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TENSORFLOW BASED PREDICTION MODEL FOR CLASSIFYING HUMAN BLOOD SMEAR MICROSCOPIC IMAGES AS INDICATING PRESENCE OF MALARIA PARASITE

Preethi N Patil[1], Andhe Dharani[2], S. Anupama Kumar[3] and Naganagouda Patil[4]
[1,2,3]*Department of Master of Computer Applications, RV College of Engineering, India*
[4]*Department of Electronics and Communication Engineering, Sri Krishna Institute of Technology, India*

Abstract

Malaria is now considered to be present in south Asian and African regions. Many countries are declared and certified as malaria free nations. But India is yet seen to be hosting with one or more indigenous cases. As per the World Health Organization (WHO) report India is one among the 25 nations expected to be malaria free by 2025. Currently the two variants out of four species of malaria parasite are prevalent in India. Falciparum and Vivax are the seen in several states of the country. The malaria detection is a manual procedure followed in the pathology laboratories. The human blood smears are collected and examined under the microscope. This process requires the experienced staff for better and accurate identification of the stages of the parasite detection. As per the standards specified for examination of a single slide is a minimum of 3 minutes and maximum of 5 minutes. But the process usually consumed by the pathology lab staff is minimum of 7 minutes with thick smears. Whereas the time duration required in case of thin smears is usually more. The proposed work aims at automating this process of detecting and identifying from thin blood smears without any compromise on the actual process adopted in detecting the parasite stages. The experiments are conducted on 200 images from Kaggle database, and the results obtained are encouraging.

Keywords:

Malaria, Microscopic Image, Blood Smear, Tensor Flow, Prediction

1. INTRODUCTION

The World Health Organization (WHO) reports 241 million malaria cases universally, with an increase of cases by 12% as compared to 2019 statistics. In India the total number of malaria cases in 2020 is 1,57,284 (till Oct 2020). This study does not consider the number in 2021 and 2022 as the cases are not clearly distinguished due to the COVID-19 pandemic.

Though there are four species of malaria parasite Falciparum, vivax, malariae and oval only two of them i.e., falciparum and vivax are found in India. This parasite travels through a life cycle phase where its life cycle begins with ring stage and progresses towards trophozoites, schizont and finally ends at gametocytes. In this work, the image processing techniques are designed and applied on the microscopic images of thin smears of human blood samples.

The state of art facilities shows the application of machine learning, artificial intelligence and deep learning techniques that do not follow the actual manual techniques that is adopted and followed by the pathologists. Also, the identification of stages is not achieved.

This motivates to carry out the work and sets the objective to design a methodology which will serve as a predictive diagnostic tool to aid physicians.

2. LITERATURE REVIEW

The major contributions by various authors are studied. Rajaraman et al. [1] have suggested feature extractors that classify healthy and parasitized blood cells using pre-trained CNN-based deep learning models. The suggested model consists of two fully connected layers, three convolutional layers that each utilize three 3 3 filters with two-pixel steps, 32 filters for the first and second convolutional layers, and 64 filters for the third convolutional layer. The segmented cells that make up the model input have a resolution of 100 100 3. They assessed how well pre-trained CNNs, AlexNet, VGG-16, Xception, ResNet-50, and DenseNet-121, extracted traits from infected and healthy cells. The Random Grid Search technique was used to optimize these models for hyperparameters.

Masud Mehedi, et. al [2] worked out a CNN model that was implemented to classify 27,588 segmented cell images of dimension 224X224X3 using Four CONV layers and two fully connected dense layers. This method suffered overfitting and hence needed refinement. Sandhya Y, et.al [3] proposed a deep learning-based CNN to overcome the overfitting of model. They used early stopping approach with number of parameters equal to 21,77,185 to optimize the training model.

