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Image Classification using Deep Neural Networks for Malaria Disease Detection

E. Laxmi Lydia[1], G. Jose Moses[2], N. Sharmili[3], K. Shankar[4] and Andino Maseleno[5]
[1] Professor & Big Data Consultant,
Computer Science and Engineering, Vignan's Institute of Information Technology, India.
[2] Professor, Computer Science and Engineering,
Raghu Engineering College (Autonomous), Viskahpatnam (Andhra Pradesh), India.
[3] Associate Professor in CSE Department,
Gayatri Vidya Parishad College of Engineering for Women, Viskahpatnam (Andhra Pradesh), India.
[4] Department of Computer Applications, Alagappa University, India.
[5] Institute of Informatics and Computing Energy, University Tenaga National, Malaysia.

(Corresponding author: E. Laxmi Lydia)

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ABSTRACT: Since the 19th century, Malaria has become a terrifying life-threating disease in most of the countries. Its been identified that five countries namely Nigeria with 25%, Congo with a ratio of 11%, Mozambique with ratio of 5%, India with ratio of 4% and Uganda with ratio of 4%. World Health Organization stated that above 90% of malaria death cases were recorded every year. Most of the Indian states like Odisha, Madhya Pradesh, Maharastra, northern countries, Chhattisgarh got affected by Malaria. India spotted death cases of malaria from millions to thousands that have reduced in recent years. Directorate of National vector Bore disease control program has started malaria control strategies using early case detection and treatments, vector control, protective measures against mosquito bites and management of Environment. The major challenge was to identify the disease at early stage. The key contributions avoid malaria disease is to provide antimalaria drugs, using indoor spray with residual insecticides, mosquito nets. For the treatment, medical technologies, deep learning architectures related to Convolutional Neural Networks to train and test performing different combinations for image classification using ResNet34 which helps patient go through prior examination for microscopic diagnosis. For patients examination, this paper considers Malaria Cell Images dataset with Parasitized and uninfected images. Thus, this clearly shows that one can easily identify person's condition whether he is infected or uninfected by enabling open-source Artificial Intelligence. It shows the start-of-the-art accuracy by checking individual details.

Keywords: Malaria, ResNet34, Convolution Neural Network, Image Classification, convolutional, neural network.

I. INTRODUCTION

Millions of people all over the world were affected by malaria. The major different Parasites that led to malaria are p.knowlesi, p.ovale, p.malariae, p.vivax and p.falciparium. These parasites are like small insects that grow through stages inside the human body and transforms into harmful bacteria, which leads to malaria. They change in their morphological behavior, size, color at each level of their stage. The main cause of malaria is due to climatic conditions in tropical region areas. Mosquitoes causing malaria, it is a parasite which gets transmitted into human blood through mosquito bites. Millions of people are getting sick from high fever to deadly states. It is a transmission process from mosquito to the human body, human body to liver, liver to red blood cells. The three different modes of malaria transmission are from mother to child (in womb, who are unborn), one to another person blood transfusions, giving similarly injected needles too other persons.

Existing approaches for malaria diseases, implemented methodologies such as automatic detection through RBC count, applying Log filters to identify unique cells, use of model variance, minimizing the variance provide solutions but not with optimal results. An automated detection system to recognize and distinguish malaria parasites in human blood varies from different stages like trophozoites; schizonts analyze blood slides through a microscope.Detection of RBC count and segmentation of cell images uses multiscale Laplacian of Gaussian, another contour-based segmentation for the detection of morphologies that detects both annular and disk-like structures among cells.Microfluidic devices used to track the red blood cells in videos to control the concentration levels of oxygen. Due to large number of varying characteristic features, the video of blood flow of RBC cells process cell classification for accurate segmentation [19]. In real-time data processing [31], implemented and performed an iterative voting-based detection of cells. To identify the local extreme and approximate centroids, multiscale LoG filter implies to know the individual cells, which help in speed up the processing and accuracy. This will result in the extraction of offline features of color and texture for further evaluation of classification and reduction of dimensionality. Some of the techniques like normalized red green blue for the extraction of color feature information and joint adaptive median binary pattern for extracting texture feature information [29]. Classifiers such as artificial neural networks result in classifying infected and uninfected cells.

