Classification of Breast Cancer Tumors Using Mammography Images Processing Based on Machine Learning

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Abstract—Using intelligent methods to identify and classify a variety of diseases, in particular cancer, has gained tremendous attention today. Tumor classification plays an important role in medical diagnosis. This study's goal was to classify breast cancer (BC) tumors using software-based numerical techniques. To determine whether breast cancer masses are benign or malignant, we used MATLAB version 2020b to build a neural network. In the first step, the features of the training images and their output classes were used to train the network. Optimal weights were obtained after several repetitions, and the network was trained to produce the best result in the test phase after several repetitions. Because of using effective and accurate features, the method suggested here, which was based on an artificial neural network, delivered the diagnostic accuracy, specificity, and sensitivity of 100%, 100%, and 100%, respectively, to discern benign from malignant BC tumors, showing a better performance compared to previously proposed methods. One of the challenges for imaging-based diagnostic techniques in medicine is the difficulty of processing dense tissues. Breast cancer is one of the most common progressive diseases among females. Early diagnosis makes treatment easier and more effective. Using AI-based methods for automated diagnosis purposes can be valuable and have a reduced error rate because accurate diagnosis by manual means is time-consuming and error-prone.

Keywords—mammography images, breast cancer, benign and malignant masses, statistical processing, machine learning

1 Introduction

There are different organs in the human body, each of which has a special function for the health of the body and the soul. The breast is one such organ unique to the feminine body. There are many different types of breast diseases, including breast cancer (BC), which is a particularly important group. Breast cancer is the most common form of cancer and the third leading cause of death among women [3], killing many women annually [1]. Today, BC is among the most devastating diseases and a serious health problem worldwide and in any society [1, 2]. Although cancer-related mortality continues to rise, early detection of benign from malignant BC tumors (i.e., earlier than

five years from the first cancerous cell division) the patient's chances for survival increase from 56% to 86% [6,]. If diagnosed early, BC can be associated with complete recovery in many cases, offering the patient a disease-free survival (without need for treatment) for years. Nowadays, diagnostic achievements offered by assistive techniques bestow the women diagnosed with this disease a survival comparable to healthy counterparts [9, 20].

All cancers begin with a single mutation in a cell, and BC, similar to other cancers, develops upon the rapid and uncontrolled growth and development of a segment of the breast tissue. The disease is generally initiated in breast ducts but can extend beyond its normal boundaries, affecting the glands and adipose tissue of the same or even other organs of the body. According to risk stratification, there are two types of BC tumors, benign and malignant [1]. Generally, various breast masses have their own specific appearance in diagnostic images. Benign elliptical masses have distinct edges without blebs, while malignant tumors have irregular and coarse shapes, indistinct edges, and unclear and angular borders that become even more vertical and sharp over time [7- 8, 10].

The diagnosis and classification of BC is difficult without the help of appropriate diagnostic techniques [1]. Several low-risk imaging techniques, such as mammography, thermography, and magnetic resonance imaging, have been employed to diagnose cancer for years [4]. Unusual pathological findings and the observation of asymmetric masses in mammography images may suggest cancer [5]. Mammography is soft-tissue radiography and an important tool for screening BC in asymptomatic women. Screening mammography along with accurate medical examinations has been reported to reduce the mortality rate of BC up to 63%. Mammography benefits from lower X-ray emission, which is why its images have a lower resolution. In addition, mammography cannot eliminate the effects of overlapping tissues or produce tomographic images such as those of CT scans, so it is required to reconstruct mammography images to boost their quality.

Extensive efforts have been dedicated in recent years to help radiologists reduce errors and timely diagnose BC. In 2013, Haddadnia proposed a method for separating mammographic images based on the density of tissues and masses, which increased the accuracy and speed of image classification by eliminating additional data in mammography images, delivering a final accuracy of around 90% [11]. In 2016, Nick Ravan et al. conducted a three-step study. In the first step (i.e., pre-processing), they managed to remove noises and background from the image. The second step (i.e., feature extraction) included the extraction of textural and geometric features of the mass. Finally, in the third step (i.e., classification), they divided masses into benign and malignant categories. The method employed in this study retrieved an accuracy of 93.3% [12].

