Final

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Introduction

With continuously changing abilities and accumulating mutations, SARS-CoV-2, the virus that causes COVID-19, have constant evolvements and accumulated mutations in its genetic code over time. The emergence and quick spread of the alpha, beta, and delta SARS-CoV-2 VOCs have generated continuous waves of infection in the past two years. The virus has brought tremendous shocks to the supply side of the economy and resulted in millions of deaths around the globe, representing an unprecedented tragic loss of the whole human society.

By analyzing the Covid-19 Case Surveillance Public Use Data from the Centers for Disease Control and Prevention, our project aims to identify the whether the hospitalized are sensible to the effects of Covid-19 under Double Robust Estimator. We mainly focus on samples in North Carolina and ignore the individual observations which have missing/unknown live status records. Focusing on a single state would help eliminate potential time-invariant effects among different states.

We hope this project will bring suggestive policy implications by identifying the most vulnerable groups against the Covid-19 virus among the population. Hopefully with our convincing results, the medical facilities would be able to allocate resources, such as hospitalization and medical aids, to the appropriate groups efficiently. Also, the government can assign social welfare benefits and designate priorities for vaccination by understanding which group is most vulnerable to the virus.

FAQ

Q1 What is Double Robust estimator and why use it?

Double Robust estimator is a estimator of average treatment effect under causal inference:

$$\begin{aligned}\tau^{DR} =& N^{-1}\sum_{i=1}^{N}\{\hat{m}_1(X_i) + \frac{Z_i\{Y_i - \hat{m}_1(X_i)\}}{\hat{e}(X_i)}\} \\ &- N^{-1}\sum_{i=1}^{N}\{\hat{m}_0(X_i) + \frac{(1-Z_i)\{Y_i - \hat{m}_0(X_i)\}}{1-\hat{e}(X_i)}\}\end{aligned}$$

Where:

- $\hat{e}(X_i)$ is the estimated Propensity score for each observation
- $\hat{m}_j(X_i)$ for $j \in \{0, 1\}$ is the estimated outcome model for each observation in either treatment or control group
- Y_i is the outcome variable `death_yn`
- Z_i is the treatment variable `hosp_yn`

- X_i is the corvariates, including sex, age, and etc.

Comparing to just focused on the estimator of any Machine Learning model, we chose the casual inference since we want to make sure the effect of hospitalization on the death rate is on itself instead of on any other confounders. Moreover, according to Bang and Robins (2005) proved both theoretically and through simulations, the double robust estimator provides two opportunities to deduce nearly correct inference on the causal effect, which indicated that even if one of the outcome model or Propensity score model is wrong, we can still accurately obtain an unbiased causal effect.

Q2 Where is the data come from?

The Data is come from CDC COVID-19-Case-Surveillance-Public-Use-Data Form, which can be found at https://data.cdc.gov/Case-Surveillance/COVID-19-Case-Surveillance-Public-Use-Data-with-Ge/n8mc-b4w4/data. The code table and introduction for each parameter can also be found at the website. After filtered all the NC 2020 observation with None-missing value of `death_yn`, there are totally 575400 observation with 19 variables, and the summary of the data set are in the appendix. Specifically,

- `res_county`: The county of the observation
- `case_month`: The Date received by CDC
- `age_group`: This is a categorical variable which has three values: 0-17 years; 18-49 years; 50-64 years; 65+years
- `race`: This is another categorical variable which has six values: American Indian/Alaska Native; Asian; Black; Multiple/Other; Native Hawaiian/Other Pacific Islander; White
- `sex`: This is a variable which has three values: Male; Female; Other
- `ethnicity`: This is a variable which has two values: Hispanic/Non-Hispanic
- `hosp_yn`: Was this patient hospitalized? Yes/No/Unknown
- `death_yn`: Did the patient die as a result of this illness? Yes/No

Q3 Why you choose this Data source than others?

We choose this data source because compared to other data sources, it includes all cases with the earliest date available in each record (date received by CDC or date related to illness/specimen collection) at least 14 days before constructing the previously updated datasets. This 14-day lag allows case reporting to be stabilized and ensure that time-dependent outcome data are accurately captured.

Moreover, most of other data source only provide the death cases without the survive, which is hard for us to build the model on the death rate.

Q4 Why choose North Carolina? Why not choose the United States?

We choose North Carolina to eliminate potential bias existing in the large volume of data. When including every state in the country, the data contains 1.8 billion observations during our time interval. To reduce the time-invariant effect lying in each state, such as the geography, population structure differences and government efficiencies, which our data has no measures of. Moreover, to include all the states, we may not only consider the fix but also random group effect caused by different states, which may cause our model too complicated to converge. Therefore, finally we choose just explore on our own states

Q5 Why 2020?

We focus on the year 2020 to eliminate the potential effects of vaccination. According to the reports from CDC, North Carolina's COVID-19 Vaccine eligibility opens for all adults on April 7. Since our data source does not contain information regarding the individual's vaccination status, we only focus on the year 2020.

