Breast Cancer Detection Using Deep Learning and Feature Decision Level Fusion

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Abstract

Among women, breast cancer has a high incidence and high fatality rate. Due to a lack of early detection facilities and barriers to accessing technological improvements in battling this illness, mortality rates are disproportionately greater in underdeveloped countries. Biopsies done by trained pathologists are the only certain approach to diagnosing cancer. With the use of computer-aided diagnostic algorithms, pathologists may improve their efficiency, objectivity, and consistency in making diagnoses. A key goal of this research is to create an accurate automated system for diagnosing breast cancer that can function in the current clinical setting. In this work, we offer an algorithm for the identification of breast cancer that uses asymmetric analysis as the basic choice and decision-level fusion. Fusion of local nuclei features extracted using convolutional neural network (CNN) models pre-trained on the database constitutes the picture feature representation. The dataset is accessible for public use, and the results are evaluated by running 25 random trials with an 80%-20% split between train and test. Overall, the suggested framework was 86%. The proposed framework is shown to outperform numerous current methods and to provide results on par with the state-of-the-art techniques without requiring extensive computing resources. Breast cancer detection from histological pictures may be greatly aided by the use of this qualitative approach based on transfer learning.

Keywords: Breast Cancer; Decision Level Fusion; Feature Fusion; Classifier Fusion; Deep Learning

1. Introduction

Noncommunicable illnesses are a leading cause of mortality worldwide (NCDs). Cancer, one of the many non-communicable diseases (NCDs), is a major reason for the rise in mortality and the greatest barrier to extending the human lifespan in the twenty-first century. Since 2018, around 2.1 million women have been told they had breast cancer. As the leading cause of cancer-related mortality in women, breast cancer is also the second most often diagnosed illness overall. By detecting breast cancer early, women may avoid having their breasts surgically removed. Diagnostic mammography (X-rays), magnetic resonance imaging (MRI), breast ultrasound (sonography), and thermography are some of the primary screening modalities used to identify breast cancer[1], [2].

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Regular checkups that include a breast exam using any of these methods may save lives by catching cancer early. If abnormalities in the breast tissues are discovered during the screening phase, therapy cannot begin until a biopsy confirms the presence of cancer. The stage of cancer identified is also determined by the results of the biopsy.

Those who have thick breasts, implants, fibrocystic breasts, or are on hormone replacement therapy may not be good candidates for mammography imaging, and the procedure may be uncomfortable or even unpleasant for the patient. The alteration of genes by electromagnetic radiation, however, has been hypothesized as a possible cause of cancer. Due to this, these patients are encouraged to try the ultrasonic technique. This imaging method does not need any invasive procedures and may help doctors figure out what kind of tumor a patient has. Neither magnetic resonance imaging (MRI) nor mammography can distinguish between a malignant mass and a benign cyst. Non-contact, radiation-free, and pain-free, digital infrared thermal imaging (DITI) is a non-invasive diagnostic tool. According to the studies, the cure rate for breast cancer rises to 85% if the tumor is found early (tumor size less than 10 mm) and drops to 10% if it is found late. In contrast to mammography, thermography imaging may identify tumors 8-10 years in advance.

To obtain at a diagnosis using radiographic images, it is necessary to evaluate and organize picture data. Because of the breast parenchyma's diversity and the structural noise induced by thick tissue masking, these techniques may be challenging to execute. These factors might lead to the concealment or disregard of cancer lesions. Serious mistakes and health consequences might result from manual diagnostic's various subjective judgments, which are further complicated by significant variances between and even among observers. Medical experts have advocated vehemently against ignoring 'false alarms'[3], [4]. In order to assist the radiologist in reducing both false-positive and false-negative instances, the creation of a CAD system as a decision support tool is very beneficial. Ground truth for the training step is represented in the radiologist labels, but the radiologist's experience is still the guideline and the ultimate decision maker[5]–[7].

