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Analysis of Breast Cancer Prediction Using Multiple Machine Learning Methodologies

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Abstract: Breast cancer has the highest fatality rate of any kind of cancer. Cancer screenings should start earlier these days. Several Machine Learning strategies are available for analysing breast cancer data for diagnosis purposes. In this research, a Machine Learning model is provided with the goal of improving breast cancer diagnosis efficiency. Disease prediction accuracy was evaluated using a variety of classifiers, including a random forest, naive bayes, decision tree, support vector machine, and k-nearest neighbours classifier. The software was put through its paces on a breast cancer detection dataset. Accuracy, recall, F1 score, and precision are used to evaluate the system's performance.

Keywords: *Breast cancer, machine learning, early detection, Quality Assurance Validation methods, K-Nearest Neighbors (KNN), SVM, Naïve Bayes, Random Forest, Decision Tree*

1. Introduction

According to the Centres for Disease Control and Prevention (CDC), Breast Cancer is the Most Common Cancer in Women. The wide variation in breast cancer survival rates may be attributed to a number of factors. The kind of cancer and its stage of development upon diagnosis are two major factors. Breast cells are the starting point for the development of breast cancer. Cancer often develops in the lobules or ducts of the breast. Breast cancer may also form in adipose tissue and fibrous connective tissue. When left untreated, breast cancer may spread to lymph nodes in the chest wall and under the arms. When cells in the breast grow abnormally and metastasis (spread to other parts of the body) at a pace equivalent to that of a Meta Size cell, medical experts call it breast cancer. If these unwanted cells can be recognised and their growth is stopped at the earliest possible stage, the consequences for the next phase may be averted. After a tumour is found, the first thing a doctor does is try to figure out whether it's benign or not. Because treating each kind of malignancy requires a unique strategy. While benign cells don't provide any health risks, malignant cells may invade other organs. The absence of an accurate cancer diagnostic test is quite worrisome, since earlier treatment would reduce the risk that carcinogenic tumours would form in the first place. If a disease is detected early enough, it may typically be treated with little intervention. Few people get an accurate diagnosis of their condition before it becomes chronic. As a result, death rates increase over the world.

One condition that may be treated if caught early enough is breast cancer, which is when it hasn't spread to other regions of the body. Doctors are hampered in their efforts to devise a treatment strategy that may increase a patient's chance of survival when prognostic models are unavailable. In order to improve precision, it will take time to perfect a method that produces little mistake. Breast cancer detection with mammography, ultrasound, and biopsy may take a lot of time, hence a computerised diagnostic system using Machine Learning approach is needed. This approach utilises algorithms that speed up the process of tumour categorization and cell detection.

Our novel method for classifying breast cancer is influenced by current advances in machine learning.

The following have made contributions:

For illness prediction, we (i) use a variety of classifier models, including random forests, naive bayes, decision trees, support vector machines, and k-nearest neighbours, and (ii) use a data preparation and data visualization strategy to lighten the classifier's burden.

In Section 2, we present the related existing researches, in Section 3, we present the architecture of the proposed suggested model; in Section 4, we present the results and discussion; and in Section 5, we present the conclusion and references.

II. Related Works

The study of classification of images using deep and

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machine learning is a hot topic right now. To show the efficacy of the suggested methods, mammography pictures were categorised using a range of methods, such as binary, multi, and dual classification. Deep learning improves deep network training by randomly removing layers from convolutional neural network (CNN) models, according to recent studies (Shen, Wu, & Suk, 2017). In order to construct their deep neural networks, the MobileNets make use of a practical architecture based on depth-wise convolutions (Howard et al., 2017). The use of ResNet for picture categorization was suggested. (Xie, Girshick, Dollár, Tu, & He, 2017) cited the high training accuracy (about 98 percent) of VGG, Xception, or ResNet as reasons to suggest them for breast cancer categorization. It has been recommended (Li, Shen, Zhou, Wang, & Li, 2020) that histological photos be combined with DenseNet and SENet for breast cancer classification. Five-fold cross-validation results for the improved InceptionV3 architecture presented in (Wang et al., 2020) showed an AUC of 0.9468, sensitivity of 0.886, and specificity of 0.876. Using the MIAS dataset, the Multiscale All Convolutional Neural Network (MA-CNN) developed by (Shin et al., 2016) achieved 96.2% sensitivity and 0.99 area under the curve (AUC). In order to classify breast cancer from histopathology pictures, (Zhu et al., 2019) propose using a Squeeze-Excitation-Pruning (SEP) block in a hybrid CNN architecture. We looked through the existing literature and discovered that the DenseNet121+ELM model has not been used to analyse mammography pictures. We were motivated to create the DenseNet121-ELM model by the dearth of high-performance, conventional CNN automated classifiers

