DEEP LEARNING MECHANISM FOR RECOGNITION OF MALARIAL PARASITE IN THICK BLOOD SMEAR

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ABSTRACT

Malaria is among the deadliest illnesses in the world. This is brought on by a female Anopheles mosquito bite that spreads Plasmodium parasites. Manual microscopic inspection and Rapid Diagnostic Test (RDT) are two modern malaria detection methodologies. These methods are susceptible to errors which made by humans. Worldwide death rates from malaria can be decreased with early detection. For accurately detect the malaria parasite, a thick blood smear examination is required. The World Health Organization (WHO) recommends thick smear screening for the primary diagnosis of malaria because it is affordable and extremely sensitive. Therefore, Deep Learning could be a highly helpful tool for identifying illnesses. This method offers a more expedient and affordable method of identifying the malaria parasite in a blood smear. In this paper, CNN-based machine learning model automatically identifies and predicts infected cells. The primary function of the custom convolutional neural network is to discriminate between blood samples that are healthy and those that are infected. Three fully connected layers plus convolutional layers make up the proposed system. A cascade of several convolutional layers with various filters contained in the layers makes up the proposed neural network, producing unusually good accuracy given the resources at hand. After the model has been trained, many blood sample images are fed into it to check the planned system's correctness. Analysis of blood smear samples can also help in the detection of a few other diseases, and the use of deep learning models will benefit the overall humanity.

Keywords: *Thick blood smear; Convolutional Neural Network; Malaria parasite; Deep learning; Iterative Global Minimum Screening (ICMS).*

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1. INTRODUCTION

The incubation time for malaria, a contagious and potentially fatal disease, is at least 7 days. The protozoan plasmodium is the cause behind malaria. In order to spread the disease, the female Anopheles mosquito, often known as the vectors of malaria, bites people. Only thirty of the 400 Anopheles mosquito species are known to transmit malaria. The most prevalent only one Plasmodium species that transmit malaria and have the potential to be hazardous are P. falciparum and P. vivax. Because of untreated malaria may cause some serious sickness and even fatality, early signs of the illness, like headaches, temperature, chills, and nausea[1].

In 2017, Worldwide there have been 219 million cases of malaria reported, resulting in 435,000 fatalities, as per the 2018 World Health Organization (WHO) malaria statistics[2]. Millions of blood smears are analysed annually by highly trained professionals in hospitals all over the world to look for disease cases. The process of manually detecting malaria cases is typically necessary, especially by counting the affected red blood

cells and parasites, which takes time and can be inaccurate [3]. Analysis of pigmented blood smears, either thick or thin, under a magnification seems to be the gold standard for recognizing malaria. The blood smear, which is 6–20 times thicker than the thin one and allows for the examination of more blood, has multiple layers of RBC as opposed to the thin one's single layer. As a result, thick smears are initially utilised to determine whether malaria parasites (MP) are present, and thin smears are next analysed to determine which species of MP they are [4].Red blood cells (RBC) and White blood cells (WBC) can both be seen clearly in thin blood smears. Standard procedures for automatically identifying parasites in thin smears involve segmenting RBC and WBC and categorising each segmented RBC and WBC as impacted or unaffected. [2].

Microscopy investigation is readily available, inexpensive, yet time-consuming[2]. Additionally, the proficiency of the parasitologist affects how well the microscope diagnosis performs. and polymerase chain reaction (PCR) and Rapid diagnostic tests (RDT) were taken into consideration to improve diagnosis. These analyses are quick but not as precise [5].Therefore, one interesting research objective for enhancing customised patient therapy and management is the creation of an automated process for identifying malaria. Automated parasite identification consists of 2 key benefits: 1) It can offer a highly appropriate analysis, particularly in field with few resources; and 2) It minimizes test expenses [6].

