Final Project: Breast Cancer Detection

Abhijit Mandal

2020-11-20

Assignment

Post the last step of your Final Project. This should be an attached file that contains each step in the final project. Include the following:.

Question A:

Overall, write a coherent narrative that tells a story with the data as you complete this section.

Answer for A

As much as data science is playing a pivotal role everywhere, healthcare also finds it prominent application. Breast Cancer is the top rated type of cancer amongst women; which took away 627,000 lives alone. This high mortality rate due to breast cancer does need attention, for early detection so that prevention can be done in time. As a potential contributor to state-of-art technology development, data mining and machine learning finds a multi-fold application in predicting Brest cancer. The objective of this project is to classify each of the tumor to be malignant or benign.

I used the dataset from Kaggle https://www.kaggle.com/uciml/breast-cancer-wisconsin-data for my research.

Question B.

Summarize the problem statement you addressed.

Answer for B:

I focused on the below problem statement:

- How do we define a tumor as malignant or benign ?
- Can any benign tumor turn to malignant at later time ?
- What are the characteristics of a malignant and benign tumor (size, mass, texture, smoothness etc)?
- Does the chances of a breast cancer varies from individual to individual?

Code

```r
## Set the working directory to the root of your DSC 520 directory

setwd("~/Documents/GitHub/dsc520")

## Loading Library
library(readr)
library(class)
library(gmodels)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
#load data
breastcancer_DF <- read.csv("data/BreastCancerData.csv")

str(breastcancer_DF)
```

```
## 'data.frame':    569 obs. of  32 variables:
##  $ id                      : int  842302 842517 84300903 84348301 84358402 843786 844359 84458202 844
##  $ diagnosis               : chr  "M" "M" "M" "M" ...
##  $ radius_mean             : num  18 20.6 19.7 11.4 20.3 ...
##  $ texture_mean            : num  10.4 17.8 21.2 20.4 14.3 ...
##  $ perimeter_mean          : num  122.8 132.9 130 77.6 135.1 ...
##  $ area_mean               : num  1001 1326 1203 386 1297 ...
##  $ smoothness_mean         : num  0.1184 0.0847 0.1096 0.1425 0.1003 ...
##  $ compactness_mean        : num  0.2776 0.0786 0.1599 0.2839 0.1328 ...
##  $ concavity_mean          : num  0.3001 0.0869 0.1974 0.2414 0.198 ...
##  $ concave.points_mean     : num  0.1471 0.0702 0.1279 0.1052 0.1043 ...
##  $ symmetry_mean           : num  0.242 0.181 0.207 0.26 0.181 ...
##  $ fractal_dimension_mean  : num  0.0787 0.0567 0.06 0.0974 0.0588 ...
##  $ radius_se               : num  1.095 0.543 0.746 0.496 0.757 ...
##  $ texture_se              : num  0.905 0.734 0.787 1.156 0.781 ...
##  $ perimeter_se            : num  8.59 3.4 4.58 3.44 5.44 ...
##  $ area_se                 : num  153.4 74.1 94 27.2 94.4 ...
##  $ smoothness_se           : num  0.0064 0.00522 0.00615 0.00911 0.01149 ...
##  $ compactness_se          : num  0.049 0.0131 0.0401 0.0746 0.0246 ...
##  $ concavity_se            : num  0.0537 0.0186 0.0383 0.0566 0.0569 ...
##  $ concave.points_se       : num  0.0159 0.0134 0.0206 0.0187 0.0188 ...
##  $ symmetry_se             : num  0.03 0.0139 0.0225 0.0596 0.0176 ...
##  $ fractal_dimension_se    : num  0.00619 0.00353 0.00457 0.00921 0.00511 ...
##  $ radius_worst            : num  25.4 25 23.6 14.9 22.5 ...
##  $ texture_worst           : num  17.3 23.4 25.5 26.5 16.7 ...
```

```
##  $ perimeter_worst        : num  184.6 158.8 152.5 98.9 152.2 ...
##  $ area_worst             : num  2019 1956 1709 568 1575 ...
##  $ smoothness_worst       : num  0.162 0.124 0.144 0.21 0.137 ...
##  $ compactness_worst      : num  0.666 0.187 0.424 0.866 0.205 ...
##  $ concavity_worst        : num  0.712 0.242 0.45 0.687 0.4 ...
##  $ concave.points_worst   : num  0.265 0.186 0.243 0.258 0.163 ...
##  $ symmetry_worst         : num  0.46 0.275 0.361 0.664 0.236 ...
##  $ fractal_dimension_worst: num  0.1189 0.089 0.0876 0.173 0.0768 ...
```

