COVID-19 Project

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Load the data and Explore the data

```
data <- read.csv("patient data.csv") # load data
str(data) # see all columns type and values
```

```
## 'data.frame':    3397 obs. of  24 variables:
##  $ id                    : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ case_in_country       : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ reporting.date        : Factor w/ 57 levels "1/13/2020","1/15/2020",..: 4 4 5 5 5 5 5 5 5 5 ...
##  $ X                     : logi  NA NA NA NA NA NA ...
##  $ summary               : Factor w/ 2103 levels "confirmed COVID-19 pneumonia patient No.11 in Tian
##  $ location              : Factor w/ 241 levels "","Aargau","Afghanistan",..: 189 186 239 207 207 38
##  $ country               : Factor w/ 39 levels "","Afghanistan",..: 10 10 10 10 10 10 10 10 10 10 ..
##  $ gender                : Factor w/ 4 levels "","20","female",..: 4 3 4 3 4 3 4 4 4 4 ...
##  $ age                   : num  66 56 46 60 58 44 34 37 39 56 ...
##  $ symptom_onset         : Factor w/ 74 levels "","1/10/2020",..: 23 7 26 NA NA 7 3 6 31 8 ...
##  $ If_onset_approximated : int  0 0 0 NA NA 0 0 0 0 0 ...
##  $ hosp_visit_date       : Factor w/ 71 levels "","1/1/2020",..: 4 8 10 12 7 NA NA 13 7 13 ...
##  $ international_traveler: int  NA NA NA NA NA NA NA NA NA NA ...
##  $ domestic_traveler     : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ exposure_start        : Factor w/ 47 levels "","1/10/2020",..: 29 NA NA NA NA NA NA 2 21 24 ...
##  $ exposure_end          : Factor w/ 64 levels "","1/10/2020",..: 26 4 23 NA NA NA NA 3 26 8 ...
##  $ traveler              : int  NA NA NA NA NA NA NA NA NA NA ...
##  $ visiting.Wuhan        : int  1 0 0 1 0 0 0 1 1 1 ...
##  $ from.Wuhan            : int  0 1 1 0 0 1 1 0 0 0 ...
##  $ death                 : Factor w/ 25 levels "","0","1","2/1/2020",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ recovered             : Factor w/ 37 levels "","0","1","1/15/2020",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ symptom               : Factor w/ 138 levels "","back pain, fever, runny nose",..: 1 1 1 1 1 1 1
##  $ source                : Factor w/ 110 levels "","1Point3Acres",..: 76 68 36 108 108 17 109 10 10
##  $ link                  : Factor w/ 534 levels "","http://behdasht.gov.ir/news/%DA%A9%D8%B1%D9%88%D9
```

```
data[data==""] <- NA #treat all blank values as missing elements of the data matrix
```

Find correlation between age, and incubation (derived)

```
data$incubation <- as.numeric(
                    as.Date(as.character(data$symptom_onset),format = "%m/%d/%Y") - as.Date(as.characte
                              ) # derive variable incubation = symptom_onset date - exposure_start date
```