The aim of the work is to provide the construction of models using neural networks by detecting the images and by decrease the model variance. This will enhance the robustness and analysis for detection. The efficiency of the CNN classifies the thin-blood smear images [22] by allowing cross-validation. Some of the performance metric calculation on finding classification accuracy is receiver-operating characteristic, mean squared error, precision, and Matthews Correlation Coefficient.

Models VGG-19 outruns the classification process on reaching optimal levels of predictions through multiple models.This has reached the real-world conditions by minimizing the variance. Computer-based diagnoses such as machine learning algorithms [25] prepared clinical assistance for decision-making. Deep learning methods work in identifying the raw pixel data of images, feature extraction, and operating end-to-end extractions and coordination. In this paper, proposed Convolution neural networks solve the existing issues in finding optimal solutions byconsidering patient blood sample features to predict the state of the patient whether the patient is parasitized and uninfected accurately.

II. LITERATURE SURVEY

In 2017, peripheral blood smear images used to detect malaria parasites through Deep Belief Networks. Bibin *et al.,* [4] introduced Boltzmann machines for pre-training using concatenated color features and texture features. The different feature extraction techniques that can be applied are color histograms, color coherence vector, Statistical method for gray level co-occurrence matrix, and textural features positioned on the gray level run length matrix and local binary pattern. The algorithm applied is backpropagation with 4 hidden layers and 600 hidden nodes. This has gained 95% specificity. Parveen *et al*., [5] also proposed an application for malaria prediction analysis using Artificial Neural Network which has given only verbal history and physical appearance of patient without any doctors and laboratory facilities showing positive and negative results.

Automatic visual diagnosis of malaria has developed through a motorized practical microscope [10]. Needed samples are collected to perform analysis using patient symptoms during curing stage. ANN techniques in [9] are applied to evaluate blood smear images. Features from RBC are collected from database with infected and non-infected RBC cells. Situated on the intensity of features, classifiers detected the images that got infected. A system architecture was designed in [11] using two processing systems (system1 and system2), system1 collects the image samples for testing and they are converted into greyscale using pre-processing techniques meanwhile system2 simultaneously collects reference samples and converts them into greyscale. System1 images are compared with the system2 images using NCC. If NCC is less than 0.7 then detection process is continued using morphological processing and detection pf RBC count. Finally, diagnosis results will be achieved.

Object detection procedures and computer vision-based approaches were implemented in [12]. The authors have suggested these approaches based on three reasons. Implemented procedure overstated raw data for color normalization using Reinhard's method. A better comparison of statistical multimodal approaches using Kalman filtersand illumination issues. Finally, pixel information using a kernel-based approach for localizing accurate infected blood samples in image processing. Peñas *et al*., [13] performed analysis-using CNN [21, 24] for problematic issues identified in rural areas for blood smears with specified pixel resolutions for p.falciparum and p.vivax ratio. Laser desorption mass spectrometry was implemented long back in the consequence of detection of malaria parasites [23] during the growth of RBC. They consider beam parameters with upgraded magnitude. It is a UV laser used to clean up entire blood samples by setting up threshold. Oguntimilehin *et al.,* [15] have mentioned all the predictive models for imaging and symptomatic approaches for the treatment of malaria detection during the process of diagnosis [14]. The different models like rough set, fuzzy logic, decision trees, analytical hierarchy process, Rule-based approach, linear programming, Mockler situation analysis through knowledge-based systems, expert systems, Neural Networks and Support Vector Machines.

