International Journal of Research Publication and Reviews

Journal homepage: www.ijrpr.com ISSN 2582-7421

AUTOMATED IMAGE PROCESSING FOR DIAGNOSING THE MALARIA SLIDES

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DOI: https://doi.org/10.55248/gengpi.2022.3.4.16

A B S T R A C T

Malaria is one of the most grievous health problems in the modern world, and it is caused by the bite of female Anopheles mosquitos. The parasite plasmodium erythrocytes are produced in the body. Malaria is caused by five Plasmodium parasites: P.falciparum, P.malariae, P.vivax, P.ovale, and P.knowlesi. In the traditional approach, blood samples are collected from the patient and then they were analyzed under a microscope further they will be sent for the manual testing procedure which consumes much time. To prevent this problem, we have proposed an efficient malaria diagnosing system which is developed using the help of a customized convolutional neural network (CNN), where we will pass the blood cells images and in return, automatically it evaluates the patient's condition parasitized or uninfected.

***Keywords**: CNN, Deep Learning, Accuracy.*

1. INTRODUCTION

The global epidemic of malaria poses a major public health threat. According to WHO estimates, 240 million people had malaria in 2020, and 6,25,000 people died from it. Many methods are available to identify malaria, including k-Nearest Neighbor, Support Vector Machine (SVM), Naive Bayes, and Artificial Neural Networks. These techniques, such as SVM, KNN, and Naive Bayes, do not provide as much accuracy as artificial neural networks. In ANN some drawbacks have existed like it would not work for large images and its computation is also very high. So, to overcome all these drawbacks we proposed the custom Convolutional neural network (CNN). Here, we are using a custom convolutional neural network; the advantage of the custom CNN is that we can apply a certain number of convolution layers to achieve the desired accuracy.

Basically, malaria is caused due to the plasmodium parasites and it passes through people by the bite of the infected female mosquitoes. If one person is infected then the sporozoites travel through the bloodstream of the liver and then there it releases another type of sporozoites will release. There are many parasites in the blood cells and those blood cells will be activated within the 48 hours to 72 hours known as the "erythrocyte cycle". In order to find malaria diseases, medical experts use the manual tasks with skilled technicians which goes through initially blood samples taken from the patients and followed the under microscopic testing and other manual tasks.

In order to find the person infected with malaria or not in less time we can use deep learning algorithms and in that convolutional neural network fits more accurately. This design works on the images of the blood spears of the person with is used by the researchers.

2. LITERATURE REVIEW

2.1 Deep learning for smartphone-based malaria parasite detection in thick blood smears:

As an alternative to a microscope, malaria parasites can be found in thick blood using a smart phone. The first step will be to develop a smart phone system based on Iterative Global Minimum Screening (IGMS) for automated parasite detection in thick blood smears. Afterwards, the method was tested on a larger collection of images taken from 150 patients, which contained 1819 thick smear images and 84,961 parasites tagged [1].

2.2 Automated image processing method for the diagnosis and classification of malaria on thin blood smears:

Here it shows morphological method has been used for identifying malaria in blood slides. To handle the problem of classifying images, pattern recognition and classification system is used. It involves four stages: the acquisition of images, the processing of images, the development of features, and the classification of the images. Using these stages as a benchmark, the performance of the method can be measured [2].

2.3 Malarial Parasite Detection and Recognition using Microscopic Images:

Here it classifies the five malaria parasites and Giemsa staining is used before acquiring the images. Here, image processing techniques are used to detect and recognize the infection in microscopic images [3].

2.4 Malaria Disease Prediction Based on Machine:

The dataset included in this study consists of images of infected red blood cells as well as images of uninfected RBCs. In this study, an extreme learning machine was used to classify and predict whether a patient was infected or not [4].

2.5 Malaria Parasite Detection and Species Identification on thin Blood Smears Using a Convolution Neural Network:

There are some problems in manual diagnosis. Using an intelligent system that recognizes malaria parasites, these issues might be addressed by automating the diagnostic procedure. Researchers propose an intelligent method for detecting malaria parasites in thin blood smear pictures [5].

