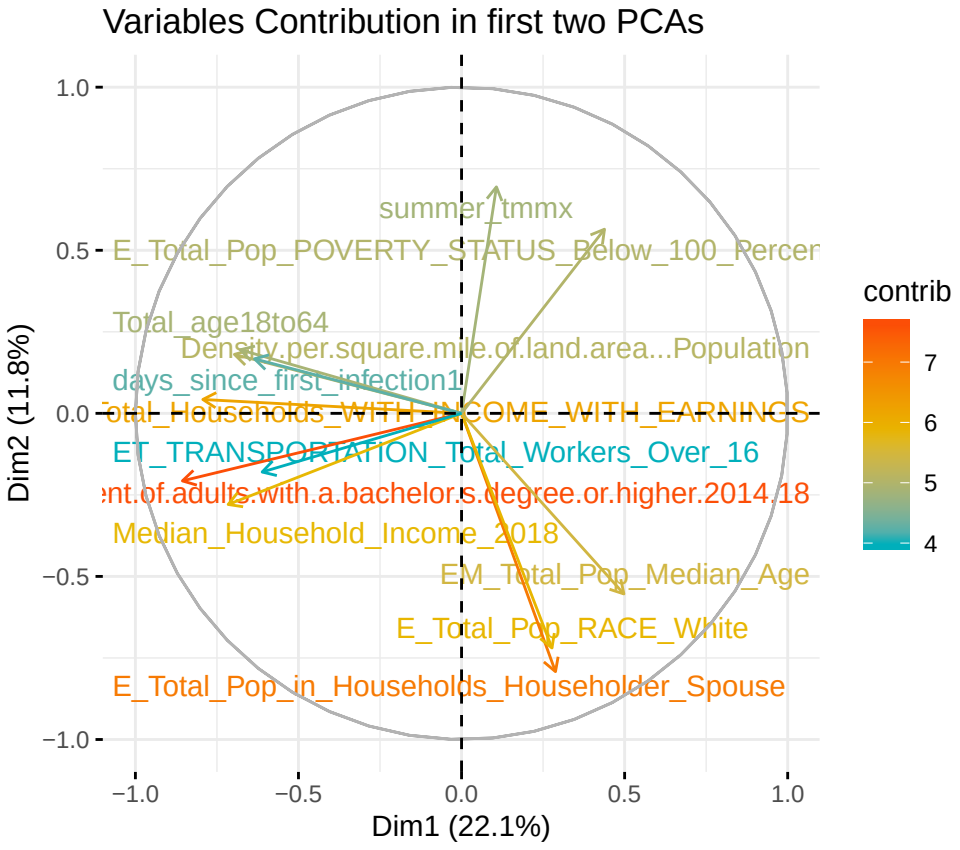
The biplot of main variables that contribute to variance is first two PCs shows that PC1 captures variation in population density, time since first case, proportion of population between 18 and 64 and change in the movement of people to their workplaces.

```
library(factoextra)
```

