Classification of Breast Cancer Using Convolution Neural Network Algorithm

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Abstract

Breast cancer is one of the utmost common diseases among women, which results in death. Detecting and classifying tumors using deep learning methods can help the diagnoses process. There are two distinct tumor classes, i.e. malignant tumors and benign ones. Doctors need an accurate diagnostic system to discriminate between certain tumors. Moreover, even the specialists usually find it difficult to identify tumors. Automation of the diagnostic system for diagnosis and treatment tumors is therefore required. This research focuses on improving the efficiency of breast cancer diagnosis through the implementation of deep convolution Neural Network (DCNN). The main experiments was carried out utilizing the dataset of Wisconsin Diagnostic Breast Cancer (WDBC). The utilized CNN technique reveals a better performance contrasted to existing methods and reaches 99.70 % accuracy for detection the breast cancer.

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

تصنيف سرطان الثدي باستخدام خوارزمية الالتفاف الشبكية العصبية

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الملخص

يعتبر سرطان الثدي من أكثر الأمراض شيوعاً بين النساء ويؤدي إلى الوفاة. يمكن أن يساعد اكتشاف الأورام وتصنيفها باستخدام طرق التعلم العميق في عملية التشخيص. هناك فئتان متميزتان من الأورام ، أي الأورام الخبيثة والأورام الحميدة. يحتاج الأطباء إلى نظام تشخيص دقيق للتمييز بين أورام معينة. علاوة على ذلك ، حتى المتخصصين عادة ما يجدون صعوبة في تحديد الأورام. لذلك ، يلزم أتمتة نظام التشخيص لتشخيص وعلاج الأورام. يركز هذا البحث على تحسين كفاءة تشخيص سرطان الثدي من خلال تنفيذ شبكة الالتواء العميق العصبية **(DCNN).** تم إجراء التجارب الرئيسية باستخدام مجموعة البيانات الخاصة بسرطان الثدي التشخيصي في ولاية ويسكونسن **(WDBC).** تكشف تقنية **CNN** المستخدمة عن أداء أفضل مقارنة بالطرق الحالية وتصل إلى دقة تصل إلى 99.70٪ للكشف عن سرطان الثدي.

الكلمات المفتاحية: الشبكة العصبية الالتفافية ، سرطان الثدي ، الكشف ، مجموعة بيانات**WDBC**

1. INTRODUCTION

One of the most prevalent diseases among women that result in to death is breast cancer. In 2017 there were 1,688,781 novel cancer cases and 600,921-cancer deaths reported in United States as per research presented in [1]. Statistics reveal that 30 % (the highest) of women cancer patients were identified as breast cancer, which causes second-highest death (14 %). Normally doctors identify breast cancer by categorizing tumors, unless they are kinds of tumors that are benign or malignant. However, even the experts find it difficult to identify tumors. Consequently physicians require an effective diagnostic procedure and automated system that has ability to differentiate between these tumors.

There is a 30% chance that the cancer can be treated effectively if it is identified in its initial phases. Medication is tougher if advanced-phase tumors are detected late [2,3]. The most common methods for early detection of breast cancer involve surgical biopsy that records nearly 100 % accuracy; Fine Needle Aspiration (FNA) used visual examination with reaching 65 % to 98 % accuracy [4], and mammography technique provides correctness of 63 to 97 % accuracy [5]. Therefore, the surgical biopsy method is credible; moreover, it is invasive and cost effective, whereas mammography and FNA methods by visual interpretation correctness differ widely [26], [28].

Many studies have decided to apply machine-learning models to identify survivability of patients with cancers and the studies proved that these algorithms work better in detecting cancer in the early stages. Borges [7] have proposed comparative analysis on two machine-learning methods (J48 and Bayesian Networks an) for classification and differentiating between malignant and benign breast tumors using Wisconsin Breast Cancer Diagnosis (WBCD) for conducting the experiments. The authors inferred that Bayesian Networks achieved a better performance (97% accuracy) when contrasted to J48 algorithm that reached 96.05 % in the term of accuracy. Moreover, Gayathri et al. [6] presented a review on breast cancer analysis based on various machine-learning techniques that target to enhance the correctness of predicting the breast cancer. This study discusses a diagnosis method that uses the FNA by means of computational interpretation through deep learning and targets to detect and classify a breast cancer with a high degree of accuracy and reduced proportion of false negatives .

