Breast cancer diagnosis system using hybrid support vector machine-artificial neural network

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ABSTRACT

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Keywords:

ANN Breast cancer CAD Classification SVM Breast cancer is the second most common cancer occurring in women. Early detection through mammogram screening can save more women's lives. However, even senior radiologists may over-diagnose the clinical condition. Machine learning (ML) is the most used technique in the diagnosis of cancer to help reduce human errors. This study is aimed to develop a computeraided detection (CAD) system using ML for classification purposes. In this work, 80 digital mammograms of normal breasts, 40 of benign and 40 of malignant cases were chosen from the mini MIAS dataset. These images were denoised using median filter after they were segmented to obtain a region of interest (ROI) and enhanced using histogram equalization. This work compared the performance of artificial neural network (ANN), support vector machine (SVM), reduced features of SVM and the hybrid SVM-ANN for classification process using the statistical and gray level co-occurrence matrix (GLCM) features extracted from the enhanced images. It is found that the hybrid SVM-ANN gives the best accuracy of 99.4% and 100% in differentiating normal from abnormal, and benign from malignant cases, respectively. This hybrid SVM-ANN model was deployed in developing the CAD system which showed relatively good accuracy of 98%.

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1. INTRODUCTION

An uncontrolled growth of cells leads to the formation of a tumor, which may later transform into cancer. If it happens in the breast, it is termed as breast cancer. A tumor can be classified into normal and pathological (or abnormal). An abnormal tumor can be of non-cancerous (benign) or cancerous (malignant). Unlike the case of the malignant condition, a benign tumor is localized and does not spread to surrounding cells or organs. Breast cancer is the number 2 cause of mortality among women [1]. According to the Global Cancer Statistics 2018, breast cancer made up about 11.6% of cancer cases in both sexes, and 24.2% of the most common cancer among women [2]. Breast cancer comprised about 1 out of 4 cancer cases diagnosed among women [2]. According to data collected from national cancer registry (NCR) conducted by [3], stage 1 to stage 4 of breast cancer has the best survival rate of 81.7%, 72.4%, 39.9% and 12.9%, correspondingly. Stage 1 is considered as the beginning-stage whereas in stage 4 cancer metastasizes to other organs/body parts [4].

One way to detect breast cancer early is through regular mammogram screening. A low-dose X-ray is used in mammograms to detect early metastases in breast cancer. There are three main types of

mammography namely screen-filming, digital mammography and digital breast tomosynthesis. A recent study in [5] proposed a combination screening of digital mammography and digital breast tomosynthesis for the diagnosis. Once cancer is detected, treatment can be given early to stop or slow down the spread of the cancerous (malignant) cells.

Mammogram screening is an early step in breast cancer detection before going into diagnosis. It was reported in [6] that around 65%–90% of positively diagnosed breast mammograms which, after undergoing a biopsy, are confirmed as negative; this situation is known as false positive (FP). FP is a test result in which the medical personnel or radiologists wrongly diagnosed the presence of a particular condition or attribute (disease) when the person does not have it. In this case, patients suffered from unnecessary pain, risk and cost of biopsy procedure for suspected lesions. Another report in [7] showed that 65%-75% of positive breast cancer cases are unable to be detected due to the difficulty in interpreting mammograms, even for experienced radiologists. This situation is considered as false negative (FN), which recognized normality or the absence of a particular condition or disease even when the person is with the disease. The incidence of FN causes patients to miss the golden opportunity to fight breast cancer, which may be life-threatening [8]. Several computer-aided design (CAD) detection systems have been used by radiologists to detect breast cancer, but they have yet to reduce the rate of false-positive cases.

The integration of information and communication technologies [9], big data [10, 11], cyberphysical system (CPS) [12] and machine learning (ML) can help in diagnosis and prognosis of breast cancer. Big data is referred to as a large volume of data which is exponentially growing [13]. Big data in this study can be obtained from medical screening, pathological data [14] or online medical database. CPS is a physical component that is linked with the simulation model, while ML is a study of computer algorithms to do prediction, pattern recognition and classification. The manipulation of big data using an optimal ML algorithm in the development of a CAD system can help radiologists in interpreting the diagnosis of cancer, and reduce the mortality rate.

There are supervised and unsupervised learning in ML. Supervised learning would supply labeled input and output for the machine to do prediction or classification, while unsupervised learning only supplies labeled input to the machine. In the latter strategy, the machine would learn from the experience in its classification. Artificial neural networks (ANN) and support vector machine (SVM) are two popular examples of supervised ML algorithms.