The dataset has 569 observation with 33 variables. Out of 33 variables or features of this dataset, One is identification Number, another is a cancer diagnosis, 30 are numerically valued laboratory measurements and the last variable is X which has all NA value. The diagnosis is coded as "M" to indicate malignant and "B" to indicate benign. By looking at the output of str command I can see that the 30 measurement numeric features include the mean, standard error and worst value for the 10 different characteristics of the cell. Radius Texture Perimeter Area Smoothness Compactness Concavity Concave points Symmetry Fractal dimension

Question C:

Summarize how you addressed this problem statement (the data used and the methodology employed).

Answer For C

In this project, I first analyzed the data and looked for any cleanups needed, then I derived correlation between the variables, after visualizing and analyzing the data I used machine learning algorithm KNN to derive at a conclusion.I considered variables such as tumor size, mass, texture, smoothness, thickness etc that can help in predicting the chances of a tumor being malignant or benign, I used K-nearest neighbor algorithm to classify the tumor, the result of this algorithm provided an accurate response.

Code

```
#The first variable is id which doesn't provide any useful information, will exclude these from the mod

breastcancer_DF <- select(breastcancer_DF,-id)

#The diagnosis variable is the outcome I want to predict. This feature indicates whether the cell is fr

table(breastcancer_DF$diagnosis)
```

```
##
##   B   M
## 357 212
```

```
round(prop.table(table(breastcancer_DF$diagnosis)) * 100, digits = 1)
```

```
##
##    B    M
## 62.7 37.3
```

```r
#The table() shows that this dataset has 357 benign cells and 212 malignant cells. The prop.table() sho

## Missing values

sum(is.na(breastcancer_DF))
```

```
## [1] 0
```

```r
# There are no missing values in the dataset so we can consider it for modeling

head(breastcancer_DF)
```

