Malaria Detection Using Red Blood Cells

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Abstract: The examination of a patient's blood sample is an important task in the medical industry. A variety of health problems are caused by abnormalities in blood cells. RBCs (red blood cells) are one of the most important components of blood. The shape and size of red blood cells can be used to distinguish them from other cells. The traditional method of manually viewing RBC under microscope is a tiresome operation that can result in incorrect interpretation. There is another method called as rapid diagnostic test where it may not be able to detect infections with lower numbers of malaria parasites[1]. To eliminate these disadvantages of traditional methods, we came up with a machine learning approach where infected and uninfected datasets of images are trained. The preprocessed images are used to train a CNN binary model to determine the pattern that may be used to categorise malaria-infected red blood cells.

Keywords: RBC, Shape, Machine-Learning, CNN, Infected RBC, Uninfected RBC

I. INTRODUCTION

Malaria is a life-threatening endemic disease caused by Plasmodium, a genus of unicellular protozoan parasites. Generally, in laboratories to detect the malaria infected cells it requires bulky equipment and it increases the chances of mortality. Malaria is commonly found in hot, humid climates near natural water sources and it is transmitted from anopheles mosquitoes[1]. Malaria cannot spread from one person to another. Infected people have symptoms that are comparable to the flu, but they can also have different symptoms like high fever, chills, septicemia, pneumonia, gastritis, enteritis, nausea and vomiting[1]. Microscopy of stained thin and thick peri blood (PB) films is used to diagnose malaria. Because this is a time-consuming method that relies on the expertise of a pathologist, healthcare professionals may have trouble identifying malaria in areas where it is not endemic. Machine learning approaches are intended to mimic the functions of data processing and decision making[2]. RBC, commonly known as erythrocytes, make up the majority of the human body's immune system. Hemoglobin is a biomolecule found in blood that gives it its red color. Shortage of oxygen is caused by a lack of normal RBC in the body. During the disease, mature red cells undergo morphological alterations. RBCs, white blood cells, platelets, and plasma are the primary components of blood. The nucleus and cytoplasm can be separated based on texture, color, size, and morphology. A blood smear, which is a thin film of blood distributed evenly on a glass slide for pathologists to examine under a microscope, is used for blood analysis. Our blood is red because we have a lot of RBCs (erythrocytes) in our bodies. These RBCs transport oxygen to different parts of our body. There are many proposed systems which can detect malaria red blood cells. The first one was proposed by Salam Shuleenda Devi; Amarjit Roy; Manish Sharma; R.H. Laskar[2016] [3] who proposed a new model by using KNN classifiers and achieved 94.2% accuracy. In KNN, the rate of prediction is slow for large data and it requires high memory to store all the training data. The second one was proposed by A. Bashir, Z. A. Mustafa, I. Abdelhameid and R.Ibrahem[2017] [4] who proposed a new model by using an Artificial Neural Network data. In ANN technique it takes more time to train The third one was proposed by Kirti Motwani, Abhishek Kanojiya, Cynara Gomes, Abhishek Yadav [2021] [5] who proposed a new model by using SVM classifier and achieved 71.2% precision and 86.3% call. In, SVM technique it takes more time to train the data. A Convolution Neural Network is most commonly applied to visual images. The CNN model is used for the preprocessing and augmentation of a given dataset. CNN has simple structure, less training parameters and is more adaptable.



II. METHODOLOGY

(a) Data set:

In this paper, we considered a data set consisting of two folders with 1500 images each. They are: **1.**Parasitized

2.Uninfected

We divided this data set into train images, validation images and test images in the ratio of 4:1:1. Figure 2 shows the sample of one of the images of both parasitized and uninfected folders.



Figure 2: Infected and uninfected cells

(b) Data processing :

Real-world data sometimes contains noise, missing values, and is in an unsuitable format that cannot be used directly in machine learning models.Data pre-processing is essential to clean the data and make it appropriate for a machine learning model, which also improves models accuracy and efficiency. Here the images are resized so that the model can be trained fastly.

(c) Data Augmentation :

Data augmentation is the process of improving the basic data in order to enhance the number of data points. It has been used to improve classification performance in a variety of medical datasets. Data augmentation is also used to train the model from all versions of the images. In data augmentation, we will take the images of different orientations of a single image to improve the training of the model. In this model, we have oriented all the images into 45° and 75° and used these images.

(d) Apply CNN model :

In this paper, we have trained our model using Convolutional Neural Networks .A Convolutional Neural Network (CNN) is a Deep Learning system that can take an input image and distinguish between the features

like shape, size and texture. When compared to other classification methods, the amount of pre-processing required by a CNN is significantly less.

(e) Evaluating the model:

After training the model, we perform evaluation by using validation data to tune hyperparameters. Validation is used to provide an unbiased evaluation of a model to fit on the training dataset while tuning model hyperparameters. So the validation set affects a model, but only indirectly. This validation set is also known as the development set.

(f) Test the model on test data:

After validation, finally we have tested our model on the test data that we have previously separated by data augmentation.

III. PERFORMANCE EVALUATION

In our proposed method, we have used CNN algorithm to identify the malaria infected cells effectively in no time with very less complexity. In our binary model, we defined the malaria infected cell as '1' and the uninfected cell as '0'. The term "true value" corresponds to the original value of the image and the term "predicted value" corresponds to the model predicted value. So, if both true value and predicted value are the same then our prediction is correct. Figure 3 shows the outputs of 49 samples from our test data.



Figure 3: Output images of dataset

IV. CONCLUSION

Malaria detection is not an easy procedure, and the availability of qualified personnel around the globe is a serious concern in the diagnosis and treatment of cases. The equipment used to detect is very bulky and costly. We developed a model to differentiate malaria-infected RBCs from healthy RBCs. Here, CNN technique is used to train the model for malaria detection. So, this model is very helpful in terms of cost, human effort and efficiency.

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