ANN is inspired by networks of human brain neurons. A collection of neuron forms a layer. ANN consists of an input layer, hidden layer and output layer. The hidden layer has an activation function that connects the input layer with the output layer. Each node X_i in the input layer has its weight, W_i . Summation of a product of each node with its weight is called a net $\sum_{i=1}^{n} X_i W_i$ [15]. The net is inputted in an activation function to give a prediction or classification as follows:

$$Y_i = f(\sum W_i X_i)$$

SVM can perform pattern recognition, classification and prediction based on statistical learning and the principle of structural risk minimization. The SVM was invented by Vapnik with colleagues at AT&T Bell Laboratories to search for optimal hyperplane ($w_0 \ x + b_0 = 0$) that separates a set of training data (x_1, y_1), ... (x_n, y_n), with a maximum margin [16] where every x_n is real pattern and y_n is either 1 or -1. When $y_n = 1$, the real pattern is in class 1, while $y_n = -1$, the real pattern is in class 2.

The real pattern is linearly separable if

 $\vec{w} \cdot \vec{x}_i + b \ge 1$, if $y_i = 1$ $\vec{w} \cdot \vec{x}_i + b \le -1$, if $y_i = -1$

The above inequality can be written as $y(\vec{w} \cdot \vec{x}_i + b) \ge 1$, $i = 1 \dots n$. The optimal hyperplane can be found by minimizing |w| subject to $y(\vec{w} \cdot \vec{x}_i + b) \ge 1$, $i = 1 \dots n$.

Hence, the linear classifier of the optimal hyperplane is given by:

 $\vec{x} \rightarrow sign(w \cdot x_i + b)$

Four models (back propagation algorithm, radial basis function networks, learning vector quantization (LVQ) and competitive learning network) of the ANN algorithms were employed on wisconsin breast cancer dataset (WBCD) in [17]. The LVQ algorithm was concluded as the best model with 95.82% accuracy [17]. The WBCD dataset contains 699 samples of biopsies, which comprises of 458 malignant and 241 benign cases with 9 features. Nonetheless, this dataset has 16 missing cases, thus it reduces to 683 cases.

A study in [18] applied the neural network pattern recognition tool in MATLAB on breast cancer data available in the MATLAB. This database has 699 biopsied samples, each with 9 features, and they obtained an accuracy of 97.6%.

SVM has been broadly employed in the classification of cancer due to its high accuracy [19]. In a study done by [20] on WBCD, it is shown that SVM gives 97.2% accuracy. Akay [21] utilized F-score to choose significant features, SVM on WBCD and obtained 99.51% in the classification accuracy. The researcher [22] utilized K-means-SVM and reduced 32 features to 6 on WBCD, which showed a classification accuracy of 97.38%. Chtihrakkannan [23] used X-ray mammogram, image processing techniques, wavelet transform and GLCM features extraction in their classification. They compared classification results from ANN, SVM, K-nearest neighbor (KNN) and deep neural network (DNN). They concluded that DNN gives the best accuracy of 96.3%.

A comparison of the performance of ANN and SVM using 64 benign, 51 malignant and 70 normal images randomly chosen from the MIAS dataset was carried out in [24]. SVM yields 95% accuracy as compared to ANN (93%). A breast cancer classification using WBCD and ML algorithm in [25] proves KNN yields 97.51% accuracy as compared to 96.19% given by the naive bayes (NB) classifier. A comparison of four ML algorithms namely SVM, logistic regression (LR), NB and random forest (RF) on WBCD in [26] showed that RF gives the best classification accuracy of 99.76%.

Omondiagbe *et al.* [27] examined the classification performance on SVM using a radial basis kernel, ANN and NB on WBCD. They later selected useful features using correlation-based feature selection (CFS) and recursive feature elimination (RFE). Principal component analysis (PCA) and linear discriminant analysis (LDA) were adopted to eliminate less useful features. SVM-LDA was chosen as the best classifier, which results in 98.82% accuracy. In [28], 11 out of 1879 online articles were selected, and the performance of five different ML algorithms namely ANN, SVM, KNN, NB and decision tree (DT) on breast cancer classification were investigated. It was concluded that SVM outperformed the others.

