

Breast Cancer: Tumor Detection in Mammogram Images Using Modified AlexNet Deep Convolution Neural Network

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Abstract

The improvement of system accuracy is a key issue in the detection and classification of tumors in digital mammographic images. This affects how radiologists make accurate analysis in the diagnosis of breast cancer. The goal of this research is to use augmentation techniques to improve system classification accuracy on a large number of datasets. A popular deep convolutional neural network (DCNN) architecture known as AlexNet was modified and used to categorize mammography images into two classes of benign (normal) and malignant (abnormal) tumors. The results demonstrated an overall system accuracy of 95.70%. It indicates an improved performance over traditional approaches in breast cancer diagnosis.

Keywords: AlexNet, benign, breast cancer, DCNN, malignant, mammographic images.

I. INTRODUCTION

Cancer causes an abnormal growth of cells and often spreads out rapidly in body tissues. It is usually named after the part of the body in which it occurs. At the early stage of development, it forms a lump or mass, often referred to as tumor. The tumor produces no significant pain at the early stage of treatment. Hence, conducting screening is crucial for early detection of the disease formation [1]. Cancerous disease occurs in both men and women but women are more susceptible to it, especially in the case of breast cancer, considered the most common type of cancer all over the world [2]. According to the American Cancer Society (ACS) in 2017 alone, about 252- 710 new cases of invasive cancer were diagnosed among women while 2,470 new cases were diagnosed in men and 40, 610 breast cancer deaths were recorded [3]. Each year, out of the about 14.1 million people who suffer from breast cancer worldwide 8.2 million result in death. 70% out of the newly reported cancer cases occur in developing countries. The figure is expected to rise due to lack of awareness on the disease, the risk factors, population growth, age and other factors such as environmental toxins, medical history, family history, genetics, exposure to radiation and infections. It is expected that by the year 2025,

there will be about 19.3 million newly reported cancer cases annually [4].

The accurate figure of cancer cases in Nigeria is unknown due to lack of adequate cancer registries, although there are research studies conducted in Abuja and Ibadan based on cancer registries. The two results show that Age Standardized Incidence Rate (ASR) for all invasive cancer is 58.3/100,000 for men while 138.6/100,000 is for women [4].

One of the ways of preventing the rapid growth of cells (benign tumor) from becoming a full-blown cancer (malignant tumor) is early detection. A lot needs to be done to educate women on the importance of self-examination and early detection of the disease. Over the years, doctors have made strides in early diagnosis and treatment of the disease resulting to significant reduction in breast cancer mortality rate using medical diagnostic imaging tools such as computer-aided detection, Digital mammography, Magnetic resonance imaging (MRI) and ultrasound. Among these, mammogram procedures is considered to be the fastest and most accurate means in detection [5]. A mammogram is an x-ray of the breast indicating changes in the breast tissues that can result to cancer. It helps in detecting very small lumps that can rarely be seen by human eyes. In the past, researchers tried to automate this procedure by reducing the huge task of the radiologist due to large volume of images as a result of increasing cancer cases all over the world. Recent studies have however shown that the use of deep learning, for example, Convolutional Neural Network (CNN) can automatically identify and extract features from mammogram images and predict the likelihood of cancer formation.

One of the key issues discussed in cancer literature is the overall accuracy improvement, as reported in the work of Saira [1]. In a similar work by Zhou on mammogram image detection using CNN the percentage accuracy is around 60% for all class detection and 75% for masses class, which is too low for a medical side solution [6]. Dina *et. al* in [7], further improved the performance accuracy to 87.2% which is a good result but can be further improved upon to get a better performance. This paper presents an optimized system in

cancer detection and classification with an overall performance accuracy of about 95%.

II. LITERATURE REVIEW

CNNs are generally 2-dimensionals of several channels data processing algorithms which have shown excellent performance in images and videos processing. The idea in CNNs is inspired by the human visual cortex organization. In a research conducted by Hubel and Wisel, they observed that the cell arrangement in the animal visual cortex in charge of light detection is in a sub-region of the visual field [8]. In CNN architecture, the complexity of the network is greatly reduced compared to the standard neural network due to the fact that the general matrix multiplication in neural network has been replaced with a convolution [9]. Furthermore, the feature extraction in the standard learning algorithm is completely truncated since raw images can be directly imported to the CNNs. It is also noteworthy that CNN model requires less pre-processing, reduced number of parameters in the network by taking advantage of spatial relationship [10]. Due to technological advancement in computation algorithm, CNNs have been successfully applied in diverse areas such as face detection, behavior recognition, speech recognition and image classifications [11].