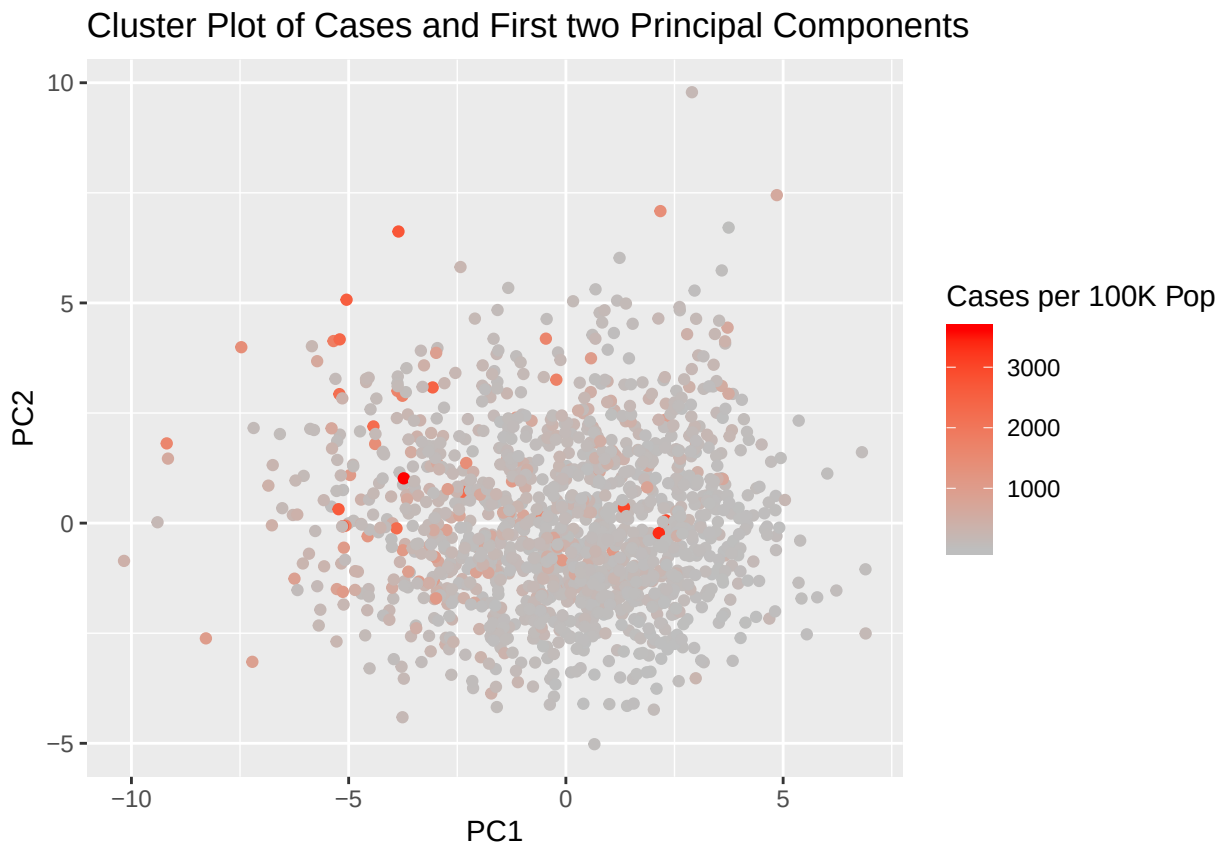
```
## Warning: package 'factoextra' was built under R version 3.6.3
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

```
covid = read.csv("covid2zargham.csv")
X= covid[,-c(1:5, 35,37)]
PCA = prcomp(X, scale. = TRUE)
fviz_pca_var(PCA, col.var="contrib",
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),select.var = list(contrib=12),
             repel = TRUE, title = "Variables Contribution in first two PCAs " )
```