2. Literature Survey

In the era of 1971s to the 1990s, many researchers analyzed medicinal images with successive application of low-level pixel handling such as edge and line indicator filters, and region growing as well as mathematical modeling such as fitting lines, ellipses and circles to build composite rule-based schemes that resolved specific tasks. The moment it was possible to digitize the medical images, scholars beginning to create automated analysis systems .

Supervised machine learning methods turn out to be more prevalent in medical images investigation in the late 1990s. These methods utilize data for training process in order to be used in a system development. Machine learning and pattern recognitions approaches are prevailing in use thru many fruitful profitable medical image analysis systems. Therefore, the systems that fully designed by humans moved to systems that are trained by computers utilizing data where feature vectors are extracted from. The features extraction from the images is a crucial step in the design of such systems. Then machine-learning algorithms select the best decision threshold in the high-dimensional feature space .

The basic concept of several deep learning techniques is as following. Models (networks) comprise of different layers that transmute input data that are images to outputs (e.g. the existing/absent of disease) through learning more and more higher-level features. After that, computers learn an attributes that optimally denote the data for the problem at hand. To date, the convolutional neural networks (CNNs) seems to be the most popular form of models for image diagnosis. CNNs involves many layers, which transform their input data with convolution filters with specific assigned values. Kim et al. [8] have presented convolutional neural network for classifying around 28,000 mammographic images collected from five several institutions. The experimental results obtained from this study were 76 %, 88 % in the terms of sensitivity, specificity respectively as well as 0.906 for AUC. Karbab et al. [9] have proposed a model based on convolutional neural network for the mobile malware recognition. As an alternative of utilizing images, the researches utilized malware marks as an input data and the Convolution Layers represent as signatures/features abstraction and after that, the last layers of CNN make a prediction of maliciousness and family of the malware .

Litjen et al. [10] review the main deep learning conceptions related to medical image analysis. As per research introduced in [10] several studies have until the late seventies conducted researches on CNNs, such as researches by Fukushima[11] and Lo et al.[12] have also adapted the CNN technique to medical image analysis. Many scholars saw their first successful actual application in LeNet [13] for hand- written digit identification. Even with these early accomplishments, the usage of CNNs did not meet momentum until end of 2012. The turning point was the contribution of Krizhevsky et al. [14] that won with large margin the ImageNet challenge in December 2012. The authors proposed AlexNet, a CNN consists of feature maps of (96; 256; 384; 384; 256) kernels with pooling on the first, second, and fifth layers and kernel sizes are (11; 5; 3; 3; 3) respectively. At network end, two completely connected layers consisting 4096 units are attached to the network edge resulting in 61 million parameters. Experts make tremendous advances in the development of deep learning CNN using deeper architectures in the years to come [15] .

3. METHDOLOGY

3.1. The Wisconsin Diagnostic Breast Cancer data.

The dataset evaluated in this research is widely accessible [20] and it was made by Dr. William H. Wo berg, doctor of medicine working at Hospital of University of Wisconsin at Madison, Wisconsin, USA. for creating the dataset, Wolberg [21] utilizes uid samples that have taken from patients with using solid breast masses [21] (see Figure 3) and an easy-to-utilize graphical computer program named as Xcyt [22], which has the capability of performing the investigation of cytological properties grounded on a digital scan. The software employs a curve-fitting algorithm, to calculate ten properties from every cells in the sample .

3.2. Deep Convolutional Neural Networks (DCNN).

Convolutional neural networks can be defined as one kind of deep learning neural networks with different of layers [16]. This is an artificial feed-forward neural network, which can be viewed as a combination of variety of functions (1) [17].