Many deep learning algorithms have recently surpassed the performance of traditional segmentation, feature extraction, and classification methods used to construct CAD systems from medical pictures. The automatic feature extraction and transfer learning capabilities of deep convolutional neural networks (CNNs) are now receiving a lot of attention[8]–[10]. However, a massive quantity of training samples is required for CNNs to be trained from scratch[11], [12]. Training takes a long time, and it's difficult to get the settings just right. If you're looking for an alternate method of feature extraction and categorization, consider transfer learning (TL). Several deep learning applications rely on transfer learning. In comparison to training a network with randomly initialized weights, fine tweaking a pretrained network saves time and effort[14]–[17].

The problem of a lack of sufficient training data may be circumvented with the use of a transfer learning strategy. For this research, we use an already-processed picture to isolate nucleus regions. Changes in the morphology and texture of nuclei are important diagnostic characteristics for malignancy. Therefore, the duty of the pre-trained CNNs as a feature extractor may be simplified by immediately inputting nucleus patches instead of the raw pictures. This eliminates the need for either scaling the input picture or using deep CNNs in order to extract high-level characteristics from the image's heterogeneous tissue arrangement. Five widely used pre-trained CNNs (ResNet-18, ResNet-50, ResNet-101, GoogleNet , and AlexNet).

In all breast cancer detection systems, feature extraction plays a vital role. Several techniques, including the wavelet transform, the lyaupon exponent, the fractal dimension, and the mutual information, have proven useful for feature extraction. To characterize the characteristics of the breast thermogram, we use the cumulative histogram, the Bezier histogram, the first order moments such as mean, skewness, and kurtosis, and the second order statistical parameters namely the co-occurrence matrix. Other methods, including fuzzy clustering, artificial neural networks, and various similarity measures, have been used to distinguish between healthy and malignant samples.

In this research, we propose using asymmetry analysis to distinguish between normal and malignant breasts in thermography pictures, and we propose using decision-level fusion to lower the FP error rate. As such, we introduce the concept of a new texture feature, the MRF-based likely texture feature, which is based on the Markov Random Field (MRF) model. To choose efficient and suitable cliques in the MRF model, this function makes use of two adapted variants of Local Binary Pattern (LBP). To further improve the MRF model for feature extraction, we also incorporate a unique potential function, the difference between co-occurrence levels (DCL). In addition, a classification

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modern with decision level fusion using Hidden Markov Model (HMM) is used to combine several retrieved characteristics from an image in order to distinguish malignant instances from normal ones. The goal of developing this decision-making framework was to reduce the frequency of FP mistakes. Different classifiers are employed to categorize the characteristics of each block, and then the results are fused using a fusion approach. To make decisions, the fusion process looks to the votes of the majority.

The remainder of this document is laid out as follows: In Section 2, we give previous studies. The suggested model is presented in Section 3. There is a thorough analysis of the experimental findings and their implications in Section 4. Section 5 presents the study's findings and suggestions for further research.

2. Related Work

Current methods for classifying breast tumors are either based on traditional feature engineering techniques or on deep learning techniques like convolutional neural networks (CNN). Indicators of the illness include abnormalities in the form, size, and extent of the nucleus. Because of this, recognizing nuclei is essential for making a breast cancer diagnosis using histological pictures. Techniques such as thresholding, active contour, Hough transform, watershed technique, region expanding, etc. are used for automated nuclei detection/segmentation from histopathology images. The identified nuclei are then processed to obtain discriminatory characteristics for categorization. The work of Filipczuk et al. for instance employs a nucleus-segmenting hybrid approach based on adaptive thresholding and k-means clustering.[18]–[20]

The nucleus was dissected to obtain its various morphological properties before being classified. This method successfully distinguished between benign and malignant breast cancers in fine needle biopsy cytological pictures 94% of the time (FNB).

Spanhol et al. were the first to show how to use the feature engineering method on the BreaKHis dataset. Six feature descriptors and many classifiers were employed in their tests. For photographs of breast tumors, the accuracy of this method ranges from 80% to 85% depending on the magnification used.

