

INDIRA GANDHI DELHI TECHNICAL UNIVERSITY FOR WOMEN



REPORT FILE

IT WORKSHOP (R PROGRAMMING)

Submitted by:

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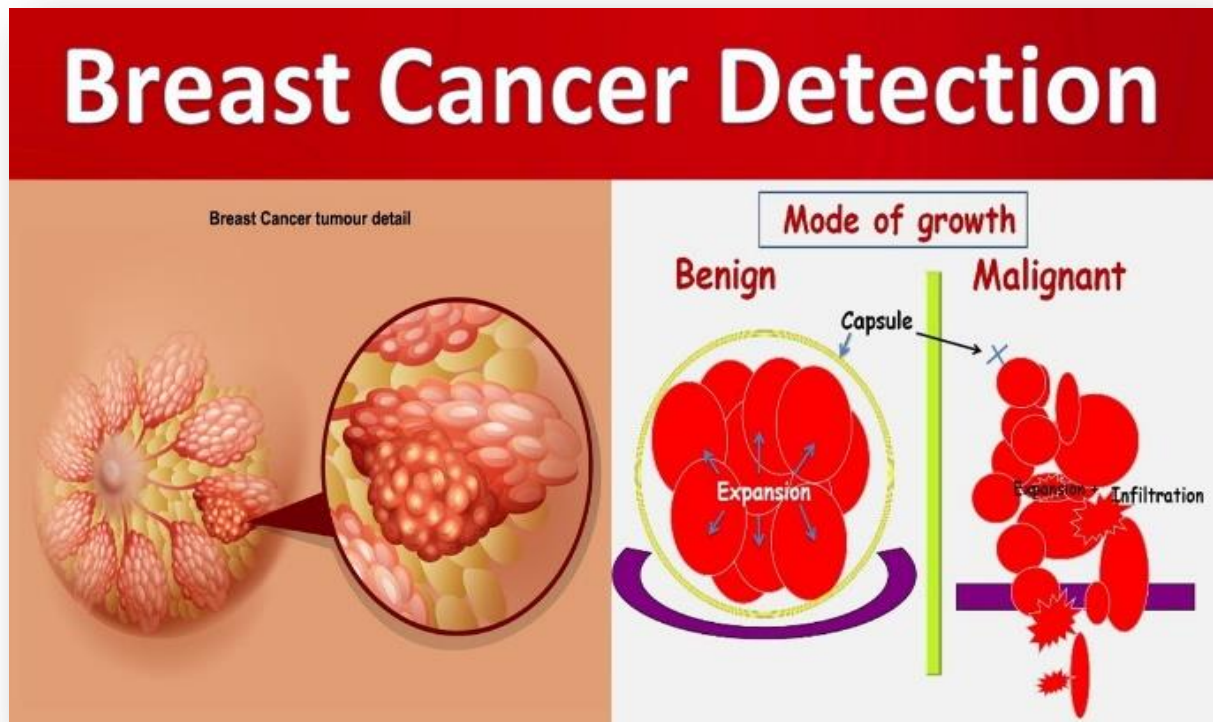
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Submitted to:

Mr. Santanoo Pattnaik

REPORT

“PREDICTING THE BREAST CANCER DETECTION OR NOT”



PROBLEM STATEMENT

Breast cancer is a significant health concern worldwide, and early detection plays a crucial role in improving patient outcomes. The problem is to develop a breast cancer detection system using the R programming language. The system should be able to accurately classify breast cancer cases as either malignant or benign based on input features.

ACKNOWLEDGMENT

We would like to take this opportunity to acknowledge everyone who has helped us in every stage of this project. We are deeply indebted to our teacher 'Mr. Santanoo Pattnaik' for his guidance and suggestions in completing this project on the topic " Video Game Sales Analysis". We came to know about so many things. We had our differences but we worked together and finalized this project within the limited time frame.

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OBJECTIVE

The objective of this project is to build a robust breast cancer classification model using R programming that achieves high accuracy in predicting the malignancy of breast tissue. The model will aid in early detection, assist in making informed treatment decisions, and contribute to improved patient outcomes in the fight against breast cancer.

- ✚ **DATA EXPLORATION:** Perform PCA(Principal Component Analysis) to gain the insight into the dataset, understand the different parameters such as cell thickness, texture , area etc. discover the correlations between features.
- ✚ **FEATURE ENGINEERING:** Prepare the dataset by handling missing values, addressing outliers, encoding categorical variables, and transforming variable if necessary.
- ✚ **MODEL SELECTION:** Evaluate and compare multiple regression techniques, such as linear regression, decision trees, support vector regression, or neural networks, to identify the most suitable models for predicting breast cancer . Consider factors like model complexity, interpretability, and performance metrics.
- ✚ **MODEL TRAINING AND EVALUATION:** Split the dataset into training and testing subsets, train the selected regression models on the training data, and evaluate their performance on the testing data.
- ✚ **MODEL IMPROVEMENT:** Fine-tune the chosen regression model by optimizing hyper parameters through techniques like grid search or randomized search. Additionally, consider applying regularization methods (e.g., L1 or L2 regularization) to prevent overfitting and improve generalization.
- ✚ **INTERPRETATION AND INSIGHTS:** Interpret the trained regression models to gain insights into the factors that significantly influence video game sales. Analyze coefficients, feature importance, or feature contribution to understand the relationships between the predictors and the sales outcome. Communicate findings and provide actionable insights based on the model interpretations.
- ✚ **FUTURE WORK:** Identify potential areas for further improvement, such as incorporating external data sources, exploring ensemble methods, or investigating advanced regression techniques like gradient boosting or deep learning models. Discuss possible extensions to the analysis and suggest future research directions.