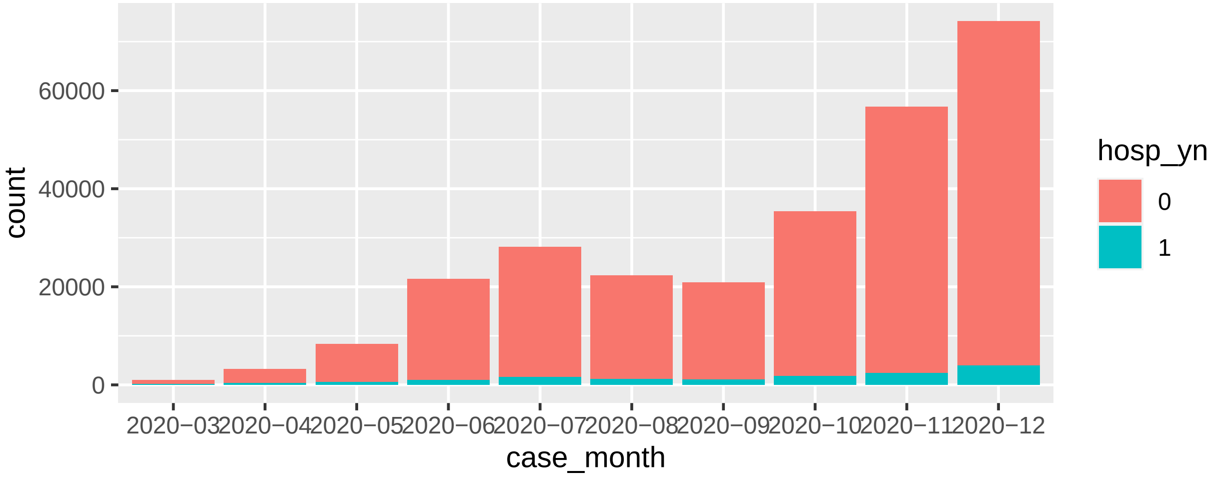
Q6 Any Data cleanning before modeling?

Data cleaning procedure:

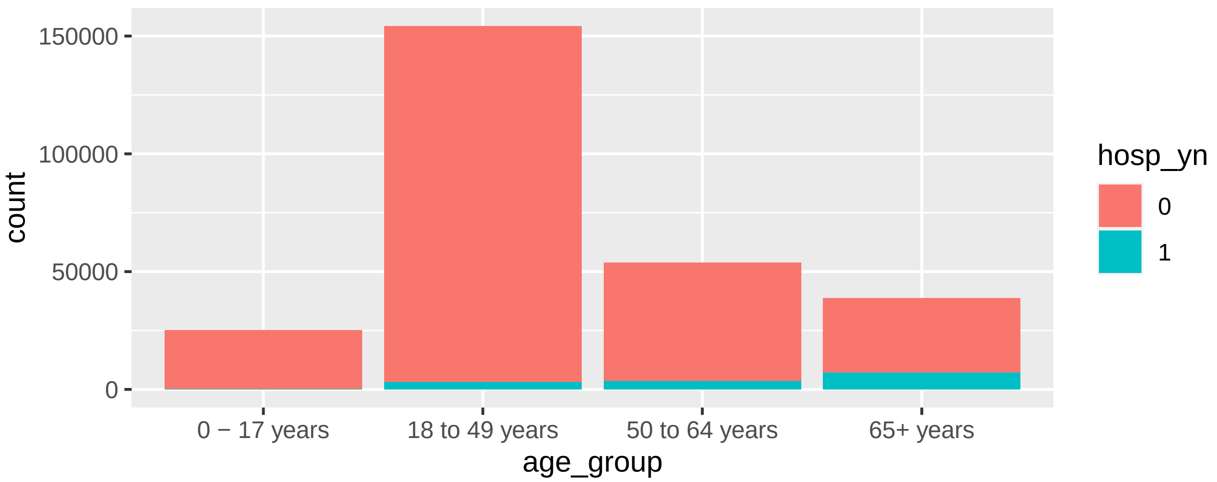
- Drop `res_state`, `state_fips_code` since all the observations come from NC
- Drop `county_fips_code` since it is redundant as `res_county`
- Drop `case_onset_interval`, `process`, `exposure_yn`, `-icu_yn`, `underlying_conditions_yn` since they have highly rate of missing or unknown
- Drop the observation with `NA`
- Combine the `Missing` and `Unknown` of `symptom_status` as `unknown`
- Drop the `Unknown` of `hosp_yn`
- Convert the `death_yn`, and `hosp_yn` as binary variable with `Yes` as 1
- Drop the`case_positive_specimen_interval`, `current_status`, `symptom_status` due to the complicity of the model
- Drop the `Missing` in `Sex` due to the limited number of observations
- Combine the county with county with 1
- Change all the categorical data as factor
- Combine the County with 2000 or less observation as `other` to reduce the group effect

