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Breast Cancer Image Classification Using the Convolution Neural Network

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ABSTRACT

Breast cancer is a type of tumour and the disease with the second-leading cause of death among women. Physicians diagnose the disease through tumour classification and decide whether it is malignant or benign. However, to accurately perform the classification is not an easy task, even by experts. Thus, diagnostic system automation is required to assist physicians in accurately diagnosing malignant tumours as cancer in the early stages. This paper attempts to improve the accuracy of breast cancer detection by utilising the deep learning convolution neural network (CNN). Experiments were conducted using the Wisconsin Diagnostic Breast Cancer (WDBC) dataset. Compared to existing techniques, the use of CNN shows a better result and achieves 99.66% in terms of accuracy.

Key words: Breast cancer, convolution neural network (CNN), feature selection, Wisconsin Diagnostic Breast Cancer (WDBC) dataset.

1. INTRODUCTION

Breast cancer is a type of tumour and a disease with the second-leading cause of death among women. Siegel et al. [1] state that, in 2017, more than 1.6 million new cases of cancer and almost 700,000 cancer deaths were reported in the United States. The statistics show that, among female cancer patients, 30% (the largest group) are diagnosed with breast cancer, the second-highest cause of death (14%). Physicians diagnose the disease through tumour classification and decide whether it is malignant or benign. Nevertheless, to accurately perform the classification is not an easy task, even by experts. Therefore, physicians need a reliable diagnostic procedure and automation of diagnostic system to distinguish between these tumours. Cancer experts can give effective treatment with a 30% probability of cure if the illness is detected in its early stages. The treatment becomes more difficult in the case of late detection of advanced-stage tumours [2,3]. The most popular techniques to detect breast cancer in the early stages include surgical biopsy, which can reach almost 100% correctness; fine needle aspiration (FNA) using visual interpretation with a correctness level of 65% to 98% [4]; and mammography with correctness percentages of 63% to 97% [5]. Thus, the surgical biopsy is reliable; however, it is invasive and costly, while FNA with visual analysis and mammography fluctuate extensively.

Machine learning algorithms for detecting the survivability of cancers patients have been implemented in many research works. Moreover, researchers have also demonstrated that the proposed algorithms perform very well on early-stage cancer detection. Borges [7] compares two machine learning techniques (Bayesian networks and J48) to classify benign and malignant breast lumps on the Wisconsin Breast Cancer Diagnosis (WBCD) dataset. The author concludes that Bayesian networks demonstrate a good performance compared to the other algorithm, J48 (97.80% versus 96.05% accuracy, respectively). Furthermore, Gayathri et al. [6] summarise previous works on breast cancer diagnosis that used different machine learning algorithms aiming to increase the cancer prediction accuracy.

This paper discusses a diagnostic tool to detect breast cancer based on the FNA and deep learning techniques. The main aim is to increase the accuracy level, at the same time providing a low rate of false negatives.

2. RELATED WORK

From the 1970s to the 1990s, researchers have analysed medical images using low-level pixel processing through sequential application, including line and edge detector filters, and region growing. They have also used fitting lines, ellipses, and circles as mathematical model to construct multiple rule-based systems that have resolved specific functions. Once it became possible to digitise the images, researchers started to develop automatic analysis systems.

Supervised techniques became more and more popular in medical image analysis in the late 1990s. Such techniques use training data to develop a system. Pattern recognition and machine learning approaches are predominantly used by many successful commercial medical image analysis systems. Thus, there is a shift in the paradigm from systems completely designed by humans to those trained by computers. The latter use data from which feature vectors are extracted, and this extraction process becomes a critical phase in the design. Subsequently, an algorithm chooses the best conclusion threshold from the feature space with high dimensionality.

Basically, deep learning algorithms constructed by models (networks) consist of layers that convert input data into outputs, and the learning process uses aggregate higher-level features. The features that optimally represent the data of the

problem are used by the system to learn. Convolutional neural networks (CNNs) are the most successful type of models for image analysis. They are constructed by multiple layers in the hidden layer that transform input data using small convolution filters. Karbab et al. [8] introduces the use of deep learning CNN on mobile malware detection. Instead of using images, the authors use malware signature as an input, the convolution layer acts as signatures or feature extraction, and then the other layers make a decision on maliciousness and the fam-ily of the malware.