In 2017, Perez et al. developed a classification method in which they used an artificial neural network (ANN) to categorize mammograms into three groups: normal, benign, and malignant, reporting a final mean accuracy of 84.72% [13]. In 2018, Torres et al., to reduce false positive diagnosis, employed a digital database for screening mammography (DDSM) based on computer-aided design (CAD). They developed a function difference index to determine the presence or absence of masses, extract their features, and classify them as benign or malignant, delivering a final accuracy of

92.29% [14]. Also, in 2018, Nahid et al. discerned benign from malignant tumors with 98% accuracy using a convolutional neural network [15]. In 2020, SamiEkici et al. presented an algorithm for extracting and analyzing prominent breast features based on biological data and statistics. These features were extracted from the data recorded by a thermal camera and used to classify breast masses as normal or suspicious using a convolutional neural network and the Bayes algorithm. The proposed method was used to assess 140 patients and offered 98.95% accuracy [16].

High diagnostic accuracy is highly important to warrant human health as an important goal of biological research. In fact, diagnostic methods should deliver the least error rate and the highest reliability. In this regard, the methods based on artificial neural networks (ANN) have attracted considerable attention in recent years. Despite great achievements in medical diagnostic technologies, due to human errors (fatigue, incompetency, etc.) and the effects of environmental factors (inaccurate equipment, etc.), there is a need to benefit from artificial intelligence to boost the accuracy of disease diagnosis [1]. The use of artificial intelligence in medicine in parallel with the clinical experiences of physicians can significantly improve diagnostic accuracy and has resulted in promising outcomes. Many parameters are needed to be examined and analyzed to correctly diagnose a disease, and the multiplicity of these parameters emphasizes the importance of widespread use of artificial intelligence to help doctors make a more accurate diagnosis and better decisions.

Although benign tumors grow abnormally, they rarely lead to death. Nevertheless, benign tumors may be associated with an increased risk of BC in some cases. Breast cancer may present with tiny protrusions and small lime and calcium particles, which are particularly hard to detect. Therefore, the aim of this study was to introduce a machine-learning diagnostic algorithm to early diagnose and classify BC to reduce its mortality rate and its extensive costs.

The rest of the paper is designed as follows. In section 2, we have presented the dataset, and the proposed method for classification. In section 3, the experimental results are shown. In section 4, a discussion of the results is describe, and i concluding remarks are given.

2 Materials and methods

2.1 Dataset

In this research, to train and test the proposed algorithm, images were obtained from a database from the University California Irvine (UCI). These pictures were related to cancer patients referred to Wisconsin Hospital. In this database, there were 699 pictures from benign and malignant BC tumors, 16 of which contained at least an inaccessible feature. Overall, 458 (65.5%) of the samples were benign, and 241 (34.5%) were malignant. For each sample, nine different properties were extracted, each of which was given a score between one and 10 (one being the closest to benign) to be able to describe images using numerical variables. Among the features used in this study were cellular

thickness, size, and shape. Each sample was finally categorized as either benign or malignant [3]. The features extracted from this data have been summarized in Table 1.

Table 1. The features extracted for each sample

Extracted features	Benign samples Mean ± SD	Malignant samples Mean ± SD
Clump Thickness	2.9640±1.6727	7.1883±2.4379
Uniformity of Cell Size	1.3063±0.8557	6.5774±2.7242
Uniformity of Cell Shape	1.4144±0.9570	6.5607±2.5691
Marginal Adhesion	1.3468±0.9171	5.5858±3.1966
Single Epithelial Cell Size	2.1081±0.8771	5.3264±2.4431
Bare Nuclei	1.3468±1.1778	7.6276±3.1167
Bland Chromatin	2.0833±1.0632	5.9749±2.2824
Normal Nucleoli	1.2613±0.9546	5.8577±3.3489
Mitosis	1.0653±0.5097	2.6025±2.5645

Clump thickness. In terms of clump thickness, it can be noted that benign cells often form a single layer, but malignant cells usually tend to create more than one layer. So, thicker clumps are more likely to be cancerous rather than benign.

Uniformity of cell size and shape. Cancer cells vary in size and shape, and one critical parameter to determine whether cells are cancerous or not is to assess cell size uniformity. This is a parameter referring to cells' nuclei (without cytoplasm). It should be noted that uniformly sized nuclei are commonly seen in benign tumors.

Marginal adhesion. Benign cells are generally connected to each other and have clear angles, whereas connections among cancerous cells are loose, and edges are indistinct.

Single epithelial cell size. Epithelial cells' diameters vary from 9 to 17 μM in 97% of measurements in different individuals. It has been noted that in malignant tumors, epithelial cells are generally markedly enlarged.