Using SVM and PFTAS characteristics, a group of researchers in 2016 (Fabio A Spanhol, Oliveira, Petitjean, & Heutte, 2015) reported an accuracy of around 85.1% at the patient level. In a 2013 study using a dataset of 500 samples from 50 patients, researchers classified nuclei using a wide variety of techniques, including K-means, fuzzy C-means, competitive learning neural networks, and Gaussian mixture models. To guarantee accurate reporting, only benign and malignant diagnoses were considered. (Kowal, Filipczuk, Obuchowicz, Korbicz, & Monczak, 2013) found that precision levels in the range of 96–100% were achieved.In 2013, researchers demonstrated 94% identification accuracy on a dataset of 92 samples for breast cancer detection using a neural network (NN) and support vector machine (SVM) based machine learning system (George, Zayed, Roushdy, & Elbagoury, 2013). Cascade-based technique with rejection option showed about 97% classification accuracy when evaluated on 361 samples from Israel Institute of Technology dataset (Zhang, Zhang, Coenen, & Lu, 2013). Most studies in this area have used little samples from obscure places to get their conclusions. Recently, a study on histological image analysis for breast cancer detection and classification addressed in detail the complexity and limits of numerous publically accessible annotated datasets (Veta, Pluim, Van Diest, & Viergever, 2014). The average recognition rate for BC categorization at the patient level using the suggested framework with colour texture characteristics and multiple classifiers employing a voting mechanism was found to be 87.53%. Support vector machines, decision trees, nearest neighbour classifiers, discriminant analysis, and ensemble classifiers were all used to arrive at this conclusion. Until 2017 (Gupta & Bhavsar, 2017), this method outperformed all others based on machine learning in terms of recognition accuracy.

Classification using CNN variations has been at the centre of several articles that investigate DL techniques for breast cancer detection. For many of these tests, the BreakHis dataset is indispensable. Using convolution kernels of varying sizes (7, 7, 5 5, and 3 3), a convolutional neural network (CNN) was suggested in 2016 as a magnification-independent method for recognising breast cancer. An 83.25% recognition rate was achieved in the classification of breast cancer patients using convolutional neural network (CNN) and multi-task CNN (MTCNN) models (Bayramoglu, Kannala, & Heikkilä, 2016). One other study from that same year classified breast cancer pictures and patients using a model comparable to AlexNet and multiple fusion approaches (sum, product, and max). Using the max fusion approach, researchers were able to increase recognition accuracy to an average of 90% for picture classification and 85.6% for patient classification (Fabio Alexandre Spanhol, Oliveira, Petitjean, & Heutte, 2016). Another deep learning-based technique saw publication this year. In this study, a convolutional neural network (CNN) was used to gather feature vectors that were fed into a classifier. DeCAF (Fabio A. Spanhol, Oliveira, Cavalin, Petitjean, and Heutte, 2017) successfully recognised patients in 86.3% of cases and 84.2% of cases in photographs.

2017 also saw the CNN model employed to categorise H&E-stained pictures from breast biopsies, another demanding dataset. Normal tissue, benign lesion, in situ malignancy, and aggressive carcinoma were the four categories used to label the photos. Images were also classified using a binary method, with the former including "normal" and "benign" tissue and the latter "in situ" and "invasive" cancer. For further information, see (Arajo et al., 2017) which contains the results of both the image-based and patch-based assessments. On the BC Classification Challenge 2015 dataset, the CNN-based method attained a about 77.8% identification accuracy for the four-class experiment and an 83.3% recognition accuracy for the binary class trial. In this study, we use a newly disclosed structured deep learning model

