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## Classifying Digital Medical Images for Breast Cancer Prediction Using Machine Learning

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### Abstract

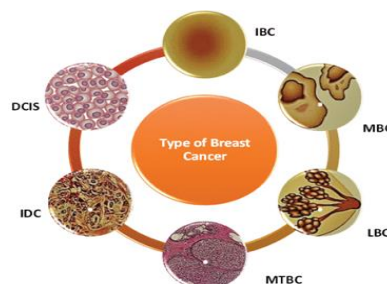
Statistics show that among the 1.67 million cancer reported cases worldwide, breast cancer is the most common cancer among women and constitutes the largest burden of the disease in developing countries. However, if detected early enough, it can be managed. Mammography is one of the best ways to identify and diagnose breast abnormalities among various medical imaging modalities. It typically detects signs and symptoms of breast cancer, including microcalcifications, lumps, nodules, architectural abnormalities, asymmetry, bilateral asymmetry, etc. These features can be benign or cancerous when they appear in the breast. Researchers have focused on creating fully automated computer-aided design methods to help radiologists combat this type of cancer. Artificial Intelligence (AI) -based algorithms have been essential in creating systems that allow for automated diagnosis, rapid response, and low mortality. In this work, several machine learning methods were compared—such as logistic regression, naive Bayesian Gaussian algorithms, support vector machines (SVM), linear support vector machines (SVM), and artificial neural networks (ANN). Processing time and accuracy were the main evaluation metrics where naive Bayes outperformed SVM, followed by linear SVM and logistic regression, with ANNs failing in accuracy. These results highlight how naive Bayes algorithms can help in early detection of breast cancer, leading to faster and more efficient treatments and ultimately better patient care.

## A. Introduction

Breast cancer is a type of cancer that develops in the breast tissue cells and ranks second as the most prevalent cancer among women in the United States, just behind skin cancer.

Although breast cancer can affect both men and women, it is more frequently diagnosed in women [1]. Significant backing for breast cancer awareness and research funding has been instrumental in driving progress in the Diagnosis and treatment of breast cancer [2]. Over time, breast cancer survival rates have shown significant improvement, and the mortality rates linked to the disease have steadily declined. Several key factors have contributed to these positive trends, including early detection practices, advancements in personalized treatment approaches, and a deeper comprehension of the disease [3].

In 2020, breast cancer emerged as the most prevalent form of cancer, with over 2.2 million reported cases. Alarmingly, about one in 12 women are projected to develop breast cancer at some point in their lives. Tragically, breast cancer also ranked as the leading cause of cancer-related deaths among women, with approximately 685,000 women succumbing to the disease in the same year. The burden of breast cancer is disproportionately higher in low- and middle-income countries. There exist significant disparities between high-income and low- and middle-income countries regarding breast cancer outcomes. In high-income countries, the 5-year survival rate after breast cancer exceeds 90%, while in India, it remains at around 66 %, and in South Africa, it is as low as 40%. Africa and Polynesia exhibit the highest age-standardized death rates from breast cancer. Notably, in sub-Saharan Africa, a concerning fact is that half of all breast cancer deaths occur among women under the age of 50. Encouragingly, substantial strides have been made in breast cancer treatment since 1980. High-income countries have witnessed a remarkable 40% decline in age-standardized death rates from breast cancer between the 1980s and 2020 [4]. Breast cancer has different types, as in Figure 1 [1]. Breast cancer encompasses different types depending on how the affected cells and tissues spread within the body. One such type is Ductal Carcinoma in Situ (DCIS), where abnormal cells spread outside the breast, but the cancer remains non-invasive. Another type is Invasive Ductal Carcinoma (IDC), also known as Infiltrative Ductal Carcinoma, which occurs when abnormal breast cells spread throughout the breast tissue. Interestingly, IDC is typically found in men as well [5]. The third type of breast cancer is Mixed Neoplasia Breast Cancer (MTBC), also referred to as Invasive Breast Cancer [6].



**Figure 1.** Demonstration of Major Types of Breast Cancer [1]

ML falls under the umbrella of AI. Is dedicated, to developing systems of learning and evolving based on data and information (Mohammed, et. al., 2023). ML along with Deep Learning (DL) methods has been widely applied across sectors in the field of healthcare. The medical industry heavily depends on analyzing data for diagnostics; automating these procedures can greatly enhance result accuracy. ML classification models have played a role in minimizing errors that inexperienced medical professionals may make and providing accurate outcomes. Nonetheless challenges can arise when employing ML techniques, including issues, like classification models, ineffective validation processes and unnecessary unweighted features. Additionally, breast cancer classification and prediction in medical imaging encounter complexities, making it a challenging and crucial task. Nonetheless, integrating ML and DL methods has shown promising potential in revolutionizing medical diagnostics and treatment [8][9].