In another work, eight ML algorithms were adopted on WBCD in [29]. These algorithms are LR, bayes network (BN), multilayer perceptron (MLP), sequential minimal optimization (SMO), J48 decision tree, NB and instance-based learner (IBK). It was concluded that BN gives 97.14% accuracy. Similarly, recently in [30], three ML algorithms: LR, RF, and DT were performed on WBCD and it was showed that LR yields the best accuracy of 99.30%. Other researchers [31] proposed a breast cancer diagnosis and prediction system using the best predictive model from the 6 ML algorithms namely NB, RF, ANN, KNN, SVM and DT. Gharibdousti [32] applied PCA, DA and LR for feature reduction together with SVM, NB, DT, LR and ANN. They proved that DA-LR performs the best.

Even though the above-mentioned previous breast cancer classification using ML techniques showed promising classification performance, those works were conducted on a WBCD dataset, which was from biopsies of abnormal cells and not from digital mammograms. Besides, these classification works were mainly to differentiate between benign and malignant cases. In this paper, we made an extra effort to provide a classification of normal-abnormal, and between benign and malignant cases from digital mammograms. On top of that, previous researchers had not tested their algorithms on new/unseen images. For this purpose, a ML-based CAD was developed in this work to classify if a digital mammogram is normal, benign or malignant. A mini-MIAS database that consists of 322 digital mammograms of normal, benign and malignant cases was chosen. A comparison of the performance of SVM, ANN, SVM with reduced features and hybrid SVM-ANN classification of digital mammograms were investigated using 80 images of normal breast, 40 benign and 40 malignant randomly chosen mammograms. All these works were accomplished using MATLAB 2019b. ANN and SVM were chosen as they are the most commonly used ML techniques to predict cancer [20]. It must also be mentioned that, as of today's date, not much works can be found on the use of the SVM classification tool in MATLAB. The best net model was deployed for use in the developed CAD system (using MATLAB graphical user interface, GUI program) to classify if a mammogram is normal, benign or malignant. The performance of the CAD program was then tested with another 100 new images.

2. RESEARCH METHOD

This study consists of two phases: the data training phase and the development of the CAD system for field application using MATLAB R2019b. The data training phase is shown in Figure 1. In the data training phase, the 160 mammograms (80 normal, 40 benign and 40 malignant) randomly chosen from mini-MIAS were first segmented to locate the region of interest (ROI). Later the ROI was preprocessed using median filtering to remove the noise and enhanced using histogram equalization. Next, statistical and gray level co-occurrence matrix (GLCM) features of these enhanced ROI images were extracted before they were used in the net model training stage. The trained net would then be deployed for use in the CAD system.

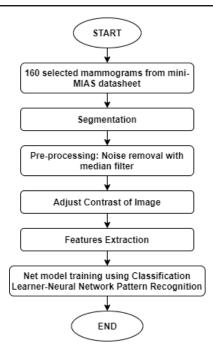


Figure 1. Preparation of data for training of ML models

The segmentation was based on the ground truth provided by the database for an abnormal case, and by locating the region of Mammograms that was considered as tumor-free for the normal case. There are a total of 21 features given from five statistical features namely mean, variance, skewness, kurtosis, and entropy, and four texture features of (GLCM) (i.e., contrast, energy, correlation and homogeneity, and at 4 different angles of 0° , 45° , 90° and 135°) considered for feature extraction. The features arrangement started from contrast, energy, correlation and homogeneity, mean, variance, skewness, kurtosis, and entropy.

Figure 2 shows the classification carried on in 2 stages via SVM implemented using *classification learner app* and ANN model from *neural network pattern recognition app* available in MATLAB R2019b. The first stage is to classify if a mammogram is normal or abnormal. The second stage is from the abnormal tumor, it was classified into benign and malignant. The SVM classification was conducted by selecting *All SVMs* in Figure 2 to run *linear, quadratic, cubic, fine gaussian, medium gaussian* and *coarse gaussian* models of SVM in one short. Later, the *optimizable SVM* was conducted too. The highest classification accuracy model was selected.

The 2-layered feedforward NN structure was created using *neural network pattern recognition app* is shown in Figure 3. The input contains 21 features, while the output is the class of mammogram either normal/abnormal in the first stage, while benign/malignant in the second stage. 15 neurons were set in the hidden layer and 1 neuron was set in the output layer. The NN was trained using 70%, 15% and 15% of training, validation and testing respectively. The classification results for both SVM and NN with 21 features were recorded and compared.