(CSDCNN) to multi-classify breast cancer using histopathological pictures. While several machine learning and deep learning strategies have been used to the BreakHis dataset, our novel DL architecture has shown to be the most effective. Our approach produces state-of-the-art outcomes on an individual patient and image level. Han et al. (2017) found that overall accuracy of patient-level breast cancer categorization was 93.2%. A number of support vector machine (SVM)-based methods were used in 2017 to detect breast cancer, however the best results were obtained by using an Adaptive Sparse SVM (ASSVM) on 40-fold-enhanced data (Kahya, Al-Hayani, & Algamal, 2017). Our research takes on the problem of BC classification by using a novel deep learning model on the BreakHis and 2015 Breast Cancer Classification Challenge datasets. The Inception Recurrent Residual Convolutional Neural Network (IRRCNN) is the model in question. An innovative hybrid DenseNet121-based Extreme Learning Machine Model (ELM) is provided in (Pattanaik, Mishra, Siddique, Gopikrishna, & Satapathy, 2022) that may improve the accuracy with which breast cancer is identified from mammography images. Preprocessing and data augmentation were applied to the mammograms to boost their quality. After first pooling and flattening traits, a second phase of classification included collecting them independently. The attributes are input at the fully connected layer of the proposed DenseNet121-ELM model. To fill in for the completely linked layer, we used a machine learning technique. AdaGrad optimisation was used to the weights of the model used in the extreme learning machine to make it more stable and efficient. AdaGrad was picked as the optimisation technique of choice since it converges quickly compared to other methods. To demonstrate these ideas, Alom, Yakopcic, Nasrin, Taha, and Asari (2019) use the Inception Recurrent Residual Convolutional Neural Network (IRRCNN) model. Combining the strengths of the Inception Network (Inception-v4), the Residual Network (ResNet), and the Recurrent Convolutional Neural Network (RCNN), the IRRCNN is a formidable deep convolutional neural network model. When compared to Residual Networks, Inception Networks, and RCNNs, the IRRCNN performs better in object recognition. Using the BreakHis and Breast Cancer (BC) classification challenge 2015 datasets, this research applies the IRRCNN method to the issue of breast cancer classification. Using deep learning techniques, several authors in this research were able to accurately anticipate the spread of disease. Yet, more time and a larger data set are required for training the classifier. The problems with traditional approaches are why we're putting greater emphasis on machine learning tactics.

III. Proposed Work

In this paper, a comparative framework approach is presented for effective identification of the cancerous image. The overall flow of the suggested methodology was illustrated in figure 1.

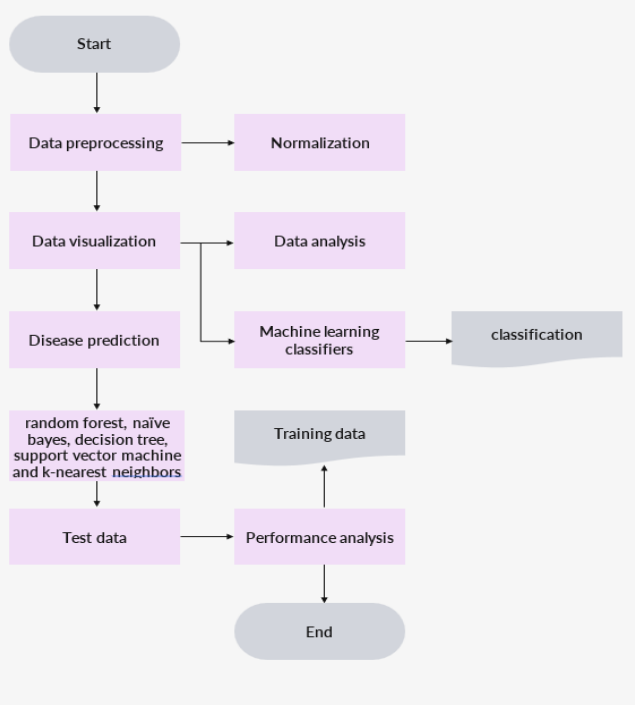

Fig 1 schematic form of the suggested approach

a. Data Source

The breast cancer patients clinical data was retrieved from the internet source which are openly available to the public. The dataset contains patients information and their clinical history.

b. Data Preprocessing and Data Visualization

"Here, we use preprocessing to enhance the quality of the data. Data preparation and data visualization are the two main components of the suggested strategy.

