Implementation of Malaria Parasite Detection and Species Classification Using Dilated Convolutional Neural Network

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***Abstract*— Malaria is an infectious disease caused by a bite of an Anopheles Mosquito which has caused a lot of death. Diagnosis of malaria is made by examining a red blood cell of an infected patient using a microscope, which takes time and requires a qualified laboratory expert to examine, read and interpret the results obtained. Convolutional Neural Network (CNN) has played important role in image classification; however, it has exhibited some problems in consuming computing resources which is one of the limitations of CNN. To reduce this problem, this paper presented a Dilated Convolution Neural Network for malaria parasites detection and species classification using blood smear images. A direct classification was carried out to detect infected and uninfected malaria parasites. Subsequently, species classification was carried out using 3 convolutional layers and Convolution2D for convolution operation while a dilation rate of 2 was used for the convolution layers. The model was trained with a publicly available dataset of 27699 images with a performance accuracy of 99.9% for parasite detection and species classification of 99.9% for falciparum, 64.6% for Malarie, 39.1% for Ovale and 37.3% for Vivax.**

Keywords*— Classification, Convolution Neural Network, Dilated, Malaria, Parasite, Species.

I. INTRODUCTION

Malaria is a dangerous parasite and very infectious disease caused by the plasmodium parasite which is transmitted by a bite of a female anopheles mosquito. Malaria disease is found all over the world but the species of each region or tropical area varies as a result of environmental conditions. Diagnosis of malaria is mostly done manually by a laboratory technician or expert by observing stained blood already on a glass slide and then counting the infected blood cells to determine its infections [1], although there are other techniques such as clinical symptoms observation and Rapid Diagnostics Test. However all the techniques take a lot of time, and skilled technicians/laboratory scientist is needed to analyse the morphological variations features and region of interest of the parasites which will enable and enhance the identification of infection and species of the malaria

There are over 20 species of plasmodium but only plasmodium malaria (p.malarie), plasmodium ovale (p.ovale), plasmodium falciparum (p.falciparum), plasmodium vivax (p.vivax) are the most common [2]. According to WHO, 2020 report, Plasmodium falciparum, and Plasmodium Vivax have a high rate of infections and as such posed a great high risk to human survival. Because of this, there is a need for continuous scientific research due to plasmodium diversity, adaptability, and co-infections with other diseases such as Dengue, Chikungunya, Zika, Tuberculosis, and HIV/AIDS to avoid re-occurrence [3] [4].

Therefore, to speed up the parasite detection and species classification a Dilated Convolutional Neural Network (DCNN) is been deployed because of its ability to expand the receptive field by maintaining the spatial resolution of the images [5] and as well as expanding the kernel receptive field without adding to the parameters but by adding zeros values weight to the filters [6].

The scope of this work is to detect malaria parasites and as well as classifying the most prevalent species (p ovale, p, malarie, p.vivax, and p.falciparum) from an infected blood image so that total elimination or eradication of this deadly disease can be achieved. The paper was structured as the introduction in section 1, section 2 is the literature review, section 3 described the methods employed and section 4 presented the results and discussions and lastly, the conclusion was then made thereafter.

II. LITERATURE REVIEW

A lot of research work has been done on malaria parasite detection and species classification to have an accurate and efficient treatment, elimination, or reduction of malaria infections. [7] used extraction based on a histogram-based surface to extract the highlighted parasite cell of plasmodium falciparum. They went further to use Multilayer perceptron backpropagation to classify the plasmodium stages of malaria parasites which accomplishes an accuracy of 87.8%, a sensitivity of 81.7%, and a specificity of 90.8%. However, the algorithm only detects if the image is infected or not and only one species was used for evaluation, hence it cannot be used for the multi-classification of species

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[8]presented an algorithm to determine the presence of plasmodium falciparum trophozoites and white blood cells from a Giemsa-stain thick blood smears image. The authors used 314 images and SVM as a classifier. The evaluation of the detection shows 80.5% sensitivity and 93.8% specificity. On the other hand, [9] applied leverage on the image spatial relations validation to limit the parameters. Using the CNN model of 16 layers to learn the two-dimensional data of the images. MATLAB was used to read the images, where the images were resized. Normalization was also carried out to improve the image with a width and height of 44 x 44 pixels. Ten-fold cross-validation was done during the training with 90:10 images for training and testing. A dataset of 27578 was used with overall accuracies of 97.37%, however, this system used single parameters which reduces the model flexibility where the model could not extract the whole features of the image for training.

