Prediction model for covid-19 patients

FINAL PROJECT FOR MACHINE LEARNING 64064-003

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Table of Contents

1. PROJECT GOAL

ABC Clinic is a non-profit medical center that provides clinical and hospital care in Northeast Ohio. It is a leader in fighting COVID-19 and is seeking consultation to better understand which COVID-positive patients have higher death rates. With the help of the ABC Clinic's historical data, we aim to develop a model to predict and identify COVID-19 patients' chance of survival. It is out of the study's scope to look at patients' survival rate who have not been identified as COVID-19 positive.

The task of our team is to apply analytics and help the management of the hospital gain understanding on covid-positive patients' survival rate based on their historic data.

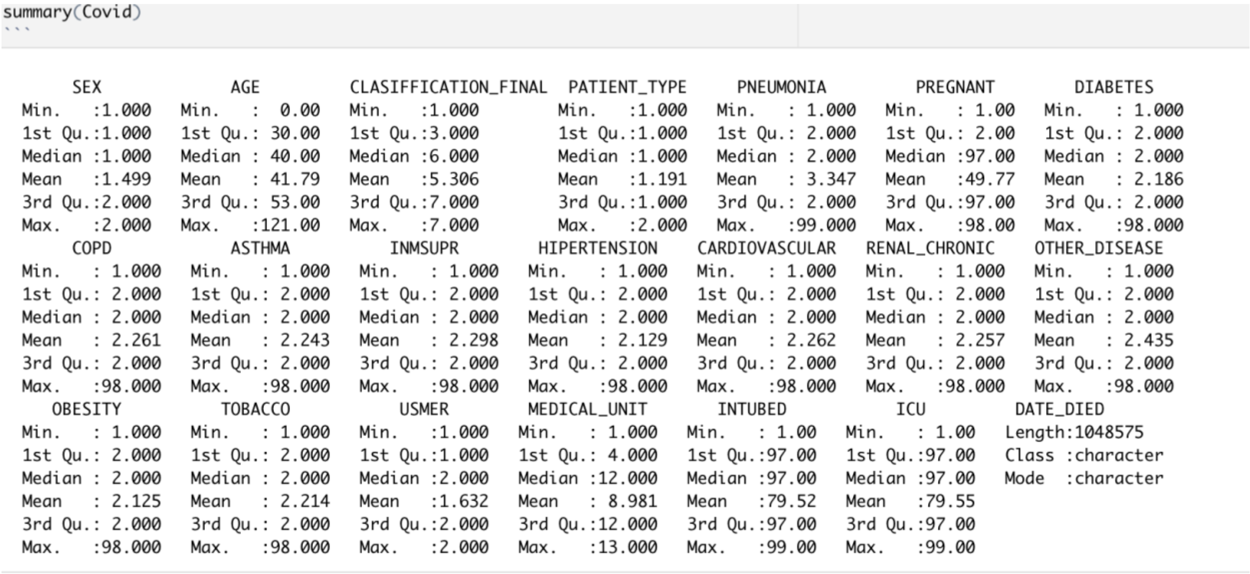
2. OVERVIEW OF THE DATA:

DATA SOURCE

The data is downloaded from Kaggle at COVID-19 dataset, original provided by the Mexican government (Kaggle COVID-19 Dataset, n.d.).

DATA EXPLORATION

The data contains over 1 million observations of patient data with their symptoms, status and medical history. There are a total of 21 variables (Figure 1) including patient general information (sex, age), symptoms (classification of covid, type of patient care received, whether or not has used ventilator or ICU), and medical history (pregnancy, pneumonia, diabetes, COPD, Asthma, inmsupr, hypertension, cardiovascular, chronic renal, other disease, obesity, tobacco). The data also has information if the patient has died.



```
summary(Covid)
```

