Classification for Diagnosis of Breast Cancer Using Machine Learning Techniques with Hyperparameter Tuning

K. K. Sreekala and Jayakrushna Sahoo

Abstract Breast cancer mortality has risen dramatically in recent years. However, early diagnosis and treatment may greatly reduce the risk of death. Cancer cells may spread from the breast to other portions of the body over the bloodstream arrangement. They will move early in the process, when the tumour is minor stage, or later in the process, when the tumour will be in major stage. The aim is to propose a method that allows use of supervised machine learning (ML) classifiers such as linear regression, Naive Bayes (NB), support vector machine (SVM) and multilayer perceptron (MLP) that classify the mammogram images as benign or Malignant. The hyperparameters scheme used for the classifiers was manually allocated in order to increase the classifier's accuracy and identify the cancer as benign or Malignant. The results show that by manually tuning the hyperparameters, all of the presented ML algorithms performed well on the classification task. In addition, the Wisconsin breast cancer (WBC) dataset was used in this analysis. The dataset was divided in the following way for the ML algorithms implement to classify the breast cancer: 60% for training and 40% for testing. The main purpose of this work is to compare multiple classifiers to discover the best classifier that provides better accuracy in breast cancer classification. The proposed model's output is evaluated using various parametric values such as precision, recall, sensitivity, and F-measure.

Keywords Machine learning classifier · Breast cancer · Classification · Benign or Malignant and hyperparameters

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1 Introduction

Healthcare is one of the most concerning fields in terms of data collection and processing. With the advent of the digital era and advancement in technology, a large amount of multidimensional data is generated about patients, which include clinical parameters, hospital resources, disease diagnostic details, patients' records and medical devices. The information about vast, voluminous and multidimensional data essentials to be processed and examined for the extraction of knowledge for effective decision-making. Cancer is the Malignant growth of cells, and it can take place in any part of the body. The malignant growth spreads and leads to crowding out of the normal cells and thereby making it difficult for the body to function [1–3]. Malignant growth of cells that is cancer cannot be categorized as a single disease. There are numerous sorts of malignant growth. It is not only one place that gets infected, but malignant growth can also occur in any internal organ and even in the blood cells.

Malignant growths are similar somehow or another, however, they are distinctive in the manners in which they develop and spread [4]. Our body functions with the aid of cells acting like building blocks. Trillions of cells in the body render shape, nutrition and energy to the body. Cells also carry out unique functions like holding on hereditary features and make copies of themselves by dividing itself into two or more cells and those daughter cells further divide into other cells. This process of cell division takes place as a part of a larger cell cycle. Cancer growth happens through the development of tumours or lumps. However, not all irregularities are malignant in nature. Doctors examine a bit of the tumour or lumps and find out whether it is Malignant or not. If it is not a Malignant growth, it is called benign. Apart from the development of tumours, there are a few malignancies, similar to leukaemia (disease of the blood), that develop in the platelets or different cells of the body not as tumours [5].

Data mining progress provides clients with methods to uncover new and unknown instances from large amounts of data. In the healthcare sector, the uncovered knowledge can be used to enhance the precision of diagnosis by medical service administrators and physicians, thus raising and lowering the level of caution. Awareness disclosure of data refers to 'the concealment of data, the retrieval of ambiguous and conceivable useful data' [6]. The aim of hypotheses in knowledge mining is to help people explore designs in data to boost their prosperity [7]. In the healthcare sector, data mining plays an important role in predicting illnesses. A data mining ideal is the forerunner of the forecast. The aftereffects of interventions were discussed in this article, and recommendations for future research were made. A health professional's diagnosis of breast cancer is not 100 per cent correct.

