

# Malaria and Dengue Disease Prediction Based On Blood Cell Image Using Machine Learning

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## ABSTRACT

The health care environment is found to be rich in information, but poor in extracting data from the knowledge. This is often due to the shortage of effective analysis tool to get hidden relationships and trends in them. By applying the machine learning algorithms and techniques, valuable knowledge are often extracted from the health care system. Malaria and Dengue fever have condition affecting the structure and functions of body and has many root causes. We tend to area unit exploitation Deep Learning algorithms to extend the accuracy of Malaria and Dengue Disease prediction System. We also expand this technique to research the actual area to maximum patient were health is weak based on hospital patient data. It is enforced as desktop application during which user submits the heterogeneous data like image of blood cells symptoms. It retrieves hidden information from stored database and deep learning model and compares the user values with trained data set.

**Keywords-** Machine learning, Disease prediction, Area detection, Malaria, Dengue

## I. INTRODUCTION

Welcome to the AI for Social Good Series, where we will be focusing on different aspects of how Artificial Intelligence (AI) including with popular open-source tools, technologies and frameworks are getting used for development and betterment of our society. "Health is Wealth" is probably a clichéd quote yet very true! During this system, we will check out how AI are often leveraged for detecting malaria, a deadly disease and therefore the promise of building a low-

cost, yet effective and accurate open-source solution. The intent of the system is two-fold understanding the motivation and importance of the deadly disease Malaria and Dengue and therefore the effectiveness of deep learning in detecting Malaria and Dengue. A major challenge facing healthcare organizations (hospitals, medical centres) is the provision of quality services at affordable costs. Quality service implies identification of diagnosing patients correctly and administering treatments that are effective. Poor clinical choices will lead to disastrous consequences

which are therefore unacceptable. Hospitals must also minimize the value of clinical tests. They can achieve these results by using acceptable computer-based information and/or decision support systems. Most hospitals nowadays use employ some sort of hospital information systems to manage their healthcare or patient data.

## II. RELATED WORK

Alif Bin Abdul Qayyum, Tanveerul Islam, Md. AynalHaque [1] Proposed three different dilation approaches were used among which Fibonacci series-wise dilated CNN model performed best altogether metrics like accuracy (96.05%), precision (95.80%), recall (96.33%) and F1 score (96.06%) while working with a dataset of 27,558 cell images.

Feng Yang\*, MahdiehPoostchi, Hang Yu, Zhou Zhou, KamolratSilamut, Jian Yu, Richard J Maude, Stefan Jaeger\*, Sameer Antani[2] This work investigates the likelihood of automated malaria parasite detection in thick blood smears with smart-phones.

They developed the primary deep learning methodology which will detect malaria parasites in thick blood smear images and might run on smart-phones.

WanchaloemNadda, WarapornBoonchieng, and EkkaratBoonchieng [3] Proposed. In this research they use machines to classify patients as dengue and non-dengue patients. They used the text of symptoms of the patients for input data. They used the dataset is that the treatment data from the patients with fever, cold, flu, pneumonia, and Dengue from the hospital.

Octave Iradukunda, HaiyingChe, JosianeUwinez, Jean Yves Bayingana, Muhammad S Bin-Imam, Ibrahim Niyonzima [4] During this paper, an appropriate model is designed to detect malaria with accuracy. A single hidden layer feedforward neural

networks methodology namely extreme machine learning(EML) model was applied to classify and predict whether a patient has been suffering from by malaria or not.

Abhas Dhaka. Prabhishek Singh [5] To implement this epidemic system four algorithms are used namely Random Forest Regression, Decision tree regression, Support vector regression, Multiple linear regression.

## III. MATERIALS AND METHODS

### A. System Architecture:

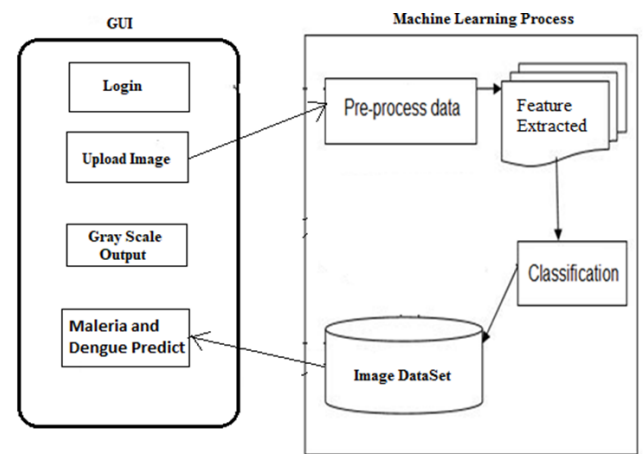


Fig 1. System architecture

The people are affected by various diseases like Dengue, Malaria. This information is collected from the various hospitals and therefore the analysis of data is completed and prediction of some diseases are often made. This technique gives the prediction as per locality of the area.