The CAD system relies heavily on feature extraction, and many techniques are shown for identifying cancerous and noncancerous tumors. Mass categorization in mammograms has been accomplished with the use of geometric parameters such as mean intensity, perimeter, diameter, centroid, and area. With just 40 Mini-MIAS pictures, a neural network (NN) with numerous hidden nodes and other characteristics supplied into the classifier achieved great accuracy. It was postulated in that mammograms may be categorized by looking at their border points and using the Hough transform to evaluate the shape's properties. It's for isolating geometric shapes in mammograms. Evaluation of this study using the support vector machine (SVM) classifier has been limited to only 95 mammography images thus far.

Recent years have seen state-of-the-art achievements in histopathology image categorization achieved via the use of deep learning with CNNs. On the other hand, to feature engineering, CNNs can automatically extract features from the raw data. Spanhol et al. utilized the patch technique to train a CNN as the first deep learning methodology on the BreaKHis database.

When starting with fewer data points, transfer learning has shown to be more effective than training CNNs from scratch. Spanhol et al. initially explored the possibility of using pre-trained CNNs on the BreaKHis dataset for feature ex- traction, and their findings were superior to those of the standard approach. On photos of varying magnifications, the average degree of accuracy was observed to be between 81% and 85%. On the BreaKHis dataset, Mehra et al. compared the results of transfer learning with those of training from scratch. When compared to VGG-19 and ResNet-50, which were both pre-trained, VGG-16 achieved a higher accuracy (91.7%).

3. Proposed Breast Cancer detection structure

There is a great deal of information packed into digital photos, and to decipher them, powerful image processing and analysis tools are required. To automatically diagnose in this model, it is required to collect key medical information, known as significant characteristics, consistently and

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accurately. A high-quality picture is essential for accurate and efficient feature extraction. While capturing a picture, though, image quality cannot be guaranteed. Therefore, improving the image's quality is essential. It is crucial to the diagnostic process to analyze the retrieved characteristics, which requires sophisticated classification tools and machine learning approaches. Figure 1 shows the proposed model.

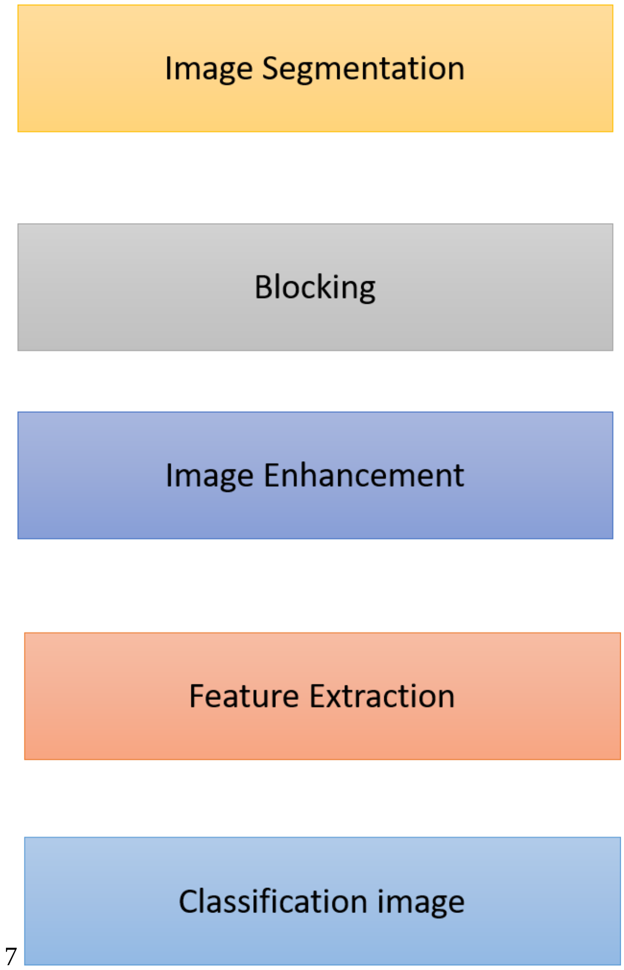

Figure 1: The proposed Model

3.1 Image Processing

H&E (hematoxylin-eosin) stains are often used to colorize tissue samples for microscopic examination of cellular architecture and other tissue components. Hematoxylin component stains nuclei a bluish purple, whereas cytoplasm, cell walls, and extracellular fibers take on a pinkish-orange hue. Because slide scanners have a range of sensitivity, the H&E pictures might seem to have a wide range of color shifts. Staining the tissue slides with varying quantities of the dye causes the tissue samples to absorb light at varied rates. Changes in the scanned photos' appearance are also caused by this. As a result, the aforementioned problems can't be resolved without first stain normalizing and color standardizing the H&E stained photos.