The present study is divided into different sections. Section (2) is about the Related Works that are being used for breast cancer prediction, section (3) is about Methods and Materials, section (4) is about the data pre-processing, section (5) is about Performance Measure Parameters, section (6) is the implementation and Result Analysis and section (7) provides the conclusion of this paper.

## **B. Related Works**

AI technologies are commonly used to find and diagnose diseases automatically. According to the authors in [5], breast cancer is the most widespread cancer in women worldwide and is considered a many-factor disease. These may be diverse social, economic, clinical and lifestyle factors[10].

In a search introduced by the authors [11], they used a dataset consisting of 569 inputs to verify the application of an LR classifier model. The primary goal of this study was the Wisconsin diagnosis of breast cancer (WDBC). Feature selection techniques were also adopted by the authors to improve the system performance, including the accuracy. Based on two selected salient features, texture and perimeter, LR model achieved accuracy of 96.5%. Thus, LR model harnessing feature selection scheme showed improved performance, comparing to LR alone.

In [12], several machine learning models were adopted to identify the cancer as benign or malignant. The authors showed that support vector machine (SVM) outperformed all other models tested in the study, with reported accuracy of 97.9% on WDBC dataset.

Using Weka data mining tool, another comparative study was conducted by the authors of [13] who compared 22 machine learning models on antenna dataset. The findings revealed that Random Forest, Random Committee, Bagging, SimpleCART and IBk algorithms achieved superior performance in terms of accuracy metric evaluated on 10-folds.

The data in [14] was used to train three machine learning models: RF, SVM, and DT. The accuracy ranking measure was used to assess the models. SVM fared the best, obtaining 98.03% and 99.68%, respectively, on both datasets, according to the results. In [15], the K-Nearest Neighbor (KNN), NB, and J48 models were assessed and their predictive power for various forms of breast cancer was compared. KNN fared better than the other two models, with an accuracy rate of 98.8%. In an Internet of Things context, the authors of [16] trained and

implemented an SVM model that incorporated several kernel types, such as polynomial, sigma, and RBF kernels, by means of a modified recursive feature selection approach. The accuracy of the SVM using the three kernel types was 84%, 97%, and 99%, in that order.

Moreover, the authors of [17] compared the performance of SVM, NB, DT, and KNN on WDBC dataset. Their findings showed that SVM outperformed all the rest models with execution time of 0.07. However, KNN reported shorter execution time comparing to SVM.

In another comparative study [18], the authors compared the performance of SVM and ANN algorithms on WDBC dataset. They found that SVM indicates better performance, reporting accuracy of 96.9%, while ANN achieved accuracy of 95.4%.

Computer aided detection system was implemented in [19] where the author used ANN, NB, SVM and WDBC dataset for breast cancer diagnosis. The reported accuracy results revealed performance of 97.0%, 91%, and 96.4% on the three classifiers, respectively. Using Weka data mining tool, the researchers in [20] trained several ML models and reported highest performance from KNN algorithm based on Kappa statistics, true positive and false positive rates, and precision evaluation metrics.

The CSSFFS approach was used by the authors of [21] to choose 15 attributes that would increase the accuracy rate of other machine learning algorithms. The results show that the Simple CART algorithm, J48, Naive Bayes, and RBF networks have accuracy rates of 92.9%, 92.6%, and 93.6%, respectively.

The authors developed a hybrid technique, integrating the K-Mean and SVM algorithms [22]. Following K-fold cross-validation, the K-SVM technique displayed exceptional performance with a low error rate, obtaining an accuracy rate of 97.38%.

The authors concluded [23] that SVM was the most effective strategy for predicting breast cancer. SVM outperformed other approaches in their research, with an accuracy rate of 97.59%.

Researchers in [24] used nonlinear machine learning methods; the MLP (Multi-Layer Perceptron) algorithm outperformed the KNN, NB, and CART algorithms with an accuracy rate of 96.70%.