Furthermore, a precise definition of a malignant tumour may prevent patients from receiving appropriate treatment. As a consequence, the proper determination and assignment of breast carcinoma to benign and malignant sets are a widely discussed subject [8, 9]. ML approaches were commonly used in the centuries to identify breast carcinoma and to draw different notions from data patterns. Machine learning

is well-known for its use in the classification and simulation of breast cancer. It is a tool for detecting previously unknown regularities and trends in a variety of datasets. It integrates a wide variety of approaches for the revelation of rules, paradigms and relations in classes of data and creates a theory of these relations that can be used to decode new secret data [10]. Various artificial learnings [8–11], deep learning scheme [12, 13] and bio-inspired computation [14] approaches have been used in many medicinal prognoses in recent years. Despite the fact that many modalities have been shown, none of them can produce a 100% right and reliable answer. The doctors must read a vast quantity of imaging data, which limits accuracy. This technique is often time taking, and in particular cases, incorrectly senses the illness.

The remaining of this paper is followed as a literature review of earlier work is focussed in Sect. 2, proposed methodology is offered in Sect. 3, result and discussion of this proposed model are labelled in Sect. 4 and finally, the paper is finished in Sect. 5.

2 Literature Review

In this section, the literature is surveyed to recognize the state of the art and to identify the problem of breast cancer identification. Numerous researches work have been conducted on the identification of breast cancer with machine learning algorithms. But the researchers have applied different ML algorithms on different breast cancer data repositories and the performance of the proposed model with various ML algorithms varies based on the algorithm and the dataset used by different researchers.

The author [11] has projected a duo-phase-SVM was showed by combining a duo-phase clustering approach with an operative probabilistic SVM in order to analyze WBC Diagnosis and achieve a classification model accuracy of 99.10%. Unlike other existing schemes, this strategy can identify the figure of the masses and provide efficient analyzes for large bodies.

Kapil and Rana [12] have projected a weight improved DT technique as a modified DT technique and applied it on WBCD dataset obtained from the UCI. Using the Chi-square test, they discovered that they had ranked the each feature and hold the features that were relevant for this classification process. Their proposed technique achieved approximately 99 per cent accuracy on the WBCD dataset, whilst it achieved approximately 85–90% accuracy on the breast cancer dataset.

Banu and Subramanian [13] have emphasized the ML scheme such as NB practises for breast cancer prediction and labelled a comparison study on tree augmented NB, boosted augmented NB and Bayes belief network (BBN). The models were implemented using SAS-EM. In their work, they use the same common WBCD dataset. According to their findings, 91.7 and 94.11% accuracy were achieved using gradient boosting.

Yue et al. [14] have presented complete analyzes on SVM, ANNs, K-NNs and DT machine learning classifier model. By this model for application of medical data diagnosis to classification of breast cancer by evaluate the system to use WBC

diagnosis dataset. This study was conducted to combining the two neural network model as ANN architecture (DBNs-ANNs) and deep belief networks (DBNs, in this combination scheme provide the better classification results achieved of 99.68% of accuracy. On other hand, the SVM classification technique achieved a 99.10% of classification accuracy, when combined with the two-step clustering algorithm. They also looked at the ensemble technique, which used to implement SVM, NB and J48. The ensemble method achieved an accuracy of 97.13%.

For the breast cancer diagnosis, a variant of SVM [15] is introduced. There are different types of SVM used for performance evaluation in this article as NSVM, SSVM, LPSVM and LPSVM. The results of typical SVM are compared to those of other types of SVM. For training and testing, four-fold cross-validation is used. In the training phase, St-SVM achieves the highest accuracy, specificity and sensitivity of 97.71, 98.9 and 97.08%, correspondingly. In the testing phase, the highest accuracy of 96.55%, sensitivity of 98.24% and specificity of 96.55% attained by are and 97.14%, respectively.

3 Proposed Methodology

In this section, we discussed the proposed scheme of breast cancer classification and detection by using Wisconsin breast cancer dataset, the proposed scheme is showed in Fig. 1. In primary, the dataset is preprocess to eliminate the noise and irrelevant data from the entire data. Then preprocessed data are given to the feature selection procedure, in this section, we proposed the PCA feature selection model to select the proper feature for better classification result and reduce the computation time. Then, apply different ML model to classify the selected data. The different ML models such as multilayer perceptron, naïve Bayes, SVM and linear regression. In this classifier, we tune the classifier parameter to tune the classifier process to improve the learning rate of the classifier. In classification section, which significantly classify the data as benign or Malignant.