Normalized the numeric variables

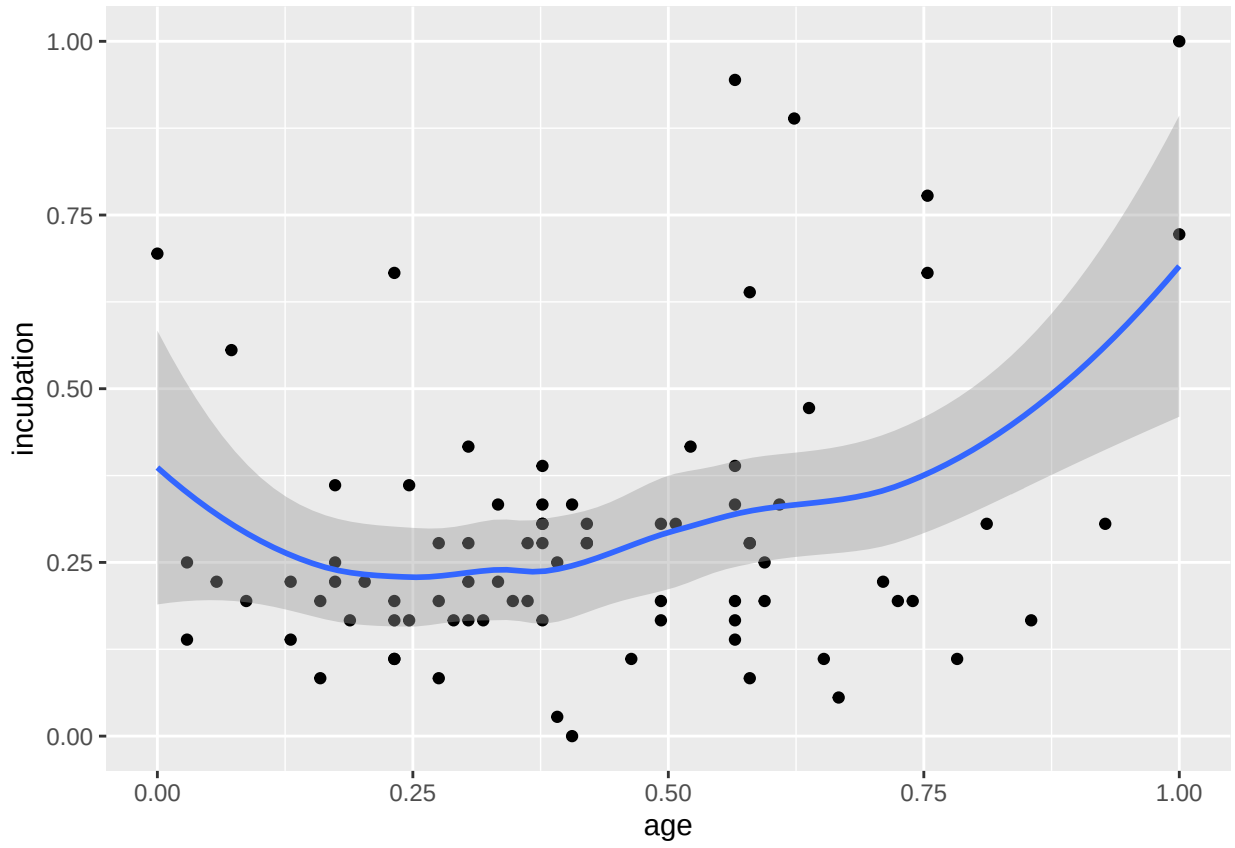
```r
normalize <- function(x){
  return((x-min(x))/(max(x)-min(x))) } # normalize function created
data1 <- data[,c(9,25)] #age and incubation selected
data1 <- na.omit(data1)
data1_n <- as.data.frame(lapply(data1,normalize))
summary(data1_n)# check if it is normalized
```

```
##       age           incubation
##  Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.2464   1st Qu.:0.1667
##  Median :0.3768   Median :0.2222
##  Mean   :0.4222   Mean   :0.2898
##  3rd Qu.:0.5797   3rd Qu.:0.3333
##  Max.   :1.0000   Max.   :1.0000
```

Find correlation between age, and incubation (derived)

```r
library(ggplot2)
ggplot(data=data1_n) +
    geom_point(mapping = aes(x=age, y=incubation)) +
  geom_smooth(mapping = aes(x=age, y=incubation))# no obvious correlation between age and incubation pe
```