The following rule was shown during the data frame phase

$$z(o,j) = \text{norma}[y(o-k,j-k),\cdots,y0,j),\cdots y(o+k,j+k)] \quad \textbf{(1)}$$

In order to compute the filtered-error output. Filtering replaces the *x(l',j')* in the right hand of Eq. (1) with *y(o',j')* if the error filtering output *y(o',j')* of pixel *x(o',j')* has been calculated.

$$z(o,j) = \text{standard data}\ [z(o-k,j-k),\cdots,y(o',j'),\cdots,y(o,j),\cdots y(o+k,j+k)] \quad \textbf{(2)}$$

The standardisation technique includes three key steps: calculating first derivatives, estimating Error parameters, and filtering. The system relies on two parameters: the variance and the reference gradient (g_{ref}).

In the first stage, the gradient vector is shown as.

$$\nabla f = \left[\frac{\partial f}{\partial x}, \frac{\partial f}{\partial y}, \frac{\partial f}{\partial z}\right]^T = \left[f_x, f_y, f_z\right]^T \quad (3)$$

where m is the gradient vector's magnitude

$$|\nabla f| = \sqrt{f_x^2 + f_y^2 + f_z^2}. \quad (4)$$

One mathematical representation of the error

filtering is, $G(\mathbf{x}) = \frac{1}{(2\pi)^{3/2}|\mathbf{V}|^{1/2}} \exp\left(-\frac{\mathbf{x}^T\mathbf{V}\mathbf{x}}{2}\right)$,

where $\mathbf{x} = [x, y, z]^T$, and $|\mathbf{V}|$ denote

the determinant of $\mathbf{V}$. Further, we assume

$$\mathbf{V} = [\mathbf{w}_1, \mathbf{w}_2, \mathbf{w}_3]^T \begin{bmatrix} \sigma & & \\ & \sigma_1 & \\ & & \sigma_1 \end{bmatrix} [\mathbf{w}_1, \mathbf{w}_2, \mathbf{w}_3] \quad (5)$$

where $\mathbf{w}_i$ is the ith eigenvector of V. Parameter estimate is as simple as finding the values of $\mathbf{w}_1$ and σ_1. because the second and third eigenvalues are the same. Phase two in which error variants are evaluated,

$$\sigma_1 = \frac{\sigma}{(1+|\nabla f|/g_{ref})} \quad (6)$$

$$\mathbf{w}_1 = \frac{\nabla f}{|\nabla f|}. \quad (7)$$

Convolve the volume information using Eqs. (7) and (6) for the third step. The value of the target class |f| is big and the anisotropy is likely to be substantial when the data is close to the error boundary. If $|\nabla f|$ is rather small, then $\sigma_1 \approx \sigma$ will normalise the data.

After that, direct data is preprocessed, Data visualization is the process of creating a visual representation of data in order to better understand its contents.There is no rigorous mathematical standard in place inside the visualization techniques by which quality may be evaluated. Separate pieces of information $z_1, z_2, \ldots, z_n$that characterise the data $z_i = (z_{i1}, z_{i2}, \ldots, z_{in}), i \in \{1, \ldots, m\}$, is displayed in a human-friendly visual format. Obtain the statistical information contained within the dataset. Use the seaborn library to display the correlation dataSklearn library ML classifier invocation.

c. Disease Prediction

For the prediction of the disease the visualized data can be spitted up into train and test data are separately given as a input for the five different types of the classifier listed below,

1. K-Nearest Neighbors:

For the purposes of prediction and classification, Using similarities to existing data sets, K-Nearest Neighbours (KNN) is a supervised machine learning technique. Diseased feature similarity between points in the test set and the training set may be calculated using the distance metric in (equ 8).

$$\text{Cosine}\,(y_i, z = y_i) = \frac{\sum_{i=1}^{n} z_i X_i}{\sqrt{\sum_{i=1}^{n} (z_i)^2}\sqrt{\sum_{j=1}^{n} (X_i)^2}} \quad (8)$$

Where X_i are numbers that should be able to categorise their disease output , Y_i are values that are known to be legitimate outputs

2. SVM:

The method is an expansion of the SVM for use in regression analysis. Depending on the kernel function, it might be linear or non-linear. Instead of looking for a hyperplane to solve the regression issue, it locates a tube around the function that is insensitive to changes of up to epsilon. To make predictions about disease, the models were first trained on the training set.

