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Malaria Parasite Species Recognition using Artificial Neural Network

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ABSTRACT: In recent years, many authors have proposed approaches related to computerization of malaria diagnosis. The malaria infection level in the blood sample images is quantified and qualified using computer vision and artificial intelligence for analysis of blood images. The degree of infection and class of species are necessary parameters for proper treatment of malaria disease. In this paper, the features extracted from the host RBCs and parasites were used to recognize the species using ANN as a classifier. In this study, MLP network achieved 92.9 % accuracy after testing the network trained using back propagation algorithm and the results were compared with radial basis neural network.

KEYWORDS: ANN, Malaria, RBC, Plasmodium

I. INTRODUCTION

Malaria continues to be one of the major global health problem, despite the massive efforts put forth by WHO in eradicating it worldwide. Almost one out of every thirty people on earth suffers from malaria yearly [1] Malaria poses a diagnostic challenge to the medical community worldwide. Correct and timely diagnosis of this disease is the prior step to control the spread of the disease[2] The disease can be treated in just 48 hours, yet it can cause fatal complications if the diagnosis and treatment are delayed.

Currently the traditional method used for the identification of Malaria parasite is a manual one. It is a gold standard [3], but requires trained technologist to examine and detect the number of parasites. Moreover, it is a very time consuming process, subjected to human errors and inconsistency. As a consequence, these disadvantages of manual microscopy bring many difficulties in mass blood screening (MSB) and controlling the spread of disease becomes a burden, especially in highly endemic and rural areas Therefore, in recent few years, many authors proposed computer aided malaria diagnosis to overcome these limitations

II. RELATED WORK

In[4], author proposed KNN classifier to detect and recognize the malaria parasite and parasite species. Various features such as Hu moments, color auto histogram, relative shape measurement, histogram were used for classification.

In [5], researcher presented MLP network as a classifier to classify malaria parasite into three species and used relative size of RBC, shape of parasite, parasite density, texture of RBC, location of chromatin dot and number of chromatin dot as features.

In [6], the author proposed back propagation feed forward neural network to identify parasite and classify the species into four types.P.falciparum, P.vivax, P.ovale and P. malariae

Kaewkamnerd *et al*. [7], presented an automated system to identify and analyze parasite species using thick blood film by image analysis technique. HSV color space was used for image segmentation. The distribution of chromatin size was then measured. The classifier classifies the parasite as P. falciparum or P. vivax based on the distribution of chromatin size. The test results of 60% success rate were obtained only for recognizing two sample blood images and the success rate was very low.

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In [8], Sutkar, Marathe developed an Artificial Neural Network (ANN) and has employed image processing techniques to automate the malaria diagnosis of blood smear images using the morphological features of erythrocytes in the bloodand achieved 75 % accuracy and sensitivity of 84.41 %.]
Neetu Ahirwar et al. [9] proposed an approach for detection of malaria parasite in thin blood smear images using Feed forward back propagation neural network. Gradient Descent algorithm was used with a learning rate of 0.2 in batch processing mode. The performance and accuracy was measured in terms of sensitivity and positive predict value.

III. METHODOLOGY

Images of thin blood smear were selected from Centre for Disease Control malaria image library available on its website.[10] These images are available in JPEG format in different sizes and magnifications. Image processing and ANN toolbox in MATLAB 2010 was used for the research study. RBCs in the red blood slide image were first segmented into individual RBC (sub image). Histogram based segmentation method [10],[11] using global and local threshold was used to separate the RBC sub images and parasites from image background and each other as shown in figure 1. Color, texture and shape based features were extracted from the host RBC and parasite. The extracted features were used as an input data to the MLP Network classifier for training using back propagation (BP) algorithm. Out of total 65 images of P. falciparum and P.vivax available, 51 thin blood images were used for training and 14 images used for validation (test set) of the classification result. The results achieved by BPNN were compared with Radial Basis Neural Network (RBNN).

(a) (b) (c)

Figure 1. (a) Original RBC Sub image**,** (b) RBC binary image after segmentation
(c) Parasite binary image after segmentation

IV. RESULTS

Table 1, shows the result of training the BPNN for the proposed approach, trained using 51 images. The training performance was measured from the confusion matrix in terms of accuracy, sensitivity, specificity as shown in the table 1.

Table 1. Training Set performance of BPNN for species classification

Classifier Type	Accuracy	Sensitivity	Specificity	PPV	NPV	Regression
BPNN	94.1 %	88.9 %	97 %	94.1 %	94.1 %	.90

Table 2, shows the test result obtained from the trained network. 14 test image samples, not used during training the network, were used for validation. Performance of Radial Basis Neural Network (RBNN) compared with BPNN and shows that BPNN performed better with species classification accuracy of 92.9 %.

Table 2. Testing set performance of BPNN & RBNN for species classification

Classifier Type	Accuracy	Sensitivity	Specificity	PPV	NPV	Regression
BPNN	92.9 %	100 %	87.5 %	85.7 %	100 %	.72
RADIAL (spread = 4)	83.3 %	100 %	75 %	66.7 %	100 %	.6667

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V. CONCLUSION

The results suggest that species recognition can be performed using back propagation neural network as a classifier using color, texture and shape based features. The species confusion mostly occurred between different species ring life stages, where species specific morphologies were less observable. The performance could also be improved, if the captured blood cell images belong to same set up.

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BIOGRAPHY

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