- ✚ By achieving these objectives, the report aims to provide a comprehensive analysis of breast cancer data and develop accurate regression models for predicting future problems.

DATA PREPARATION

- ✚ **SELECTING DATA:** For this we researched and visualized different data of breast cancer with different parameters and finally we select the 'wisconsin breast cancer data'.

- `library(readxl)`
- `wbcd <- read_excel("C:/Users/dell/Downloads/wbcd.xlsx", n_max = 50)`
- `View(wbcd)`

- ✚ **NORMALIZING DATA :** When we use this wisconsin breast cancer data(wbcd) it has some irregularities like in the place of types of cancer it has 1 & 2 so for clearing this issue we normalise the data and in place of 1 = Malignant & 2 = Benign . This helped us to visualise and use the data properly for further processes.

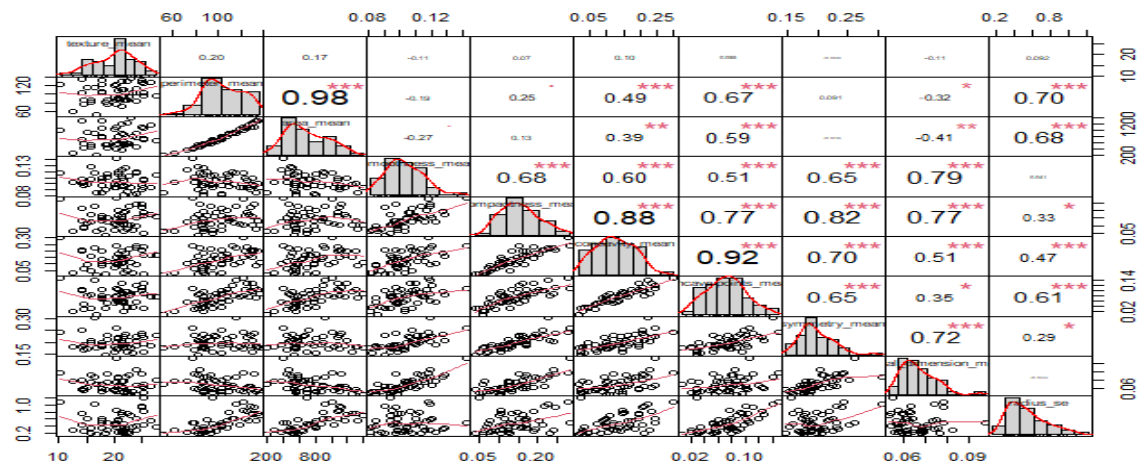
- `wbcd <- wbcd[,-1]`
- `wbcd$diagnosis <- factor(ifelse(wbcd$diagnosis=="B","Benign","Malignant"))`

DATA EXPOLRATION

ANALYZE THE CORRELATION BETWEEN VARIABLES

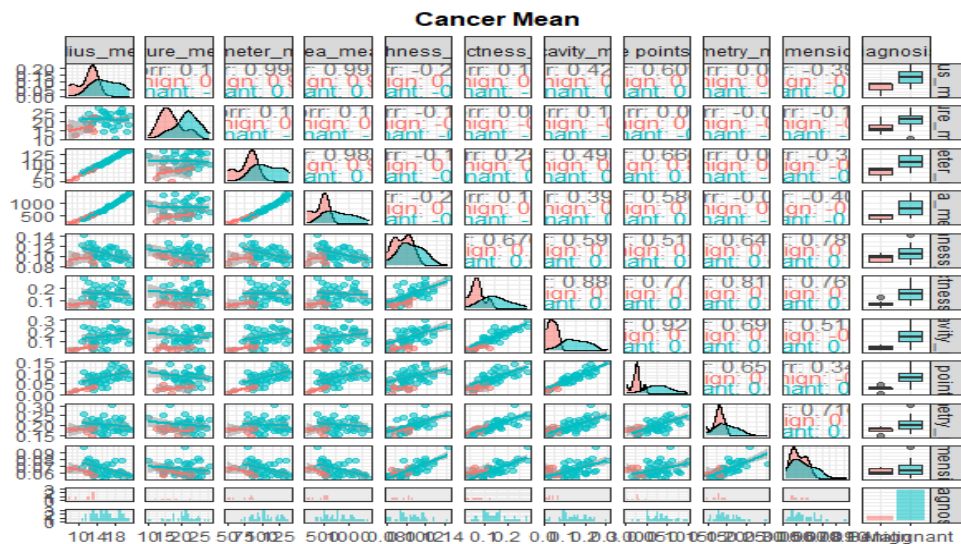
- ✚ Correlation between each variables

- `library(PerformanceAnalytics)`
- `chart.Correlation(wbcd[,c(2:11)], histogram=TRUE, col="grey10", pch=1, main="Cancer Mean")`