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

The function $g(x)$ that presented in the above formula (1) has three processes: first process is taking a data xl as input a second process is transforming an input data to vector wt and the last process is producing the output $xl+1$. Though the form and structure of functions is typically handcrafted, the variable $\boldsymbol{w = (w1,\dots,wI)}$ are trained by the input data as to resolve a categorizations or other aimed problems. The representation of the input data in CNN will be 2 dimensional array, for example the data $\mathbf{x1, x2, \dots xn}$ in general will be in 2D arrays. Every **xi** will be represented as $Mx\ NxC$ in matrix of $M *N$ rows and columns inputs and K channel for each input. Therefore, the first two rows and columns of the array are used as span space, where the final dimension acts as span channel. All input data that represent by $\boldsymbol{x\ l}$ are intermediary feature maps excepting $x = x1$ as an real input data to the network layers. The functions $\boldsymbol{gt}$ have a convolutional layer that is the first layer of the networks. $\boldsymbol{gt}$ utilize an operational that is local and transformation fixed to the input map xl. The first layer of convolutional neural networks is linear convolution with different size of filter bank. A single function relationship as displayed in (2.3).

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

1. An overall Construction of convolutional Neural Network

This module presents the overall construction of convolutional Neural Network summarized from [17]. The overall architecture of CNN comprises of 3 layers: (1) Convolutional Layer (2) Max and global Pooling Layer (3) Completely Connected Layer.

1.1. Convolutional Layer

This is the first layer in CNN structure and called as feature extraction layer. Furthermore, it is used to extract important features from input data by using particular set of convolution filters. . The rectified linear unit (RLU) is activation function employed to the product of the activation formed thru the earlier layer. The ReLU function is applied to presents nonlinearities to the model and represented the positive part of convolution layer parameters.

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

1.2. Max Pooling Layer

This layer carry out down sampling beside the spatial dimensionality of the given input, which more reducing the number of factors thru that activation .

1.3. Completely (Full) Connected Layer

This is the last layer in CNN and used to accomplish the same tasks presented in standard ANNs and attempt to produce the classification scores from the activation function. In order to improve performance, the activation function ReLu is possible to be utilized between these layers. CNN have the ability to transform the given input using convolution layer and down sampling methods to yield class scores for the classification and regression purposes. This section introduces the CNN framework and its contains utilized in the experiments. Figure 1 demonstrates the overview of the method of this research that adapted from the study presented in [9]. The CNN has a modest structure and utilizes smallest of possible preprocessing steps in order to acquire the breast cancer information. The exemplification knowledge and detection are depend on the actual neural network. A concept used in the CNN is supervised artificial machine learning, consequently it is required to train the CNN. After that, the CNN is evaluated by utilizing new part of the dataset. The experiments use the identical preprocessing process for the training and the testing steps to ensure an accuracy of the identification results .

This work decides to utilize the presented methodology because of its effectiveness and capability to use the proposed model on resource-controlled systems. The recognition process requires only unit neuron in the final layer since the network detect whether the input image is malignant or benign tumor. As depicted in Figure 1, the initial layer is a convolutional layer [18] with rectified linear unit (ReLU) activation function as presented in (3). Later, we utilize global and local max pool layer [18] besides that it attached to a fully connected layer then Dropout layer [19] is employed to avoid over fitting, this work also uses Bench normalization [19] for improving the experiment results .

