WJARR

World Journal of Advanced Research and Reviews

World Journal Series INDIA

(REVIEW ARTICLE)

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Malaria disease detection system based on convolutional neural network (CNN)

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Abstract

Traditionally to diagnose malaria and compute the parasitemia, a microscope is being used, which involves the use of thick and thin blood smears. However, the efficiency in examining the blood smear depends on the expertise of the laboratory technician in classifying the blood smear using the natural eye, through observation on the microscope as this may produce inaccurate reports due to human errors and offer less classification accuracy for novice laboratory technicians with less experience. In order to carry out a highly, accurate diagnosis of malaria. This paper presents a mobile malaria disease detection system based on Convolutional Neural Network (CNN), a class of Deep Learning (DL) algorithm with end-to-end feature extraction and classification. It is highly scalable and offers superior results in image classification problems, this would be used in training a classification model and deploying the model in a Mobile App. The Mobile App would then be used to diagnose malaria by using the device camera to take photo of patient blood smears for the model to classify, and give result output. Structured System Analysis and Design Methodology (SSADM) was adopted in the design of the research. The Malaria diagnosis system was developed using the JAVA Mobile Edition (ME) programming language and Python programming language to train the model and deployed in the developed software. The developed software meets the objectives of the system.

Keyword: Malaria Disease Detection; Convolutional Neural Network; Machine Learning; Deep Learning

1. Introduction

Malaria is a parasitic illness caused by female anopheles' mosquitoes carrying the plasmodium parasite. In severe instances, red blood cells infected with the plasmodium parasite can cause symptoms such as headaches, malaise, seizures, and coma. Urgent and reliable diagnosis and early treatment of malaria is among the most effective ways of fighting the disease, together with better treatments and mosquito control (Mahdieh et al., 2018).

The assessment of micro blood smear images is still the standard method for diagnosing malaria. It has the ability to identify parasitic organism species, measure parasite intensity, and evaluate the efficacy of anti-malarial treatment, among other things. Regrettably, due to the high costs of training professionals in our traditional institutions, malaria-affected areas frequently lack qualified personnel who can conduct high-quality microscopy examinations (Hang et al., 2020).

Diagnosis of malaria can be difficult, where malaria is not endemic anymore, health-care providers may not be familiar with the disease. Clinicians while examining a malaria patient tend to forget to consider malaria among a potential disease and hence don't suggest the necessary diagnostic tests. Detecting parasites while examining blood smears under the microscope requires experience, which the laboratorians may lack and thus fail to detect (Mohd et al., 2020).

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In some malaria-endemic areas, a large section of the population is infected by the parasites but are still not ill or sick. Such carriers have the malaria infection but they have developed just enough immunity to not get the malaria illness or to show any symptoms in their system. In that case, finding malaria parasites in an ill person doesn't necessarily mean that malaria is the root cause of the person's illness or the parasites are solely responsible for the illness. The proposed system would sense the presence of malaria parasites on a regular blood-smeared slide. A phone camera can be attached to the microscope's ocular to take the blood smear photographs and then analyze it. Traditional malaria detection approaches are very time consuming, may produce inaccurate reports due to human errors, and are laborious for extensive diagnoses. Based on the weaknesses of the state-of-the-art solution, a Deep learning technique is being proposed (Faza et al., 2021).

Deep learning techniques are now generally used for image classification and medical image analysis. It has been a proven method which increases the performance in any field. A Convolutional Neural Network (CNN), a type of deep neural networks, is essentially considered for research in the computer vision field. The deep architecture of CNN is its main power. The convolutional layer in the CNN works as an automatic feature extract-tor that extracts hidden and important features. Extracted features are passed to a fully connected neural network which performs classification images by maximizing the probability scores. In this research, a mobile based classification system, for classifying red blood cell smears, for either being infected or not, of plasmodium parasite is proposed using Convolutional Neural Network (Çinar et al., 2020).