Bare nuclei. The term refers to the nuclei that are not surrounded by cytoplasm (or other cells). Generally, the presence of a single nucleus without any other cellular components within the epithelial layers of the breast tissue biopsy indicates a benign lesion.

Bland chromatin. This feature describes a uniform tissue with homogenous nuclei observed in benign lesions. In malignant tumors; on the other hand, chromatin is coarse.

Normal Nucleoli. Nucleoli, which are seen in the nucleus of cells, appear small and invisible in benign and large and prominent in malignant cells.

Mitosis. Mitosis is the most common form of cell division and necessary for growth and repair, during which a cell produces an exact copy of itself. To ascertain cancer grade, the number of cell divisions is counted.

2.2 The proposed method

In this study, for cancer classification based on the features extracted, a multilayer perceptron (MLP) neural network, as one of the most renowned and practical artificial

neural networks, was employed. Also, the error back-propagation algorithm was used to teach the network based on different architectures [21-22]. As the type of each sample (i.e., benign or malignant) was known, a supervised teaching method for this network was utilized. The MLP network used in this research employed a Feed-Forward architecture consisting of an input, an output layer, and one or more hidden layers. Each layer contained a number of neurons linked with the neurons of other layers. It should be noted that as the number of layers increases, the number of connections and unknown parameters of the network also increases. In addition, increasing the number of hidden layers boosts the ability to learn complex functions. The aim of this study was to develop an optimal neural network architecture to increase the efficiency of the MLP network in the diagnosis and classification of BC and upgrade the results obtained in previous studies.

Considering the nature of learning-based systems, in each neural network, the data that are selected for training the network are chosen in a way that after training, the network would be ready to be tested with the data that have not been previously used in network training. In this study, a matrix of the features mentioned in the previous section was used as the input of the neural network. Around 70% of the data (310 benign, 167 malignant) were randomly applied for training the MLP neural network. The output was also regarded as a matrix equivalent to the input matrix. The matrix consisted of the numbers of zero and one (zero indicating benign and one indicating malignant). The input and output matrices were applied under various architectures to ensure effective training of the neural network and obtaining plausible test results. Then, to test the neural network, 30% of the data (134 benign and 72 malignant) that had an equal distribution were randomly used to evaluate the performance of the network and receive the output. The structure of the perceptron neural network with two hidden layers has been shown in Figure 1.

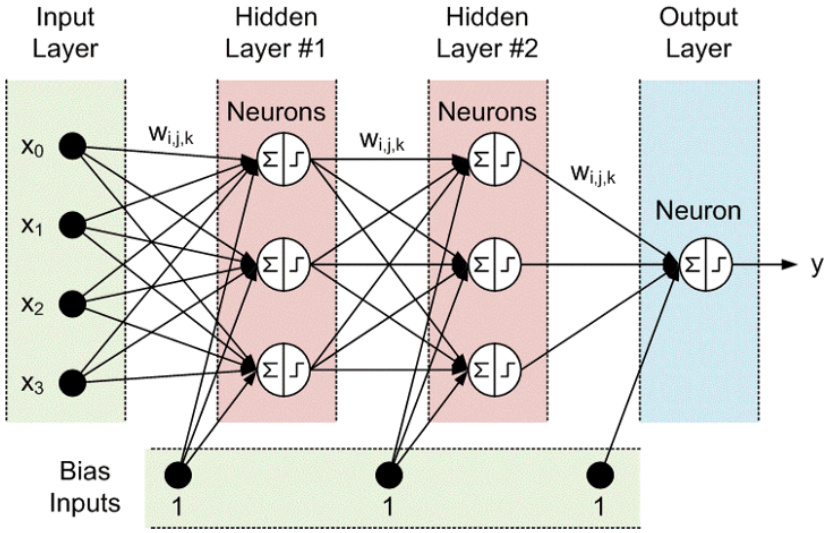

Fig. 1. The structure of the perceptron neural network with two hidden layers

The different steps taken in this study to diagnose and categorize BC have been summarized in Figure 2. In the preprocessing phase, the data were initially examined to exclude those with insufficient information about the sample. Then, different features were extracted from each sample, and in order to increase the efficiency of the diagnostic system, some differentiating diagnostic features, which were obtained by statistical tests, were utilized. Then, with the help of the MLP neural network and data, the network was trained and finally assessed based on test results. The performance of the neural network was determined by calculating sensitivity, specificity, and accuracy and compared with other studies.

