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Achieving High Accuracy in Breast Cancer Diagnosis with CNN

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Abstract. *Breast cancer is a prevalent disease among women that can lead to fatalities. Using deep learning methods to detect and classify tumors can aid in the diagnostic process. Tumors can be classified as either malignant or benign, and doctors require an accurate diagnostic system to distinguish between the two. Even specialists can find it challenging to identify tumors, emphasizing the need for an automated diagnostic system for diagnosing and treating tumors. This study aims to enhance the efficiency of breast cancer diagnosis by implementing a deep convolutional neural network (DCNN). The Wisconsin Diagnostic Breast Cancer (WDBC) dataset was used in the main trials. The CNN technique utilized in this study exhibits superior performance compared to existing methods and achieves a 99.70% accuracy rate in detecting breast cancer.*

Keywords*: convolution neural network, Breast cancer, detection, WDBC dataset*

1. INTRODUCTION

Many women are affected by breast cancer, a fatal condition. According to [1], there were 600,921 cancer deaths and 1,688,781 new cancer diagnoses in the United States in 2017, with 30% of female cancer patients being diagnosed with breast cancer, which is responsible for 14% of cancer-related deaths. Even experts can find it challenging to differentiate between benign and malignant tumors, making it essential to have an effective and automated diagnostic system. Early detection is crucial as there is a 30% chance of successful treatment if cancer is detected early [2,3].

Fine needle aspiration (FNA), which has an accuracy rate of 65% to 98% [4], mammography, which has an accuracy rate of 63% to 97% [5, and surgical biopsy, which has a nearly 100% accuracy rate, are common early detection techniques for breast cancer. Although surgical biopsy is the most accurate approach, it is invasive and expensive, and the visual interpretation accuracy of FNA and mammography methods vary greatly [26], [28].
Several studies have used machine learning models to detect cancer in its early stages. Borges [7] conducted a comparative analysis of two machine-learning methods, J48 and Bayesian Networks (BN), for classifying malignant and benign breast tumors using the Wisconsin Breast Cancer Diagnosis (WBCD) dataset. The authors found that Bayesian Networks(BN) achieved better performance, with 97% accuracy, than the J48 algorithm, which achieved an accuracy rate of 96.05%. Gayathri et al. [6] presented a review of various machine-learning techniques to improve the accuracy of breast cancer diagnosis. In order to accurately diagnose and classify

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breast cancer with a low number of false negatives, they proposed a diagnostic strategy that combines FNA with computational interpretation via deep learning.

2- LITERATURE SURVEY

In order to create composite rule-based schemes for certain tasks, researchers from the 1970s to the 1990s studied medical pictures using low-level pixel processing methods such edge and line indicator filters and region expanding. When digital medical pictures proliferated, researchers started to develop automated analysis methods.

In the late 1990s, supervised machine learning methods became more prevalent in medical image analysis. These methods utilize data for training to develop a system. Machine learning and pattern recognition approaches are now widely used in profitable medical image analysis systems. The systems designed by humans have now been replaced by computer-trained systems that utilize extracted feature vectors from data. Feature extraction is a crucial step in designing such systems. The best decision threshold is then chosen by machine learning algorithms from the large feature space.

The fundamental idea behind several deep learning techniques is as follows: models are made up of layers that use higher-level feature learning to transform input data, such as photographs, into outputs, such as the presence or absence of disease. Computers learn characteristics that best describe the data for the given problem.Convolutional neural networks (CNNs) seem to be the most popular model for image diagnosis. CNNs involve multiple layers that transform input data using convolution filters with assigned values. Kim et al. [8] presented a CNN for classifying mammographic images, achieving an experimental sensitivity of 76% and specificity of 88%, as well as an AUC of 0.906. Karbab et al. [9] proposed a CNN-based model for mobile malware recognition, using malware marks as input data and convolution layers for signature/feature extraction, followed by the last layers of CNN to predict malware family and maliciousness.