Litjen et al. [9] review medical image analysis research that uses main deep learning concepts. According to [9], many researchers have carried out studies on CNNs since the late 1970s. Works by Fukushima [10] and Lo et al. [11], for example, have already applied the CNN to medical image analysis. The researchers successfully showed the first real-world application for hand-written digit recognition in LeNet [12]. These early achievements did not even meet the momentum for the use of CNNs until the end of 2012. In December 2012, work by Krizhevsky et al. [13] that won the ImageNet contest with a significant margin became the turning point. The authors introduced AlexNet, a CNN with an architecture that consists of (96; 256; 384; 384; 256) feature map kernels and pooling of the first, second, and fifth layers and (11; 5; 3; 3; 3) of kernel sizes, respectively. Two fully connected layers with 4096 units are added to the end of the network, giving rise to 60 million parameters. In the following years, researchers have made great progress in deep learning CNN development using deeper architectures [14]. Deep convolutional networks have gained enough popularity to become the technique of choice.

3. METHODOLOGY

3.1 Wisconsin Diagnostic Breast Cancer (WDBC) Dataset

The authors use the disease dataset from the University of Wisconsin Hospital at Madison, Wiscon-sin, USA, which is available to the public [20]. Wolberg et al. [21] created the dataset using UID sam-ples from the solid breast masses of patients (see Figure 1) and a computer program named Xcyt [22], which analysed cytological features from scanned digital images. Ten features of each cell in the image samples resulted from the application of a curve-fitting algorithm.

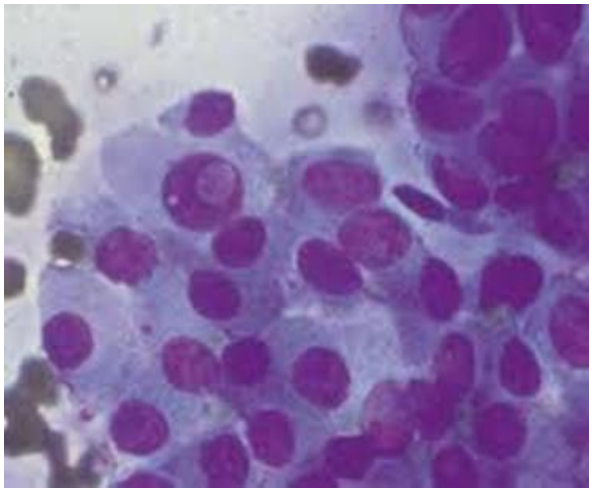

Figure 1: Magnified image of a malignant breast fine needle aspirate

There are 569 entries in the WDBC dataset [20], consisting of 357 benign and 212 malignant cases. Experts have derived 10 characteristics for evaluating the size, shape, and texture of each cell nucleus. The following are descriptions of these characteristics, summarised from [22,23].

- Radius: the average length of the radial line segments from the centre of mass of the boundary to each of the boundary points.
- Perimeter: the sum of the distances between consecutive boundary points.
- Area: count of the number of pixels on the interior of the boundary, adding one-half of the pixels on the perimeter to correct for error caused by digitisation.
- Compactness: a combination of the perimeter and the area to give a measurement of the compact-ness of the cell.
- Smoothness: the difference between the length of each radial line and the mean length of the two radial lines surrounding it.
- Concavity: the size of any indentations in the boundary of the cell nucleus.
- Concave points: similar to concavity, but counts only the number of boundary points lying on the concave regions of the boundary, not the magnitude of the concavities.
- Symmetry: the relative difference in length between pairs of line segments perpendicular to the major axis of the contour of the cell nucleus.
- Texture: the variance of the grayscale intensities in the component pixels.
- Fractal dimension: the perimeter of the nucleus.

3.2 Convolution Neural Networks (CNN)

Convolution neural networks are a type of deep artificial neural networks (ANNs) [15]. It is a feed-forward ANN that can be considered a composition of a number of functions (1) [16]:

$$g(x) = g_L(\ldots g_2(g_1(x;w_1);w_2)\ldots),w_L) \quad (1)$$

Each function g_l takes as input a value x_l and a parameter vector w_l, producing x_{l+1} as output. While the type and sequence of functions is usually handcrafted, the parameters $w = (w_1,\ldots,w_l)$ are learned from the data in order to solve a classification or other target problem.