Poostchi *et al.,* (2018) [2] described that they discovered an automated system that identifies the infected blood cells using Blood Smears. They used the extraction method to segment the RBC in blood. The algorithm used for segmentation is C-EPAC Geodesic Active Contour Based Segmentation Algorithm. Their experiment analysis was tested [30] on human blood cells of malaria-infected and mouse blood cells of malaria-infected. The implemented procedure is they initially considered microscopy thin smears of blood images, detection of RBC and its segmentation, computational evaluation of Cell features like texture features and RBC color, cell classification performance, and evaluation, finally to achieve parasite quantification.Thusthe model has outperformed automatic counting of parasites. This was already tested by [3] based on the histogram features. But the classification techniques implemented are from Artificial Neural Networks and experiment analysis tested using clinical database. Before that Chakrabortya *et al*., [6] have merged algorithms for classification for a thick blood smear. Techniques like pixel discrimination and color based on segmentation. In this approach they didn't use training data, implemented using unsupervised approach [32].

Later based on mathematical morphology detection systems are introduced for malaria parasites in [7]. They have identified certain issues in the diagnosis of malaria and performed a practical implementation over spatial structures with impressive image processing techniques. In this, they have selected morphological mathematical operators that successfully gained image analysis and pre-processing tasks using Non-linear transformation computer-aided architectures suggested for the diagnosis in visual inspection [8]. Image analysis using deep learning for vision-based has obtained fast identification of malaria disease.

Poostchi *et al.,* (2018) [16] has deep concern over these diseases to make use of technology. They have implemented an analysis of images and machine learning approaches [18]. They concentrated on automatic cell classification and cell segmentation. Malaria image acquisition techniques like light, Binocolor, Fluorescent, Polarized, Multi-spectral, multi-modal, image-based cytometer, sub-pixel resolving optofluidic microscopy, quantitative phase imaging, quantitative cartridge-scanner, scanning electron, fiber array-based Raman imaging, serial block-face scanning electron microscopy, and sightDx digital imaging scanning.

Dharpal and Malviya (2018) [17] suggested the work analyses on image processing for the treatment of malaria disease. Parasites are recognized from tainted and non-contaminated red platelets using local binary patterns. Here the Plasmodium parasites are detected using support vector machine [28].

Sajana and Narasingarao (2017) [18] worked for the improvement of malaria disease detection using R programming and weka software by establishing a model-based decision support system on 165 patients from distinct groups collected from Narasaraopet using Naive Bayesian technique. SMOTE is applied to transform unbalanced dataset to achieve balanced dataset.

In 2019, infectious malaria disease has been analyzed using machine learning approaches. The authors [1] have selected spatial features through microscopic images and trained using the Neural network model. Using these images as input, the model needs to recognize the infected area. Exposure of the malaria parasite in the images performed testing the transfer-learning method. This method is an expert learning model that is used as the Unification of VGG network and SVM. Top layers are trained and the rest of the layers are frozen. Images of blood smear samples are tested using VGG19-SVM. This model has shown its potentiality above CNN [20].

Raut and Marathe (2019) [25] identified the rapid usage of multimedia websites that transmit videos and retrieve information from images using a classification system. Applied modules to retrieve image information such as word-level textual cue encoding, visual cue encoding, finally classification. Singh and Singh (2019) [26] analyzed image classification through SVM, and Convolution based PSO. They progressed these techniques for the detection of diseases that occur on leaves. Rao *et al.,* (2019) [27] determined the count of blood cell images from the proposed convolution neural network models using color split channel, binary, mathematical morphology for segmentation. Experimental results were counted based on the hierarchical multiclass Support vector machine.

A. Methodology

Convolution neural networks designed based on some samples through periodic downsampling with the increase of feature maps. Many computer vision problems have identified through machine learning image processing progress through image classification, object detection, and image segmentation. Various Deep Convolution Neural Networks are Spatial exploitation based Convolution Neural Networks, Depth based Convolution Neural Networks, Multi-path basedConvolution Neural Networks, width based multi-connection Convolution Neural Networks, feature map (channel$_{\text{fmap}}$) exploitation based Convolution Neural Networks, channel$_{\text{(Input Channels)}}$ exploitation based Convolution Neural Networks, Attention-based Convolution Neural Networks.