```
scores = PCA$x
scores= cbind(covid$cases1, scores)
scores = as.data.frame(scores)
qplot(PC1,PC2, data=scores, color= V1)+scale_color_gradient(low = "grey", high= 'red')+ggtitle("Cluster
```



Plotting the scatter plot with first two components with color scaling the number of cases, we see that there is no specific clustering of high cases counties but generally, we see that there are more red points in the upper left quadrant of the graph. Which means that variables mentioned above are correlated with higher number of covid-19 cases in counties. Similarly, lower right quadrant has less number of high case counties and from the biplot we saw that this is associated with higher proportion of white population, higher median age and higher proportion of spouse households in total households. Interestingly, we cannot say much about the effect of temperature on virus spread but there does seems to be a slight negative correlation between temperature and virus spread.

Negative Binomial Logistic Model

Since our outcome is count of cases with overdispersion, we fit a negative binomial logistic model on our data. As we have only those counties that reported the any cases, we use zero truncated negative binomial logistic model. This model has been used by Wu,Nethery,Sabath (2020) in their study of exposure to air pollution and its effect on covid death rate in US counties. We include all the explanatory variables in our model to which of them are correalted with cases count. The summary of the model is provided in the appendix.

We can clearly see that infection start date is positively correlated with the log count of cases. Along with it, stay at home orders are linked negatively to cases growth which is also theoretically correct. Another important variable is population density per square mile area which means that congested counties see higher number of cases. Counties with higher percentage of educated people and people with race as white also observe lower cases. Higher proportion of people employed in educational and health services and lower

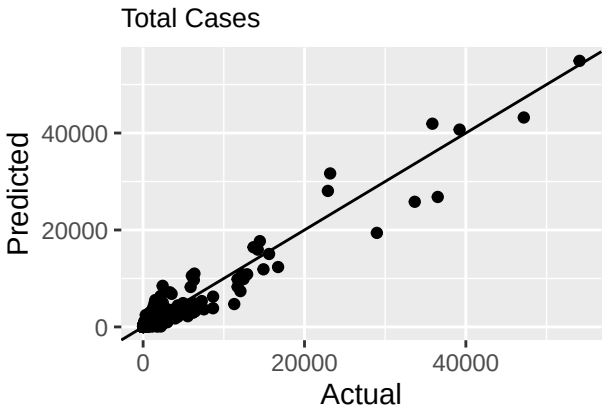
proportion of people in arts, recreational, accommodation and public administration industries are correlated with higher cases of virus. The signs for these co-efficient are consistent with our PCA analysis.
We have a problem of small sample and it would have been better if the sample size could have been bigger. We have Hauck-Donner effect in two variables: % of population age 18 to 64 and E_Total_Households_TYPE_Family. The co-efficient magnitude cannot be considered as casual effect. However, the signs of co-efficient points towards some plausible correlation between number of cases and different variables. To check the predictive power of our model, we do 300 test/ train splits of our sample and run the model. We get a RMSE of around 240 cases per hundred thousand people. Plotting the predicted values against the actual values, we see that the model on average underpredicts the number of cases for counties with high number of cases and overpredicts for counties with lower number of cases. Overall, we do not think this model does a good job at prediction.

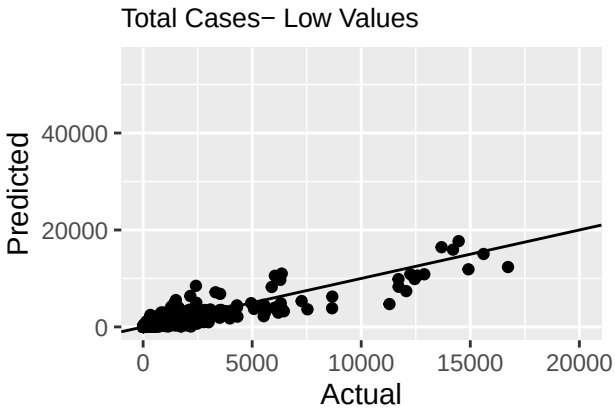
```
## [1] 242.3946
```

```
yhat1 = predict(m12, type = 'response')
modelfit1= as.data.frame(cbind(yhat1, covid$cases1))

b1=ggplot(modelfit1, mapping = aes(V2, V1))+geom_point()+geom_abline(slope = 1,intercept = 0)+ labs(x="

b2= ggplot(modelfit1, mapping = aes(V2, V1))+geom_point()+geom_abline(slope = 1,intercept = 0)+ labs(x=

