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A Deep Learning Model for Malaria Disease Detection and Analysis using Deep Convolutional Neural Networks

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ABSTRACT: Malaria is a very infectious disease that is caused by female anopheles mosquito. This disease not only harms humans but also animals. If this disease not diagnosed properly in the early stage than it can cause muscular paralysis or even death of the patient in worst case. Due to lack of highly technical expertise in industry, it becomes very difficult to confirm the presence of disease. In this context, the intervention of IT must be involved for proper and rapid detection of disease. Modern day IT sectors are putting their blood and sweat for fighting this disease by taking the help of IT sector buzz words technologies like Machine Learning, Deep Learning and Artificial Intelligence. These technologies have been a backbone for healthcare since the last few years and will continue to be if used properly. This paper uses the CNN algorithm on the microscopic image of the malaria infected blood cells to predict if an organism is suffering from malaria or not. Our proposed model got accuracy of 95.23% and out of 16 random images, 15 are always predicted correctly.

Keywords: Deep Convolutional Neural Network, Image Processing, Malaria Detection, Artificial Neural Network, Deep Learning, Medical Imaging, Disease Detection.

I. INTRODUCTION

Improvement in the system of healthcare is the need of the hour. Using AI in the field of healthcare can solve the problems associated in the field of healthcare up to some extent. Artificial Intelligence is a sophisticated technique which uses complex algorithms to emulate human like behavior in case of the analysis of complex data. It also has the interesting ability to predict without the interference of any direct human contact. The reason is that makes AI technology better than obsolete technologies in the field of medical and healthcare are its power to acquire information, take action and give correct output to the user. Artificial Intelligence does this by the use of various Machine Learning and Deep Learning algorithm [1].

The father and the founding member of modern computer and AI is Sir Alan Turning. The year which saw an increase in the amount of interest in the technique of AI was 1980s and 1990s. The complex techniques like Fuzzy expert systems, Bayesian Networks, ANN were used in healthcare systems. In the year 2016 people all over the world saw a huge amount of investments that were in the field of healthcare as compared to the other sectors. AI in medical can be useful in many ways like in virtual section, use of neural network to develop a model which can recognize brain tumor and in physical part and help robots to perform surgery. AI is whooshing its way into the public sector. It can help physicians to identify which patient will require more attention. By doing this the doctor can provide personalized rules and regulation for treatment for each individual. Artificial Intelligence can be used by primary care physicians for preparing their records, study their discourse with patients and feed the relevant information to EHR systems directly. These AI driven systems helps to gather the patient data and then analyze it and present it to physicians to get analysis of medical needs of patients [2].

AI has a very vast application in the case of medicine and healthcare. It can be used to detect disease like malaria, tumors and can also provide personalized medical care. For a person it can become a very tedious work to correctly classify a disease. Here AI plays an important role, as it can perform these tasks with ease. It can be used to detect lung cancer or heart strokes based on CT scan. AI proves to be very helpful to classify skin cancer based on skin images. Developing an AI product which detects a disease takes very less amount of time in comparison with a doctor. Similarly developing a drug is a very notorious and very costly process. It can take many years of hard work and it has the potential to shave off years of hard work. If it fails then it can result in the loss of millions of dollars. AI can similarly be used to design drugs. The other application of AI in medical are providing personalized treatments and improving gene editing [3]. Use of AI in the field of health care can transform the field magically. It can create wonders. There has been quite a few works in AI like detecting lung cancer, pneumonia and other diseases. AI proves itself more accurate and faster at diagnosis than real life doctors [4].

Malaria is the disease which can prove very fatal for the organism if not diagnosed in early stages and is caused by parasites. It can be transmitted to people if bitten by the female anopheles mosquitoes. This disease can be completely prevented and cured provided precautions must be taken well before the matter gets out of our

hands. In 2017 there was a total of 219 million people were infected due to malaria in total 87 countries which was roughly expected. There were a pretty high number of deaths due to malaria [5]. A parasite named plasmodium is the root cause of malaria. When an infected female mosquito bites a person, and after sucking bloods the saliva of the mosquito gets into the person's blood. The infected parasite enters into the human blood by means of infected mosquito saliva which it injects while biting onto the surface of the human skin. There are five parasites species which causes malaria in human.