Magotra, V, et. al [4] projected customized CNN with six convolutional layers, filter sizes ranging from 16 to 128 and an activation function dubbed "Relu" to reduce overfitting and increase the model's robustness in real-time applications. They used a dropout function three times at various stages of the training process. The custom CNN includes 332,577 parameters in total, 332,161 of which are trainable and 416 of which are not.

Roy, Kishor, et al. [5], proposed a model based on the two segmentation techniques of watershed segmentation and HSV segmentation to accurately detect malaria parasite. These are the processes that make up the HSV (Hue, Saturation, and Value) procedure: (1) converting the image to HSV form and calculating parasite indices; (2) enhancing the image; and (3) binary image conversion. About Watershed Segmentation, it is utilized to address the HSV issue since, because to some color distortion in the input photos, all parasites cannot be spotted. Before using this technique, the following stages must be completed: (1) grayscale conversion, (2) morphological transformation, (3) image adjustment, and (4) conversion to black and white image.

Adenowo, A. A, et. al [6] deployed a software-based diagnostic approach to detect Malaria Parasite in Blood. This system associates a set of image processing techniques like image acquisition, image pre-processing, image segmentation, feature extraction and classification applied to 92 Plasmodium parasite

images were acquired in three categories: downloaded, captured, and digitally acquired images.

Madhu, Golla et. al [7] designed a classification strategy using Enormously Randomized Trees classifier experimented on a locally created dataset containing 400 images. The design involved several steps such as image denoising using modified K-SVD, segmentation using fuzzy type-2 functions, feature extraction by local and global features, feature selection by Extra Trees Classifier, classification using Extra Trees Classifier, and diagnosis.

Gopakumar et. al [8] designed a customized CNN model and analysed videos containing parasites. The process used complete field of view of stained microscopic images which were acquired by scanner.

3. METHODOLOGY

The proposed work is experimented on the dataset of microscopic images of human blood smear from public domain Kaggle repository. This dataset consists of 200 images, with 100 images infected by malaria parasite and 100 uninfected images.

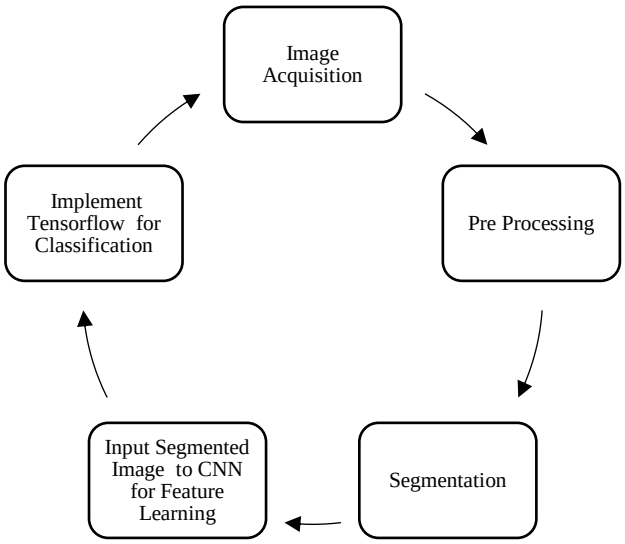


Fig.1. Architecture diagram for proposed work

The phases followed in implementation of TensorFlow for CNN:

Step 1: Bind TensorFlow models and dataset models with the work environment

Step 2: Set the optimization parameters to learning_rate=0.001, epoch=20 and batch_size=16

Step 3: Define the input parameters as (-1, 512,384,1) where the first parameter defines the TensorFlow output can take up dynamic shape depending on the input data, the second and third parameters indicate the dimension of the input image.

