# Final Project Report
# Breast Cancer Classification

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*27th April 2020*

# Business Understanding

## Business Problem

Breast cancer is the top cancer in women both in the developed and the developing world. The incidence of breast cancer is increasing in the developing world due to increase life expectancy, increase urbanization and adoption of western lifestyles. Although some risk reduction might be achieved with prevention, these strategies cannot eliminate the majority of breast cancers that develop in low- and middle-income countries where breast cancer is diagnosed in very late stages. Therefore, early detection in order to improve breast cancer outcome and survival remains the cornerstone of breast cancer control. It is practically impossible for doctors to look at the data of each patient for breast cancer prediction. Thus, the business problem here is, to automate the task of classify the patients into 2 groups – malignant and benign for breast cancer, so that the doctors would only have to cross check the data about those patients who are classified as malignant for breast cancer.

## Dataset

For this problem, we will be using Breast Cancer Wisconsin (Diagnostic) Data Set provided by UCI Machine Learning Repository. Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image.

This data set is created by Dr. William H. Wolberg from University of Wisconsin, W. Nick Street from University of Wisconsin and Olvi L. Mangasarian from University of Wisconsin.

Attribute Information:

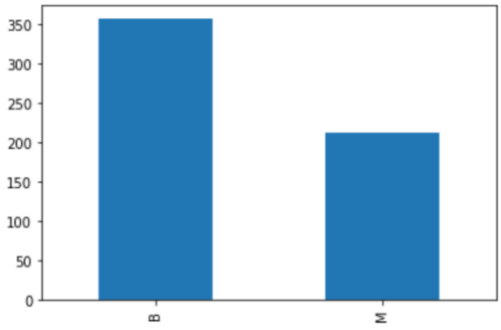
- Link to the data set: https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+%28Diagnostic%29
- Data Set Characteristics: Multivariate
- Number of attributes: 32
- Number of missing values: 0
- Class distribution: 357 benign, 212 malignant
- Target Variable: The diagnosis of breast tissues (M = malignant, B = benign)

## Proposed Analytics Solution

We can train machine model on the previous data about the patients who had and didn't have breast cancer, so that it learns to classify the new patient based upon his or her data. This will help in early diagnosis of breast cancer which can improve the chances of patients getting good treatment from the beginning and thus increasing chances of their survival.

