Breast Cancer Detection Using Machine Learning



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Abstract Through studies and statistics, it has been found that these days, breast cancer is the most common cancer leading to frequent deaths among women. Early screening and subsequent treatment can raise the chances of survival. Through this paper, we aim to demonstrate the ability to detect breast cancer cases using MRI scan data by analyzing the given data with machine learning algorithms. Using machine learning, we hope to ease the process of cancer detection in the hospitals so the patient can be afforded the right treatment as soon as possible before the situation can become critical. It also opens the door toward new possibilities in cancer detection for other different types of cancers as well as other diseases by use of machine learning in medical science, where detection using conventional means is usually laborious and time-taking.

1 Introduction

During the past years, doctors have classified breast cancer into various subtypes. In 2020, there were 2.3 million women diagnosed with breast cancer and 685,000 deaths globally. At the end of 2020, there were 7.8 million women alive who were diagnosed with breast cancer in the past 5 years. According to GLOBOCAN, breast cancer is the predominant cancer in women, making up to 25.1% of all cancers. There has been a significant decline in the amount of cases of breast cancer because of improvement in the medical sector with the help of advanced technology and software. Over a period of time, machine learning has helped a lot in improving the accuracy of detection of breast cancer in early stages. Breast cancer is more difficult and costly to treat as it reaches upper stages, hence, proper machinery and technology for detection and treatment are called for. This paper lays out a machine learning algorithm that helps to detect breast cancer in women efficiently and with great accuracy.

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2 Related Works

This section gives the review of literature work in the field of "Breast cancer detection using machine learning." Multiple sources were reviewed by the authors for the literature which have been referred for the analysis of breast cancer using machine learning. Further, the authors reviewed datasets from reliable sources for testing purposes of the methods reviewed. The most popular methods [1] of breast cancer detection, namely Naive Bayes classifier, K-nearest neighbors (KNN) [2], logistic regression, decision tree classifier, support vector machine (SVM) classifier [3] and random forest classifier [4, 5], which are given in Table 1.

3 Proposed Methodology

The purpose of this work is to analyze the dataset using random forest classifier, logistic regression and decision tree classifier and compare the efficiency of the respective algorithms in terms of accuracy in detecting cancer in the subject.

3.1 Experimental Setup

The program was made using Python programming language on Jupyter Notebook application. We have used the Wisconsin Breast Cancer datasets [14] from the UCI machine learning repository for our analysis regarding the scope of our work.

We imported NumPy library for working with data using arrays. We imported Pandas library to analyze, clean and manipulate the given dataset. We imported Matplotlib and Seaborn libraries for data visualization of the statistics. We made use of Sclearn which is a machine learning library for Python to import and implement logistic regression, random forest classifier and decision tree classifier algorithms on the given data.

Logistic Regression: It uses a logistic function to for modeling data using dependent and independent variable. It is used for binary data and it is efficient to train. Logistic regression algorithm performs efficiently when the given dataset is separable linearly.

Decision Tree Classifier: A decision tree consists of decision nodes and leaf nodes. It begins with the root node and finds the best attribute using attribute selection measure so as to divide it into multiple subsets. From these, a decision tree node is generated. The process repeats recursively until no further classification of nodes is possible. It makes predictions from all types of outcomes.

Random Forest Classifier: It uses the functionality of a group of decision trees. It is an ensemble algorithm. Individual trees are generated by attribute selection indication. Greater number of trees lead to computation of a better average and thus

S. No	Study	Technique used	Strength	Weakness		
1	Tahmooresi et al. [6]	Artificial neural network (ANN) Support vector machine (SVM) K-nearest neighbors (KNN)	SVM is a performant algorithm and produces accurate results	Large datasets not suitable for SVM algorithm		
2	Nallamala et al. [7]	NumPy Pandas	Powerful libraries for representation and manipulation of data	None		
3	Bazazeh et al. [8]	Random forest (RF) Bayesian networks (BN)	Stable and unbiased algorithm producing accurate results	Heavy use of computational resources		
4	Agarap et al [9]	GRU-SVM Linear regression	Used for predictive analysis	Performs poorly in nonlinear relationships between variables		
5	Vaka, Soni et al. [10]	R-CNN (convolutional neural networks) classifier Bidirectional recurrent neural networks (HA-BiRNN)	Deep learning models with unsupervised feature extraction	Computationally taxing and big dataset required for training		
6	Chaurasia et al. [11]	Sequential minimal optimization (SMO) BF tree	Resolves quadratic programming problem that arises during training of SVM	Necessary to solve QP scaling with number of SVMs		
7	Gayathri et al. [12]	Supervised, unsupervised, semi-supervised and reinforcement learning	Optimize performance in case of supervised algorithm and implement real-world problems	Preprocessing required. Computation time is vast for supervised algorithms		
8	Ganggayah et al. [13]	Support vector machine neural networks logistic regression	Outperforms most of the machine learning algorithms	Unpredictable output and computationally its very expensive		

 Table 1
 Literature work

increases the accuracy of the making predictions on the given dataset. It resolves the overfitting problem that arises with decision trees.

