Data Science: Capstone - Create Your Own Project (Prediction of Breast Cancer)

KLC

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Objective

The aim of this project is to build a machine learning algorithm to predict whether a breast mass cell is "benign" or "malignant". Breast lumps that are benign are mostly non-cancerous and not life threatening. They do not spread outside of the breast. Malignant lumps are cancerous however. Such kind of prediction algorithm could help medical practitioners to detect and diagnose breast cancer.

We will train a few machine learning models and measure their performance with their prediction sensitivity and F1 score. Our aim is to choose a model which yields the highest sensitivity (i.e. low false-negative) and F1 score.

This report will first explore the dataset, then analyse several models, compare their performance and conclude the result.

Dataset

Breast Cancer Wisconsin (Diagnostic) DataSet obtained from Kaggle (https://www.kaggle.com/lbronchal /breast-cancer-dataset-analysis) is used for this project. Such data, collected in 1993 by the University of Wisconsin, contains 569 samples of measurements on cells in suspicious lumps in a women's breast. 20% of the data will be used for testing, while the remaining will be used for training the machine learning algorithm.

Description of data: The dataset contains 569 observations with 33 variables including 30 "features" as listed below. "Features" are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass, which describe characteristics of the cell nuclei present in the image.

Attribute Information:

1) ID number
2) Diagnosis (M = malignant, B = benign) 3-32)

Ten real-valued features are computed for each cell nucleus:

a) radius (mean of distances from center to points on the perimeter)
b) texture (standard deviation of gray-scale values)
c) perimeter
d) area
e) smoothness (local variation in radius lengths)
f) compactness (perimeter^2 / area - 1.0)
g) concavity (severity of concave portions of the contour)
h) concave points (number of concave portions of the contour)
i) symmetry
j) fractal dimension ("coastline approximation" - 1)

The mean, standard error and “worst” or largest (mean of the three largest values) of these features were computed for each image, resulting in 30 features. All feature values are recorded with 4 significant digits.

```r
################################
# Load dataset
################################

data <- read.csv("https://raw.githubusercontent.com/happycheers/BreastCancer/master/data.csv")
```