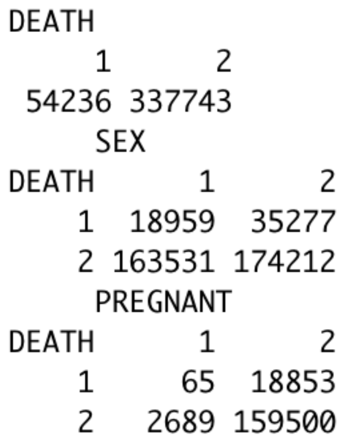
```
      SEX             AGE          CLASIFFICATION_FINAL  PATIENT_TYPE     PNEUMONIA        PREGNANT        DIABETES    
 Min.   :1.000   Min.   :  0.00   Min.   :1.000        Min.   :1.000   Min.   : 1.000   Min.   : 1.00   Min.   : 1.000  
 1st Qu.:1.000   1st Qu.: 30.00   1st Qu.:3.000        1st Qu.:1.000   1st Qu.: 2.000   1st Qu.: 2.00   1st Qu.: 2.000  
 Median :1.000   Median : 40.00   Median :6.000        Median :1.000   Median : 2.000   Median :97.00   Median : 2.000  
 Mean   :1.499   Mean   : 41.79   Mean   :5.306        Mean   :1.191   Mean   : 3.347   Mean   :49.77   Mean   : 2.186  
 3rd Qu.:2.000   3rd Qu.: 53.00   3rd Qu.:7.000        3rd Qu.:1.000   3rd Qu.: 2.000   3rd Qu.:97.00   3rd Qu.: 2.000  
 Max.   :2.000   Max.   :121.00   Max.   :7.000        Max.   :2.000   Max.   :99.000   Max.   :98.00   Max.   :98.000  
      COPD             ASTHMA           INMSUPR         HIPERTENSION     CARDIOVASCULAR   RENAL_CHRONIC    OTHER_DISEASE   
 Min.   : 1.000   Min.   : 1.000   Min.   : 1.000   Min.   : 1.000   Min.   : 1.000   Min.   : 1.000   Min.   : 1.000  
 1st Qu.: 2.000   1st Qu.: 2.000   1st Qu.: 2.000   1st Qu.: 2.000   1st Qu.: 2.000   1st Qu.: 2.000   1st Qu.: 2.000  
 Median : 2.000   Median : 2.000   Median : 2.000   Median : 2.000   Median : 2.000   Median : 2.000   Median : 2.000  
 Mean   : 2.261   Mean   : 2.243   Mean   : 2.298   Mean   : 2.129   Mean   : 2.262   Mean   : 2.257   Mean   : 2.435  
 3rd Qu.: 2.000   3rd Qu.: 2.000   3rd Qu.: 2.000   3rd Qu.: 2.000   3rd Qu.: 2.000   3rd Qu.: 2.000   3rd Qu.: 2.000  
 Max.   :98.000   Max.   :98.000   Max.   :98.000   Max.   :98.000   Max.   :98.000   Max.   :98.000   Max.   :98.000  
    OBESITY           TOBACCO           USMER        MEDICAL_UNIT       INTUBED           ICU          DATE_DIED        
 Min.   : 1.000   Min.   : 1.000   Min.   :1.000   Min.   : 1.000   Min.   : 1.00   Min.   : 1.00   Length:1048575    
 1st Qu.: 2.000   1st Qu.: 2.000   1st Qu.:1.000   1st Qu.: 4.000   1st Qu.:97.00   1st Qu.:97.00   Class :character  
 Median : 2.000   Median : 2.000   Median :2.000   Median :12.000   Median :97.00   Median :97.00   Mode  :character  
 Mean   : 2.125   Mean   : 2.214   Mean   :1.632   Mean   : 8.981   Mean   :79.52   Mean   :79.55                     
 3rd Qu.: 2.000   3rd Qu.: 2.000   3rd Qu.:2.000   3rd Qu.:12.000   3rd Qu.:97.00   3rd Qu.:97.00                     
 Max.   :98.000   Max.   :98.000   Max.   :2.000   Max.   :13.000   Max.   :99.00   Max.   :99.00                     
```

Figure 1 Covid-19 data summary

Across the dataset, **1 is used for positive** and **2 for negative**.

There are a few early observations from the dataset:

- The death rate is about 13.8% (54236 death cases) of all COVID patients (391917 cases)
- Positive male (sex=2) death rate is almost double of the death rate of female (sex =1) (Figure 2).
- The death for pregnancy cases is very few and pregnancy is not a focus for our study.
- High percentage of data are missing for INTUBED and ICU. As INTUBED and ICU are only used in extreme conditions, let's assume all the missing data as negative.
- The rest of NAs in each column are normal (<1% are missing) and will be imputed with median values.