Parameter sharing in CNNs is such that instead of learning a different set of parameters at each location as the case in standard learning algorithm, it only needs to learn one set of them and apply it to the whole image. This approach often leads to reduction in computational time, thereby improving system performance. In mammogram images, the CNN algorithm is used to detect and classify images by scanning to find out the possible abnormal tissues, tumor formation, lumps and masses. Mammography is currently widely used in the medical field to predict the likelihood of breast cancer and has shown huge success in that area [12]. Although architectural distortions are also used as an indicator of breast cancer, they are less significant [13]. There are basically two forms of mass tumor, the benign tumor which often appears round or oval shape and malignant tumor (cancerous) which is partially rounded and has irregular outline that is white in color [14]. Over the years, researchers have proposed several methods for breast mass classification in mammography images but one of the most important parameters for consideration is the classifier accuracy [15]. Dina *et al.*, worked on breast cancer detection using deep CNNs and support vector machines for classifying mammography images into benign and malignant mass tumors. The aim of the work was to extract features from the image using two different techniques: the region of interest (ROI) and threshold, and the last fully connected layer of the DCNN architecture was replaced with support vector machine. The work was implemented using two different databases, the digital database for screening mammography (DDSM) and Curated Breast Imaging Subset (CBIS). The result showed that the overall accuracy was improved to 87.2% when support vector machine was used as a classifier in combination with DCNN as against 71.01% when feature extraction was done manually [7]. In a similar work by Ghongade and Wakde, the aim was to detect breast tumor from mammograms using random forest (RF) and a combination of RF-ELM (Extreme Learning Machine) classifier implemented on MIAS database. The classifiers worked by sending an irregular specimen down in each tree and at the end of the process, the vote of all trees indicate

classification into either benign tumor or malignant tumor. The result shows that RF classifier works well with large datasets and high dimensional data but the combination of RF-ELM gives a better result [16]. The overall accuracy achieved for the work is 89%.

In a work proposed by A-Masni, a computer-aided diagnose (CAD) system was used with a combination of CNN. The work is broken down into four stages: feature extraction using CNN, mass detection with confidence model and mass classification using CNN fully and it is implemented using public available mammograms images from DDSM on YOLO-based CAD system. The image pre-processing was done using the multi-threshold peripheral equalization techniques to remove the noise background from the images. The YOLO-based CAD system performs two basic operations to find the mass locations and classify them according to their features into benign or malignant. A total of 600 breast images were used for both training and testing purposes containing 300 benign images and 300 malignant images. The results for both detection and classification were evaluated and about 85.52% overall accuracy was achieved [17].

In a study conducted by Duraisamy and Emperumal, the presence of tumor tissues in a mammogram images was modeled using the Chan-Vese level set method to first extract the contour and the DCNN algorithm to learn the specific features from the contour of mammograms images. The classification of the mammogram images into ten different classes by a full complex-valued relaxation network (FCRN) classifier was because the suspicious areas in the ROI are so dense with varying characteristics. The FCRN will learn and generalize them into normal, benign or malignant-calcification [18]. Results show that this classifier achieved 85% overall accuracy and performed better than most classifiers using the same system parameters. The summary of the reviewed literature is shown in Table I.

TABLE I. SUMMARY OF THE REVIEWED LITERATURES

Author	Metric parameters		
	Neural Network	Database	Accuracy
Dina.et al, (2019)	DCNN classify masses	DDSM	87.2%
Jiang (2017)	DCNN classify tumors	BCDR	79.1%
Duraisamy (2017)	DCNN classify masses	MIAS	85%
Ghongade (2017)	CNN classifier	MIAS	89%
Jain et al., (2016)	DCNN classify tumors	DDSM	66%

III. METHODOLOGY

The proposed technique in this research was implemented using images from Mammographic image analysis society (MIAS) database. The MIAS images undergo enhancement in preparation for feature segmentation. The processed images are then assigned to a modified Alex-Net CNN model for feature extraction during training as well as image classification. The different stages of the process are illustrated in Fig.1, which is followed by brief discussion of the various stages.