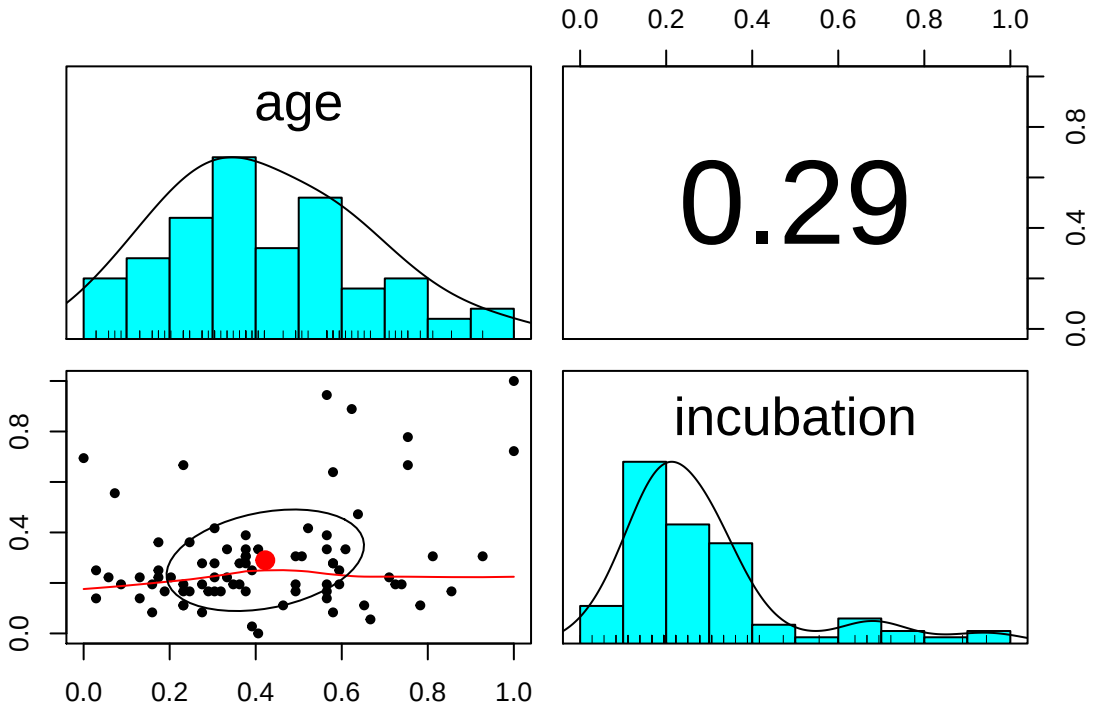
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