After the first part of cleaning, we got 271822 observations with 270088 survivors and 1734 deaths which can be found in the appendix. Thus, the death rate from the population is 1734/271822 = 0.00638

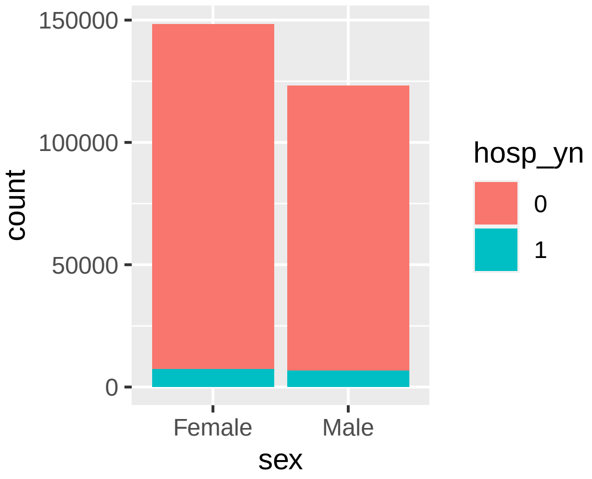
Q8 Any finding during the EDA?

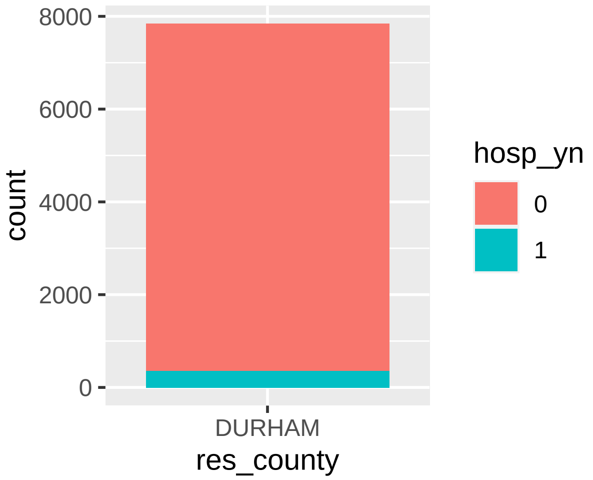


From this stacked bar chart we can observe the surge of active cases and death cases in December 2020.