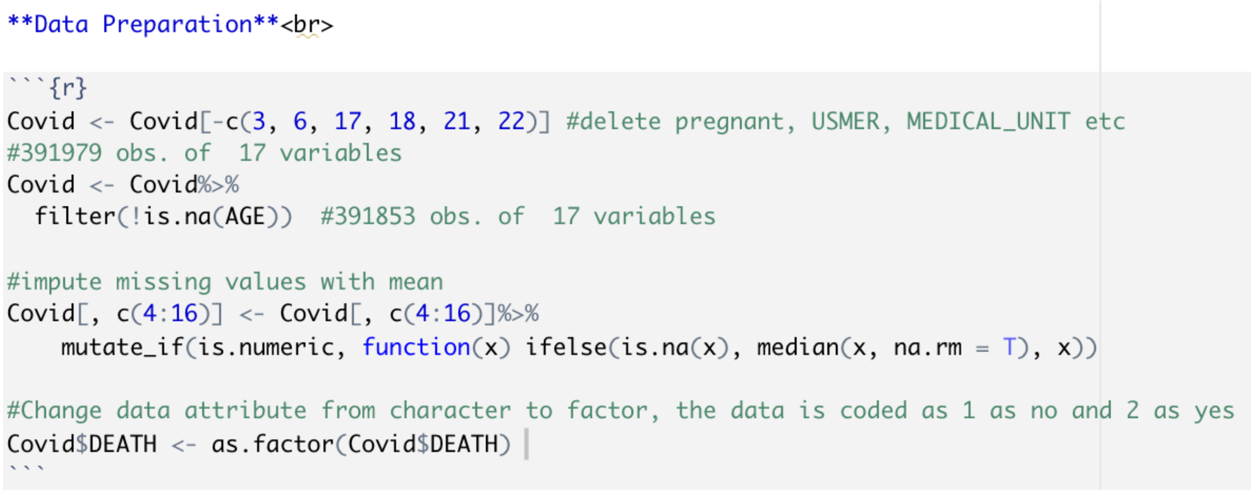


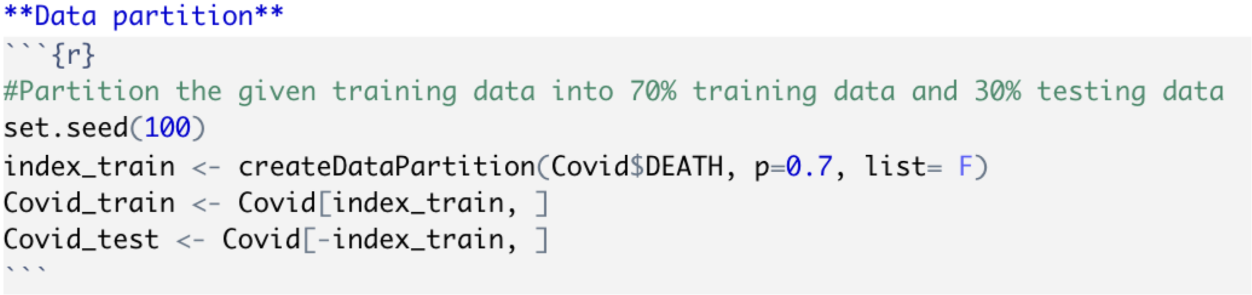
```
DEATH
     1      2
 54236 337743
     SEX
DEATH      1      2
    1  18959  35277
    2 163531 174212
     PREGNANT
DEATH      1      2
    1     65  18853
    2   2689 159500
```

Figure 2 Distribution of Death, by sex and by pregnancy

DATA PREPARATION

- Convert all binary data: Since most of the columns use 1 for “Yes” and 2 for “No”, convert CLASSIFICATION and DEATH columns to binary
- Filter only COVID positive cases
- Convert other forms to NA: convert 97, 98, 99 to NAs
- Change attribute: Convert DEATH from date to factor
- Remove unnecessary variables: removed pregnancy, USMER, MEDICAL_UNIT, DEATH_DATE, CLASIFICATION_FINAL
- Delete NA records for age
- Impute the NAs with medians: We replaced NAs with median values for 13 columns (Figure 3)
- By this step, there are 391979 observations of 17 variables left



~~~
**Data Preparation**<br>