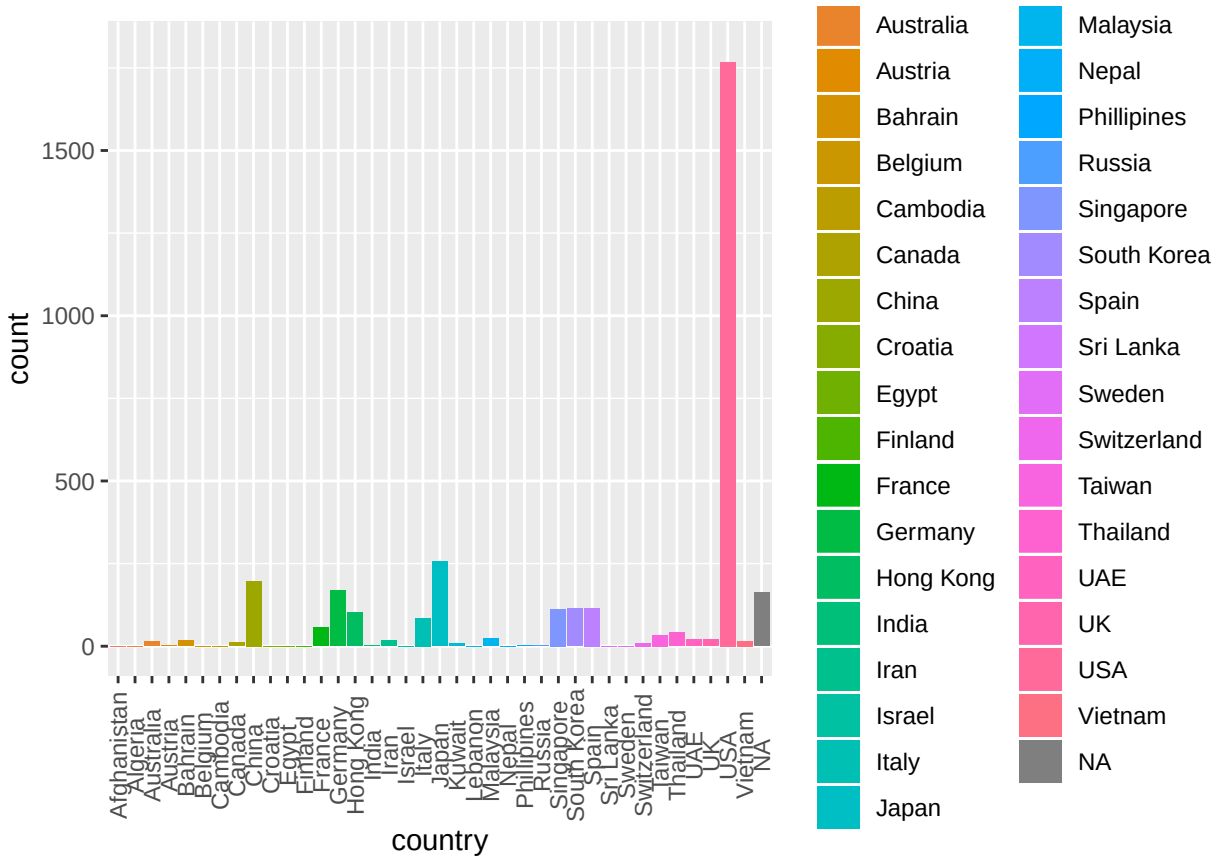
```r
cor(data1_n$age,data1_n$incubation,use="complete.obs", method = "pearson") # 0.3 indicates 1 weak posit
```

```
## [1] 0.2917508
```

```r
psych::pairs.panels(data1_n[,c(1,2)]) # correlation visualization between age and incubation.
```




```r
ggplot(data, aes(x=country, fill=country)) +
    ylim(0,1800) +
    geom_bar() +
    theme(axis.text.x = element_text(angle = 90, vjust = 0.5))
```



Predict the probability of death using different prediction models: MODEL 1: multiple regression model - lm from stats package

```
library(data.table)

data$death<- as.numeric(fifelse(data$death==0, 0, 1, na=NA)) # changing death to numeric variable

library(stringr)

for (i in 1:nrow(data)){
  data$n_symptom[i] <- (str_count(data$symptom[i], ',')+1)
} # assuming more number of symptoms there are, more severe the problem is.

data$gender1 <- ifelse(data$gender!="female"&
                         data$gender!="male",
                       NA,data$gender);

for (i in 1:nrow(data)){
  data$gender1[i] <- (data$gender1[i]-3)
}; # 0 is female; 1 is male

lm <-lm(death~case_in_country+country+gender1+age+incubation+n_symptom,data) # creating multiple linear

summary(lm); # model r-squared value is around 15%, which is quite small; only 15% of variances are exp

##
```

```
## Call:
## lm(formula = death ~ case_in_country + country + gender1 + age +
##     incubation + n_symptom, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.16615 -0.05438 -0.01293  0.00372  0.82968
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -0.1949904  0.4215324  -0.463    0.649
## case_in_country    -0.0007051  0.0010175  -0.693    0.497
## countryHong Kong    0.2858215  0.3267511   0.875    0.393
## countryJapan        0.2148380  0.3363094   0.639    0.531
## countryMalaysia     0.2153029  0.4041220   0.533    0.601
## countrySingapore    0.1812980  0.3774848   0.480    0.637
## countrySouth Korea  0.2322287  0.4234381   0.548    0.590
## countryTaiwan       0.1601536  0.3479455   0.460    0.651
## countryUSA          0.1413528  0.3856444   0.367    0.718
## countryVietnam      0.1800077  0.3510145   0.513    0.614
## gender1             0.0765412  0.0853975   0.896    0.382
## age                -0.0015201  0.0026254  -0.579    0.570
## incubation          0.0004375  0.0062654   0.070    0.945
## n_symptom           0.0335138  0.0725135   0.462    0.649
##
## Residual standard error: 0.2147 on 18 degrees of freedom
##   (3365 observations deleted due to missingness)
## Multiple R-squared:  0.1436, Adjusted R-squared:  -0.475
## F-statistic: 0.2321 on 13 and 18 DF,  p-value: 0.9949
```

```
test <- data.frame(case_in_country=210, country="USA",gender1=0, age=70, n_symptom=6, incubation=4) # m

test$death.p <- predict(lm,test)
test$death.p
```

```
## [1] -0.1052773
```

```
# the likelihood of patient death is close to 0.
```