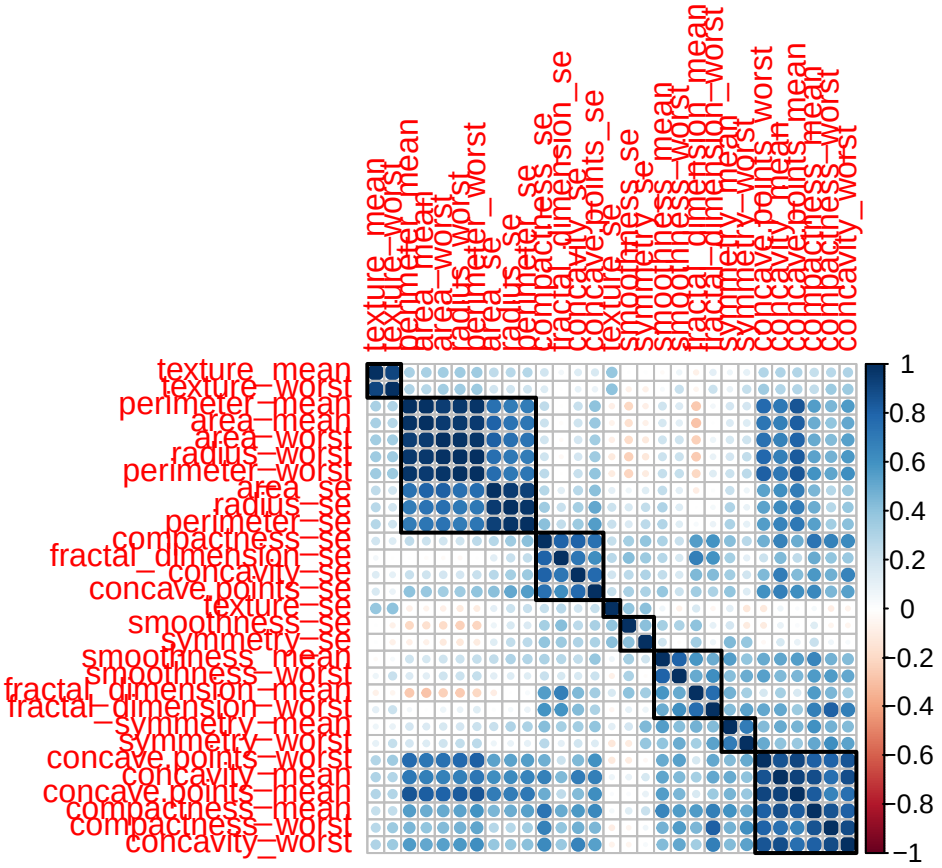
```
##   diagnosis radius_mean texture_mean perimeter_mean area_mean smoothness_mean
## 1         M       17.99        10.38         122.80    1001.0         0.11840
## 2         M       20.57        17.77         132.90    1326.0         0.08474
## 3         M       19.69        21.25         130.00    1203.0         0.10960
## 4         M       11.42        20.38          77.58     386.1         0.14250
## 5         M       20.29        14.34         135.10    1297.0         0.10030
## 6         M       12.45        15.70          82.57     477.1         0.12780
##   compactness_mean concavity_mean concave.points_mean symmetry_mean
## 1          0.27760         0.3001             0.14710        0.2419
## 2          0.07864         0.0869             0.07017        0.1812
## 3          0.15990         0.1974             0.12790        0.2069
## 4          0.28390         0.2414             0.10520        0.2597
## 5          0.13280         0.1980             0.10430        0.1809
## 6          0.17000         0.1578             0.08089        0.2087
##   fractal_dimension_mean radius_se texture_se perimeter_se area_se
## 1                0.07871    1.0950     0.9053        8.589  153.40
## 2                0.05667    0.5435     0.7339        3.398   74.08
## 3                0.05999    0.7456     0.7869        4.585   94.03
## 4                0.09744    0.4956     1.1560        3.445   27.23
## 5                0.05883    0.7572     0.7813        5.438   94.44
## 6                0.07613    0.3345     0.8902        2.217   27.19
##   smoothness_se compactness_se concavity_se concave.points_se symmetry_se
## 1      0.006399        0.04904      0.05373           0.01587     0.03003
## 2      0.005225        0.01308      0.01860           0.01340     0.01389
## 3      0.006150        0.04006      0.03832           0.02058     0.02250
## 4      0.009110        0.07458      0.05661           0.01867     0.05963
## 5      0.011490        0.02461      0.05688           0.01885     0.01756
## 6      0.007510        0.03345      0.03672           0.01137     0.02165
##   fractal_dimension_se radius_worst texture_worst perimeter_worst area_worst
## 1             0.006193        25.38         17.33          184.60     2019.0
## 2             0.003532        24.99         23.41          158.80     1956.0
## 3             0.004571        23.57         25.53          152.50     1709.0
## 4             0.009208        14.91         26.50           98.87      567.7
## 5             0.005115        22.54         16.67          152.20     1575.0
## 6             0.005082        15.47         23.75          103.40      741.6
##   smoothness_worst compactness_worst concavity_worst concave.points_worst
## 1           0.1622            0.6656          0.7119               0.2654
## 2           0.1238            0.1866          0.2416               0.1860
## 3           0.1444            0.4245          0.4504               0.2430
## 4           0.2098            0.8663          0.6869               0.2575
## 5           0.1374            0.2050          0.4000               0.1625
```

```
## 6           0.1791            0.5249          0.5355               0.1741
##   symmetry_worst fractal_dimension_worst
## 1         0.4601                 0.11890
## 2         0.2750                 0.08902
## 3         0.3613                 0.08758
## 4         0.6638                 0.17300
## 5         0.2364                 0.07678
## 6         0.3985                 0.12440
```

```
## Corelation
library(corrplot)
```

```
## corrplot 0.84 loaded
```

```
corr_mat <- cor(breastcancer_DF[,3:ncol(breastcancer_DF)])
corrplot(corr_mat, order = "hclust", tl.cex = 1, addrect = 8)
```




```
#cor(select(breastcancer_DF,-diagnosis))

summary(breastcancer_DF)
```

```
##   diagnosis          radius_mean      texture_mean   perimeter_mean
##  Length:569         Min.   : 6.981   Min.   : 9.71   Min.   : 43.79
##  Class :character   1st Qu.:11.700   1st Qu.:16.17   1st Qu.: 75.17
```

```