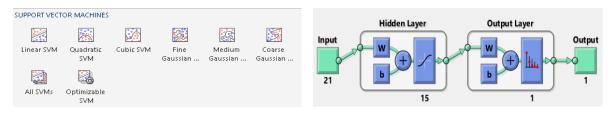


Figure 2. Type of SVM in MATLAB classification learner app

Figure 3. ANN structure

To improve the SVM classification accuracy, the *features selection* tab from *classification learner* app which comprises all 21 features were unchecked all. Later, the first feature was checked on and its

classification accuracy was recorded. The second feature was checked on next and the accuracy for both features was recorded and compared with only the first feature. If the newly added feature increases the accuracy then this newly added feature was kept, otherwise it was removed. The process was repeated for the subsequent features until the last feature to get the highest accuracy. The highest accuracy with selected features was recorded lastly. The reduced features will be input into ANN to get a hybrid SVM-ANN net model.

Figure 4 shows the flow diagram of the prediction using the developed CAD system. The functions of this CAD system are almost similar to that of the training phase, this is, however, with the addition of the binarization of the image to remove unwanted objects to display the largest detected region, and thresholding process to show possible tumor region for segmentation. The process of the CAD started with importing the SVM-ANN-trained net followed by a random selection of 100 digital mammograms from the directory. This is followed by the filtering of the selected mammogram using a median filter before the filtered image is binarized to remove unwanted objects like tag in the mammograms. Next, the largest detected region was cropped. After that, a threshold value was applied to this region; image pixels of high intensity (white region) (higher than that of the threshold value) will be shown as the possible tumor regions. This guides its users to click the mammogram region with suggestive tumor lesions. Once a point of interest was selected from the possible tumor region, the ROI would be segmented. Later, a histogram equalization was adopted to enhance the ROI followed by features extraction and lastly classification using the imported hybrid SVM-ANN from the data training process. The performances of the training and testing phases were evaluated based on the calculation of the confusion matrix as shown in Table 1.

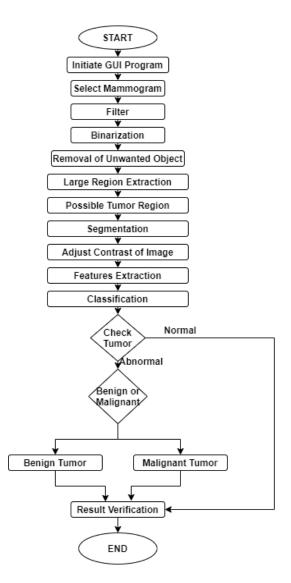


Figure 4. Operation flow diagram of the developed CAD system

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	Т	Cable 1. Confusion matrix	
	Non-cancerous	Cancerous	
Negative diagnosis	TN	FN	Negative Precision $= \frac{TN}{TN + FN}$
Positive diagnosis	FP	TP	Positive Precision = $\frac{TP}{FP+TP}$
U	Specificity = $\frac{TN}{TN+FP}$	Sensitivity $= \frac{TP}{FN+TP}$	Accuracy = $\frac{TN+TP}{TN+TP+FN+FP}$

3. RESULTS AND DISCUSSION

Table 2 shows the comparison of the performance of SVM, ANN, SVM with reduced features and hybrid SVM-ANN models. The performance of the SVM model in the classification of normal and abnormal cases is 78.8%, while between benign and malignant is 71.3%. On the other hand, the performance of the ANN model for normal and abnormal classification work is slightly higher, which is 83.1%, but there is a reduction in its performance in the classification of benign and malignant to 78.8%.

Table 2. Comparison of performance of SVM, ANN, SVM with reduced features and hybrid SVM-ANN models

	SVM model	ANN model	SVM model (reduced features)	Hybrid SVM-ANN model
Normal/Abnormal	78.8%	83.1%	80%	99.4%
Benign/ Malignant	71.3%	78.8%	73.8%	100%

Some of the features were then removed to improve the accuracy of the SVM for classification of the normal and abnormal cases. This is through manual identification of 12 unwanted features that caused a decline in accuracy; these features were removed leaving 9 (third feature of contrast, first to third features of energy, first, second and fourth features of homogeneity, skewness, and entropy) features remained. Meanwhile, 10 features that caused a decline in accuracy (in differentiating benign from malignant) were removed, while the other 11 features (contrast, first to third features of energy, first and third feature of correlation, third feature of homogeneity and kurtosis) were kept for the training model used in the classification of benign and malignant cases. The kept features can be referred to as given in Figure 5. The highest accuracies obtained for the SVM model with reduced features are given by 80 % and 73.8 % for classification of normal-abnormal and benign-malignant cases, respectively as display in Figure 6.

