Performance assessment of Deep Learning procedures: Sequential and ResNet on Malaria Dataset

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***Abstract*—Malaria detection is a time-consuming procedure. Only blood sample investigation is the practice which provides the confirmation. Now numerous computational methods have been used to make it faster. The proposed model uses the conception of Convolutional Neural Network (CNN) to lessen the time complexity in the identification of Malaria. The prototypical model uses different deep learning algorithms that uses the same dataset to validate stability. The model uses the two various components of CNN like Sequential and ResNet. ResNet uses more number of hidden layers rather than sequential. The ResNet model achieved 96.50% accuracy on training data, 96.78% accuracy on validation data, and 97% accuracy on testing data. The sequential model on the other hand achieved 98% accuracy on the training data, 96% accuracy on the validation data, and 96% accuracy on the testing data. From this initial hypothesis, we get to know that there is no significant difference in accuracy when we have too many layers.**

Keywords*—CNN, Computational Methods, ResNet, Sequential

I. INTRODUCTION

Malaria is bred by the parasite Plasmodium, which attacks red blood cells & is transfused by mosquitoes. Malaria's severity ranges from mild to highly serious, which eventually leads to the death of humans. In 2018, an estimated 228 million cases of malaria have occurred worldwide, compared to 251 million cases in 2010 and 231 million cases in 2017. WHO South-East Asia Region constitutes 53% globally for being burdened with P. vivax, with the majority being in India (47%). In 2018, children below 5 years of age accounted for almost 67% (272,000) of all malaria worldwide making them the most vulnerable group affected by malaria. Traditional Methods of Malaria diagnosis is time-consuming [1] and requires highly trained lab technicians. Cure for malaria is of high success if it is detected in the early stages. The limitations of the traditional methods affect the success rates for the cure of malaria. This gives a need to propose an automated system that reduces the time for malaria detection with great accuracy. Sir Ronald Ross discovered that mosquitoes transfer malaria in 1897 and even after so many years' malaria has still proven to be one of the major health problems in the World [2]. In India, more than 50% of the population resides in areas prone to malaria and the remaining population resides in hilly or remote areas. India is ranked fourth in the number of malaria cases according to the latest Lancet Commission report [3]. Out of the 219 million cases that occurred in 2017, as many as 9.6 million occurred in India.

The malaria statistics for India is calculated using several indices. This can be seen in figure 1. The World malaria report 2017 is shown in figure 2.

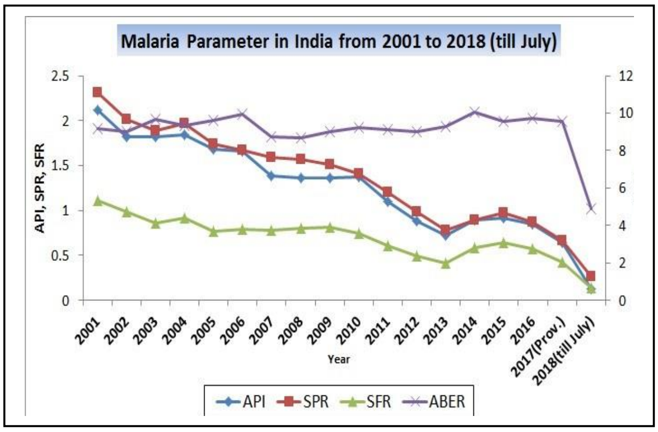


Fig. 1. Malaria Parameter in India from 2001 to 2018 [26]

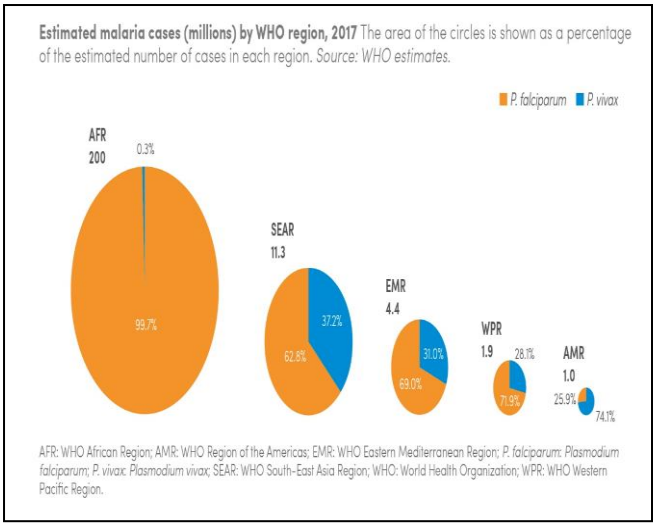


Fig. 2. Malaria cases by WHO estimates, 2017 [31]