### B. Description:

#### Module 1:

During this system we tend to notice the malaria and dengue diseases-based blood cell dataset and apply image processing with the help of machine learning technique.

**Model 2:**

Here offer the module for detecting diseases.

**C. Mathematical Model:**

Let 'S' be the system  $S = \{I, O, P, Fs, Ss\}$

where,

I = Set of input

O = Set of Output

P = Set of technical processes Fs = Set of Failure state

Ss = Set of Success state

Identify the input data  $I_1, I_2, \dots, I_n$

$I = \{(\text{Input Data (Image), Dataset (Dengue, Malaria)})\}$

Identify the output applications as  $O_1, O_2, \dots, O_n$

$\{(\text{Malaria Detection, Dengue Detection})\}$

Identify the Process as P

$P = \{(\text{Image pre-processing, Image Processing, Grey-scale, smoothing, Edging, segmentation, feature extraction, classification, show result})\}$

Identify the Failure state as Fs

$Fs = \{(\text{If data set not loaded, If not predicted, if more time required to predict})\}$

Identify the Success state as Ss

$P = \{(\text{Correct prediction within time})\}$

**D. Algorithm:**

1. Classify dataset under labeled folders such as malaria and dengue images
2. Read dataset
3. Read features of all images and label (here name of dataset folder) of it
  - a. Conv2D
  - b. Maxpool2D
  - c. RELU activation for layers
  - d. Sigmoid activation for dense layer
  - e. Binary Cross entropy for loss calculation
4. Store it in model file
5. Get input image
6. Read features of input image
7. Compare features of stored features

8. Show label as prediction of nearly matched features.

**Algorithm Details****Step 1 : Convolution Operation**

Here are the three elements which include in the convolution operation:

1. Input image
2. Feature detector
3. Feature map

**Step 2 : ReLU Layer**

The reason we would like to try to to that's that images are naturally non-linear.

When you check out any image, you will find it contains tons of non-linear features (e.g. transition in the middle of pixel, borders, colours etc.). The rectifier serves to interrupt up the linearity even further so as to form up for the linearity that we'd impose a picture once we put it through the convolution operation.

**Step 3 : Pooling**

Again, max pooling cares with teaching your convolutional neural network to acknowledge that despite all of those differences that we mentioned, they're all images are same. In order to try to to that, the network must acquire a property that's referred to as "spatial variance." This property makes the network capable of detecting the thing in the image without rambling by the differences within the image's textures, the distances from where they're shot, their angles, or otherwise.

**Step 4 : Flattening**

This will be a brief breakdown of the flattening process and how data move from pooled to flattened layers when working with Convolutional Neural Networks.

**Step 5 : Pooling**

What happens after the flattening step is that you simply simply find yourself with an extended vector of input file that you then undergo the synthetic neural network to possess it processed further which is called pooling.

Types of pooling: Mean, Max, Sum

**Step 6 : Full Connection**

In this part, everything that we trained throughout the section will be merged together. By learning this, you will get to determine a fuller picture of how Convolutional Neural Networks operate and thus the way the "neurons" that are finally produced learn the classification of images.

**Step 7 : Summary**

In the end, it'll wrap everything up and provides a fast recap of the concept covered within the training.

**Step 8 : SoftMax & Cross-Entropy**

Optimization Functions for model file. To calculate final accuracy and losses.

**IV. RESULTS AND DISCUSSION**

Fig 2(a) and fig 2(b) represents the GUI and login window respectively.