3. PURPOSE OF THE WORK

The proposed project works to find whether the person is infected with malaria or not. Malaria can be diagnosed using a variety of techniques, including k-Nearest Neighbor, Support Vector Machine (SVM), Naive Bayes, and Artificial Neural Networks. In these techniques, there were some drawbacks are there such as SVM, KNN, and Naïve Bayes are not as much as accurate as of the Artificial neural network. In ANN some drawbacks have existed like it would not work for large images and its computation is also very high. So, to overcome all these drawbacks we proposed the custom convolutional neural network (CNN). By using a custom CNN, we can apply as many convolution layers as we need to obtain the required accuracy.

4. PROPOSED WORK

In this project, the following modules are present they are Data loading and Exploration, Normalization and Splitting Dataset, Model Building, Training the model, and evaluating the model. We have proposed a new convolutional neural network (CNN). In the phase of Data loading and Exploration, images will be taken and resized into (64,64) and then these images are stored in an array, and finally, all the images are stored either in files or folders or lists. Basically, the images are displayed using RGB Values of the pixel. In the phase of Normalisation and Splitting of Dataset, all the images' pixels will be in the range of 0 to 1. Splitting of Dataset will be done where data will be split into the Training and Testing dataset in the ratio80:20. Basically here we have taken 27,000 RBC images.