3. Naïve Bayes:

Here, Bayes's theorem has been used for classification, with the underlying assumption being that classification is independent of predictors. Naive Bayes classifier assumes that a feature in a class has no correlation with any other features in the class.

The Naive Bayes model may be used to construct and analyse very large datasets. This model is a very effective classification approach despite its apparent simplicity, and it can handle complex circumstances with ease. The following equation may be used to get the posterior probability using Bayes' theorem

$$M(b/y) = (M(y/b)M(b))/M(y) \quad (9)$$

where M(a/y) is the predictor's prior probability and M(y) is the observed value's prior probability. The posterior probability of a class is indicated by v(a), whereas the likelihood, or possibility that the prediction is right, is shown by w(y/a).

4. Random Forest

In Machine Learning, the Random Forest Classifier is utilized as a Regression and Classification Algorithm.0 To improve projected accuracy and restrict over-fitting, this meta estimator takes the average of the results from fitting several decision tree classifiers to distinct subsamples of the dataset. L is the score range that results from,

$$\mathrm{L}: \{(\mathrm{z_i}, \mathrm{x_i}), \mathrm{i} = 1, \ldots, \mathrm{n}\} \quad (10)$$

where yi $\in \{1, \ldots, c\}$ represents the kind of sample i and the features of sample i are represented by the vector $\mathrm{xi} = (\mathrm{x_{i1}}, \ldots, \mathrm{x_{ip}})$

The d(..,) distance function is used to determine the nearest neighbour. To determine the Euclidean distance between a sample point xi and an assigned point xj in P variables, we compose:

$$d\left((y_{i1}, y_{i2}, \ldots, y_{ip}), (y_{j1}, y_{j2}, \ldots, y_{jp})\right) = \sqrt{(y_{i1} - y_{j1})^2 + (y_{i2} - y_{j2})^2 + \cdots + (y_{ip} - y_{jp})^2} \quad (11)$$

The observation of the sample subset (y, x) by the nearest neighbor $(y(1), x(1))$ in the learning sample is determined by:

$$d(y_i, y_j) = \min_j \left(d(y_i, y_j)\right) \quad (12)$$

The closest neighbor's predicted class is denoted by y = y(i). This group has been chosen to make y forecasts.

By substituting 2 for p in Minkowski's formula (12), we get the Euclidean distance in equation (13).

The closest neighbor's predicted class is denoted by$\hat{y} = y(i)$. This group has been chosen to make y forecasts.

By substituting 2 for p in Minkowski's formula (12), we get the Euclidean distance in equation (13).

$$d(y_i, y_j) = \left(\sum_{s=1}^{p} |y_{is} - y_{js}|^p\right)^{\frac{1}{p}}$$

$$d(y_i, y_j) = \left(\sum_{s=1}^{p} (y_{is} - y_{js})^2\right)^{\frac{1}{2}} \quad (13)$$

5. Decision Tree

One kind of supervised machine learning models is the decision tree classifier. This implies that they use the usage of tagged data to train a prediction algorithm. For the following input vector to be generated:

$$\mathrm{X} = [C_x, C_y] \quad (14)$$

where C_x and C_y are the components that are calculated as,

$$C_x = \frac{1}{3} \frac{\sum_{i=0}^{n-1} (y_i + y_{i+1})(x_i y_{i+1} - x_{i+1} y_i)}{\sum_{i=0}^{n-1} (x_i y_{i+1} - x_{i+1} y_i)} \quad (15)$$

And

$$C_y = \frac{1}{3} \frac{\sum_{i=0}^{n-1} (y_i + y_{i+1})(y_i x_{i+1} - y_{i+1} x_i)}{\sum_{i=0}^{n-1} (y_i x_{i+1} - y_{i+1} x_i)} \quad (16)$$