Data exploration

First, let’s grab an overview of the dataset.

```r
#Structure of the dataset
str(data)
```

```
## 'data.frame':    569 obs. of  33 variables:
##  $ id                     : int  842302 842517 84300903 84348301 84358402 843786 844359 84458202 8449
##  $ diagnosis              : Factor w/ 2 levels "B","M": 2 2 2 2 2 2 2 2 2 2 ...
##  $ 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 ...
##  $ X                      : logi  NA NA NA NA NA NA ...
```

```r
# First 6 rows and header
head(data)
```

```
##         id diagnosis radius_mean texture_mean perimeter_mean area_mean
## 1   842302         M       17.99        10.38         122.80    1001.0
## 2   842517         M       20.57        17.77         132.90    1326.0
## 3 84300903         M       19.69        21.25         130.00    1203.0
## 4 84348301         M       11.42        20.38          77.58     386.1
## 5 84358402         M       20.29        14.34         135.10    1297.0
## 6   843786         M       12.45        15.70          82.57     477.1
##   smoothness_mean compactness_mean concavity_mean concave.points_mean
## 1         0.11840          0.27760         0.3001             0.14710
## 2         0.08474          0.07864         0.0869             0.07017
## 3         0.10960          0.15990         0.1974             0.12790
## 4         0.14250          0.28390         0.2414             0.10520
## 5         0.10030          0.13280         0.1980             0.10430
## 6         0.12780          0.17000         0.1578             0.08089
##   symmetry_mean fractal_dimension_mean radius_se texture_se perimeter_se
## 1        0.2419                0.07871    1.0950     0.9053        8.589
## 2        0.1812                0.05667    0.5435     0.7339        3.398
## 3        0.2069                0.05999    0.7456     0.7869        4.585
## 4        0.2597                0.09744    0.4956     1.1560        3.445
## 5        0.1809                0.05883    0.7572     0.7813        5.438
## 6        0.2087                0.07613    0.3345     0.8902        2.217
##   area_se smoothness_se compactness_se concavity_se concave.points_se
## 1  153.40      0.006399        0.04904      0.05373           0.01587
## 2   74.08      0.005225        0.01308      0.01860           0.01340
## 3   94.03      0.006150        0.04006      0.03832           0.02058
## 4   27.23      0.009110        0.07458      0.05661           0.01867
## 5   94.44      0.011490        0.02461      0.05688           0.01885
## 6   27.19      0.007510        0.03345      0.03672           0.01137
##   symmetry_se fractal_dimension_se radius_worst texture_worst perimeter_worst
## 1     0.03003             0.006193        25.38         17.33          184.60
## 2     0.01389             0.003532        24.99         23.41          158.80
## 3     0.02250             0.004571        23.57         25.53          152.50
## 4     0.05963             0.009208        14.91         26.50           98.87
## 5     0.01756             0.005115        22.54         16.67          152.20
## 6     0.02165             0.005082        15.47         23.75          103.40
##   area_worst smoothness_worst compactness_worst concavity_worst
## 1     2019.0           0.1622            0.6656          0.7119
## 2     1956.0           0.1238            0.1866          0.2416
## 3     1709.0           0.1444            0.4245          0.4504
## 4      567.7           0.2098            0.8663          0.6869
## 5     1575.0           0.1374            0.2050          0.4000
## 6      741.6           0.1791            0.5249          0.5355
##   concave.points_worst symmetry_worst fractal_dimension_worst  X
## 1               0.2654         0.4601                 0.11890 NA
## 2               0.1860         0.2750                 0.08902 NA
## 3               0.2430         0.3613                 0.08758 NA
## 4               0.2575         0.6638                 0.17300 NA
## 5               0.1625         0.2364                 0.07678 NA
## 6               0.1741         0.3985                 0.12440 NA
```

```r
# Summary of statitics
summary(data)
```

```