3.2 Feature Analysis

First up, the features are analyzed for their frequency count [15], and then, their pairwise correlation is computed. The code is given below.

```
In [1]: #This program detects breast cancer using data.
In [2]: #import libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
In [3]: #Load the data
df = pd.read_csv('data.csv')
In [4]: #count the number of rows and coloumns
df.shape
Out[4]: (569, 32)
```

The plot for the count of diagnosis for malignant (M) and benign (B) is shown in Fig. 1. The pairwise correlation is shown with the help of a heat map [15-17] as in Fig. 2.

```
In [8]: #get a count of Malignant (M) or Begnin(B) cells
df['diagnosis'].value_counts()
Out[8]: B 357
```

```
M 212
Name: diagnosis, dtype: int64
```

```
In [9]: #visualize the count
sns.countplot(df['diagnosis'], label = 'count')
```



Fig. 1 Frequency plot for two classes-malignant (M) and benign (B)

												-10
diagnosis -	100%	73%	42%	74%	71%	36%			78%	33%	-1%	-10
radius_mean -	73%	100%	32%	100%	99%	17%			82%	15%	-31%	- 0.8
texture_mean -	42%	32%	100%	33%	32%	-2%	24%	30%	29%	7%	-8%	
perimeter_mean -	74%	100%	33%	100%	99%	21%		72%	85%	18%	-26%	- 0.6
area_mean -	71%	99%	32%	99%	100%	18%			82%	15%	-28%	
smoothness_mean -	36%	17%	-2%	21%	18%	100%						- 0.4
compactness_mean -			24%				100%	88%	83%			- 0.2
concavity_mean -			30%	72%			88%	100%	92%	50%	34%	
concave points_mean -	78%	82%	29%	85%	82%		83%	92%	100%	46%	17%	- 0.0
symmetry_mean -	33%	15%	7%	18%	15%					100%	48%	
fractal_dimension_mean -	-1%	-31%	-8%	-26%	-28%			34%	17%	48%	100%	0.2
	diagnosis -	- radius_mean -	texture_mean _	perimeter_mean -	area_mean -	smoothness_mean -	compactness_mean -	concavity_mean -	concave points_mean -	symmetry_mean -	fractal_dimension_mean -	

Fig. 2 Heat map plot for pairwise correlation among features

```
In [11]: #Encode the catogorical data values
from sklearn.preprocessing import LabelEncoder
labelencoder_Y = LabelEncoder()
df.iloc[:,1] = labelencoder_Y.fit_transform(df.iloc[:,1].values)
In [12]: #Create a pair plot
sns.pairplot(df.iloc[:,1:8], hue = 'diagnosis')
```

In [13]: #get the correlation of the cloumns df.iloc[:, 1:12].corr()

Out[39]:									
		diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean	compactness_mean	concevity_mean
1	diagnosis	1.000000	0.730029	0.415185	0.742636	0.708984	0.358560	0.596534	0.696360
	radius_mean	0.730029	1.000000	0.323782	0.997855	0.987357	0.170581	0.506124	0.676764
	texture_mean	0.415185	0.323782	1.000000	0.329533	0.321086	-0.023389	0.236702	0.302418
	perimeter_mean	0.742636	0.997855	0.329533	1.000000	0.986507	0.207278	0.556936	0.716136
	area_mean	0.708984	0.987357	0.321086	0.986507	1.000000	0.177028	0.498502	0.685983
	smoothness_mean	0.358560	0.170581	-0.023389	0.207278	0.177028	1.000000	0.659123	0.521984
	compactness_mean	0.596534	0.506124	0.236702	0.556936	0.498502	0.659123	1.000000	0.883121
	concavity_mean	0.696360	0.676764	0.302418	0.716136	0.685983	0.521984	0.883121	1.000000
	concave points_mean	0.776614	0.822529	0.293464	0.850977	0.823269	0.553695	0.831135	0.921391
	symmetry_mean	0.330499	0.147741	0.071401	0.183027	0.151293	0.557775	0.602641	0.500667

```
In [14]: #Visualize the correlation
    plt.figure(figsize = (10,10))
    sns.heatmap(df.iloc[i, 1:12].corr(), annot = True, fmt='.0%')
```

