MIDTERM PROJECT

1. Exploratory Data Analysis
   a. What variables look most promising for predicting cancer mortality from exploratory data analysis? Why?

Ans-The variables that look promising for predicting cancer are incidenceRate, medIncome, PctHS18_24, PctBachDeg18_24, PctPrivateCoverage, PctPublicCoverageAlone, PctOtherRace. This can be seen by comparing the p-values that are calculated by fitting a linear regression model using the Cancer Data dataset. This can also be seen for the co-relation plot and co-relation matrix.

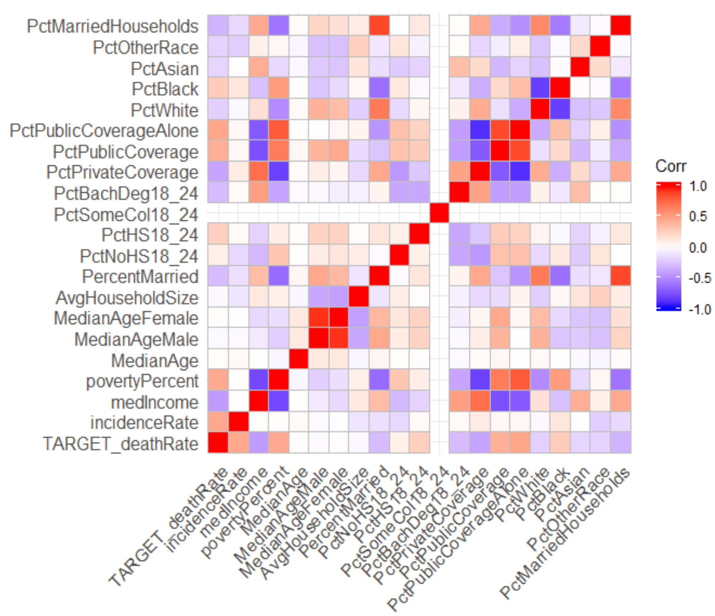


Figure 1-Co-relation graph

   b. Are there any outliers? Can they be detected and addressed? How does addressing outliers affect model performance?

Ans-Yes there are outliers, this can be seen by plotting a box plot. Outliers can be treated by replacing them with the column mean or mode. They can also be treated using capping technique. In percentile capping, the value at 1st percentile, and values that are greater than the value at 99th percentile are replaced by the value at 99th percentile. In this following code, I used a for loop to replace the outliers in every feature.

Code-

```
#finding outliers

OutVals = boxplot(train, plot=FALSE)$out

OutVals1 = boxplot(medIncome, plot=FALSE)$out

plot(OutVals1)

plot(OutVals)

boxplot(train)

library(outliers)

outlier(medIncome)

#treating outlies- by using capping

y = c(1,2,3,4,5,6,7,9,10,11,12,14,15,16,17,18,19,20,21,22)

for (i in y)

{

x <- train[,i]

qnt <- quantile(x, probs=c(.25, .75))

caps <- quantile(x, probs=c(.05, .95))

H <- 1.5 * IQR(x)

x[x < (qnt[1] - H)] <- caps[1]

x[x > (qnt[2] + H)] <- caps[2]

train[,i] = x
```

```
}
for (i in y)
{
  x <- test[,i]
  qnt <- quantile(x, probs=c(.25, .75))
  caps <- quantile(x, probs=c(.05, .95))
  H <- 1.5 * IQR(x)
  x[x < (qnt[1] - H)] <- caps[1]
  x[x > (qnt[2] + H)] <- caps[2]
  test[,i] = x
}
```

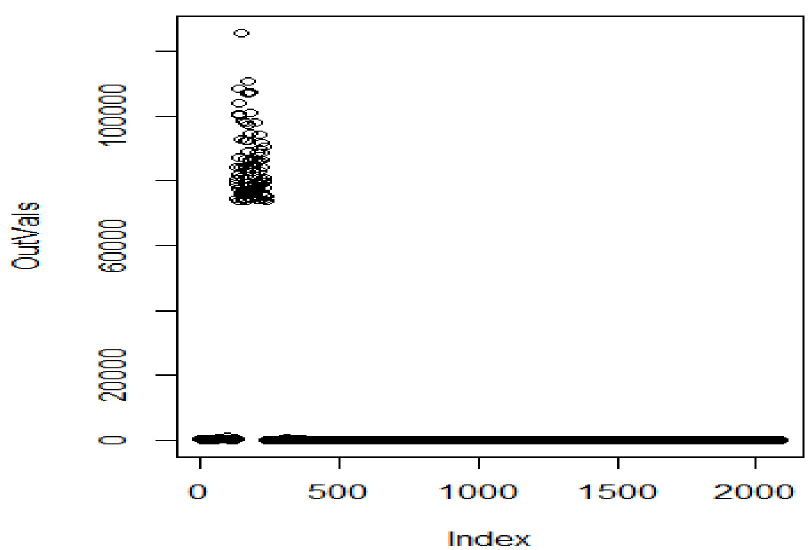


Figure 2- Outliers Plot

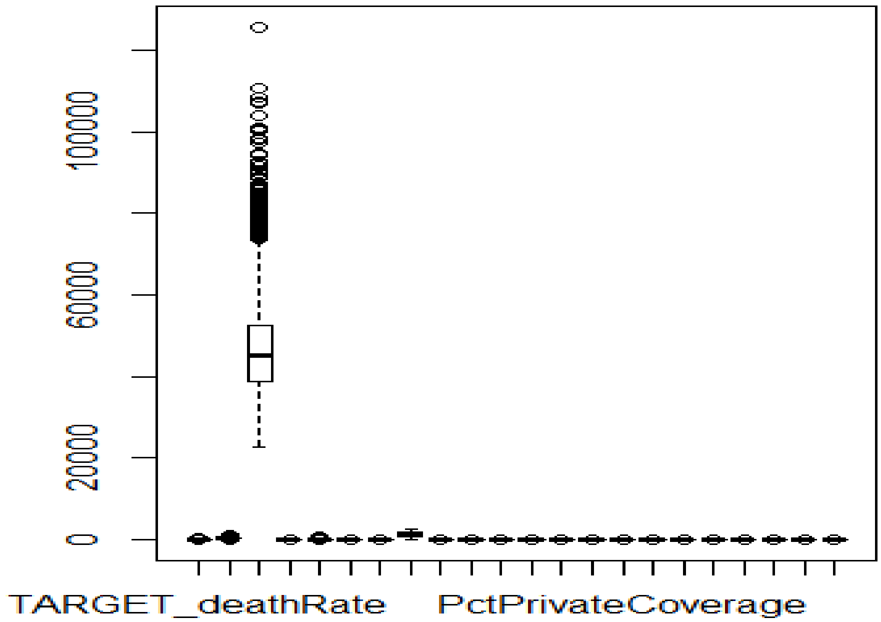


Figure 3-Box plot

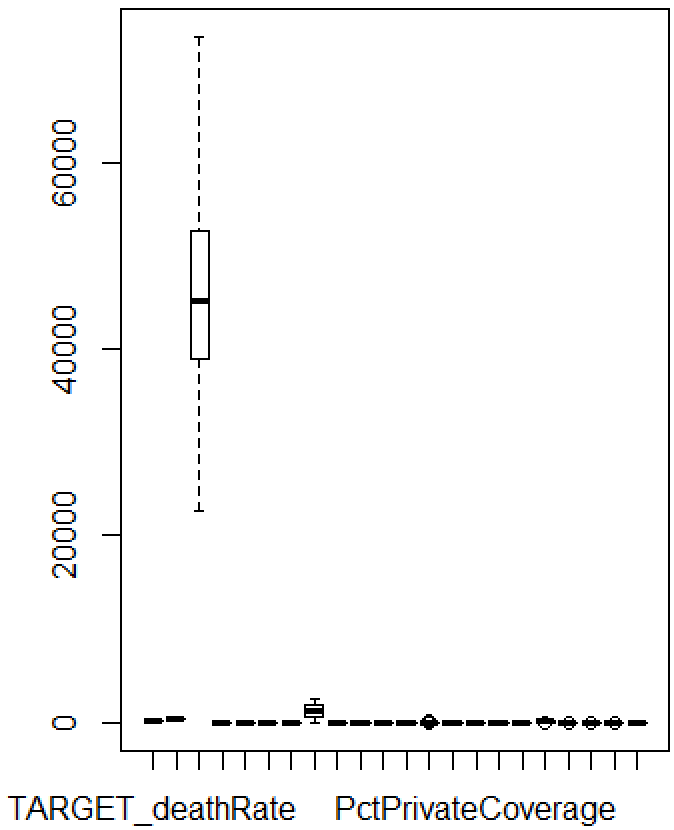


Figure 4- Box pot after capping

c. Are there any missing values? Research and explore techniques to handle missing values. Note that the approach to handle missing data might be different for different variables. Document model performance improvement obtained by missing data handling.