[10]proposed a model which consists of pre-processing for sample level global white balance method, multiple focal planes based on novel adaptive non-linear grayscale intensity. It also consists of features extraction and CNN which was incorporated to introduce a new gamma-transform colour augmentation while a classification module was used to compute patient's level diagnosis and quantification. However, 1452 images were used and only falciparum parasites were identified. [11] on the other hand, developed a system to detect malaria parasites and species by using morphological transformations for pre-processing to give better contrast of the region of the images between the parasitized and non-parasitized ones. The image segmentation was also carried out by rescaling the image to 299x299 pixels and data augmentation was also performed to reduce imbalance as a result of classifiers relying on the minimization of some loss function. Finally, classification was carried out to detect infected and non-infected with an accuracy of 92.4% while species classification was 87.9%. In contrast, only 363 images of P. vivax and P. falciparum were considered.

In [12] a model was made for the detection of the plasmodium falciparum parasite where CNN was used to perform a focus stack using thin blood smear images which were acquired from a custom-built slide camera. The system used hand-engineered features for processing the image patches. The model achieves a sensitivity of 97.06% and a specificity of 98.50%. While dried blood spots (DBS) were attenuated by [13] using a total reflection –Fourier transform (ATR-FTIR) spectrometer to obtain high resolution, a supervised machine learning (MIR-ML) was used to screen the parasites from the blood spot which helped in screening plasmodium infections. The model achieved an accuracy of 92% for predicting P. Falciparum from a sample collected using PCR while 85% for predicting mixed infections of P. falciparum and P. Ovale for the sample collected from the field. Meanwhile, 296 people's samples were collected and used for the model

[14] deployed dilated CNN in malaria diagnosis to classify infected and uninfected. A 5- layer CNN model was used but a 4-dilated convolution element with each kernel element having a receptive field of 15x15. The system achieved 96.5% and a comparison with other approaches shows higher results than others. [15] method consists of intensity-based iterative global minimum screening (IGMS) for screening of images and then a customized CNN to classify the parasite either as infected or uninfected. A dataset of 1819 images was used for the training. The system achieves 93.4% accuracy, but the method was only applied to only falciparum species.

[16] worked on Attentive Dense Circular Net (ADCN) which is related to residual and dense networks. The system used 27558 images which is a public dataset from NIH public dataset. The system compared its results with other state-of-the-art methods and the performance shows high results in comparison. Their accuracy was 97.68% which is higher than those compared with. [17] on the hand modified YOLOV3 and YOLOV4 to identify small objects by increasing the features scale and by extension adding more layers such that the model can have a better capability for small object detection than the original model. The system was only demonstrated for the P.falciparum parasite while other species were not considered.

In summary, these related works showed a high level of performance but some images used are patches where some affected areas were not captured because they were far away from the region which might not be easy for their model to detect. In addition, their work does not have a complete system that detects infected, uninfected, and classification of species of malaria parasites in a single model. Therefore, to overcome some downsides of the related works we focused on using fewer layers of networks, images, and training. In addition, we are optimizing some of the hyper-parameters such as learning rate, epochs, and dropout which will help in fine-tuning the designed model and as well as extract very important features from the image.

III. METHODS

The workflow diagram of this work is shown in figure 1. Stage one is the acquisition of images which involves image pre-processing and normalization. The second stage is the classification of images into infected and uninfected. The next stage is the classification of species into different types (P.Ovale, P.falciparum, P.Vivax, and P.malarie), while the last stage is to evaluate the performance of the model. To improve the performance, the network needs to be enhanced because there might be the presence of plasmodium in some infected images or not because of the key features of the infected images which greatly affect the accuracy expected from the evaluation.

As shown in figure 2, normal CNN architecture was used without any dilation rate but the inner architecture was

based on the dilation rate of the layer which was fixed at 2 for the model performance. The addition of the dilation rate as a hyperparameter is by introducing zeroes between the elements which makes the network cover more information that is relevant by increasing the receptive field. The input images used for the model were fixed at 150x150 which is a feature indicator. The hidden layers of the model consist of 3 convolution layers with neurons and have a connection link with input and output which is made up of Convolution2D object as used in this work which performs convolution operation on the image. In the architecture, it shows Layer 1 has 146 feature maps, layer 2 with 71, and last layer 3 with 33 feature maps respectively