In this study, a completely customized CNN model was employed to identify the presence of malaria using images of tiny blood smears. As well as offering a useful technique for separating infected from uninfected malaria cells, The efficiency of the proposed deep learning technique for identifying malaria from tissue images will be investigated in this paper. All existing deep learning models are outperformed by the suggested customised[7] CNN-based algorithm. The suggested approach makes use of bilateral filtering to enhance image quality and image augmentation methods to increase model generalisation. On a dataset consisting for malaria, the performance of the suggested method is assessed, and the outcomes are contrasted with those of other similar procedures already in use. The outcomes demonstrate that our method outperforms the compared strategies and delivers great performance. The rest of this paper is summarized as follows: Section I presents specifics of the suggested technique for automatically identifying parasites. Section II, Related works are presented. Section III contains the problem statement. In Section IV, the dataset and the experimental strategy are presented. Section V presents a summary of the results, and Section VI presents the conclusion.

2. RELATED WORKS

The parasite Plasmodium causes the life threatening disease malaria. Trained microscopists examine tiny blood smear images to find it. This analysis might be carried out automatically using contemporary deep learning techniques. Web-based and mobile-based applications were created to show the robustness and compatibility of the established approach. This advancement demonstrates unequivocally how useful this methodology may be for malaria automated diagnosis in a resource-constrained setting. The various classification models presented in this study for the identification of malaria parasites, however, take into account both classification accuracy and processing efficiency. The fact that their approach may be used with mobile phones is also noteworthy, as their demonstration omitted the low-cost mobile phones that are commonly used in the world's poorer regions [8].

In this study, the proposed CNN method that makes utilization of supervised learning, segmented affected and unaffected red blood cells were identified [3]. The earlier diagnosis of parasites utilizing smeared images has been made possible by a range of machine learning and image processing methods. The CNN model with the maximum rapidity and minimum input size of all those utilized before, the experimental findings demonstrate that the proposed architecture is successful in detecting malaria with high accuracy rate. Furthermore, the proposed architecture requires improvement, and applying the genetic algorithm (GA) The test set will be aided by increasing the model parameters.

A successful patient recovery depends on the early detection of malaria disease and an accurate and exact diagnosis. In order to find the existence of malarial parasites in smear images, a comprehensive computer-aided diagnosis(CAD) approach is proposed in this study[9]. The functional link artificial neural network is used to pre-train the system's parameters, which is followed by a sparse stacked auto encoder. The work utilizes microscopic thick blood smear images to implement a novel fast processing technique that produces improved outcomes in terms of precision and prediction time. Also, Malaria in smear blood cells has not been classified more deeply.

The world is plagued by the fatal disease known as malaria. A quick diagnosis of this ailment will be highly helpful to patients because current approaches need substantial work for its identification. Recently, a number of automated techniques that benefit from expertly built feature selection techniques have been created,

however their reliability cannot be trusted. Deep learning approaches boost technology because of their improved to enhance method. CNN is highly accessible for image classification applications toselect the features via hidden layers of the method with no manual coding. It is possible to utilise convolutional neural networks to recognise malaria-infected RBC from segmentation blood smear images, which can expedite diagnosis and be useful in regions with a shortage of medical experts[10].

In this paper, a fresh method for leveraging a deep belief network to recognize the existence of malaria parasites in pictures of human peripheral blood smears is proposed (DBN). This paper presents the classification of 4100 pictures of peripheral blood smears into the parasite or uninfected class using a trained set based on a DBN[11]. The proposed system is constructed by loading finite Boltzmann machines and pre-training them with contrastive divergence. This work builds a revolutionary DBN classifier model gives significantly higher sensitivity and specificity than past works in the field. The study covered in this article, however, is the first to employ DBN images of blood smears could be used to detect malaria. This study may lead to improvements in the machine supported pattern classification of malaria parasites. This technique is expensive.

3. PROBLEM STATEMENT

The parasite that causes malaria spreads from person to person in areas where the disease is endemic through the sting of a particular kind of mosquito. Pregnant women and kids under the age of 5 are those most at possibility for developing severe forms of the disease and dying from it. The proposed solution uses Deep Learning study procedures to find the malarial parasite in thick blood smears to solve this issue. Since, to make precise predictions on a tiny no. of pixel spots. The task may be processed more quickly by being split into a selection and classification phase. This also reduces the overall processing cost.