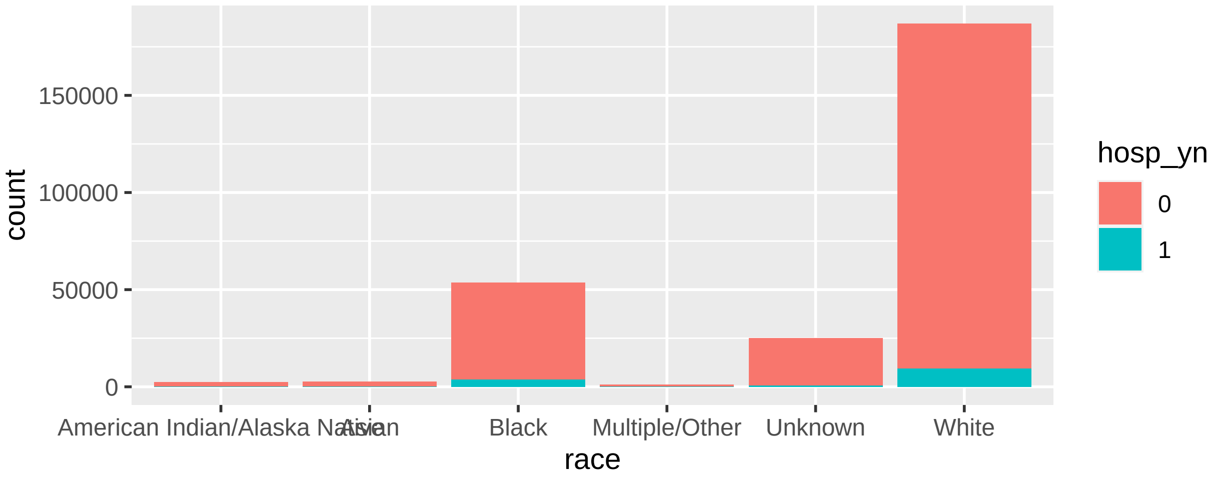


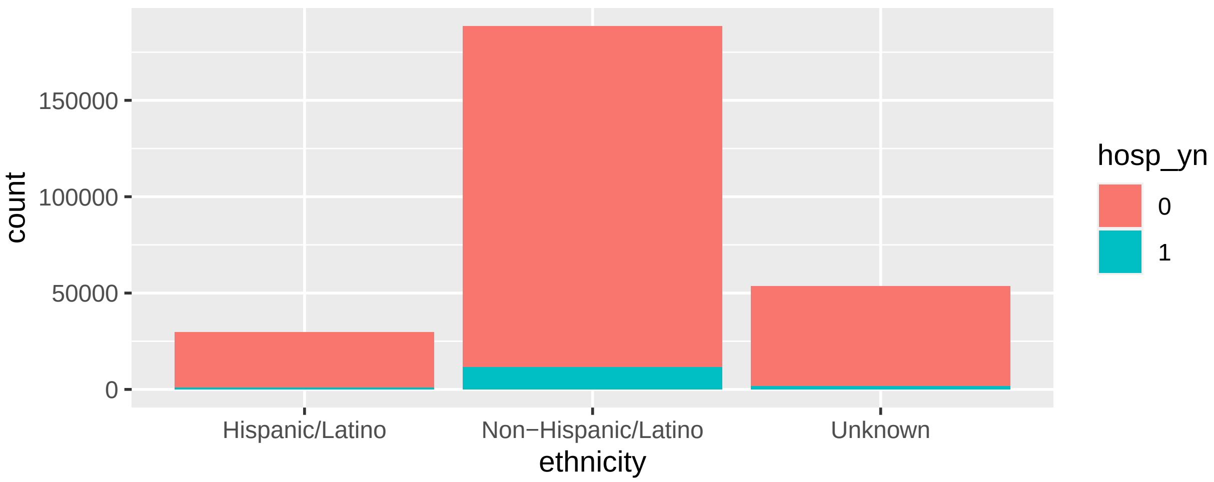
Most of the cases are people who are 18-49 years old, while the group whose ages are above 65 years old tends to have the highest number of death cases.

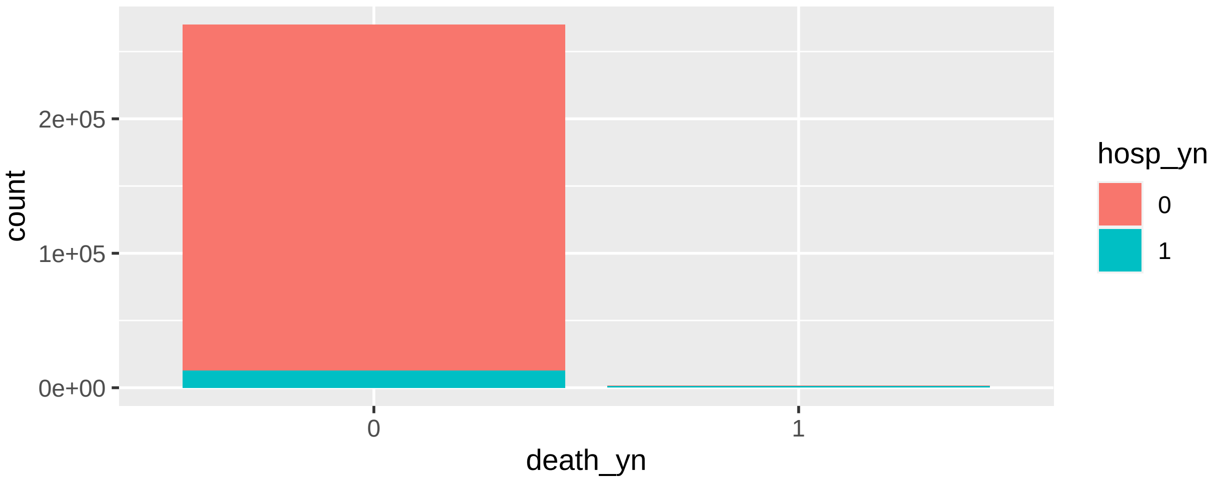




There is not a clear gender effect on the mortality of COVID based on this stacked bar chart.