Step 4: Define the convolve layer for feature extraction and selection, the number of CONV layers is decided empirically

Step 5: In pooling strategy, a square mean pooling defined by as

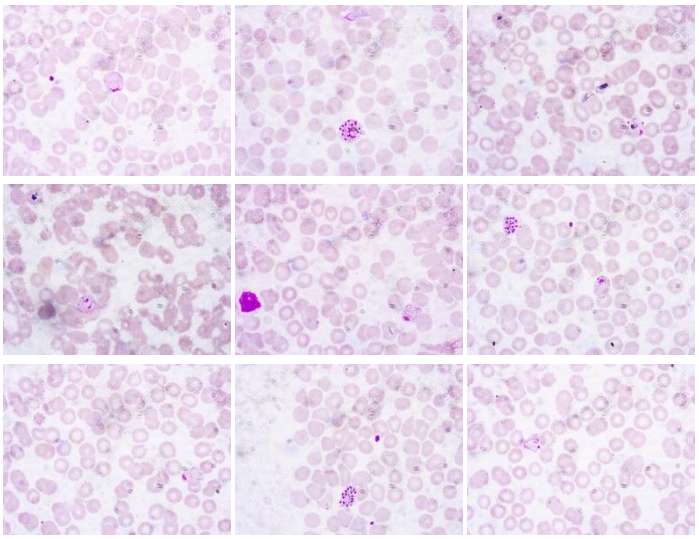
$$\frac{1}{m}\sqrt{\sum_{i=1}^{m} U_{ij}^2}$$

Step 6: The activation function ReLu is defined with the empirically calculated bias weights to have fully connected dense layers for training phase.

4. EXPERIMENT RESULTS

The proposed work has yielded encouraging results. Further this encourages to carry out the research using larger dataset and local real-time dataset.

Malaria Infected images



Un Infected Images

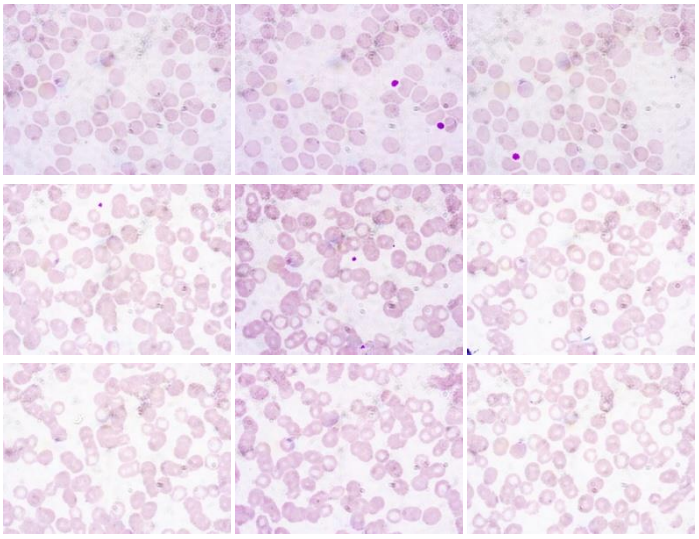


Fig.2. Sample microscopic Images of Human Blood Smears

The experiments were implemented pipeline strategy to achieve model parallelism and evaluate the stability of the trained model. The results show the model is stable up to 87% of the times.

The learning rate of the algorithm is shown for specific setting of the optimization parameters.

Table.1. Accuracy

Class	# of Training samples	# of validation samples	# of Test sample	Epoch and learning rate	Accuracy
No_ Malaria	74	12	14	20, 0.001	93%
					91%
				30, 0.001	94%
					90%
				40, 0.001	87%
					88%
Malaria	72	17	11	20, 0.0001	94%
					93%
				30, 0.0001	94%
					90%
				40, 0.0001	91%
					88%