3.2 Feature Extraction

In medical imaging, especially breast imaging, asymmetric analysis is a commonly used tool for finding abnormal situations. This method involves comparing a patient's left and right breasts. Each patient's risk of developing breast cancer is increased if the degree of asymmetry between their left and right breasts is greater than a predetermined cutoff. Since breast cancer often spreads from its original site to other parts of the patient's body, this assessment makes sense. Furthermore, cases of cancer in both breasts at the same time are exceedingly rare. Thus, it is acceptable to use an asymmetric analytical approach. To get respectable outcomes with this technique, it is important to focus on efficient feature extraction. Two different sets of picture characteristics, based on MRF and modified LBP, are retrieved in this research.

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3.3 Transfer Learning

The objective behind a transfer learning model is to use a trained model's weighted layers for feature extraction without re-training the model's layers. One of the used networks is an AlexNet variant that was honed on the ImageNet data set. When the original network's last classification layer is removed, a 4096-dimensional feature vector is generated from the final feature layer. Next, a binary SVM classifier layer is applied to the features, which is trained using data from the BreaKHis database, and the characteristics are classed as benign or malignant. As a consequence, it's a low-complexity model since the training time for feature extraction is drastically cut down.

3.4 Classifier Fusion

With its probabilistic model and criteria for combining data from many sources, belief theory can account for the unknown and facilitate the fusion of previously siloed pieces of knowledge. It's excellent for use in any kind of classification system because of this. Dempster's rule for fusion is discussed in our study.

3.5 Fusion

Binary choices are generated to determine if the chosen ROI is cancerous or benign, and these decisions are used in the fusion process. After all, blocks have been tested, the fusion stage may make a final determination on the breast cancer class of the ROI based on the findings of five blocks. A measure of the certainty with which a diagnosis is made, as indicated in the assessment of malignancy risk. The fusion process raises the level of confidence in the diagnosis, which in turn leads to more precise diagnoses. Cases, where classifiers disagree, need more examination because of the inherent uncertainty introduced by the fusion process. The final choice is reached by fusing the five individual ROI votes using the majority vote fusion method. Next, a majority vote is taken to determine the outcome for each ROI. At the highest decision level, a decision is obtained by fusing the outputs of five separate decision-based trained classifiers.

3.6 Ablation Study

To ensure that our performance assessment is accurate and reliable, we use a cross-validation approach to calculate the outcome for each dataset. The classification effectiveness of this research is measured by using the performance metrics sensitivity (Sn), specificity (Sp), accuracy (AC), and F-measure.

Since the dataset depends largely on false negatives, the sensitivity (true positive rate) metric is the fraction of accurate strong texture indicators for classification. When sensitivity is increased, the proportion of correctly detected positive instances to the total number of positive cases rises, while the proportion of false negatives falls. By comparing the number of false positives to the total number of real images in the dataset, we can calculate the specificity (true negative rate). This ratio represents how effective the texture signs for classification are at enhancing and segmenting breast cancer mammogram images. The efficacy of the suggested detection approach is denoted by the accuracy (classification rate)). The degree of accuracy reveals how well the anticipated assessment outcomes match reality. To conclude, we get the F-measure.

3.7 ML Algorithms

As was mentioned up top, this paper's study used a binary classification model that was then applied to a pattern recognition classification issue. The method included randomly selecting 90% of the data set to serve as the training set and 10% as the test set. Logistic Regression, Nearest Neighbor, Naive Bayes, Support Vector Machine, Decision Tree Algorithm, and Random Forests Classification are just a few of the numerous techniques available for accomplishing classification problems. SVM, K-nearest neighbors (kNN), Naive Bayes (NGB), and a decision tree were the four approaches tested in this study (DT).