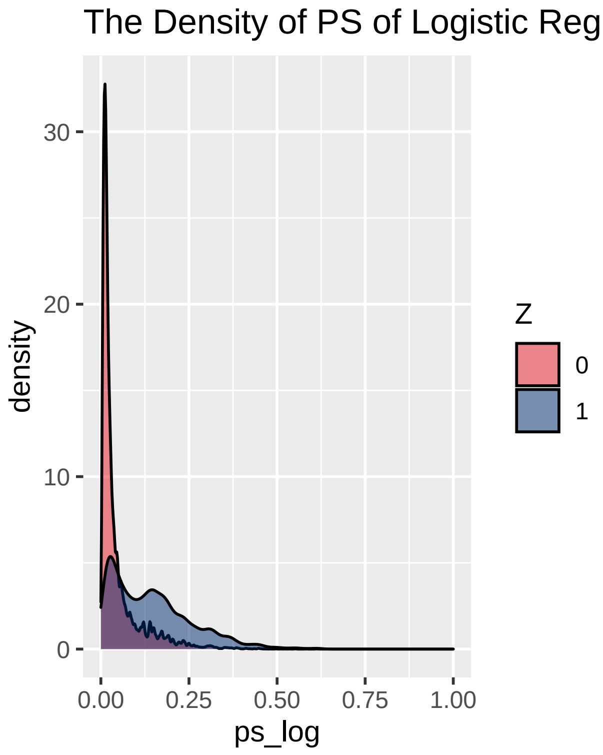


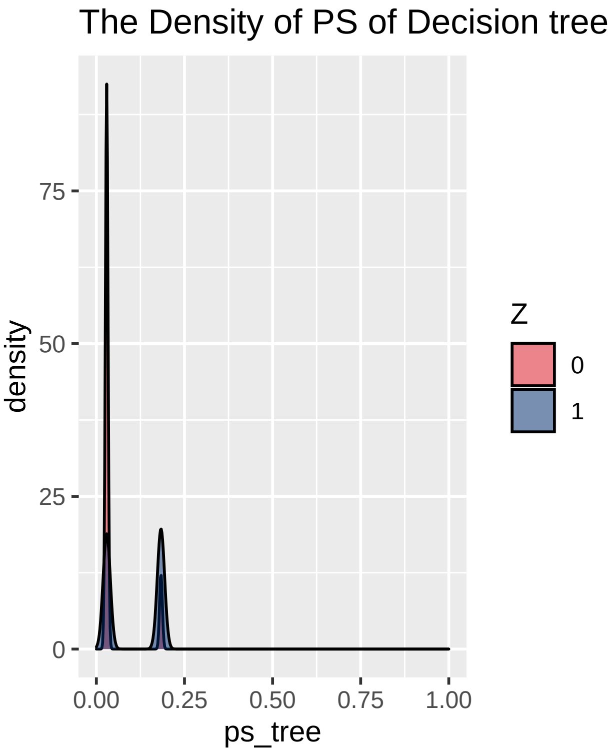


Most of the observations in this data set are Caucassians. Such imbalance may downplay the potential racial effect. Most of the death cases were hospitalized.

Q9 How do you build the model and what is your result?

For both outcome model and PS model, we apply two algorithms: Logistic Regression and Decision Tree. We want to compare the result of all four combinations.





The density plot of PS in different algorithm are plot here to check the overlap. As we obvioused, both PS model has relative nice overlap, so we do not clean any data out.

Table 1: The four different estimator treatment effect of Covid death rate

τ_1	τ_2	τ_3	τ_4
0.0170229	0.0172924	0.0178099	0.0181142

The table here illustrate our result, where:

- τ_1 applied the Logistic Regression in both PS model and outcome model
- τ_1 applied the Logistic Regression in outcome model and Decision Tree in PS model
- τ_1 applied the Logistic Regression in PS model and Decision Tree in outcome model
- τ_4 applied the Decision Tree in both PS model and outcome model

Q10 How Do you interpretate your reuslt?

All of the four estimators illustrate that the τ^{DR} is about 0.018, which means people were sent to the hospital has about 0.018 higher rate to die than people who were not. Compared to the average death rate 0,0063, it is a very significant difference. It seems to be reliable, since we can assume people who were sent to the hospital had a more serious symptom. And, since we do not have the seriousness of each observation in our corvariates, such information may be concluded to the difference of the death rate. Moreover, the 4 estimators shows very close results, which is consistent with Bang and Robin's (2005) idea about how the Double Robust Estimator works. However, since we have a very lower death rate, it may also be caused by the random probability.

Q11: Are there any past literature? What are the differences between this project and them?

In the past two years, several papers have discussed the potential determinants of Covid-19 death rates. Lan Feinhandler and four other authors offer several predictors that lead to the death rate during the first eight months of 2020. They implement the OLS model/Two-stage regression model/Lasso regression model and conclude that the national Covid-19 death rate is greater than that of other flu pandemics. Also, the increase in the reported death rate in states with Democratic governors is higher than the increase in states with Republican governors. (Feinhandler et al., 2020). Besides, in the paper Determinants of COVID-19 Death Rate in Europe: Empirical Analysis, six authors use the OLS models to test multiple hypotheses. They finally prove that the population density in European countries does not affect the COVID-19 death rate. Also, the COVID-19 death rate will not drastically raise mortality statistics since people already at risk are susceptible to the disease. (Kozlovskyi et al., 2021)

Comparing to other method, we focus on the 2020 NC data, and we choose to build the model under the causal inference, which allow us to explore the effect of hospitalization on death rate without the effects of other parameter. If we use a regression, for example, directly, it is hard for us to address the cor variance between the death rate the the hospitalization is because of themselves, or because they are just both correlated to any other parameter.

Q12 Are there any limitations?