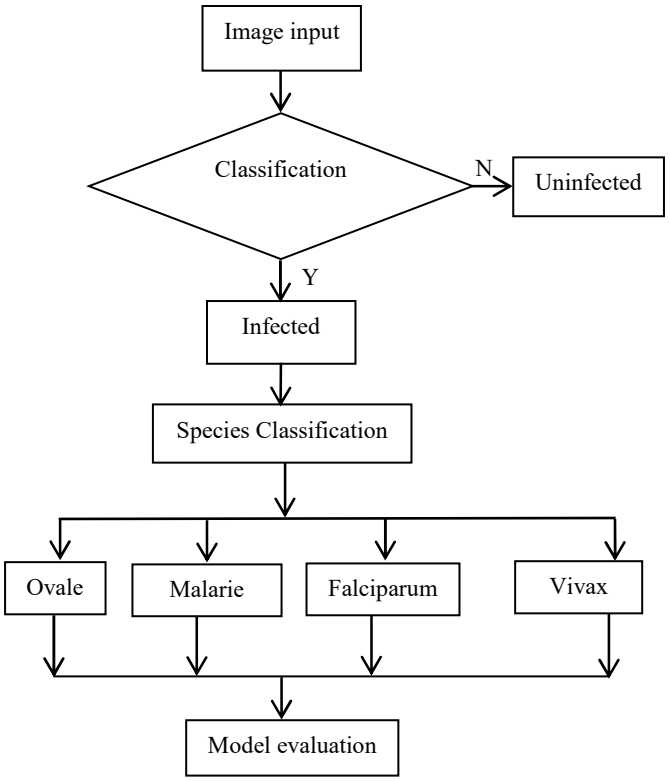


Fig 1: Flow diagram of the methodology

The pooling type used was max-pooling which the Maxpool2D object is. We used a pool size of 2x2 for the whole layers. The pooling operation gives an overview of the features gotten from the convolution operation by sliding a filter over the feature of an input image and as well select the highest or maximum value from the region, which is purposely meant to reduce computational time and reduction of feature map used for the convolution layer.

Rectified Linear Unit (ReLU) was used as an activation function for all the layers which helped in preventing gradient problems that do occur during training. The final layer has flattened and 3 dense layers which the model needs for the training after the feature maps have been generated. The Dense layer which is a fully connected neural network is connected to the last layer. In addition to the model, the batch size was set at 64, and the epoch was set at 10, while, the Adam optimizer was used for the binary cross-entropy of the loss function and the sigmoid was used for species classification which has more than one category. Finally, categorical cross-entropy for the loss function and softmax for the activation function was used.

A. Data description

Malaria images were sourced from a publicly available dataset available from the USA National Institutes of Health (NIH), which is good in terms of comparative analysis of other related work to arrive at a standard, however, a Microbiologist was involved to ascertain the data samples due to observation found in the labeling of the data as some were wrongly labelled as infected and uninfected. A total of 27699 data images (Table 1) were used with 14394 as infected and 13305 as uninfected while that of species (Table 2) was 134 for p.ovale, 65 for p.malarie, 1316 for p.falciparum, and 80 for p.vivax. The normalization was also carried out to prepare the data for training and testing. The images were then split into training and testing with the width and height normalized as 150 by 150 pixels. All the images have three color channels.

Table 1: Data size for Infected and uninfected Parasites

Infected	14394
Uninfected	13305
Total	27699

Table 2: Data size for species

P.Falciparum	P. Malarie	P. Ovale	P. Vivax
1316	65	134	80

B. Image pre-processing

Images are acquired through a high-resolution digital camera connected to a microscope and most of this data has different resolutions, given this, Python 3.7 functions were used to convert the image from coloured to grayscale to improve and enhance the quality of the input image for processing activities, such that any noise present in the image is removed or reduced. Figure 3 shows the original image used for the pre-processing. Figure 4 is the final image after the pre-processing has been carried out.