# Data Exploration and Preprocessing

## Distribution of the target variable




Data Quality Report

| | feature | count | missing % | unique values | mean | std | min | Q1 | median | Q3 | max | IQR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | radius_mean | 569 | 0.000000 | 456 | 14.127292 | 3.524049 | 6.981000 | 11.700000 | 13.370000 | 15.780000 | 28.110000 | 4.080000 |
| 1 | texture_mean | 569 | 0.000000 | 479 | 19.289649 | 4.301036 | 9.710000 | 16.170000 | 18.840000 | 21.800000 | 39.280000 | 5.630000 |
| 2 | perimeter_mean | 569 | 0.000000 | 522 | 91.969033 | 24.298981 | 43.790000 | 75.170000 | 86.240000 | 104.100000 | 188.500000 | 28.930000 |
| 3 | area_mean | 569 | 0.000000 | 539 | 654.889104 | 351.914129 | 143.500000 | 420.300000 | 551.100000 | 782.700000 | 2501.000000 | 362.400000 |
| 4 | smoothness_mean | 569 | 0.000000 | 474 | 0.096360 | 0.014064 | 0.052630 | 0.086370 | 0.095870 | 0.105300 | 0.163400 | 0.018930 |
| 5 | compactness_mean | 569 | 0.000000 | 537 | 0.104341 | 0.052813 | 0.019380 | 0.064920 | 0.092630 | 0.130400 | 0.345400 | 0.065480 |
| 6 | concavity_mean | 569 | 0.000000 | 537 | 0.088799 | 0.079720 | 0.000000 | 0.029560 | 0.061540 | 0.130700 | 0.426800 | 0.101140 |
| 7 | concave points_mean | 569 | 0.000000 | 542 | 0.048919 | 0.038803 | 0.000000 | 0.020310 | 0.033500 | 0.074000 | 0.201200 | 0.053690 |
| 8 | symmetry_mean | 569 | 0.000000 | 432 | 0.181162 | 0.027414 | 0.106000 | 0.161900 | 0.179200 | 0.195700 | 0.304000 | 0.033800 |
| 9 | fractal_dimension_mean | 569 | 0.000000 | 499 | 0.062798 | 0.007060 | 0.049960 | 0.057700 | 0.061540 | 0.066120 | 0.097440 | 0.008420 |
| 10 | radius_se | 569 | 0.000000 | 540 | 0.405172 | 0.277313 | 0.111500 | 0.232400 | 0.324200 | 0.478900 | 2.873000 | 0.246500 |
| 11 | texture_se | 569 | 0.000000 | 519 | 1.216853 | 0.551648 | 0.360200 | 0.833900 | 1.108000 | 1.474000 | 4.885000 | 0.640100 |
| 12 | perimeter_se | 569 | 0.000000 | 533 | 2.866059 | 2.021855 | 0.757000 | 1.606000 | 2.287000 | 3.357000 | 21.980000 | 1.751000 |
| 13 | area_se | 569 | 0.000000 | 528 | 40.337079 | 45.491006 | 6.802000 | 17.850000 | 24.530000 | 45.190000 | 542.200000 | 27.340000 |
| 14 | smoothness_se | 569 | 0.000000 | 547 | 0.007041 | 0.003003 | 0.001713 | 0.005169 | 0.006380 | 0.008146 | 0.031130 | 0.002977 |
| 15 | compactness_se | 569 | 0.000000 | 541 | 0.025478 | 0.017908 | 0.002252 | 0.013080 | 0.020450 | 0.032450 | 0.135400 | 0.019370 |
| 16 | concavity_se | 569 | 0.000000 | 533 | 0.031894 | 0.030186 | 0.000000 | 0.015090 | 0.025890 | 0.042050 | 0.396000 | 0.026960 |
| 17 | concave points_se | 569 | 0.000000 | 507 | 0.011796 | 0.006170 | 0.000000 | 0.007638 | 0.010930 | 0.014710 | 0.052790 | 0.007072 |
| 18 | symmetry_se | 569 | 0.000000 | 498 | 0.020542 | 0.008266 | 0.007882 | 0.015160 | 0.018730 | 0.023480 | 0.078950 | 0.008320 |
| 19 | fractal_dimension_se | 569 | 0.000000 | 545 | 0.003795 | 0.002646 | 0.000895 | 0.002248 | 0.003187 | 0.004558 | 0.029840 | 0.002310 |
| 20 | radius_worst | 569 | 0.000000 | 457 | 16.269190 | 4.833242 | 7.930000 | 13.010000 | 14.970000 | 18.790000 | 36.040000 | 5.780000 |
| 21 | texture_worst | 569 | 0.000000 | 511 | 25.677223 | 6.146258 | 12.020000 | 21.080000 | 25.410000 | 29.720000 | 49.540000 | 8.640000 |
| 22 | perimeter_worst | 569 | 0.000000 | 514 | 107.261213 | 33.602542 | 50.410000 | 84.110000 | 97.660000 | 125.400000 | 251.200000 | 41.290000 |
| 23 | area_worst | 569 | 0.000000 | 544 | 880.583128 | 569.356993 | 185.200000 | 515.300000 | 686.500000 | 1084.000000 | 4254.000000 | 568.700000 |
| 24 | smoothness_worst | 569 | 0.000000 | 411 | 0.132369 | 0.022832 | 0.071170 | 0.116600 | 0.131300 | 0.146000 | 0.222600 | 0.029400 |
| 25 | compactness_worst | 569 | 0.000000 | 529 | 0.254265 | 0.157336 | 0.027290 | 0.147200 | 0.211900 | 0.339100 | 1.058000 | 0.191900 |
| 26 | concavity_worst | 569 | 0.000000 | 539 | 0.272188 | 0.208624 | 0.000000 | 0.114500 | 0.226700 | 0.382900 | 1.252000 | 0.268400 |
| 27 | concave points_worst | 569 | 0.000000 | 492 | 0.114606 | 0.065732 | 0.000000 | 0.064930 | 0.099930 | 0.161400 | 0.291000 | 0.096470 |
| 28 | symmetry_worst | 569 | 0.000000 | 500 | 0.290076 | 0.061867 | 0.156500 | 0.250400 | 0.282200 | 0.317900 | 0.663800 | 0.067500 |
| 29 | fractal_dimension_worst | 569 | 0.000000 | 535 | 0.083946 | 0.018061 | 0.055040 | 0.071460 | 0.080040 | 0.092080 | 0.207500 | 0.020620 |

