



MALARIA DETECTION USING IMAGE PROCESSING AND MACHINE LEARNING

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ABSTRACT: Plasmodium parasites, which are spread by mosquito bites, are responsible for malaria. Microscopical analysis of stained blood cells is the standard diagnostic method for malaria. The quantity of infected RBCs may be determined by placing a drop of blood on a microscope slide and counting them. One may imagine the experienced technician's focused attention as he or she examines the slide. It's a tedious and lengthy procedure. In this research, I build a novel image processing system to identify and quantify plasmodium parasites in blood smear slides, and then I use Machine Learning to train the system to recognise different kinds of infected cells based on their unique characteristics. In order to identify malaria in photos, I am using support vector machine (SVM), convolutional neural network (CNN), and SVM incorporated CNN techniques. As can be shown from the experiments, the suggested models perform well and provide reliable outcomes.

Keywords - *Malaria, support vector machine (SVM), convolutional neural network (CNN)*

1. INTRODUCTION

Malaria is a very dangerous parasitic illness spread by mosquitoes. Around 3.2 billion individuals worldwide are at high risk (annual risk of malaria of >1 in 1000). There were 212 million new cases of malaria in 2015, the study said (range 148–304 million). The WHO African Region was responsible for 90% of all malaria cases worldwide; the next highest regions were

South-East Asia (7%) and the Eastern Mediterranean (2%). [1]. Chemical processes allow for the detection and visual identification of Plasmodium in RBC [2]. The red blood cells are slightly tinted by the stain, while the parasite Plasmodium, white blood cells, and platelets stand out. To identify Plasmodium, one must examine stained samples. However, further analysis of stained items is required to establish

whether or not they are parasites. There are a number of malaria detection techniques available. Image segmentation and feature extraction using a minimal distance classifier [3] may be used to identify malaria parasite (MP) in a blood sample. Images are acquired, preprocessed, smoothed, thresholded, and expanded before being segmented.

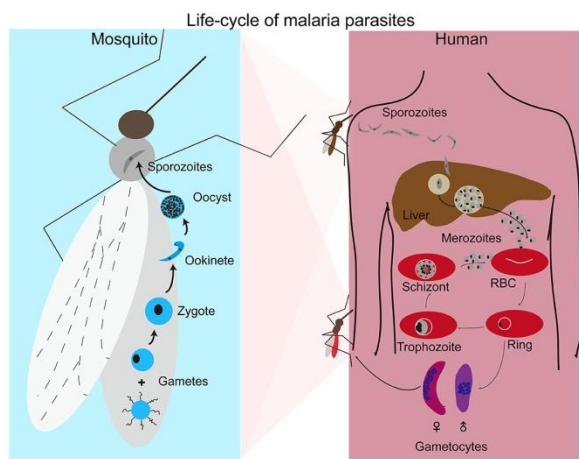


Fig.1: Example figure

The architectural model for feature extraction consists of two stages: 1) a training phase, during which the MP is learned to be recognised, and 2) a recognition phase, during which the MP is actually recognised. We concentrate on 1) developing methods for automatic malaria detection and quantification, and 2) developing methods for identifying infected images via the use of machine learning. 3)

Talk about ways to boost the test's ability to predict whether or not a cell is contaminated.

Malaria is a mosquito-borne life threatening disease caused by Plasmodium parasite. Globally, an estimated 3.2 billion people are at high risk (>1 in 1000 chance of getting malaria in a year). According to the report, there were 212 million new cases of malaria worldwide in 2015 (range 148–304 million). The WHO African Region accounted for most global cases of malaria (90%), followed by the South-East Asia Region (7%) and the Eastern Mediterranean Region (2%). [1]. Visual detection and recognition of Plasmodium in RBC is possible via chemical process [2]. The staining process somewhat colorizes the RBCs but highlight Plasmodium, WBCs and platelets. The detection of Plasmodium requires detection of the stained objects. However, we need to analyzed stained objects further to determine if they are parasites or not to prevent false diagnosis. Several methods exist for malaria detection. Malaria parasite (MP) in blood sample can be identified by using image segmentation and feature extraction using minimum distance classifier [3]. Based on Image Acquisition, Image Preprocessing,



Image Smoothing, Thresholding and Dilation image segmentation is done. Feature extraction uses two phases in architectural model: 1) Training Phase and 2) Recognition Phase which helps to recognize the MP.