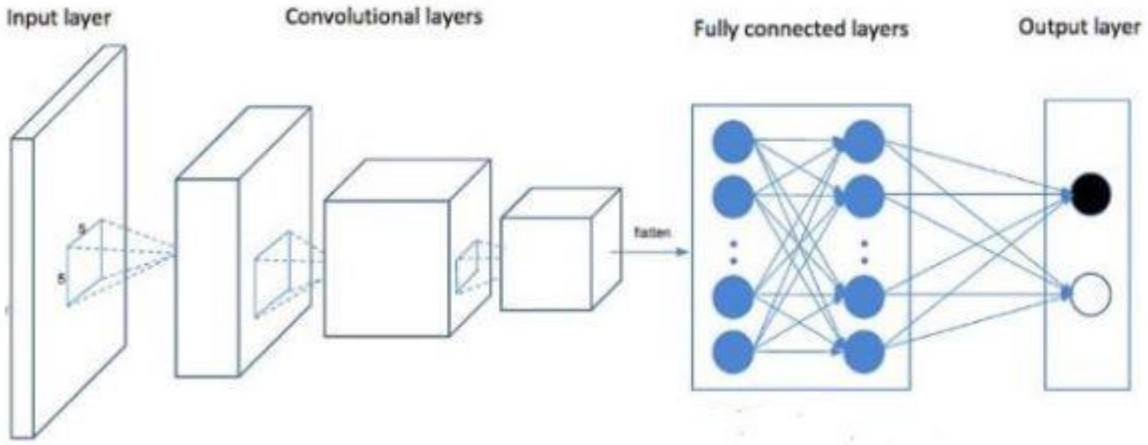

Figure 1: Structure of convolution neural network

This subsection undertakes the convolutional neural network structure and its fundamentals elements that have employed in the experiments. Figure 1 shows the structure of CNN presented in this research that extended from the work in [8]. The CNN has a modest design and utilizes smallest preprocessing to attain the breast cancer data. The attributes extraction and identification are constructed on the definite neural network. The type of learning used in convolution neural network is supervised learning; hence, it is important to train the CNN. Then, the CNN is evaluated based on unseen dataset that is test set. The proposed experiments use the similar preprocessing ways for both, the training and the testing stages to confirm the accuracy of the detection results. The proposed model has reliability and ability to work on resource-constrained systems hence this works chooses to use that same proposed model. The detection process only involves one neuron in the product layer, since the network determines that whether input image is malignant (cancer) or benign image (non-cancer). As depicted in Figure 2.3, the first layer is a convolution layer [18] with rectified linear unit (ReLU) activation function as introduced in (3). Later, we use global max pool [18] and attach it to a fully connected layer in addition to Dropout [19] that used for avoiding the model over-fitting; this work also utilizes Bench normalization [19] to improve the performance of the CNN model. The figure (2) below shows the framework for the proposed methodology in this research .

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

Name of the layer	Options and [illegible]	The used activation function
convolutional	[illegible]	RLU
Max pooling	[illegible]	RLU
Completely (full) connected	[illegible] Drop out=2.0	Sigmoid