6. Performance Analysis

Testing sets used to evaluate performance in a Python environment were utilized to assess the likelihood of breast cancer

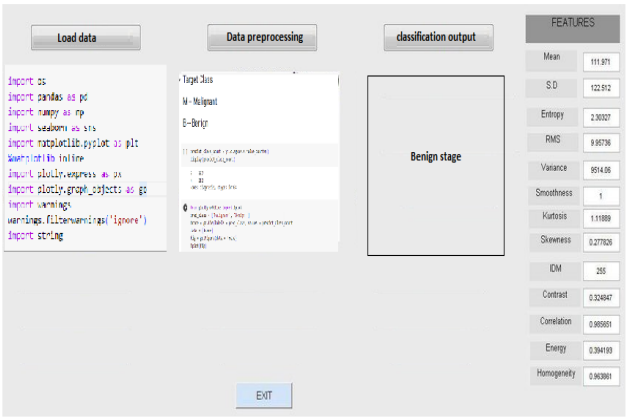

Fig 2 Simulated output

The overall simulation output was illustrated in figure 2

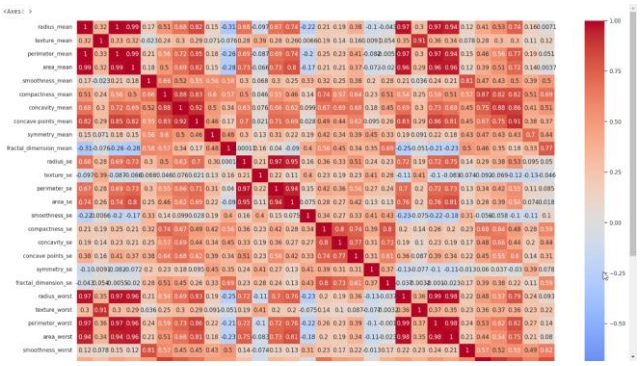

Fig 3 Data visualization

The overall data and its features can be visualized using the process of data visualization as depicted in figure 3.

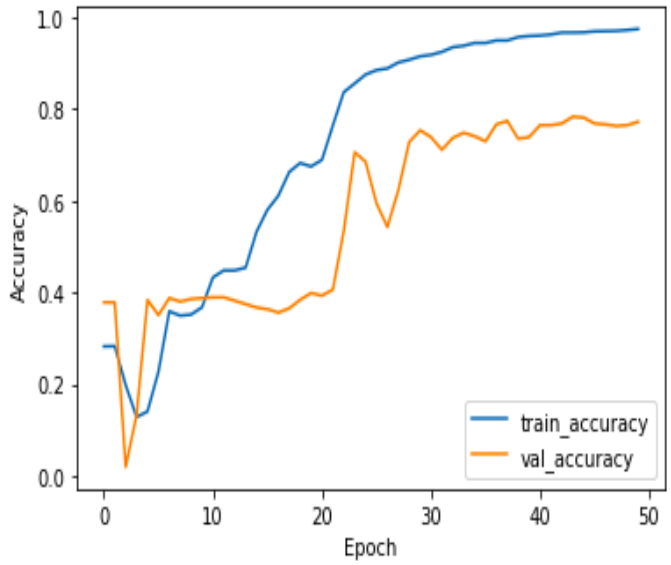

Fig 4 accuracy percentile calculation

As can be seen in Figure 4, this drop in precision is to be anticipated after the model has been trained using the training data. The model is validated using data that was not utilized in the training process.

The optimal densely connected graphical neural network for classification is proposed for accurately identifying metastatic breast cancer (see Figure 4). The effectiveness of the proposed strategy may be shown using the illustrated performance measures.