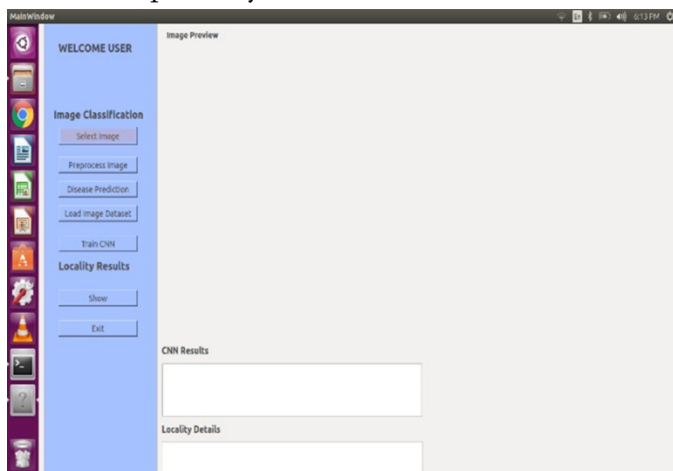


Fig 2(a). GUI

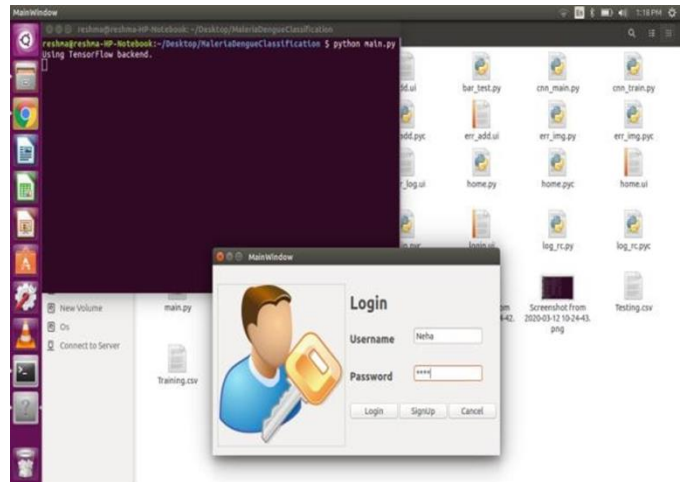


Fig 2(b). Log-In window

After successful authentication for operating the application, the user can input the data (i.e. images of blood cell dataset) to be processed. Then the input images are pre-processed in which the original image is converted into grayscale image, canny edge image and bilateral image. As shown figure 3(a) represents malaria blood cell image dataset which is pre-processed and converted into grayscale image, canny edge image and bilateral image. Similarly figure 3(b) represents dengue blood cell image dataset which is pre-processed and converted into grayscale image, canny edge image and bilateral image.

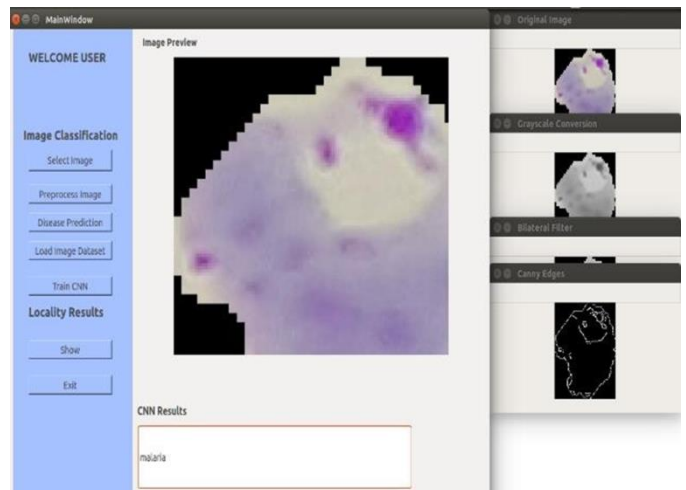


Fig 3(a). Malaria disease Prediction.

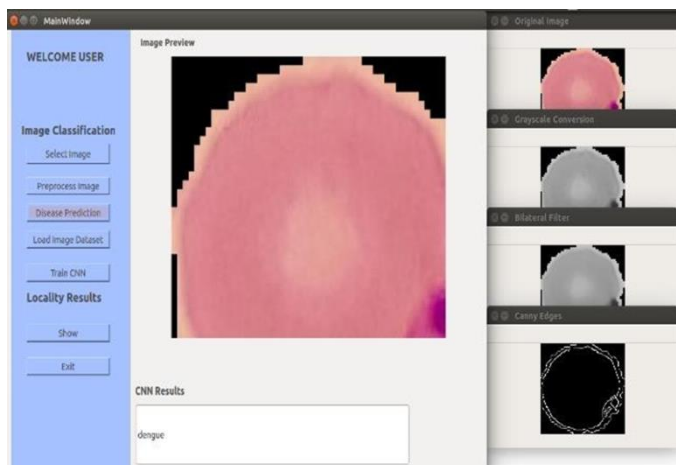


Fig 3(b). Dengue disease Prediction

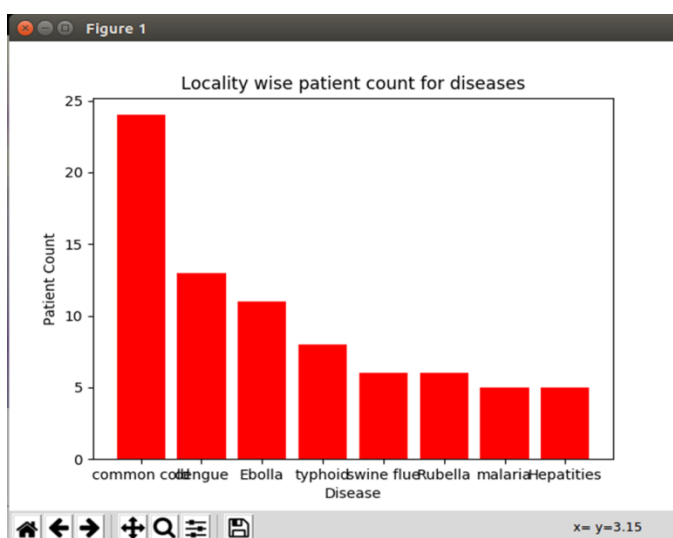


Fig 4. Graph of diseases as per locality.