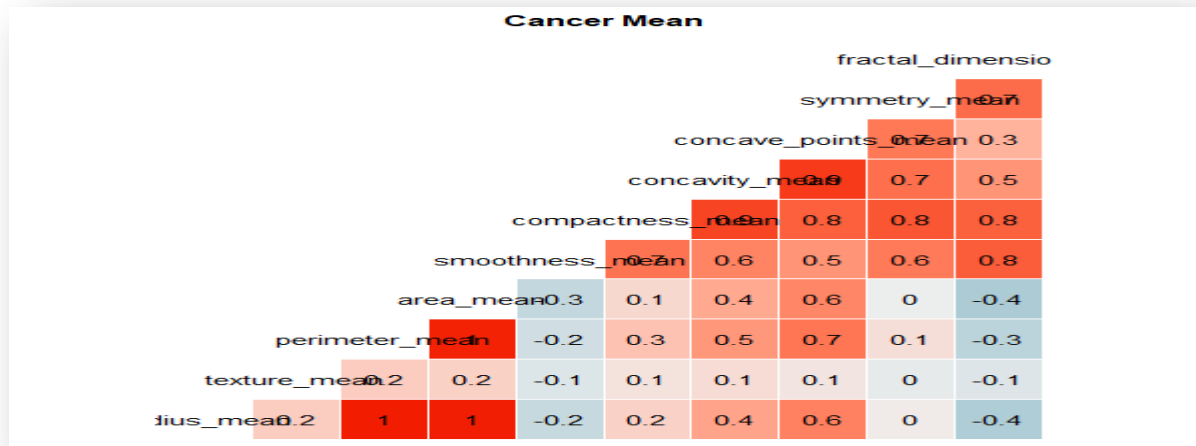
Relation between each variables (diagnosis included)

- `library(ggplot2)`
- `library(GGally)`
- `ggpairs(wbcd[,c(2:11,1)], aes(color=diagnosis, alpha=0.75), lower=list(continuous="smooth"))+ theme_bw()+`
- `labs(title="Cancer Mean")+`
- `theme(plot.title=element_text(face='bold',color='black',hjust=0.5,size=12))`



ggcorr plot

- `ggcorr(wbcd[,c(2:11)], name = "corr", label = TRUE)+`
- `theme(legend.position="none")+`
- `labs(title="Cancer Mean")+`
- `theme(plot.title=element_text(face='bold',color='black',hjust=0.5,size=12))`



PRINCIPAL COMPONENT ANALYSIS

Too many variables can cause such problems below

- ✚ Increased computer throughput
- ✚ Too complex visualization problems
- ✚ Decrease efficiency by including variables that have no effect on the analysis
- ✚ Make data interpretation difficult

If you see the ggcorr plot above high correlation value means it has “multicollinearity” between variables. -> Use one main component for model development by reduce the variables with high correlation. **PCA uses standardized data so that it can avoid data distortion caused by scale difference.** In the results of PCA, if the cumulative proportion is 85% or above, it can be determined by the number of principal components. The cumulative proportion from PC1 to PC6 is about 88.7%. (above 85%). It means that PC1~PC6 can explain 88.7% of the whole data.

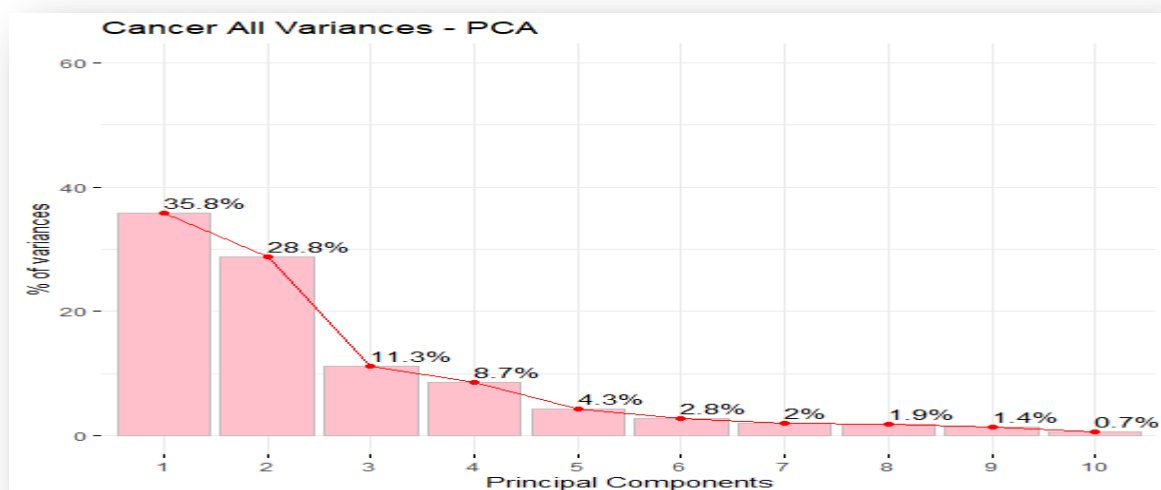
- `library(factoextra)`
- `all_pca <- transform(wbcd)`
- `all_pca <- prcomp(wbcd_pca[, -2], scale = TRUE)`
- `summary(all_pca)`