The concept of introducing the Deep-learning image analysis techniques [4] into the diagnosis procedure introduces advantages like saving time and giving confidence in making the diagnosis. Deep learning is a type of machine learning that utilizes layered architecture in large for analyzing data. It is also referred to in different terminologies as hierarchical or structured learning. The layered architecture or strategies allow deep learning models for classification tasks [5]. These tasks can range from highlighting relationships between a large number of unstructured data and symptoms to identifying subtle abnormalities in medical images. Deep learning has many advantages over other types of learning such as it requires fewer humans for training and also has a reduced amount of pre-processing data.

Several key processing steps are required for the quantification of parasitemia automatically. First, digital blood slide images should be acquired, which often requires pre-processing to normalize for lighting and staining variations. In the second step, the detection of blood cells and parasites is done. This involves cell segmentation in which we identify individual cells in cell clumps to obtain accurate cell counts. In the third step, features are extracted to visualize the infected and uninfected blood cells. In the final step, a trained classifier is used to differentiate between infected and uninfected cells [1].

Since the diagnosis of malaria is a tedious task if done manually, automation of this is an essential task. Automatic parasite counting has various benefits over manual counting [6]: (a) it gives more accurate and standardized interpretation of the blood films, (b) more number of patients can be served, this reduces the burden on the malaria field workers, and (c) it is much cheaper.

Deep learning techniques, in specific convolutional networks [7], have developed a methodology for investigating medical images. Computer-aided diagnosis has been contributing to the quantitative characterization of diagnostic markers in the medical imaging field and subsequently augmented decision making towards disease diagnosis and prognosis.

In deep learning models [4], data is passed through various layers where each consequent layer uses the output produced by the preceding layer. Deep learning models improve their accuracy by learning from previously processed data by enhancing their capacity to find out relations and connections.

Deep learning is inspired by the working of biological neurons in the brain, how they connect to transmit information from one part to another. Analogous to the way electrical signals advance across the cells when the successive layers are activated on receiving stimuli from the adjacent neurons.

In artificial neural networks (ANNs), which forms the basis of deep learning, each layer performs a particular segment of the whole task, and the data passes through the layers several times to reform and optimize the output.

These "hidden" layers are present in between the input and output layers. They convert the raw input into meaningful output.

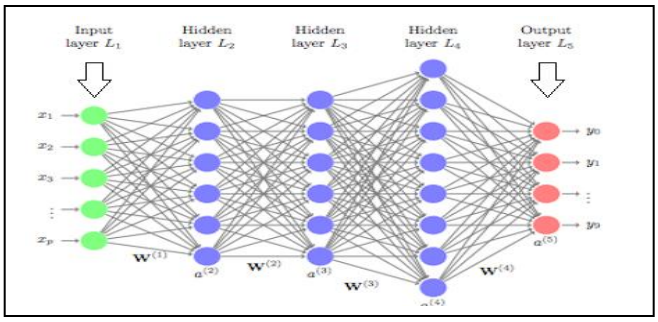


Fig. 3. An illustration of a Deep Learning Neural Network [25]

II. LITERATURE SURVEY

Jahanzaib Latif et.al in their paper "Medical Imaging using Machine Learning and Deep Learning Algorithms: A Review" [8] intends to provide a framework to discuss the existing techniques for medical imaging and gives a comparison of these techniques with their limitations and advantages. The main types of learning are supervised, unsupervised, semi-supervised, active, and reinforcement. Deep learning is an advancement of machine learning algorithms which are more accurate and reliable using CNNs for prediction.[7].

Young Im Cho et.al in his paper "An Improvement for Medical Image Analysis Using Data Enhancement Techniques in Deep Learning" [9] proposed several algorithms for medical imaging. Recent advancements in deep learning especially, deep convolutional neural networks (CNN), enhanced the performance of medical image [6] classification methods. Training a deep CNN with medical images is a complex task. To overcome this many methods were suggested. Firstly, a deep CNN model with twelve layers for image classification [29] is created. Then the network was trained using a CT scan image dataset and new datasets were generated from the original set. Then the comparison of results on different datasets were analyzed. Data augmentation [30] methods improve the performance and provide better results. Techniques for Augmentation such as Data warping, Geometric and colour augmentation, flipping the image horizontally or vertically, rotating 90 degrees, Use of multi-column deep neural network algorithm (already used in MNIST) large datasets were used to solve the problem of overfitting.