##        id             diagnosis  radius_mean      texture_mean
##  Min.   :     8670   B:357     Min.   : 6.981   Min.   : 9.71
##  1st Qu.:   869218   M:212     1st Qu.:11.700   1st Qu.:16.17
##  Median :   906024            Median :13.370   Median :18.84
##  Mean   : 30371831            Mean   :14.127   Mean   :19.29
##  3rd Qu.:  8813129            3rd Qu.:15.780   3rd Qu.:21.80
##  Max.   :911320502            Max.   :28.110   Max.   :39.28
##  perimeter_mean     area_mean      smoothness_mean   compactness_mean
##  Min.   : 43.79   Min.   : 143.5   Min.   :0.05263   Min.   :0.01938
##  1st Qu.: 75.17   1st Qu.: 420.3   1st Qu.:0.08637   1st Qu.:0.06492
##  Median : 86.24   Median : 551.1   Median :0.09587   Median :0.09263
##  Mean   : 91.97   Mean   : 654.9   Mean   :0.09636   Mean   :0.10434
##  3rd Qu.:104.10   3rd Qu.: 782.7   3rd Qu.:0.10530   3rd Qu.:0.13040
##  Max.   :188.50   Max.   :2501.0   Max.   :0.16340   Max.   :0.34540
##  concavity_mean    concave.points_mean symmetry_mean    fractal_dimension_mean
##  Min.   :0.00000   Min.   :0.00000     Min.   :0.1060   Min.   :0.04996
##  1st Qu.:0.02956   1st Qu.:0.02031     1st Qu.:0.1619   1st Qu.:0.05770
##  Median :0.06154   Median :0.03350     Median :0.1792   Median :0.06154
##  Mean   :0.08880   Mean   :0.04892     Mean   :0.1812   Mean   :0.06280
##  3rd Qu.:0.13070   3rd Qu.:0.07400     3rd Qu.:0.1957   3rd Qu.:0.06612
##  Max.   :0.42680   Max.   :0.20120     Max.   :0.3040   Max.   :0.09744
##    radius_se        texture_se      perimeter_se       area_se
##  Min.   :0.1115   Min.   :0.3602   Min.   : 0.757   Min.   :  6.802
##  1st Qu.:0.2324   1st Qu.:0.8339   1st Qu.: 1.606   1st Qu.: 17.850
##  Median :0.3242   Median :1.1080   Median : 2.287   Median : 24.530
##  Mean   :0.4052   Mean   :1.2169   Mean   : 2.866   Mean   : 40.337
##  3rd Qu.:0.4789   3rd Qu.:1.4740   3rd Qu.: 3.357   3rd Qu.: 45.190
##  Max.   :2.8730   Max.   :4.8850   Max.   :21.980   Max.   :542.200
##  smoothness_se      compactness_se      concavity_se     concave.points_se
##  Min.   :0.001713   Min.   :0.002252   Min.   :0.00000   Min.   :0.000000
##  1st Qu.:0.005169   1st Qu.:0.013080   1st Qu.:0.01509   1st Qu.:0.007638
##  Median :0.006380   Median :0.020450   Median :0.02589   Median :0.010930
##  Mean   :0.007041   Mean   :0.025478   Mean   :0.03189   Mean   :0.011796
##  3rd Qu.:0.008146   3rd Qu.:0.032450   3rd Qu.:0.04205   3rd Qu.:0.014710
##  Max.   :0.031130   Max.   :0.135400   Max.   :0.39600   Max.   :0.052790
##   symmetry_se       fractal_dimension_se  radius_worst   texture_worst
##  Min.   :0.007882   Min.   :0.0008948    Min.   : 7.93   Min.   :12.02
##  1st Qu.:0.015160   1st Qu.:0.0022480    1st Qu.:13.01   1st Qu.:21.08
##  Median :0.018730   Median :0.0031870    Median :14.97   Median :25.41
##  Mean   :0.020542   Mean   :0.0037949    Mean   :16.27   Mean   :25.68
##  3rd Qu.:0.023480   3rd Qu.:0.0045580    3rd Qu.:18.79   3rd Qu.:29.72
##  Max.   :0.078950   Max.   :0.0298400    Max.   :36.04   Max.   :49.54
##  perimeter_worst    area_worst     smoothness_worst  compactness_worst
##  Min.   : 50.41   Min.   : 185.2   Min.   :0.07117   Min.   :0.02729
##  1st Qu.: 84.11   1st Qu.: 515.3   1st Qu.:0.11660   1st Qu.:0.14720
##  Median : 97.66   Median : 686.5   Median :0.13130   Median :0.21190
##  Mean   :107.26   Mean   : 880.6   Mean   :0.13237   Mean   :0.25427
##  3rd Qu.:125.40   3rd Qu.:1084.0   3rd Qu.:0.14600   3rd Qu.:0.33910
##  Max.   :251.20   Max.   :4254.0   Max.   :0.22260   Max.   :1.05800
##  concavity_worst  concave.points_worst symmetry_worst   fractal_dimension_worst
##  Min.   :0.0000   Min.   :0.00000      Min.   :0.1565   Min.   :0.05504
##  1st Qu.:0.1145   1st Qu.:0.06493      1st Qu.:0.2504   1st Qu.:0.07146
##  Median :0.2267   Median :0.09993      Median :0.2822   Median :0.08004
##  Mean   :0.2722   Mean   :0.11461      Mean   :0.2901   Mean   :0.08395
##  3rd Qu.:0.3829   3rd Qu.:0.16140      3rd Qu.:0.3179   3rd Qu.:0.09208
##  Max.   :1.2520   Max.   :0.29100      Max.   :0.6638   Max.   :0.20750
##     X
##  Mode:logical
##  NA's:569
##
##
##
##
```

```
# Summarize number of diagnosis ("B" and "M") in the dataset
data %>% group_by(diagnosis) %>% summarize(n())
```

```
## # A tibble: 2 x 2
##   diagnosis `n()`
##   <fct>     <int>
## 1 B           357
## 2 M           212
```