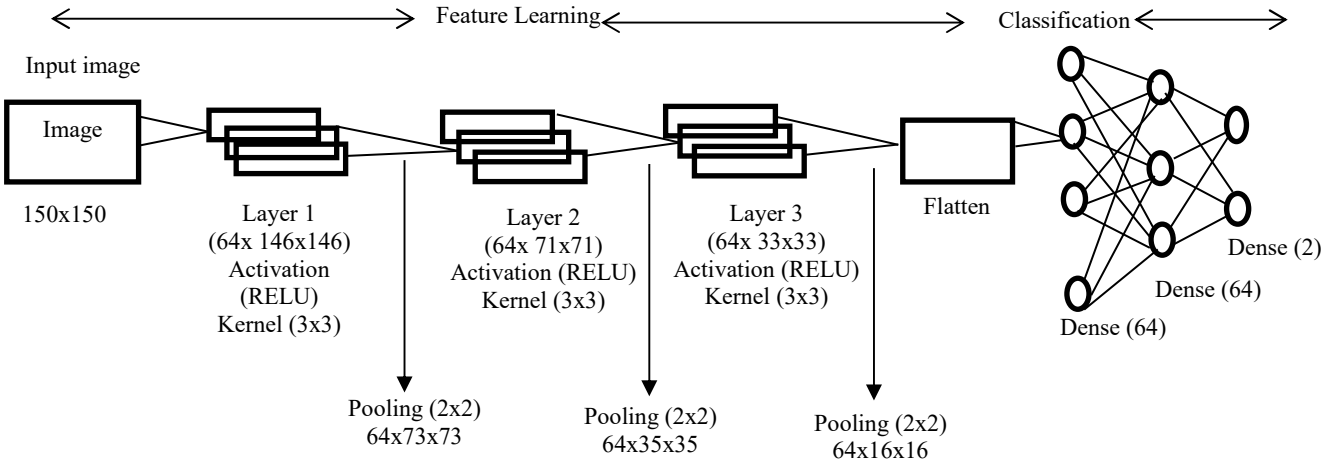
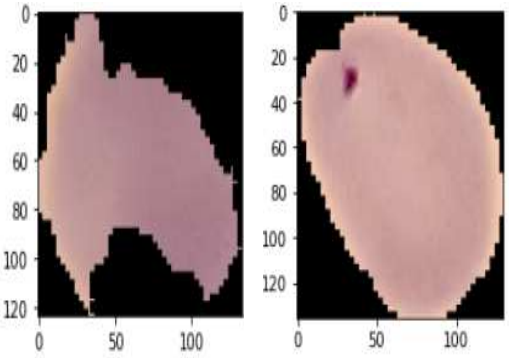
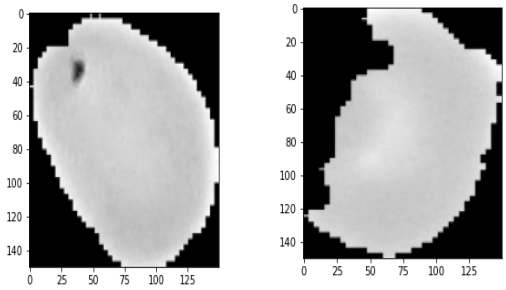


Fig 2: System architecture



(a) (b)

Fig 3: Original Image for uninfected (a) and infected (b)



(a) (b)

Fig 4: Images after pre-processing (a. Infected, b- Uninfected)

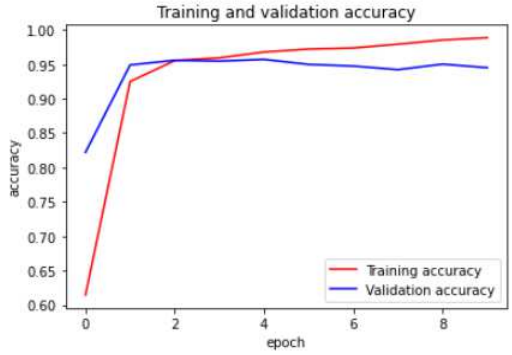


Fig 5: (a) Training and validation Accuracy

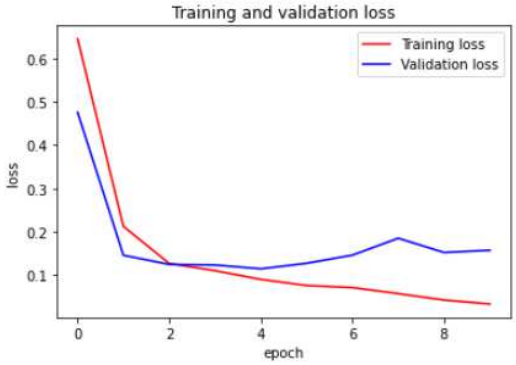


Fig 5: (b) Training and Validation loss

IV. RESULTS

A. Malaria Parasites Classification

The work was carried out using a simple and less costly PC for deployment. Figure 5a shows the training accuracy of 0.99 while the validation accuracy was 0.95. Figure 5b shows the training loss of 0.03 and validation loss of 0.15.