Lipo Wang et.al in his paper "Deep Learning Applications in Medical Image Analysis" [10] proposed that Medical records are increasingly digitized (eg. EHR already being used). Medical imaging tasks need to be automated by using efficient machine learning algorithms. AI algorithms improved from heuristic to manual and now supervised learning. CNN can process both 2-dimensional as well as 3-dimensional images. Cognitive Vision Techniques [11] is a new way of linguistic algorithm applications for semantic data analysis in the medical industry. Methodology of linguistic analysis based on graph grammars. The main mechanism is the stage of cognitive resonance (comparing expected vs. experimented).

Saiprasath G et.al in his paper "Performance comparison of machine learning algorithms for malaria detection using microscopic images" [12] proposed the traditional method needs the considerable expertise of microscopists or laboratory technicians. In regions majorly affected by malaria, diagnosis is very difficult & treatments are given based on symptoms alone. Image processing & computer vision methods can be implemented for diagnosis. A new computer vision method based on the approach to identify the MP (Malaria Parasite) from the light microscopy images. This is a pixel-based approach, which uses the K-means clustering algorithm [13] for the segment identification of malaria parasite tissue.

Soner Can Kalka et.al in their paper "Deep Learning-Based Classification of Malaria from Slide Images, IEEE-May,2019"[14] has suggested a malaria detection system based on image processing which is trained using deep learning [4]. Huge data is available for improving the accuracy and the acquired accuracy showed that this system has an excellent rate of classification and hence, should be used for real-world detection.

III. DATASET DESCRIPTION

The dataset was grabbed from the U.S National Library of Medicine [15] and which contains 27,558 cell images. The dataset is split in the ratio of 50% into two classes—infected and uninfected. Researchers of the Lister Hill National Center for Biomedical Communications (LHNCBC) [16], and also the National Library of Medicine (NLM), has developed an Android application which was attached to a light microscope. Giemsa-stained thin blood smear slides from 150 P. falciparum-infected and 50 healthy patients were collected and photographed at Chittagong Medical College Hospital [17]. Using the camera in the smartphone images of these slides from different microscopic angles were obtained. Mahidol-Oxford Tropical Medicine Research Unit in Bangkok, Thailand elucidated these images [18]. The de-identified images and annotations are archived at NLM (IRB#12972).

TABLE I. DATASET EXAMPLE

Dataset Name	**Source**	**Example of infected**	**Example of uninfected**
Cell images	American National Library of Medicine		

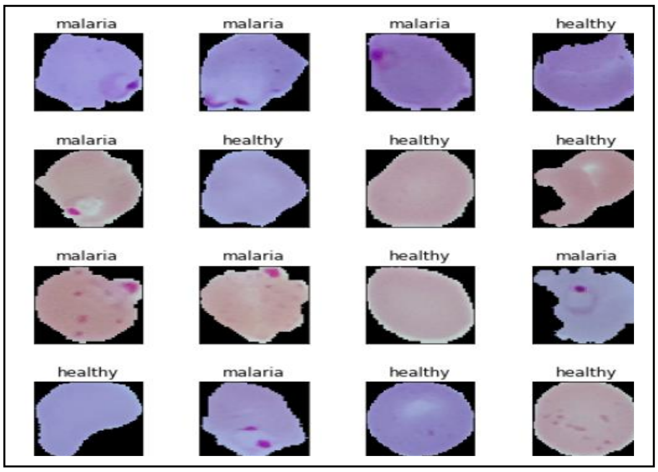
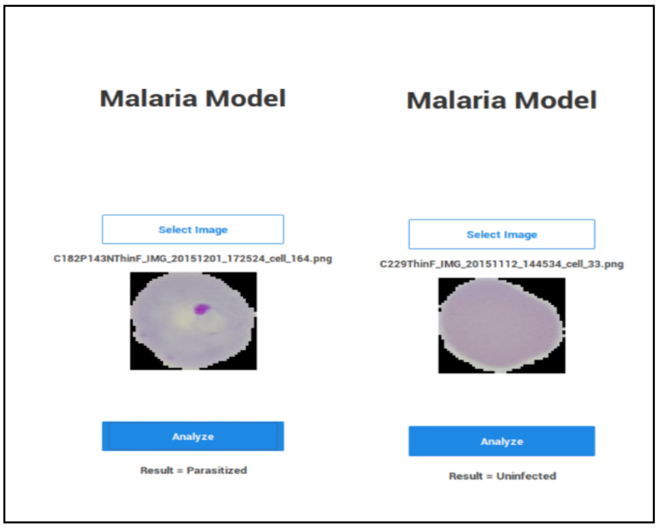