	Feature Selection	Feature Selection	
eature Selection		✓ row_1	Feature Selection
row_1	row_8		
	row_9	✓ row_2	row_8
	row_10	row_3	✓ row_9
✓ row_3	row_11	✓ row_4	row_10
row_4		✓ row_5	✓ row_11
✓ row_5	row_12	✓ row_6	row_12
🗹 row_б	✓ row_13		row_13
	✓ row_14	✓ row_7	
✓ row_7	row_15	row_8	row_14
row_8	✓ row_16	row_9	✓ row_15
row_9		row_10	row_16
row_10	row_17	✓ row_11	row_17
 row_11	row_18	row_12	row_18
_	✓ row_19		 row_19
row_12	row_20	row_13	
✓ row_13	✓ row_21	row_14	✓ row_20
✓ row_14		✓ row 15	row_21
	(a)		(b)

Figure 5. Feature selection of: (a) Normal-abnormal cases, (b) Benign-malignant cases

50 ☆ SVM Last change:		Accuracy: 80.0% 9/21 features
	(a)	
27 🏠 SVM Last change:		Accuracy: 73.8% 11/21 features
	(b)	

Figure 6. Accuracy of reduced features: (a) Normal-abnormal cases, (b) Benign-malignant cases

Lastly, the reduced featured obtained from SVM were supplied into ANN to give a hybrid SVM-ANN model. This hybrid model achieved the highest performance results, which are 99.4% for classification of normal and abnormal cases whereas the accuracy of 100% is obtained for benign and malignant classification. Therefore, the hybrid SVM-ANN model was chosen as the net model in the CAD system.

In the efforts to test the performance of the CAD system, 100 mammograms that have not involved in the training phase were randomly chosen for classification. The use of the CAD system in the classification of normal, benign and malignant breasts is shown in Figures 7-9. The left side of the GUI shows the functionality buttons, which starts from image loading (*select mammogram*) to preprocessing (*filter, binarization, removal of unwanted objects* as shown in Figure 10, *large region extraction, possible tumor region*), to *segmentation* of 256 x 256 pixels of ROI and *adjust image contrast* of the ROI before extracting the features. Once all the preprocessing functions on the left, *segmentation* and *adjust image contrast* panel have been executed, the processed/resulting figure would be displayed on the right side of the GUI. The default thresholding value is set 0.65 as shown in the GUI. Once *adjust image contrast* is clicked, the *feature extraction* button located on the left bottom panel would enable its users to view all 21 of the values of the calculated features. Lastly in the classification panel, the results would indicate whether the mammogram is normal, benign or malignant after the *classification* button is pressed.

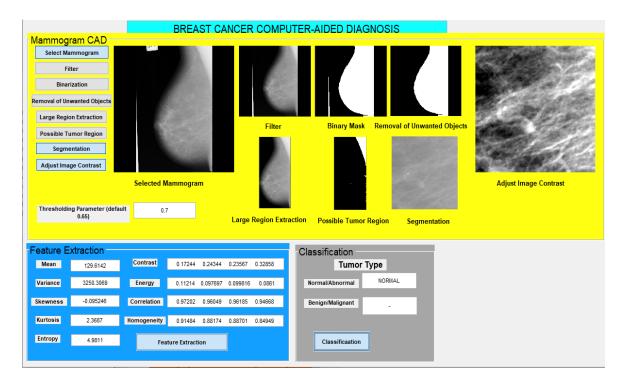


Figure 7. An example of the developed CAD application in identifying normal breast

			BREA	ST CA	NCER		UTER-AIDED DIAGNOSIS
Mammo	gram CAD				_		
Select I	Mammogram	1				100	2748 TSR COLL 1008 29 20
	Filter	10				100	
Bin	arization	1907					
	Unwanted Objects						
	gion Extraction					Filter	Binary Mask Removal of Unwanted Objects
Possible	Tumor Region						TOTAL CONTRACTOR OF TAXABLE CONTRACTOR
Segr	mentation	Street Second					A REAL A GLEVERS AND A REAL AND A
Adjust In	nage Contrast					188	
						1993	
		Selected N	lammogra	m			Adjust Image Contrast
Threshold	ding Parameter (defau 0.65)	ult 0.7	7				
					Large	Region Ex	traction Possible Tumor Region Segmentation
Feature	Extraction						-Classification
Mean	184.1288	Contrast	0.067349	0.09993	0.076149	0.096817	Tumor Type
Variance	2171.7924	Energy	0.29389	0.2771	0.28788	0.28217	Normal/Abnormal ABNORMAL
Skewness	-1.8497	Correlation	0.98414	0.97624	0.98197	0.97698	Benign/Malignant BENIGN
Kurtosis	6.7737	Homogeneity	0.96633	0.95004	0.96193	0.95167	
Entropy	6.112	Fea	ture Extracti	on]		Classification