B. Species classification

Figure 6a shows that of the species classification, the model training accuracy was 0.89, and the validation accuracy was 0.90. figure 6b shows a training loss of 0.24 while the validation loss was 0.22

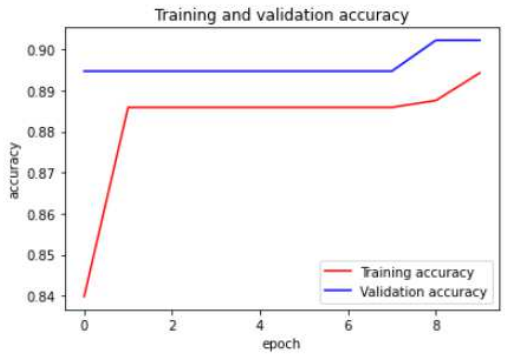


Fig 6: (a) Training and validation Accuracy

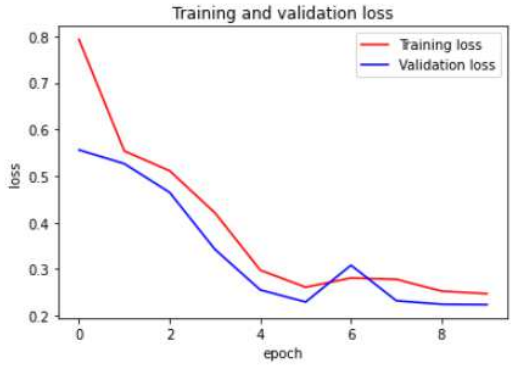


Fig 6: (b) Training and Validation loss

In summary, the model performed effectively, this clearly shows that it is not necessary to accomplish or attained all the epochs for a model to get a better result. The performance of this system accuracy for parasite classification was 99.9% while as shown in figure 7, Plasmodium falciparum achieved a higher rate of 99.9%, plasmodium malarie 64.6.3%, Plasmodium ovale 39.1%, and plasmodium Vivax 37.3%.

```
Falciparum: 0.9997912049293518
Malariae: 0.6463150978088379
Ovale: 0.3907793462276459
Vivax: 0.37322527170181274
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Fig 7: Results of Species classification

Table 3: Comparison of the proposed method with existing methods of Classifications

Author	Methods	Parasite Classification	Species Classification				Dataset	Results
			M	O	F	V		
Nugroho et al. [7]	ANN	✓	✗	✗	✓	✗	60	87.8%
Rosado et al. [8]	SVM	✓	✗	✗	✓	✓	314	80.59% Parasite classification
Liang et al. [9]	CNN	✓	✗	✗	✗	✗	27578	97.37% Parasite classification
Mehanian et al. [10]	CNN	✓	✗	✗	✓	✗	1452	Not Stated
Penas et al. [11]	CNN	✓	✗	✗	✓	✓	363	92.4% parasite classification
Qayyum et al. [14]	Dilated CNN	✓	✗	✗	✗	✗	27558	96.5% classification
Yang et al. [15]	CNN	✓	✗	✗	✓	✗	1819	93.4% species classification
Quan et al. [16]	CNN	✓	✗	✗	✗	✗	27558	97.68% classification
Proposed model	Dilated CNN	✓	✓	✓	✓	✓	27699	99.9% classification

Key: ✓ Represent activity carried out: ✗ Represent activity not carried out
M: P. Malarie **O**: P.Ovale **F**: P.Falciparium **V**: P.Vivax

Table 3 gives a comparison of the performance metrics of the model and other state-of-the-art approaches. This model shows an improvement over others for accuracy and classification in terms of coverage of infected and uninfected and as well as species classification which clearly shows that with little size of the model, less number of parameters, few layers and epochs used for training we have achieved a better result.

In addition to using a less costly and simple PC, the CPU environment for training; the model still used an average training time of 1921 seconds, although the time is much

higher but still better for areas where there is no network infrastructure and also it makes it easier, accessible and useage for rural areas.

V. CONCLUSION

Diagnosis of malaria involves knowing if the blood sample is infected or not and subsequently knowing the species is very important before administering drugs or vaccine to the infected person. This study has shown that malaria parasites can be effectively detected and species classified on infected blood images by using a Dilated Convolutional Neural Network which reduces laboratory technicians' errors and as well computational time. The model was built using 3 convolution layers, ReLU for activation function and a dilation rate of 2 as hyper-parameters. The Database consists of infected and uninfected parasites while species consist of P. falciparum, P. Vivax, P. Ovale and P. Malarie. The system achieved performance accuracy of 99.9% for parasite detection and species classification of 99.9% for falciparum, 64.6% for Malarie, 39.1% for Ovale, and 37.3% for Vivax. Because of its high result and simplicity in implementation, it has reduced the errors observed in using manual methods in diagnosis and also assists in the ongoing trial vaccine development for all the species. However, the limitation of the work is enough species datasets which would have improved the overall performance of the species classification.

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