The malaria disease is a major health issue and is often found in more than 107 countries [6]. Even the WHO is very much worried about the disease. It comes under a life threatening disease category which can result in death of a person if she/he is not given proper health care in time. When the female mosquito bites you, the parasite enters into the stream of your blood and once it is inside your blood they travel to your liver where they spend some time to mature themselves. After they mature completely they start affecting your Red blood cells. Within two days to three days, the parasites which are present inside the RBCs starts to multiply themselves and that causes the infected blood cells to burst open [18].

Malaria shows it's symptoms within ten days to four weeks after the blood cells are infected. In very rare cases there is a delay in symptoms for several months. There are some cases when the parasites will enter the body and will stay dormant for long period of time. The symptoms of malaria are person suffering from an attack which will shiver him and he will suffer from high fever, diarrhea, anemia, bloody stools, muscular coma etc. It is a need of an hour to recognize this disease properly to diagnose the infected person in time to prevent the disease for spreading further.

This paper focuses on the implementation of a deep CNN algorithm for the detection of malaria disease using thin blood smear images. The deep CNN algorithms are the neural network-based algorithms used for solving these kinds of complex image-related problems. The advantage of these algorithms is that it analyzes the image in a proper way through the core of the algorithm which is the mathematical convolution operation. Due to this, the algorithm becomes more and more efficient and powerful which is the main reason for using this algorithm here.

The rest of the paper is organized as follows: Section II briefs about the literature survey done in the paper, Background study about malaria and the model discussed in Section III and IV discusses about the proposed architecture, Model implementation is elaborated in Section V and VI is about the result and discussion and lastly Conclusion and future scope is described in section.

II. LITERATURE SURVEY

Bairagi and Chrape (2016) has proposed a model for detection of the malaria parasite life stages using blood images. They have used approach of image processing for detection of malaria parasite in the blood cell and detect their stages. The paper detects the parasite's life stage that is present in the blood by using features like statistical features and textural features of the parasite. The authors have also made a comparison based on accuracy, sensitivity, and specificity of the features [7].

Ahiwar *et al.*, (2012) has formulated an automated technique for detection and classification of parasites which causes malaria in blood using blood cell images. They have tried an automated diagnostic technique for fast and accurate diagnosis of disorders in RBC and have proposed a model for detection and classification of malaria parasites in blood samples captured from light microscopes. This paper also used Image classification to positively identify the parasite that causes malaria inside thin blood smears. The features are generated on the basis of color texture and the geometry of the cells and parasites. The paper taken the help of neural network classifier to distinguish between normal and parasitized blood cells [8].

Tek *et al.*, (2009) suggested in their paper that makes a clear cut review of image analysis and computer vision techniques for automation of diagnosis of malaria infection in thin blood film smear microscopic images [9].

Das *et al.*, (2013) recommended a technique which follows an automated approach of machine learning on microscopic peripheral blood smear images. In their analysis, they have found 6 classes which can be determined by ninety four features. They have used a classification scheme-cum-feature selection by combining Bayesian learning and Support Vector Machine for providing higher accuracy in classification [10].

Pan *et al.*, (2018) has suggested an approach for detecting the cells that are infected by malaria using DCNN. They have used Image processing that is used segment red blood cells [11]. The problem of over fitting is solved by the use of data augmentation as well as deep neural networks. The above mentioned dataset contains the original dataset and the augmented data which are obtained using automatically extracted features obtained by stacked auto-encoders.

Dong *et al.*, (2017) in their paper has examines the DCNN for automatic identification of the cells that are infected by malaria. The dataset that they have used contains blood slide images of RBCs which can be categorized into two labels which are infected and non-infected. They have evaluated three types of popular architectures of CNN that are LeNet, AlexNet and GoogleNet [12].