3.1 Dataset Description

In this study, WBC dataset is used for the breast cancer identification process. The dataset is accessible from UCI ML repository website as https://www.kaggle.com/uciml/breast-cancer-wisconsin-data. In the clump depth, benign cells appear to form monolayers, whilst cancerous cells often form multilayers [16]. Cancer cells, on the other hand, differ in size and structure in the standardization of cell size/shape. As a result, these criteria are useful in deciding whether or not the cells are cancerous. Normal cells tend to stay together in the case of marginal adhesion, whilst cancer cells tend to lose this capacity. As a result, lack of adhesion is a symptom of cancer. The scale of a single epithelial cell is linked to the previously described uniformity.

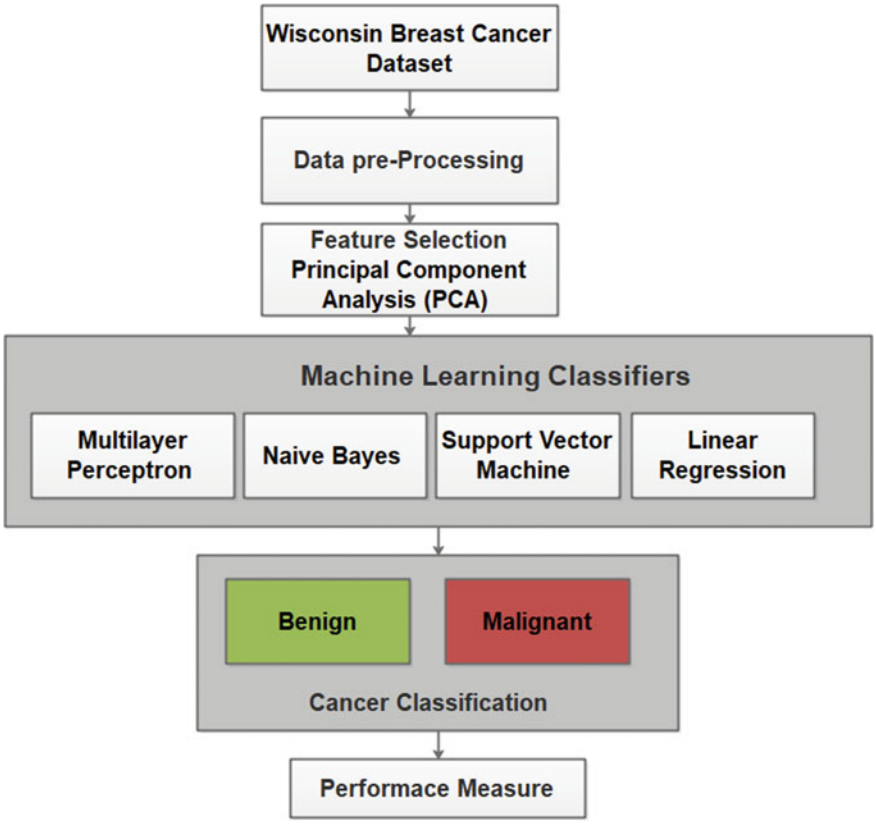

Fig. 1 Proposed method for breast cancer detection

Significantly, swollen epithelial cells may be Malignant cells. The word 'bare nuclei' refer to nuclei that are not enclosed by cytoplasm. These are commonly seen in benign tumours (Table 1).

In benign cells, the bland chromatin represents a 'texture' of the nucleus. The chromatin in cancer cells is coarser. Normal nucleoli are minor size structures that can be found in the nucleus. If the nucleolus is visible in normal cells, it is typically very thin. The nucleoli become more evident in cancer cells, and there are sometimes more of them. As a final stage, Mitoses is known as nuclear division plus cytokines, which result in the development of two identical descendant cells during prophase. It refers to the mechanism by which a cell splits and replicates. By measuring the number of mitoses, pathologists may assess the grade of cancer. Figure 2 depicts an extract from the dataset.