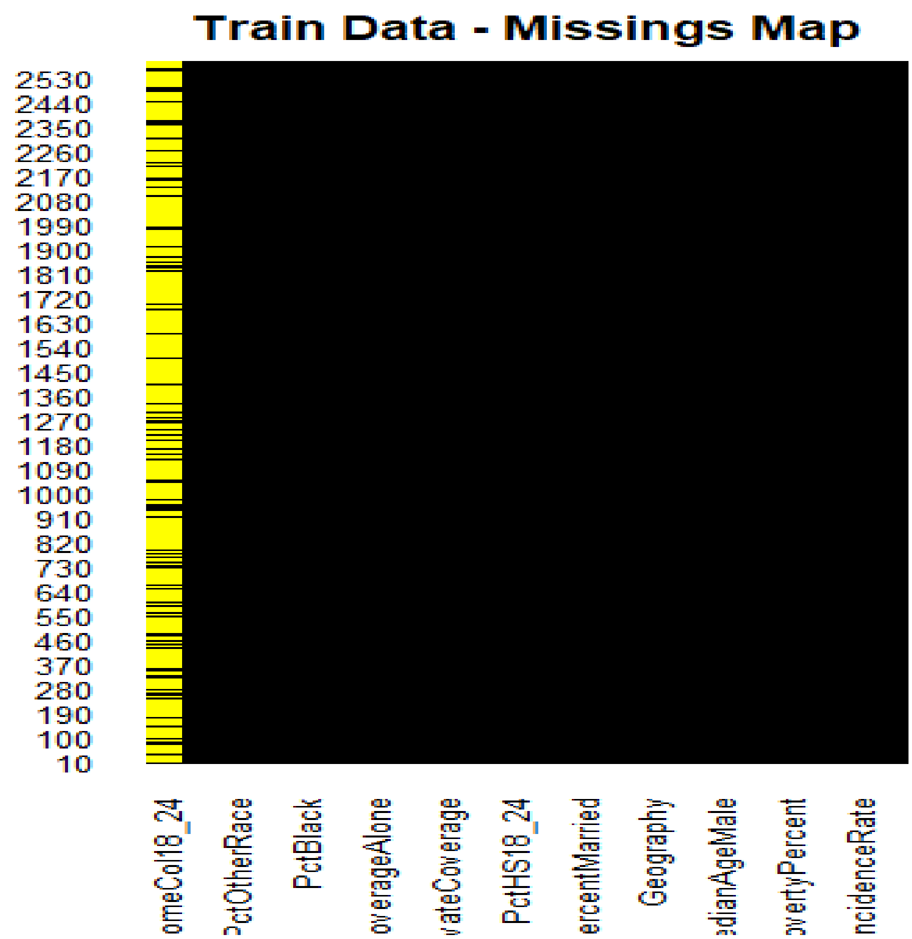
Ans – By observing the test and the train dataset, one can observe that there are a lot of missing values in PctSomeCol18_24. This can also be observed by plotting a Missing Map of the datasets. There are a total of 1938 missing values in PctSomeCol18_24. Missing values can be treated by replacing them with mean, median or mode of that column or ignoring the column if there are a lot of missing values. In this case, since there are a lot of missing values PctSomeCol18_24 can be neglected from model fitting. Documentation of model performance improvement obtained by missing data handling is done in question 2.

Code-

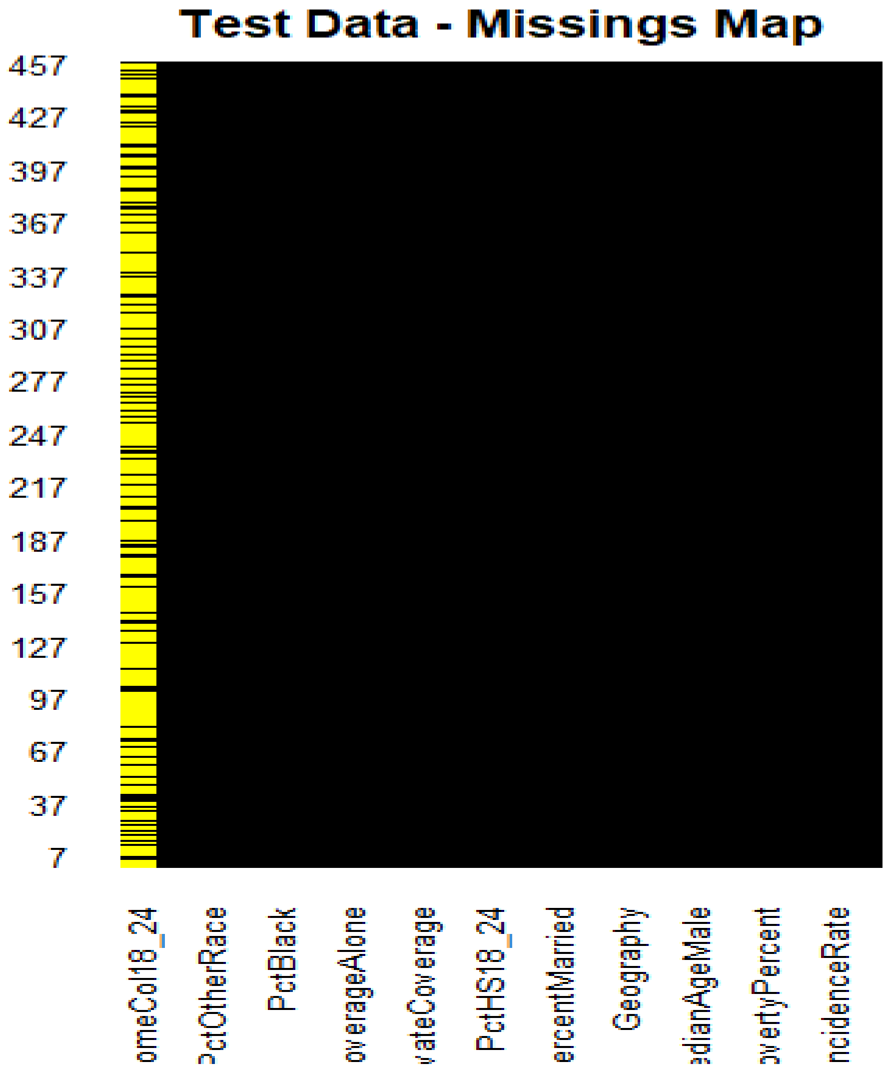
```
#missing values
library(Amelia)
sum(is.na(train$PctSomeCol18_24))
missmap(train, main="Train Data - Missings Map",
    col=c("yellow", "black"), legend=FALSE)
```

Output-

```
> sum(is.na(train$PctSomeCol18_24))
[1] 1938
```



Train Data - Missings Map
2530
2440
2350
2260
2170
2080
1990
1900
1810
1720
1630
1540
1450
1360
1270
1180
1090
1000
910
820
730
640
550
460
370
280
190
100
10
omeCol18_24
PctOtherRace
PctBlack
overageAlone
vateCoverage
PctHS18_24
ercentMarried
Geography
edianAgeMale
overtyPercent
ncidenceRate



d. Is there any collinearity between variables? Can it be detected? Document how addressing collinearity affects model performance?
e. Ans- There is collinearity between the variables. It can be detected by observing the VIF values of the variables after fitting them in linear regression using the olsrr library. Documentation on how addressing collinearity affects the model performance is discussed in question 2. Any variable with VIF value above 4 should be neglected because of collinearity.

Code-

#finding collinearity

install.packages('olsrr')

train = read.csv("C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

train$PctSomeCol18_24[is.na(train$PctSomeCol18_24)]= median(train$PctSomeCol18_24, na.rm= TRUE)

test$PctSomeCol18_24[is.na(test$PctSomeCol18_24)]= median(test$PctSomeCol18_24, na.rm= TRUE)

library(olsrr)

ols_vif_tol(LR3)

Output-

```
> ols_vif_tol(LR3)
                 Variables  Tolerance       VIF
1            incidenceRate 0.82900494  1.206265
2                medIncome 0.17124026  5.839748
3           povertyPercent 0.13454213  7.432616
4                MedianAge 0.98189629  1.018437
5            MedianAgeMale 0.11254315  8.885481
6          MedianAgeFemale 0.09976550 10.023505
7         AvgHouseholdSize 0.68497668  1.459904
8           PercentMarried 0.13710069  7.293909
9             PctNoHS18_24 0.63776768  1.567969
10              PctHS18_24 0.72733607  1.374880
11         PctBachDeg18_24 0.54450499  1.836530
12      PctPrivateCoverage 0.10992638  9.096997
13       PctPublicCoverage 0.05668669 17.640825
14 PctPublicCoverageAlone 0.05545882 18.031395
15                PctWhite 0.14668757  6.817210
16                PctBlack 0.19471208  5.135788
17                PctAsian 0.57515070  1.738675
18            PctOtherRace 0.71566391  1.397304
19    PctMarriedHouseholds 0.15894287  6.291569
```

2. Linear Regression
    a. Develop a linear regression model.

Ans- Multiple linear regression models are developed after refining the data at each step.

<u>After treating the missing values-</u>

- Three models are built after treating the missing by replacing them with mean, median and by neglecting the column. The train MSE obtained by neglecting the column, replacing it with median and mean is 411.3217, 411.3189, 411.3217 respectively and the test MSEs obtained are 414.5908, 414.54, 414.5908. Neglecting the column is a better choice in this situation since there are a lot of missing values even though the test MSE and train MSE are better when replaced by median.

<u>After treating the outliers-</u>

- The fourth model is developed after replacing the outliers using percentile capping and neglecting the PctSomeCol18_24 column. The train and test MSE are 351.1055 and 348.365 respectively. This model performs well on the training data set since the train MSE is lower than the other three models but it has a higher test MSE compared to the other models.

<u>After treating collinearity-</u>

- The fifth model is developed after removing the collinear variables and neglecting the PctSomeCol18_24 column. The train and test MSE are 459.1824 and 460.9086 respectively. This model doesn't perform as good as the other models because it has a higher test and train MSE.

<u>After treating everything -</u>

- The last model is developed after treating the missing values, outliers and collinearity. The train and test MSE are 381.06 and 361.6792 respectively.