R 4.2.3 . ~/				
Importance of components:				
	PC1	PC2	PC3	PC4
Standard deviation	3.3305	2.9891	1.8681	1.6385
Proportion of Variance	0.3578	0.2882	0.1126	0.0866
Cumulative Proportion	0.3578	0.6461	0.7586	0.8452
	PC5	PC6	PC7	
Standard deviation	1.15439	0.93427	0.79569	
Proportion of Variance	0.04299	0.02816	0.02042	
Cumulative Proportion	0.88820	0.91636	0.93678	
	PC8	PC9	PC10	
Standard deviation	0.77054	0.66026	0.46339	
Proportion of Variance	0.01915	0.01406	0.00693	
Cumulative Proportion	0.95594	0.97000	0.97692	
	PC11	PC12	PC13	PC14
Standard deviation	0.43000	0.40579	0.29732	0.2612
Proportion of Variance	0.00596	0.00531	0.00285	0.0022
Cumulative Proportion	0.98289	0.98820	0.99105	0.9932

SCREEPLOT

The percentage of variability explained by the principal components can be ascertained through screeplot.

```
fviz_eig(all_pca, addlabels=TRUE, ylim=c(0,60), geom = c("bar", "line"), barfill = "pink", barcolor="grey",linecolor = "red", ncp=10)+
labs(title = "Cancer All Variances - PCA",
      x = "Principal Components", y = "% of variances")
```



GET PCA VARIABLES

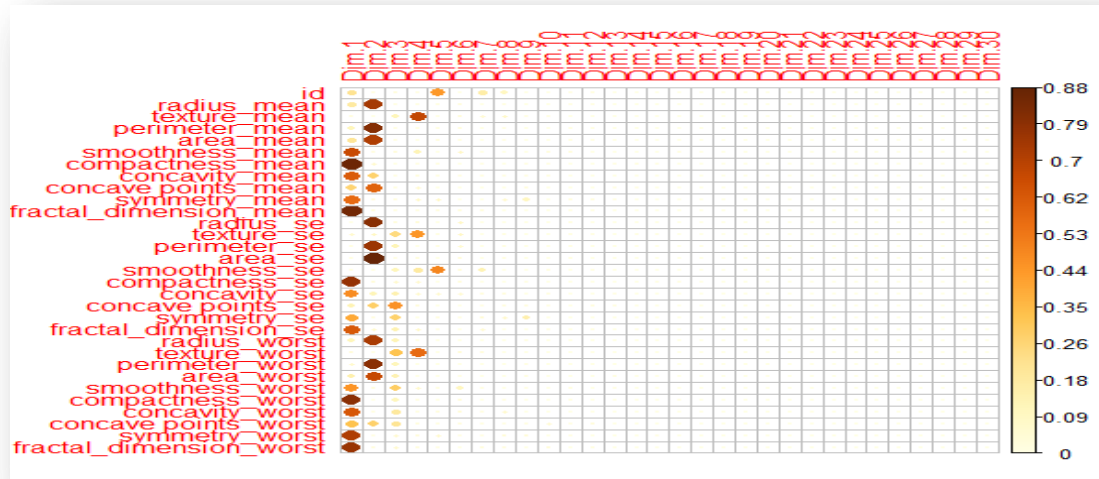
```
all_var <- get_pca_var(all_pca)

all_var
```

QUALITY OF REPRESENTATION OF PCA

Correlation between variables and PCA

```
library("corrplot")  
  
corrplot(all_var$cos2, is.corr=FALSE)
```



METHODOLOGY

MODELS & ALGORITHM :

Make test & train dataset for testing classification ML methods

```
nrows <- NROW(wbcd)  
  
set.seed(218)  
  
index <- sample(1:nrows, 0.7 * nrows)  
  
train <- wbcd[index,]  
  
test <- wbcd[-index,]
```

CHECK THE PROPORTION OF DIAGNOSIS (BENIGN / MALIGNANT)

#Train Data

```
prop.table(table(train$diagnosis))
```

```
Benign Malignant  
0.1428571 0.8571429
```

Test Data

```
prop.table(table(test$diagnosis))
```

```
Benign Malignant  
0.1333333 0.8666667
```

NAIVE BAYES

Given a new instance (test sample) , calculate the posterior probability of each class using Baye's theorem and the Naive Bayes assumptions . The class with the highest posterior probability is assigned as the predicted class for instance.

WITH LAPLACE

```
library(e1071)
```

```
acc_test <- numeric()
```

```
accuracy1 <- NULL; accuracy2 <- NULL
```

```
for(i in 1:30){
```

```
  learn_imp_nb <- naiveBayes(train[,-1], train$diagnosis, laplace=i)
```

```
  p_nb <- predict(learn_imp_nb, test[,-1])
```

```
  accuracy1 <- confusionMatrix(p_nb, test$diagnosis)
```

```
  accuracy2[i] <- accuracy1$overall[1]
```

```
}
```

```
acc <- data.frame(l= seq(1,30), cnt = accuracy2)
```

```
opt_l <- subset(acc, cnt==max(cnt))[1,]
```

```
sub <- paste("Optimal number of laplace is", opt_l$l, "(accuracy :", opt_l$cnt,") in
```

```
naiveBayes")
```

```
library(highcharter)
```

```
hchart(acc, 'line', hcaes(l, cnt)) %>%
```