```{r}
Covid <- Covid[-c(3, 6, 17, 18, 21, 22)] #delete pregnant, USMER, MEDICAL_UNIT etc
#391979 obs. of  17 variables
Covid <- Covid%>%
  filter(!is.na(AGE))  #391853 obs. of  17 variables

#impute missing values with mean
Covid[, c(4:16)] <- Covid[, c(4:16)]%>%
    mutate_if(is.numeric, function(x) ifelse(is.na(x), median(x, na.rm = T), x))

#Change data attribute from character to factor, the data is coded as 1 as no and 2 as yes
Covid$DEATH <- as.factor(Covid$DEATH)
~~~
```

Figure 3 Data preparation

DATA PARTITION:

Once the data has no missing values, we partition the data using the CARET package in R in training and test sets. The partition index is set at "0.70," which refers to the training set of 70% of the whole dataset and the test set of 30% (Figure 4).



```
**Data partition**
```{r}
#Partition the given training data into 70% training data and 30% testing data
set.seed(100)
index_train <- createDataPartition(Covid$DEATH, p=0.7, list= F)
Covid_train <- Covid[index_train, ]
Covid_test <- Covid[-index_train, ]
```
```

Figure 4 Data Partition
```

# 3. DETAILS OF MODELLING STRATEGY

We developed four models (Logistic regression, KNN, Naïve bayes and Decision Tree) (**Error! Reference source not found.**) based on the 70% of the training data to determine the most accurate model for predicting the death of COVID-19 patients

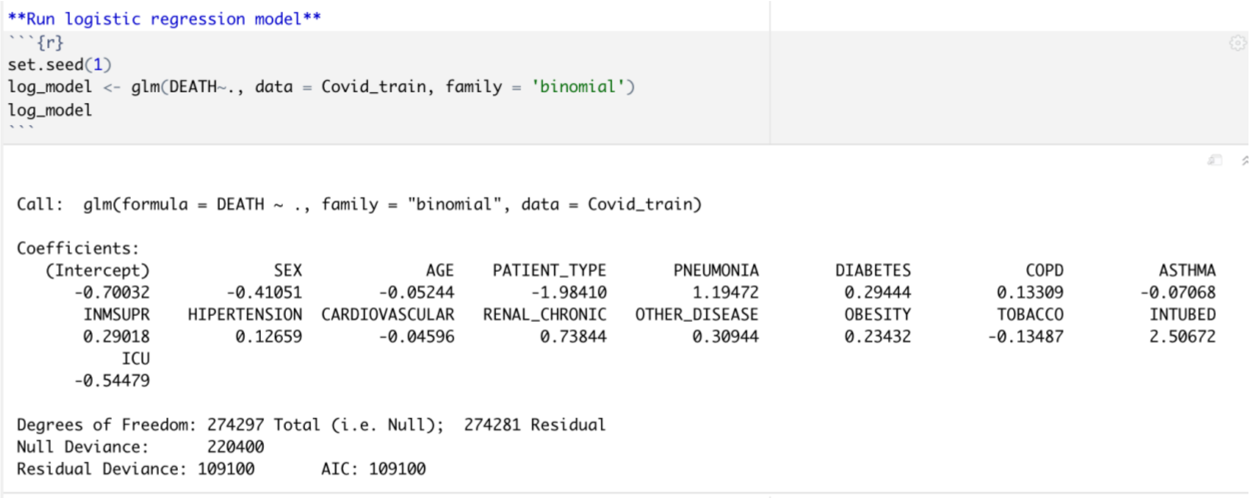
## LOGISTIC REGRESSION MODEL

A logistic regression model is considered since the data's target variable is categorical. When predicting a binomial attribute, a linear regression model is less optimal since its performance likelihood can be negative or more than 1. Logistic regression, ranging between 0 and 1, is the desired outcome for this model.

From the model output (Figure 5), we can interpret information similar to what we have observed before. Among all the factors, the red ones tend to show a higher death rates and blue ones are correlated to lower death rates in COVID-positive patients. Correlation is not causation and we do not conclude red factors lead to a higher death rate.

- SEX: male, female
- AGE: old, young
- PATIENT_TYPE: home care, hospitalized
- PNEUMONIA: if the patient already has air sacs inflammation
- DIABETES: if the patient already has diabetes
- COPD: if the patient has Chronic obstructive pulmonary disease
- ASTHMA: : if the patient has asthma
- INMSUPR: if the patient is immunosuppressed

- HIPERTENSION: if the patient has hypertension
- CARDIOVASCULAR: the patient has heart or blood vessels related disease
- RENAL_CHRONIC: if the patient has chronic renal disease
- OTHER_DISEASE: if the patient has other disease
- OBESITY: if the patient is obese
- TOBACCO: if the patient is a tobacco user
- INTUBED: if the patient has been connected to the ventilator
- ICU: if the patient has been admitted to an intensive care unit