4. PROPOSED (IGMS - CNN) METHOD

The proposed approach utilizes intensity-based iterative global minimum screening (IGMS) to quickly choose and analyse parasite trainees. A system specifically designed to classify parasite trainees as parasites or backgrounds is the basis for spontaneous parasite screening. To our knowledge, this study is based on deep learning strategies and uses Tensor Flow and Keras packages for the implementation process. Moreover, the proposed system is a quick process. Typically, it takes approximately 10 secs to identify the parasites in a 3024 x 4032 image. Finally, the method was tested using a very large data set, consisting of 84,961 identified parasites and 1819 thick smear images found in 150 people. This method requires three stages such as 1. Pre-selection, 2. Feature Extraction, 3. Classification. Figure 1 shows the Block diagram of the proposed system.

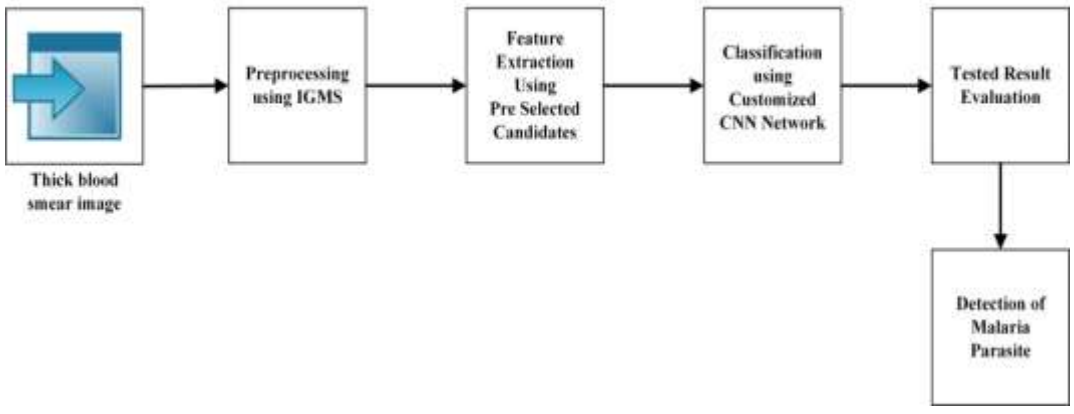


Figure 1: Block diagram of the proposed method

4.1 Dataset

In this study, 1819 thick blood smear images from 150 samples were used. Giemsa blood smear slides implanted with 150 samples of people infected with P. falciparum was filmed with various minimalist views at Chittagong Medical College Hospital in Bangladesh. To perform statistical analysis a total of 150 patient

databases were used. There are 84,961 annotation parasites in total, with a total radius of 22 pixels and a radius variation from 2 to 96 pixels. Phase-based diagnostic tests and performance tests are performed to detect automatic blood smears. In addition, patient-level datasets were divided into test sets and training sets, and five-fold analysis was used to examine the CNN method's effectiveness. To improve the effectiveness of the suggested system, use a reliable training data set with an equivalent number of positive and negative areas. [10].

4.2 Iterative Global Minimum Screening (IGMS) for Parasite Pre selection

Detecting low levels of intensity in the gray image, IGMS creates RGB insect candidates. If only 1 pixel is made locally, a circular circuit with a pre-determined parasites range of 22 pixels is sliced from first RGB image and chosen as the parasite candidates. If the total distance between the i^{th} image and the pre-trained pixels is greater than 22, the additional parasite candidate in the center of that pixel is added if there are more pixels created locally. To ensure that the IGMS method is compliant, after parasite selection, the strength values within this gray area region will be subtracted by zero. Once a certain number of parasite candidates have been completed, the testing phase ends. To adequately represent the real parasites in our experiment, we selected 500 parasites for each image. Each parasite candidate is a 44 by 44 RGB pool image, with more than 22 pixels from the center set to zero. IGMS flowchart for processing and images of good and bad patches issued by the system.