2. Literature survey

2.1. Detection of Malarial Parasites in Blood using Image Processing

One of the most infectious and a highly transmissible disease caused by a blood parasite which belongs to genre of Plasmodium is Malaria. Considering the traditional and the general microscopy method, which is "The Gold Standard" for malaria detection has been proven to be inconsistent, because the process requires significant amount of time and the results are difficult to reproduce as and when required. Malaria is causing a serious global health issue, and the appraised process is of high significance. The system developed here represents a model that uses image processing techniques and algorithms that are, definite, rapid and cost-effective detection of malaria by training and testing over the acquired stained thin blood smear images. Datasets consisting of images of affected and non-affected erythrocytes are collected, preprocessed, closely connected features are extracted from the acquired images and finally, it is confirmed whether the sample image is infected or not based on the features that are extracted from them. A set of characteristics depending on the features are suggested, and the performance from the created database of the features on the erythrocyte (Neha et al., 2019).

2.2. Detection of Malaria Parasites in Thick Blood Smear

The researchers proposed a clinical diagnosis of malaria as one of the traditional malaria detection methods. The researchers state that, diagnosis is clinically done by observing the visible physical symptoms and characteristics of patient's body. Medics try to identify disease though early symptoms, such as fever, headache, diarrhea, cold, chills, myalgia, abdominal pain, and vomiting. The number of symptoms that experts need to consider in clinical diagnosis is leading to the difficulty for accurate identification of the disease, because the symptoms of the disease are likely still too general to determine whether that the patient has malaria or not. The diagnosis of malaria using PBS (Peripheral Blood Smear) is based on blood smear. The presence of malaria parasites in blood smears were observed using microscope. The researchers observe that the blood smear can be thick and thin. The thick blood smear is used to detect the presence of plasmodium parasites, whereas the thin blood preparation is used to detect the type and phase of plasmodium. The results of sensitivity and specificity depended on the technique used, the reagent, and the expertise of medical personnel. The required time to do the diagnosis is about 30-60 minutes (Faza et al., 2021).

2.3. Malaria Cell Image Classification Using Deep Learning

Malaria is a disease that has to be detected promptly for on time treatment of the patient and for preventing it from spreading in the community via mosquitoes. Malaria should be treated as a medical emergency and not just a regular illness, the researchers proposed the use of machine learning (ML) techniques on the microscopic images of red blood smears using features that demand expertise in analyzing textural, morphological and positional variations of the region of interest (ROI). They used Convolutional Neural Networks (CNN) which is a sub-class of deep learning (DL) models. It is highly scalable, superior and gives better results with end-to-end feature extraction and classification. It therefore, serve as an effective diagnostic aid in automated malaria detection. In the research, the researchers evaluate the performance of pre-trained CNN based Deep Learning models as feature extractors towards classifying parasitized and uninfected cells to aid in improved disease screening. From the underlying data, the researchers determine the optimal

model layers for feature extraction of the statistical validation of the results and demonstrates the use of pre-trained CNNs as a promising tool for optimal feature extraction (Mohd et al., 2020).

2.4. Malaria Parasite Detection and Cell Counting for Human and Mouse Using Thin Blood Smear Microscopy

Accurate parasite identification is essential for diagnosing and treating malaria correctly. Parasite counts are used for monitoring treatment effect. Despite the remarkable progress that has been made to reduce global malaria mortality by over 29% in the past years, malaria is still a serious global health problem. Inadequate diagnostics is one of the major obstacles in fighting the disease. The researchers proposed an automated system for malaria diagnosis, that can help to make malaria screening faster and more reliable. They presented an automated system to detect and segment red blood cells (RBCs) and identify infected cells in Wright–Giemsa-stained thin blood smears. Specifically, using image analysis and machine learning techniques, they process digital images of thin blood smears to determine the parasitemia in each smear. using a cell extraction method to segment RBCs, in particular overlapping cells. they show that a combination of RGB color and texture features outperforms other features. They evaluate our method on microscopic blood smear images from human and mouse and show that it outperforms other techniques. For human cells, they measure an absolute error of 1.18% between the true and the automatic parasite counts. For mouse cells, their automatic counts correlate well with expert and flow cytometry counts, which also makes their system the first one to work for both human and mouse (Poostchi et al., 2018).