~~~
**Run logistic regression model**
```{r}
set.seed(1)
log_model <- glm(DEATH~., data = Covid_train, family = 'binomial')
log_model
```
~~~

```
Call:  glm(formula = DEATH ~ ., family = "binomial", data = Covid_train)

Coefficients:
   (Intercept)             SEX             AGE    PATIENT_TYPE       PNEUMONIA        DIABETES            COPD          ASTHMA
      -0.70032        -0.41051        -0.05244        -1.98410         1.19472         0.29444         0.13309        -0.07068
       INMSUPR    HIPERTENSION  CARDIOVASCULAR   RENAL_CHRONIC   OTHER_DISEASE         OBESITY         TOBACCO         INTUBED
       0.29018         0.12659        -0.04596         0.73844         0.30944         0.23432        -0.13487         2.50672
           ICU
      -0.54479

Degrees of Freedom: 274297 Total (i.e. Null);  274281 Residual
Null Deviance:	    220400
Residual Deviance: 109100 	AIC: 109100
```

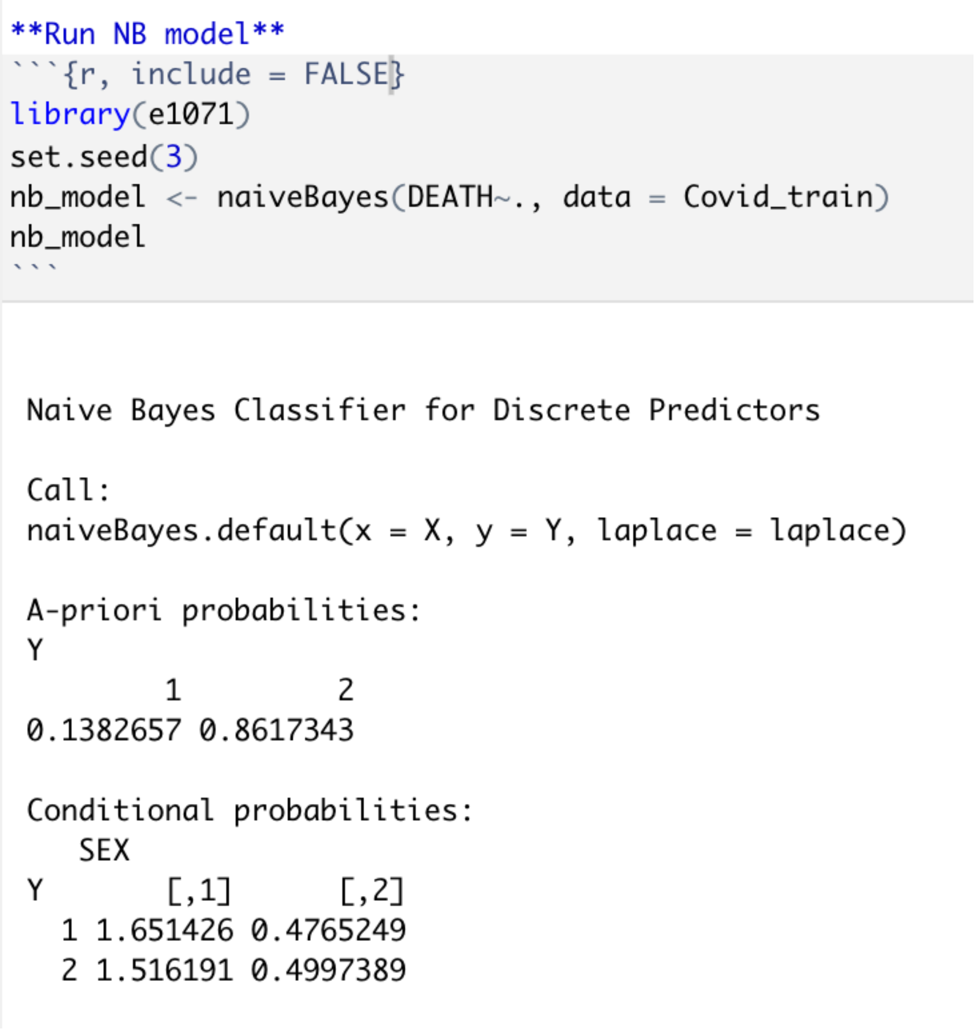
Figure 5 Logistic Regression Model

KNN MODEL

KNN model failed to run as there are too many ties in the result which KNN can't deal with. This means that there are many similar data points and it is hard for KNN to tell which are the nearest since many points have the same distance. We will forgo KNN model for this use case.

NAÏVE BAYES MODEL

Naïve Bayes model can show the conditional probabilities of each variable (Figure 6).