If there is a greater than 50% difference between the parasite produced by IGMS and the parasite described by hand, the parasite is considered to have been accurately detected. Depending on the balance between the sensitivity of the previous selection and the level of accuracy, this range of variance is legally chosen. Then, calculate IGMS sensitivity as a measure of the overall number of parasites with annotations to the no. of parasites actually found. The proposed IGMS method has 97.04 percent sensitivity at the patch level, 97.49 percent and 5.40 percent at the image level, and 96.59 percent and 5.52 percent at the patient level, respectively, in previous selections.

4.3 Classification of Parasites Using CNN

After identifying parasites, classify them as real parasites or parasites using the Convolutional neural network. In this proposed system, a customized CNN model with 7 flexible layers, three layers using max-pooling, three layers fully integrated, and softmax. After each layer of flexibility, the Adjusted Line (ReLU) unit is used as an activation function, which allows for high quality and makes the system less susceptible to initial values. To select sub-sets, the mass consolidation layers are added after all 2 conversion layers. 3 fully integrated layers with 50 units. The 2 hidden units each connected to a final map of the conversion feature. To reduce the model over installation, two dropping layers with a drop-out rate of 0.5 are used between 3 fully connected layers. The first 6 flexible layers and the three associated layers of high-density integration from the VGG19 structure are selected to complete the feature maps of 64 @ 55, and then fully integrated and downgrade layers are added thereafter. The CNN model produces the vector of a point that indicates the probability that the inserted image clip is in the background or parasite. By using the flexibility limit on the point's vector, we can detect a large or small number of expected parasites. The CNN method generates a point vector indicating the probability that the inserted image clip is in the background or parasite. By using the threshold of the variable variables in the points vector, to obtain the maximum or a minimum number of parasites expected.

Five-fold analysis used to test the performance of CNN's customized model. There are 24 patients in each set. The AUC School rating for our customized CNN model is 98.39 percent, with a standard deviation of 0.18 percent, indicating its reliability and efficiency. 93.46 percent, 93.40 percent, 94.33 percent, 92.59 percent, 94.25 percent and 92.74 percent respectively, standard values for our customized CNN model acc, spec, sens, prec, F-score and negative predicted values.

4.4 CNN Algorithm

Algorithm : Evaluation of CNN process

```
loadImage();
dataAugmentation();
splitData();
loadModel();
for each epoch in epochNumber do
    for each batch in batchSize do
    Y = (No. of iterations * batchSize) / overall no. of images in training.
    Loss = crossEntropy(y,Y)
    BestAccuracy = max(bestAccuracy,Accuracy);
```

Return

5. RESULT AND DISCUSSION

To assess the effectiveness and efficiency of the customised CNN architecture, RBC were classified as either parasitized or uninfected [3]. The acc, sensi, prec, and spec values measure how accurately the RBC are categorized. The effectiveness of the classification is evaluated using four statistical metrics. True Positive (T_P), True Negative (T_N) and False Positive (F_P) , False Negative (F_N) are the indices in question. The precision, sensitivity, sensitivity, and accuracy were determined in Eqs. (1) , (2), (3), (4) and (5) respectively.