Table 1 WBC dataset attributes [14]

Attribute	Domain
Sample code number (SCN)	Id number
Clump thickness (CT)	1 to 10
Marginal adhesion (MA)	1 to 10
Uniformity of cell shape—(UCSh)	1 to 10
Single epithelial cell size (SECS)	1 to 10
Uniformity of cell size (UCS)	1 to 10
Bare nuclei—(BN) 1–10	1 to 10
Mitoses	1 to 10
Bland chromatin (BC)	1 to 10
Normal nucleoli (NN)	1 to 10
Class	2 as benign, 4 as Malignant

sample code number	clump thickness	uniformity of cell size	uniformity of cell shape	marginal adhesion	single epithelial cell size	bare nuclei	bland chromatin	normal nucleoli	mitoses	class
1000025	5	1	1	1	2	1	3	1	1	benign
1002945	5	4	4	5	7	10	3	2	1	benign
1015425	3	1	1	1	2	2	3	1	1	benign
1016277	6	8	8	1	3	4	3	7	1	benign
1017023	4	1	1	3	2	1	3	1	1	benign
1017122	8	10	10	8	7	10	9	7	1	malignant
1018099	1	1	1	1	2	10	3	1	1	benign
1018561	2	1	2	1	2	1	3	1	1	benign
1033078	2	1	1	1	2	1	1	1	5	benign
1033078	4	2	1	1	2	1	2	1	1	benign
1035283	1	1	1	1	1	1	3	1	1	benign
1036172	2	1	1	1	2	1	2	1	1	benign
1041801	5	3	3	3	2	3	4	4	1	malignant
1043999	1	1	1	1	2	3	3	1	1	benign
1044572	8	7	5	10	7	9	5	5	4	malignant
1047630	7	4	6	4	6	1	4	3	1	malignant
1048672	4	1	1	1	2	1	2	1	1	benign
1049815	4	1	1	1	2	1	3	1	1	benign
1050670	10	7	7	6	4	10	4	1	2	malignant
1050718	6	1	1	1	2	1	3	1	1	benign

Fig. 2 Breast cancer Wisconsin (BCW) dataset

3.2 Dataset Preprocessing

Data preprocessing is a salient step in data mining which deals with the renovation of raw data into a clean, precise and understandable format. Preprocessing activities involve but are not restricted to issues related to cleaning, transformation, mapping, reduction, organization and selection of data. Amongst all the issues, feature selection is of prime importance. To evade inappropriate task of significance, the dataset was uniform using Eq. 1.

$$z = X - \mu\sigma \tag{1}$$

where X is identified as a feature to be standardized, mean value of the feature is specified as μ, and the standard deviation of the feature is represented as σ. The preprocessing process was implemented using the code as below.

```
• from sklearn.preprocess import StandardScaler
• scaler = Standard Scaler()
• X = scaler.fit_transform(X)
```

3.3 Feature Selection

Choosing features are a significant phase in creating a classification model. To attain the better classification results of the model, it is beneficial to limit the sum of input attributes in a classifier. Instead of using the whole attribute collection, a few dominant features that are good enough to execute the classification task with the same or much better precision is used. Choosing a feature subset not only improves precision, but it also cuts computation time and model complexity [17].

Principal Component Analysis (PCA).

PCA is a technique for evaluating principal components by using them to perform information-based adjustments, often using only the main principal components and skipping the respite. Knowledge may be extracted from a high-dimensional (include) space by predicting it into a low-dimensional subspace. It attempts to preserve the fundamental parts with greater data diversity whilst removing redundant parts with less diversity.

This paper proposes function selection methods based on principal component analysis. The benefits of fit test decides, if an empirical frequency distribution corresponds to a theoretical frequency distribution. PCA is a scientific technique that employs an orthogonal transformation to turn a series of potentially clustered measurements into a set of values of linearly uncorrelated variables known as PCA. The amount of PCA is equal to or less than the number of initial variables.