We note from the above that the diagnosis is slightly unbalanced. We may have to adjust the data when using some models so that they can work properly.

Data cleaning

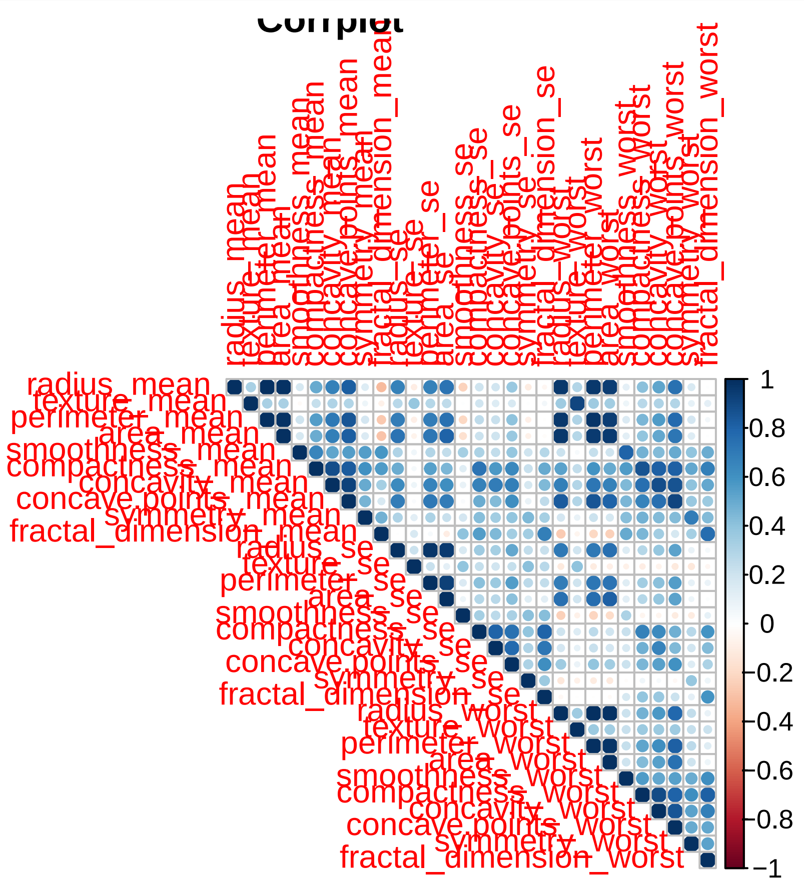
```
################################
# Data cleaning
################################

# Remove columns 1 and 33 as irrelevant
data <- data[,-33]
data <- data[,-1]

# Check if there are missing values
map_int(data, function(.x) sum(is.na(.x)))
```

```
##               diagnosis             radius_mean            texture_mean
##                       0                       0                       0
##          perimeter_mean               area_mean         smoothness_mean
##                       0                       0                       0
##        compactness_mean          concavity_mean     concave.points_mean
##                       0                       0                       0
##           symmetry_mean  fractal_dimension_mean               radius_se
##                       0                       0                       0
##              texture_se            perimeter_se                 area_se
##                       0                       0                       0
##           smoothness_se          compactness_se            concavity_se
##                       0                       0                       0
##       concave.points_se             symmetry_se    fractal_dimension_se
##                       0                       0                       0
##            radius_worst           texture_worst         perimeter_worst
##                       0                       0                       0
##              area_worst        smoothness_worst       compactness_worst
##                       0                       0                       0
##         concavity_worst    concave.points_worst          symmetry_worst
##                       0                       0                       0
## fractal_dimension_worst
##                       0
```

We now have removed the 1st coloumn "id" and the 33rd coloumn "X" as they appear irrelevant to our prediction. We have also checked that there are no missing values in the dataset.

Some models such as naive bayes do not work well with highly-correlated variables as they assume the predictor variables are independent with each other. Therefore, we will check if the variables of the dataset are highly correlated and will remove them if their correlation coefficients are higher than 0.9 or lower than -0.9.

```
# Plot the correlation among variables
corrplot(cor(data[,2:31]) , main=" Corrplot" , method = "circle" , type = "upper")
```



```
# Identify variables with correlation coefficient higher than 0.9 or lower than -0.9
to_drop_col <- findCorrelation(cor(data[,2:31]), cutoff=0.9)

# Adjust the result by one column shift
to_drop_col <- to_drop_col + 1

# Remove highly correlated variables
new_data <- data[,-to_drop_col]

# Cross-check if highly correlated variables have been removed
findCorrelation(cor(new_data[,2:21]), cutoff=0.9)
```

```
## integer(0)
```

Now, we are going to divide the dataset into training (80%) and testing (20%) datasets.

```
###################################
# Create training and testing sets
```

```
###################################

# Divide the data set into training (80%) and testing (20%) sets
set.seed(1234, sample.kind="Rounding")
```

```
## Warning in set.seed(1234, sample.kind = "Rounding"): non-uniform 'Rounding'
## sampler used
```

```
index <- createDataPartition(new_data$diagnosis, times=1, p=0.8, list = FALSE)
train <- new_data[index, ]
test <- new_data[-index, ]
```