Fig. 4. Dataset example [27]



C182P143NThinF_IMG_20151201_172524_cell_164.png

Result = Parasitized

C229ThinF_IMG_20151112_144534_cell_33.png

Result = Uninfected

Fig. 5. Dataset example of infected and uninfected cells [27]

IV. METHODOLOGIES ADOPTED

In this project, we intend to compare the performance of the disease diagnostic systems under different deep learning techniques [4]. The proposed model is going to be implemented using the same dataset across various deep learning techniques. During the comparisons, the model will take care of parameters such as time complexity & accuracy from the diagnosis of malaria disease.

Training of convolutional neural networks and its' specification

Convolutional neural networks [7] are a type of neural network and widely used for image processing. In traditional networks like multi-layered perceptron [5], the layers are connected densely. The receptive field in CNN are small regions in the input space. Various convolutional filters are present and each responds to different patterns in input, the initial layers respond to simple patterns like edges or colors whereas the layers in the upper levels respond to more complex patterns.

Computation of the layers is done by taking a sliding window across the inputs and the response function is calculated. Every filter captures various patterns.

To reduce the input size, pooling is carried out. Max pooling [28] is a type of pooling in which neighbors are merged and the maximum is considered as an example. Pooling helps in reducing not only, the input size but also, number of parameters and the number of computations required.

The layers in which all activations from previous layers are connected with all the outputs are called as fully connected layers.

This is almost the same as a convolutional layer having only one filter which is equal in size as the input size. A fully connected layer makes up the last layer in a CNN. The output consists of each class label having one element.

We are comparing two networks because ResNet has more layers as compared to sequential which has as short layers as possible (2 layers). So, we see that increasing the number of layers does not affect the accuracy of the same dataset.

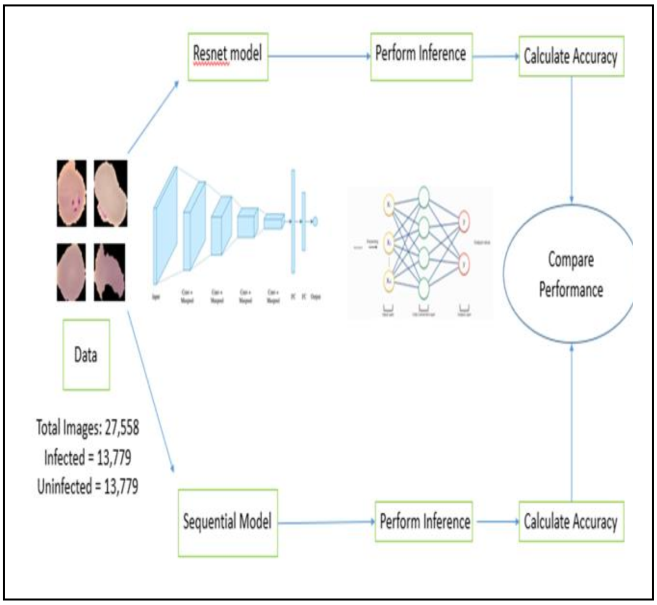


Fig. 6. Proposed Model Diagram

Infected and uninfected samples of cells in image form are broken into arrays of pixels. These images are sent to both the models, Sequential as well as ResNet. These models are then trained and accuracies are calculated. Based on the accuracies, the performance of both the models is compared.

V. MODEL DESCRIPTION

An image-based classification structure is used for the diagnosis of malaria after the cells have been thoroughly examined. CNN is widely used in the field of deep learning, hence, we have used CNNS for classification. First, the system performs feature selection in which the relevant features are selected based on the separating properties of the input images. These features go through the layers of ANN. Then comparison of values obtained with the expected values is done and the network is optimized.