The first limitation is that although we have a large number of observations with solid values, there are still observations with missing values up to twenty thousand that we have to delete. As a result, there might exist a loss of "explanality" inside the observation with missing values of death rates. Besides, our data has no access to the severity of symptoms the patient experiences. Thus, when testing the casual relationship between hospitazation and death rates, we can not exclude the possibility that patients with severer symptoms would go to hopstials and patients with less severe symptoms would stay home, leading to the case that death rates of former would be higher than that of later.

Q13 Are there any future directions/Perspective?

With access to data regarding the severity of the illness, we can futher test the selection bias mentioned above and future test the effectiveness of hospitalization and therapy received inside. Also, if we can acquire data related to the severity of other illnesses which share similar medical-source-occupation patterns with Covid-19, we are able to determine whether the virus is as severe as we expect.

Reference

Bang, H. and Robins, J. (2005). Doubly Robust Estimation in Missing Data and Causal Inference Models, Biometrics, Volume 61, Pages 962–972. DOI: 10.1111/j.1541-0420.2005.00377.x

CDC. COVID 19 Case Surveillance Public Use Data Form. https://data.cdc.gov/Case-Surveillance/COVID-19-Case-Surveillance-Public-Use-Data-with-Ge/n8mc-b4w4/data

Robins, J. M., Rotnitzky, A., Zhao, L. P. (1994). Estimation of regression coefficients when some regressors are not always observed. Journal of the American statistical Association, 89(427), 846-866

Feinhandler, Ian, et al. "Predictors of Death Rate during the Covid-19 Pandemic." Healthcare, vol. 8, no. 3, 2020, p. 339., https://doi.org/10.3390/healthcare8030339.

Kozlovskyi, Serhii, i in. „Determinants of COVID-19 Death Rate in Europe: Empirical Analysis". Problemy Ekorozwoju, t. 16, nr 1, 1, Polska Akademia Nauk. Komitet Człowiek i Środowisko PAN, 2021, s. 17–28.

Knittel, Christopher, and Bora Ozaltun. "What Does and Does Not Correlate with Covid-19 Death Rates." NBER, 2020, https://doi.org/10.3386/w27391.

Centers for Disease Control and Prevention. “COVID-19 Case Surveillance Public Use Data.” 7 Apr. 2022, https://data.cdc.gov/Case-Surveillance/COVID-19-Case-Surveillance-Public-Use-Data-with-Ge/n8mc-b4w4/data. Accessed 10 Apr. 2022.

Appendix

Summary of Original Data

```
##    case_month     res_state   state_fips_code       res_county    
##  2020-12:195568   NC:575400   Min.   :37      MECKLENBURG: 66644  
##  2020-11:103453               1st Qu.:37      WAKE       : 45793  
##  2020-10: 63455               Median :37      GUILFORD   : 26375  
##  2020-07: 54015               Mean   :37      FORSYTH    : 21623  
##  2020-08: 43620               3rd Qu.:37      GASTON     : 16321  
##  2020-06: 42996               Max.   :37      (Other)    :382586  
##  (Other): 72293                               NA's       : 16058  
##  county_fips_code          age_group           sex        
##  Min.   :37001    0 - 17 years  : 64882   Female :292579  
##  1st Qu.:37063    18 to 49 years:311481   Male   :254172  
##  Median :37109    50 to 64 years:114004   Missing:   563  
##  Mean   :37105    65+ years     : 76362   NA's   : 28086  
##  3rd Qu.:37151    NA's          :  8671                   
##  Max.   :37197                                            
##  NA's   :16058                                            
##                            race                       ethnicity     
##  White                        :282065   Hispanic/Latino    : 38215  
##  Black                        : 81269   Non-Hispanic/Latino:257526  
##  Unknown                      : 79637   Unknown            :140826  
##  Asian                        :  4735   NA's               :138833  
##  American Indian/Alaska Native:  4110                               
##  (Other)                      :  1884                               
##  NA's                         :121700                               
##  case_positive_specimen_interval case_onset_interval
##  Min.   :-40.000                 Min.   :-16        
##  1st Qu.:  0.000                 1st Qu.:  0        
##  Median :  0.000                 Median :  0        
##  Mean   :  0.193                 Mean   :  0        
##  3rd Qu.:  0.000                 3rd Qu.:  0        
##  Max.   :105.000                 Max.   : 22        
##  NA's   :195                     NA's   :298698     
##                            process        exposure_yn    
##  Clinical evaluation           :    46   Missing:264105  
##  Contact tracing of case patient:     8   Missing:264105  
##  Missing                       :575334   Yes    : 51698  
##  Multiple                      :     6                   
##  Other                         :     6                   
##                                                          
##                                                          
##                   current_status        symptom_status      hosp_yn      
##  Laboratory-confirmed case:520209   Asymptomatic: 58823   Missing:    52  
##  Probable Case            : 55191   Missing     :   117   No     :354159  
##                                     Symptomatic :333915   Unknown:200548  
##                                     Unknown     :182545   Yes    : 20641  
##                                                                           
##                                                                           
##                                                                           
##      icu_yn       death_yn     underlying_conditions_yn
##  Missing:   235   No :573258      :476449              
##  No     :  6291   Yes:  2142   Yes: 98951
##  Unknown:566279
##  Yes    :  2595
##
##
##
```