The classification models are constructed. After training the model with the given algorithms, we computed accuracy and confusion matrix from Sclearn library to ascertain the performance of the algorithms on the constructed model.

```
In [15]: #split the data set into independent (X) and dependent (Y) data sets
    X = df.iloc[:, 2:31].values
    Y = df.iloc[:, 2:31].values
    Y = df.iloc[:, 2:31].values
    In [16]: #split the data set into 80% training and 20% testing
    from sklearn.model_selection import train_test_split
    X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size = 0.20, random_state=0)
In [17]: #Scale the data (Feature Scaling)
    from sklearn.preprocessing import StandardScaler
    sc = StandardScaler()
    X_train = sc.fit_transform(X_train)
    X_test = sc.fit_transform(X_train)
    X_test = sc.fit_transform(X_test)
In [18]: #Create a function for the models
    def models(X_train, Y_train):
    #Logistic Regression
        log = LogisticRegression(random_state = 0)
        log.fit(X_train, Y_train)
    #Readom forest classifier(criterion= 'entropy', random_state = 0)
        tree.fit(X_train, Y_train)
    #Readom forest classifier
        from sklearn.ensemble import RandomForestClassifier
        from stlearn.ensemble import to the training data
        print('Logistic Regression fields:fiter(regression = 0)
        forest.fit(X_train, Y_train)
        #Print the models accuracy on the training daccuracy ', log.score(X_train, Y_train))
        print('Logistic Regression gives a Training Accuracy ', forest.score(X_train, Y_train))
        print('Reandom forest Classifier gives a Training Accuracy ', forest.score(X_train, Y_train))
        print('Reandom forest Classifier gives a Training Accuracy ', forest.score(X_train, Y_train))
        print('Reandom forest Classifier gives a Training Accuracy ', forest.score(X_train, Y_train))
        print('Reandom forest Classifier gives a Training Accuracy ', forest.score(X_train, Y_train))
        print('Reandom forest Classifier gives a Training Accuracy ', forest.score(X_train, Y_train))
        print('Reandom forest Classifier gives a Training Accuracy ', forest.score(X_train, Y_train))
        print('Reandom forest Classifier gives a Training Accuracy
```

```
In [19]: #Getting all of the models
    model = models(X_train, Y_train)
```

We calculated the accuracy of each model using a confusion matrix:

```
TrPoTrue PositiveTrNeTrue NegativeFaNeFalse NegativeFaPoFalse positive
```

Accuracy = (TrPo + TrNe)/(TrPo + TrNe + FaNe + FaPo)

```
In [20]: #test model accuracy on test data on confussion matrix
from sklearn.metrics import confusion_matrix
for i in range(len(model)):
    print('Model ', i)
    cm = confusion_matrix(Y_test, model[i].predict(X_test))
    TP = cm[0][0]
    TN = cm[1][1]
    FN = cm[1][0]
    FP = cm[0][1]
    print(cm)
    print('testing accuracy =',(TP + TN ) / (TP + TN + FN + FP ))
    print()
```

Fig. 3 Confusion matrix for	TrPo = 66	FaPo = 1
logistic regression	FaNe = 3	TrNe = 44
Fig. 4 Confusion matrix for	TrPo = 64	FaPo = 3
decision tree	FaNe = 4	TrNe = 43
Fig. 5 Confusion matrix for	TrPo = 67	FaPo = 0
random forest classifier	FaNe = 3	TrNe = 44

4 Results and Discussions

We were successful in detection of breast cancer in patients through the use of machine learning algorithms. To assess the performance of all the algorithms, we used a confusion matrix to provide the best evaluation. We took 80% of the dataset to train each of the model and 20% of the dataset to test the precision of each model.

Logistic regression algorithm has an accuracy of 96.49%, while the decision tree algorithm has an accuracy of only 93.85%. However, the best results were shown by random forest classifier algorithm with an accuracy of 97.36%. Hence, we are able to tell with high accuracy if the cancer is benign or malignant in the subject (Figs. 3, 4 and 5).

5 Conclusions

Breast cancer is one of the most predominant cancers found in women. Detection at an early stage and diagnosis of this disease can save lives and the patient can undergo suitable treatment. Machine learning has vast applications in the modern healthcare system. One such use of machine learning is detection and diagnosis of diseases that has been thoroughly discussed in this paper. Integration of machine learning with medical databases and devices will make healthcare system more efficient and help in better organization of data. Healthcare industries such as tempus are using machine learning on their clinical data to provide personalized treatments for patients. Hence, an increased adoption of machine learning technology is expected in medical fields in the future.

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