III. BACKGROUND STUDY

A. Deep CNN

Deep Convolutional Neural Networks (DCNN) is the complex neural network architecture widely used in the industry to solve complex real world problems. DCNNs are capable of handling and processing audio, video and images etc. DCNN proves as a very good feature extractor among all kinds of data as it has a complex set of hidden convolutional layers within it. Real world problems in the domains like medical science, human activities, object detection, sound classification and many more are solved by Deep CNN. Gu *et al.*, (2018) has explained all the recent advances in the field of Deep CNN [17].

The productiveness of deep learning techniques is evolved by the continuous invention and evolution in the area of neural networks. Khan *et al.*, (2019) has explained some of the evolving modern day Deep CNN

architectures like AlexNet, VGG and LeNet-5. Deep CNNs are one of the major reasons that the industry and whole world has woken up to believe in the amazing power of Deep learning. Here is an example for a complex deep CNN architecture [16].

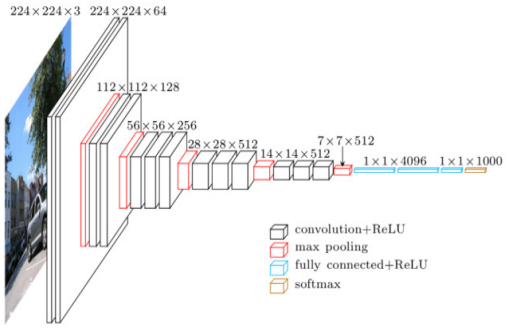

Fig. 1. A Deep CNN Architecture (VGG-16).

B. Mathematics behind CNN

x : Input
a^k : After convoluted image
k : Index of kernel (weight filter)
W : Kernel (weight filter)
b : Bias
E : Cost function

C. Convolution Layer

We have taken a filter/kernel matrix for feature extraction and convolve that to the original image matrix. This layer is mainly responsible for feature extraction [13].

For forward propagation

$$a_{ij}^{(k)} = \sum_{s=0}^{p-1}\sum_{t=0}^{q-1} W_{st}^{(k)} x_{(i+s)(j+t)} + b^{(k)} \quad (1)$$

For backward propagation

$$\frac{\partial E}{\partial W_{st}^{(k)}} = \sum_{i=0}^{P-p}\sum_{j=0}^{Q-q} \frac{\partial E}{\partial a_{ij}^{k}} \frac{\partial a_{ij}^{k}}{\partial W_{st}^{(k)}} = \sum_{i=0}^{P-p}\sum_{j=0}^{Q-q} \frac{\partial E}{\partial a_{ij}^{k}} x_{(i+s)(j+t)} \quad (2)$$

$$\frac{\partial E}{\partial b^{(k)}} = \sum_{i=0}^{P-p}\sum_{j=0}^{Q-q} \frac{\partial E}{\partial a_{ij}^{k}} \frac{\partial a_{ij}^{k}}{\partial b^{(k)}} = \sum_{i=0}^{P-p}\sum_{j=0}^{Q-q} \frac{\partial E}{\partial a_{ij}^{k}} \quad (3)$$

D. Pooling Layer

In this layer, we pick up the important features or the features which we require to extracted from the convolution layer. The size of the matrix gets reduced after it passes from this layer [14].

Forward Propagation:

$$a_{ij} = max(0, x_{(i+s)(j+t)})$$

Backward Propagation:

$$\frac{\partial E}{\partial x_{(i+s)(j+t)}} = \frac{\partial E}{\partial a_{ij}^{(k)}} \frac{da_{ij}^{(k)}}{dx_{(i+s)(j+t)}} = \begin{cases} \dfrac{\partial E}{\partial a_{ij}^{(k)}} & (a_{ij}^{(k)} = x_{(i+s)(j+t)}) \\ 0 & (\text{Otherwise}) \end{cases}$$

E. Fully Connected Layer

This layer is very crucial as it converts the previously processed matrix to the 1-dimensional vector which will be further used for classification [15].