Cell radius, compactness, concavity, perimeter, area and concave points mean values can be used to define cancer. Higher values of these parameters are associated with Malignant tumours. ii) Mean texture, symmetry, smoothness, or fractal dimension values do not imply a preference for one diagnosis over another. There are no apparent large outliers in any of the histograms that need further cleaning. Table 2 shows the significance of the characteristics in determining whether tumours are malignant or benign.

Table 2 Feature importance

Features importance mean (%)	Importance (%)
Concavity	18.2823
Texture	3.8492
Symmetry	1.6371
Fractal dimension	0.9043
Area	17.3446
Smoothness	1.9023
Radius	11.5543
Perimeter	20.45614
Concave points	19.7067
Compactness	4.3632

3.4 Classification

Classification of diseases is a majorly focussed challenge in medical data mining. When it comes to breast cancer, the main concern is to categorize the occurrences into benign and Malignant cases with high accuracy. Several ML systems for classification of breast cancer data.

3.5 Linear Regression

Despite the fact that, there is an algorithm for the regression problem by using a ML scheme of linear regression classifier in this analysis. This was accomplished by setting a threshold for the contribution of Eq. 2, i.e. subjecting the regress and to Eq. 3.

$$h_\theta(x) = \sum_{i=0}^{n} \theta i \cdot xi + b \tag{2}$$

$$fh_\theta(x) = \begin{cases} 1h_\theta(x) \geq 0.5 \\ 0h_\theta(x) < 0.5 \end{cases} \tag{3}$$

The mean squared error (MSE) was used in Eq. 4 to calculate the loss of the model.

$$L(y, \theta, x) = 1/N \sum_{i=0}^{N} (y_1 - (\theta i \cdot x_i + b))2 \tag{4}$$

where y denotes the real class and (θ x + b) denotes the expected class. The SGD algorithm, which knows the constraints of Eq. 7, is used to minimize this deficit. The same loss minimization approach was used for Softmax regression and MLP.

3.6 Support Vector Machine

The SVM was designed specifically for binary classification. Its main goal is to find the best hyperplane $f(w, x) = w \cdot x + b$ for separating two groups in a given dataset with input features x R p and labels $yi + 1$ by resolving the guarded optimization problem in the SVM is derived below:

$$min1/pw^T w + \sum_{i=1}^{p} \xi i \tag{5}$$

$$s.t\, y'\, i\, (w \cdot x + b) \geq 1 - \xi i \tag{6}$$

$$\xi i \geq 0, i = 1, ..., p \tag{7}$$

where w^T w is identified as Manhattan norm, ξ represented as a cost function, its problem of unconstrained optimization is derived in the following as

$$\min\ 1/p\ w^T w\ +\ \sum\nolimits_{i=1}^{p} \max\ (0, 1 - y'i(w_i x_i\ +\ b)) \tag{8}$$

The predictor function is wx + b. Equation 9's target is known as the primitive form dilemma of L1-SVM with the regular hinge loss. The downside of L1-SVM is that it is not distinguishable, as opposed to its variant, L2-SVM:

$$\min\ 1/p\ ||\ w\ ||_2^2\ +\ C\ \sum\nolimits_{i=1}^{p} \max(0, 1 - y'i(w_i x_i\ +\ b))^2 \tag{9}$$

The L2-SVM delivers better stable outcomes than its L1 counterpart.

3.7 Multilayer Perceptron

The most commonly used for pattern recognition is MLP, which is known as a feedforward backpropagation neural network system. MLPs are supervised learning classifiers composed compressed a different layers that extract valuable information during learning and allocate modifiable weighting coefficients to input layer components. The preceding words are represented in Fig. 3. Weighted input is allocated to the input units, as well as the nodes in the hidden layer and the output specify the output in the first (forward) pass. The result is compared to the desired result. An