##  Mode  :character   Median :13.370   Median :18.84   Median : 86.24
##                     Mean   :14.127   Mean   :19.29   Mean   : 91.97
##                     3rd Qu.:15.780   3rd Qu.:21.80   3rd Qu.:104.10
##                     Max.   :28.110   Max.   :39.28   Max.   :188.50
##    area_mean      smoothness_mean   compactness_mean  concavity_mean
##  Min.   : 143.5   Min.   :0.05263   Min.   :0.01938   Min.   :0.00000
##  1st Qu.: 420.3   1st Qu.:0.08637   1st Qu.:0.06492   1st Qu.:0.02956
##  Median : 551.1   Median :0.09587   Median :0.09263   Median :0.06154
##  Mean   : 654.9   Mean   :0.09636   Mean   :0.10434   Mean   :0.08880
##  3rd Qu.: 782.7   3rd Qu.:0.10530   3rd Qu.:0.13040   3rd Qu.:0.13070
##  Max.   :2501.0   Max.   :0.16340   Max.   :0.34540   Max.   :0.42680
##  concave.points_mean symmetry_mean    fractal_dimension_mean   radius_se
##  Min.   :0.00000     Min.   :0.1060   Min.   :0.04996        Min.   :0.1115
##  1st Qu.:0.02031     1st Qu.:0.1619   1st Qu.:0.05770        1st Qu.:0.2324
##  Median :0.03350     Median :0.1792   Median :0.06154        Median :0.3242
##  Mean   :0.04892     Mean   :0.1812   Mean   :0.06280        Mean   :0.4052
##  3rd Qu.:0.07400     3rd Qu.:0.1957   3rd Qu.:0.06612        3rd Qu.:0.4789
##  Max.   :0.20120     Max.   :0.3040   Max.   :0.09744        Max.   :2.8730
##    texture_se      perimeter_se       area_se        smoothness_se
##  Min.   :0.3602   Min.   : 0.757   Min.   :  6.802   Min.   :0.001713
##  1st Qu.:0.8339   1st Qu.: 1.606   1st Qu.: 17.850   1st Qu.:0.005169
##  Median :1.1080   Median : 2.287   Median : 24.530   Median :0.006380
##  Mean   :1.2169   Mean   : 2.866   Mean   : 40.337   Mean   :0.007041
##  3rd Qu.:1.4740   3rd Qu.: 3.357   3rd Qu.: 45.190   3rd Qu.:0.008146
##  Max.   :4.8850   Max.   :21.980   Max.   :542.200   Max.   :0.031130
##  compactness_se      concavity_se     concave.points_se   symmetry_se
##  Min.   :0.002252   Min.   :0.00000   Min.   :0.000000   Min.   :0.007882
##  1st Qu.:0.013080   1st Qu.:0.01509   1st Qu.:0.007638   1st Qu.:0.015160
##  Median :0.020450   Median :0.02589   Median :0.010930   Median :0.018730
##  Mean   :0.025478   Mean   :0.03189   Mean   :0.011796   Mean   :0.020542
##  3rd Qu.:0.032450   3rd Qu.:0.04205   3rd Qu.:0.014710   3rd Qu.:0.023480
##  Max.   :0.135400   Max.   :0.39600   Max.   :0.052790   Max.   :0.078950
##  fractal_dimension_se  radius_worst   texture_worst   perimeter_worst
##  Min.   :0.0008948    Min.   : 7.93   Min.   :12.02   Min.   : 50.41
##  1st Qu.:0.0022480    1st Qu.:13.01   1st Qu.:21.08   1st Qu.: 84.11
##  Median :0.0031870    Median :14.97   Median :25.41   Median : 97.66
##  Mean   :0.0037949    Mean   :16.27   Mean   :25.68   Mean   :107.26
##  3rd Qu.:0.0045580    3rd Qu.:18.79   3rd Qu.:29.72   3rd Qu.:125.40
##  Max.   :0.0298400    Max.   :36.04   Max.   :49.54   Max.   :251.20
##    area_worst     smoothness_worst  compactness_worst concavity_worst
##  Min.   : 185.2   Min.   :0.07117   Min.   :0.02729   Min.   :0.0000
##  1st Qu.: 515.3   1st Qu.:0.11660   1st Qu.:0.14720   1st Qu.:0.1145
##  Median : 686.5   Median :0.13130   Median :0.21190   Median :0.2267
##  Mean   : 880.6   Mean   :0.13237   Mean   :0.25427   Mean   :0.2722
##  3rd Qu.:1084.0   3rd Qu.:0.14600   3rd Qu.:0.33910   3rd Qu.:0.3829
##  Max.   :4254.0   Max.   :0.22260   Max.   :1.05800   Max.   :1.2520
##  concave.points_worst symmetry_worst   fractal_dimension_worst
##  Min.   :0.00000      Min.   :0.1565   Min.   :0.05504
##  1st Qu.:0.06493      1st Qu.:0.2504   1st Qu.:0.07146
##  Median :0.09993      Median :0.2822   Median :0.08004
##  Mean   :0.11461      Mean   :0.2901   Mean   :0.08395
##  3rd Qu.:0.16140      3rd Qu.:0.3179   3rd Qu.:0.09208
##  Max.   :0.29100      Max.   :0.6638   Max.   :0.20750
```

```r
#I will be using KNN algorithm, after looking at the output of the summary() , the range for radius_mea

normalize <- function(x) {
    return ((x - min(x)) / (max(x) - min(x)))
}


updated_breastcancer_DF <- as.data.frame(lapply(select(breastcancer_DF,-diagnosis), normalize))

summary(select(updated_breastcancer_DF,radius_mean,smoothness_mean))
```

```
##   radius_mean     smoothness_mean
##  Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.2233   1st Qu.:0.3046
##  Median :0.3024   Median :0.3904
##  Mean   :0.3382   Mean   :0.3948
##  3rd Qu.:0.4164   3rd Qu.:0.4755
##  Max.   :1.0000   Max.   :1.0000
```