ReLU Activation Function: It is an activation function which adds non-linearity to the graph.

$$a_{ij} = ReLU(x) = max(0, x_{ij})$$

F. Output Layer

As depicted by the name, the output layer is used for demonstration of output of our model.

Sigmoid activation function:

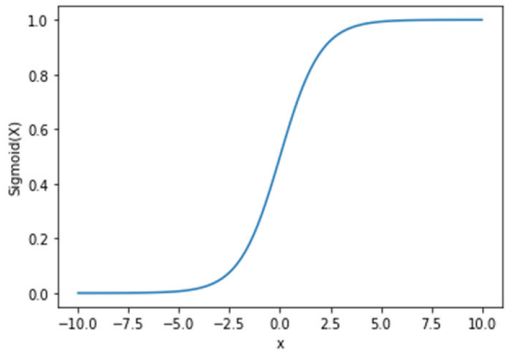

Fig. 2. Graph for Sigmoid activation function.

IV. PROPOSED ARCHITECHTURE

Deep CNN architectures are very complex in nature as it contains multiple layers inside it. Here's the description of our proposed DCNN architecture.

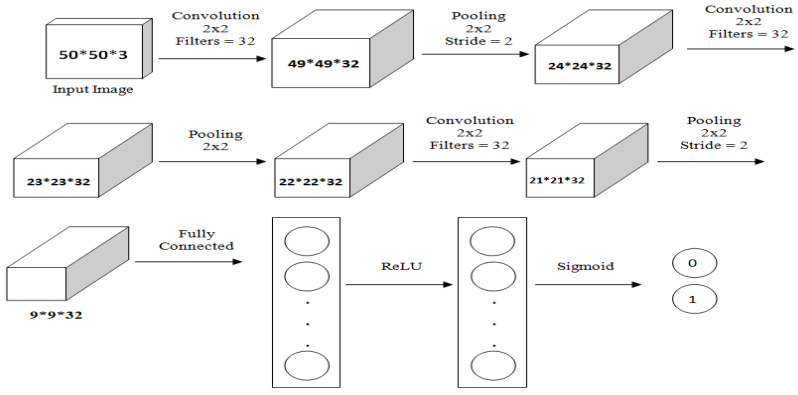

Fig. 3. Proposed Architecture for Malaria Disease detection.

V. MODEL IMPLEMENTATION

A. Dataset Description

We have used dataset from the official website of NIH [20]. We have used a balanced dataset of blood cells. There are total number of 27560 images which are equally divided into two classes that are Parasitized and Uninfected cells. We have divided the dataset into 3 categories known as training sets, test set and validation sets. The model is trained using the train set and validated using the validation set [23]. After the training phase is over, we have used the test set to test the model to verify the accuracy. The dataset contained thin blood smear images of infected and uninfected blood cells. Below are the some samples images from the dataset which is categorized in to two classes i.e. parasitized and uninfected.

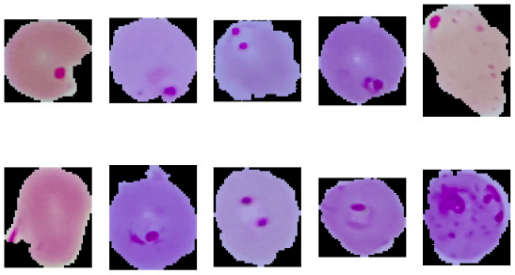

Fig. 4. Parasitized Blood Smear Images.

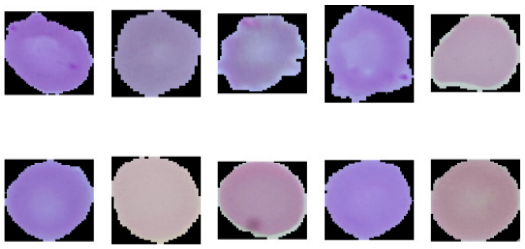

Fig. 5. Uninfected Blood Smear Images.

B. Image Augmentation:

Image data generator is basically used to expand our dataset artificially to prevent the model from over fitting and to get better training results. What image data generator does is, it augments the data artificially by performing various methods like brightening, shearing the image, and rotating it left and right. It also increases and decreases the brightness and contrast level of the image in order to artificially create new training images [19].