MODEL 2 K-Means Clustering (to discover any unknown subtypes of patients who have being diagnosed with COVID)

```
# removing unnecessary columns
interests<- data[,c(2,9,25,26)]
# The kmeans() function requires a data frame containing only numeric data and a parameter specifying t

# removing non-existing values
interests <- na.omit(interests)

# apply as.interger to all vectors
data.interest_int <- as.data.frame(lapply(interests,as.integer))
summary(data.interest_int)
```

```
##  case_in_country       age          incubation      n_symptom
##  Min.   :  1.00   Min.   :16.00   Min.   :-1.00   Min.   :1.000
##  1st Qu.: 10.75   1st Qu.:35.00   1st Qu.: 5.75   1st Qu.:1.000
##  Median : 17.00   Median :42.50   Median : 8.50   Median :2.000
##  Mean   : 36.81   Mean   :47.16   Mean   :10.44   Mean   :1.781
##  3rd Qu.: 52.25   3rd Qu.:55.50   3rd Qu.:12.00   3rd Qu.:2.000
##  Max.   :169.00   Max.   :85.00   Max.   :34.00   Max.   :5.000
```

```
# apply z-score standardization
data_int_z <- as.data.frame(lapply(data.interest_int,scale))

# Set the seed, so results are reproducible
set.seed(1234)

# create index for randomly selecting 75% rows of the original data set
index <- sample.int(n = nrow(interests), size = floor(.75*nrow(interests)), replace = F)

# create training dataset, which accounts for 75% of the data set
data.train_z <- data.interest_int[index, ]
# create testing dataset, which accounts for 25% of the data set
data.test_z  <- data.interest_int[-index, ]

# set specific starting point for k-means algorithm
RNGversion("3.5.2")
```

```
## Warning in RNGkind("Mersenne-Twister", "Inversion", "Rounding"): non-uniform
## 'Rounding' sampler used
```

```
# building clustering model
patient_clusters <- kmeans(data.interest_int,3) # 3 for 3 clusters
```

Evaluating Model 2- Check machine learning performance evaluation for k-means clustering

```
# check size of all 3 groups
patient_clusters$size
```

```
## [1]  8  2 22
```

```
# examine cluster centroids
patient_clusters$centers
```

```
##   case_in_country      age incubation n_symptom
## 1        70.75000 51.50000  14.750000  1.750000
## 2       158.50000 55.00000   6.500000  1.500000
## 3        13.40909 44.86364   9.227273  1.818182
```

```
# Comment: we can see that group 2 and 3 are mostly alders, and group 1 is younger people. For elders h
```