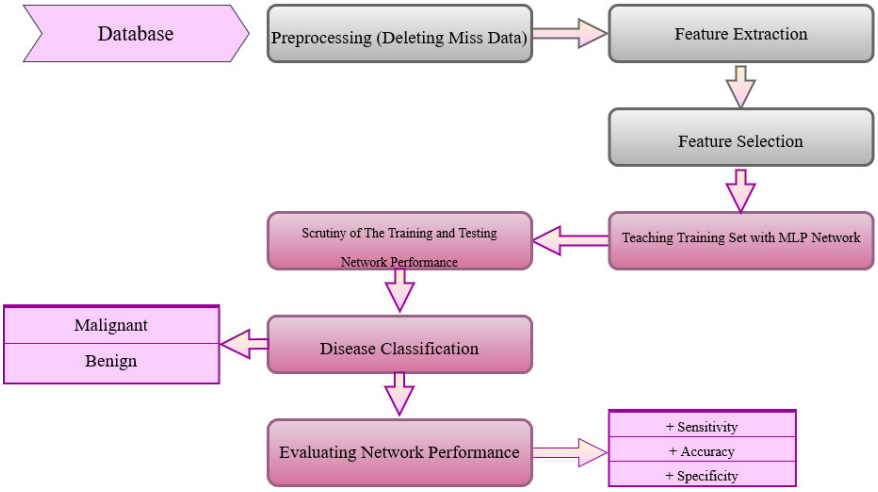

Fig. 2. The block diagram of the algorithm suggested in this study

3 Simulation results

To obtain simulation results, MATLAB R2020b software was used. The results highlighted the importance of selecting correct inputs (i.e., the features) to increase the accuracy and efficiency of the neural network and significantly decrease the convergence time. In this study, we used the MLP neural network and changed some structural parameters in the artificial neural network, such as training function, adaptation learning function, performance function, the number of hidden layers, and the number of neurons in each layer, and transfer function, to boost its efficiency in the diagnosis of BC [23]. Statistical analysis was performed on the different features extracted to evaluate their ability to differentiate benign from malignant lesions. The value of each feature and its differentiation capacity have been shown in Table 2. A P value of <0.05 indicated differentiation between the two groups. Figure 3 shows the box plots (including minimum, first quartile, median, third quartile, and maximum) of the values related to each feature in the two groups. This diagram is a standard method for scrutinizing the distribution of data and can also show the existence of outliers and symmetry in the data.

Table 2. The statistical analysis of the features

Extracted features	Benign samples Mean ± SD	Malignant samples Mean ± SD	P value
Clump Thickness	2.9640 ± 1.6727	7.1883 ± 2.4379	6.9102×10^{-65}
Uniformity of Cell Size	1.3063 ± 0.8557	6.5774 ± 2.7242	3.3883×10^{-76}
Uniformity of Cell Shape	1.4144 ± 0.9570	6.5607 ± 2.5691	4.8863×10^{-76}
Marginal Adhesion	1.3468 ± 0.9171	5.5858 ± 3.1966	2.5268×10^{-53}
Single Epithelial Cell Size	2.1081 ± 0.8771	5.3264 ± 2.4431	8.4978×10^{-46}
Bare Nuclei	1.3468 ± 1.1778	7.6276 ± 3.1167	3.8906×10^{-79}
Bland Chromatin	2.0833 ± 1.0632	5.9749 ± 2.2824	2.4293×10^{-52}
Normal Nucleoli	1.2613 ± 0.9546	5.8577 ± 3.3489	2.4221×10^{-51}
Mitosis	1.0653 ± 0.5097	2.6025 ± 2.5645	1.0053×10^{-16}

