New York City Demographic Dataset (Prediction of Gender Ratio)

R Code

```
#### Setting The Working Directory ####
setwd("D:/01. B.TECH 3rd YEAR/04. Mini Project/MINI")
#### Reding The Dataset ####
ny <- read.delim("New_York.dat")</pre>
#### EXPLORATORY DATA ANALYSIS ####
# Count of NA values
sapply(ny, function(x) sum(is.na(x)))
# Count of empty strings
sapply(ny, function(x) length(which(x==")))
# Counting the Count of Number of Unique values in every Column
sapply(ny, function(x) length(unique(x)))
summary(ny)
# Here we find that the median population is 4013 but Max population is coming very high i.e 7322563.
# Therefore we can sense that there might be outliers present in this column.
# Now we'll see which place has such a high value
new_york[which(new_york$TOT_POP==7322564),]
# Hence we come to know that this population is of New York City
# After Cross Checking on the Internet, in 2015 which was when the book in which this dataset is given was
published,
# the population of New York City was 8.2 million but since here we have the population as 7.32 million which
# was the population of New York City in 1990. So maybe this dataset is of 1990.
# install.packages("ggplot2")
library(ggplot2)
```

ggplot(data = ny, aes(y=ny\$TOT_POP)) + geom_boxplot() + ggtitle("Boxplot of TOT_POP")

```
ggplot(data = ny, aes(y=ny$PCT_U18)) + geom_boxplot() + ggtitle("Boxplot of PCT_U18")
ggplot(data = ny, aes(y=ny$PC_18_65)) + geom_boxplot() + ggtitle("Boxplot of PC_18_65")
ggplot(data = ny, aes(y=ny$PCT_O65)) + geom_boxplot() + ggtitle("Boxplot of PCT_O65")
ggplot(data = ny, aes(y=ny$MALE_FEM)) + geom_boxplot() + ggtitle("Boxplot of MALE_FEM")
# install.packages("psych")
library(psych)
pairs.panels(ny[c("MALE_FEM","TOT_POP","PCT_U18","PC_18_65","PCT_O65")],method = "pearson",lm=TRUE,
ellipses = FALSE)
#### Data Cleaning ####
# TOT_POP
boxplot(ny$TOT_POP,main="TOT_POP")$stats[c(1,5),] #1000 #19750
length(which(ny$TOT_POP>19750)) #81
length(which(ny$TOT_POP<1000)) #0</pre>
ny <- ny[-which(ny$TOT_POP>19750),]
summary(ny$TOT_POP)
# PCT_U18
boxplot(ny$PCT_U18,main="PCT_U18")$stats[c(1,5),]
length(which(ny$PCT_U18>33.7)) #9
length(which(ny$PCT_U18<15.1)) #23
ny <- ny[-which(ny$PCT_U18>33.7),]
ny <- ny[-which(ny$PCT_U18<15.1),]
# PC_18_65
boxplot(ny$PC_18_65,main="PC_18_65")$stats[c(1,5),]
length(which(ny$PC_18_65>72.4)) #4
length(which(ny$PC_18_65<49.5)) #2
ny <- ny[-which(ny$PC_18_65>72.4),]
ny <- ny[-which(ny$PC_18_65<49.5),]
```

PCT_O65

boxplot(ny\$PCT_O65,main="PCT_O65")\$stats[c(1,5),]

```
length(which(ny$PCT_O65>26.2)) #10
length(which(ny$PCT_O65<2.7))</pre>
ny <- ny[-which(ny$PCT_065>26.2)]
# MALE_FEM
boxplot(ny$MALE_FEM,main="MALE_FEM")$stats[c(1,5),]
length(which(ny$MALE_FEM<69.7)) #3
length(which(ny$MALE_FEM>107.4)) #5
ny <- ny[-which(ny$MALE_FEM<69.7),]</pre>
ny <- ny[-which(ny$MALE_FEM>107.4),]
# Scatterplot Matrix
pairs(ny[c("MALE_FEM","TOT_POP","PCT_U18","PC_18_65","PCT_O65")])
# Correlation Matrix (Pearson)
cor(ny[c("MALE_FEM","TOT_POP","PCT_U18","PC_18_65","PCT_O65")])
pairs.panels(ny[c("MALE_FEM","TOT_POP","PCT_U18","PC_18_65","PCT_O65")],method = "pearson",lm=TRUE)
ny$TOT_POP <- log(ny$TOT_POP)</pre>
pairs.panels(ny[c("MALE_FEM","TOT_POP","PCT_U18","PC_18_65","PCT_O65")],method = "pearson",lm=TRUE,
ellipses = FALSE)
#### Splitting The Dataset ####
ny1 <- ny[,c(6,2,3,4,5)]
#install.packages('caTools')
library(caTools)
set.seed(123)
#Split of dataset into training dataset and test dataset
split <- sample.split(ny1$MALE_FEM,SplitRatio = 0.8)</pre>
training_set <- subset(ny1, split==TRUE)</pre>
```

```
test_set <- subset(ny1, split == FALSE)
```

```
#Scaling
```

```
#For putting variables in same scale
training_set[,2:5] <- scale(training_set[,2:5])
test_set[,2:5] <- scale(test_set[,2:5])</pre>
```

Model Building

Using all variables

```
model1 <- Im(MALE_FEM ~ TOT_POP + PCT_U18 + PC_18_65 + PCT_O65,data = training_set)
summary(model1)
y_pred1 = predict(model1,newdata=test_set)
cor(y_pred1,test_set$MALE_FEM)*cor(y_pred1,test_set$MALE_FEM)
# 48.08</pre>
```

Eliminating PCT_O65

FINAL MODEL

```
model2 <- Im(MALE_FEM ~ TOT_POP + PCT_U18 + PC_18_65,data = training_set)
summary(model2)
y_pred2 = predict(model2,newdata=test_set)
cor(y_pred2,test_set$MALE_FEM)*cor(y_pred2,test_set$MALE_FEM)
# 48.48</pre>
```

Removing the PCT_U18 in model2

```
model22 <- Im(MALE_FEM ~ PCT_U18 + PC_18_65,data = training_set) summary(model22)
```

Calculating Variance Inflation Factor

library(caret)

varImp(model1)

Error Rate

sigma(model2)/mean(training_set\$MALE_FEM)*100

```
# Calculating the No of rows in training set
nrow(training_set)
# Eliminating PC_18_65
model3 <- Im(MALE_FEM ~ TOT_POP + PCT_U18 + PCT_065,data = training_set)
summary(model3)
y_pred3 = predict(model3,newdata=test_set)
cor(y_pred3,test_set$MALE_FEM)*cor(y_pred3,test_set$MALE_FEM)
# 48.24
# Eliminating PC_18_65 and PCT_O65
model4 <- Im(MALE_FEM ~ TOT_POP + PCT_U18,data = training_set)
summary(model4)
y_pred4 = predict(model4,newdata=test_set)
cor(y_pred4,test_set$MALE_FEM)*cor(y_pred4,test_set$MALE_FEM)
# 0.1
#### Different Plots ####
# Histogram of residuals
resid = test_set$MALE_FEM-y_pred2
ggplot() + aes(resid)+ geom_histogram(binwidth=1, colour="black", fill="white") +
geom_density(aes(y=1*..count..)) +
ggtitle("Overlay Histogram of Residuals") +
xlab("Residuals") +
ylab("")
# Homoscedasticity
ggplot(data=NULL,aes(x=y_pred2,y=resid))+geom_point() +
ggtitle("Predicted Values VS Residuals") +
ylab("Residuals") +
xlab("Predicted Values")
```