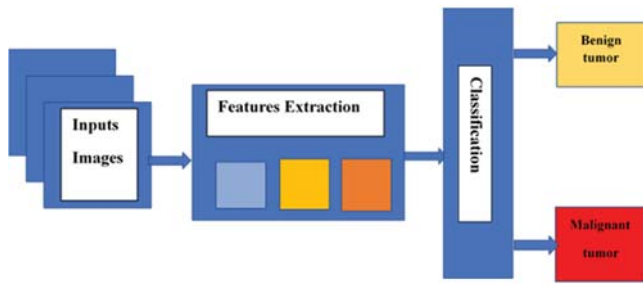


Fig. 1. Project block diagram

A. Pre-processing of images

This involves the process of preparing the mammogram images for feature extraction. Mammogram images contain noise, different resolutions, high and low contrasts which make the location of the tumor tissue difficult. In this work, Gaussian filter is used for pre-processing purposes to remove the image noise. At the end, data augmentation is applied to increase the amount of data needed to effectively train the CNN model.

B. Data Augmentation

In image processing, data augmentation is a way of creating new training data from the existing training data. This is done by creating transformed copies of the original images in the training dataset that belong to the same class as the original image. In this study, the original image from MIAS database comes in a portable gray map file (*.pgm) format with a resolution of 1024 x 1024 dimensions which makes training on this dataset not feasible. In order to overcome this challenge, the image was downsampled by a factor of 16 reduced to 64 x 64 dimensions for faster image processing. The down sampled images are then imported directly to the MATLAB directory for the augmentation operation. Each of the 322 down sampled images were flipped horizontally (reflection operation) giving different copies of the images. The down sampled images and the reflected images were then augmented through rotation by the application of different transformation angles ranging from 0 to 360 degrees. The transformation angles used in this study are 90, 180 and 270 degrees; both the down sampled images and reflected copies were each rotated through these angles thus, the original database was augmented by a factor of eight (8) leading to 2,576 images for training and testing the samples.

C. Deep Convolution Neural Network

The convolutional layers consist of neurons that have learnable weights and biases [19]. Each neuron receives some inputs then performs a new set of matrix operation known as dot product to generate a single value in the output [20]. To perform the convolution operation, we implemented the concept of kernel. A kernel or filter as referred to in the literature review is a small matrix that is selected to perform the feature extraction of the image. To do this, the kernel is slid along the image horizontally and the dot product of pixels that falls in the window of the kernel is performed along with the kernel weight. The model has an input of 64 x 64 matrix and kernel size of 3 x 3.

The proposed system architecture consists of five convolutional layers. The first layer is used to detect large features or patterns that differ from their immediate surroundings in texture, color and intensity. The next layers

detect smaller features that have irregular shape and size without a definite pattern. The last layer combines all the features detected by the previous layers and used the information to make detailed classification into distinct group of two classes: Benign and Malignant (cancerous tumor). The configuration of the network is as shown in Table II.

TABLE II. ARCHITECTURE OF THE MODIFIED ALEXNET

Input image, grayscale (64 x 64)		
2	Conv1	96, 5 x 5 convolution with Stride=2 and zero padding
3	ReLu	Rectifier linear unit
4	Cross channel normalization	cross channel normalization with 5 channels per element
5	Max pooling layer	3x3 max pooling with stride [2 2] and zero padding
6	Conv2	256, 5 x 5 convolution filter, with Stride=1, and Padding = 2
7	ReLu	Same as previous
8	Cross channel normalization	Same as previous
9	Max pooling layer	Same as previous
10	Conv3	384, 3 x 3 convolution filter with Stride=1, and Padding = 1
11	ReLu	Same as previous
12	Conv4	Same as Conv3
13	ReLu	Same as previous
14	Conv5	256, 3 x 3 convolution filter with Stride=1, and Padding=1
15	ReLu	Same as previous
16	Max pooling layer	Same as previous
17	FC1	Fully connected layer with 4096 neurons
18	ReLu	Same as previous
19	Dropout	Dropout layer of 50%
20	FC2	Fully connected layer with 4096 neurons
21	ReLu	Same as previous
22	Dropout	Dropout layer of 50%
23	FC3	Fully connected layer of 2 neurons
24	Softmax	softmax
25	Classification layer	Output layer into two classes (Benign vs Malignant)