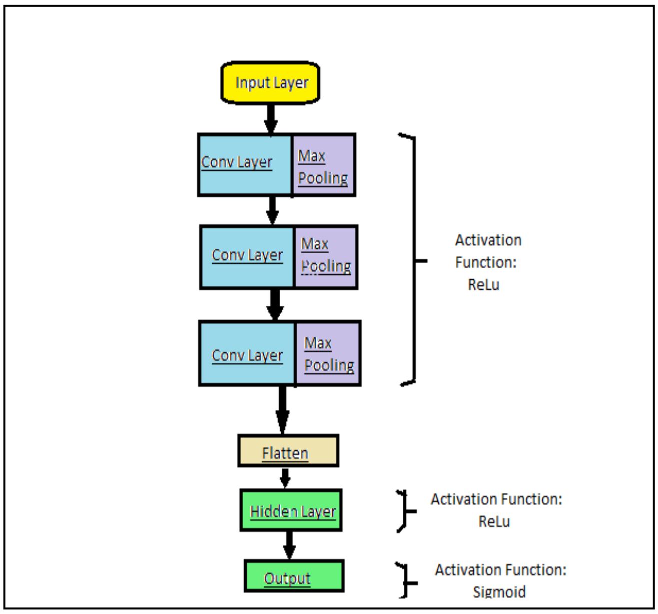


Fig. 7. Sequential Model [14]

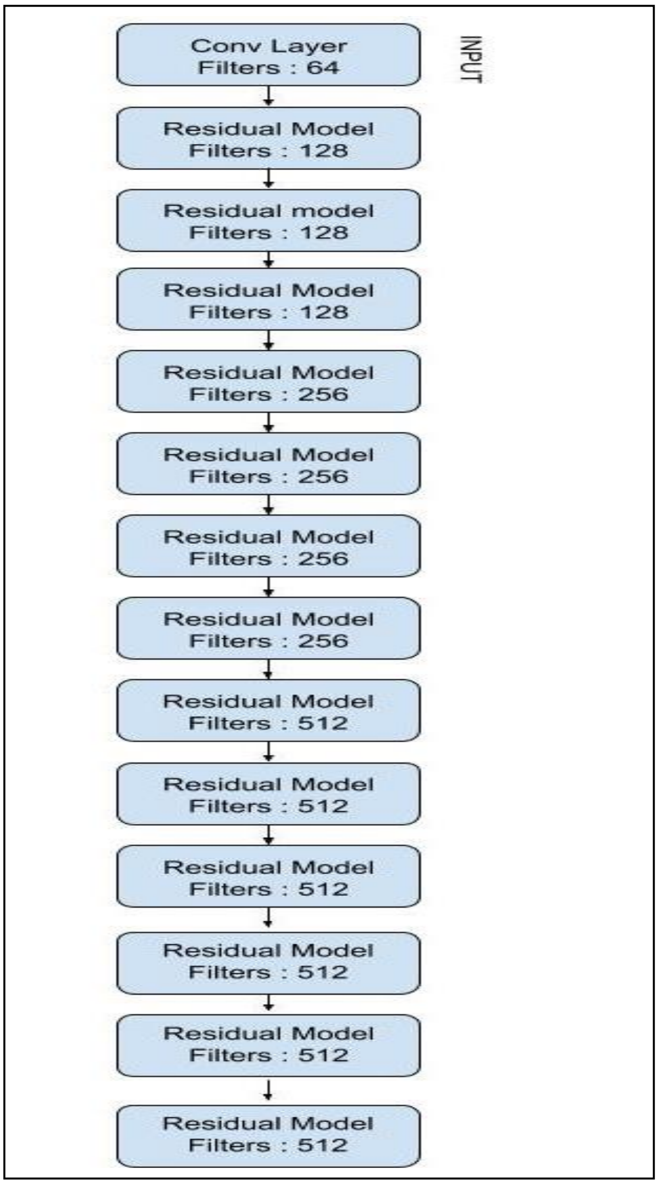


Fig. 8. ResNet Model

Relevant mathematical models associated with the Project:

- Input Data:

$$x_{in} \in R^3$$

$$x_{in} \in \{(i, j, 3) | i \in R, j \in R, 0 \leq i \leq m, 0 \leq j \leq n\} \tag{1}$$

Where x_{in} is the input matrix, $m \times n$ is the max resolution of the image.

- Down Sampling & Gray Scale Functions:

$$f_{downsample}: R^3 \rightarrow R^2$$

$$f_{downsample}: (x) = x_0$$

$$x_0 \in \{(i_0, j_0) | i_0 \in R, j_0 \in R, 0 \leq i_0 \leq i, 0 \leq j_0 \leq j\} \tag{2}$$

Where x is the input matrix, and x_0 is the matrix containing the down-sampled image.