Finding the optimal separating hyperplane in the feature space to maximize the spacing among positive and negative values on the training set is the foundational model for Support Vector Machine. A support vector machine (SVM) is a supervised training approach for dealing with dual

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classification issues. The K-nearest neighbor classification technique is one of the easiest ml algorithms, yet it is also one of the most well-established in theory. The premise behind this technique is that if the majority of the k closest (i.e. the nearest neighbors in the higher dimensional space) samples around a particular sample belong to a specific category, then the sample in question must also belong to this category. Supervised learning models like Naive Bayes are generative. With minimal iteration required and high efficiency for learning, it is both easy to deploy and effective. It will do well in a statistically significant dataset. But it can't be used in situations where the input vector's feature conditions are intertwined since the assumption is too strong (that the feature criteria are independent). The chance that the net present value is larger than zero, the risk of the project, and whether or not it is feasible may be calculated using a decision tree based on the known probabilities of occurrence of different events. Intuitive users of probability analysis will find DT's graphical technique to be very helpful.

We ranked the approaches' efficiency to get the top-scoring algorithm and then analyzed their results. We ran the model building procedure 10 times for each approach and presented the classifier performance in a confusion matrix (CM). As the data sets were rather small, we conducted a 10-fold cross-validation assessment to ensure the accuracy of our classification results. Also, we compared the four utilized different classifiers by computing and analyzing their accuracy, sensitivity, and specificity.

4. Experimental Results

4.1 Image Achievement

In this research, we utilize two datasets to evaluate the suggested method against state-of-the-art techniques. Evaluating mammography classification performance methods requires using pictures from the mammogram dataset culled from a representative sample of the population. Protocols for splitting the mammography dataset into test and training sets for categorization are followed during the testing of such systems. Experiments may benefit from having access to many datasets of mammograms for comparison purposes. Mini Mammographic Image Processing Society (Mini-MIAS), Digital Dataset for Screening Mammography (DDSM), INbreast, and Breast Cancer Digital Registry (BCDR) were utilized for this analysis. Figure 2 shows the binary class images.