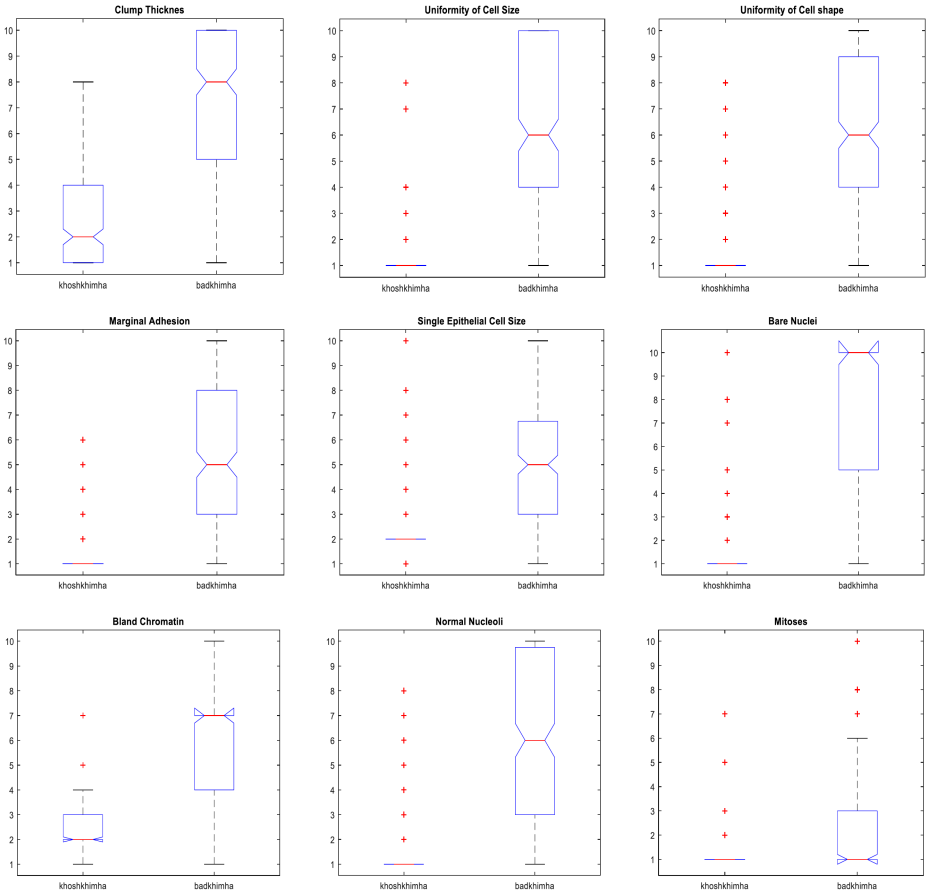

Fig. 3. A comparison of various features to detect breast cancer

3.1 Evaluating the proposed system

The essential criteria used for evaluating the performance of the diagnostic system (i.e., accuracy, sensitivity, and specificity) have been shown in Figure 4. To calculate these parameters, the rates of true positive (TP), true negative (TN), false negative (FN), and false positive (FP) were determined for each feature.

Specificity: This indicator shows the efficiency of the proposed diagnostic system in discerning benign lesions.

Sensitivity: This indicator shows the efficiency of the proposed diagnostic system in discerning malignant lesions.

Accuracy: This indicator shows the efficiency of the proposed diagnostic system in differentiating malignant from benign lesions. In fact, the accuracy of a diagnostic system that involves normal and abnormal groups reflects the rate of correct detection of each group.

TP: The system has detected the case as patient, which indeed is true.

TN: The system has detected the case as healthy, which indeed is true.

FN: The system has detected the case as healthy, but the case actually belongs to the patient group.

FP: The system has detected the case as a patient, but the case is actually healthy.