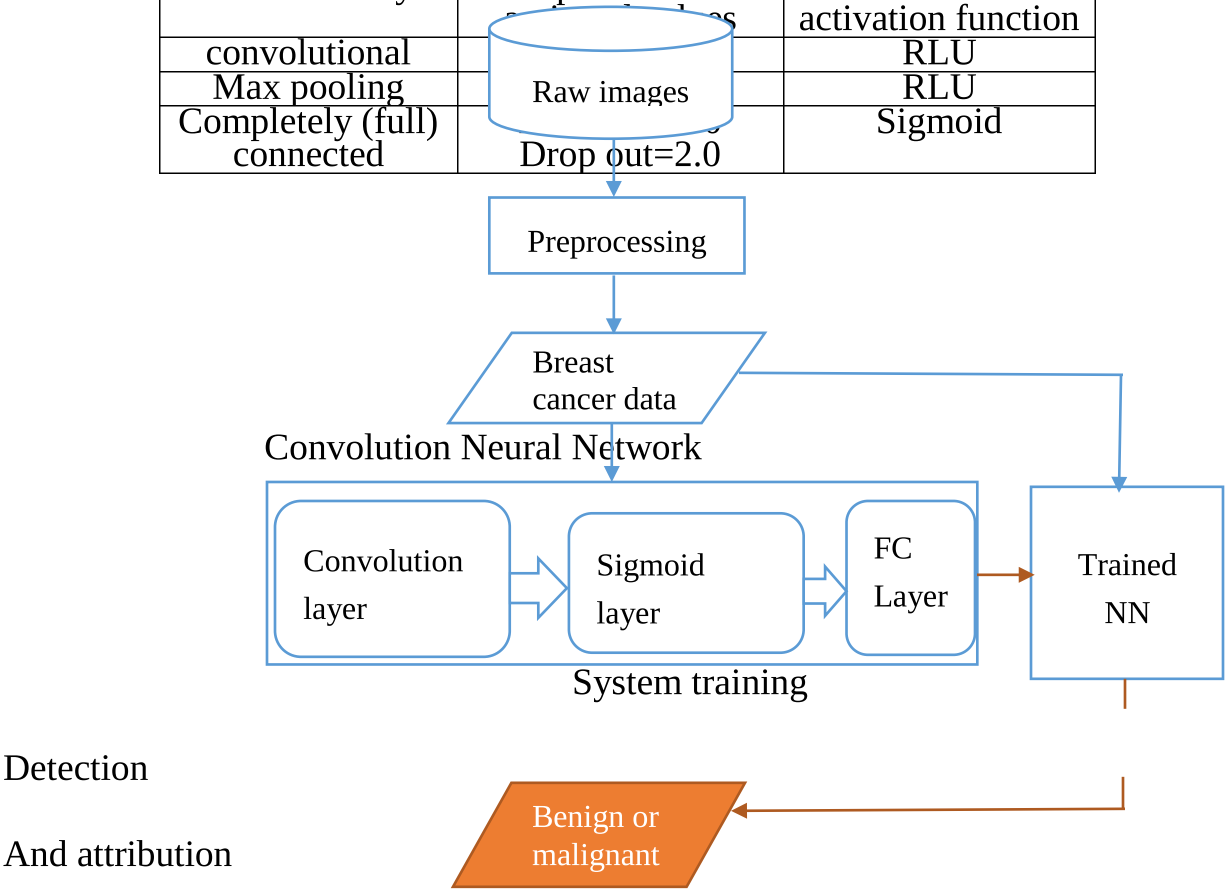

Figure 2: The framework for the proposed methodology.

Fig 2.2.: The framework of the proposed methodology.

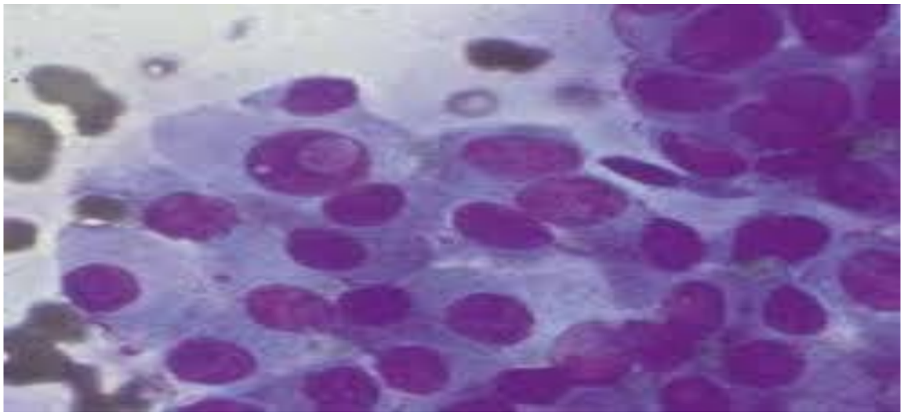

Image 1. A magnified image of a malignant breast fine needle aspirate (FNA).

The Wisconsin Diagnostic Breast Cancer (WDBC) dataset [20] includes 569 breast images with 357 benign and 212 malignant cases. As to estimate the size, shape, and texture of each cell nuclei, ten features were extracted and described as following [23, 24].

a. Radius: average of distance of the radial line portions from the middle of volume of the border to every of the boundary points.
b. Perimeter: addition of the differences across following boundary points.
c. Area: Measure the number of pixels within the border and adding one-half of the perimeter pixels in order to correct the errors created by digitalization.
d. Compactness: Integration of area and perimeter to provide measurement of cell compactness. Smoothness: Amount of the differentiation among the length within each radial line as well as the mean length including its two adjacent radial lines.
e. Concavity: Length and width of any indentation that is in the cell nucleus boundary.
f. Concave points: Closely related to concavity, it only calculates the number of boundaries points located on the boundary concave areas, not its magnitude of concavities.
g. Symmetry: the related variation in length among couple of line divisions orthogonal to the main axis of the shade of the cell nucleus.
h. Fractal measurement: it represent the perimeter of the nucleus.
i. Texture: the deviation of the grayscale level intensities in the pixels elements.