2. LITERATURE REVIEW

Automatic detection of malaria parasite from blood images

The Plasmodium parasite is responsible for malaria. The female Anopheles mosquito is responsible for transmission. A skilled pathologist uses a microscope to physically inspect both thick and thin blood smears of the patient to make a diagnosis. Many sections of the globe may lack access to such highly trained pathologists owing to a lack of adequate medical infrastructure. In addition to being a time-consuming and laborious method, hand examination demands the pathologist's undivided attention. As a result, it is crucial to rapidly and accurately identify malaria that automated technologies be developed. It may aid in reducing the number of false negatives and finding diseases at an early, treatable stage. In this study, we provide a computer-assisted approach for identifying

malaria parasites in blood micrographs. Bilateral filtering is used in the suggested approach to get rid of the noise and improve the quality of the picture. In order to find malaria parasites inside a single cell, researchers use adaptive thresholding and morphological image processing methods. We have evaluated the effectiveness of the suggested algorithm using a dataset provided by the National Institutes of Health (NIH) and compared the findings to those obtained by other, comparable approaches. We were able to outperform rival algorithms with a detection accuracy of over 91% using our approach. The results demonstrate the validity of the proposed algorithm and its potential usefulness to pathologists and haematologists in the identification of malaria parasites.

Advanced Image Analysis-Based System for Automatic Malaria Parasite Detection and Classification in Blood Images

This work presents a technique for automatically detecting and classifying malarial parasites in blood sample pictures collected using light microscopes, and it explores the potential for speedy and accurate automated diagnosis of red blood cell diseases. Because malaria is an



infectious illness, most diagnoses are made by the microscopic examination of Giemsa-stained blood smears. Automation of the assessment process is crucial because it represents a major threat to world health. This image classification technique was developed specifically for the purpose of recognising the malaria parasite in very small samples of blood. Red blood cells (erythrocytes) and any parasites they could be harbouring can be picked out of a slide of blood by using a combination of conventional morphological analysis and cutting-edge threshold selection methods. Generated image characteristics include those based on colour, texture, and the geometry of the cells and parasites, as well as features that make use of a priori knowledge of the classification issue and features that mirror features utilised by human technicians. Parasite-infected and uninfected blood samples are distinguished using a classifier based on a back propagation feed forward neural network.

Otsu Algorithm for Improved Identification of Malaria-Infected Objects from Thin Smear Digital Images

In order to effectively combat malaria, a prompt and precise diagnosis is essential. In

this work, we create an algorithm for automatic malaria detection in blood pictures using image processing. Experts are required for the laborious and time-consuming task of manually counting parasitaemia. Here, we create an image classification method to positively detect malaria parasites in thin blood smears. We propose an automated method for detecting Malaria parasites in blood pictures by first identifying and categorising red blood cells (RBCs) as either normal or infected. In this method, blood cell segmentation may be accomplished by the use of Otsu thresholding on either the green or blue channel of the RGB blood picture. The binary picture is segmented, and then morphological processing is given to it so that parasites and blood cells may be detected with high precision. The proportion of parasitaemia is determined by summing the parasite counts and the RBC counts, which is a two-step procedure.

Cell Detection in Digital Micrographs Using a Hybrid System

Advanced image processing methods are required for accurate, reproducible analysis of vast collections of digital micrographs from high-throughput screening



investigations. Systems using model-based fitting methods, morphological operators, and artificial neural networks have been suggested in the literature (ANN). Due of the low performance of stand-alone methods, we suggest a hybrid system that combines the Hough transform with a multi-layer perceptron (MLP) network. The locations of cell bodies are acquired with higher sensitivity and positive predictive value, as shown by our findings, when the two methods are combined.

3. METHODOLOGY

To detect the MP in light microscopy pictures, N.A.Khan and colleagues presented a computer vision based technique. In this study, we focus on the difficulties inherent in the automated identification of malaria parasite tissues. It employs a pixel-based technique. In order to segment and recognise malaria parasite tissue, they employed K-means clustering, an unsupervised method. K-means clustering is used to find groups of objects that belong to the same goal category. To make predictions about undiscovered data, we assume that it is similar to existing data and is geographically close to the cluster's epicentre. Permeabilization, fixing, mounting, and

staining are all chemical processes that are somewhat more challenging to carry out in rural locations due to a lack of resources and trained personnel.

Disadvantages:

1. Malaria detection has always required the use of a microscope, a process that is both time-consuming and labor-intensive.
2. Requiring a high level of laboratory technician experience.

Image segmentation and feature extraction using a minimal distance classifier may be used to identify malaria parasite (MP) in a blood sample. Images are acquired, preprocessed, smoothed, thresholded, and expanded before being segmented. To identify malaria in photos, we are using Support Vector Machines (SVMs), Convolutional Neural Networks (CNNs), and a CNN integrated inside an SVM. As can be shown from the experiments, the suggested models perform well and provide reliable outcomes.