Among the methods studied, the CART algorithm was determined by the authors in [25] to be the most appropriate for breast cancer analysis. While J48 and A DT algorithms obtained 98.10% and 97.70% accuracy rates, respectively, CART achieved 98.50%.

The authors employed [26] the J48 DT algorithm and NB, which handles class numbers based on probabilistic theory. The accuracy rate of J48 DT was measured at 94.2%, while Naive Bayes achieved an accuracy rate of 82.6%.

In another study [27] the authors provided a comparative analysis of various algorithms for breast cancer prediction, considering accuracy rates, efficiency, and effectiveness. SVM stood out with the highest accuracy rate of 97.13% and the lowest error rate.

In [28], ML and DL techniques were utilized to predict breast cancer. Regular ML models and optimized deep RNN were applied to selected features,

with the univariate method showing the best performance for cross-validation and testing results when applied to the optimized deep RNN with selected features. The authors, through [29], employed ML algorithms and utilized two test modes: 10-fold cross-validation and percentage split. They also used several performance measures. The results showed that the ontological model exhibited superior accuracy, even without feature selection.

[30] Also tackled the problem using ML techniques. The findings revealed that SVM achieved an accuracy of 97.14%, precision of 95.65%, and F1 score of 0.9777, while ANN obtained the highest accuracy of 98.57%, precision of 97.82%, and F1 score of 0.9890.

Another paper in [31], the performance of three different ML algorithms was evaluated and compared. The results indicated that all three ML algorithms outperformed LR in accuracy. Notably, XGBoost emerged as the best choice for predicting breast cancer.

In [32], ML algorithms were used, and the findings showed that SVM achieved the highest accuracy of 97.2% among all other classifiers. Similarly, The reference [33] ML algorithms were employed, and the results demonstrated that SVM was the best classifier, surpassing even the stack classifier with an accuracy of 97.7% and classification errors of 0.019 false positive (FP) and 0.029 false negative (FN).

Despite of great effort already made by the researchers in the literature for automatic breast cancer detection, we believe that there are still open rooms for further improvements.

### **C. Material and Methods**

Various ML techniques are available to aid in predicting whether an individual is affected by benign or malignant cancer, ensuring an efficient and error-free process.

#### **Linear Support Vector Machine (LSVM)**

Linear SVM is employed to handle linearly separable data, which means data that can be divided into two classes using a single straight line. A dataset is said to be linearly separable when it can be clearly divided in this way [34], [35]. In these kinds of situations, the Linear SVM classifier is the best option.

#### **Support Vector Machine (SVM)**

SVM algorithms are among the most powerful AI algorithms for prediction, particularly in supervised learning [36]. To forecast point scores, SVM algorithms create a sample from a dataset during training. To discriminate between two classes based on a set of binaries, they develop a linear decision boundary known as a training vector. The model is then tested using a derived linear classification rule to categorize more test instances. Linear SVM algorithms are effective at addressing optimization issues, and the hard margin classifier is the most basic type of SVM algorithm, which uses a linear classification rule to select the most important geometric margin [37], [38]. Real-world datasets frequently contain linearly irreparable data, needing SVM method adjustments. Using the Soft margin principle, this adjustment strikes a compromise between improving the geometric margin and reducing the classification error on training data points. The soft margin enables a superplane to accept inaccurate classifications of complicated

states while increasing the distance between them and the next fully separated data samples [39].

### Artificial neural networks (ANNs)

The multi-layer perceptron architecture known as ANNs [39] is used to train and categorize input samples to create the desired output. In our ANN model, we employed a three-layer network with 32 neurons in the input layer, 34 in the hidden layer, and two in the output layer. The number of neurons in the hidden layer was chosen empirically to produce the best performance. The ANN model was trained on the data, and backpropagation was used as an optimization strategy to alter the network weights via gradient descent, lowering error at each stage and improving the model's performance [40]. Soft-max activation was used in the output layer to generate the final prediction. The network's input included thirty-two criteria, while the output layer differentiated between breast cancer presences (0) and absences (1). Equation (1) is defined the cross-entropy loss function as follows:

$$L = -\sum_{i=1}^2 t_i \log(p_i) \quad (1)$$

In the context of a specific sample (i) of the ground truth value (t) and the probability (p) obtained through the soft-max activation function [39] for that sample, the following relationship holds.