$$Acc = \frac{T_P + T_N}{T_P + F_P + T_N + F_N} \quad (1)$$

$$Sens = \frac{T_P}{T_P + F_N} \quad (2)$$

$$Spec = \frac{T_N}{T_N + F_P} \quad (3)$$

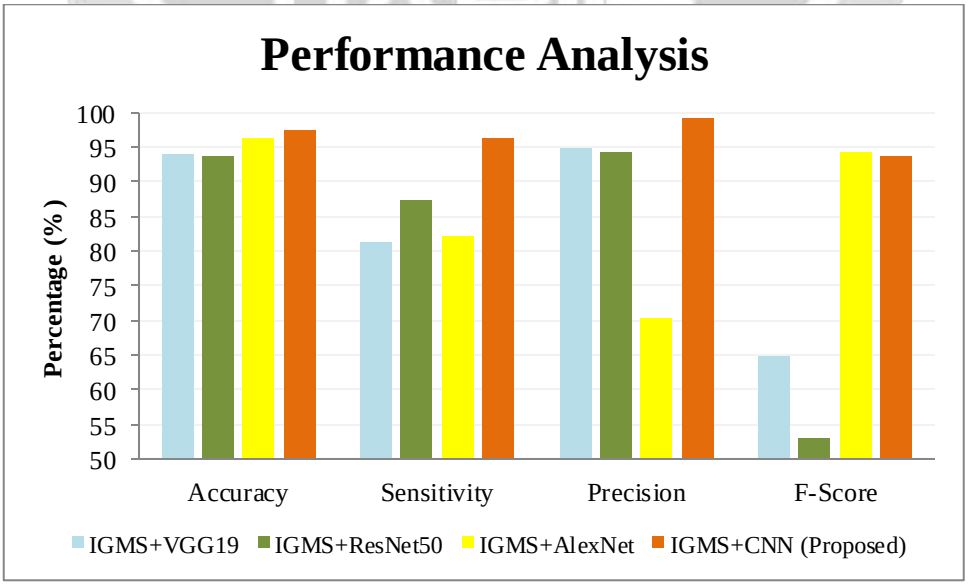
$$Prec = \frac{T_P}{T_P + F_P} \quad (4)$$

$$F1 - Score = 2 * \frac{Precision * Sensitivity}{recision + Sensitivity} \quad (5)$$

Table 1. Performance evaluation of Proposed and existing methodologies

Network	Accuracy	Sensitivity	Precision	F-Score
IGMS+VGG19	93.88%	81.34%	94.82%	64.94%
IGMS+ResNet50	93.72%	87.31%	94.20%	52.99%
IGMS+AlexNet	96.33%	82.15%	70.23%	94.39%
IGMS+CNN (Proposed)	97.44%	96.45%	99.07%	93.56%

Figure 2: Performance comparison of Existing and Proposed Method



The performance evaluations contrast our approach's efficiency with those of trained networks like VGG19, ResNet50 and AlexNet. Utilize IGMS to first remove patch candidates, and then use several models to identify

the real parasites. Performances evaluation are compared for a particular specificity in terms of acc, sensi, spec, prec, F-score. The customised CNN model's accuracy is around4% higher than VGG19's and ResNet50 and 1% higher than AlexNet about, as shown in Table 1.Also, the graphical representation of the performance analysis is given in Figure 2.

5.1 Discussion

This program uses the IGMS method and deep learning to simulate parasite identification using Tensor Flow and Keras packages. The proposed system achieves a correlation coefficient of more than 98 percent at both image level and patient level, and achieves 98.26 percent accuracy and AUC of 97.78 percent data level. This is mainly determined by two things: First, the pre-selection of IGMS for parasite eaters adequately counts parasites in the basic fact. Second, the CNN model can accurately classify pre-selected candidates using customized input sizes and network layers. Based on a comparison of our custom CNN architecture with three pre-trained systemsVGG19, ResNet50, and AlexNet, in Table 1 find: 1) The custom CNN model is faster than VGG19 and ResNet50 2) Custom CNN network accuracy is much higher in Set A, between 1 and 2 %, and the precision of existing AlexNet (p0.01)and VGG19 (p0.001). In Set A, ResNet50 gets an accuracy of about 92.50 percent. ResNet50 performs worse than VGG19, ResNet50 and AlexNet from 7% to 29% in terms of specificity given, according to the ROC curve; however, ResNet50 is much bigger and slower in our Smartphone system. In order to identify potential parasites, we have also used RCNN and YOLO instant detection networks. With standard pixels of 4032 × 3024in a picture with size of 44 × 44, parasites are too small for these detected applications to be able to detect them effectively, leading to many false positives.

6. CONCLUSION

The proposed system uses a deep learning study method to detect malaria parasites in dense smears. Insect testing and classification of parasites are the first two steps to evaluate the automatic malaria pest identification pipe. A complete thick smear image is quickly detected using intensity IGMS to identify potential parasites. Each candidate is then classified as a background or parasite by a modified CNN partition model. Our simulation results show how effective our approach is in automatically detecting malaria parasites. Studies using tensor flow and deep learning study methods for detecting parasites in dense smears also examined the results at the patient level. As a service to the scientific community, a collection comprising 1819 images from 150 patients will help solve the problem of lack of training set up for automated recognition of malaria in congested smears in blood. The recommended system produced special accuracy when compared to all related functions .