2.5. Automated Identification and Classification of Malarial Parasites in Thin Blood Smear Images

Malaria is a dreadful disease in the hematological field causing millions of deaths. Fast diagnosis and acute treatment of malaria is important to reduce the death rate. Hence the rapid diagnosing and proper medication is the intense need of the era. Malaria analysis is based on microscopic examination of blood films. In the research, image processing techniques are used for detection of malaria from microscopic images of Giemsa stained thin blood smear. Here, blood smear images are analyzed based on two methods. First, by extracting Scale-invariant Feature Transform (SIFT) features from preprocessed images and lead to the classifier for recognition. A comparative analysis of SVM (Support Vector Machine) and ANN (Artificial Neural Network) was carried out for recognition of extracted SIFT features. Second method comprises of leading the image directly without any preprocessing to CNN based network. SIFT based feature extraction method produces recognition efficiency of 94% with SVM and 96% efficiency with ANN. CNN based feature extraction method produces recognition efficiency of 98% (Soumya et al., 2018).

2.6. Classification of Malaria Cell Images with Deep Learning Architectures

Malaria is a contagious disease caused by the infection of erythrocytes by Plasmodium parasites, which are transmitted to human by parasitic female anopheles' mosquitoes during feeding. Malaria is a type of infection that can be fatal if left untreated. It is very important to classify malaria virus images quickly and accurately using computer-aided systems. Because there are not enough personnel in each health unit to perform this procedure, traditional methods are both time consuming and open to errors. Once malaria images have been classified, it will be easier to diagnose malaria virus related diseases. Multiple methods have been developed to process large amounts of data. In particular, deep learning methods are frequently used for classification. In the research, Convolutional Neural Networks (CNN) have been used to classify malaria images as healthy and parasited. Then, medium filter and gauss filter were applied to the original dataset. When classifying malaria data, the highest accuracy rate was achieved in the DenseNet201 architecture with gaussian filtered data of 97.83%. It was observed that the result obtained with the preprocessed data are higher. The application is implemented in the Matlab environment and works independently of the size of the images in the data set (Çinar et al., 2020).

2.7. Classification of White Blood Cells by Deep Learning Methods for Diagnosing Disease

White blood cells, also known as Leukocytes, are a group of cells that protect the body against infections, unlike the red blood cells, it's an important part of the immune system. The classification of white blood cells is widely used to diagnose various diseases, such as AIDS, leukemia, myeloma and anemia. However, the conventional methods to classify white blood cells are time consuming and prone to errors. In the research, one of the most popular neural networks, Convolutional Neural Network (CNN) was selected to differentiate between different types of white blood cells, namely, eosinophil, lymphocyte, monocyte and neutrophil. The CNN was coupled with Alexnet, Resnet50, Densenet201 and GoogleNet in turn, and trained with the Kaggle Dataset. Then, Gaussian and median filters were applied separately to the images in the database. The new images were classified again by the CNN with each of the four networks. The results obtained after applying the two filters to the images were better than the results obtained with the original data. The research results make it easier to diagnose blood related diseases (Yildirim et al., 2019).

2.8. Unsupervised Identification of Malaria Parasites Using Computer Vision

Malaria in human is a serious and fatal tropical disease. The disease results from Anopheles mosquitoes that are infected by Plasmodium species. The clinical diagnosis of malaria based on the history, symptoms and clinical findings must always be confirmed by laboratory diagnosis. Laboratory diagnosis of malaria involves identification of malaria parasite or its antigen/products in the blood of the patient. Manual diagnosis of malaria parasite by the pathologists has proven to become cumbersome. Therefore, there is a need of automatic, efficient and accurate identification of malaria parasite. In the research, the researchers proposed a computer vision-based approach to identify the malaria parasite from light microscopy images. This research deals with the challenges involved in the automatic detection of malaria parasite tissues. The proposed method was based on the pixel-based approach. K-means clustering was used (unsupervised approach) for the segmentation to identify malaria parasite tissues (Khan et al., 2014).

2.9. Automated Status Identification of Microscopic Images Obtained from Malaria Thin Blood Smears Using Bayes Decision

In the control of malaria, diagnosing its symptoms, has been the first step to control the spread of the infectious disease, which can be significantly optimized with a Computer Aided Diagnosis system. The researchers proposed to develop a novel image processing algorithm to reliably detect the presence of malaria parasites from Plasmodium falciparum species in the smears of Giemsa-stained peripheral blood sample.