Code-

```
#missing values
library(Amelia)
sum(is.na(train$PctSomeCol18_24))
missmap(train, main="Train Data - Missings Map",
        col=c("yellow", "black"), legend=FALSE)
missmap(test, main="Test Data - Missings Map",
        col=c("yellow", "black"), legend=FALSE)


#treating missing values
#method1 - neglecting the coloumn
LR3 =
lm(TARGET_deathRate~incidenceRate+medIncome+povertyPercent+MedianAge+MedianAgeMale+MedianAgeFemale+AvgHouseholdSize+PercentMarried+PctNoHS18_24+PctHS18_24+PctBachDeg18_24+PctPrivateCoverage+PctPublicCoverage+PctPublicCoverageAlone+PctWhite+PctBlack+PctAsian+PctOtherRace+PctMarriedHouseholds
        , data =train)
summary(LR3)
LR3.pred= predict(LR3 ,newdata= test )
msetrain_n=mean((train$TARGET_deathRate-fitted(LR3))^2)
msetrain_n
msetest_n=mean(((test$TARGET_deathRate) - (LR3.pred))^2)
```

```
msetest_n

#Method2 - inputing median

train = read.csv("C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

train$PctSomeCol18_24[is.na(train$PctSomeCol18_24) ]= median(train$PctSomeCol18_24, na.rm= TRUE)

test$PctSomeCol18_24[is.na(test$PctSomeCol18_24)]= median(test$PctSomeCol18_24, na.rm= TRUE)

LR2 = lm(TARGET_deathRate~incidenceRate+medIncome+povertyPercent+MedianAge+MedianAgeMale+MedianAgeFemale+AvgHouseholdSize+PercentMarried+PctNoHS18_24+PctHS18_24+PctSomeCol18_24+PctBachDeg18_24+PctPrivateCoverage+PctPublicCoverage+PctPublicCoverageAlone+PctWhite+PctBlack+PctAsian+PctOtherRace+PctMarriedHouseholds

    , data =train)

summary(LR2)

LR2.pred= predict(LR2 ,newdata= test)

LR2.pred

msetrain_median=mean((train$TARGET_deathRate-fitted(LR2))^2)

msetrain_median

msetest_median=mean(((test$TARGET_deathRate) - (LR2.pred))^2)
```

```
msetest_median


#method3- Inputing the mean

train = read.csv("C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

train$PctSomeCol18_24[is.na(train$PctSomeCol18_24) ]= mean(train$PctSomeCol18_24, na.rm= TRUE)

test$PctSomeCol18_24[is.na(test$PctSomeCol18_24)]= mean(test$PctSomeCol18_24, na.rm= TRUE)

LR1 = lm(TARGET_deathRate~incidenceRate+medIncome+povertyPercent+MedianAge+MedianAgeMale+MedianAgeFemale+AvgHouseholdSize+PercentMarried+PctNoHS18_24+PctHS18_24+PctBachDeg18_24+PctPrivateCoverage+PctPublicCoverage+PctPublicCoverageAlone+PctWhite+PctBlack+PctAsian+PctOtherRace+PctMarriedHouseholds

        , data =train)

summary(LR1)

LR1.pred= predict(LR1 ,newdata= test)

msetrain1=mean((train$TARGET_deathRate-fitted(LR1))^2)

msetrain1

msetest1=mean(((test$TARGET_deathRate) - (LR1.pred))^2)

msetest1
```

```
attach(train)

#removing insignificant variables

fix(train)

LR4 = lm(TARGET_deathRate~incidenceRate+medIncome+PctHS18_24+PctOtherRace+PctBachDeg18_24+PctPrivateCoverage+PctPublicCoverageAlone+povertyPercent, data =train)

LR4.pred= predict(LR4 ,newdata= test)

msetrain_sign=mean((train$TARGET_deathRate - fitted(LR4))^2)

msetrain_sign

msetest_sign=mean(((test$TARGET_deathRate) - (LR4.pred))^2)

msetest_sign


#finding outliers

OutVals = boxplot(train, plot=FALSE)$out

OutVals1 = boxplot(medIncome, plot=FALSE)$out

plot(OutVals1)

plot(OutVals)

boxplot(train)

library(outliers)

outlier(medIncome)
```

```
#treating outlies- by using capping

y = c(1,2,3,4,5,6,7,9,10,11,12,14,15,16,17,18,19,20,21,22)

for (i in y)

{

x <- train[,i]

qnt <- quantile(x, probs=c(.25, .75))

caps <- quantile(x, probs=c(.05, .95))

H <- 1.5 * IQR(x)

x[x < (qnt[1] - H)] <- caps[1]

x[x > (qnt[2] + H)] <- caps[2]

train[,i] = x

}

for (i in y)

{

  x <- test[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  test[,i] = x
```

```
}

boxplot(train)

LR5 =
lm(TARGET_deathRate~incidenceRate+medIncome+povertyPercent+MedianA
ge+MedianAgeMale+MedianAgeFemale+AvgHouseholdSize+PercentMarried+P
ctNoHS18_24+PctHS18_24+PctBachDeg18_24+PctPrivateCoverage+PctPublic
Coverage+PctPublicCoverageAlone+PctWhite+PctBlack+PctAsian+PctOtherRa
ce+PctMarriedHouseholds


    , data =train)

summary(LR5)

LR5.pred= predict(LR5 ,newdata= test)

msetrain2=mean((train$TARGET_deathRate-fitted(LR5))^2)

msetrain2

msetest2=mean(((test$TARGET_deathRate) - (LR5.pred))^2)

msetest2


#finding collinearity


#install.packages('olsrr')

train = read.csv("C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')
```

```
train$PctSomeCol18_24[is.na(train$PctSomeCol18_24) ]= median(train$PctSomeCol18_24, na.rm= TRUE)

test$PctSomeCol18_24[is.na(test$PctSomeCol18_24)]= median(test$PctSomeCol18_24, na.rm= TRUE)

library(olsrr)

ols_vif_tol(LR3)

#treating collinearity - neglecting the variables


LR6 = lm(TARGET_deathRate~incidenceRate+medIncome+MedianAge+AvgHouseholdSize+PctBlack+PctAsian+PctOtherRace, data =train)

summary(LR6)

LR6.pred= predict(LR6 ,newdata= test)

msetrain3=mean((train$TARGET_deathRate-fitted(LR6))^2)

msetrain3

msetest3=mean(((test$TARGET_deathRate) - (LR6.pred))^2)

msetest3




#after treating everything

train = read.csv("C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerData.csv ")
```

```
test = read.csv('C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

y = c(1,2,3,4,5,6,7,9,10,11,12,14,15,16,17,18,19,20,21,22)

for (i in y)

{

  x <- train[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  train[,i] = x

}

for (i in y)

{

  x <- test[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  test[,i] = x
```

}

LR7 = lm(TARGET_deathRate~incidenceRate+medIncome+MedianAge+AvgHouseholdSize+PctBlack+PctAsian+PctOtherRace

, data =train)

summary(LR7)

LR7.pred= predict(LR7 ,newdata= test)

msetrain4=mean((train$TARGET_deathRate-fitted(LR7))^2)

msetrain4

msetest4=mean(((test$TARGET_deathRate) - (LR7.pred))^2)

