

# CANCER PREDICATION

## 1)Initial Variables

age  
ethnicity  
ER  
PR  
RT  
CT  
HT  
N  
tumorStage  
tumorSize  
grade

## 2)Pre-processing

1) Checked the summary of data

| age           | ethnicity    | ER             | PR             |
|---------------|--------------|----------------|----------------|
| Min. :31.00   | Min. :0.00   | Min. :0.0000   | Min. :0.0000   |
| 1st Qu.:43.00 | 1st Qu.:1.00 | 1st Qu.:0.0000 | 1st Qu.:0.0000 |
| Median :51.00 | Median :2.00 | Median :1.0000 | Median :1.0000 |
| Mean :54.04   | Mean :1.57   | Mean :0.6579   | Mean :0.5702   |
| 3rd Qu.:62.00 | 3rd Qu.:2.00 | 3rd Qu.:1.0000 | 3rd Qu.:1.0000 |
| Max. :88.00   | Max. :2.00   | Max. :1.0000   | Max. :1.0000   |

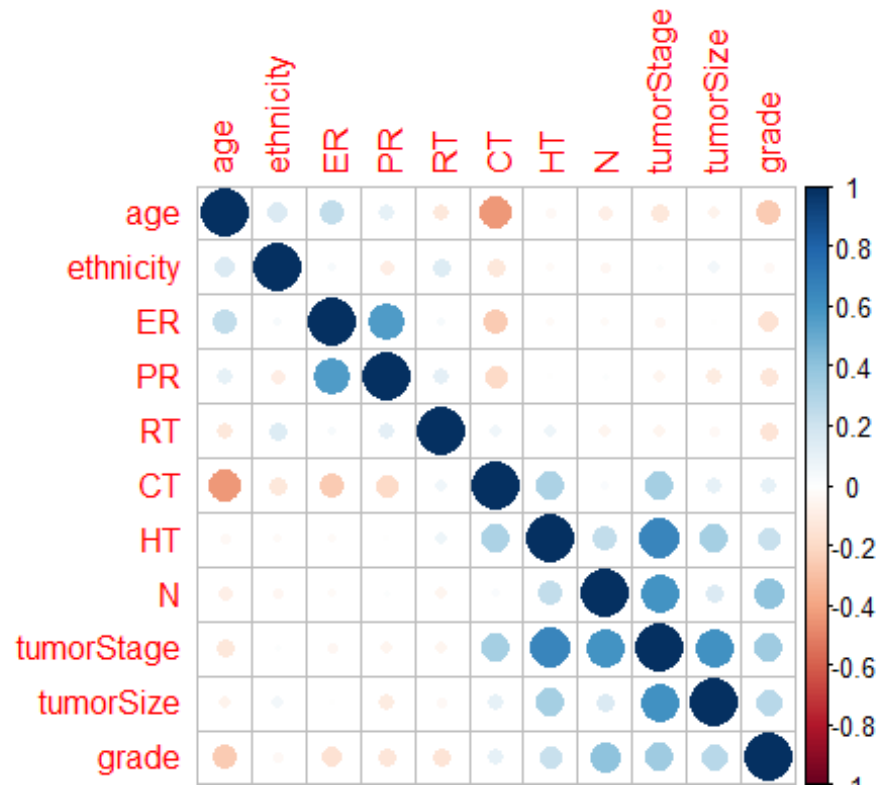
  

| RT             | CT             | HT             | N               |
|----------------|----------------|----------------|-----------------|
| Min. :0.0000   | Min. :0.0000   | Min. :0.0000   | Min. :0.00000   |
| 1st Qu.:0.0000 | 1st Qu.:0.0000 | 1st Qu.:0.0000 | 1st Qu.:0.00000 |
| Median :1.0000 | Median :1.0000 | Median :1.0000 | Median :0.00000 |
| Mean :0.5351   | Mean :0.5439   | Mean :0.5702   | Mean :0.04386   |
| 3rd Qu.:1.0000 | 3rd Qu.:1.0000 | 3rd Qu.:1.0000 | 3rd Qu.:0.00000 |
| Max. :1.0000   | Max. :1.0000   | Max. :2.0000   | Max. :1.00000   |