- Resizing Function:

$$f_{resize}: R^2 \rightarrow R^2$$

$$f_{resize}(x_0) = x_1$$

$$x_1 \in \{(i_1, j_1) | i_1 \in R, j_1 \in R, 0 \leq i_1 \leq m', 0 \leq j_1 \leq n'\} \tag{3}$$

Where x_1 is the matrix containing the resized image, and $m' \times n'$ is the new resolution after resizing.

- Output Data:

$$x_{out} \in R^2$$

$$x_{out} \in \{(i', j') | i' \in R, j' \in R, 0 \leq i' \leq m', 0 \leq j' \leq n'\} \tag{4}$$

Where x_{out} is the containing output of the preprocessing module; this matrix is provided an input to the layer of Neural Network. Using the Template

VI. MODEL EVALUATION

A. Performance Metrics

Minimum for ResNet [19] it was found that 50 epochs, that is the number of training iterations, were sufficient to get desirable results. A batch size of 32 is adequate for most systems. The initial learning rate is set to 1e-1 which further decays in response to the poly decay functions.

The ResNet model was defined in the following manner:

Images are of the dimension 64 x 64 x 3 i.e. 3-channel RGB images. There are 2 classes. ResNet will perform with (3, 4, 6) stacking along with (64, 128, 256, 512) CONV layers, the first CONV layer has 64 total filters. There are 3 sets of residual modules and each set has 3 CONV layers. The first and second layers have 32 filters and the third layer has 128 CONV filters. After these dimensions are further reduced spatially.

In the residual model stack 4 sets has three layers in which the first and second layer will have 64 filters and the third layer will have 256 filters. Dimension reduction is again carried out spatially. In the final step that is the stack 6 of the model, each CONV layer learns 128,128 and 512 filters. Spatial dimension reduction is done for the last time and then average pooling is carried out followed by softmax classifier [20].

The SGD optimizer [21] was used with 1e-1 which was the initial learning rate and with momentum of 0.9. Finally, the ResNet model [19] is compiled with the loss function as binary cross-entropy.

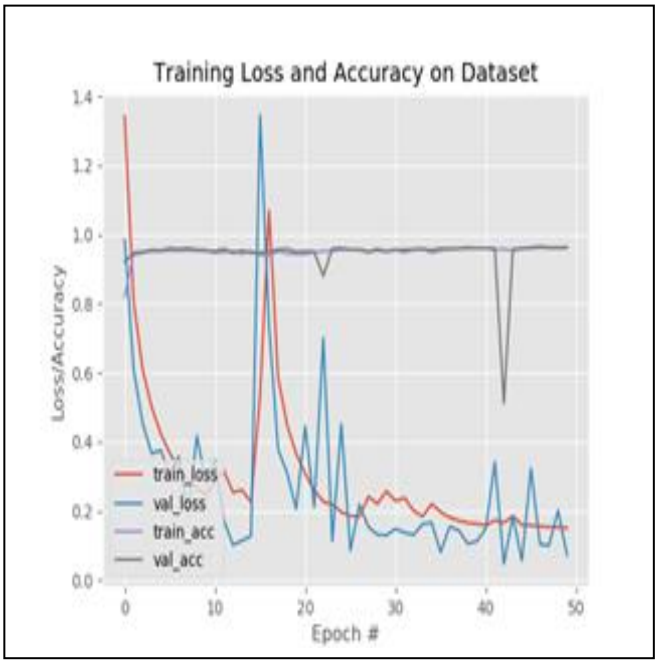


Fig. 9. Result of ResNet Model

Results for ResNet CNN model:
96.50% accuracy for the training data,
96.78% accuracy for the validation data
97% accuracy for the testing data

Now, by using the Sequential CNN model [22] we introduced Cov2D - MaxPooling2D - Cov2D - MaxPooling2D – Cov2D - MaxPooling2D layers with activation function as "ReLu "[23] and pool size as (2,2). Sigmoid function was used for classification purposes. Finally, the sequential CNN model was compiled with an optimizer as adam and binary cross-entropy was used as a loss function. 10 epochs were sufficient in the case of a sequential model to generate acceptable results.