D. Training the model

Alex-Net architecture is among the most used pre-trained CNN models for image classification. The architecture was initially designed for 1000 classes using the ImageNet dataset [7]. In this study, the Alex-Net architecture was adopted since it has the potential of training large networks of dataset faster with the available graphical processing units (GPU).

We modified the Alex-Net architecture by removing the last three layers of a standard Alex-Net architecture and replaced them with fully connected layer (FC), soft-max layer and classification layer respectively. Thus, the architecture was modified to suit a two-class problem. The input and convolution layers were also modified to suit the problem at hand.

The CNN model was trained using the stochastic gradient descent (SGDM) algorithm. The dataset from MIAS was split into 31% and 69% for training and testing respectively. To train the model we started with some specified vector parameters. In the process of training, parameters like

iteration number, learning rate and weight decay were updated so that the loss function was reduced at each iteration of the algorithm. The training algorithm stopped when the specified condition was satisfied.

IV. RESULTS AND DISCUSSION

The results obtained in this study are in two phases: tumor classification without augmentation and with augmentation of the original MIAS database. In both cases, the system performance was evaluated using all the evaluation parameters. The architecture presented in Table II was implemented using MATLAB computer vision and machine learning toolboxes. First, all images in the MIAS database were resized to a dimension of 64 by 64 to match the input size of the CNN as well as to reduce the computation complexity. As it had earlier been stated, the program was simulated on two cases: without augmentation and with data augmentation (by adding reflection and rotational version of the original images to the database). In both cases, a learning rate of 0.1 and maximum epoch of 100 were used. The SGD training function (optimizer) was used with a PC specification of 8GB RAM, Core i5, 2.5GHz. The obtained results are thus presented.

A. Tumor Classification Without Augmentation

In this section, the training and testing of the CNN model was carried out using the original image data obtained from the MIAS dataset containing 322 images of which 207 samples are normal breast mammogram while 115 samples are abnormal. The data was divided into training and testing sets where 100 samples (31%) out of the 322 were used for training and the rest for testing. The percentage of training samples was low to avoid the training phase from being over fitted to normal breast samples which are more in number than the abnormal samples. Randomly selected samples from the database are shown in Fig. 2.

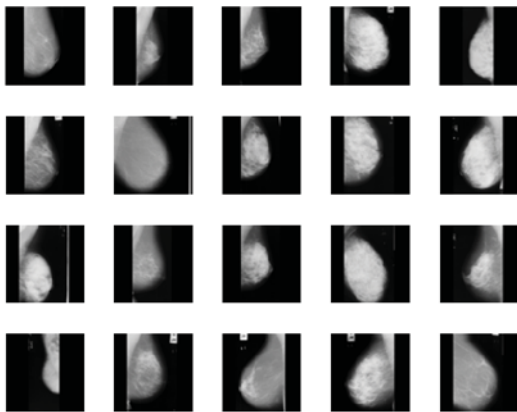


Fig. 2. Samples from original MIAS database

Obtained results using a single CPU for simulation is thus presented as follows. The percentage accuracy for training and validation are shown in Fig. 3. In addition, the training and validation loss is shown in Fig. 4.