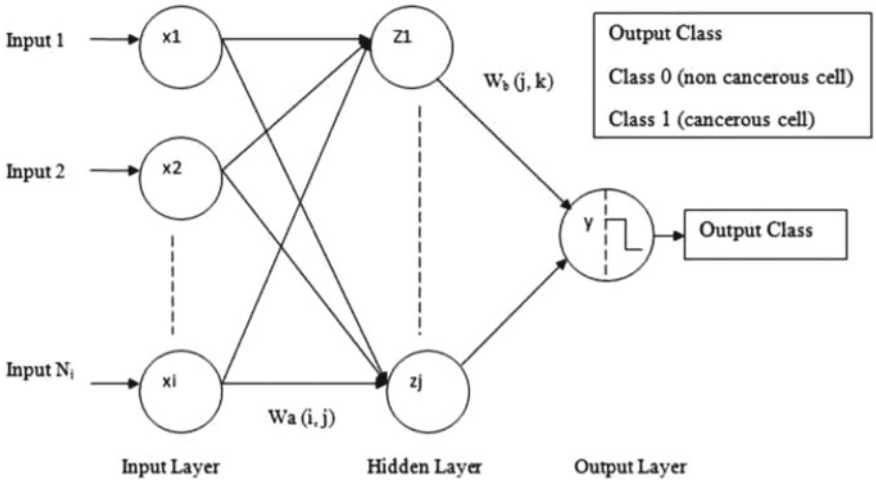

Fig. 3 Architecture of multilayer perception feedforward neural network

error signal is then returned, and the link weights are modified accordingly. During preparation, MLPs create a multidimensional space identified by the activation of secret nodes, in order to separate the three groups (Malignant or benign) as far as possible. The separating surface changes in response to the results.

3.8 Naive Bayes

Bayesian learning methods are important to the ML research for two reasons. First, Bayesian learning algorithms, such as the Naive Bayes classifier, that compute explicit probabilities for hypotheses, are amongst the most effective alternatives to certain kinds of learning problems. The Bayes theorem-based NB classifier is called as a probabilistic classifier. The Nave Bayes classifier provides probability approximations rather than forecasts. They measure the chance that a given example belongs to a given class for each class value. The Naive Bayes classifier has the advantage of having only a limited training data to approximate the parameters used for classification. It is presumed that the influence of an attribute rate on a given class is liberated of the other attributes' values.

4 Simulation Results and Analysis

In this simulation study, we conducted by evaluate the classification and identification of breast cancer by using WBC dataset. The experimentation was compiled by using a Python platform and further materials required as PC with 4 GB RAM Windows

Table 3 Hyperparameter tuning in machine learning model

Hyperparameter	SVM	MLP	NB	Linear regression
Batch size	128	128	128	128
Cell size	128	500	-	500
Dropout rate	1.0	0.5	-	-
Learning rate	0.01	0.001	0.01	0.01
Normal	L2	-	-	L1
Epochs	1500	1500	1500	1500

10. The performance of the machine learning classifier obtained and analysis by using different parameter as accuracy, precision recall and F-measure, which are mathematically expressed in following section. The choice of classifier is based on the percentage of correct prediction. There are at least three machine learning techniques which are generally used to calculate classifier accuracy. First one is to divide the whole dataset in two parts by 60:40 ratio for training and testing dataset. Table 3 demonstrations that the manually allocated the hyperparameters used for the machine learning algorithm.

4.1 Performance Measures

This proposed system in which different classifier performances is measure by using different parametric. The developed system is assessed using evaluation metrics such as TP, FP, TN, FN, sensitivity, precision, specificity, F-measure and accuracy.

- TP—Sum of normal sample is correctly categorized as noncancerous sample.
- TN—Sum of abnormal sample is correctly categorized as cancerous sample.
- FP—Sum of normal sample is wrongly categorized as cancerous sample.
- FN—Sum of abnormal sample is wrongly categorized as noncancerous sample.