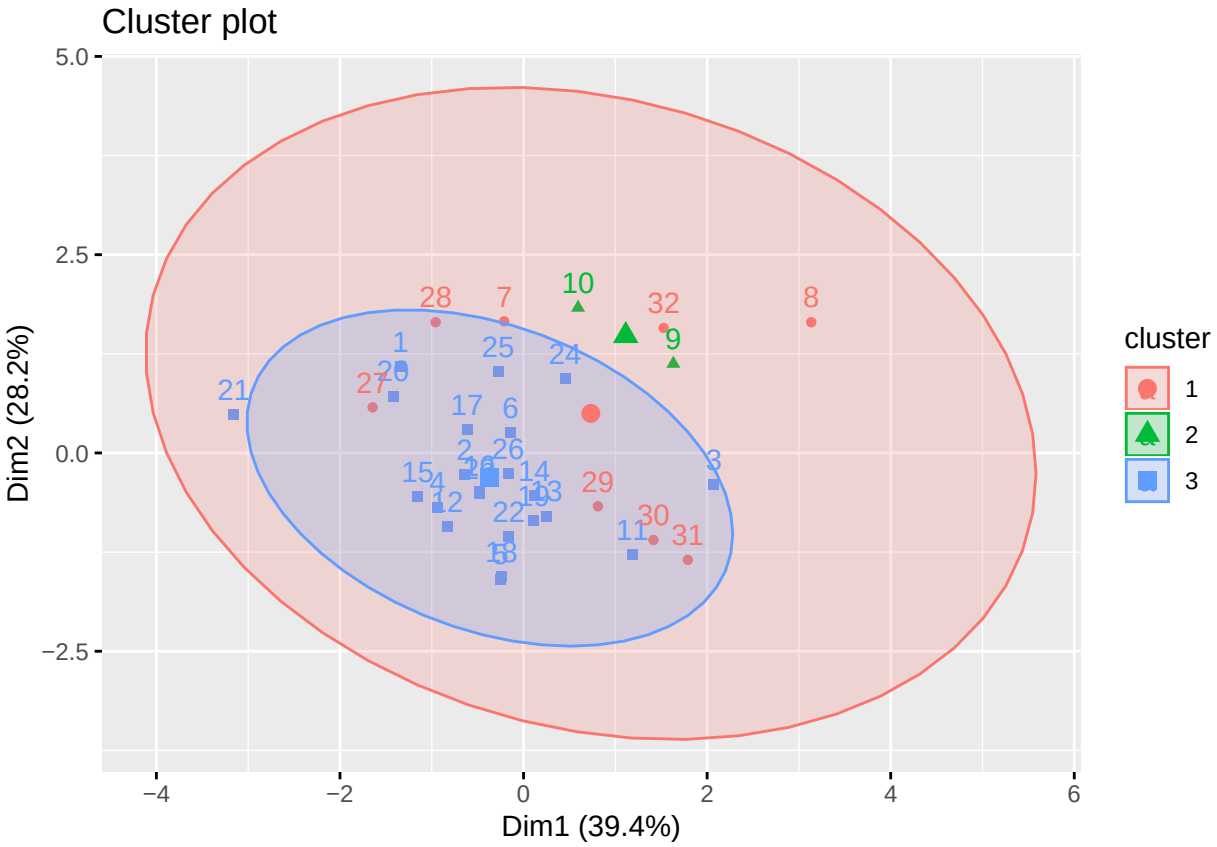
Visualize the clusters

```
# load necessary package
library(factoextra)
```

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

```
# function fviz_cluster can be used to visualize the 3 clusters created previously.
fviz_cluster(patient_clusters,data.interest_int,ellipse.type = "norm")
```

```
## Too few points to calculate an ellipse
```




```
# Comment: Given the graph, we would have a clear dipictions of 3 groups of patients related to COVID-1
# shortcoming of the model: after missing values being omitted, there are too little data points availa
```