Data and functions in CNNs have extra structures. The datapoints $x_1, x_2, \ldots, x_n$, in general, form 2D arrays. Every x_i is an $MxNxC$ real array of MxN entries and K channels per entry. Thus, the first two dimensions of the array span space, whereas the last dimension spans channels. All the data points x_l are intermediate feature maps, except $x = x_1$, which is an actual input into the network.

The functions g_l have a convolution structure as well. They use an operator that is local and translation invariant to the input map x_l. The first CNN is the regular linear convolution by a filter bank. A sample of the single function relation is shown in (2):

$$g: RM\times N\times C \rightarrow RM'\times N'\times K',\ x \mapsto y \quad (2)$$

A. The General Architecture of the CNN

This subsection provides the general architecture of the CNN summarised from [17]. The general structure consists of three layers: the convolution, MaxPooling, and fully connected (FC) layers.

B. The Convolution Layer

This layer governs the output of neurons connected to local parts of the input by calculating the scalar product between their weights and the region connected to the input volume. An activation function called the rectified linear unit (ReLU) is applied to the output of the activation produced by the previous layer. The ReLU function is defined as the positive part of its argument [17]:

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

C. The MaxPooling Layer

MaxPooling is a process of discretisation based on a sample. The aim is to down-sample an input presentation, thus dropping its dimensionality and allow assumptions about features contained in the ditched sub-regions. This layer decreases the parameters within an activation.

D. The Fully Connected Layer

This layer carries out the same functions as in conventional ANNs. It attempts to yield class scores from the activations so as to perform classification task. To improve performance, the ReLU activation function may be used between these layers. After executing the modest transformation method, the CNNs are able to transform the original input layer by layer using convolution and to class scores for regression and classification using down-sampling techniques.

Figure 2 shows an overview of the approach of this work, adapted from [8]. The CNN has a simple design and uses minimum pre-processing to obtain the breast cancer information. Representation learning (feature extraction) and detection/attribution are based on the actual neural network. The CNN uses supervised machine learning, thus it requires training. Subsequently, it is tested using a different part of the dataset. During the experiments, the training and the testing phases used the same pre-processing procedure to guarantee the correctness of the detection outcomes.

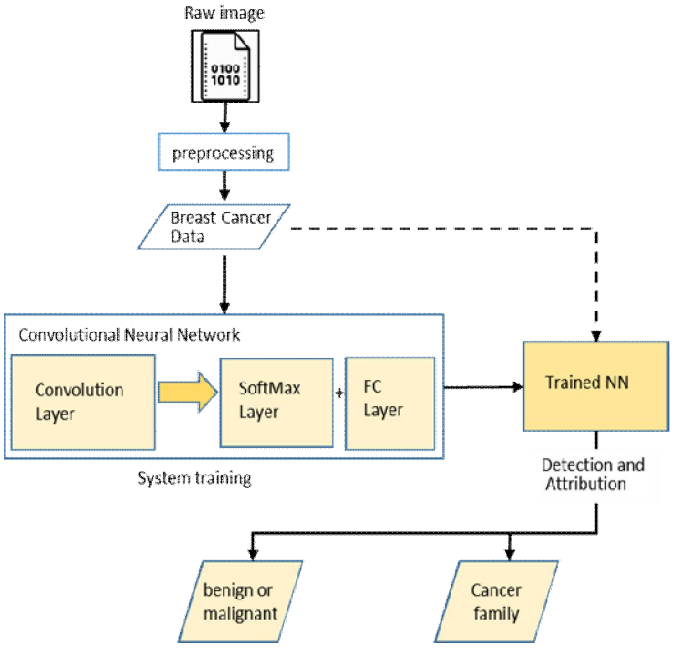

Figure 2: Overview of the research approach

Figure 3 presents the CNN framework and its components as used in the experiments. The rationale behind using the proposed model is that this model has the efficiency and capability to run on resource-constrained machines. Since the network only decides whether the image is of a benign or malignant tumour, the detection task needed one neuron in the output layer. Figure 2 shows the CNN used. The first layer is the input, followed by a convolution layer [18] with ReLU activation function, presented in (3). Afterwards, this work used the global MaxPooling function [18] and connected it to a fully connected layer. Besides the use of dropout [19] to avoid overfitting, this work utilised bench normalisation [19] as well to produce better accuracy detection. Table 1 shows the attributes of the proposed.