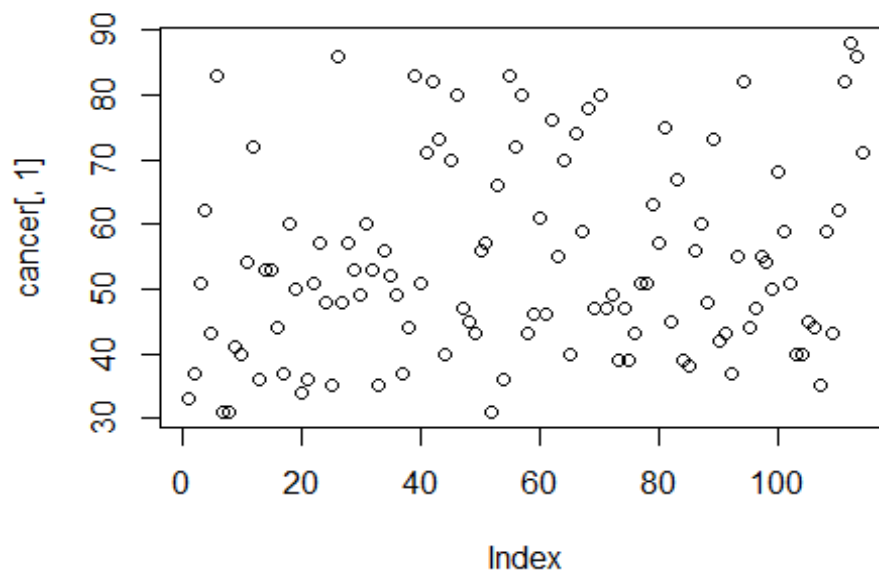
  

| tumorStage    | tumorSize     | grade          |
|---------------|---------------|----------------|
| Min. :1.000   | Min. :0.000   | Min. :0.0000   |
| 1st Qu.:2.000 | 1st Qu.:1.625 | 1st Qu.:0.0000 |
| Median :2.000 | Median :2.300 | Median :0.0000 |
| Mean :1.956   | Mean :2.689   | Mean :0.2193   |
| 3rd Qu.:2.000 | 3rd Qu.:3.475 | 3rd Qu.:0.0000 |
| Max. :4.000   | Max. :7.500   | Max. :1.0000   |

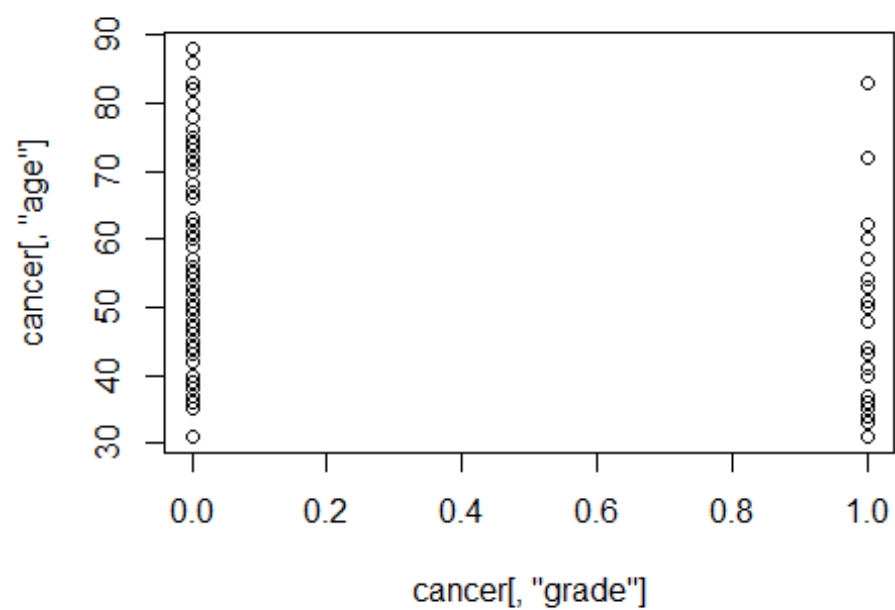
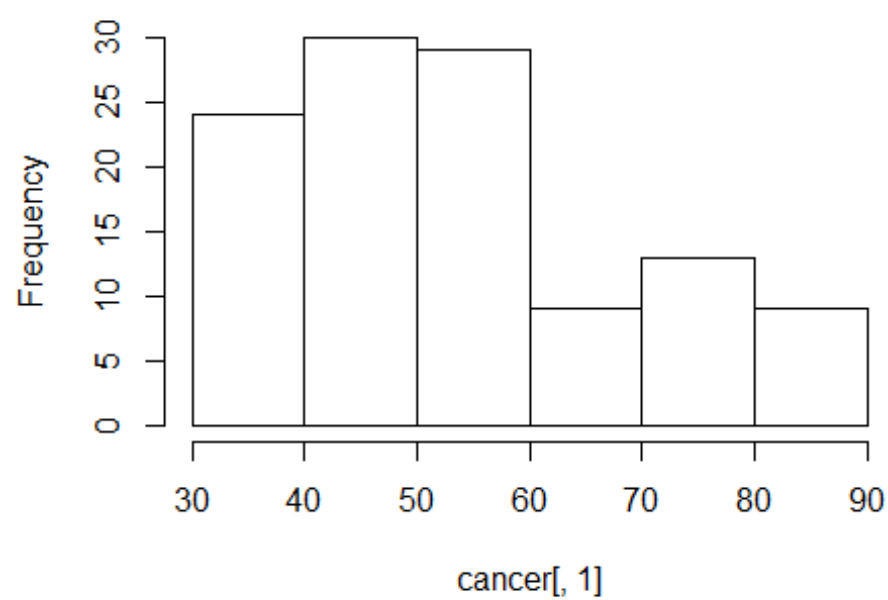
- 2) Checked the correlation of data
- 3) Some Variables are scaled for Normalization of data