## Missing Values

There are no missing values in the data.

```
[17]: data.isnull().sum().sum()

Out[17] 0
```

## Normalization

Some classifiers require normalized data to work on. We have performed minmax normalization for each feature of the data set except class variable. We have used MinMaxScaler from the sklearn's preprocessing package.
*Note: We will be feeding normalized data to all classifiers except Random Forest Classifier.*

## Feature Selection and Transformations

To avoid the overfitting caused by the curse of dimensionality, we have performed feature selection. In the original data set, there are total 32 features. After removing the Unnamed:32 feature which doesn't have any values, there are still 31 features. We have used chi2 test to select k=10 best features.
These are the 10 best features selected after ch2 test. There is off-course class variable 'diagnosis' with us.

```
Out[52] array(['radius_mean', 'texture_mean', 'perimeter_mean', 'area_mean',
       'perimeter_se', 'area_se', 'radius_worst', 'texture_worst',
       'perimeter_worst', 'area_worst'], dtype=object)
```

We have mapped our class variable – diagnosis (M, B) into 0 and 1.

# Model Selection and Evaluation

## Evaluation Metrics

In this problem, precision is the most important metric. Other important metrics are f1 score, accuracy and recall. If 2 models are having the same accuracy, we would select the one with the higher precision as there shouldn't be any patient who has cancer and our model classifies him/her as malignant for breast cancer.

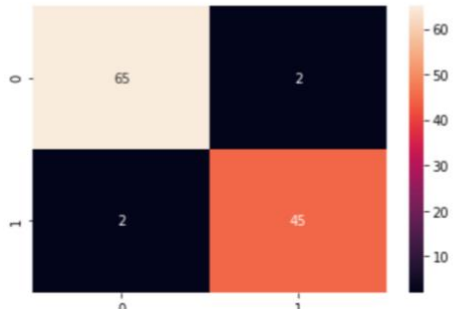
## Models

We have developed at least 1 model from each category of supervised learning algorithms.

**Information Based Learning:** Random Forest Classifier
We have built Random Forest Classifier with criterion='gini', number of estimators=1000, max_depth=3, random_state=0, n_jobs=-1.

```
Accuracy on test set is 0.9649122807017544
f1 score on test set is 0.9574468085106385
Precision on test set is 0.9574468085106383
Recall on test set is 0.9574468085106383
```

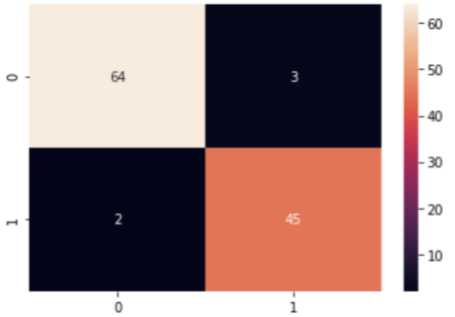
```
<matplotlib.axes._subplots.AxesSubplot at 0x7fa7d3d62748>
```




**Error Based Learning:** SVM, Logistic Regression
1. **SVM**
These are the results that SVM classifier gave on the test set.

```
Accuracy on test set is 0.956140350877193
f1 score on test set is 0.9473684210526315
Precision on test set is 0.9375
Recall on test set is 0.9574468085106383
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fa7d45fc080>
```