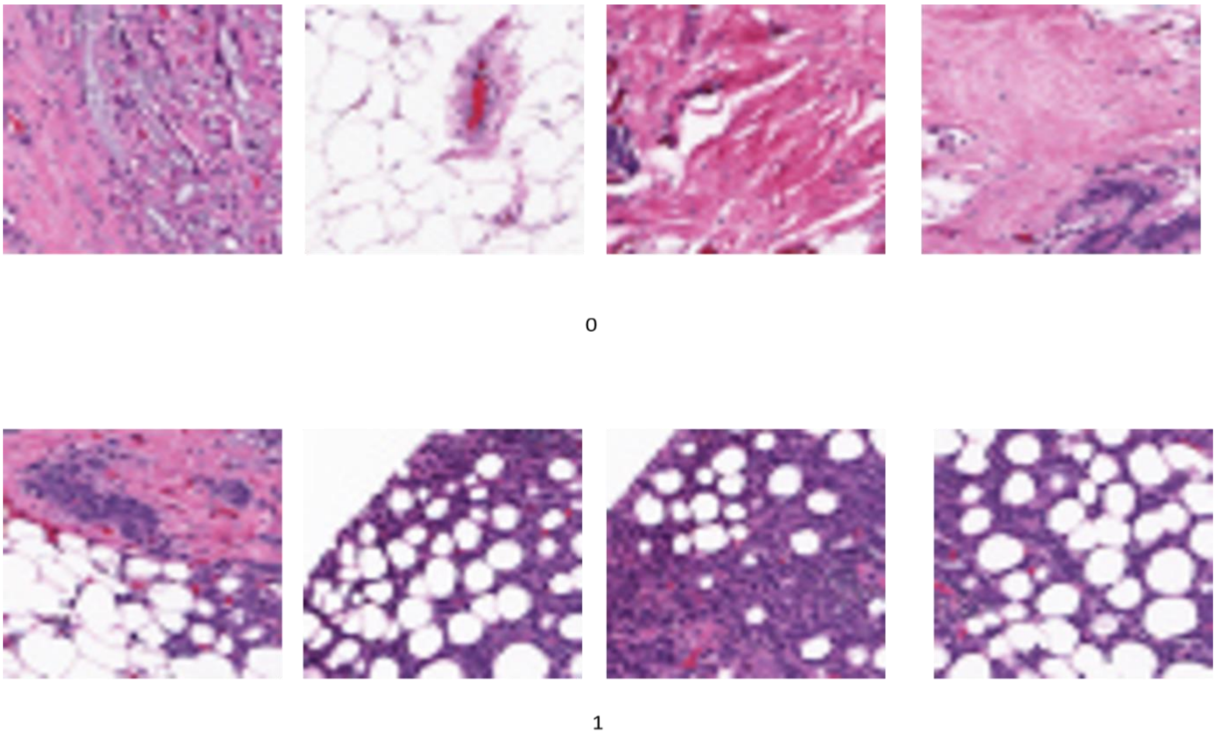

Figure 2: The two classes of images.

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Images from the databases have been digitalized and used in this research. Therefore, to assess and verify the suggested technique, a total of 20000 breast cancer mammograms are culled from various databases, consisting of 12000 benign and 8000 malignant cases.

Experts have gathered the ground truth labels, and they've diagnosed these instances (named them) using their knowledge and various diagnostic tools, such as mammograms. The sample sizes of the datasets used to create Table 1 are for mammography pictures. Before performing an assessment, each dataset's photos are split into two categories: training and testing.

Table 1: Distribution of the dataset

Data set	Total number of images		Training		Testing	
	Benign	Malignant	Benign	Malignant	Benign	Malignant
Data	12000	8000	1000	6000	2500	1500
Total	20000		16000		4000	

4.2 Binary Classification

In this part, we show you how well the suggested approach, which employs feature extraction and the ANN classifier, can distinguish between benign and malignant breast cancer mammograms. When training an artificial neural network (ANN) to distinguish malignant from benign cases, the multilayer perceptron was used as the ANN classifier because it follows the generalized least mean square (LMS) rule and employs the gradient search method to minimize the average difference between the output and the target value. The ANN was constructed with three layers: input, hidden, and output. Both the input and the hidden layers have the same number of nodes (125 nodes). In the training phase, ANN can make adjustments to the weights, and our results show an error of less than 0.1.

Using the suggested method, we extract 25 features from each ROI block and 125 features altogether. According to these results, not all retrieved characteristics are useful for categorization. Since characteristics were taken from each block, and blocks were categorized independently, the derived features may exhibit some connected traits. What's more, the proposed model's overall performance assessment does not rely on the ANN classifier being fed all extracted features. As a result, we begin by excluding associated characteristics, choose features of interest from each block using GA as the feature selection approach, and then incorporate the results. Each block's worth of mammography instances was used to train the ANN classifier. Values of 0.05, 0.5, and 8 are used for the ANN classifier's learning rate, momentum, and some hidden nodes, respectively. At this point, we had five trained ANN classifiers and generated five results for the full ROI. Once all the data was collected, a fusion procedure was carried out to arrive at a conclusive verdict. In Table 2, we can see the results of a comparison of three models used to evaluate the proposed model's performance.

Table 2: The ablation study of this work.

	Accuracy	Validation Accuracy	Precision	Recall	F1-Score
ANN	81%	82%	84%	81%	86%
CNN1	83%	84%	84%	86%	87%
CNN2	85%	86%	85%	88%	86%

Experiments reveal that our proposed model outperforms some prior research across a dataset in terms of assessment performance measures including accuracy, sensitivity, specificity, and the F-measure. Our suggested model incorporates several algorithms ANN, and CNN that together give a wide range of benefits.