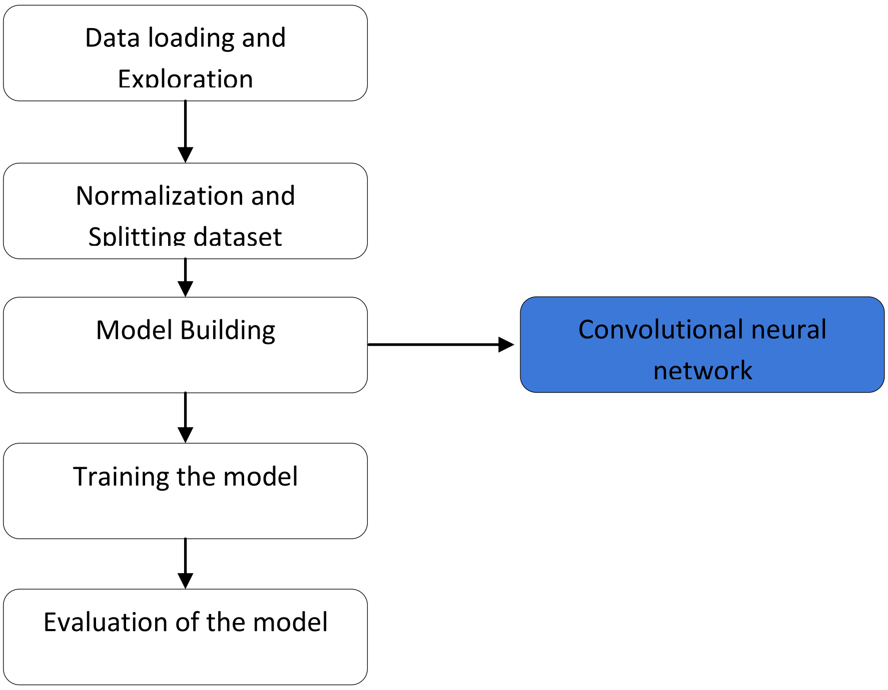

Fig-1. Overall Architecture of Proposed System

5. METHODOLOGY

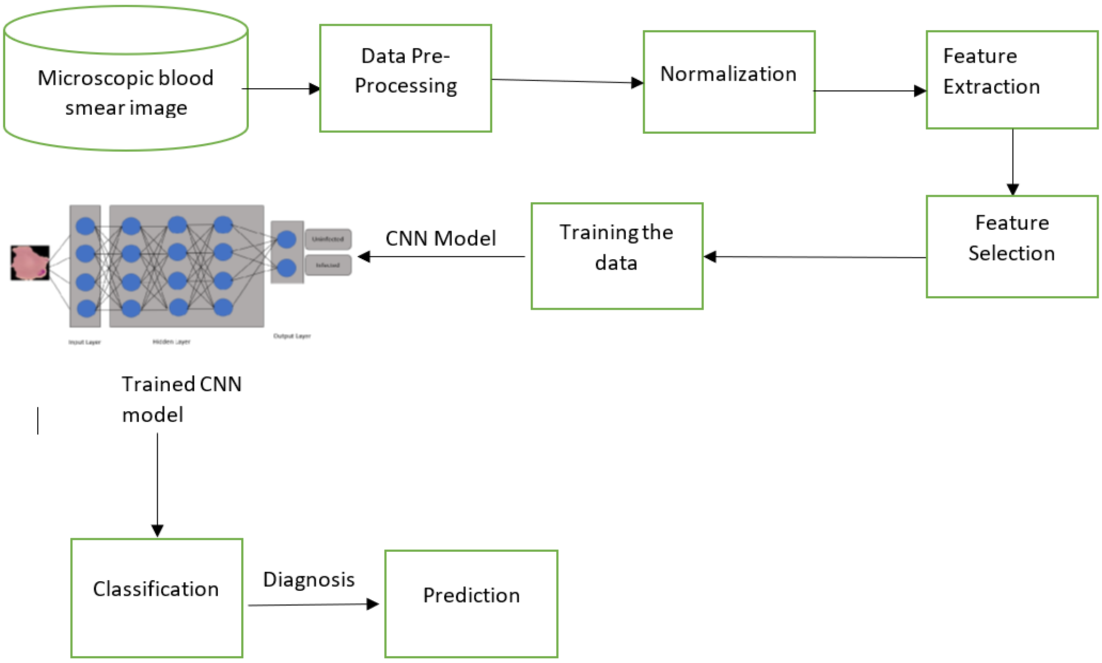

Fig-2: Methodology of Convolution neural network

5.1.2 Normalization

Upon picture pre-processing, the region of interest, namely the erythrocyte, must be retrieved for further analysis. Using the global thresholding technique, the erythrocytes are segregated from the complex backdrop. Within the segmented region of interest, we kept the entire stained component, along with the clump of erythrocytes. A morphological filtering mechanism separates the undesired stained components from the erythrocyte.

5.1.3 Feature Extraction

Previously segmented erythrocyte characteristics must be removed in order to distinguish between normal and infected erythrocytes. The histogram features of distinct colour channels have been considered to improve the effectiveness of the classification of normal and diseased erythrocytes. Histograms include the colour channel histogram, the red-green histogram, the green channel histogram, and the saturation level histogram.

5.1.4 Feature Selection

The technique for selecting the best collection of features for erythrocyte classification is detailed in this section. Feature selection is the most critical phase in image analysis. The saturation level histogram, the green channel histogram, the chrominance channel histogram, and the R-G histogram are explored, and several feature combinations are tested in order to determine which feature set provides the highest accuracy for erythrocyte categorization.

5.1.5 Classification

In the phase of Model Building, the image of size 64*64*3 is taken as input and passed to the first layer of the convolution neural network which is a convolution layer. In the max-pooling layer, the output from the convolution layer is transferred, which minimizes the number of parameters that must be taught at each level of the network. This pair of convolution and max-pooling layer is repeated for 4 consecutive times. The extracted features are then flattened using a flattened layer. The flattened features are then used for classification with the help of fully connected layers i.e., dense layers. Between thick layers, dropout layers prevent the model from overfitting. Only one neuron is involved in the final dense layer, which determines whether the blood cell images is affected.

6. RESULT AND DISCUSSION

Classification	**Performance Metrics**
k-NN Based Classification	Prescision : 86.25 Recall : 93.49 Accuracy : 91.29 F1- score : 80.75
SVM Based Classification	Prescision : 90.11 Recall : 91.89 Accuracy : 92.09 F1- score : 84.14
ANN Based Classification	Precision : 92.65 Recall : 91.75 Accuracy : 94.32 F- score : 85.32
NaïveBayes Based Classification	Precision : 90.48 Recall : 92.62 Accuracy : 92.86 F- score : 83.33
CNN Classification	Precision : 95.64 Recall : 97.85 Accuracy : 93.69 F- score : 95.73

Fig-3. Comparison table for k-NN, SVM, ANN, Naïve Bayes based, CNN Classifications

The above table shows that how the performance metrics for different algorithms to find the malaria disease. Apart from CNN, ANN is more accurate than others. But CNN is more accurate than ANN and also CNN can be used for large images as well as low computation comparatively to ANN. Hence, a convolution neural network is the best algorithm for diagnosing malaria.

7. CONCLUSION

The outcome is a process useful for finding whether the person is infected with malaria based on the patient's red blood cells. This project leads to the identification and detection of malaria diseases. The algorithm which has been used here i.e., the convolutional neural network helps to give the high accurate i.e., 95.11 for the dataset.

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