msetest4

Output-

```
> summary(LR3)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + medIncome + povertyPercent +
    MedianAge + MedianAgeMale + MedianAgeFemale + AvgHouseholdSize +
    PercentMarried + PctNoHS18_24 + PctHS18_24 + PctBachDeg18_24 +
    PctPrivateCoverage + PctPublicCoverage + PctPublicCoverageAlone +
    PctWhite + PctBlack + PctAsian + PctOtherRace + PctMarriedHouseholds,
    data = train)

Residuals:
    Min      1Q  Median      3Q     Max
-86.338 -12.160  -0.137  11.656 127.254

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
(Intercept)             1.057e+02  1.422e+01   7.435 1.42e-13
incidenceRate           2.177e-01  8.218e-03  26.494  < 2e-16
medIncome              -2.648e-04  7.983e-05  -3.317 0.000922
povertyPercent          3.093e-01  1.697e-01   1.823 0.068467
MedianAge               2.215e-03  9.630e-03   0.230 0.818095
MedianAgeMale          -2.048e-01  2.292e-01  -0.893 0.371682
MedianAgeFemale        -1.382e-01  2.392e-01  -0.578 0.563459
AvgHouseholdSize        6.104e-01  1.201e+00   0.508 0.611419
PercentMarried          1.748e-01  1.565e-01   1.117 0.264197
PctNoHS18_24           -4.513e-02  6.158e-02  -0.733 0.463691
PctHS18_24              4.582e-01  5.217e-02   8.782  < 2e-16
PctBachDeg18_24        -3.448e-01  1.182e-01  -2.918 0.003553
PctPrivateCoverage     -2.744e-01  1.135e-01  -2.417 0.015711
PctPublicCoverage       2.896e-02  2.136e-01   0.136 0.892171
```

```
PctPublicCoverageAlone  5.627e-01  2.780e-01   2.024 0.043095
PctWhite               -4.835e-02  6.361e-02  -0.760 0.447280
PctBlack                3.708e-02  6.232e-02   0.595 0.551899
PctAsian               -2.683e-01  1.989e-01  -1.349 0.177477
PctOtherRace           -9.938e-01  1.293e-01  -7.687 2.12e-14
PctMarriedHouseholds   -2.982e-01  1.531e-01  -1.947 0.051613

(Intercept)            ***
incidenceRate          ***
medIncome              ***
povertyPercent         .
MedianAge
MedianAgeMale
MedianAgeFemale
AvgHouseholdSize
PercentMarried
PctNoHS18_24
PctHS18_24             ***
PctBachDeg18_24        **
PctPrivateCoverage     *
PctPublicCoverage
PctPublicCoverageAlone *
PctWhite
PctBlack
PctAsian
PctOtherRace           ***
PctMarriedHouseholds   .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 20.36 on 2570 degrees of freedom
Multiple R-squared:  0.4728,   Adjusted R-squared:  0.4689
F-statistic: 121.3 on 19 and 2570 DF,  p-value: < 2.2e-16

Warning messages:
1: In doTryCatch(return(expr), name, parentenv, handler) :
  display list redraw incomplete
2: In doTryCatch(return(expr), name, parentenv, handler) :
  invalid graphics state
3: In doTryCatch(return(expr), name, parentenv, handler) :
  invalid graphics state
> summary(LR2)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + medIncome + povertyPercent +
    MedianAge + MedianAgeMale + MedianAgeFemale + AvgHouseholdSize +
    PercentMarried + PctNoHS18_24 + PctHS18_24 + PctSomeCol18_24 +
    PctBachDeg18_24 + PctPrivateCoverage + PctPublicCoverage +
    PctPublicCoverageAlone + PctWhite + PctBlack + PctAsian +
    PctOtherRace + PctMarriedHouseholds, data = train)

Residuals:
    Min      1Q  Median      3Q     Max
-86.368 -12.179  -0.142  11.648 127.281

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
(Intercept)             1.051e+02  1.497e+01   7.022 2.79e-12
incidenceRate           2.177e-01  8.222e-03  26.484  < 2e-16
medIncome              -2.647e-04  7.985e-05  -3.314 0.000931
povertyPercent          3.094e-01  1.697e-01   1.823 0.068440
MedianAge               2.211e-03  9.632e-03   0.230 0.818497
MedianAgeMale          -2.055e-01  2.293e-01  -0.896 0.370160
MedianAgeFemale        -1.377e-01  2.393e-01  -0.576 0.564976
```

```
AvgHouseholdSize        6.071e-01  1.202e+00   0.505 0.613465
PercentMarried          1.758e-01  1.568e-01   1.122 0.262074
PctNoHS18_24           -4.241e-02  6.492e-02  -0.653 0.513636
PctHS18_24              4.610e-01  5.636e-02   8.181 4.39e-16
PctSomeCol18_24         1.112e-02  8.397e-02   0.132 0.894639
PctBachDeg18_24        -3.423e-01  1.197e-01  -2.860 0.004277
PctPrivateCoverage     -2.747e-01  1.136e-01  -2.419 0.015653
PctPublicCoverage       2.916e-02  2.137e-01   0.136 0.891447
PctPublicCoverageAlone  5.624e-01  2.781e-01   2.022 0.043271
PctWhite               -4.830e-02  6.362e-02  -0.759 0.447871
PctBlack                3.724e-02  6.234e-02   0.597 0.550318
PctAsian               -2.683e-01  1.990e-01  -1.348 0.177667
PctOtherRace           -9.937e-01  1.293e-01  -7.685 2.17e-14
PctMarriedHouseholds   -2.991e-01  1.533e-01  -1.951 0.051200

(Intercept)            ***
incidenceRate          ***
medIncome              ***
povertyPercent         .
MedianAge
MedianAgeMale
MedianAgeFemale
AvgHouseholdSize
PercentMarried
PctNoHS18_24
PctHS18_24             ***
PctSomeCol18_24
PctBachDeg18_24        **
PctPrivateCoverage     *
PctPublicCoverage
PctPublicCoverageAlone *
PctWhite
PctBlack
PctAsian
PctOtherRace           ***
PctMarriedHouseholds   .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 20.36 on 2569 degrees of freedom
Multiple R-squared:  0.4728,	Adjusted R-squared:  0.4687 
F-statistic: 115.2 on 20 and 2569 DF,  p-value: < 2.2e-16

> summary(LR1)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + medIncome + povertyPercent + 
    MedianAge + MedianAgeMale + MedianAgeFemale + AvgHouseholdSize + 
    PercentMarried + PctNoHS18_24 + PctHS18_24 + PctBachDeg18_24 + 
    PctPrivateCoverage + PctPublicCoverage + PctPublicCoverageAlone + 
    PctWhite + PctBlack + PctAsian + PctOtherRace + PctMarriedHouseholds, 
    data = train)

Residuals:
    Min      1Q  Median      3Q     Max 
-86.338 -12.160  -0.137  11.656 127.254 

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)    
(Intercept)             1.057e+02  1.422e+01   7.435 1.42e-13
incidenceRate           2.177e-01  8.218e-03  26.494  < 2e-16
medIncome              -2.648e-04  7.983e-05  -3.317 0.000922
povertyPercent          3.093e-01  1.697e-01   1.823 0.068467
MedianAge               2.215e-03  9.630e-03   0.230 0.818095
```

```
MedianAgeMale          -2.048e-01  2.292e-01  -0.893 0.371682
MedianAgeFemale        -1.382e-01  2.392e-01  -0.578 0.563459
AvgHouseholdSize        6.104e-01  1.201e+00   0.508 0.611419
PercentMarried          1.748e-01  1.565e-01   1.117 0.264197
PctNoHS18_24           -4.513e-02  6.158e-02  -0.733 0.463691
PctHS18_24              4.582e-01  5.217e-02   8.782  < 2e-16
PctBachDeg18_24        -3.448e-01  1.182e-01  -2.918 0.003553
PctPrivateCoverage     -2.744e-01  1.135e-01  -2.417 0.015711
PctPublicCoverage       2.896e-02  2.136e-01   0.136 0.892171
PctPublicCoverageAlone  5.627e-01  2.780e-01   2.024 0.043095
PctWhite               -4.835e-02  6.361e-02  -0.760 0.447280
PctBlack                3.708e-02  6.232e-02   0.595 0.551899
PctAsian               -2.683e-01  1.989e-01  -1.349 0.177477
PctOtherRace           -9.938e-01  1.293e-01  -7.687 2.12e-14
PctMarriedHouseholds   -2.982e-01  1.531e-01  -1.947 0.051613

(Intercept)            ***
incidenceRate          ***
medIncome              ***
povertyPercent         .
MedianAge
MedianAgeMale
MedianAgeFemale
AvgHouseholdSize
PercentMarried
PctNoHS18_24
PctHS18_24             ***
PctBachDeg18_24        **
PctPrivateCoverage     *
PctPublicCoverage
PctPublicCoverageAlone *
PctWhite
PctBlack
PctAsian
PctOtherRace           ***
PctMarriedHouseholds   .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 20.36 on 2570 degrees of freedom
Multiple R-squared:  0.4728,	Adjusted R-squared:  0.4689 
F-statistic: 121.3 on 19 and 2570 DF,  p-value: < 2.2e-16

> summary(LR5)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + medIncome + povertyPercent + 
    MedianAge + MedianAgeMale + MedianAgeFemale + AvgHouseholdSize + 
    PercentMarried + PctNoHS18_24 + PctHS18_24 + PctBachDeg18_24 + 
    PctPrivateCoverage + PctPublicCoverage + PctPublicCoverageAlone + 
    PctWhite + PctBlack + PctAsian + PctOtherRace + PctMarriedHouseholds, 
    data = train)

Residuals:
    Min      1Q  Median      3Q     Max 
-83.779 -11.131  -0.023  11.414  65.958 

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
(Intercept)             1.323e+02  1.807e+01   7.321 3.26e-13
incidenceRate           2.170e-01  8.710e-03  24.917  < 2e-16
medIncome              -4.402e-04  9.907e-05  -4.443 9.24e-06
povertyPercent         -1.032e-01  1.873e-01  -0.551 0.581676
MedianAge              -1.362e-01  3.321e-01  -0.410 0.681805
```

```
MedianAgeMale          -2.303e-01  2.864e-01  -0.804 0.421302
MedianAgeFemale        -3.389e-02  2.821e-01  -0.120 0.904381
AvgHouseholdSize        4.789e+00  3.261e+00   1.468 0.142096
PercentMarried          2.915e-02  1.632e-01   0.179 0.858288
PctNoHS18_24           -5.393e-02  6.269e-02  -0.860 0.389773
PctHS18_24              4.371e-01  5.080e-02   8.605  < 2e-16
PctBachDeg18_24        -3.876e-01  1.333e-01  -2.908 0.003667
PctPrivateCoverage     -4.026e-01  1.087e-01  -3.705 0.000216
PctPublicCoverage       1.773e-02  1.774e-01   0.100 0.920388
PctPublicCoverageAlone  2.791e-01  2.398e-01   1.164 0.244722
PctWhite                2.749e-02  5.928e-02   0.464 0.642868
PctBlack                1.165e-01  5.352e-02   2.176 0.029659
PctAsian               -5.868e-01  3.859e-01  -1.521 0.128486
PctOtherRace           -1.757e+00  1.959e-01  -8.968  < 2e-16
PctMarriedHouseholds   -3.523e-01  1.778e-01  -1.982 0.047610

(Intercept)            ***
incidenceRate          ***
medIncome              ***
povertyPercent
MedianAge
MedianAgeMale
MedianAgeFemale
AvgHouseholdSize
PercentMarried
PctNoHS18_24
PctHS18_24             ***
PctBachDeg18_24        **
PctPrivateCoverage     ***
PctPublicCoverage
PctPublicCoverageAlone
PctWhite
PctBlack               *
PctAsian
PctOtherRace           ***
PctMarriedHouseholds   *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 18.81 on 2570 degrees of freedom
Multiple R-squared:  0.4695,	Adjusted R-squared:  0.4656 
F-statistic: 119.7 on 19 and 2570 DF,  p-value: < 2.2e-16

> summary(LR6)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + medIncome + MedianAge + 
    AvgHouseholdSize + PctBlack + PctAsian + PctOtherRace, data = train)

Residuals:
    Min      1Q  Median      3Q     Max 
-79.812 -13.020  -0.769  12.190 122.468 

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)    
(Intercept)       1.074e+02  4.924e+00  21.813  < 2e-16 ***
incidenceRate     2.263e-01  8.180e-03  27.666  < 2e-16 ***
medIncome        -9.349e-04  4.053e-05 -23.067  < 2e-16 ***
MedianAge        -2.352e-03  1.008e-02  -0.233    0.815    
AvgHouseholdSize  5.421e+00  1.096e+00   4.948 7.98e-07 ***
PctBlack          2.004e-01  3.082e-02   6.504 9.33e-11 ***
PctAsian         -1.709e-02  1.804e-01  -0.095    0.925    
PctOtherRace     -6.210e-01  1.231e-01  -5.044 4.87e-07 ***
---
```