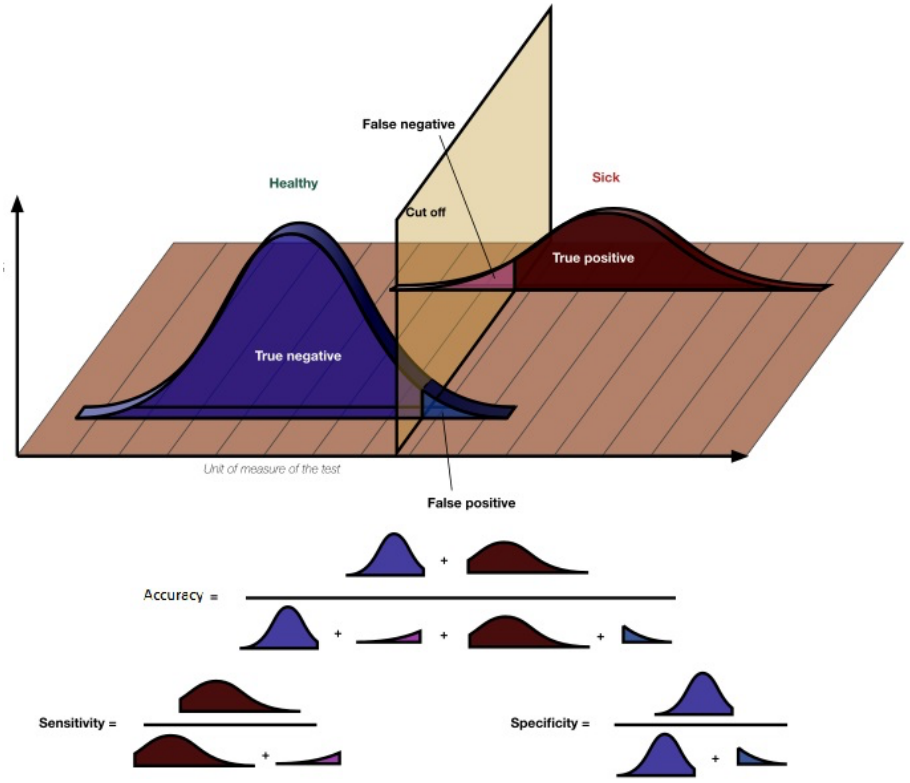

Fig. 4. The definition of sensitivity, specificity, and accuracy

These assessment criteria were calculated at the two stages of training and testing to discover the best answer. The results obtained at the training and testing steps have been shown in Tables 2 and 3, respectively, according to different types of training functions. The best answer in the training and testing steps was retrieved using the TRAINLM function. Using a three-layered neural network with four neurons in the hidden layers delivered the highest accuracy, specificity, and sensitivity in the testing step (100%, 100%, and 100%, respectively).

Table 3. The results of training the neuronal network using different training functions

Training function	SEN	SEP	ACC
TRAINOSS	97%	96%	97%
TRAINLM	95%	97%	96%
TRAINLM	100%	100%	100%
TRAINGDM	91%	98%	95%
TRAINGDA	93%	97%	95%
TRAINR	94%	98%	97%
TRAINRP	97%	97%	97%

Table 4. The results of testing the neuronal network using different training functions

Training function	SEN	SEP	ACC
TRAINOSS	93%	94%	63%
TRAINLM	100%	100%	100%
TRAINLM	95%	97%	97%
TRAINGDM	88%	97%	94%
TRAINGDA	97%	96%	96%
TRAINR	83%	98%	93%
TRAINRP	94%	98%	97%

4 Discussion and conclusion

Breast cancer is the most common neoplasm in women, which is triggered, like other cancers, by the rapid and uncontrolled growth and proliferation of a part of the breast tissue. Researchers have conducted numerous studies to employ ANNs to extract various features to successfully discern malignant from benign tumors. In this study, the data were initially entered into a preprocess phase to eliminate those including incomplete and unclear information. Then, in order to detect and classify BC, features such as breast shape and tumor mass density, volume, and boundaries were used. Afterward, by processing the information and designing different classifiers in MATLAB software, benign and malignant tumors would be identified. A software loaded with mammography images (containing the defined features) was finally employed to report the presence or absence of the disease [24].

Breast cancer diagnosis using ANNs has acquired great interest in recent years. It is critical for physicians to choose the correct treatment for cancer patients, which requires

cancer cells to be properly characterized. For a correct diagnosis, BC tumors need to be properly classified, and ANN-based diagnostic algorithms can be a great help to upgrade the accuracy and speed of diagnosis in this area.

The results of previous studies in this field have shown inferior performance compared to that of the system proposed in the present study. There are several methods for the pre-processing and classification of diagnostic images, and we here provide a brief review of the algorithms already employed for differentiating malignant tumors from other tumors to better understand the importance of the system proposed in this study. Marcano-Cedeno *et al.*, in 2011 employed an AM-MLP algorithm (inspired by Shannon's theory) to improve neural network training for classifying patterns and reported an accuracy of 99.26% [18]. Chaurasia and Chakrabarti (2013), using a support vector machine and the data available at the WBCD database, developed a BC diagnostic method with 96.4% accuracy [19]. To discern malignant from benign tumors, Dehghan *et al.* (2017) also utilized multilayer perceptron neural networks, Learning Vector Quantization (LVQ), and Bayesian (with an average of 10 tests), which delivered 97.5%, 97.6%, and s98.3% accuracy, respectively [17].

Mammography is currently the most commonly used method to diagnose BC and provides a simple radiograph of the breast, allowing for the early detection of intangible breast tumors. However, this method suffers from a number of limitations, including low sensitivity (especially in dense breasts). For this reason, other methods such as 3D mammography, sonography, and magnetic resonance imaging have been suggested to obtain more and accurate information. Recently, computer-assisted or intelligent diagnostic systems have been developed to help radiologists boost diagnostic accuracy.

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