The study set out to find the genes that may reliably differentiate TNBC from other types of breast cancer, and to do so using an ML-based classification system. The premise behind this approach was that DNA methods categorization utilizing ML algorithms may offer a framework to correctly interpret women at risk of developing TNBC, who could then be given priority for specialist therapy. We used the 5502 substantially differently expressed genes found from gene expression differences analysis with varying thresholds to assess the efficacy of four classification techniques designed to fill this gap (p values). Classifiers such as the KNNs, NGB, DT, and SVM were tested and compared. Ten separate models were created for each of these classifiers. Accuracy, sensitivity/recall, and specificity were calculated as mean values depending on the number of times every method was used to simulate a given dataset. Table 3 displays the averaged accuracy, recall, and specificity values for the four different categorization methods. Following is a definition and calculation of these performance measures:

$$Accuracy = \frac{Tp + TN}{TP + TN + FP + FN}$$

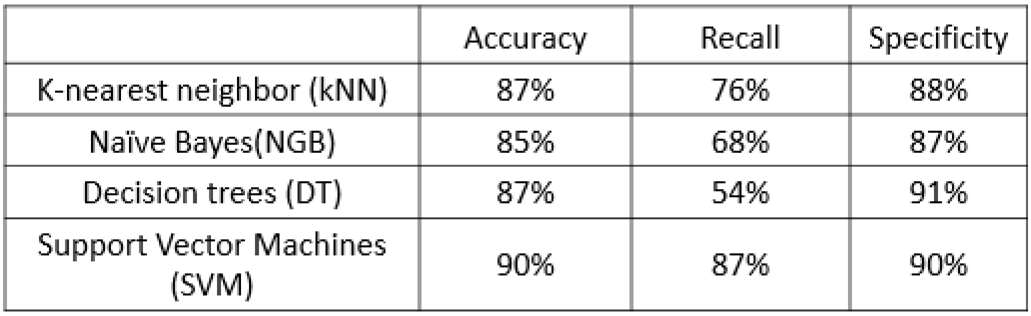
$$Recall = \frac{Tp}{TP + FN}$$

$$Specificity = \frac{TN}{TN + FP}$$

$$Precision = \frac{Tp}{TP + FP}$$

$$F1\,Score = 2 * \frac{Recall * Precision}{Recall + Precision}$$

Table 3. Ml algorithms accuracy.



	Accuracy	Recall	Specificity
K-nearest neighbor (kNN)	87%	76%	88%
Naïve Bayes(NGB)	85%	68%	87%
Decision trees (DT)	87%	54%	91%
Support Vector Machines (SVM)	90%	87%	90%

With 90% correctness, 87% recall, and 90% specificity, SVM outperformed the other three examined classification techniques, which achieved 87% accuracy, 76% recall, and 88% specificity, respectively. NGB and DT had decent precision, but terrible recall. There was a lot of variation in the assessment parameters because of the huge number of characteristics and the uneven distribution of the samples.

It has been shown that the classification algorithms' efficacy might be hampered by the excessive quantity of features (5502 genes). Therefore, we conducted a series of additional experiments on the methods using fewer genes picked at varying thresholds to establish which algorithm worked best. Using this method, the 5502 transcripts were sorted according to their FDR-adjusted p-values. Using the same metrics as before (accuracy, recall, and specificity), we choose the best 200, 150, 100, and 50 genes to utilize in the performance assessment of each model. We put all four algorithms through their paces for each group of genes.

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6. Conclusion

Both the methods used and the picture itself have an impact on what can be extracted most accurately. The extracted features, however, need to be consistent in terms of noises and artifacts while being resilient in terms of size, translation, illumination, and orientation. This research suggests a reliable method for finding breast cancer in mammograms. Specifically, this research improves upon previous efforts by creating a novel model for feature extraction in mammography images. This new framework was able to reach an accuracy of 96.91 percent, making it competitive with state-of-the-art methods. The experimental findings and the resulting simplicity validate the concept as a viable method for developing low-cost CAD systems for breast cancer diagnosis. The model is based on histopathological pictures taken using photomicroscopy, which are both readily accessible and reasonably inexpensive, suggesting further clinical implications in terms of the suggested system's compatibility to work in the current clinical settings of the hospitals. It has already been shown that training a CNN with exceptionally big-size histological images is not feasible for clinical use.

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