7. REFERENCES

[1] M. Umer, S. Sadiq, M. Ahmad, S. Ullah, G. S. Choi, and A. Mehmood, “A Novel Stacked CNN for Malarial Parasite Detection in Thin Blood Smear Images,” *IEEE Access*, vol. 8, pp. 93782–93792, 2020, doi: 10.1109/ACCESS.2020.2994810.

[2] F. Yang *et al.*, “Deep Learning for Smartphone-Based Malaria Parasite Detection in Thick Blood Smears,” *IEEE J. Biomed. Health Inform.*, vol. 24, no. 5, pp. 1427–1438, May 2020, doi: 10.1109/JBHI.2019.2939121.

[3] A. Alqudah, A. M. Alqudah, and S. Qazan, “Lightweight Deep Learning for Malaria Parasite Detection Using Cell-Image of Blood Smear Images,” *Rev. Intell. Artif.*, vol. 34, no. 5, pp. 571–576, Nov. 2020, doi: 10.18280/ria.340506.

[4] L. Rosado, J. M. C. da Costa, D. Elias, and J. S. Cardoso, “Automated Detection of Malaria Parasites on Thick Blood Smears via Mobile Devices,” *Procedia Comput. Sci.*, vol. 90, pp. 138–144, 2016, doi: 10.1016/j.procs.2016.07.024.

[5] D. Shah, K. Kawale, M. Shah, S. Randive, and R. Mapari, “Malaria Parasite Detection Using Deep Learning : (Beneficial to humankind),” in *2020 4th International Conference on Intelligent Computing and Control Systems (ICICCS)*, Madurai, India, May 2020, pp. 984–988. doi: 10.1109/ICICCS48265.2020.9121073.

[6] F. Yang *et al.*, “Deep Learning for Smartphone-Based Malaria Parasite Detection in Thick Blood Smears,” *IEEE J. Biomed. Health Inform.*, vol. 24, no. 5, pp. 1427–1438, May 2020, doi: 10.1109/JBHI.2019.2939121.

[7] K. E. Delas Penas, P. T. Rivera, and P. C. Naval, “Malaria Parasite Detection and Species Identification on Thin Blood Smears Using a Convolutional Neural Network,” in *2017 IEEE/ACM International Conference on Connected Health: Applications, Systems and Engineering Technologies (CHASE)*, Philadelphia, PA, Jul. 2017, pp. 1–6. doi: 10.1109/CHASE.2017.51.

[8] K. M. F. Fuhad, J. F. Tuba, Md. R. A. Sarker, S. Momen, N. Mohammed, and T. Rahman, "Deep Learning Based Automatic Malaria Parasite Detection from Blood Smear and Its Smartphone Based Application," *Diagnostics*, vol. 10, no. 5, p. 329, May 2020, doi: 10.3390/diagnostics10050329.

[9] P. A. Pattanaik, M. Mittal, and M. Z. Khan, "Unsupervised Deep Learning CAD Scheme for the Detection of Malaria in Blood Smear Microscopic Images," *IEEE Access*, vol. 8, pp. 94936–94946, 2020, doi: 10.1109/ACCESS.2020.2996022.

[10] A. Maqsood, M. S. Farid, M. H. Khan, and M. Grzegorzek, "Deep Malaria Parasite Detection in Thin Blood Smear Microscopic Images," *Appl. Sci.*, vol. 11, no. 5, p. 2284, Mar. 2021, doi: 10.3390/app11052284.

[11] D. Bibin, M. S. Nair, and P. Punitha, "Malaria Parasite Detection From Peripheral Blood Smear Images Using Deep Belief Networks," *IEEE Access*, vol. 5, pp. 9099–9108, 2017, doi: 10.1109/ACCESS.2017.2705642.