grid.arrange(b1,b2, widths=c(0.5, 0.5) , heights=c(0.7, 0.7),ncol = 2)
```

We try the same model with actual number of cases rather than number of cases per hundred thousand people and include log of population in the model to control for community size. The RMSE of 300 test and train split comes out to be around 1500 and the prediction graph is more balanced as compared to the model with cases per hundred thousand population. Therefore, we prefer using total number of cases in the model

for prediction purpose.





Analysis using Random Forest and Boosting Trees

In this section we perform an anlysis over the county level data of Covid-19 reports. We know that the tree models are characterized to be flexible fitters that can capture non-linearity and interactions between the variables. Tree models also are useful when we have information in different magnitudes as this case, where we have variables that are values while others are proportions. Specifically, we will work with with a Random Forest model and a Boosting Tree mode. The first, model mainly fit many large trees to bootstrap-resampled versions of the training data by relevance, while the second fits several trees to reweighted versions of the training dataset and then classifies by weighted majority relevance.

Our goal in this section will be fittin models on cases per 100k population. As in the previous section, our data set includes a set of socieconomic, demographic and geographical variables for many US states. The data set includes information about the Covid crisis such as tests per 100k population and policies issued to fight the pandemic. By the use of this sort of models we can get information about variable relevance, that can shed light about what variables make more likely the presence of the disease in a community and to improve the understanding of this pandemic. To run our models, we first splitted our sample in a training and test subsamples in order to confirm the model performance. After this, We created 1000 trees by random forest including a minimum of 5 features per bucket, and later we compute the out of sample RMSE.

Table XX summarizes the variable importance information derived from the random forest model (RF). We can notice that as expected the population density per square mile plays an importante role as expected. It suggest that Counties more dense must expect a higher number of people infected, as happened in New York state. The RF model also suggets that the number of test performed in county matters, this goes in the direction of people that support the lower initial of reported cases in the US was due to the lack of testing. The RF model shows that the variable that measures the decrease in number of people at work places is

relevant, which may suggest two things, one that places that started the lockdown earlier could have more cases or the lockdown did stop the virus expansion, since variable importance here does not gives us the impact sign. From the variable importance table we can also see covariates related with the population that have had more exposition the the virus, such as occupation. We can see that the proportion of people working at food services in a county explains the number of cases, which make sense since this sort of jobs are likely to have contact with many people, increasing the probability to get sick. As mentioned, we fit a Boosting Tree(BT) that allows us to validate the results of the RF model. The BT model generate a variable importance output as well, the result in this case are close with those released by the RF and are summarized in table XX.

```
## Warning in rug(quantile(xv, seq(0.1, 0.9, by = 0.1)), side = 1): some values
## will be clipped