~~~
**Run NB model**
```{r, include = FALSE}
library(e1071)
set.seed(3)
nb_model <- naiveBayes(DEATH~., data = Covid_train)
nb_model
```
~~~

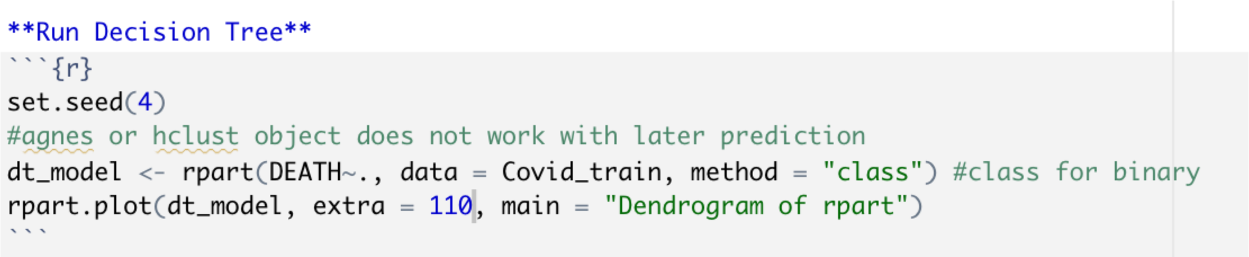
```

Naive Bayes Classifier for Discrete Predictors

Call:
naiveBayes.default(x = X, y = Y, laplace = laplace)

A-priori probabilities:
Y
        1         2 
0.1382657 0.8617343 

Conditional probabilities:
   SEX
Y       [,1]      [,2]
  1 1.651426 0.4765249
  2 1.516191 0.4997389
```

Figure 6 Naive Bayes model

DECISION TREE MODEL

From the DT model, we can tell that covid-positive patients that have higher death rate are those (Figure 7, Figure 8)

1) who have been hospitalized and connected to a ventilator (6%)
2) who have been hospitalized, age >=71, and has past medical history of pneumonia (3%)