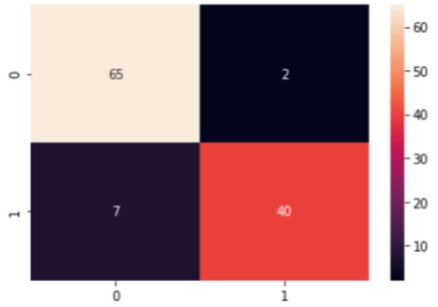


2. **Logistic Regression**

These are the results that Logistic Regression classifier gave on the test set.

```
Accuracy on test set is 0.9210526315789473
f1 score on test set is 0.898876404494382
Precision on test set is 0.9523809523809523
Recall on test set is 0.851063829787234
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fa7d38aeb38>
```

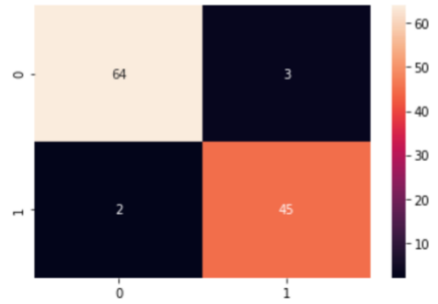



**Similarity Based Learning:** kNN Classifier

We have built kNN classifier with k=19. These are the results that kNN classifier gave on the test set.

```
Accuracy on test set is 0.956140350877193
f1 score on test set is 0.9473684210526315
Precision on test set is 0.9375
Recall on test set is 0.9574468085106383
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fa7d34497b8>
```

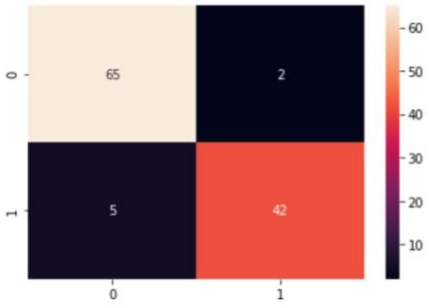



**Probability Based Learning:** Naïve Bayes Classifier

We built Naïve Bayes classifier. These are the results that Naïve Bayes classifier gave on the test set.

```
Accuracy on test set is 0.9385964912280702
f1 score on test set is 0.9230769230769231
Precision on test set is 0.9545454545454546
Recall on test set is 0.8936170212765957
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7fa7d32e9e10>
```



## Sampling and Evaluation Settings

We divided the entire data set into 3 parts – Training set, Validation set and Test set. Test is 20% of the entire data set, train set is 64% of the entire data set and validation set is 16% of the entire data set.
We performed cross-validation to make sure that our models aren't overfitting.

## Evaluation

Following is the table for comparing the evaluation metrics of all the models that we have built.

| | Accuracy | f1 score | Precision | Recall |
|---|---|---|---|---|
| **RandomForest** | 0.964912 | 0.957447 | 0.957447 | 0.957447 |
| **SVM** | 0.956140 | 0.947368 | 0.937500 | 0.957447 |
| **LogisticRegression** | 0.921053 | 0.898876 | 0.952381 | 0.851064 |
| **kNN** | 0.956140 | 0.947368 | 0.937500 | 0.957447 |
| **Naive Bayes** | 0.938596 | 0.923077 | 0.954545 | 0.893617 |

As discussed earlier, with all things being equal, the model that gives high precision is best choice for the breast cancer classification problem. Thus, Random Forest classifier is the best of model.

# Results and Conclusion

As discussed earlier, precision is the most important metric for evaluation in this task. Other very important metrics for evaluation are f1 score, accuracy and recall.

| | Accuracy | f1 score | Precision | Recall |
|---|---|---|---|---|
| **RandomForest** | 0.964912 | 0.957447 | 0.957447 | 0.957447 |

Random Forest classifier outperforms all other models in terms of precision, f1 score, accuracy and recall. Thus, we propose this model for this task.

The Early detection in order to improve breast cancer outcome and survival remains the cornerstone of breast cancer control. The proposed analytics model – Random Forest classifier seems to be promising model for this task after carefully comparing it with other models based on the selected metrics for evaluation.

Therefore, health care practitioners can make use of this model to classify patients into malignant and benign for breast cancer. After getting classification results from the model, they themselves can check those data to make sure it is correctly classified.