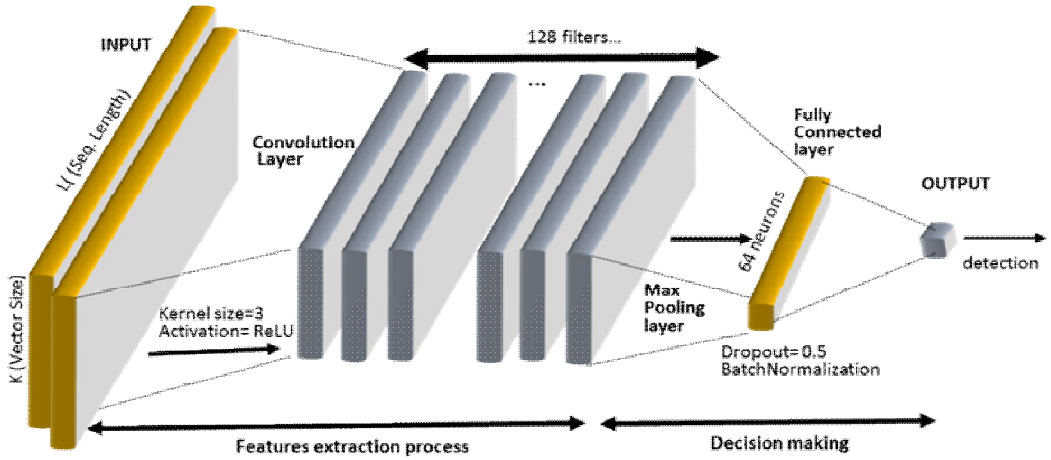

Figure 3: The architecture of the proposed CNN

Table 1: Attributes of the CNN

Layer	Options	Activate function

Convolution
MaxPooling
Full-connected
	Fitter:128
	Filer size = 3
	#Neurons = 64
	Dropout = 0.5
		ReLU
		-
		ReLU

Table 2 shows the 10 characteristics of the cells and their values. These characteristics were used as the feature parameters of the cells. For each image of the cells, three parameters (mean, standard deviation, and the maximum or minimum) of each characteristic were calculated. This resulted in (3x10) features of 569 images, giving rise to a database of 569×30 entries.

Table 2: Features parameters

Features	**Domain, Value**
Radius	Numeric, 1–10
Perimeter	Numeric, 1–10
Area	Numeric, 1–10
Compactness	Numeric, 1–10
Smoothness	Numeric, 1–10
Concavity	Numeric, 1–10
Concave points	Numeric, 1–10
Symmetry	Numeric, 1–10
Texture	Numeric, 1–10
Fractal dimension	Numeric, 1–10
Class distribution	*Malignant: 212* *Benign: 357*
Number of instances	*569*

4. EXPERIMENTAL SET-UP, RESULTS, AND DISCUSSION

The proposed CNN was implemented on a high-end server machine with the following specifications: VPS 16-core processor, 512GB RAM, and 3TB SSD storage using Java, Python Version 3.5.1, Keras and Tensorflow utilities/libraries [24]. Out of 569 samples, 260 were randomly selected to be used for training (110 malignant and 150 benign masses), and the rest were used for training.

A. Performance measurement

This section evaluates how effectively the proposed CNN is able to recognise malignant and benign images by measuring the false positive rate (FPR). Table 3 depicts the metrics used to measure performance.

Table 3: Performance metrics

Metric	**Measurement**
True positive (TP)	Number of successfully detected malignant masses
False negative (FN)	Number of incorrectly classified malignant masses
False positive (FP)	Number of incorrectly classified benign masses
True negative (TN)	Number of successfully classified benign masses
False positive rate (FPR)	Ratio of FPs to total number of false detections

$$FPR = FP/(FP + TN) \quad (4)$$

$$Accuracy = (TP + TN)/(TP + TN + FP + FN) \quad (5)$$

The trained CNN performed the malignancy detection on the WDBC dataset, and the experiments were repeated 10 times.

B. Results analysis

The graph in Figure 4 shows that the accuracy during the training achieved 96% after 160 epochs. Figure 5 presents the accuracy of the test, which reached 98.1% after 160 epochs. The results are considered good enough, because losses during training and testing are unavoidable.