Data Analysis - Modelling Approach

In the following, we will train a naive bayes model, logistic regression model, k-nearest neighbor model and random forest model.

```
# Cross validatin with 10 folds
tc <- trainControl(method="cv", number = 10, classProbs=TRUE, summaryFunction = twoClassSummary)
```

Naive Bayes Model

```
#################################
# Naive bayes model
#################################

# Train a naive bayes model
naiveb_model <- train(diagnosis~.,
                      train,
                      method="nb",
                      metric = "ROC",
                      preProcess=c('center','scale'),
                      trControl=tc)

# Predict testing set
naiveb_pred <- predict(naiveb_model, test)

# summarize results (set positive as "M" so that the sensitivity is correct)
naiveb_result <- confusionMatrix(naiveb_pred, test$diagnosis, positive = "M")
naiveb_result
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##          B 67  3
##          M  4 39
##
##                Accuracy : 0.9381
##                  95% CI : (0.8765, 0.9747)
##     No Information Rate : 0.6283
##     P-Value [Acc > NIR] : 1.718e-14
##
##                   Kappa : 0.868
```

```
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9286
##             Specificity : 0.9437
##          Pos Pred Value : 0.9070
##          Neg Pred Value : 0.9571
##              Prevalence : 0.3717
##          Detection Rate : 0.3451
##    Detection Prevalence : 0.3805
##       Balanced Accuracy : 0.9361
##
##        'Positive' Class : M
##
```

Logistic Regression Model

```r
#################################
# Logistic regression model
#################################

# Train a logistic regression model
glm_model <- train(diagnosis~.,
                      train,
                      method="glm",
                      metric = "ROC",
                      preProcess=c('center','scale'),
                      trControl=tc)

# Predict testing set
glm_pred <- predict(glm_model, test)

# summarize results (set positive as "M" so that the sensitivity is correct)
glm_result <- confusionMatrix(glm_pred, test$diagnosis, positive = "M")
glm_result
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##          B 69  1
##          M  2 41
##
##                Accuracy : 0.9735
##                  95% CI : (0.9244, 0.9945)
##     No Information Rate : 0.6283
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9434
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9762
##             Specificity : 0.9718
##          Pos Pred Value : 0.9535
##          Neg Pred Value : 0.9857
##              Prevalence : 0.3717
##          Detection Rate : 0.3628
##    Detection Prevalence : 0.3805
##       Balanced Accuracy : 0.9740
##
##        'Positive' Class : M
##
```

K-nearest Neighbor Model

```
################################
# K-nearest neighbor model
################################

# Train a KNN model
knn_model <- train(diagnosis~.,
                      train,
                      method="knn",
                      metric = "ROC",
                      preProcess=c('center','scale'),
                      tuneLength=10,
                      trControl=tc)

# Predict testing set
knn_pred <- predict(knn_model, test)

# summarize results (set positive as "M" so that the sensitivity is correct)
knn_result <- confusionMatrix(knn_pred, test$diagnosis, positive = "M")
knn_result
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##          B 71  3
##          M  0 39
##
##                Accuracy : 0.9735
##                  95% CI : (0.9244, 0.9945)
##     No Information Rate : 0.6283
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9423
##
##  Mcnemar's Test P-Value : 0.2482
##
##             Sensitivity : 0.9286
##             Specificity : 1.0000
##          Pos Pred Value : 1.0000
##          Neg Pred Value : 0.9595
##              Prevalence : 0.3717
##          Detection Rate : 0.3451
##    Detection Prevalence : 0.3451
##       Balanced Accuracy : 0.9643
##
##        'Positive' Class : M
##
```