The proposed system was built using malaria samples that were specifically prepared by Eijkman Institute for Molecular Biology. Digital microphotographs were acquired using a digital camera connected to a light microscope. Global thresholding and connected component extraction were implemented to identify blood cell components. Two stage classification using separate set of features were built based on Bayes Decision Theory. Infected erythrocytes were identified with sensitivity of 92.59%, specificity of 99.65%, and PPV of 67.56%. The system provided an F_1 measure of 0.78 (Anggraini et al., 2011).

2.10. Image Analysis and Machine Learning for Detecting Malaria

As Malaria remains a major burden on global health, with roughly 200 million cases worldwide and more than 400,000 deaths per year. Besides biomedical research and political efforts, modern information technology is playing a key role in many attempts at fighting the disease. One of the barriers toward a successful mortality reduction has been inadequate malaria diagnosis in particular. To improve diagnosis, image analysis software and machine learning methods have been used to quantify parasitemia in microscopic blood slides. This article gives an overview of these techniques and discusses the current developments in image analysis and machine learning for microscopic malaria diagnosis. The researchers organize the different approaches according to the techniques used for imaging, image preprocessing, parasite detection and cell segmentation, feature computation, and automatic cell classification. Also, the researchers discussed the latest developments in sections devoted to deep learning and smartphone technology for future malaria diagnosis (Poostchi et al., 2018).

2.11. Automatic Detection of Malarial Parasite Using Microscopic Blood Images

Machine learning, especially deep learning based malarial parasite analysis and recognition has opened a new area for early malaria detection that showed potential to overcome the drawbacks of manual strategies. The researchers analyze, categorize and address the recent developments of machine assisted malarial parasite recognition using machine learning approach based on microscopic images of peripheral blood smears. Although, malaria cell segmentation and morphological analysis is a challenging problem due to both the complex cell nature uncertainty in microscopic videos. To improve the performance of malaria parasite segmentation and classification, many researchers have presented camera-based approach. The researchers intend to bring the current state of art, future directions and summarize the open problems. The literature was reviewed in an explicit segmentation and machine learning framework, the components of which are preprocessing, feature extraction and selection, classification, and evaluation. The researchers proposed that the accuracy can be improved by using hyper-spectral imaging and adding the expert knowledge through Neuro-fuzzy (Imran et al., 2012).

2.12. Malaria Parasite Detection from Peripheral Blood Smear Images Using Deep Belief Networks

The researchers proposed a novel method to identify the presence of malaria parasites in human peripheral blood smear images using a deep belief network (DBN). They introduce a trained model based on a DBN to classify 4100 peripheral blood smear images into the parasite or non-parasite class. The proposed DBN is pre-trained by stacking restricted Boltzmann machines using the contrastive divergence method for pre-training. To train the DBN, they extract features from the images and initialize the visible variables of the DBN. A concatenated feature of color and texture was used as a feature vector in the research. Finally, the DBN is discriminatively fine-tuned using a back propagation

algorithm that computes the probability of class labels. The optimum size of the DBN architecture used in the research was 484-600-600-600-600-2, in which the visible layer has 484 nodes and the output layer has two nodes with four hidden layers containing 600 hidden nodes in every layer. The proposed method has performed significantly better than the other state-of-the-art methods with an F-score of 89.66%, a sensitivity of 97.60%, and specificity of 95.92% (Bibin et al., 2017).

3. Methodology

The methodology adopted for the implementation of this study is Structured System Analysis and Design Methodology (SSADM). This methodology was selected because it allows the researcher to design the system by creating objects which are able to interact with each other and accomplish the required aim. Also, it allows the researcher to depict the system easily with the help of special diagrams which includes use case diagrams, activity diagrams, and class diagrams. The steps involved in this kind of methodology are requirements specification; Analysis; Design; Implementation (coding); Testing; Maintenance.