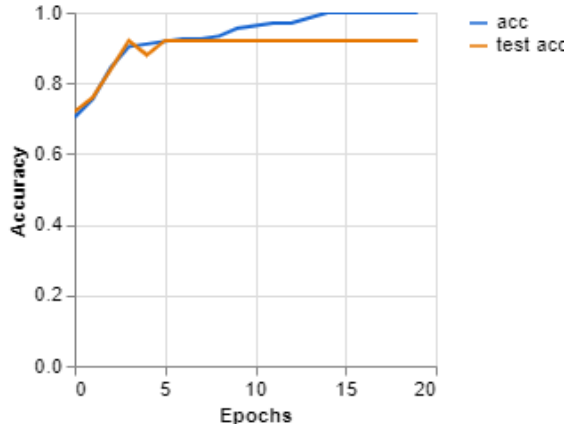


Fig.3. Accuracy per Epoch: trained with 20 Epoch

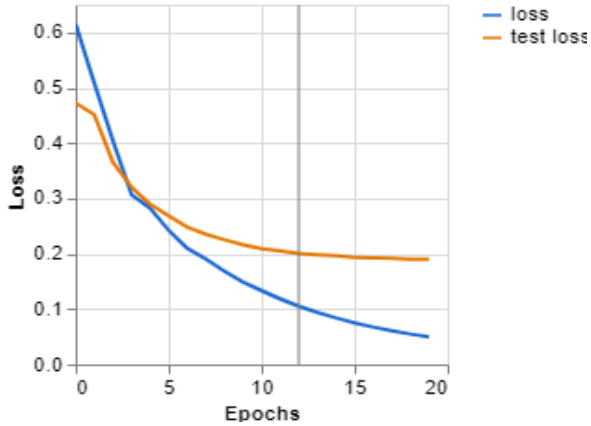


Fig.4. Loss per Epoch: trained with 20 Epoch

5. CONCLUSION

The proposed work has successfully implemented the classification of human blood smear into two class as not_infect_with_malaria and infected_malaria. The methodology has shown results of accuracy of 94% and stability of 87%. The results are encouraging and hence the extension of this work is carried out to classify the malaria into different stages.

5.1 FUTURE ENHANCEMENT

The parasite detected in the proposed work will further be used to identify the parasite stage and thereby determine the severity of the infection. This identification is helpful in prescribing the line of treatment of the malaria disease.

REFERENCES

[1] Sivaramakrishnan Rajaraman, Stefan Jaeger and Sameer K. Antani, "Performance Evaluation of Deep Neural Ensembles Toward Malaria Parasite Detection in Thin-Blood Smear Images", *PeerJ*, Vol. 7, pp. 1-13, 2019.

[2] Mehedi Masud, "Leveraging Deep Learning Techniques for Malaria Parasite Detection using Mobile Application", *Wireless Communications and Mobile Computing*, Vol. 2020, pp. 1-14, 2020.

[3] Yamala Sandhya, Prasanta Kumar Sahoo and K. Eswaran. "Malaria Disease Detection using Deep Learning Technique", *International Journal on Advance Science and Technology*, Vol. 29, No. 2, pp. 7736-7745, 2020.

[4] Varun Magotra and Mukesh Kumar Rohil, "Malaria Diagnosis using a Lightweight Deep Convolutional Neural Network", *International Journal of Telemedicine and Applications*, Vol. 2022, pp. 1-9, 2022.

[5] Kishor Roy, "Detection of Malaria Parasite in Giemsa Blood Sample using Image Processing", *SSRN*, Vol. 10, pp. 55-65, 2018.

[6] A.A. Adenowo, Adesoji A. Awobajo and Sheriff Alimi, "Software-based Diagnostic Approach for Detection of Malaria Parasite in Blood", *International Journal of Computer Applications*, Vol. 975, pp. 8887-8898, 2020.

[7] Golla Madhu, "Computer Vision and Machine Learning Approach for Malaria Diagnosis in Thin Blood Smears from Microscopic Blood Images", *Machine Learning for Intelligent Decision Science*, Vol. 87, pp, 191-209, 2020.

[8] G.P. Gopakumar, M. Swetha and G.R.K. Sai Subrahmanyam, "Convolutional Neural Network-Based Malaria Diagnosis from Focus Stack of Blood Smear Images acquired using Custom-Built Slide Scanner", *Journal of Biophotonics*, Vol. 11, pp. 1-16, 2018.