Random Forest Model

```
################################
# Random forest model
################################

# Train a random forest model
rf_model <- train(diagnosis~.,
                      train,
                      method="rf",
                      metric = "ROC",
                      preProcess=c('center','scale'),
                      trControl=tc)

# Predict testing set
rf_pred <- predict(rf_model, test)

# summarize results (set positive as "M" so that the sensitivity is correct)
rf_result <- confusionMatrix(rf_pred, test$diagnosis, positive = "M")
rf_result
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##          B 67  3
##          M  4 39
##
##                Accuracy : 0.9381
##                  95% CI : (0.8765, 0.9747)
##     No Information Rate : 0.6283
##     P-Value [Acc > NIR] : 1.718e-14
##
##                   Kappa : 0.868
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9286
##             Specificity : 0.9437
##          Pos Pred Value : 0.9070
##          Neg Pred Value : 0.9571
##              Prevalence : 0.3717
##          Detection Rate : 0.3451
##    Detection Prevalence : 0.3805
##       Balanced Accuracy : 0.9361
##
##        'Positive' Class : M
##
```

Results

The results of each model developed above are summarized below:

```
#################################
# Results
#################################

# Summarize the confusion matrixes of each model
result_list <- list (naive_bayes = naiveb_result,
                     logistic_regression = glm_result,
                     KNN = knn_result,
                     random_forest = rf_result)
results <- sapply (result_list, function(x) x$byClass)

# Print the results in a table format
results %>% knitr::kable()
```

	naive_bayes	logistic_regression	KNN	random_forest
Sensitivity	0.9285714	0.9761905	0.9285714	0.9285714
Specificity	0.9436620	0.9718310	1.0000000	0.9436620
Pos Pred Value	0.9069767	0.9534884	1.0000000	0.9069767
Neg Pred Value	0.9571429	0.9857143	0.9594595	0.9571429
Precision	0.9069767	0.9534884	1.0000000	0.9069767
Recall	0.9285714	0.9761905	0.9285714	0.9285714
F1	0.9176471	0.9647059	0.9629630	0.9176471
Prevalence	0.3716814	0.3716814	0.3716814	0.3716814
Detection Rate	0.3451327	0.3628319	0.3451327	0.3451327
Detection Prevalence	0.3805310	0.3805310	0.3451327	0.3805310
Balanced Accuracy	0.9361167	0.9740107	0.9642857	0.9361167

```
# Identify the best results for each metric in confusion matrix
best_results <- apply(results, 1, which.is.max)

# Match the best results with corresponding model
report <- tibble (metric = names(best_results),
                    best_model = colnames(results)[best_results],
                    value=mapply(function(x,y) {results[x,y]},
                    names(best_results),
                    best_results))
rownames(report)<-NULL

# Print the best model identified for each metric
report
```

```
## # A tibble: 11 x 3
##    metric               best_model          value
##    <chr>                <chr>               <dbl>
##  1 Sensitivity          logistic_regression 0.976
##  2 Specificity          KNN                 1
##  3 Pos Pred Value       KNN                 1
##  4 Neg Pred Value       logistic_regression 0.986
##  5 Precision            KNN                 1
##  6 Recall               logistic_regression 0.976
##  7 F1                   logistic_regression 0.965
##  8 Prevalence           KNN                 0.372
##  9 Detection Rate       logistic_regression 0.363
## 10 Detection Prevalence random_forest       0.381
## 11 Balanced Accuracy    logistic_regression 0.974
```

There has been discussion which metric, say accuracy, precision, recall or F1 score, we should use to select the "best model". There is no one-size-fit-all answer. **For our case on prediciting whether a breast mass cell is cancerous, undoubtedly the cost associated with false negative is high**. The consequence can be very serious for a patient where his/her cell is predicted as negative (benign) while it is actually positive (malignant). In this regard, **the sensitivity, which calculates how many of actual positives a model capture, would be more relevant in this case**. While false positives appear to cause less serious consequence in our case, it does not mean costless. A healthy person diagnosed with cancer will result in stress and high medical costs. To this end, we should consider F1 score as well, which seek a balance between sensitivity and specificity.

Based on the result table above, the **best model should be logistic regression model** which has the highest sensitivity and F1 score.

Conclusion

In this project, We have developed four machine learning models to predict classification of a breast mass cell as "benign" or "malignant". Then, we have discussed which metric we should use to select the best model. Finally, we have selected logistic regression model as the most optimal one given its good sensitivity and F1 score. To further improve our prediction, we can in fact build more models such as neutral network and support vector machine to explore if there are any better models than the one we chose.

This kind of classification prediction will have a wide use across industries, such as prediciting no-shows for medical appointments, spam emails or fradulent transactions.