3.1. Neural Network

Neural network is a series of algorithms that endeavors to recognize underlying relationships in a set of data through a process that mimics the way the human brain operates. In this sense, neural networks refer to systems of neurons, either organic or artificial in nature. Neural networks can adapt to changing input; so, the network generates the best possible result without needing to redesign the output criteria. neural network works similarly to the human brain's neural network. A "neuron" in a neural network is a mathematical function that collects and classifies information according to a specific architecture. The network bears a strong resemblance to statistical methods such as curve fitting and regression analysis. A neural network contains layers of interconnected nodes. Each node is a perceptron and is similar to a multiple linear regression. The perceptron feeds the signal produced by a multiple linear regression into an activation function that may be nonlinear.

3.2. CNN Training Algorithm

Convolution is represented mathematically with an asterisk * sign. If we have an input image represented as X and a filter represented with f, then the expression would be:

$$Z = X * f$$

The algorithm for the training of an image dataset is given as thus;

Step 1: Load the input images in a variable (say X)
Step 2: Define (randomly initialize) a filter matrix. Images are convolved with the filter $Z_1 = X * f$
Step 3: Apply the Sigmoid activation function on the result

$$A = sigmoid(Z_1)$$

Step 4: Define (randomly initialize) weight and bias matrix. Apply linear transformation on the values

$$Z_2 = W^T.A + b$$

Step 5: Apply the Sigmoid function on the data. This will be the final output

$$O = sigmoid(Z_2)$$

The CNN model treats these values as parameters, which are randomly initialized and learned during the training process.

3.3. Proposed CNN Model Framework

CNN is a type of Neural Network Model which allows us to extract higher representations of an image content. Unlike the classical image recognition where images features are being defined manually, CNN takes the image's raw pixel data, trains the model, then extracts the features automatically for better classification, the proposed system CNN model is as shown in Figure 1.
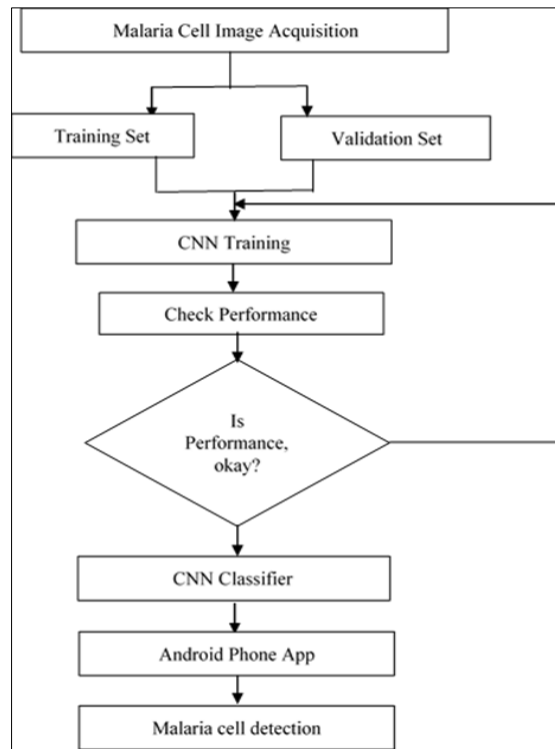
Figure 1 Framework of the Proposed System

3.4. Dataflow Diagram of the Existing System

A dataflow diagram (DFD) is a way of representing a flow of data through a process or a system. The DFD also provides information about the outputs and inputs of each entity and the process itself. The Yourdon and Coad dataflow diagram of the proposed system is depicted in Figure 2.
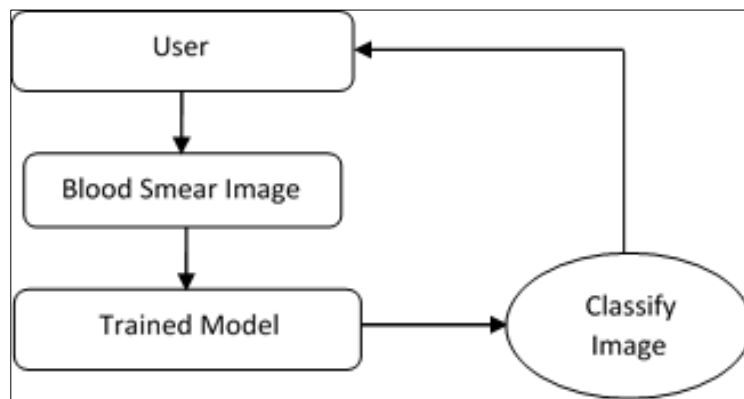