Model 3 - kNN algorithm

```
# load necessary packages
library(caret)
```

```
## Loading required package: lattice
```

```r
library(ISLR)

# removing unnecessary columns
interests<- data[,c(2,9,19,20,26,27)]  # includes columns: case_in_country, age, from.wuhan, death, n_s

# removing non-existing values
interests <- na.omit(interests)

# normalize data
data_n <- as.data.frame(lapply(interests,normalize))
summary(data_n)# check if it is normalized
```

```
##  case_in_country        age           from.Wuhan          death
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.00000   Min.   :0.00000
##  1st Qu.:0.07843   1st Qu.:0.4505   1st Qu.:0.00000   1st Qu.:0.00000
##  Median :0.32941   Median :0.5604   Median :0.00000   Median :0.00000
##  Mean   :0.37894   Mean   :0.5503   Mean   :0.08182   Mean   :0.02424
##  3rd Qu.:0.65784   3rd Qu.:0.6703   3rd Qu.:0.00000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.00000   Max.   :1.00000
##    n_symptom         gender1
##  Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.0000   1st Qu.:0.0000
##  Median :0.2000   Median :1.0000
##  Mean   :0.2103   Mean   :0.5697
##  3rd Qu.:0.4000   3rd Qu.:1.0000
##  Max.   :1.0000   Max.   :1.0000
```

```r
# set seed
set.seed(12378)

# create index for randomly selecting 75% rows of the original data set
index <- sample.int(n = nrow(data_n), size = floor(.75*nrow(data_n)), replace = F)

# create training dataset, which accounts for 75% of the data set
data.train <- data_n[index, ]
# create testing dataset, which accounts for 25% of the data set
data.test  <- data_n[-index, ]

# column bind labels to the normalized test and train dataset
data_train_label <- as.data.frame(data.train$death)
data_test_label <- as.data.frame(data.test$death)
names(data_train_label) <- "death"
names(data_test_label) <- "death"
data_train1 <- cbind(data_train_label,data.train)
data_test1 <- cbind(data_test_label,data.test)
```

```r
# set up control object which controls the computational nuances of the train function.
ctrl <- trainControl(method="repeatedcv", repeats = 3)  #Cross-Validated (10 fold, repeated 3 times)

# training the model
knnFit <- train(death~., data=data_train1,method="knn",trControl=ctrl,preProcess=c("center","scale"),tu
```

```
## Warning in train.default(x, y, weights = w, ...): You are trying to do
```