ResNet34 architecture followed deep residual networks, which are adequate with a large number of complex functionalities and input descriptions. A large number of layers indicate mapping and a deeper model that generates no further training error than empty its counterpart. Residual connections initiate network architectures by enabling all the deeper structures. Image recognition through deep neural networks is hard to train but using ResNet 34 training networks is easy by reformulated formulae. This architecture calculates from layer 1 to layer 152 having minimum complexity. This pre-trained model consumes less time and obtains more features. This will train the input dataset and maintain all its weights and bias that reflects the corresponding features. Furthermore, these are transferred and tested by other datasets. Special features of ResNet are to avoid network and rapid use of batch normalization. This further avoids fully connected layers at the extreme. In Convolution Neural Networks for the image reorganization, uses ConvNets. Procedure for ResNet34 Architecture needs residual blocks trained to achieve deeper networks. Initially calculate activations from layer 1 to end of the layers. This reduces the error in-network and assumes weight and bias for computing layers of predictions.The mathematical form of ResNet can be evaluated using $g(a_i)$ and $f(a_i)$.

$f(x_i)$ in which the incoming original input a_i is combined to $f(a_i)$. where $f(a_i)$ is $g(a_i) - a_i$ (results in residual learning).

i.e, $f(a_i) = g(a_i) - a_i$ (1)

and $g(a_i) = f(a_i) + a_i$ (2)

Eqns. 1 and 2 are the ResNet calculations on network layers to make connections among layers and enable cross-layer connectivity.

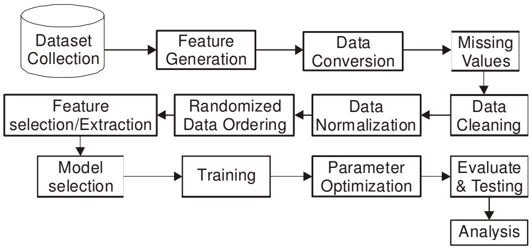

Fig. 1. Block diagram of Convolution Neural Networks.

Convolution Neural Networks process in different layers of execution. For the model selection, the Convolutional layer involvesa group of convolutional kernels that associates with small image regions (receptive field) by dividing the image and convolving those values withset of weights.Represented as

$$F_l^k = I_{x,y} * K_l^k \tag{3}$$

Eqn. (3) represents the operation of the convolution. The input of the image to the network is represented by $I_{x,\ y}$, K_l^k shows the kernel *l* and the k^{th} layer of the convolution and spatial locality are given by x, y. This implementation additionally performs categorization with respect to various filters, padding, and direction. Pooling layer downsamples the features pointing to a specific local region which is represented as below

$$Z_l = f_p(F_{x,y}^l) \tag{4}$$

Equation (4) represents the operation of the pooling by determining the output feature map which reduces the overfitting problem.

Activation Function helps to work on complex patterns and provide decision function. Such as

$$T_l^k = f_A(F_l^k) \tag{5}$$

Eqn. (5) represents the activation function, activation function can use different functions like maxout, ReLU (ELU, PReLU), tanh, sigmoid.

Fig. 1 describes the procedure for image classification using a convolution neural network at three different stages. Initially at first stage data is collected andperformed feature generation, at second stage data will be pre-processed and feature selection will be performed, at third stagea supervised model has been selected, apply to tune on parameters and finally analyze the prediction data.

III. RESULT ANALYSIS

In this paper, the malaria disease dataset was collected from the website, which has images of Parasitized and Uninfected blood samples. Parasitized and Uninfected datasets each consists of 13,779 cell images of blood samples. Considered malaria disease dataset was implemented over a Python environment using Anaconda.

Fig. 1 demonstrates the plot using lr.find() function between learning rate and loss to achieve a good learning rate. Fig. 2 demonstrates the plot for the learning rate over fit_one_cycle at stage_1. Fig. 3 demonstrates the plot on losses at stage-2

Table 1 shows overall accuracies for fit_one_cycle for six epochs. Table 2 shows overall accuracies for fit_one_cycle for four epochs with maximum learning rate.