Figure 8. An illustration of CAD detection result for benign case

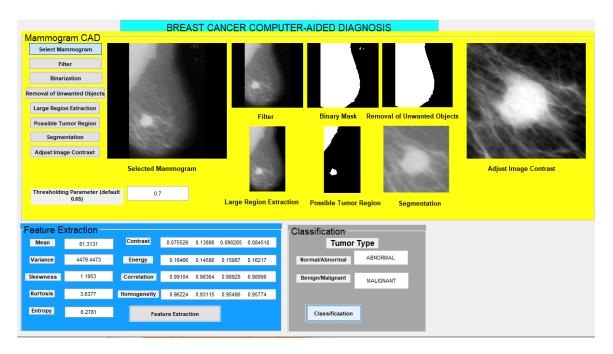
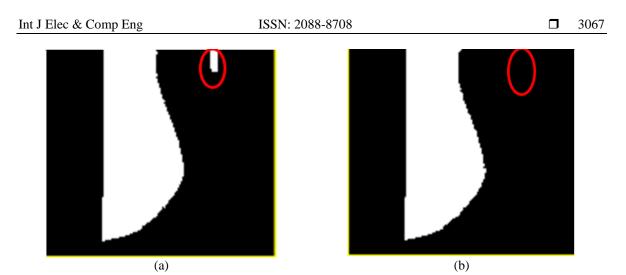
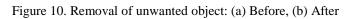


Figure 9. An illustration of CAD detection result for malignant case

Once the *Segmentation* button is clicked, two images appear with the binary masked image on the left and the original largest extracted breast region on the right as seen in Figure 11. Other than that, there will be a crosshair or guiding axis for the users to locate and select the possible tumor region. Once, the possible tumor region is clicked, a 256x256 ROI will be segmented as seen on top of the *Segmentation* button in Figures 7-9.

Meanwhile, the accuracy, specificity, sensitivity, negative precision and positive precision obtained following validation of the system using the unseen 100 mammograms are given by 98% (i.e., 98/100*100), 97.70% (85/87*100%), 100% (13/13*100%), 100% (85/85*100%) and 86.67% (13/15*100%) as given in Table 3. The detail of normal, benign and malignant classification can be referred to in Table 4.





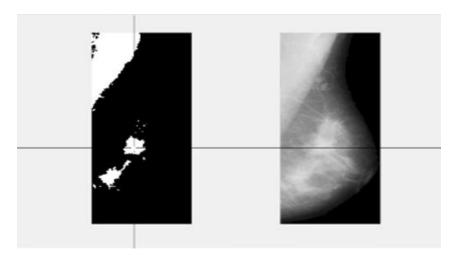


Figure 11. Segmentation of tumor region using a crosshair

	Noncancerous	Cancerous	
Negative diagnosis	85	0	Negative Precision 100%
Positive diagnosis	2	13	Positive Precision 86.67%
	Specificity	Sensitivity	Accuracy
	97.70%	100%	98%

Table 3. Confusion matrix of CAD program's performance

Table 4. Classification results of CAD program's performance

			Real	
		Normal	Benign	Malignant
Predicted	Normal	62	0	0
	Benign	0	23	0
	Malignant	0	2	13

4. CONCLUSION

In this study, a comparison of the performance of SVM, ANN, SVM with reduced features and hybrid SVM-ANN model in the breast cancer diagnosis was carried out. The hybrid SVM-ANN net model was chosen to be imported into the CAD system for the testing of the new data owing to its high accuracy of 99.4% and 100% for classification of normal-abnormal and benign-malignant cases, respectively. The developed CAD system starts with the functions *select mammogram*, *filter*, *binarization*, *removal of unwanted objects*, *large region extraction*, *possible tumor region*, *segmentation*, *adjust image contrast, feature extraction* and *classification*. This system can classify a tumor image into either normal, benign or

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malignant. This was confirmed using 100 randomly chosen new samples; the results showed relatively good performance of 98%, 97.70%, 100%, 100% and 86.67% for accuracy, specificity, sensitivity, negative precision and positive precision, respectively.

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