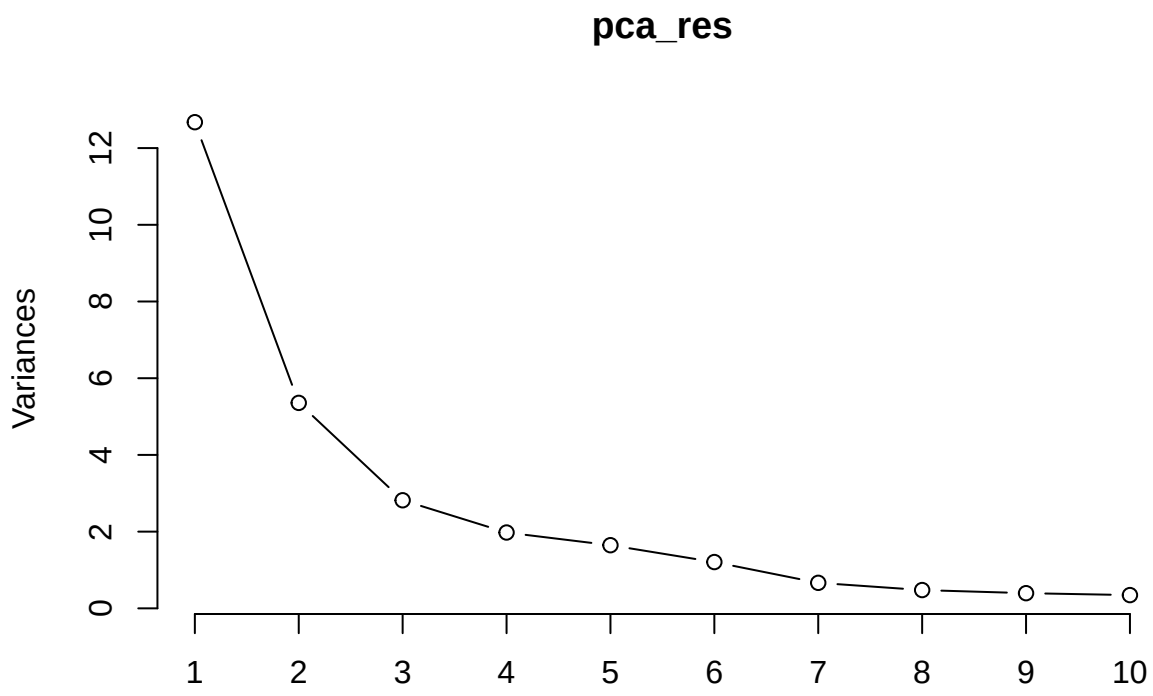
```r
#Creating a training set for building the KNN model and testing set for checking the accuracy of the mo
#I will use the 80% for training and 20% to simulate the new patients.

binaryClassifier_split <- sample(1:nrow(updated_breastcancer_DF), 0.8 * nrow(updated_breastcancer_DF))
trainds <- updated_breastcancer_DF[binaryClassifier_split,]
testds <- updated_breastcancer_DF[-binaryClassifier_split,]

trained_dataset <- breastcancer_DF[binaryClassifier_split,1]
test_dataset <- breastcancer_DF[-binaryClassifier_split,1]

#Data preprocessing

#Because there is so much correlation, some machine learning models can fail. We are going to create a
pca_res <- prcomp(breastcancer_DF[,3:ncol(breastcancer_DF)], center = TRUE, scale = TRUE)
plot(pca_res, type="l")

summary(pca_res)
```

```
## Importance of components:
##                           PC1    PC2     PC3     PC4     PC5     PC6     PC7
## Standard deviation     3.5602 2.3145 1.67860 1.40601 1.28301 1.09859 0.81534
## Proportion of Variance 0.4371 0.1847 0.09716 0.06817 0.05676 0.04162 0.02292
## Cumulative Proportion  0.4371 0.6218 0.71895 0.78712 0.84388 0.88550 0.90842
##                           PC8     PC9    PC10    PC11    PC12    PC13    PC14
## Standard deviation     0.69036 0.62876 0.58783 0.54148 0.51013 0.49123 0.39543
## Proportion of Variance 0.01643 0.01363 0.01192 0.01011 0.00897 0.00832 0.00539
## Cumulative Proportion  0.92485 0.93849 0.95040 0.96051 0.96948 0.97781 0.98320
##                           PC15   PC16    PC17    PC18    PC19    PC20    PC21
## Standard deviation     0.30645 0.2796 0.23982 0.22774 0.21104 0.17623 0.17248
## Proportion of Variance 0.00324 0.0027 0.00198 0.00179 0.00154 0.00107 0.00103
## Cumulative Proportion  0.98644 0.9891 0.99111 0.99290 0.99444 0.99551 0.99654
##                           PC22    PC23    PC24    PC25    PC26    PC27    PC28
## Standard deviation     0.16495 0.15477 0.13050 0.12436 0.08933 0.08164 0.03850
```