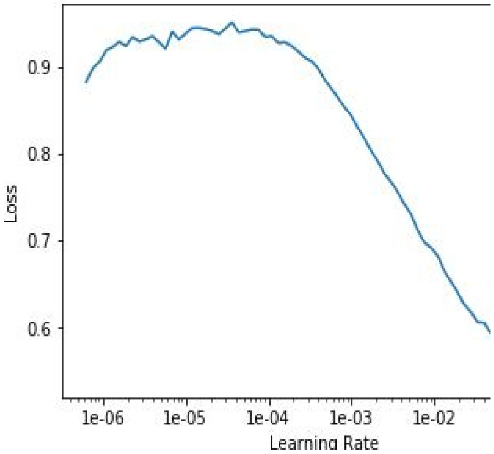

Fig. 2. Plot for Learning rate versus Loss using Learning Rate Finder.

Table 1: Over all accuracy for fit_one_cycle for six epochs.

epoch	Train-Loss	Valid-loss	accuracy
1	0.171754	0.129417	0.956632
2	0.154249	0.116933	0.958447
3	0.146585	0.153310	0.950100
4	0.130996	0.105276	0.961350
5	0.101642	0.091105	0.966975
6	0.090302	0.083954	0.969153

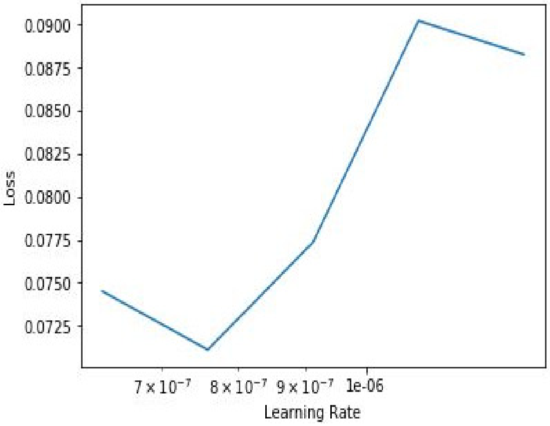

Fig. 3. Learning rate fit_one_cycle at stage_1.

Table 2: Accuracy for fit_one_cycle on four epochs with maximum learning rate.

epoch	Train-Loss	Valid-loss	Accuracy
1	0.100960	0.081042	0.970967
2	0.103197	0.082964	0.972600
3	0.086624	0.080855	0.972600
4	0.087902	0.079658	0.973870

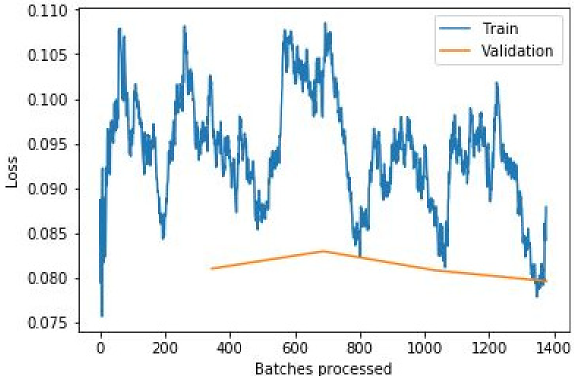

Fig. 4. Plot on losses at stage_2.

IV. CONCLUSION

Image classification on blood samples for the detection of malaria disease. This paper proposed Convolution neural networks for the detection of malaria over 13,779 Parasitized and Uninfected blood cell images. The learning rate at different stages is calculated and identified that 97% of the learning rate is accurate for classification. This involves the identification of parasites in blood sample images. The proposed Deep Convolution Neural Networks predicts the patient conditions for further diagnosis. Therefore, computer predictive models took prior place in medical diagnosis and treatment. Implementation of Deep Convolution Neural Networks results ina good performance on image datawhile estimating its optimal features, orientation and location of the cells (object).

Conflict of Interest. Nil.

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