Table 2 that is below depicts the ten features of the cells and their kinds of standards. These features will utilized as feature constraints of the cells therefore for every image of the cells, the average, standard error, and the greatest (largest or “worst”) threshold value of each feature was calculated that produced in 30 features of 570 images, resulting a database of 570×30 inputs. The table 2 presented below shows the factors of image’s features.

Table 2: Factors of features.

Features	Range
Compactness	1:11
concavity	1:11
Radius	1:11
Symmetry	1:11
length	1:11
Fractal dimension	1:11
Perimeter	1:11
Concave points	1:11
Area	1:11
Softness	1:11
Texture	1:11
Class distribution	Malignant: 213 Benign: 357
Number of samples	570

4. Experiments results and ddiscussions.

For experiments purpose, the offered method is performed and executed on high-end computer which having the configurations such as. cores i3 processor, 8GB RAM, and 1TB SSD storage using Python programming language version 3.7.1, Keras and Tensor flow library [25]. The dataset is divided into 456 as training set (256 benign images and 200 malignant images tumors), and the remaining 114 samples as test set.

4.1 Performance evaluation .

This subsection provides an evaluation of how effectively the proposed system can distinguish between malicious and benign images in terms of false positive rate. The performance evaluation process have performed to evaluate the results of presented model. We have used different evaluation metrics such as False Positive, Precision accuracy, Precision and True Positive. The formulas of the evaluation performance are as follow:

$$\text{False Positive Rate (FPR)} = \frac{FP}{TN+Fp}\%100 \qquad (4)$$

$$\text{True Positive Rate (TPR)} = \frac{TP}{TP+FN}\%100 \qquad (5)$$

$$\text{Accuracy}= \frac{TP+TN}{TP+FP+TN+FN}\%100 \qquad (6)$$

$$\text{Precision}=\frac{TP}{TP+FP}\%100 \qquad (7)$$

True negative (TN): the total numbers of samples that classified correctly as malignant images.

True positive (TP): the total numbers of samples that classified correctly as benign images.

False positive (FP): the total numbers of benign images that classified as malignant image.

False negative (FN): the total numbers of malignant images that classified as benign image.

2.4 Results analysis

From 570 samples 456 were arbitrarily chosen as training set (256 benign masses and 200 malignant tumors), and 114 samples as test set. Table 3 illustrates performance results. As shown in the table 3 an accuracy during the training achieved 99.70 % after 25 epochs. The results are seemed good enough, due the fact that the losses during the training and during the testing are very less. The proposed CNN model performed the detection of malignant images on the

WDBC dataset faultlessly. The presented experiments are performed 10 times. Table 3 shows the results obtained by the CNN model

Table 3: An experiment results of CNN model

Method	**Data**	**Train data**	**Testing data**	**Accuracy (%)**	**Sensitivity (%)**	**Specificity (%)**	**Precision (%)**	**Time second/**
CNN	Images	70 %	20%	99.70	98.90	99.60	99.30	2.3

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The author compares the accuracy of the proposed model with previous works that use same dataset [7]. The table 4 depicts the comparative analysis between the proposed system and existing works.

Table 4: Comparative analysis of existing methods.

Method Name	**Accuracy**	**Reference &Year**
Back propagation	93.90%	[25]/1992
Back propagation	97.00%	[21]/1993
MSM-T	97.50%	[22]/1995
GRNN	99.51%	[29]/2008
Fuzzy+ KNN	99.28%	[30]/2011
Proposed system	99.70	

5. Conclusions.

One of the most prevalent diseases among women that result in to death is breast cancer. Designing and developing reliable system can help doctors in diagnosing process of breast tumor. This paper has presented the using of CNN for detection the breast cancer. The evaluated dataset collected from Wisconsin

University. With compared to existing methods, our proposed model is relatively provides better accuracy for detection the breast cancer. The CNN gives more accurate identification results because it has convolution layer nature that filters the features of input images in depth details.

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