~~~
**Run Decision Tree**
```{r}
set.seed(4)
#agnes or hclust object does not work with later prediction
dt_model <- rpart(DEATH~., data = Covid_train, method = "class") #class for binary
rpart.plot(dt_model, extra = 110, main = "Dendrogram of rpart")
```
~~~

Figure 7 Decision Tree model

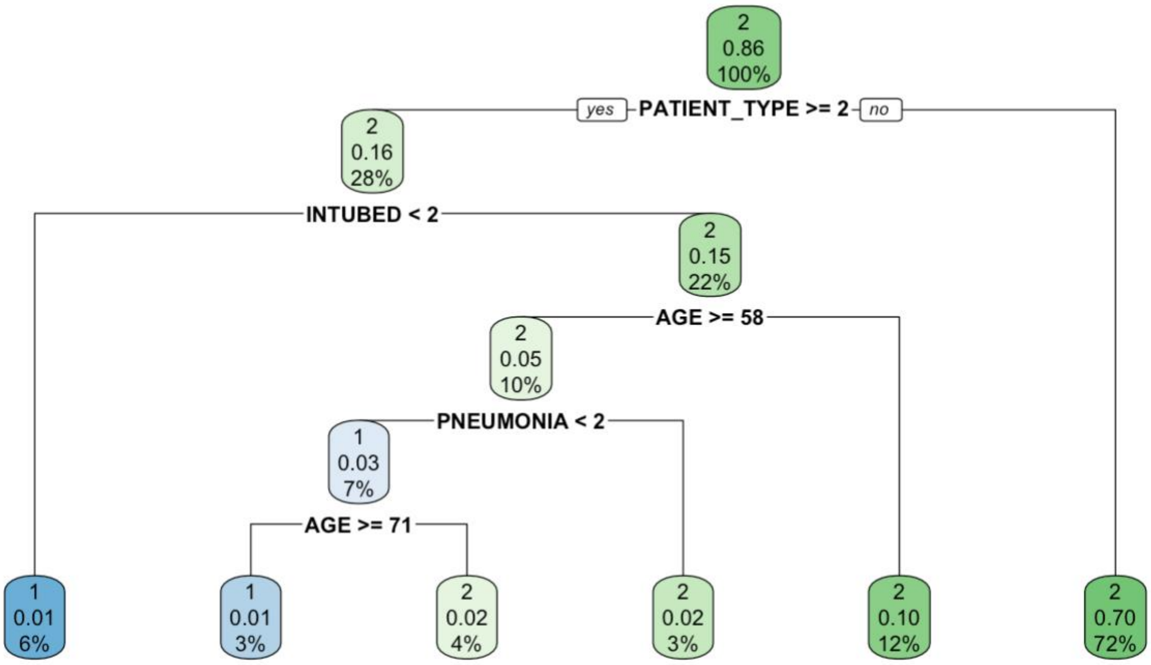


Figure 8 DT Dendrogram

4. ESTIMATION OF MODEL’S PERFORMANCE

MODEL ACCURACY

- We apply the model on the test data to calculate the ROC curve to examine the algorithm's effectiveness and determine the best threshold based on our tolerance for false negatives and desire for true positives. The area under the curve determines the model accuracy where a perfect classifier would be 1. Therefore, the higher the AUC, the more confident we are in our model's predictive ability

MODEL PERFORMANCE

- Confusion matrix are created to balance the trade-off between false positive and false negative. It reveals information on sensitivity (how good the model can detect a positive patient) and specificity (how good the model can detect a negative patient). We need to choose a model that balance the sensitivity and specificity while also have a AUC > 0.85. If sensitivity is similar to specificity, we emphasize more on reaching a good sensitivity as it is more important to reduce false negative than false positive.
- Below is example of ROC plot (Figure 9) and confusion matrix (Figure 10) from Logistic Regression.

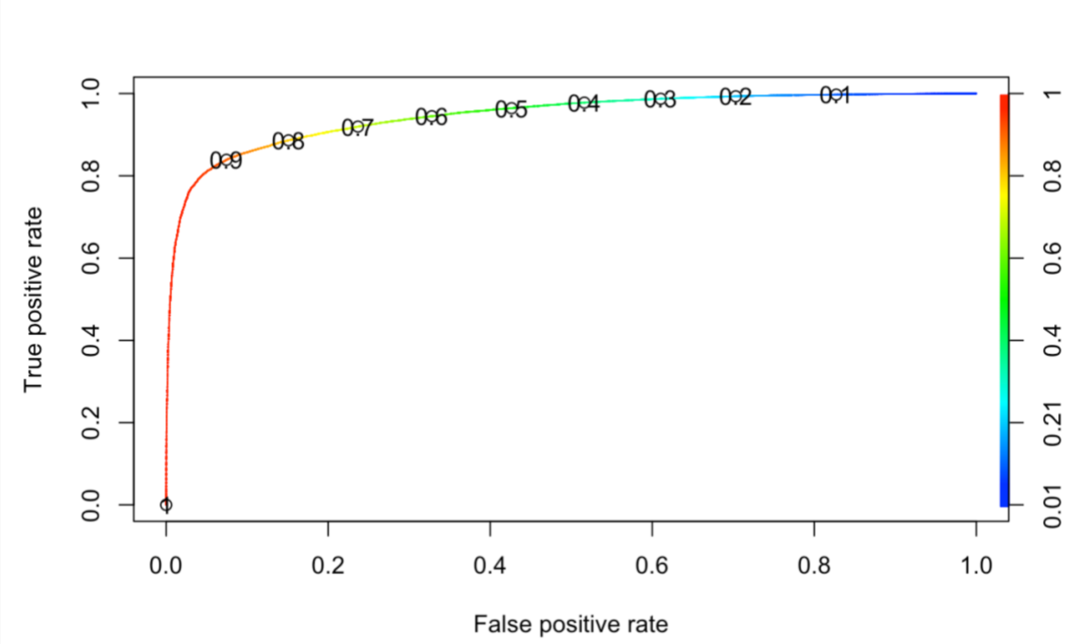
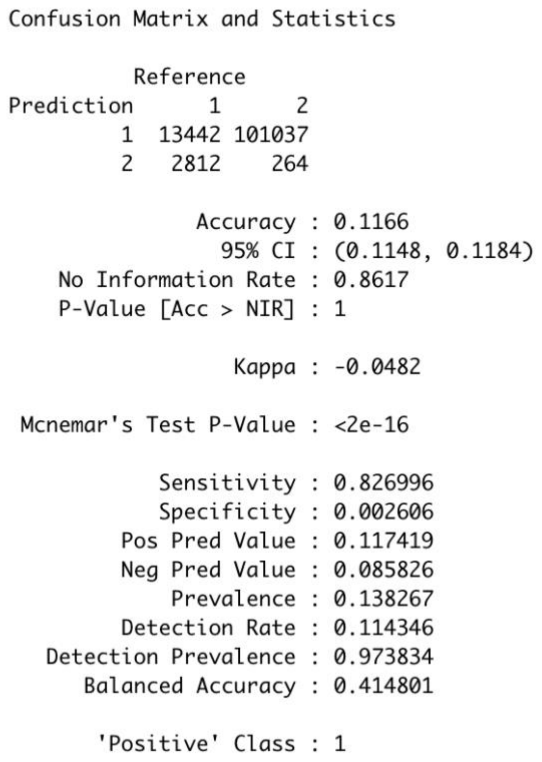


Figure 9 ROC Curve for Logistic Regression