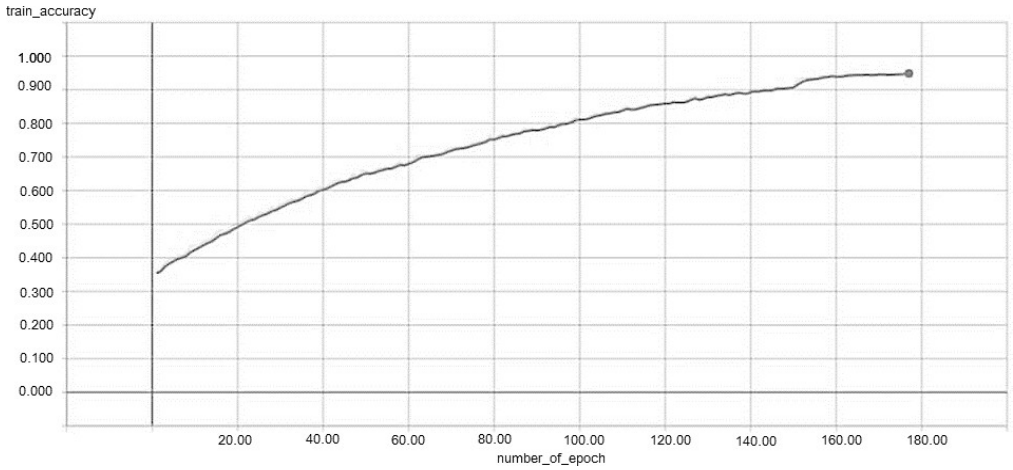

Figure 4: Accuracy results during training

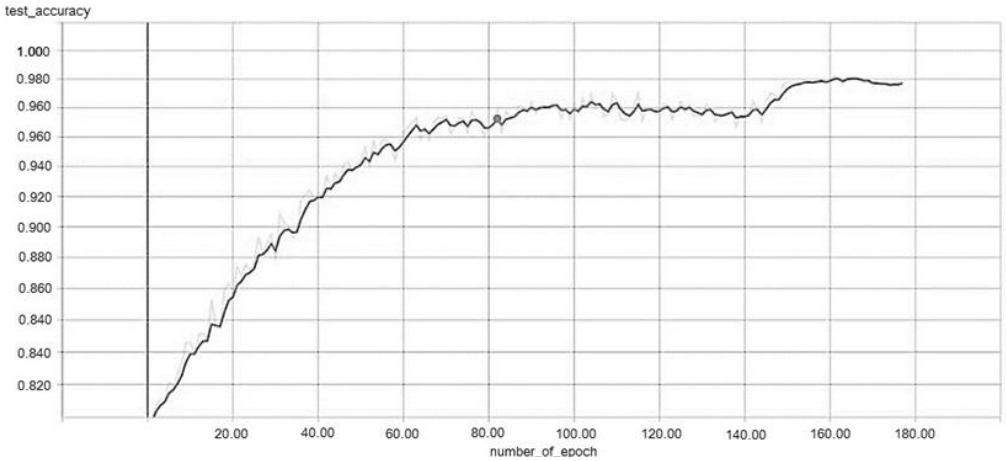

Figure 5: Accuracy results during testing

Table 4 shows the TP, FP, FN, TN, and accuracy results. The authors then compared the accuracy of this study with other works that have used same dataset [7]. Table 5 depicts the comparison results.

Table 4: Experiment results on malignant tumour detection

Experiment #	**TP**	**FP**	**FN**	**TN**	**Accuracy**
1	210	2	2	35	0.9894
2	212	0	2	355	0.9964
3	212	0	0	357	1.000
4	211	1	2	355	0.9947
5	212	0	0	354	1.000
6	211	1	0	357	0.9982
7	210	2	1	356	0.9947
8	212	0	1	356	0.9982
9	212	0	1	356	0.9964
10	212	0	1	356	0.9982
Total					99.662

Table 5: Comparison of the accuracy (Source [7])

Algorithm	Accuracy	Reference & Year
Back propagation	94.90%	[25]/1992
MSM-T	97.00%	[21]/1993
MSM-T+	97.50%	[22]/1995
Pre-processing	98.80%	[26]/1999
Fuzzy-genetic	97.80%	[27]/2004
GRNN	99.14%	[28]/2006
Fuzzy+ KNN	99.51%	[29]/2008
Hybrid SVM	99.28%	[30]/2011
BP-MLP		
Proposed system	**99.66%**	

5. CONCLUSION

This work has shown the adaptation of CNNs for assessing a breast cancer dataset from Wisconsin University. The detection performance is relatively better than that of existing available methods. The proposed CNN provides more accurate detection results due to the nature of its convolution layer, which filters the features in more detail.

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