Summary of the cleaning Data

```
##    case_month          res_county              age_group          sex
##  2020-12:74139   OTHER      : 38023   0 - 17 years  : 25183   Female:148469
##  2020-11:56715   MECKLENBURG: 33373   18 to 49 years:154162   Male  :123353
##  2020-10:35374   WAKE       : 19589   50 to 64 years: 53730
##  2020-07:28173   GUILFORD   : 11579   65+ years     : 38747
##  2020-08:22296   CUMBERLAND :  8979
##  2020-06:21578   FORSYTH    :  8484
##  (Other):33547   (Other)    :151795
##                              race                      ethnicity
##  American Indian/Alaska Native:  2334   Hispanic/Latino    : 29868
##  Asian                        :  2772   Non-Hispanic/Latino:188461
##  Black                        : 53636   Unknown            : 53493
##  Multiple/Other               :  1086
##  Unknown                      : 25048
##  White                        :186946
##
##     hosp_yn           death_yn            ps_log             ps_tree
##  Min.   :0.00000   Min.   :0.000000   Min.   :0.001228   Min.   :0.02927
##  1st Qu.:0.00000   1st Qu.:0.000000   1st Qu.:0.012096   1st Qu.:0.02927
##  Median :0.00000   Median :0.000000   Median :0.022454   Median :0.02927
##  Mean   :0.05122   Mean   :0.006379   Mean   :0.051221   Mean   :0.05122
##  3rd Qu.:0.00000   3rd Qu.:0.000000   3rd Qu.:0.057002   3rd Qu.:0.02927
##  Max.   :1.00000   Max.   :1.000000   Max.   :0.615006   Max.   :0.18327
##
```

The number of death and suvivor for the cleaning data

```
## # A tibble: 2 x 2
##   death_yn  ‘n()‘
##      <dbl>  <int>
## 1        0 270088
## 2        1   1734
```