```
Confusion Matrix and Statistics

          Reference
Prediction      1      2
         1  13442 101037
         2   2812    264

               Accuracy : 0.1166
                 95% CI : (0.1148, 0.1184)
    No Information Rate : 0.8617
    P-Value [Acc > NIR] : 1

                  Kappa : -0.0482

 Mcnemar's Test P-Value : <2e-16

            Sensitivity : 0.826996
            Specificity : 0.002606
         Pos Pred Value : 0.117419
         Neg Pred Value : 0.085826
             Prevalence : 0.138267
         Detection Rate : 0.114346
   Detection Prevalence : 0.973834
      Balanced Accuracy : 0.414801

       'Positive' Class : 1
```

Figure 10 Confusion matrix for logistic regression

PERFORMANCE METRICS

Performance of the four models are compared against each other (see .

).

Metric\Model	Logistic Regression	Naïve Bayes	Decision Tree
ROC value	0.95	0.92	0.91
True Positive (TP)	13442	13857	14752
True Negative (TN)	264	85337	82584
False Positive (FP)	101037	15964	18717
False Negative (FN)	2812	2397	1502
Miscalculations	103849	18361	20219
Accuracy	11.66%	84.38%	82.80%
Sensitivity	82.70%	85.25%	90.76%
Specificity	0.26%	84.24%	81.52%

Table 1 Performance metric by model

Based on TABLE1, we will choose decision tree model as the best model to predict patient survival situation. Decision Tree model has the best sensitivity rate while not compromising too much on specificity therefore it is the best model to use. It also has good capability reducing number of false negatives among all three models.

5. INSIGHTS AND CONCLUSION

We recommend the Decision Tree model to ABC Clinic to use on future patient data and identify if the patient have a higher death rate. We aim to help ABC Clinic predict COVID patients survival situation beforehand so they take into account the additional information when treating the patient in order to increase patient survival rate. The model intend to reduce false negatives (correctly identify all positive patients) but produce more false positives (some patients with good survival will be marked with higher death rate).

If we are provided with the cost for treating each false positive and false negative patient, the total cost of saving for the hospital could also be calculated.

APPENDIX