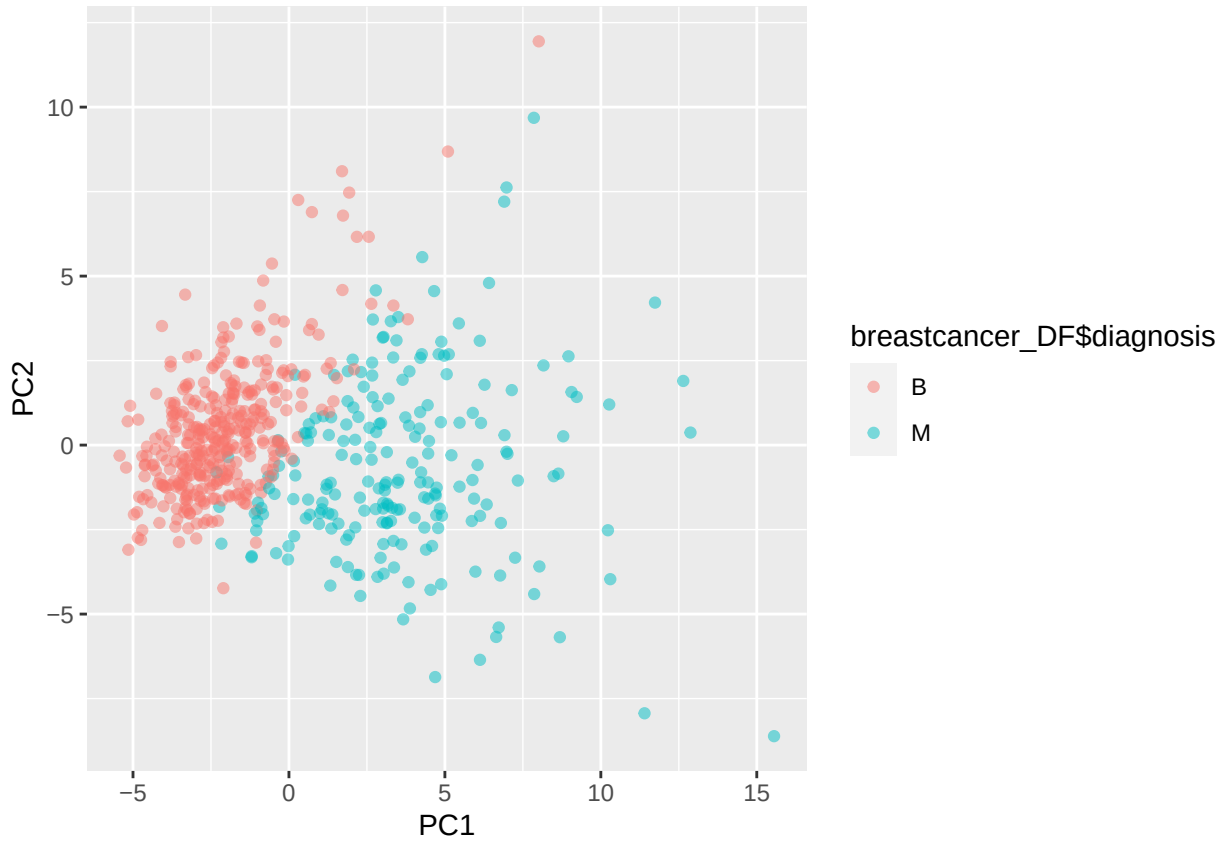
```
## Proportion of Variance 0.00094 0.00083 0.00059 0.00053 0.00028 0.00023 0.00005
## Cumulative Proportion  0.99747 0.99830 0.99889 0.99942 0.99970 0.99992 0.99998
##                            PC29
## Standard deviation     0.02635
## Proportion of Variance 0.00002
## Cumulative Proportion  1.00000
```

```
#The two first components explains the 0.6324 of the variance. We need 10 principal components to expla
```

```
library(ggplot2)
```




```
pca_df <- as.data.frame(pca_res$x)
ggplot(pca_df, aes(x=PC1, y=PC2, col=breastcancer_DF$diagnosis)) + geom_point(alpha=0.5)
```