Table 1 performance metrics for evaluation

"value of Accuracy"	"The percentage of samples with accurate forecasts. ."	"A = $\frac{TP+TN}{TP+FP+TN+FN}$,"
"value of Recall"	"Predictions where every characteristic was spot on, expressed as a percentage."	"Rec = $\frac{TP}{TP+FP}$ "
"value of Precision"	"Accuracy of a forecast as a function of the total number of features."	"Prec = $\frac{TP}{TP+FN}$,"
"value of F1 score"	"There are just two inputs needed for the F-measure (precision and recall) ."	"F score = $2* \frac{(Precision * Recall)}{(Precision+Recall)}$,"

```
df_model_eval = pd.DataFrame({'model': model_names, 'feature_count': feature_counts,
                              'acc': model_acc_scores,
                              'prc': model_prc_scores, 'rec': model_rec_scores,
                              'f1': model_f1_scores})
df_model_eval
```

	model	feature_count	acc	prc	rec	f1
0	rfc_model_1	30	0.935673	0.935673	0.936040	0.935952
1	dtc_model_1	30	0.906433	0.906433	0.912675	0.907368
2	nbc_model_1	30	0.912281	0.912281	0.907929	0.912415
3	svc_model_1	30	0.923977	0.923977	0.901577	0.922261
4	knc_model_1	30	0.935673	0.935673	0.929761	0.935569

Fig 5 Output analysis

As of from the Figure 5 and figure 6, among the classifier implemented random forest and KNN outperforms well by obtaining high range of precision, recall, accuracy and F score

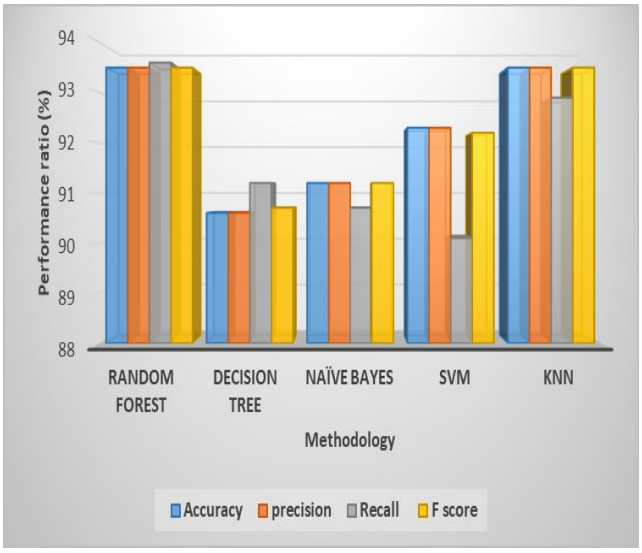

Fig 6 Performance analysis of the suggested methodology

The effectiveness of the proposed strategy may be shown by contrasting it with currently used approaches [22,23].

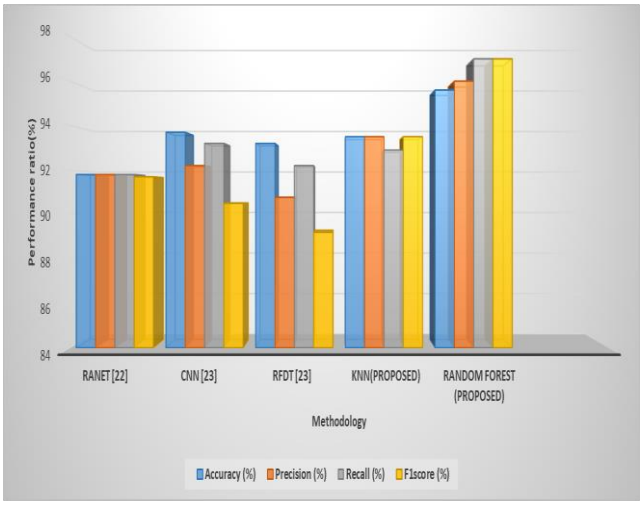

Fig 7 Comparative performance analysis

Based on the findings, it was determined that the proposed KNN and RF approach performs better than the alternatives.

IV. Conclusion

Breast cancer survival rates of 80% or more may be achieved with early diagnosis. The breast cancer dataset undergoes data mining with a 70% training/30% testing split. Through the use of comparative analysis, this study implements five distinct kinds of classifiers, each of which simplifies the classification process. Based on the results, RF scored very well in all categories (F1 score = 93.5%, Precision = 93.5%, Recall = 93.6%, and Accuracy = 93.5%). Results demonstrated that the machine learning methodology was more appropriate for breast cancer prediction than other deep learning methods. Implementing a variety of feature extraction techniques in the future may help boost the classifiers' precision.

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