Figure 4 represents the diseases and patient count for those diseases as per the locality in graphical form. The graph shows patient count for different diseases including malaria and dengue as per the locality.

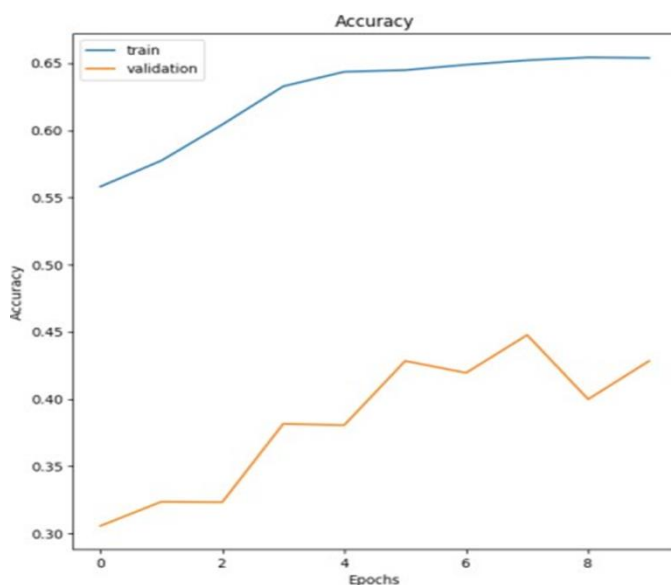


Fig 5(a). Accuracy Graph

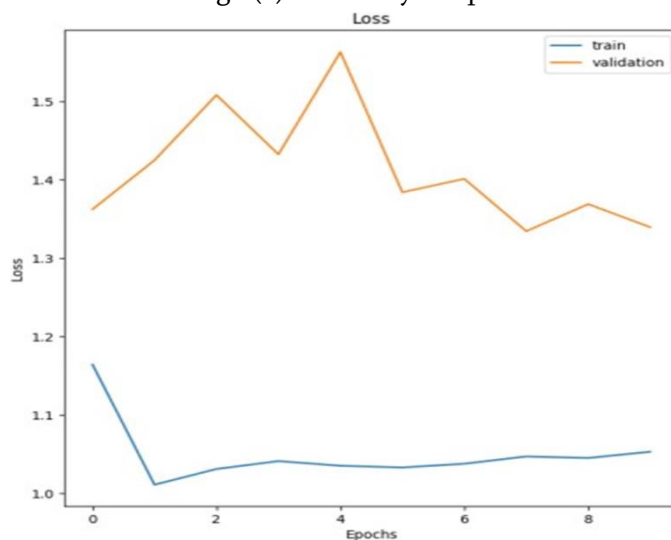


Fig 5(b). Loss graph.

Figure 5(a) and Figure 5(b) represents the accuracy and loss respectively in graphical form. In fig 5(a), the accuracy increases as the epochs increase. In fig 5(b), loss decreases as epochs increases.

## V. FUTURE SCOPE

For future work, in addition to input just as images of blood cell dataset of malaria or dengue, we could also accept textual data as input consisting of symptoms and predict the disease based on symptoms algorithm other than malaria and dengue as well. Further it would predict the diseases and count of patients as per

locality using textual input data. Also, instead of just predicting results for malaria and dengue dataset we can additionally can also predict results of normal dataset.

## VI. CONCLUSION

A robust and novel method by using machine learning for diagnoses malaria and dengue has been implemented during this paper. By using this method, we obtain the less than 60 seconds time to offer diagnosis as compared to other clinical laboratories. The prediction algorithm rule is design to predict the area in danger zone of particular disease by considering the locality from the database to calculate the results. The results need to be the same as the Python output, also as keeping to a suitable processing speed and duration. The research will focus on the benefits it can provide for the successful diagnosis of malaria, dengue and therefore the supportive treatment. The system prediction is extremely important within the awareness about the viral disease spreading within the locality as people get alerted by the system about any particular disease in order that they take precautions about that.

## VII. REFERENCES

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