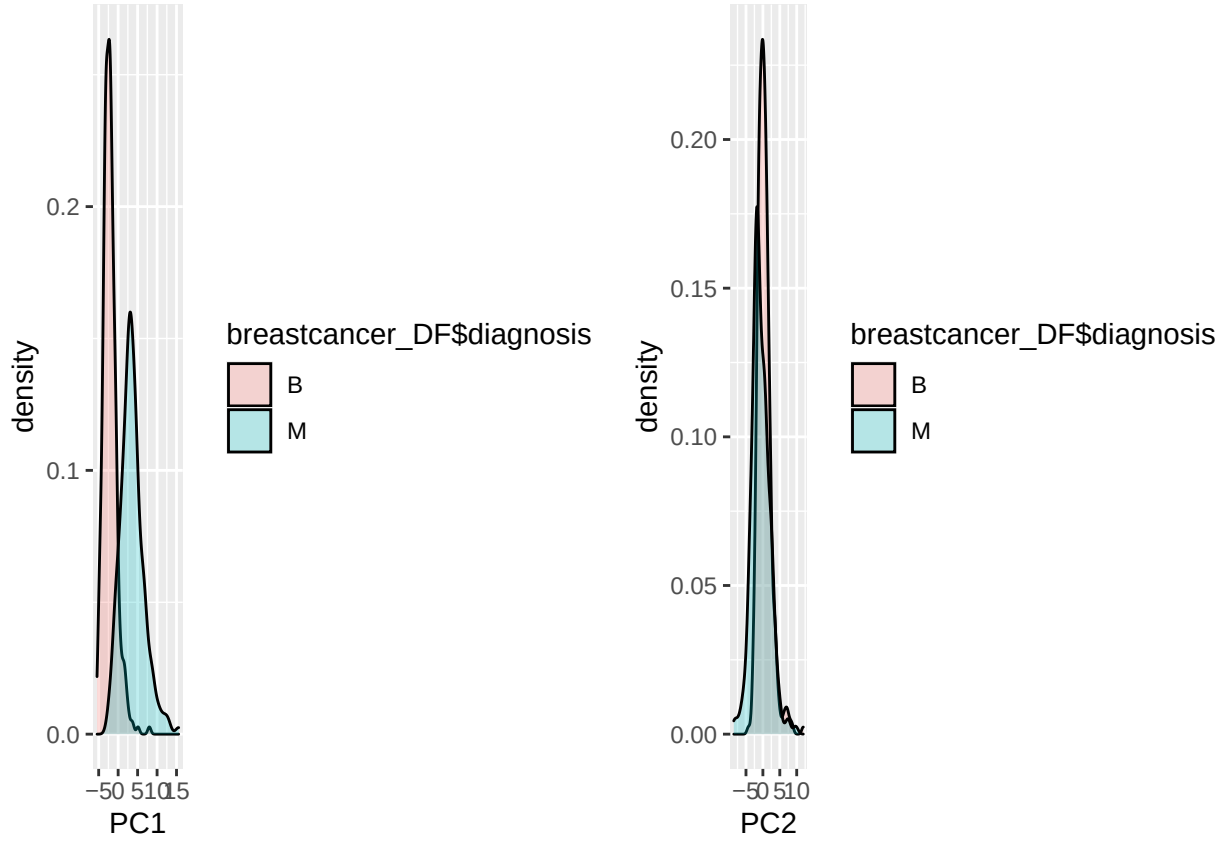



```
#The data can be easly separated.
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
g_pc1 <- ggplot(pca_df, aes(x=PC1, fill=breastcancer_DF$diagnosis)) + geom_density(alpha=0.25)
g_pc2 <- ggplot(pca_df, aes(x=PC2, fill=breastcancer_DF$diagnosis)) + geom_density(alpha=0.25)
grid.arrange(g_pc1, g_pc2, ncol=2)
```




```
# Applying k nearest neighbour algorithm, using K as 23
knnTestprediction <- knn(trainds,testds,cl=trained_dataset,k=23)

#Model Performance
#After the modeling of the data in knn algorithm, checking the performance of the model using confusion
confusionMatrix <- table(test_dataset,knnTestprediction)
confusionMatrix
```

```
##              knnTestprediction
## test_dataset  B  M
##            B 70  0
##            M  6 38
```

```
modelaccuracy <- (confusionMatrix[[1,1]] + confusionMatrix[[2,2]]) / sum(confusionMatrix)
modelaccuracy
```

```
## [1] 0.9473684
```

```
#The classification the model is divided into four categories
# Top Left      - True negative : predicted value was benign and identified as benign
# Bottom Right  - True positive : predicted value was malignant and identified as malignant
# Top Right     - False Positive: predicted value was malignant but cancer was actually benign
# Bottom Left   - False negative: predicted value was benign but the cancer was actually malignant
```

```
#False negative should be as much less as possible for our model as it is misleading to the patient and
#False positive is less dangerous than the false negative but it can add an extra financial burden on t
```