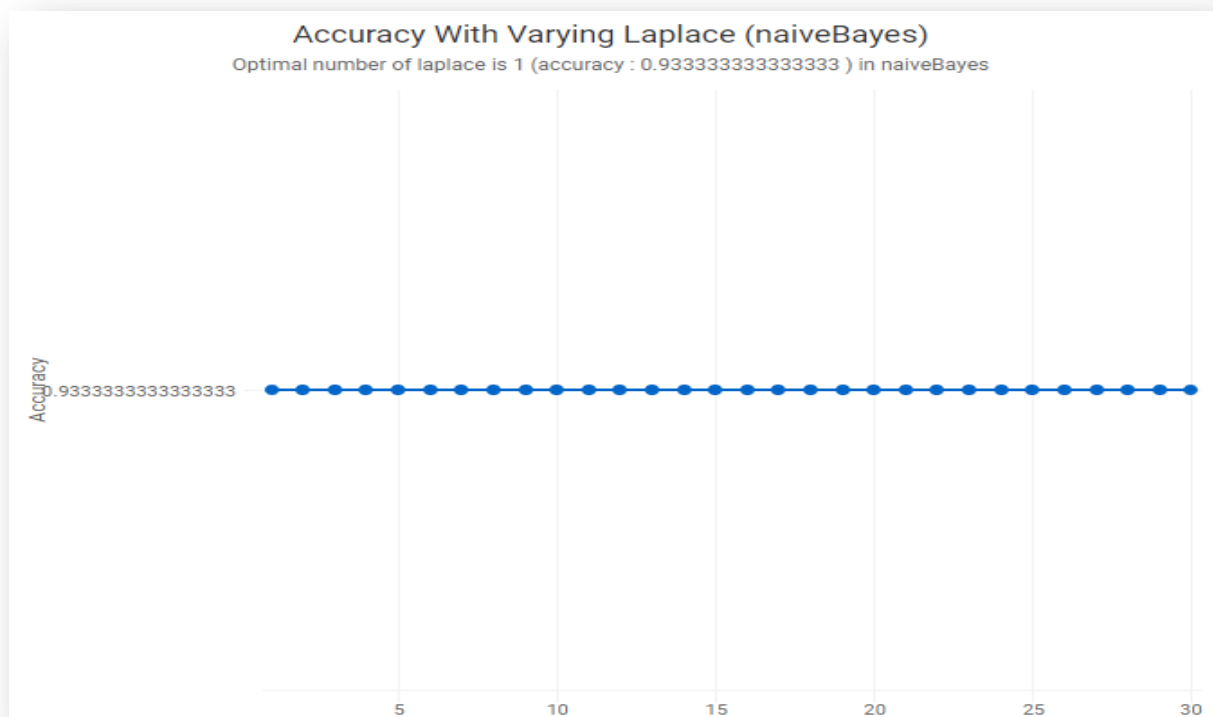
```
  hc_title(text = "Accuracy With Varying Laplace (naiveBayes)") %>%
```

```
  hc_subtitle(text = sub) %>%
```

```
  hc_add_theme(hc_theme_google()) %>%
```

```
  hc_xAxis(title = list(text = "Number of Laplace")) %>%
```

```
  hc_yAxis(title = list(text = "Accuracy"))
```



```
## WITHOUT LAPLACE
```

```
learn_nb <- naiveBayes(train[,-1], train$diagnosis)
```

```
pre_nb <- predict(learn_nb, test[,-1])
```

```
cm_nb <- confusionMatrix(pre_nb, test$diagnosis)
```

```
cm_nb
```

K – MEANS

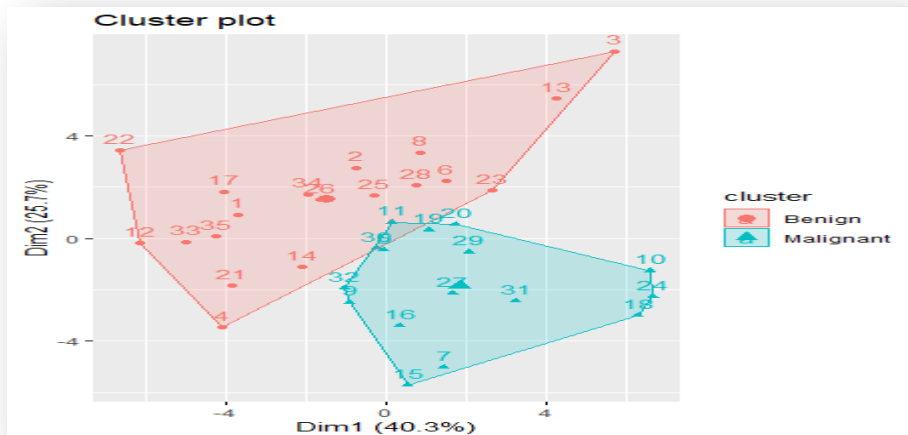
K – Means is a clustering algorithm that is typically used for unsupervised learning tasks, where the goal is to partition a dataset into distinct groups or clusters based on the similarity of data points.

```
## INPUT
predict.kmeans <- function(newdata, object){
  centers <- object$centers
  n_centers <- nrow(centers)
  dist_mat <- as.matrix(dist(rbind(centers, newdata)))
  dist_mat <- dist_mat[-seq(n_centers), seq(n_centers)]
  max.col(-dist_mat)
}
library(caret)
learn_kmeans <- kmeans(train[,-1], centers=2)
pre_kmeans <- predict.kmeans(test[,-1], learn_kmeans)
pre_kmeans <- ifelse(pre_kmeans == 1, "Benign", "Malignant")
cm_kmeans <- confusionMatrix(pre_kmeans, test$diagnosis)
cm_kmeans
```

```
## OUTPUT

Confusion Matrix and Statistics
Reference
Prediction Benign Malignant
Benign      2      7
Malignant   0      6
Accuracy : 0.5333
95% CI : (0.2659, 0.7873)
No Information Rate : 0.8667
P-Value [Acc > NIR] : 0.99973
Kappa : 0.186
McNemar's Test P-Value : 0.02334
Sensitivity : 1.0000
Specificity : 0.4615
Pos Pred Value : 0.2222
Neg Pred Value : 1.0000
Prevalence : 0.1333
Detection Rate : 0.1333
Detection Prevalence : 0.6000
Balanced Accuracy : 0.7308
'Positive' Class : Benign
```

```
## INPUT
library(factoextra)
learn_kmeans$cluster <- ifelse(learn_kmeans$cluster == 1, "Benign", "Malignant")
fviz_cluster(learn_kmeans, data = train[,-1])
```