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 21.46 on 2582 degrees of freedom
Multiple R-squared:  0.4115,	Adjusted R-squared:  0.4099 
F-statistic: 257.9 on 7 and 2582 DF,  p-value: < 2.2e-16

> summary(LR7)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + medIncome + MedianAge + 
    AvgHouseholdSize + PctBlack + PctAsian + PctOtherRace, data = train)

Residuals:
    Min      1Q  Median      3Q     Max 
-82.077 -11.678  -0.145  11.731  73.401 

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)    
(Intercept)       8.689e+01  9.921e+00   8.758  < 2e-16 ***
incidenceRate     2.284e-01  8.602e-03  26.548  < 2e-16 ***
medIncome        -1.006e-03  4.437e-05 -22.683  < 2e-16 ***
MedianAge        -6.065e-02  1.044e-01  -0.581  0.56134    
AvgHouseholdSize  1.610e+01  2.363e+00   6.815 1.17e-11 ***
PctBlack          1.651e-01  3.080e-02   5.361 9.01e-08 ***
PctAsian         -1.086e+00  3.556e-01  -3.055  0.00228 ** 
PctOtherRace     -1.350e+00  1.911e-01  -7.062 2.10e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 19.55 on 2582 degrees of freedom
Multiple R-squared:  0.4242,	Adjusted R-squared:  0.4226 
F-statistic: 271.8 on 7 and 2582 DF,  p-value: < 2.2e-16

msetrain_n
[1] 411.3217
> msetest_n
[1] 414.5908
> msetrain_median
[1] 411.3189
> msetest_median
[1] 414.54
> msetrain1
[1] 411.3217
> msetest1
[1] 414.5908
> msetrain2
[1] 351.1055
> msetest2
[1] 348.3685
> msetrain3
[1] 459.1824
> msetest3
[1] 460.9086
> msetrain4 #optimum msetrain
[1] 381.0683
> msetest4   #optimum msetest
[1] 361.6792
```

b. What variables are significant? Insignificant? How does removing insignificant variables affect model performance?

Ans- The variables incidenceRate, medIncome, PctHS18_24, PctBachDeg18_24, PctPrivateCoverage, PctPublicCoverageAlone, PctOtherRace are significant.

The model performs better than the original model because it has a lower test and train MSE compared to the original model .

Code-

```
#removing insignificant variables

fix(train)

LR4 =
lm(TARGET_deathRate~incidenceRate+medIncome+PctHS18_24+PctOtherRace+PctBachDeg18_24+PctPrivateCoverage+PctPublicCoverageAlone+povertyPercent, data =train)

summary(LR4)

LR4.pred= predict(LR4 ,newdata= test)

msetrain_sign=mean((train$TARGET_deathRate - fitted(LR4))^2)

msetrain_sign

msetest_sign=mean(((test$TARGET_deathRate) - (LR4.pred))^2)

msetest_sign
```

Output-

```
> LR4  = lm(TARGET_deathRate~incidenceRate+medIncome+PctHS18_24+PctOtherRace+
PctBachDeg18_24+PctPrivateCoverage+PctPublicCoverageAlone+povertyPercent, dat
a =train)
> summary(LR4)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + medIncome + PctHS18_24 +
    PctOtherRace + PctBachDeg18_24 + PctPrivateCoverage + PctPublicCoverageAl
one +
    povertyPercent, data = train)

Residuals:
    Min      1Q  Median      3Q     Max
-85.564 -11.515   0.276  11.721  67.194

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
(Intercept)             9.595e+01  1.034e+01   9.281  < 2e-16
incidenceRate           2.292e-01  8.517e-03  26.907  < 2e-16
medIncome              -2.451e-04  7.516e-05  -3.261  0.00113
PctHS18_24              3.882e-01  4.899e-02   7.925 3.38e-15
PctOtherRace           -1.625e+00  1.823e-01  -8.915  < 2e-16
PctBachDeg18_24        -3.301e-01  1.239e-01  -2.664  0.00777
PctPrivateCoverage     -4.743e-01  9.692e-02  -4.893 1.05e-06
PctPublicCoverageAlone  1.762e-01  1.492e-01   1.181  0.23782
povertyPercent          5.723e-01  1.463e-01   3.912 9.38e-05

(Intercept)            ***
incidenceRate          ***
medIncome              **
PctHS18_24             ***
PctOtherRace           ***
PctBachDeg18_24        **
PctPrivateCoverage     ***
PctPublicCoverageAlone
povertyPercent         ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 18.98 on 2581 degrees of freedom
Multiple R-squared:  0.4577,   Adjusted R-squared:  0.456
F-statistic: 272.3 on 8 and 2581 DF,  p-value: < 2.2e-16
```

```
> msetrain_sign
[1] 358.9149
> msetest_sign=mean(((test$TARGET_deathRate) - (LR4.pred))^2)
> msetest_sign
[1] 352.1031

>
```

c. Present and interpret model diagnosis. What insights did you obtain to improve the model from diagnosis?

Ans-

Code-

```
# model diagnosis
par(mfrow=c(2,2))
plot(LR3)
```

Output-

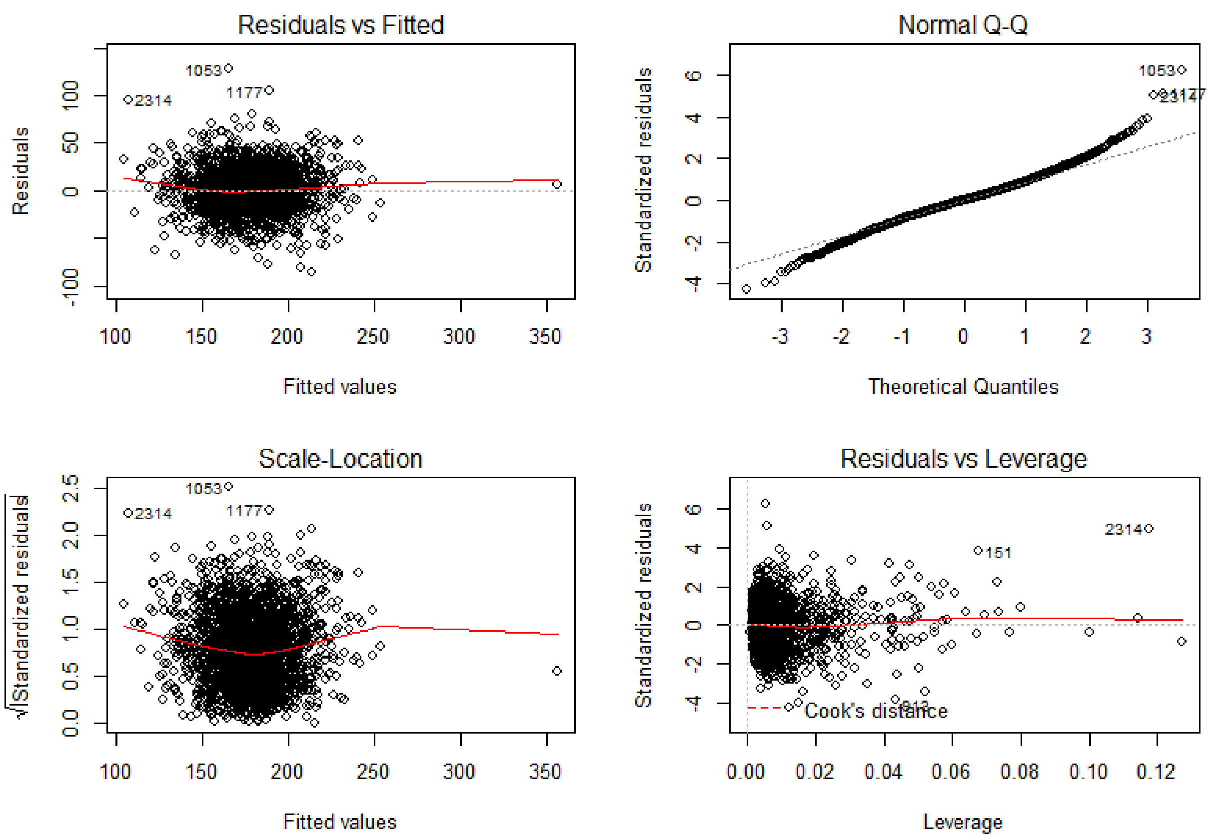


Figure 5-Diagnostics Plot

1. Plot-1 (Residual vs Fitted)- - This plot is used to check the linear relationship assumptions (This plot shows if residuals have non-linear patterns). From the diagnostic plot drawn, the residuals have a linear relationship.
2. Plot-2 (Normal Q-Q)- This plot shows if the residuals are normally distributed. They are normally distributed if all the points fall on a straight line. From the plot obtained, the residuals are normally distributed.

3. Plot-3 (Scale- Location)- It's also called Spread-Location plot. This plot shows if residuals are spread equally along the ranges of predictors (homogeneity of variance of the residuals). From the plot obtained the residuals are spread equally along the range of the predictors.
4. Plot-4(Residuals vs leverage)- This plot helps us to find if the outliers are influential in linear regression analysis. This can be found out by Cook's distance. From our plot we can infer that the outliers are not influential since we can't see cook's distance line (since its well inside the Cook's distance line).

d. Include few non-linear and interaction terms and evaluate how they affect model performance and diagnosis.

Ans-

Code-

```
#inputing non-linear terms

attach(train)

LR8 = lm(TARGET_deathRate~incidenceRate+sqrt(medIncome)+povertyPercent+MedianAge+sqrt(MedianAgeMale)+MedianAgeFemale+AvgHouseholdSize+(PercentMarried)^2+PctNoHS18_24^3+PctHS18_24+PctBachDeg18_24+PctPrivateCoverage+PctPublicCoverage+PctPublicCoverageAlone+PctWhite+PctBlack+PctAsian+PctOtherRace+PctMarriedHouseholds

    :medIncome, data =train)

summary(LR8)