Question D:

Summarize the interesting insights that your analysis provided. As out of interest I looked at using various other models for comparison with KNN, the areas where KNN is certified as best model were Specificity, Positive Prediction Value and Precision.

Answer For D

Question E:

Summarize the implications to the consumer (target audience) of your analysis

Answer For E

The intent of this project is to assist doctors in diagnosing breast cancer for patients, allowing physicians to spend more time on treating the disease.Using machine learning methods for diagnostic can significantly increase processing speed and on a big scale can make the diagnostic significantly cheaper.

Question F:

Discuss the limitations of your analysis and how you, or someone else, could improve or build on it.

Answer For F

We have features of a tumor but I was not sure what does they mean or actually how much do we need to know about these features I believe that we do not need to know meaning of these features however in order to imagine in our mind we should know something like variance, standard deviation, number of sample (count) or max min values. These type of information helps to understand about what is going on data. For example , the question is appeared in my mind the area_mean feature's max value is 2500 and smoothness_mean features' max 0.16340. Also, it would have been great if i could compare the result of my data model vs other machine learning algorithms like Random Forest, SVM etc. In future we can look into the implementation of artificial neural net and deep learning for predictive model development with a larger and un- structured data set. This will use unsupervised learning algorithms such SVM etc. to first label the data and distributing them over training set, cross-validation set and test set.