Sensitivity

Sensitivity is also called as recall. Sensitivity is distinct as the percentage of sample with abnormal, whose output is positive, and it is calculated using the Eq. 10 as

$$Sensitivity = TP/(TP + FN) \tag{10}$$

Specificity

Specificity is defined as percentage of sample with normal, whose output is negative, and it is calculated using the Eq. 11 as

$$Specificity = TN/(TN + FP) \tag{11}$$

Classification accuracy

Classification accuracy is defined as the sum of correctly classified images, which are separated by the total sum of samples, and then, it is multiplied by 100 to turn it into a percentage. It is calculated using the Eq. 12 as

$$Classification Accuracy = (TP + TN)/(TP + FP + TN + FN) \quad (12)$$

Precision

Precision is distinct as the sum of true positives, which is divided by the number of TP and false positives, and it is calculated using the Eq. 13 as

$$Precision = TP/(TP + FP) \quad (13)$$

False positive rate

FPR is distinct as the sum of false positives, which is divided by the sum of false positives and true negative, and it is calculated using the Eq. 14 as

$$FPR = FP/(FP + TN) \quad (14)$$

F-measure

This is the kind of parameter measure, which association of recall and precision. The F-measure is determined by using the Eq. 15 as

$$F - measure = 2 * Recall * Precision/Recall + Precision \quad (15)$$

In Tables 4, 5 and Fig. 4, they show that the performance analysis of different machine learning classifier with and without feature selection method. In SVM classifier, achieved the 97.01% accuracy on with without feature selection and 99.07% of accuracy achieved at combination of feature selection algorithm. Then, MLP achieved 98.89% accuracy and PCA-MLP achieved 99.07% of accuracy. NB classifier achieved the accuracy of 96.13% and PCA-NB achieved 98.00% of accuracy.

Table 4 Comparison analysis of different classifier model without feature selection

Methods	Precession (%)	Recall (%)	F-measure (%)	Accuracy (%)
SVM	97.46	95.32	97.21	97.01
MLP	97.20	96.89	96.45	98.89
Linear regression	94.52	95.99	96.21	96.13
NB	96.33	95.15	94.15	97.33

Table 5 Comparison analysis of different classifier with feature selection technique

Methods	Precession (%)	Recall (%)	F-measure (%)	Accuracy (%)
PCA-SVM	97.99	96.42	98.92	97.92
PCA-MLP	97.85	97.48	97.13	99.07
PCA-linear regression	98.54	97.84	97.88	97.35
PCA-NB	97.82	96.58	98.55	98.00

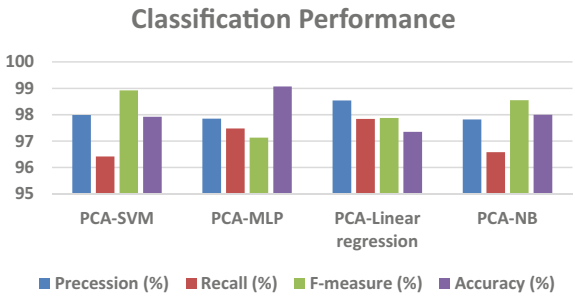

Fig. 4 Graphical representation of classifier performance

PCA-linear regression achieved the accuracy of 97.35% of accuracy. By this comparison, conclude that the PCA-MLP achieved better accuracy than other classifier model.

5 Conclusion

To reduce the mortality rate caused by breast cancer by increasing the accuracy of early detection of breast cancer and achieving effective Remote Diagnosis System through improved Machine Learning and Data Mining Mechanism. In this study, we increased the learning rate of the machine learning classifier by tuning the hyperparameter of the classifier to classify the breast cancer as begin or malignant efficiently. And also, on other hand, we implemented the PCA scheme to select the important feature from the large dataset. By combing the classifier with feature selection algorithm to get better classification result in breast cancer classification and identification. In this experimentation, Wisconsin breast cancer is used to evaluate the performances of the model by obtaining the different parametric values. In testing and training process, by choosing, 60% of data for training process and 40% testing process. And also we set the parameter of each machine learning classifier to train and test the model effectively to get the better result. By this comparative study of different machine learning classifier, principal component analysis with multilayer perceptron achieved the better classification accuracy as 99.07%.

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