### Naive Bayes (NB) classifier

The Naive Bayes (NB) method, a statistical pattern recognition technique, was applied to detect breast cancer cases by utilizing Bayesian probability. It relies on an acceptable assumption about the data generation process, assuming that all sample attributes are independent [41]. However, if this assumption is incorrect, the classification hypothesis becomes a mere approximation. Despite this limitation, the NB classifier has demonstrated high accuracy in its predictions, even though the evaluation of the function may be achieved with lower accuracy [42], [43], [44].

### Logistic Regression

Logistic Regression, a significant analytical modelling technique, is prominent among various ML algorithms. It relates the probability level to a set of explanatory variables, making it suitable for analysing datasets with one or more independent variables to determine a binary outcome with two possible results. This method is commonly used for binary predictions (1/0, Yes/No, True/False). The LR model can be described using the following equations (2) and (3):

$$x = c_0 + \sum_{i=1}^n c_i x_i \quad (2)$$

$$p(x) = \frac{e^x}{1+e^x} \quad (3)$$

In the context of Logistic Regression, the participation quantity of variables  $x_i$  (where  $i = 1, n$ ) and their corresponding regression coefficients  $c_i$  are used to determine the highest probability of an event along with its regular errors. In LR, a specific event's probability (P) is calculated using the Bernoulli test and is associated with the sampling event [45].

### Data Pre-processing Data Set Description

The dataset of breast cancer was uploaded from the UCI ML repository [46] There are 569 persons with thirty-two attributes representing symptoms that may cause breast cancer, where the Diagnosis is either benign (B) or malignant (M). For such situations, 357 (62.741%) are benign, and 212 (37.258%) are malignant. Table (1) shows examples of data applied in the research.

**Exploratory Data Analysis (EDA)**

In statistics, exploratory data analysis (EDA) is used to thoroughly examine data sets and succinctly represent their essential characteristics, frequently utilizing visual methods. Whether or not a statistical model is used, the main objective of EDA is to reveal and identify significant insights within the data that go beyond formal modelling or hypothesis testing [47]; below table 1 that shows the results after applied EDA.

**Table 1.** The Data set after EDA [46]

	count	mean	std	min	25%	50%	75%	max
id	569	3.04E+07	1.25E+08	8670	869218	906024	8.81E+06	9.11E+08
radius mean	569	1.41E+01	3.52E+00	6.981	11.7	13.37	1.58E+01	2.81E+01
texture mean	569	1.93E+01	4.30E+00	9.71	16.17	18.84	2.18E+01	3.93E+01
perimeter mean	569	9.20E+01	2.43E+01	43.79	75.17	86.24	1.04E+02	1.89E+02
area mean	569	6.55E+02	3.52E+02	143.5	420.3	551.1	7.83E+02	2.50E+03
smoothness means	569	9.64E-02	1.41E-02	0.05263	0.08637	0.09587	1.05E-01	1.63E-01
compactness means	569	1.04E-01	5.28E-02	0.01938	0.06492	0.09263	1.30E-01	3.45E-01
concavity means	569	8.88E-02	7.97E-02	0	0.02956	0.06154	1.31E-01	4.27E-01
concave points mean	569	4.89E-02	3.88E-02	0	0.02031	0.0335	7.40E-02	2.01E-01
symmetry mean	569	1.81E-01	2.74E-02	0.106	0.1619	0.1792	1.96E-01	3.04E-01
fractal_dimension_mean	569	6.28E-02	7.06E-03	0.04996	0.0577	0.06154	6.61E-02	9.74E-02
radius_se	569	4.05E-01	2.77E-01	0.1115	0.2324	0.3242	4.79E-01	2.87E+00
texture_se	569	1.22E+00	5.52E-01	0.3602	0.8339	1.108	1.47E+00	4.89E+00
perimeter_se	569	2.87E+00	2.02E+00	0.757	1.606	2.287	3.36E+00	2.20E+01
area_se	569	4.03E+01	4.55E+01	6.802	17.85	24.53	4.52E+01	5.42E+02
smoothness_se	569	7.04E-03	3.00E-03	0.001713	0.005169	0.00638	8.15E-03	3.11E-02
compactness_se	569	2.55E-02	1.79E-02	0.002252	0.01308	0.02045	3.25E-02	1.35E-01