SVM (SUPPORT VECTOR MACHINES)

INPUT

```
learn_svm <- svm(diagnosis~., data=train)
pre_svm <- predict(learn_svm, test[,-1])
cm_svm <- confusionMatrix(pre_svm, test$diagnosis)
cm_svm
```

output

Confusion Matrix and Statistics

Reference

Prediction Benign Malignant

Benign 2 0

Malignant 0 13

Accuracy : 1

95% CI : (0.782, 1)

No Information Rate : 0.8667

P-Value [Acc > NIR] : 0.1169

Kappa : 1

Mcnemar's Test P-Value : NA

Sensitivity : 1.0000

Specificity : 1.0000

Pos Pred Value : 1.0000

Neg Pred Value : 1.0000

Prevalence : 0.1333

Detection Rate : 0.1333

Detection Prevalence : 0.1333

Balanced Accuracy : 1.0000

'Positive' Class : Benign

INPUT

```
gamma <- seq(0,0.1,0.005)
```

```
cost <- 2^(0:5)
```

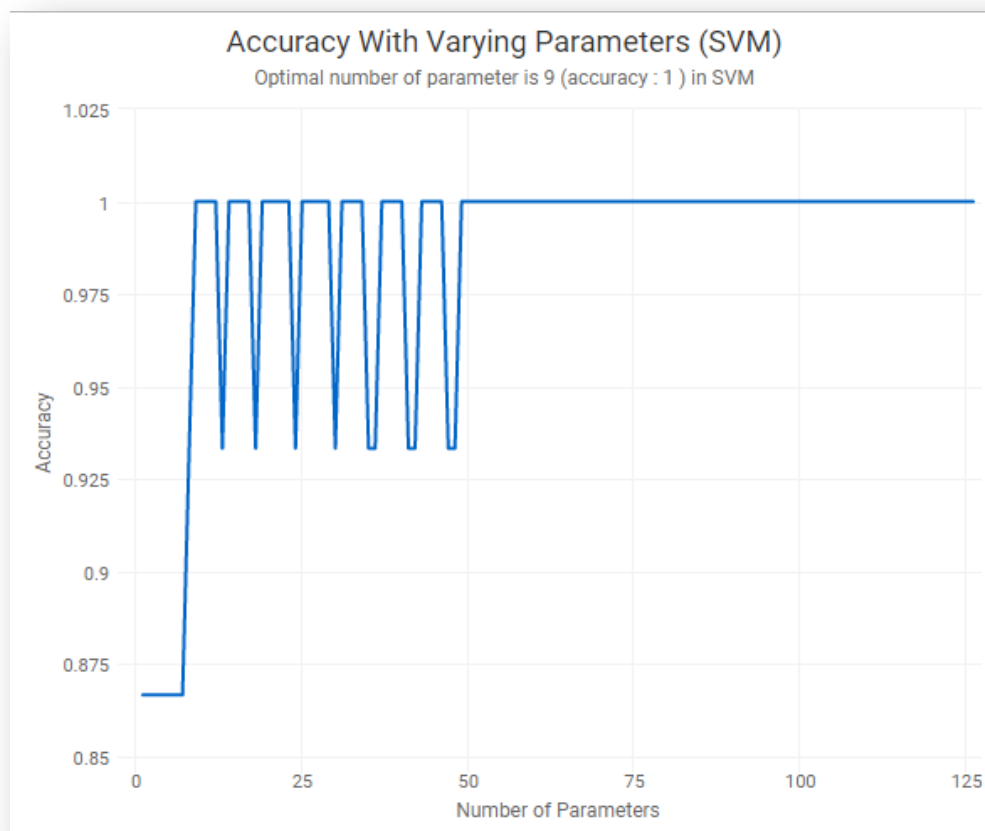
```
parms <- expand.grid(cost=cost, gamma=gamma) ## 231
```



```

acc_test <- numeric()
accuracy1 <- NULL; accuracy2 <- NULL
for(i in 1:NROW(parms)){
  learn_svm <- svm(diagnosis~., data=train, gamma=parms$gamma[i],
cost=parms$cost[i])
  pre_svm <- predict(learn_svm, test[,-1])
  accuracy1 <- confusionMatrix(pre_svm, test$diagnosis)
  accuracy2[i] <- accuracy1$overall[1]
}
acc <- data.frame(p= seq(1,NROW(parms)), cnt = accuracy2)
opt_p <- subset(acc, cnt==max(cnt))[1,]
sub <- paste("Optimal number of parameter is", opt_p$p, "(accuracy :", opt_p$cnt,")
in SVM")
library(highcharter)
hchart(acc, 'line', hcaes(p, cnt)) %>%
  hc_title(text = "Accuracy With Varying Parameters (SVM)") %>%
  hc_subtitle(text = sub) %>%
  hc_add_theme(hc_theme_google()) %>%
  hc_xAxis(title = list(text = "Number of Parameters")) %>%
  hc_yAxis(title = list(text = "Accuracy"))