The benefits of this suggested system are:

1. Efficient performance.
2. Provable forecasting

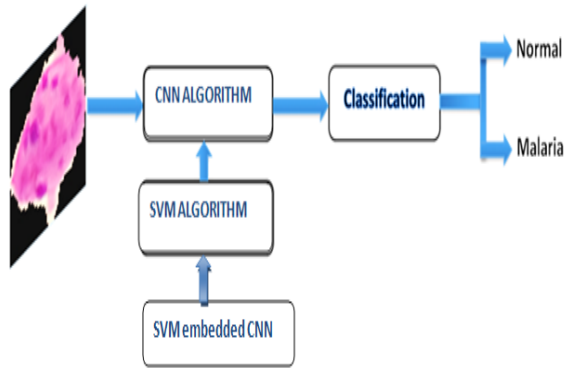


Fig.2: System architecture

MODULES:

To implement aforementioned project we have designed following modules:

- User signup and signin: Using this module user will register & login into the application
- User gives input : Using this module user gives input
- Algorithms: using this module algorithms generated
- Prediction: Using this prediction result displayed

4. IMPLEMENTATION

CNN ALGORITHM:

A Convolutional Neural network (ConvNet/CNN) is a Deep Learning method that can take in an input picture, give relevance (learnable weights and

biases), and then distinguish between distinct objects or features within the input image. By comparison to other classification methods, ConvNet requires much less pre-processing work. Although filters must be hand-engineered when using basic techniques, ConvNets may be trained to acquire the necessary properties automatically. ConvNets' design takes cues from the visual cortex's structure, which is why it is so similar to the human brain's pattern of neuronal connection. The Receptive Field is the portion of the visual field to which each individual neuron is sensitive. When several of these fields overlap, they may protect a whole field of view.

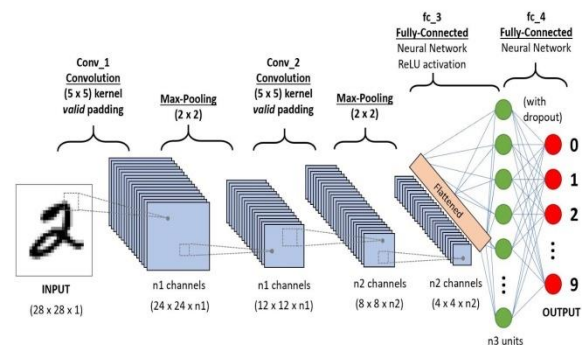


Fig.3: CNN model

SVM ALGORITHM:

One of the most widely used Supervised Learning techniques, Support Vector



Machine (SVM) is also effective when used to Regression situations. The primary use of this technique, however, is in the field of Machine Learning, where it is employed for Classification tasks. The SVM algorithm's objective is to find the optimal line or decision boundary that divides the n-dimensional space into classes, making it simple to assign the new data point to the right class in the future. A hyperplane describes this optimal choice boundary. For the purpose of constructing the hyperplane, SVM picks the most extreme points and vectors. These outlier examples are referred to as support vectors, which is how the corresponding method got its name: Support Vector Machine. Take a look at the picture below, which uses a decision boundary (or hyperplane) to classify two groups of objects:

An example of SVM may be found in the KNN classifier, which can be utilised to better grasp SVM. So, if we encounter a peculiar cat that has characteristics with dogs, and we want a model that can reliably determine which species it belongs to, we may use the SVM technique to construct such a model. First, we'll put our model through its paces using a large dataset consisting of cat and dog photographs so it can get familiar with the species and its characteristics, and then we'll put it to the test with this out-of-the-ordinary animal. To this end, support vector builds a decision boundary between these two data (cat and dog) and selects extreme instances (support vectors), which leads it to the conclusion that cats and dogs are, respectively, the two most extreme examples. It will be identified as a cat based on the support vectors.