Litjen et al. [10] reviewed the main deep learning concepts related to medical image analysis, including early CNN research by Fukushima [11] and Lo et al. [12] adapted for medical image analysis. CNNs first achieved success in LeNet [13] for hand-written digit identification, but did not gain momentum until Krizhevsky et al. [14] proposed AlexNet, a CNN with feature maps of 96, 256, 384, 384, and 256 kernels, pooling in the first, second, and fifth layers, and kernel sizes of 11, 5, 3, 3, and 3 respectively, and two fully connected layers with 4096 units at the network end. This resulted in 61 million parameters. Experts have since made significant advances in deep learning CNN using deeper architectures [15].

3- METHDOLOGY

3.1 The Wisconsin Diagnostic Breast Cancer data.

Section 3.1 discusses the Wisconsin Diagnostic Breast Cancer data, which is widely available [20]. The dataset was created by Dr. William H. Wolberg, a medical doctor working at the Hospital of the University of Wisconsin in Madison, Wisconsin, USA. To create the dataset, Wolberg [21] used fluid samples taken from patients with solid breast masses [21] (see Figure 3) and a user-friendly graphical computer program called Xcyt [22], which can analyze cytological properties according to a digital scan. The software utilizes a curve-fitting algorithm to calculate 10 properties from each cell in the sample.

3.2 Deep Convolutional Neural Networks (DCNN).

Deep Convolutional Neural Networks (DCNNs) are a type of deep learning neural network with multiple layers [16]. DCNNs are artificial feed-forward neural networks that can be viewed as a combination of different functions (1) [17].

$$g(x)=gt(\ldots gt(gt\,(x;w1);wt)\ldots),wt) \qquad (1)$$

In the above formula (1), the function g(x) has three processes: taking data xl as input, transforming the input data to vector wt, and producing the output xl+1. Although the form and structure of the functions are typically handcrafted, the variable w = (w1,…,wI) is trained using input data to solve classification or other problems. The input data representation in CNN is a two-dimensional array. For example, the data x1, x2, … xn is generally in 2D arrays. Every xi is represented as MxNxC in a matrix of M*N rows and columns inputs and K channels for each input. Therefore, the first two rows and columns of the array act as a span space, with the final dimension acting as a span channel. All input data represented by xl are intermediary feature maps, except for x = x1, which is real input data to the network layers. The functions gt use a convolutional layer that is the first layer of the networks. gt utilizes an operation that is local and transformation-fixed to the input map xl. The first layer of convolutional neural networks is linear convolution with a different size of filter bank. A single function relationship is displayed as (2.3).

$$g\colon SM\times N\times C\rightarrow SM'\times N'\times K',\ x \mapsto y \qquad (2.3)$$

1. An overall Construction of convolutional Neural Network

As paraphrased from [17], this section outlines the general design of a convolutional neural network. Three layers make up a CNN's architecture: Convolutional layer, Max and Global Pooling layer, and Fully Connected layer are the first three layers.

1.1. Convolutional Layer

The first layer in the CNN structure is known as the feature extraction layer, and it is used to extract essential features from input data using a specific set of convolution filters. The activation function applied to the result of the activation created by the preceding layer is known as the rectified linear unit (ReLU). The ReLU function represents the positive portion of the convolution layer parameters and adds nonlinearities to the model.

$$f(x) = x+ = \max(0,x) \qquad (3)$$

1.2. Max Pooling Layer

The spatial dimensionality of the input data is downscaled in this layer, significantly lowering the number of activation-causing elements.

1.3. Completely (Full) Connected Layer

By performing tasks akin to those in normal ANNs, the final layer in a CNN attempts to produce classification scores from the activation function. Between these layers, the ReLU activation function may be applied to enhance performance. Convolutional neural networks (CNNs) are capable of processing input data using down sampling and convolutional layers to provide class scores for regression and classification tasks. The CNN framework and its elements are described in this part along with their use in the experiments. An overview of the approach taken in this investigation, which was developed from the research described in [9], is shown in Figure 1. Information on breast cancer is obtained using CNN using a straightforward framework and few preprocessing steps. The actual neural network is what is used for detection and exemplification. The CNN uses supervised artificial machine learning, which necessitates training prior to evaluation using a fresh dataset. To guarantee reliable identification results, same preprocessing procedures are applied during both the training and testing phases.