LR8.pred= predict(LR8 ,newdata= test)

msetrain5=mean((train$TARGET_deathRate-fitted(LR8))^2)
```

msetrain5 #optimum msetrain

msetest5=mean(((test$TARGET_deathRate) - (LR8.pred))^2)

msetest5   #optimum msetest

par(mfrow=c(2,2))

plot(LR8)

Output-

```
summary(LR8)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + sqrt(medIncome)
 +
    povertyPercent + MedianAge + sqrt(MedianAgeMale) + MedianAg
eFemale +
    AvgHouseholdSize + (PercentMarried)^2 + PctNoHS18_24^3 +
    PctHS18_24 + PctBachDeg18_24 + PctPrivateCoverage + PctPubl
icCoverage +
    PctPublicCoverageAlone + PctWhite + PctBlack + PctAsian +
    PctOtherRace + PctMarriedHouseholds:medIncome, data = trai
n)

Residuals:
    Min      1Q  Median      3Q     Max
-82.478 -11.177  -0.031  11.233  64.401

Coefficients:
                                Estimate Std. Error t value
(Intercept)                    1.692e+02  3.031e+01   5.583
incidenceRate                  2.195e-01  8.667e-03  25.324
sqrt(medIncome)               -2.316e-01  8.678e-02  -2.669
povertyPercent                -2.853e-01  1.961e-01  -1.455
MedianAge                     -2.739e-01  3.293e-01  -0.832
sqrt(MedianAgeMale)            8.192e-01  3.599e+00   0.228
MedianAgeFemale               -1.785e-01  2.826e-01  -0.632
AvgHouseholdSize               1.866e+00  3.171e+00   0.588
PercentMarried                -2.252e-01  1.448e-01  -1.555
PctNoHS18_24                  -5.272e-02  6.269e-02  -0.841
PctHS18_24                     4.306e-01  5.080e-02   8.476
PctBachDeg18_24               -3.674e-01  1.319e-01  -2.785
PctPrivateCoverage            -4.055e-01  1.084e-01  -3.741
PctPublicCoverage             -3.973e-02  1.773e-01  -0.224
PctPublicCoverageAlone         3.303e-01  2.397e-01   1.378
PctWhite                      -3.537e-03  5.789e-02  -0.061
PctBlack                       1.048e-01  5.354e-02   1.958
PctAsian                      -5.315e-01  3.844e-01  -1.383
PctOtherRace                  -1.705e+00  1.975e-01  -8.633
PctMarriedHouseholds:medIncome -8.017e-07  2.829e-06  -0.283
                              Pr(>|t|)
(Intercept)                   2.62e-08 ***
incidenceRate                  < 2e-16 ***
sqrt(medIncome)               0.007653 **
povertyPercent                0.145806
MedianAge                     0.405539
```

```
sqrt(MedianAgeMale)             0.819968
MedianAgeFemale                 0.527553
AvgHouseholdSize                0.556344
PercentMarried                  0.120070
PctNoHS18_24                    0.400444
PctHS18_24                       < 2e-16 ***
PctBachDeg18_24                 0.005395 **
PctPrivateCoverage              0.000187 ***
PctPublicCoverage               0.822709
PctPublicCoverageAlone          0.168301
PctWhite                        0.951277
PctBlack                        0.050344 .
PctAsian                        0.166922
PctOtherRace                     < 2e-16 ***
PctMarriedHouseholds:medIncome  0.776871
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 18.8 on 2570 degrees of freedom
Multiple R-squared:   0.47,    Adjusted R-squared:  0.4661
F-statistic:   120 on 19 and 2570 DF,  p-value: < 2.2e-16

> LR8.pred= predict(LR8 ,newdata= test)
> msetrain5=mean((train$TARGET_deathRate-fitted(LR8))^2)
> msetrain5 #optimum msetrain
[1] 350.7415
> msetest5=mean(((test$TARGET_deathRate) - (LR8.pred))^2)
> msetest5   #optimum msetest
[1] 346.4466

>
```

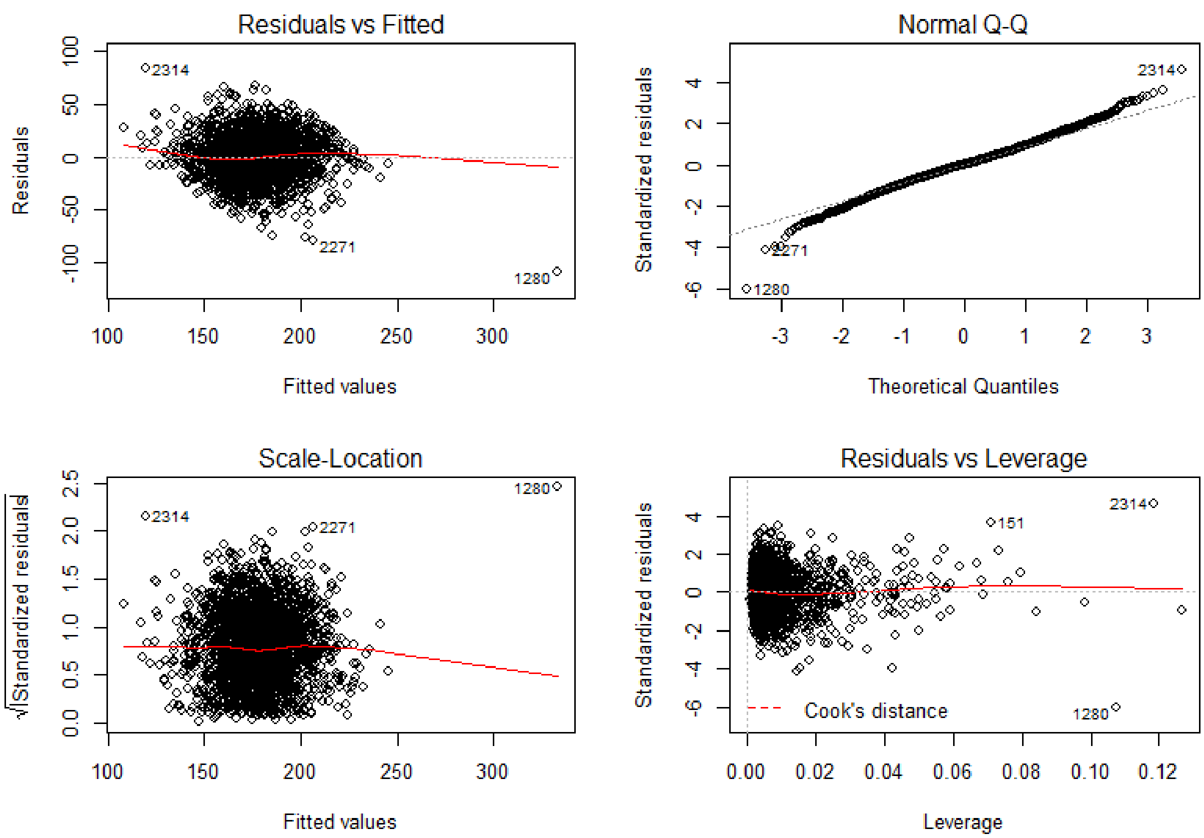


Figure 6-Diagnostics Plot

Summary- The model performance increases due to the addition of interaction terms and non-linear terms since the test and train MSE (350.74 and 346.446 respectively) are lower when compared to the test and train MSE of the original model.

1.Plot-1 (Residual vs Fitted)- - This plot is used to check the linear relationship assumptions (This plot shows if residuals have non-linear patterns). From the diagnostic plot drawn, the residuals have a linear relationship.

2.Plot-2 (Normal Q-Q)- This plot shows if the residuals are normally distributed. They are normally distributed if all the points fall on a straight line. From the plot obtained, the residuals are normally distributed.

3.Plot-3 (Scale- Location)- It’s also called Spread-Location plot. This plot shows if residuals are spread equally along the ranges of predictors (homogeneity of variance of the residuals). From the plot obtained the residuals are spread equally along the range of the predictors.

4.Plot-4(Residuals vs leverage)- This plot helps us to find if the outliers are influential in linear regression analysis. This can be found out by Cook's distance. From our plot we can infer that the outliers are not influential since we can't see cook's distance line (since its well inside the Cook's distance line).

3. KNN-
   a. Split CanverData.csv data into 70% training and 30% testing.

Code-

```
#question 3

library(FNN)

library(class)

set.seed(1)

train = read.csv("C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

for (i in y)

{

  x <- train[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)
```

```
  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  train[,i] = x

}

for (i in y)

{

  x <- test[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  test[,i] = x

}

n <- nrow(train) * 0.7

T <- sample(nrow(train), size = n)

train1 <- train[T,-c(1,8,13)]

test1 <- train[-T,-c(1,8,13)]

test1_full <- train[-T,]

train.Y = train$TARGET_deathRate

#fix(train1)
```

b. Develop KNN model for predicting Cancer Mortality. Evaluate test MSE for at least 5 different values of K and find the K that minimizes test MSE.

Ans- KNN model is developed after splitting the train into test and train data.

The K that minimizes test MSE is K=5, with a test MSE of 764.3161

Code-

```
knn <- knn.reg(train1, test1, train.Y, k=1)

knntestmse =mean(((test1_full$TARGET_deathRate) - (knn$pred))^2)

error = c(0,0,0,0,0)

for(i in 1:5)

{

 knn <- knn.reg(train1, test1, train.Y, k=i)

 knntestmse =mean(((test1_full$TARGET_deathRate) - (knn$pred))^2)

 error[i] = knntestmse

}

error
```

Output-

```
> error
[1] 1259.7968  965.2434  836.5874  807.6674  764.3161
```

c. KNN is a non-linear technique, but does not work well with high dimensional data. Try to identify important variables from Linear Regression model and use only a subset of important features in the KNN model. Document impact on test performance.

Ans- The variables incidenceRate, medIncome, PctHS18_24, PctBachDeg18_24, PctPrivateCoverage, PctPublicCoverageAlone, PctOtherRace are significant. This can be found out using the p-values obtained from the linear regression. The test MSE for K = 1,2,3,4,5 is 1299.8198, 961.2180, 844.4425, 805.0395 and 760.8135. Using significant variables improved the performance of the KNN model since the test MSE for the same seed is less when compared to the KNN model when all the variables are used. K=5 is the optimum K values since the test MSE is 760.8135.

Code-