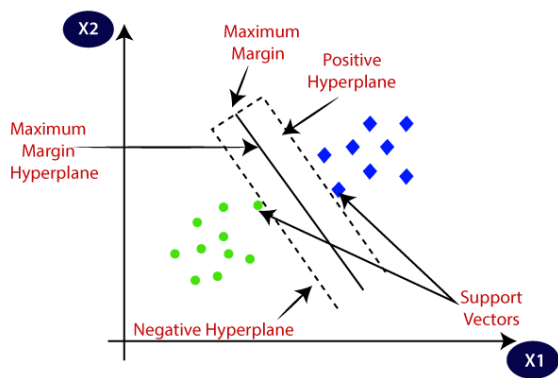


Fig.4: SVM model

5. EXPERIMENTAL RESULTS

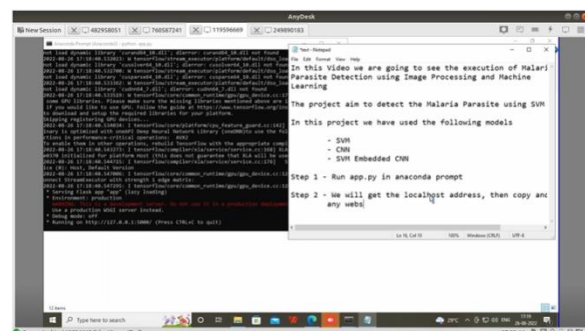


Fig.5: Web page address

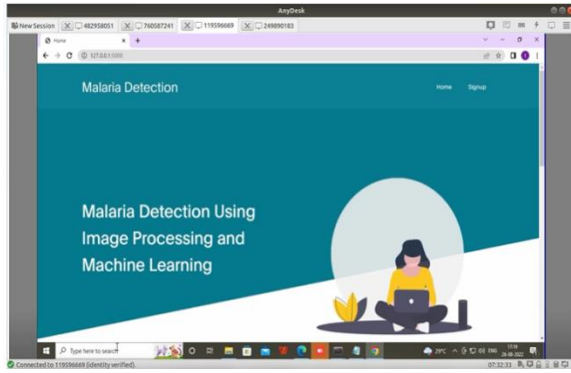


Fig.6: Main page

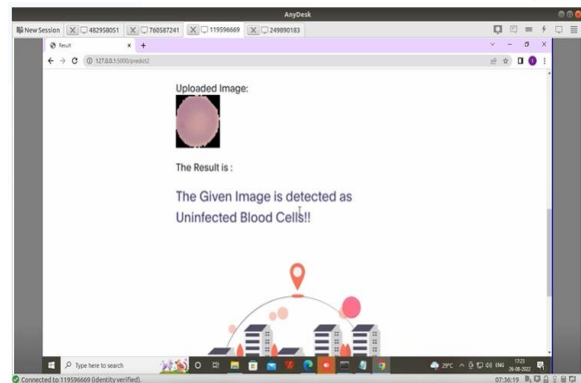


Fig.9: Prediction result

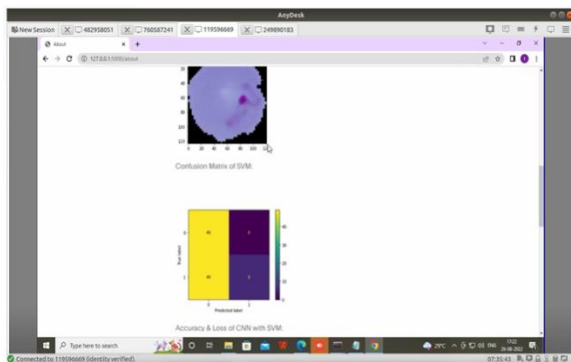


Fig.7: Confusion matrix

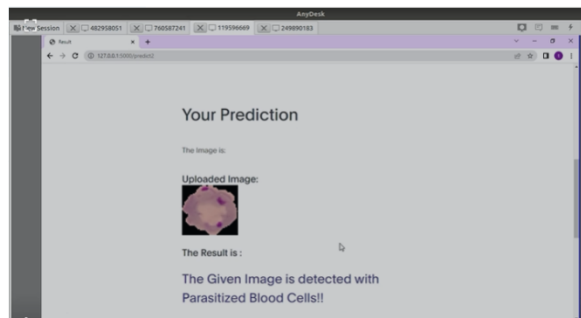


Fig.10: Prediction result

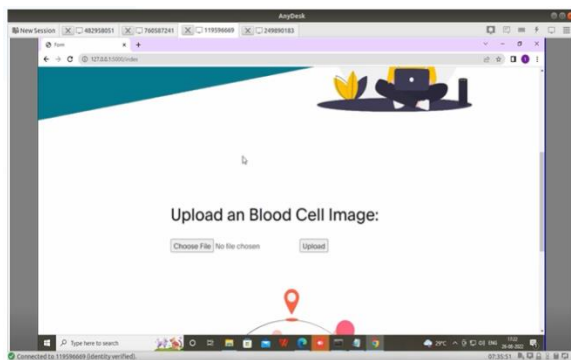


Fig.8: User input

6. CONCLUSION

We have given a method, and constructed an algorithm, for identifying malaria, automating the detection of malaria, and quantifying malaria infection. To improve the prediction value of our findings, we also devised a machine learning training technique that is generalizable to the identification of malaria parasites of different kinds.

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