Result for Sequential CNN model:
98% accuracy for the training data,
96% accuracy for the validation data
96% accuracy for the testing data

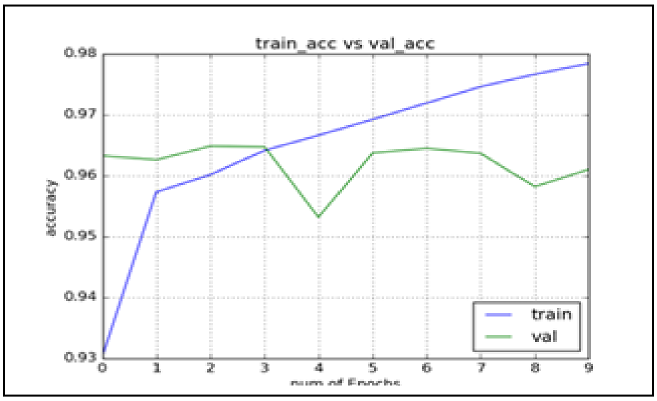


Fig. 10. Sequential Result (Accuracy)

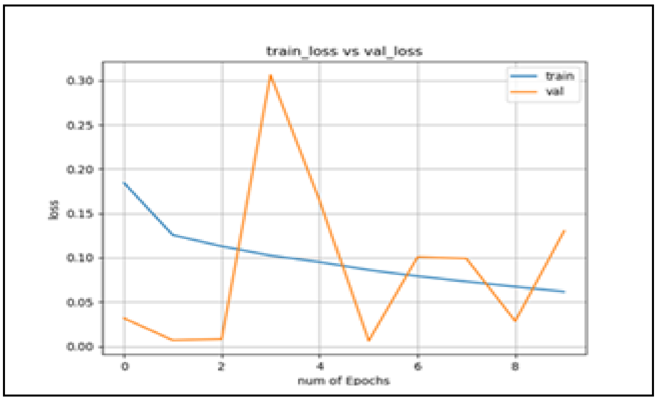


Fig. 11. Sequential Result (Loss)

B. Discussion

The proposed system aims to check if the number of layers in a convolutional neural network will affect the performance in the diagnosis of malaria. It is absolutely important to perform tests on the training of the neural network to obtain as accurate results from the convolutional neural network as possible. Appropriate testing environment is required for performing the tests. This section will discuss the results of the experimental environment.

TABLE II. ENVIRONMENT

Environment	**Specification**
Operating System	64 bit Windows
Python	Version 3.6.8
Tensorflow	Version 2.0.0
Nvidia Driver	Version 441.87
Cuda Toolkit	Version 10
cuDNN	Version 7.6.5
GPU	1060 (6GB)

We are using Keras [24] as our backend to train the deep learning models. The dataset was split into 80% training data and the rest of the 20 percent for testing purposes. And 10% of training data was used for validation purposes. The dataset was applied with data augmentation to artificially expand the dataset. Data augmentation involved rescaling, rotation, zoom, width and height shift, shear, horizontal flip, and fill mode. To load images from the directory Keras generators are created. Class mode is taken as categorical to perform one-hot encoding on the labels. All images are resized to 64 x 64-pixel dimensions and color mode is set to RGB. Image paths are to be shuffled only for the training generator. A batch size of 32 is required.

From the literature survey it found that the machine learning algorithms, which was performed on different malaria dataset, they are:

TABLE III. EXISTING ALGORITHMS

Algorithm	**Accuracy**
Ada Boost	0.962
Decision Tree	0.946
KNN	0.940
Linear Regression	0.943
Naïve Bayes	0.858
Random Forest	0.965
Extra Trees	0.956

And the deep learning model, training accuracy rate of 0.97, and testing accuracy of 0.95, which was referred to, the model performed very similar to our proposed model. That is the reason why it was decided to see how having a large number of layers in a model affects the performance.

VII. CONCLUSION AND FUTURE WORK

From the initial hypothesis, we get to know that there is no significant difference in accuracy when we have too many layers.

Malaria detection is a very time-consuming process and its' efficiency is impacted by the type of hardware and software used and also on the experience of pathologists. Deep learning has been widely accepted and thus the need for huge annotated data image repositories is essential for training. This will allow more patients to be evaluated and extensive field testing can be carried out efficiently.

Parallel computing devices such as multicore computers and GPUs can be used to reduce the training time. Setting parameters in an appropriate way may result in better accuracies. Implementing the methodology on devices like mobiles can further improve the functionality and ease the use and access of the tools.

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