```



```

## INPUT
learn_imp_svm <- svm(diagnosis~., data=train, cost=parms$cost[opt_p$p],
gamma=parms$gamma[opt_p$p])
pre_imp_svm <- predict(learn_imp_svm, test[,-1])
cm_imp_svm <- confusionMatrix(pre_imp_svm, test$diagnosis)

```

cm_imp_svm

##output

Confusion Matrix and Statistics

Reference

Prediction Benign Malignant

Benign 2 0

Malignant 0 13

Accuracy : 1

95% CI : (0.782, 1)

No Information Rate : 0.8667

P-Value [Acc > NIR] : 0.1169

Kappa : 1

Mcnemar's Test P-Value : NA

Sensitivity : 1.0000

Specificity : 1.0000

Pos Pred Value : 1.0000

Neg Pred Value : 1.0000

Prevalence : 0.1333

Detection Rate : 0.1333

Detection Prevalence : 0.1333

Balanced Accuracy : 1.0000

'Positive' Class : Benign

VISUALIZE TO COMPARE THE ACCURACY OF ALL METHODS

INPUT

```
col <- c("#ed3b3b", "#0099ff")
```

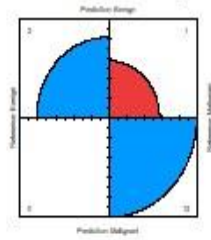
```
par(mfrow=c(3,5))
```

```
fourfoldplot(cm_nb$table, color = col, conf.level = 0, margin = 1, main=paste("NaiveBayes", round(cm_nb$overall[1]*100), "%"), sep="")
```

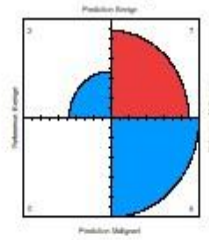
```
fourfoldplot(cm_kmeans$table, color = col, conf.level = 0, margin = 1, main=paste("KMeans", round(cm_kmeans$overall[1]*100), "%"), sep="")
```

```
fourfoldplot(cm_svm$table, color = col, conf.level = 0, margin = 1, main=paste("SVM", round(cm_svm$overall[1]*100), "%"), sep="")
```

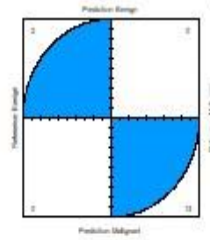
NaiveBayes (93%)



KMeans (53%)



SVM (100%)



PREPARE PATIENT DATA FOR TESTING FUNCTION

```

## INPUT
patient <- read_excel("C:/Users/dell/Downloads/wbcd.xlsx", n_max = 50)
patient$X <- NULL
## MALIGNANT
M <- patient[19,]
M[,c(1,2)]

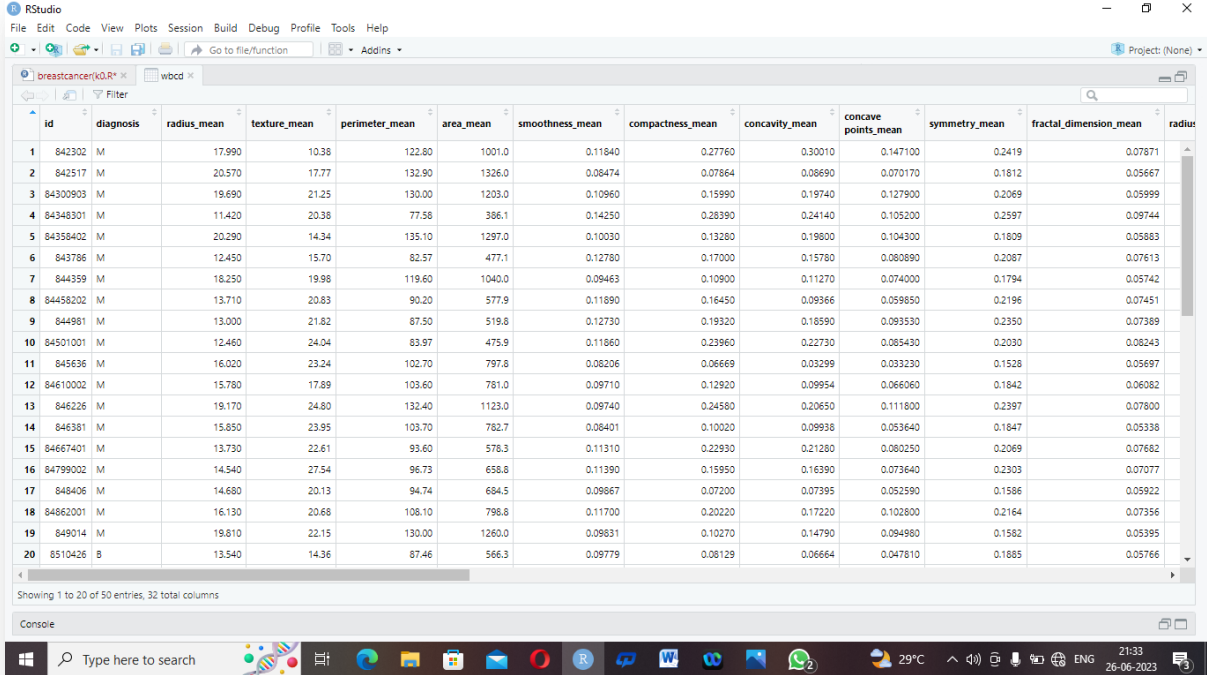
## OUTPUT
id diagnosis
1 849014 M
## BENIGN
B <- patient[20,]
B[,c(1,2)]

##OUTPUT
id diagnosis
1 8510426 B