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## will be clipped

## Warning in rug(quantile(xv, seq(0.1, 0.9, by = 0.1)), side = 1): some values
## will be clipped
```

From Random Forest model and Boosting Trees we have the posibility to generate partial dependence functions. This functions show the marginal effect of one feature on the predicted outcome of our model. A partial dependence function can be represented as:

Where x_i are the variables for which we are computing the function and matrix X the other variables used in the model $\hat{g}$. Then, the partial function tell us for a given value of covariate i what the average marginal effect on the prediction is. Then by the calculation of the partial depence functions we can look for the effect of the County level features over the number of Covid cases per 100k. Figure **??** shows the partial depence function derived of the RF for some features we found intuitive, for example we can observe the can confirm the positive relation of population density over number of cases. We also can evaluate the effect of a socioeconomic variable such as poverty level, specifically we can see that an increase of poverty level has a positive impact over number of cases. In the case of proportion of population being white has a negative effect on number of cases. This finding goes in line with the last reports of New York State that suggest that the most affected ethnicity or race are Hispanic and Black. It is also interesting to see how warmer summer temperatures have a negative effect over Covid cases. Finally, we can see how a higher median age has a positive effect and more people driving alone to work has a negative one.

Regarding to the predictive performance of the models, we got an out of sample RMSE of 203.1140734 for the RF model and 236.0619057 for the BT. This values sugget that these models are reasonable tools for prediction even tough they do not outperform the result of the Negative Binomial model on cases per 100k.

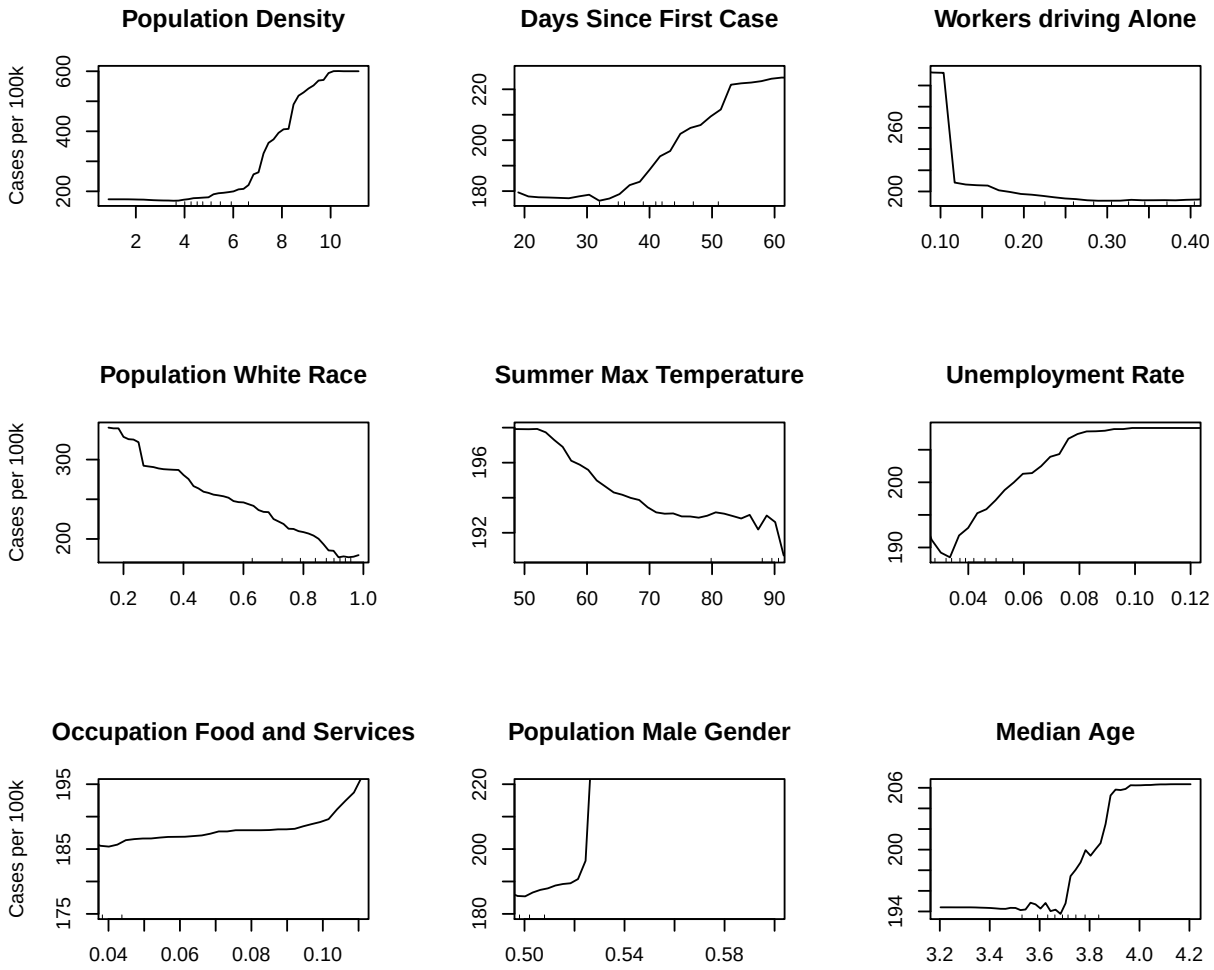

Figure 3: Partial Dependence From Random Forest Model