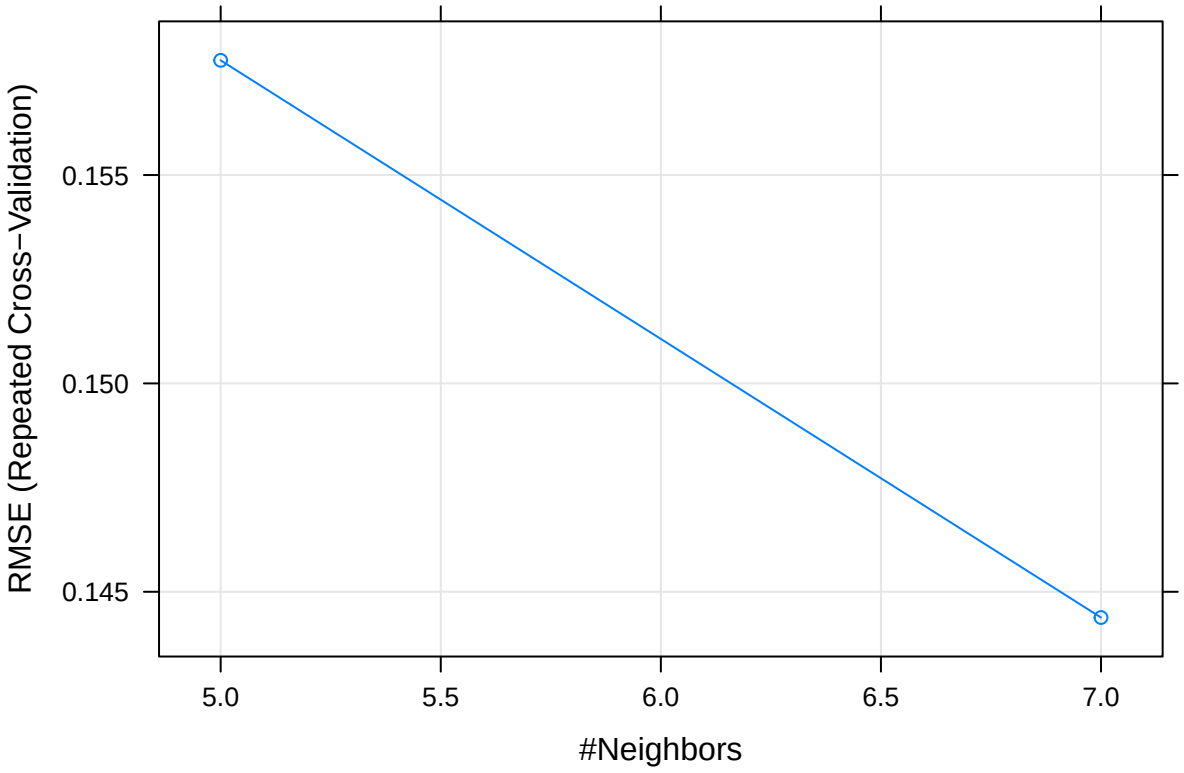
```
## regression and your outcome only has two possible values Are you trying to do
## classification? If so, use a 2 level factor as your outcome column.
```

```
## Warning in nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainInfo, :
## There were missing values in resampled performance measures.
```

```
# output of the kNN fit
knnFit
```

```
## k-Nearest Neighbors
##
## 247 samples
##   5 predictor
##
## Pre-processing: centered (5), scaled (5)
## Resampling: Cross-Validated (10 fold, repeated 3 times)
## Summary of sample sizes: 223, 223, 222, 222, 223, 222, ...
## Resampling results across tuning parameters:
##
##   k  RMSE       Rsquared    MAE
##   5  0.1577519  0.01190423  0.05233148
##   7  0.1443826  0.04507728  0.04845139
##
## RMSE was used to select the optimal model using the smallest value.
## The final value used for the model was k = 7.
```

```
# plotting yields number of neighbours vs accuracy (based on repeated cross valdiation)
 plot(knnFit)
```




```
# predict using testing data
knnPredict <- predict(knnFit,newdata=data_test1)
knnPredict <- as.factor(ifelse(knnPredict>0,1,0))
knnPredict
```

```
##  [1] 0 1 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [39] 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 1 1 0 0 0 0 1 0 1 1 0 0 0 1 0
## [77] 0 0 0 0 1 0 0
## Levels: 0 1
```

```
#data_test1$death <- as.factor(data_test1$death)
data_test1$death
```

```
##  [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [39] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [77] 0 0 0 0 0 0 1
```

```
death_label <- as.factor(data_test1$death)
# use confusion matrix to calculate accuracy for caret algorithm
confusionMatrix(knnPredict,death_label)
```

```
## Confusion Matrix and Statistics
##
##           Reference
```

```
## Prediction  0  1
##          0 71  1
##          1 11  0
##
##                Accuracy : 0.8554
##                  95% CI : (0.7611, 0.923)
##     No Information Rate : 0.988
##     P-Value [Acc > NIR] : 1.000000
##
##                   Kappa : -0.0226
##
##  Mcnemar's Test P-Value : 0.009375
##
##             Sensitivity : 0.8659
##             Specificity : 0.0000
##          Pos Pred Value : 0.9861
##          Neg Pred Value : 0.0000
##              Prevalence : 0.9880
##          Detection Rate : 0.8554
##    Detection Prevalence : 0.8675
##       Balanced Accuracy : 0.4329
##
##        'Positive' Class : 0
##
```

```
mean(knnPredict==death_label)
```

```
## [1] 0.8554217
```

```
# comment: the accuracy for caret is 86%.
```

Comparison of models

```
# According to evaluations for each model, the one with the most accurate data is k-NN algorithm, which
```