code

```
knitr::opts_chunk$set(echo = TRUE)
library(tidyverse)
library(ggplot2)
library(dplyr)
library(zoo)
library(readxl)
library(cobalt)
library(sandwich)
library(PSweight)
library(knitr)
library(lme4)
library(boot)
library(stan4bart)
library(rstan)
library(kableExtra)
library(tree)
library(rpart)
library(gridExtra)
covid=read.csv("COVID-19_Case_Surveillance_Public_Use_Data_with_Geography.csv",header = TRUE)
factor_covid <- as.data.frame(unclass(covid),stringsAsFactors=TRUE)
covid_clean=covid%>%
  select(-res_state,-state_fips_code,-county_fips_code,-case_onset_interval,-process,-exposure_yn, -icu_
  drop_na()%>%
  filter(hosp_yn!="Unknown")%>%
  mutate(death_yn=ifelse(death_yn=="Yes",1,0),
         hosp_yn=ifelse(hosp_yn=="Yes",1,0))%>%
  filter(sex!="Missing")
county_list=covid_clean%>%
  group_by(res_county)%>%
  summarise(observation=n())
covid_clean=covid_clean%>%
  mutate(res_county=ifelse(res_county %in% county_list$res_county[county_list$observation < 2000],"OTHE
covid_clean=as.data.frame(unclass(covid_clean),stringsAsFactors=TRUE)
stackedbar_case_month_hosp_yn=ggplot(covid_clean, aes(x = as.factor(case_month),
           fill = as.factor(hosp_yn))) +
  geom_bar(position = "stack") +
  guides(fill=guide_legend(title="hosp_yn")) +
  scale_x_discrete(name="case_month")
stackedbar_res_county_hosp_yn=ggplot(covid_clean[covid_clean$res_county=="DURHAM",], aes(x = as.factor(r
           fill = as.factor(hosp_yn))) +
  geom_bar(position = "stack") +
  guides(fill=guide_legend(title="hosp_yn")) +
  scale_x_discrete(name="res_county")
stackedbar_age_group_hosp_yn=ggplot(covid_clean, aes(x = as.factor(age_group),
           fill = as.factor(hosp_yn))) +
  geom_bar(position = "stack") +
  guides(fill=guide_legend(title="hosp_yn")) +
  scale_x_discrete(name="age_group")
stackedbar_sex_hosp_yn=ggplot(covid_clean, aes(x = as.factor(sex),
           fill = as.factor(hosp_yn))) +
  geom_bar(position = "stack") +
  guides(fill=guide_legend(title="hosp_yn")) +
  scale_x_discrete(name="sex")
stackedbar_race_hosp_yn=ggplot(covid_clean, aes(x = as.factor(race),
           fill = as.factor(hosp_yn))) +
  geom_bar(position = "stack") +
  guides(fill=guide_legend(title="hosp_yn")) +
  scale_x_discrete(name="race")
stackedbar_ethnicity_hosp_yn=ggplot(covid_clean, aes(x = as.factor(ethnicity),
           fill = as.factor(hosp_yn))) +
```

```r
  geom_bar(position = "stack") +
  guides(fill=guide_legend(title="hosp_yn")) +
  scale_x_discrete(name="ethnicity")
stackedbar_death_yn_hosp_yn=ggplot(covid_clean, aes(x = as.factor(death_yn),
           fill = as.factor(hosp_yn))) +
  geom_bar(position = "stack") +
  guides(fill=guide_legend(title="hosp_yn")) +
  scale_x_discrete(name="death_yn")
stackedbar_case_month_hosp_yn
stackedbar_age_group_hosp_yn
grid.arrange(stackedbar_sex_hosp_yn, stackedbar_res_county_hosp_yn,
             ncol=2)
stackedbar_race_hosp_yn
stackedbar_ethnicity_hosp_yn
stackedbar_death_yn_hosp_yn
att=data.frame(tau1=numeric(1),tau2=numeric(1),tau3=numeric(1))
## get the PS
ps_model_log=glm(hosp_yn~.-death_yn,family="binomial",data=covid_clean)
ps_model_tree=rpart(hosp_yn~.-death_yn,method="anova",data=covid_clean)

covid_clean=covid_clean%>%
  mutate(ps_log=ps_model_log$fitted.values,
         ps_tree=predict(ps_model_tree,covid_clean))
q1=ggplot(covid_clean, mapping = aes(x = ps_log, fill = factor(hosp_yn)))+
  geom_density(alpha = .5) +
  scale_fill_manual(values = c("#E81828", "#002D72"))+
  xlim(c(0,1))+
  guides(fill=guide_legend(title="Z"))+
  ggtitle("The Density of PS of Logistic Regression for different group ")
q2=ggplot(covid_clean, mapping = aes(x = ps_tree, fill = factor(hosp_yn)))+
  geom_density(alpha = .5) +
  scale_fill_manual(values = c("#E81828", "#002D72"))+
  xlim(c(0,1))+
  guides(fill=guide_legend(title="Z"))+
  ggtitle("The Density of PS of Decision tree for different group ")
grid.arrange(q1, q2, ncol=2)
##seperate the data
covid_clean_1=covid_clean%>%
  filter(hosp_yn==1)
covid_clean_0=covid_clean%>%
  filter(hosp_yn==0)
## generate the outcome model
m1_log=glm(death_yn~.-hosp_yn-ps_log-ps_tree,family = "binomial",
           data=covid_clean_1)
m0_log=glm(death_yn~.-hosp_yn-ps_log-ps_tree,family = "binomial",
           data=covid_clean_0)

m1_tree = rpart(death_yn~.-hosp_yn-ps_log-ps_tree,
           data=covid_clean_1)
m0_tree = rpart(death_yn~.-hosp_yn-ps_log-ps_tree,
           data=covid_clean_0)

## predict m1,m1
## calculate the result
result=covid_clean%>%
  mutate(m1_log=predict.glm(m1_log,covid_clean,type = "response"),
         m0_log=predict.glm(m0_log,covid_clean,type = "response"),
         m1_tree=predict(m1_tree,covid_clean),
         m0_tree=predict(m0_tree,covid_clean))%>%
  mutate(tau1=m1_log+hosp_yn*(death_yn-m1_log)/ps_log-m0_log-(1-hosp_yn)*(death_yn-m0_log)/(1-ps_log),
         tau2=m1_log+hosp_yn*(death_yn-m1_log)/ps_tree-m0_log-(1-hosp_yn)*(death_yn-m0_log)/(1-ps_tree)
         tau3=m1_tree+hosp_yn*(death_yn-m1_tree)/ps_log-m0_tree-(1-hosp_yn)*(death_yn-m0_tree)/(1-ps_log
         tau4=m1_tree+hosp_yn*(death_yn-m1_tree)/ps_tree-m0_tree-(1-hosp_yn)*(death_yn-m0_tree)/(1-ps_t
  summarise(tau1=mean(tau1),
            tau2=mean(tau2),
            tau3=mean(tau3),
            tau4=mean(tau4))
result%>%
  kable(caption = "The four different estimator treatment effect of Covid death rate",
        col.names = c("$\\tau_1$",
                      "$\\tau_2$",
                      "$\\tau_3$",
                      "$\\tau_4$"),
        align = "c", booktabs = TRUE, escape = FALSE)%>%
  kable_styling(latex_options = "HOLD_position")

summary(factor_covid)
summary(covid_clean)
covid_clean%>%
  group_by(death_yn)%>%
  summarise(n())
```