```
train2 <- train[T,-c(1,4,5,7,8,9,10,12,13,15,17,22)]

test2 <- train[-T,-c(1,4,5,7,8,9,10,12,13,15,17,22)]

test2_full<-train[-T,]

train.Y1 = train$TARGET_deathRate

#fix(train2)

knn3 <- knn.reg(train2, test2, train.Y1, k=1)

knntestmse3 =mean(((test2_full$TARGET_deathRate) - (knn3$pred))^2)

error2 = c(0,0,0,0,0)

for(i in 1:5)

{

  knn3 <- knn.reg(train2, test2, train.Y1,k=i)

  knntestmse3 =mean(((test2_full$TARGET_deathRate) - (knn3$pred))^2)

  error2[i] = knntestmse3
```

}

error2

Output-

```
error2
[1] 1299.8198  961.2180  844.4425  805.0395  760.8135
```

4. Feature Selection
    a. Write an "Executive Summary" section documenting your interpretation of the important features impacting cancer mortality and how they influence cancer mortality.

Ans – The feature selection from a data set in R can be done creating a correlation matrix. Visually it can also be done by plotting a correlation plot from the matrix.

In this project correlation matrix and correlation plot are used to select the features in the initial stages. Later the p-values obtained from the linear regression are used to select the significant features that are used to improve the model performance.

Interpreting Correlation plot-

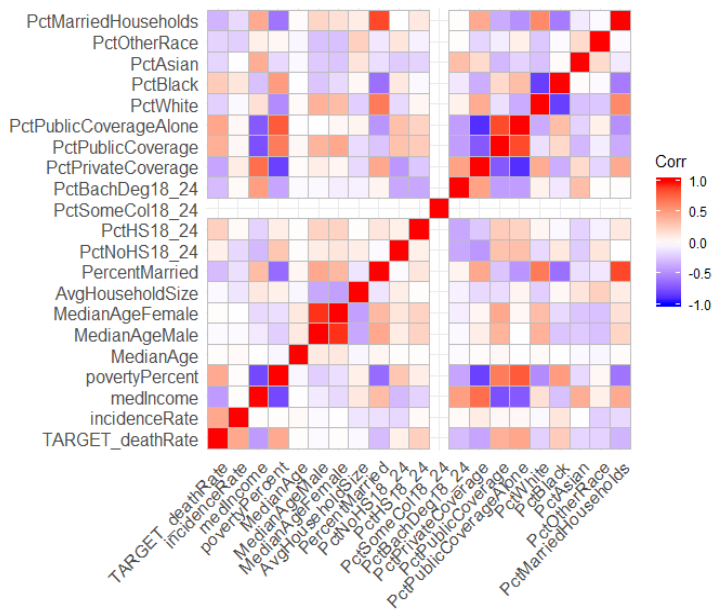


Figure 7-Correlation graph

In this correlation plot, correlation scale which is displayed in the right hand corner of the plot is used to select a feature(darker the color, the higher the correlation).

<u>Interpreting Linear Regression-</u>

```
> summary(LR3)

Call:
lm(formula = TARGET_deathRate ~ incidenceRate + medIncome + povertyPercent +
    MedianAge + MedianAgeMale + MedianAgeFemale + AvgHouseholdSize +
    PercentMarried + PctNoHS18_24 + PctHS18_24 + PctBachDeg18_24 +
    PctPrivateCoverage + PctPublicCoverage + PctPublicCoverageAlone +
    PctWhite + PctBlack + PctAsian + PctOtherRace + PctMarriedHouseholds,
    data = train)

Residuals:
    Min      1Q  Median      3Q     Max
-86.338 -12.160  -0.137  11.656 127.254

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
(Intercept)             1.057e+02  1.422e+01   7.435 1.42e-13
incidenceRate           2.177e-01  8.218e-03  26.494  < 2e-16
medIncome              -2.648e-04  7.983e-05  -3.317 0.000922
povertyPercent          3.093e-01  1.697e-01   1.823 0.068467
MedianAge               2.215e-03  9.630e-03   0.230 0.818095
MedianAgeMale          -2.048e-01  2.292e-01  -0.893 0.371682
MedianAgeFemale        -1.382e-01  2.392e-01  -0.578 0.563459
AvgHouseholdSize        6.104e-01  1.201e+00   0.508 0.611419
PercentMarried          1.748e-01  1.565e-01   1.117 0.264197
PctNoHS18_24           -4.513e-02  6.158e-02  -0.733 0.463691
PctHS18_24              4.582e-01  5.217e-02   8.782  < 2e-16
```

```
PctBachDeg18_24        -3.448e-01  1.182e-01  -2.918 0.003553
PctPrivateCoverage     -2.744e-01  1.135e-01  -2.417 0.015711
PctPublicCoverage       2.896e-02  2.136e-01   0.136 0.892171
PctPublicCoverageAlone  5.627e-01  2.780e-01   2.024 0.043095
PctWhite               -4.835e-02  6.361e-02  -0.760 0.447280
PctBlack                3.708e-02  6.232e-02   0.595 0.551899
PctAsian               -2.683e-01  1.989e-01  -1.349 0.177477
PctOtherRace           -9.938e-01  1.293e-01  -7.687 2.12e-14
PctMarriedHouseholds   -2.982e-01  1.531e-01  -1.947 0.051613

(Intercept)            ***
incidenceRate          ***
medIncome              ***
povertyPercent         .
MedianAge
MedianAgeMale
MedianAgeFemale
AvgHouseholdSize
PercentMarried
PctNoHS18_24
PctHS18_24             ***
PctBachDeg18_24        **
PctPrivateCoverage     *
PctPublicCoverage
PctPublicCoverageAlone *
PctWhite
PctBlack
PctAsian
PctOtherRace           ***
PctMarriedHouseholds   .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Features can be selected from linear regression by observing the corresponding p-values. Smaller the p-value, higher the significance. Significance code displayed at the bottom can be used to interpret the p-value.

5. Performance reporting on Holdout data-
   a. Summarize and compare the model performance (MSE) of LR and KNN on holdout dataset as a table.

Code-

#question-5

set.seed(1)

train = read.csv("C:¥¥Users¥¥KIRAN KONDISETTI¥¥Desktop¥¥CancerData.csv ")

```
test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

for (i in y)

{

  x <- train[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  train[,i] = x

}

for (i in y)

{

  x <- test[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  test[,i] = x

}
```

```
trainn <- train[,-c(1,8,13)]

testn <- test[,-c(1,8,13)]

y = train$TARGET_deathRate

error1 = c(0,0,0,0,0)

for(i in 1:5)

{

  knn1<- knn.reg(trainn, testn, train$TARGET_deathRate, k=i)

  knntestmse1 =mean(((test$TARGET_deathRate) - (knn1$pred))^2)

  error1[i] = knntestmse1

}

error1
```

Output-

```
> error1
[1] 732.3953 589.5190 524.3679 514.2016 516.9247
```

SR. No	Model name	Test MSE
1	Linear Regression	414.5908
3	KNN	514.2016

Summary-

The Test MSE for Linear Regression and KNN are 414.5908, 514.2016 respectively. Linear Regression perform better than KNN since KNN doesn't work when multi-dimensional data and also when the variables are linearly separable.