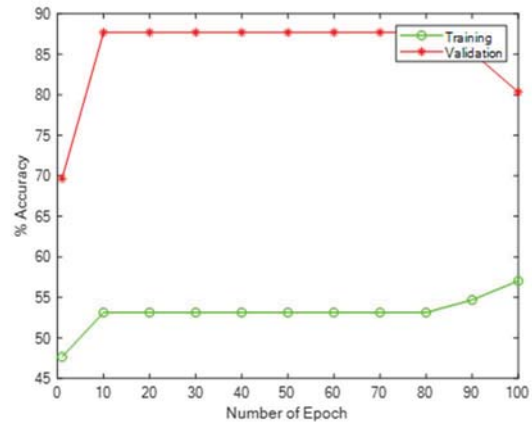


Fig. 3. Percentage accuracy for training and validation (without augmentation)

TABLE III. CONFUSION MATRIX OF THE SYSTEM

		MODEL	
		Benign	Malignant
Classified as	Actual Benign	0.95	0.05
	Actual Malignant	0.054	0.946

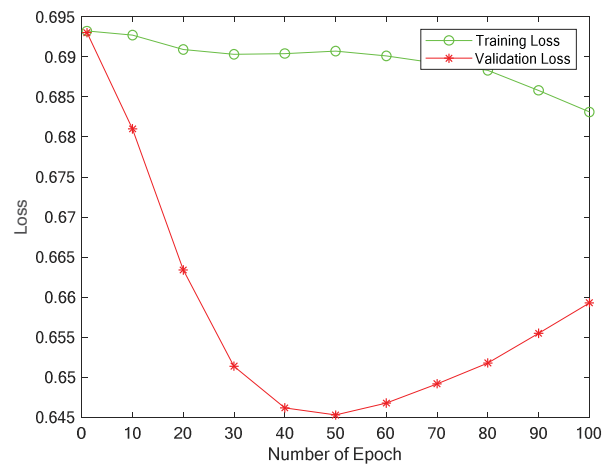


Fig. 4. Training and Validation Loss function (without augmentation)

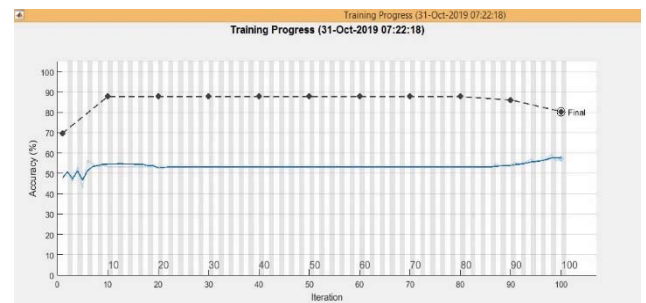


Fig. 5. Percentage accuracy of the system model (without augmentation)

In this case, an average system accuracy of 80.32% was obtained. The next section presents the results obtained when data augmentation is used.

B. Tumor Classification With Augmentation

The second case involves augmentation of the original MIAS database using the augmentation approach previously discussed. With augmentation, the total samples of images become 2,576 samples, out of which 800 samples (31%) were used for training and the rest for testing. Some of the randomly selected samples are shown in Fig.6.

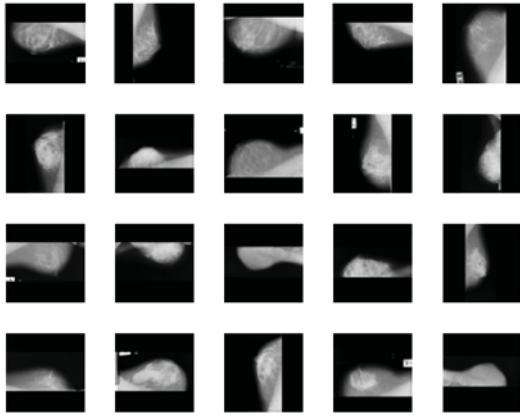


Fig. 6. Randomly selected samples from the augmented data

With augmentation, the obtained results show some level of improvement and this is presented as follows. The training and validation accuracies are shown in Fig. 7. while the training and validation loss are shown in Fig. 8.