<b>concavity_se</b>	569	3.19E-02	3.02E-02	0	0.01509	0.02589	4.21E-02	3.96E-01
<b>concave points_se</b>	569	1.18E-02	6.17E-03	0	0.007638	0.01093	1.47E-02	5.28E-02
<b>symmetry_se</b>	569	2.05E-02	8.27E-03	0.007882	0.01516	0.01873	2.35E-02	7.90E-02
<b>fractal_dimension_se</b>	569	3.79E-03	2.65E-03	0.000895	0.002248	0.003187	4.56E-03	2.98E-02
<b>radius_worst</b>	569	1.63E+01	4.83E+00	7.93	13.01	14.97	1.88E+01	3.60E+01
<b>texture_worst</b>	569	2.57E+01	6.15E+00	12.02	21.08	25.41	2.97E+01	4.95E+01
<b>perimeter_worst</b>	569	1.07E+02	3.36E+01	50.41	84.11	97.66	1.25E+02	2.51E+02
<b>area_worst</b>	569	8.81E+02	5.69E+02	185.2	515.3	686.5	1.08E+03	4.25E+03
<b>smoothness_worst</b>	569	1.32E-01	2.28E-02	0.07117	0.1166	0.1313	1.46E-01	2.23E-01
<b>compactness_worst</b>	569	2.54E-01	1.57E-01	0.02729	0.1472	0.2119	3.39E-01	1.06E+00
<b>concavity_worst</b>	569	2.72E-01	2.09E-01	0	0.1145	0.2267	3.83E-01	1.25E+00
<b>concave points_worst</b>	569	1.15E-01	6.57E-02	0	0.06493	0.09993	1.61E-01	2.91E-01
<b>symmetry_worst</b>	569	2.90E-01	6.19E-02	0.1565	0.2504	0.2822	3.18E-01	6.64E-01
<b>fractal_dimension_worst</b>	569	8.39E-02	1.81E-02	0.05504	0.07146	0.08004	9.21E-02	2.08E-01

### Training and Testing Phase

Divide the data set into the training set and the test set and the percentage (95%, Number of Instances (540)) for training and (0.05%, Number of Instances (29)) for testing.

### Normalize Data

Data normalization is an essential pre-processing before modelling. The scaling is as follows:

$$y = ((x - \min) / (\max - \min)) \quad (4) \quad [48].$$

### Normalized Data with Min\_Max\_Scaler

Several techniques exist for data normalization, such as min-max normalization, z-score normalization, and normalization by decimal scaling. Min-max normalization involves applying a linear transformation to the original data, using the minimum value (min) and the maximum value (max) of the attribute [49].

### Performance Measure Parameters

ML algorithm's baseline performance was evaluated using a confusion matrix (CM), to measure the performance of the classification model [50], which is an ML structure that aims to predict information about a classification model's actual and expectant classifications. The CM matrix has two dimensions to index the class: the object's actual class index and the classifier's predicted class index [51]. The sample number categorized as class  $A_j$  but actually belonging to class  $A_i$  is acted by  $N_{ij}$  in the confusion matrix [52].

The number of classification performance measures is evaluated using different evaluation factors. Accuracy or classification Rate, Recall or Sensitivity, specificity, Precision, and F1-score or F-measure are among the evaluation metrics, which are defined as: [53].

**Accuracy or Classification Rate**

The relationship between the actual accurate classification numbers and the total number of test samples applied during training and testing refers to accuracy and is calculated by using equation (5).

$$Accuracy = \frac{TP+TN}{TP+FP+TN+FN} \tag{5} [54]$$

Where truth positive (TP), false positive (FP), true negative (TN), and false negative (FN), each one has a particular meaning in the confusion matrix.

**Implementation and Result Analysis**

**Experimental Setup**

To classify cells as benign or malignant, we employed five ML techniques: LR, SVM, linear SVM, GNB, and ANN. Each method was individually implemented under specific system requirements, including hardware processor with Core i7-CPU 8550U running at 2.00 GHz, 8 GB of RAM and the Windows-10 operating system. The programming language used for the implementation was Python (version 3.7.10, 64-bit).

**Results and Discussion**

The data set was divided into 95% for training and 0.05 for testing for all five methods, where we used 29 cases to test all models. The CM of the ML strategies used is shown in Tables (2), (3), (4), (5), and (6), which provide predictive results for LR, SVM, linear SVM, GNB, and ANN, respectively.