```

SAMPLE DATASET

```
library(readxl)
wbcd <- read_excel("C:/Users/dell/Downloads/wbcd.xlsx", n_max = 50)
View(wbcd)
```



	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	symmetry_mean	fractal_dimension_mean	radius
1	842302	M	17.990	10.38	122.80	1001.0	0.11840	0.27760	0.30010	0.147100	0.2419	0.07871	
2	842517	M	20.570	17.77	132.90	1326.0	0.08474	0.07864	0.08690	0.070170	0.1812	0.05667	
3	84300903	M	19.690	21.25	130.00	1203.0	0.10960	0.15990	0.19740	0.127900	0.2069	0.05999	
4	84348301	M	11.420	20.38	77.58	386.1	0.14250	0.28390	0.24140	0.105200	0.2597	0.09744	
5	84358402	M	20.290	14.34	135.10	1297.0	0.10030	0.13280	0.19800	0.104300	0.1809	0.05883	
6	843786	M	12.450	15.70	82.57	477.1	0.12780	0.17000	0.15780	0.080890	0.2087	0.07613	
7	844359	M	18.250	19.98	119.60	1040.0	0.09463	0.10900	0.11270	0.074000	0.1794	0.05742	
8	84458202	M	13.710	20.83	90.20	577.9	0.11890	0.16450	0.09366	0.059850	0.2196	0.07451	
9	844981	M	13.000	21.82	87.50	519.8	0.12730	0.19320	0.16590	0.093530	0.2350	0.07389	
10	84501001	M	12.460	24.04	83.97	475.9	0.11860	0.23960	0.22730	0.085430	0.2030	0.08243	
11	845636	M	16.020	23.24	102.70	797.8	0.08206	0.06669	0.03299	0.033230	0.1528	0.05697	
12	84610002	M	15.780	17.89	103.60	761.0	0.09710	0.12920	0.09954	0.066060	0.1842	0.06082	
13	846226	M	19.170	24.80	132.40	1123.0	0.09740	0.24580	0.20650	0.111800	0.2397	0.07800	
14	846381	M	15.850	23.95	103.70	782.7	0.08401	0.10020	0.09938	0.053640	0.1847	0.05338	
15	84667401	M	13.730	22.61	93.60	578.3	0.11310	0.22930	0.21280	0.080250	0.2069	0.07682	
16	84799002	M	14.540	27.54	96.73	658.8	0.11390	0.15950	0.16390	0.073640	0.2303	0.07077	
17	848406	M	14.680	20.13	94.74	684.5	0.09867	0.07200	0.07395	0.052590	0.1586	0.05922	
18	84862001	M	16.130	20.68	108.10	798.8	0.11700	0.20220	0.17220	0.102800	0.2164	0.07356	
19	849014	M	19.810	22.15	130.00	1260.0	0.09831	0.10270	0.14790	0.094980	0.1582	0.05395	
20	8510426	B	13.540	14.36	87.46	566.3	0.09779	0.08129	0.06664	0.047810	0.1885	0.05766	

RESULT

The Report on Breast Cancer yielded the promising results . The dataset, comprising a diverse range of patient samples as shown in sample dataset , was effectively preprocessed to remove noise & ensure data quality. Three machines learning algorithm i.e. Naïve Bayes , K-Means , SVM . were implemented & evaluated using appropriate performance metrics. The models demonstrated high accuracy rates , with SVM achieving the highest performance with 100% of accuracy rates.





SCOPE OF IMPROVEMENT

The report on breast cancer detection using R programming has a strong foundation, highlighting the importance of early diagnosis and the potential of machine learning techniques. However, there are areas that can be further improved. Firstly, the report could benefit from a more detailed explanation of the dataset used, including its size, characteristics, and any preprocessing steps applied. Secondly, the evaluation metrics used for assessing the performance of the models could be expanded to include additional measures such as precision, recall, and F1 score to provide a more comprehensive analysis. Lastly, incorporating visualizations and comparative analysis with other existing methods would enhance the report's impact and provide a broader context for the findings.

CONCLUSION

The effectiveness of machine learning algorithms in accurately identifying breast cancer. By employing Naïve Bayes, K – Means, and support vector machines, the Report achieved high accuracy rates and demonstrated the potential of R programming for this task. The preprocessing steps ensured the quality of the dataset, and the evaluation metrics provided a comprehensive assessment of the models' performance. The inclusion of visualizations enhanced the report's clarity and highlighted the important features and predictive capabilities of the models. These findings underscore the importance of early detection and the role of R programming in advancing breast cancer diagnosis. Further research and exploration in this field can lead to improved detection methods and ultimately contribute to better patient outcomes.

REFERENCES

-  ChatGpt
-  Google
-  Kaggle
-  WBCD (wisconsin breast cancer data) Dataset