C. Training the model

After finishing the data preprocessing and image augmentation we have trained the model on the training set and validated the model on the validation set. We have taken a total of 22046 training samples divided into 2 classes and a total of 2756 validation samples also divided into 2 classes.

Loss Function Cross-entropy loss function is a type of function or parameter that is often used to measure the performance of the model in terms of loss. For a problem which has binary labels as its output (often termed as binary classification) the binary cross-entropy loss function is used [21]. For a multiclass problem having multiple labels as its output (often coined as multiclass classification) the categorical cross-entropy loss function is used. In our model we have used the binary cross-entropy loss function because our dataset has two labels which is a binary classification problem.

Activation Function The activation function is considered as a gateway in between the input layer and its output layer. In other words it a type of function that limits the output signals to a finite value [24]. So it is important to put an activation function just to stop the output value to a certain finite value. We have used a Rectified Linear Unit (ReLU) as an activation function in the input and hidden layers. The sigmoid function is used in the output layers as the activation function as our data has binary label.

Optimizer Optimizers are considered as a group of certain algorithms that are used to change the feature of the neural network such as weights and the learning rate in order to reduce the loss. There are various optimizers like SGD, RMSprop, Adam, Adamax etc. [22]. Out of all these optimizers we have chosen the Adam optimizer for our model. We can look at the Adam optimizer as a combination of the both RMSprop and Stochastic Gradient Descent with the momentum.

Validation and Testing After training our model in each epoch, we are validating our model on the random batches of 30 samples. This validation occurs after the training of each epoch. After validating the model, we are testing our model by taking random images from the test set and the testing accuracy after final evaluation is coming out to be 95.44%.

VI. RESULT AND ANALYSIS

After training our model for 30 epochs, we have tested our model on a test dataset which is giving us an accuracy of 95.23% and the model is working well as a whole. We are evaluating our model in various parameters which are very important for analysis of results.

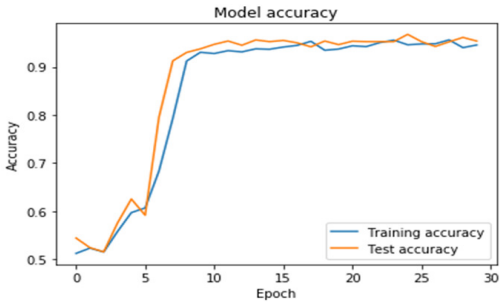

Fig. 6. Accuracy Curve.

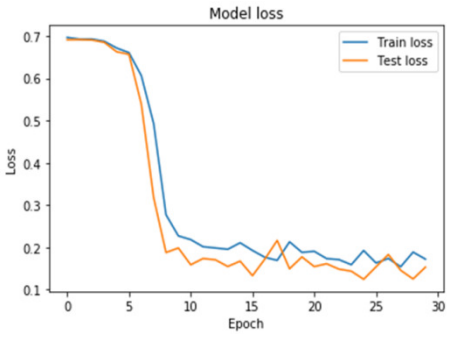

Fig. 7. Loss Curve.

From the above graphs, it is evident that our training and testing accuracy are increasing progressively which means the model is learning very well with time. It can also be seen that the loss in our model is decreasing.

Table 1: Classification Results after completion of testing and training.

Class	Precision	Recall	F1-Score	Support
Parasitized(0)	0.97	0.92	0.95	1370
Uninfected(1)	0.93	0.98	0.95	1385

From the above table, it is clear that our model has achieved a precision of 97% for the parasitized class and 93% for the uninfected class. The recall for both classes is 92% and 98% respectively, F1-Score for the both classes are 95% respectively. The supports are 1370 and 1385 respectively. After in-depth analysis, we have tested our model on randomly generated images from the test set. For a current instance of 12 images we get 11 correctly classified images and 1 incorrect result (denoted by red colored text). The image is displayed below for reference.