**Table 2.** CM for LR

		<b>Malignant</b>	<b>Benign</b>
<b>Actual</b>	Malignant	14	2
	Benign	2	11
		<b>Predicted</b>	

**Table 3.** CM for SVM

		<b>Malignant</b>	<b>Benign</b>
<b>Actual</b>	<b>Malignant</b>	12	4
	<b>Benign</b>	0	13
		<b>Predicted</b>	

**Table 4.** CM for Linear SVM

		Malignant	Benign
ctual	<b>Malignant</b>	13	2
	<b>Benign</b>	1	13

		Predicted	
<b>Table 5. CM for GB</b>			
		Malignant	Benign
Actual	Malignant	14	2
	Benign	0	13
		Predicted	

		Predicted	
<b>Table 6. CM for ANN</b>			
		Malignant	Benign
Actual	Malignant	7	7
	Benign	12	3
		Predicted	

In table (7) The combined CM depicts that the GNB and LR model predicts the highest number of true positives (14 out of 29 test samples) among the five techniques. In addition, the SVM and GNB models predict the highest number of true negatives and the lowest number of false negatives (13 of 29 test samples) and (0 of 29 test samples), respectively.

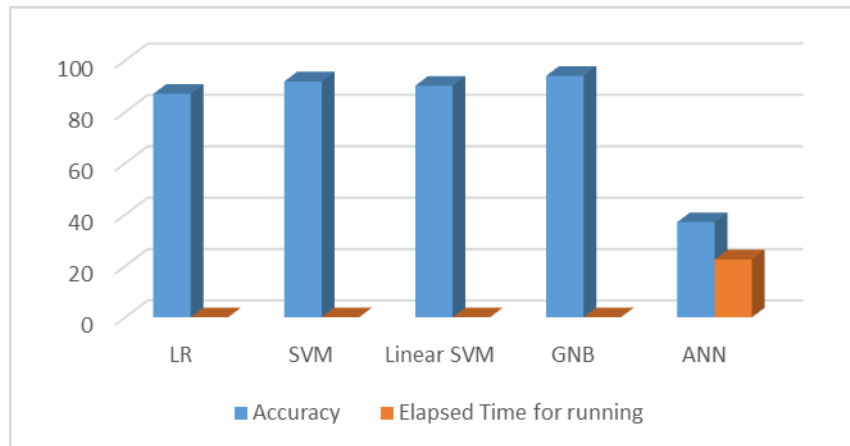
**Table7.** The Combined Confusion Matrix

	LR	SVM	Linear SVM	GNB	ANN
TP	14	12	13	14	7
TN	11	13	13	13	3
FP	2	4	2	2	7
FN	2	0	1	0	12

The measures of calculated performance are shown in Figure 2. and Table( 8), where they show that GNB has outperformed all other ML techniques in terms of accuracy and elapsed time for execution then the other four algorithms are, respectively SVM, Linear SVM, LR, and ANN, which are considered to have failed to build this model with the least accuracy and the highest execution time, according to the values in Table(8).

**Table 8.** ML Techniques in Accuracy and Elapsed Time

NO.	Algorithm	Accuracy	Elapsed Time
1.	LR	87.04	0.020136
2.	SVM	91.85	0.016133
3.	Linear SVM	90.19	0.007103
4.	GNB	94.07	0.005495
5.	ANN	37.04	22.523813



**Figure 2.** Comparison of Algorithms

#### D. Conclusion

The current research compared five machine learning (ML) techniques for breast cancer prediction: LR, SVM, linear SVM, GNB, and ANN. The study provided an overview of each ML approach's fundamental features and working principles. Among the five techniques, GNB achieved the highest accuracy of 94.57%, while ANN showed the lowest accuracy of 37.04%. It's worth mentioning that ANN excels in accuracy when dealing with image-related tasks. For the remaining three algorithms, SVM achieved an accuracy of 91.85%, linear SVM achieved 90.19%, and LR achieved 87.04%. Diagnostics in the medical field is costly and time-consuming. The system suggested that the ML technology could act as a clinical assistant for breast cancer diagnosis and would be very useful to Medical diagnostics are known for being costly and time-consuming. However, the introduction of ML technology as a clinical assistant for breast cancer diagnosis has shown promising potential to benefit physicians and new doctors, particularly in misdiagnosis cases. Among the ML models studied, the one developed by GNB displayed remarkable consistency, surpassing other technologies. This advancement has the potential to revolutionize breast cancer prediction practices. The research findings lead to the conclusion that ML techniques can automatically detect diseases with high accuracy.

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