R-CODE(FULL)-

```
#question 2

#promising variables

train = read.csv("C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

library(ggplot2)

mydata <- train[, -c(8)]

cormat<-signif(cor(mydata),2)

cormat

install.packages("ggcorrplot")

library(ggcorrplot)

ggcorrplot(cormat)

#missing values

library(Amelia)

sum(is.na(train$PctSomeCol18_24))

missmap(train, main="Train Data - Missings Map",
```

```
        col=c("yellow", "black"), legend=FALSE)
missmap(test, main="Test Data - Missings Map",
        col=c("yellow", "black"), legend=FALSE)

#treating missing values
#method1 - neglecting the coloumn
LR3 =
lm(TARGET_deathRate~incidenceRate+medIncome+povertyPercent+MedianA
ge+MedianAgeMale+MedianAgeFemale+AvgHouseholdSize+PercentMarried+P
ctNoHS18_24+PctHS18_24+PctBachDeg18_24+PctPrivateCoverage+PctPublic
Coverage+PctPublicCoverageAlone+PctWhite+PctBlack+PctAsian+PctOtherRa
ce+PctMarriedHouseholds
         , data =train)
summary(LR3)
LR3.pred= predict(LR3 ,newdata= test )
msetrain_n=mean((train$TARGET_deathRate-fitted(LR3))^2)
msetrain_n
msetest_n=mean(((test$TARGET_deathRate) - (LR3.pred))^2)
msetest_n

#Method2 - inputing median
train = read.csv("C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerData.csv ")
```

```
test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

train$PctSomeCol18_24[is.na(train$PctSomeCol18_24) ]=
median(train$PctSomeCol18_24, na.rm= TRUE)

test$PctSomeCol18_24[is.na(test$PctSomeCol18_24)]=
median(test$PctSomeCol18_24, na.rm= TRUE)

LR2 =
lm(TARGET_deathRate~incidenceRate+medIncome+povertyPercent+MedianA
ge+MedianAgeMale+MedianAgeFemale+AvgHouseholdSize+PercentMarried+P
ctNoHS18_24+PctHS18_24+PctSomeCol18_24+PctBachDeg18_24+PctPrivate
Coverage+PctPublicCoverage+PctPublicCoverageAlone+PctWhite+PctBlack+P
ctAsian+PctOtherRace+PctMarriedHouseholds

        , data =train)

summary(LR2)

LR2.pred= predict(LR2 ,newdata= test)

LR2.pred

msetrain_median=mean((train$TARGET_deathRate-fitted(LR2))^2)

msetrain_median

msetest_median=mean(((test$TARGET_deathRate) - (LR2.pred))^2)

msetest_median


#method3- Inputing the mean

train = read.csv("C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerData.csv ")
```

```
test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

train$PctSomeCol18_24[is.na(train$PctSomeCol18_24) ]=
mean(train$PctSomeCol18_24, na.rm= TRUE)

test$PctSomeCol18_24[is.na(test$PctSomeCol18_24)]=
mean(test$PctSomeCol18_24, na.rm= TRUE)

LR1  =
lm(TARGET_deathRate~incidenceRate+medIncome+povertyPercent+MedianA
ge+MedianAgeMale+MedianAgeFemale+AvgHouseholdSize+PercentMarried+P
ctNoHS18_24+PctHS18_24+PctBachDeg18_24+PctPrivateCoverage+PctPublic
Coverage+PctPublicCoverageAlone+PctWhite+PctBlack+PctAsian+PctOtherRa
ce+PctMarriedHouseholds

       , data =train)

summary(LR1)

LR1.pred= predict(LR1 ,newdata= test)

msetrain1=mean((train$TARGET_deathRate-fitted(LR1))^2)

msetrain1

msetest1=mean(((test$TARGET_deathRate) - (LR1.pred))^2)

msetest1



#finding outliers

OutVals = boxplot(train, plot=FALSE)$out

OutVals1 = boxplot(medIncome, plot=FALSE)$out
```

```
plot(OutVals1)

plot(OutVals)

boxplot(train)

library(outliers)

outlier(medIncome)


#treating outlies- by using capping

y = c(1,2,3,4,5,6,7,9,10,11,12,14,15,16,17,18,19,20,21,22)

for (i in y)

{

x <- train[,i]

qnt <- quantile(x, probs=c(.25, .75))

caps <- quantile(x, probs=c(.05, .95))

H <- 1.5 * IQR(x)

x[x < (qnt[1] - H)] <- caps[1]

x[x > (qnt[2] + H)] <- caps[2]

train[,i] = x

}

for (i in y)

{

  x <- test[,i]

  qnt <- quantile(x, probs=c(.25, .75))
```

```
  caps <- quantile(x, probs=c(.05, .95))
  H <- 1.5 * IQR(x)
  x[x < (qnt[1] - H)] <- caps[1]
  x[x > (qnt[2] + H)] <- caps[2]
  test[,i] = x
}
boxplot(train)
LR5 =
lm(TARGET_deathRate~incidenceRate+medIncome+povertyPercent+MedianA
ge+MedianAgeMale+MedianAgeFemale+AvgHouseholdSize+PercentMarried+P
ctNoHS18_24+PctHS18_24+PctBachDeg18_24+PctPrivateCoverage+PctPublic
Coverage+PctPublicCoverageAlone+PctWhite+PctBlack+PctAsian+PctOtherRa
ce+PctMarriedHouseholds

        , data =train)
summary(LR5)
LR5.pred= predict(LR5 ,newdata= test)
msetrain2=mean((train$TARGET_deathRate-fitted(LR5))^2)
msetrain2
msetest2=mean(((test$TARGET_deathRate) - (LR5.pred))^2)
msetest2

#finding collinearity
```

```
#install.packages('olsrr')

train = read.csv("C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

train$PctSomeCol18_24[is.na(train$PctSomeCol18_24) ]=
median(train$PctSomeCol18_24, na.rm= TRUE)

test$PctSomeCol18_24[is.na(test$PctSomeCol18_24)]=
median(test$PctSomeCol18_24, na.rm= TRUE)

library(olsrr)

ols_vif_tol(LR3)

#treating collinearity - neglecting the variables


LR6  =
lm(TARGET_deathRate~incidenceRate+medIncome+MedianAge+AvgHousehol
dSize+PctBlack+PctAsian+PctOtherRace, data =train)

summary(LR6)

LR6.pred= predict(LR6 ,newdata= test)

msetrain3=mean((train$TARGET_deathRate-fitted(LR6))^2)

msetrain3

msetest3=mean(((test$TARGET_deathRate) - (LR6.pred))^2)

msetest3
```

```
#after treating everything

train = read.csv("C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

y = c(1,2,3,4,5,6,7,9,10,11,12,14,15,16,17,18,19,20,21,22)

for (i in y)

{

  x <- train[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  train[,i] = x

}

for (i in y)

{

  x <- test[,i]
```

```
  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  test[,i] = x

}

LR7  =
lm(TARGET_deathRate~incidenceRate+medIncome+MedianAge+AvgHousehol
dSize+PctBlack+PctAsian+PctOtherRace

         , data =train)

summary(LR7)

LR7.pred= predict(LR7 ,newdata= test)

msetrain4=mean((train$TARGET_deathRate-fitted(LR7))^2)

msetrain4

msetest4=mean(((test$TARGET_deathRate) - (LR7.pred))^2)

msetest4


#removing insignificant variables

fix(train)

LR4  =
lm(TARGET_deathRate~incidenceRate+medIncome+PctHS18_24+PctOtherRa
```

```
ce+PctBachDeg18_24+PctPrivateCoverage+PctPublicCoverageAlone+povertyP
ercent, data =train)

summary(LR4)

LR4.pred= predict(LR4 ,newdata= test)

msetrain_sign=mean((train$TARGET_deathRate - fitted(LR4))^2)

msetrain_sign

msetest_sign=mean(((test$TARGET_deathRate) - (LR4.pred))^2)

msetest_sign



#inputing non-linear terms

attach(train)

LR8  =
lm(TARGET_deathRate~incidenceRate+sqrt(medIncome)+povertyPercent+Me
dianAge+sqrt(MedianAgeMale)+MedianAgeFemale+AvgHouseholdSize+(Perce
ntMarried)^2+PctNoHS18_24^3+PctHS18_24+PctBachDeg18_24+PctPrivateC
overage+PctPublicCoverage+PctPublicCoverageAlone+PctWhite+PctBlack+Pct
Asian+PctOtherRace+PctMarriedHouseholds

        :medIncome, data =train)

summary(LR8)

LR8.pred= predict(LR8 ,newdata= test)

msetrain5=mean((train$TARGET_deathRate-fitted(LR8))^2)

msetrain5
```

```
msetest5=mean(((test$TARGET_deathRate) - (LR8.pred))^2)

msetest5

par(mfrow=c(2,2))

plot(LR8)



# model diagnosis

par(mfrow=c(2,2))

plot(LR1)




#trainmse vs testmse

trainMSE= c(459,411,409,409)

testMSE= c(460,414,416,416)

#1= collinearity,2= neglecting,  3= optimum in x, 4= outliers,

x= c(1,2,3,4)

plot(x,trainMSE, ylab='trainMSE and testMSE')

lines(testMSE, col = 'red')

lines(trainMSE, col='blue')


#question 3
```

```
library(FNN)

library(class)

set.seed(1)

train = read.csv("C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

for (i in y)

{

  x <- train[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  train[,i] = x

}

for (i in y)

{

  x <- test[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))
```

```
  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  test[,i] = x

}

n <- nrow(train) * 0.7

T <- sample(nrow(train), size = n)

train1 <- train[T,-c(1,8,13)]

test1 <- train[-T,-c(1,8,13)]

test1_full <- train[-T,]

train.Y = train$TARGET_deathRate

#fix(train1)

knn <- knn.reg(train1, test1, train.Y, k=1)

knntestmse =mean(((test1_full$TARGET_deathRate) - (knn$pred))^2)

error = c(0,0,0,0,0)

for(i in 1:5)

{

  knn <- knn.reg(train1, test1, train.Y, k=i)

  knntestmse =mean(((test1_full$TARGET_deathRate) - (knn$pred))^2)

  error[i] = knntestmse

}

error
```

```
train2 <- train[T,-c(1,4,5,7,8,9,10,12,13,15,17,22)]

test2 <- train[-T,-c(1,4,5,7,8,9,10,12,13,15,17,22)]

test2_full<-train[-T,]

train.Y1 = train$TARGET_deathRate

#fix(train2)

knn3 <- knn.reg(train2, test2, train.Y1, k=1)

knntestmse3 =mean(((test2_full$TARGET_deathRate) - (knn3$pred))^2)

error2 = c(0,0,0,0,0)

for(i in 1:5)

{

  knn3 <- knn.reg(train2, test2, train.Y1,k=i)

  knntestmse3 =mean(((test2_full$TARGET_deathRate) - (knn3$pred))^2)

  error2[i] = knntestmse3

}

error2




#question-5

set.seed(1)
```

```
train = read.csv("C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerData.csv ")

test = read.csv('C:¥¥Users¥¥KIRAN
KONDISETTI¥¥Desktop¥¥CancerHoldoutData.csv ')

for (i in y)

{

  x <- train[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]

  train[,i] = x

}

for (i in y)

{

  x <- test[,i]

  qnt <- quantile(x, probs=c(.25, .75))

  caps <- quantile(x, probs=c(.05, .95))

  H <- 1.5 * IQR(x)

  x[x < (qnt[1] - H)] <- caps[1]

  x[x > (qnt[2] + H)] <- caps[2]
```

```
  test[,i] = x
}
trainn <- train[,-c(1,8,13)]
testn <- test[,-c(1,8,13)]
y = train$TARGET_deathRate
error1 = c(0,0,0,0,0)
for(i in 1:5)
{
  knn1<- knn.reg(trainn, testn, train$TARGET_deathRate, k=i)
  knntestmse1 =mean(((test$TARGET_deathRate) - (knn1$pred))^2)
  error1[i] = knntestmse1
}
error1
```