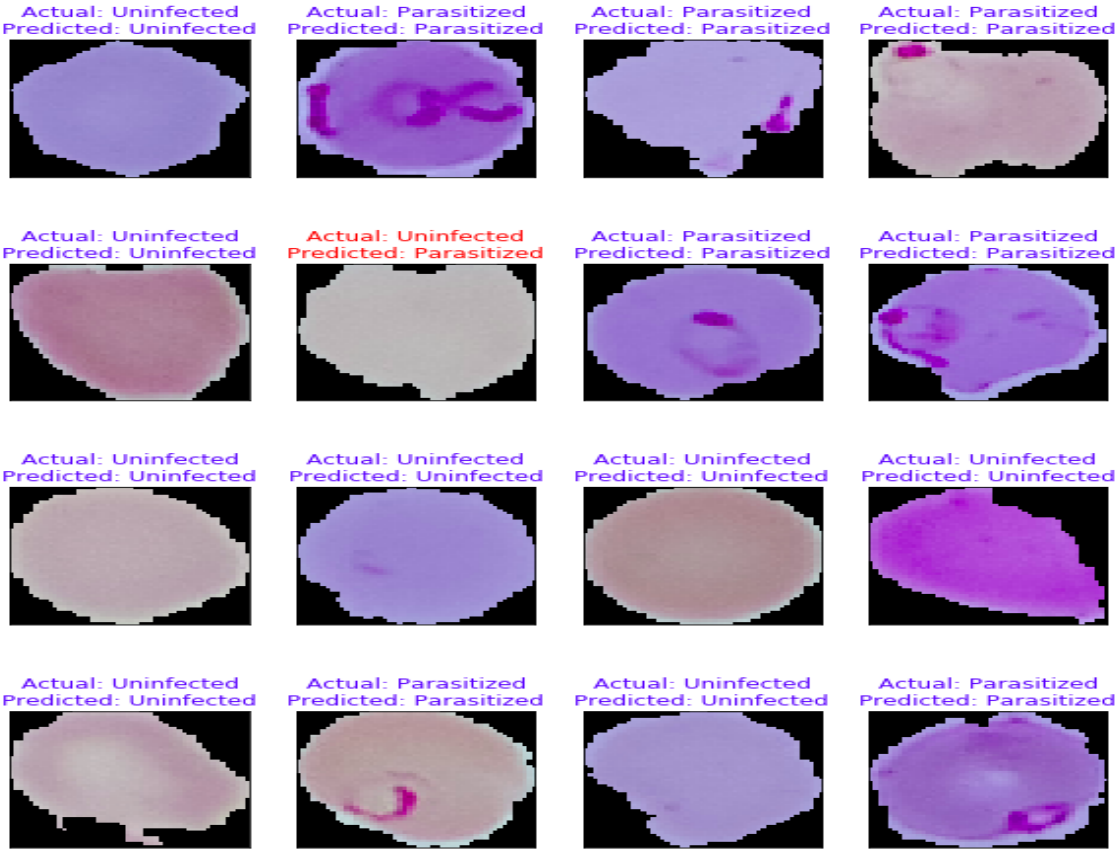

Fig. 8. Predicted results for randomly taken thin blood smears.

VII. CONCLUSION AND FUTURE SCOPE

Malaria is a deadly disease that has taken countless lives and is on a verge to take more. It not only affects humans but also affects a lot of organisms. It is a type of disease for which even the World Health Organization is concerned about. The early detection of malaria is very important to save someone life. Our proposed model has used a famous deep learning technique popularly known as Deep Convolutional Neural Network (DCNN). The proposed mode takes the images of a microscopic blood samples which are the thin blood smear images and detects whether malaria is present in that smear or not. This model can be very helpful in curing the malaria disease at the earliest. Disease detection and healthcare applications using Artificial Intelligence can be a new step towards the modern industrial revolution and digitization. In future, we can build a full-fledged and working application and website which will work for detecting malaria disease. We can also embed a sensor along with the camera device to capture the microscopic images in the microscope for detection of malaria.

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Conflict of Interest: No conflicts of interest are there

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