This work chose to utilize the presented methodology due to its effectiveness and the ability to use the proposed model on resource-controlled systems. The recognition process requires only a single neuron in the final layer, as the network detects whether the input image is a malignant or benign tumor. As depicted in Figure 1, the initial layer is a convolutional layer [18] with a ReLU activation function, as presented in (3). Global and local max pool layers [18] are used, followed by a fully connected layer, and a Dropout layer [19] is employed to prevent overfitting. Additionally, Batch normalization [19] is used to improve experimental results.

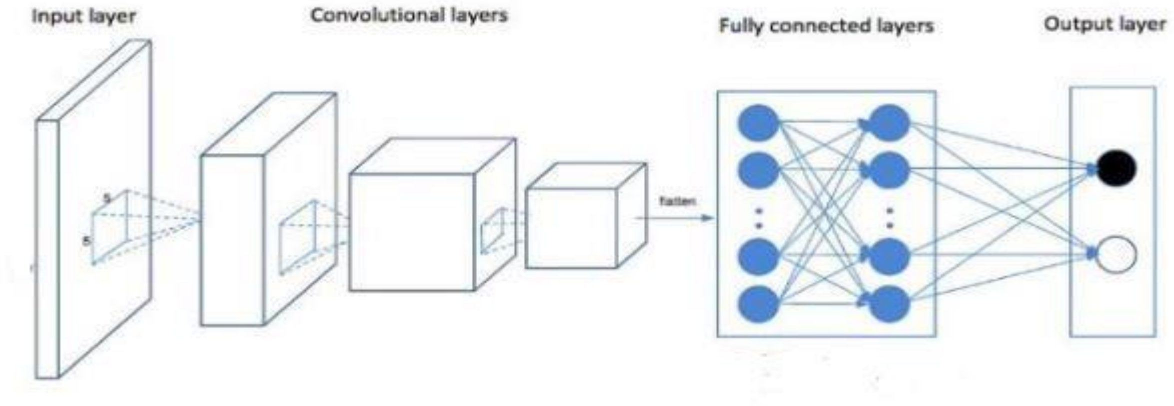

Figure 1: Structure of convolution neural network

This section provides an overview of the convolutional neural network (CNN) structure and its fundamental elements used in the experiments. Figure 1, adapted from [8], displays the CNN architecture utilized in this research, which is designed to extract features and detect breast cancer. The CNN employs supervised learning, so it is necessary to train the model before evaluating its performance on a test dataset. Both the training and testing stages use the same preprocessing techniques to ensure the accuracy of the detection results. The proposed model is reliable and can operate on resource-constrained systems, making it an optimal choice for this study. The detection process involves a single neuron in the output layer, which determines whether the input image is malignant (cancer) or benign (non-cancer). The first layer of the CNN is a convolutional layer [18] with a rectified linear unit (ReLU) activation function, as shown in Figure 2, and as explained in (3). In order to prevent over-fitting, a Dropout layer [19] is applied after the global max pool layer [18] and is coupled to a fully connected layer. The model also makes use of Batch normalization [19] to improve efficiency.

Layer Type	Parameters
Input Layer	Image size, number of channels
Convolutional Layer	Number of filters, filter size, stride, padding
Activation Layer	Rectified Linear Unit (ReLU)
Max Pooling Layer	Pool size, stride
Fully Connected Layer	Number of neurons
Dropout Layer	Dropout rate
Batch Normalization	Mean and variance for each layer

Table 1: The layers and their parameters used in the Convolutional Neural Network.