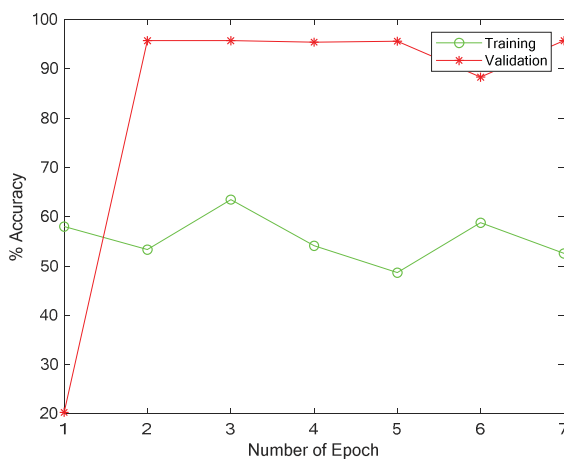


Fig. 7. Percentage accuracy training and validation

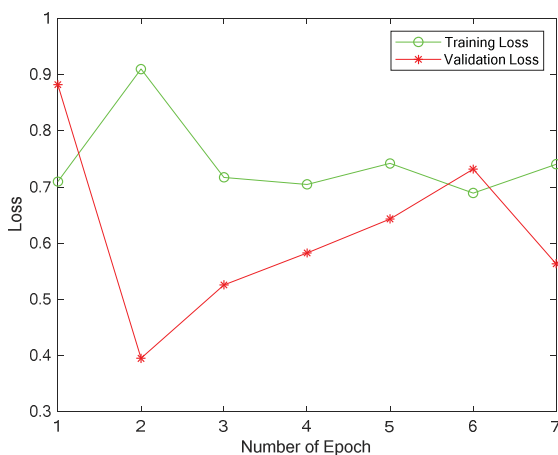


Fig. 8. Training and Validation loss function

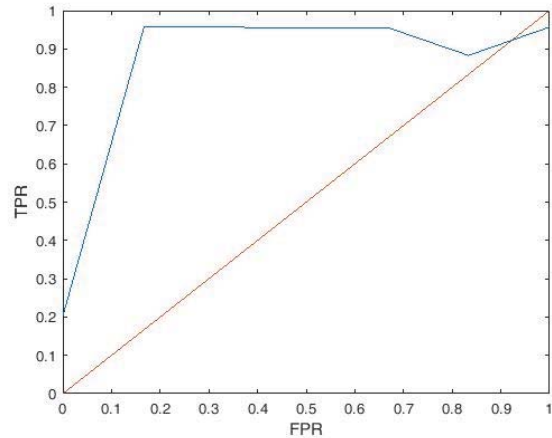


Fig. 9. ROC for evaluated model

The True Positive Rate (TPR) is also known as sensitivity (precision) and it tells what proportion of the tumor samples are correctly classified while False Positive Rate (FPR) or (1- specificity) indicates the non-tumor samples that are incorrectly classified.

The ROC curve summarizes all the confusion matrices that each of the threshold produced. The threshold was set at the optimum point of 0.5. As one moves along the ROC curve upward it shows that there are more proportions of accurately predicted tumor samples than incorrectly predicted samples. At the high point (0.9) of correctly predicted samples on the TPR axis there is the indication of a lower point of 0.15 incorrectly predicted samples on the FPR axis.

The straight line indicates a direct proportionality relationship between TPR and FPR, and all points on the line mean that the proportion of correctly classified tumor samples (malignant) are the same as the proportions of incorrectly classified samples that are not tumors (benign). The Area under curve (AUC) of the ROC curve from the graph shown in Fig. 9, is 0.957 (95.7%). Using data augmentation, Fig. 7 and Fig. 9 give an indication that the average recognition rate of 95.7% was obtained which shows an improvement over the use of the original database without augmentation.

CONCLUSION

In this paper, a modified AlexNet DCNN was used for the classification of breast cancer into benign and malignant tumor using the MIAS database. The deep convolution neural network automatically learn and extract features from mammographic images in order to classify breast tumor into two distinct class of benign (normal) and malignant (abnormal). The implementation of the work requires the use of different convolutional filter sizes of 5x5 and 3x3 for the first four layers respectively. In order to remove noise factor and reduce the amount of computational time, a pre-processing algorithm was employed. The results demonstrate that the fully connected layer used as the classifier in the modified AlexNet architecture give an overall classification accuracy of 95.70%, showing improvement over the traditional methods used for mammogram analysis. This is made possible by leveraging

on augmentation techniques involving both reflection and rotation.

ACKNOWLEDGMENT

This work was supported partly by the National Space Research and Development Agency under the Federal Ministry of Science and Technology, Nigeria.

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