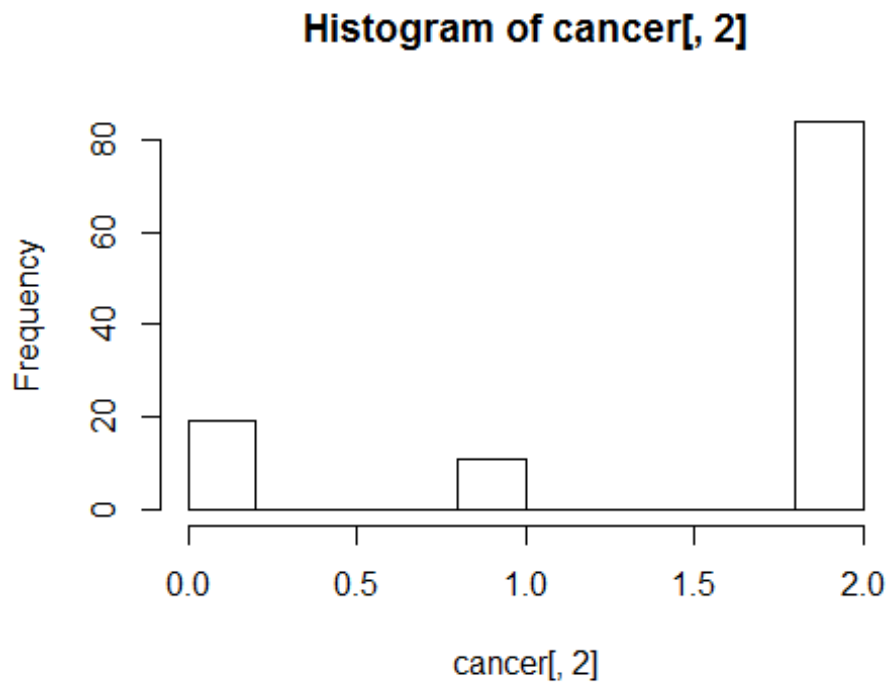


- 4) Observed the data by all means



**Histogram of cancer[, 1]**





- 5) Checked for missing values
- 6) Outlier treatment is not done since most of them were categorical variables

### ***3)Feature Selection***

- 1) First of all, all the variables are taken into consideration
- 2) Then according step() function number of variables are reduced

### ***4)Model Development***

- 1) Generalized Linear Model (GLM) algorithm have been run

### ***5)Model Testing and Accuracy Checking***

- 1) RMSE is checked for developed model
- 2) Accuracy also is calculated

## 6) Codes

```
#Set working directory where my dataset resides
setwd("C:/Users/DELL/Desktop/Aegis/Machine Learning/Data")

#Read the .csv file of cancer dataset
cancer=read.csv("cancer.csv")

#checking the structure of data
head(cancer)

#checking summary of data
summary(cancer)

#Checking the Correlation of the cancer dataset's features
library("corrplot")
corrplot(cor(cancer))

#Plotting the first column i.e age of cancer dataset
plot(cancer[,1])

#Histogram of age column
hist(cancer[,1])

#plot grade vs age column of cancer dataset
plot(cancer[, "grade"],cancer[, "age"])

#Correlation of age and grade of cancer dataset
cor(cancer[, "grade"],cancer[, "age"])

#Histogram of ethnicity column of cancer dataset
hist(cancer[,2])
```

```

#correlation of ethnicity and grade of cancer dataset
cor(cancer[,2],cancer[, "grade"])

#checking is there any NA data in row
anyNA(cancer)

#if any NA then its row and column number i.e its position
which(is.na(cancer),T)

#Divide the grade 1 and grade 0 data
class1=subset(cancer,grade==1)
class0=subset(cancer,grade==0)

#taking sample of 70% grade 1 and grade 0 data
ind0=sample(1:nrow(class0),round(0.70*(nrow(class0))))
ind1=sample(1:nrow(class1),round(0.70*(nrow(class1))))

train1=class1[ind1,]
train0=class0[ind0,]
test1=class1[-ind1,]
test0=class0[-ind0,]

#creating final train and test data
train=rbind(train1,train0)
test=rbind(test1,test0)

#logistic model of cancer data
fit1=glm(grade ~ sqrt(age) + ethnicity + ER + PR + RT + CT + HT + factor(tumor
Stage) + tumorSize ,family=binomial("logit"),train)#71.651

#step function applied on fit1 model
step(fit1)

```

```

#created the new logistic model according to step() function

fit=glm(grade ~ sqrt(age) + RT + factor(tumorStage) + tumorSize ,family=binomial("logit"),train)#63.269


#plot of logistic model

plot(fit)


#checking is there any multicollinearity in logistic model

library("car")

vif(fit)


#predicting the grade of our test data

out=predict(fit,test,type="response")


#checking summary of our logistic model

summary(fit)


#Rounding of the grade vaue

out=ifelse(out>0.5,1,0)

out


#checking the accuracy

count=0

accuracy=0

for(i in 1:nrow(test)){
  if(out[i]==test[i,11]){
    count=count+1
  }
}

accuracy=c(accuracy,count/nrow(test))

}

accuracy


#checking root mean square error

RMSE=sqrt(mean((out-test["grade"])^2))

RMSE

```