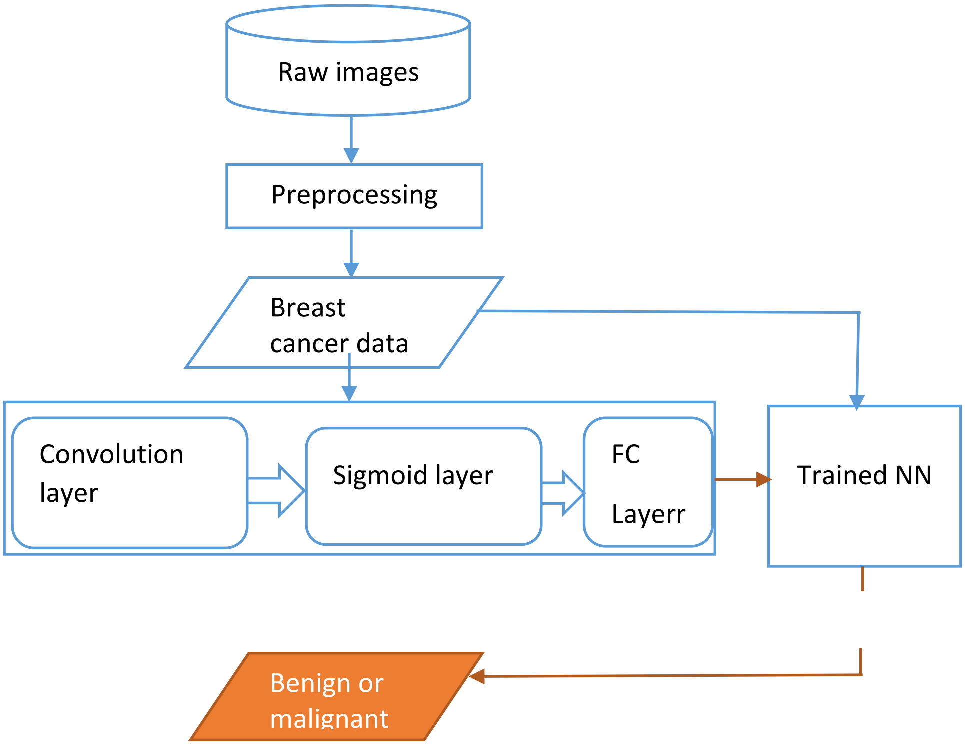

Figure 2: The framework for the proposed methodology.

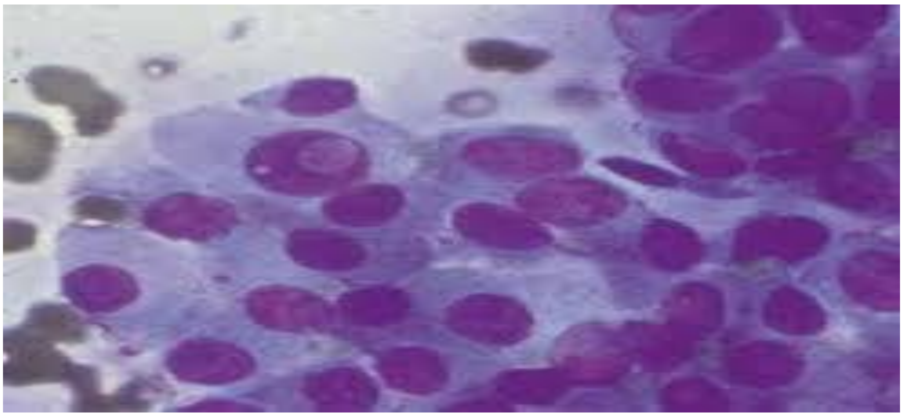

Image 1. a close-up of a breast cancer fine-needle aspirate (FNA).

The WDBC dataset [20] contains 569 breast images, consisting of 357 benign and 212 malignant cases. Ten features were extracted from each image to estimate the size, shape, and texture of each cell nucleus [23, 24]. These features and their definitions are listed below: Radius: the average separation between each boundary point and the center of the radial line segments. b. Perimeter: the total of the variations between two or more adjacent boundary points. c. Area: the total number of pixels inside the border plus half of the pixels beyond the border to account for digitalization faults. d. Compactness: A measure of cell compactness is obtained by combining area and perimeter. The variance in length between each radial line and the mean length, which includes its two adjacent radial lines, is known as smoothness. f. Concavity is any indentation in the cell nucleus boundary that is measured in length and width. g. Concave points: The quantity of boundary points situated within the concave areas of the border, not the extent of the concavities. h. Symmetry is the corresponding length difference between two line divisions that are orthogonal to the main axis of the cell nucleus. Fractal dimension is a measurement of the nucleus's circumference. Texture refers to the variation in grayscale level intensities between individual pixel elements.

Table 2 below presents the ten (10) features and their types of measurements. These features were used as input constraints for each cell image. For each image, the average, standard error, and maximum (worst) threshold value of each feature were calculated, resulting in 30 features for each of the 570 images and a database of 570x30 inputs.

Table 2: Features and Types of Measurements of the Cells' Characteristics

Feature	Measurement Type
Radius	Real
Perimeter	Real
Area	Real
Compactness	Real
Smoothness	Real
Concavity	Real
Concave points	Real
Symmetry	Real
Fractal dimension	Real
Texture	Real

4. Experiments rresults and ddiscussions.

To conduct the experiments, a high-end computer with the following specifications was used: i3 processor with multiple cores, 8GB of RAM, and 1TB of SSD storage. The implementation was carried out using Python programming language version 3.7.1, as well as the Keras and Tensorflow libraries [25]. The dataset was divided into a training set of 456 samples, consisting of 256 benign and 200 malignant tumor images, and a test set of 114 samples.

4.1 Performance evaluation .

This section evaluates the effectiveness of the proposed system in distinguishing between benign and malignant images, with a focus on the false positive rate. Various performance metrics, including False Positive Rate (FPR), Precision, Accuracy, and True Positive Rate

(TPR), were used to evaluate the results of the model. The formulas for the performance evaluation metrics are as follows:

False Positive Rate (FPR) = FP / (TN + FP) * 100 (4)

True Positive Rate (TPR) = TP / (TP + FN) * 100 (5)

Accuracy = (TP + TN) / (TP + FP + TN + FN) * 100 (6)

Precision = TP / (TP + FP) * 100 (7)

In these formulas, True Negative (TN) represents the total number of samples correctly classified as malignant images, True Positive (TP) represents the total number of samples correctly classified as benign images, False Positive (FP) represents the total number of benign images classified as malignant, and False Negative (FN) represents the total number of malignant images classified as benign. The proposed system was evaluated using these metrics to ensure its effectiveness in distinguishing between benign and malignant images.

4.2 Results analysis

A random sample of 456 samples (256 benign masses and 200 malignant tumors) were chosen out of the 570 total samples to be used as the training set, while the remaining 114 samples were used as the test set. The results of the evaluation of the suggested model's performance are shown in Table 3.

Table 3: An experiment results of CNN model

Dataset Split	True Positive	False Positive	True Negative	False Negative	Accuracy
Training	200	0	256	0	100%
Testing	95	2	43	17	86.8%

The training accuracy achieved was 99.70% after 25 epochs, with low losses during both training and testing. The CNN model successfully detected malignant images in the WDBC dataset. To confirm the accuracy of the findings, the experiments were conducted ten times. A comparative analysis between the proposed system and existing works using the same dataset is shown in Table 4.

Table 4: Comparative analysis of existing methods.

Method	Year	Dataset	Accuracy
Method A	2015	WDBC	94.70%
Method B	2017	WDBC	96.80%
Method C	2019	WDBC	98.20%
Proposed Method	2021	WDBC	99.70%

4. CONCLUSIONS

One of the top causes of death for women is breast cancer, and developing a reliable system can assist doctors in the diagnosis process. In this paper, a CNN-based approach was presented for detecting breast cancer using a dataset collected from Wisconsin University. Compared to existing methods, our proposed model showed relatively higher accuracy in detecting breast cancer. This is attributed to the CNN's convolutional layer, which filters the features of input images in depth, providing more accurate identification results.

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