Figure 2 Dataflow Diagram of the Proposed System

3.5. System Flowchart

The program flowchart depicts the step-by-step sequence of instructions, workflow or process, showing the steps as boxes of various kinds, and their order by connecting them with arrows. The diagrammatic representation illustrates a solution model to the existing system indicating the start operation and series of activities that occurred before the termination of the system processes by the stop operation as shows Figure 3.
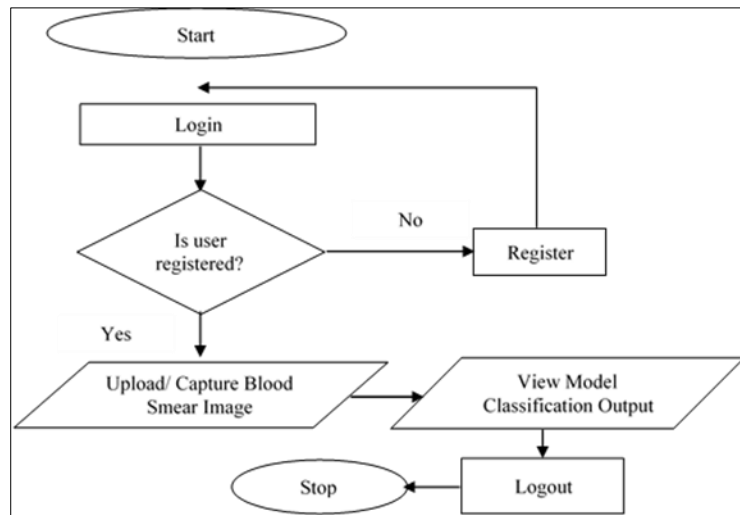
Figure 3 Program Flowchart of the Proposed System

3.6. High Level Model of the Proposed System

A data model is a conceptual representation of the data structures that are required by a database. The data structures include the data objects, the associations between data objects, and the rules which govern operations on the objects. As the name implies, the data model focuses on what data is required and how it should be organized rather than what operations will be performed on the data. To use a common analogy, the data model is equivalent to an architect's building plans. Hence the data model is the database structural plan of a system. Figure 4 is the high-level model of the proposed system.
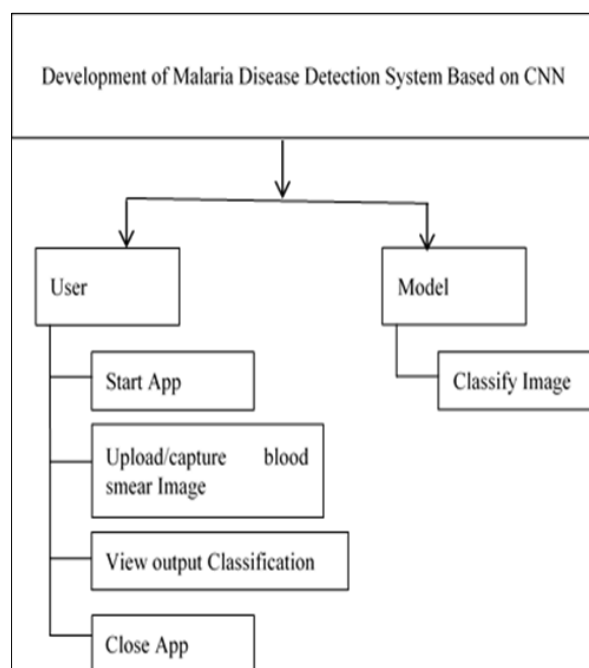

Figure 4 High Level Modeling of the Proposed System

3.7. Use Case Diagram

A use case diagram is a type of UML diagram that is used to graphically depict the interactions among elements of a system. With a use case diagram, the individual roles of a system are assigned use cases to show operations they can perform. In the proposed system, there is one (1) user role which is most times referred to as an actor. This actor is the user that will make use of the system. Figure 5 shows the use case diagram of the system.
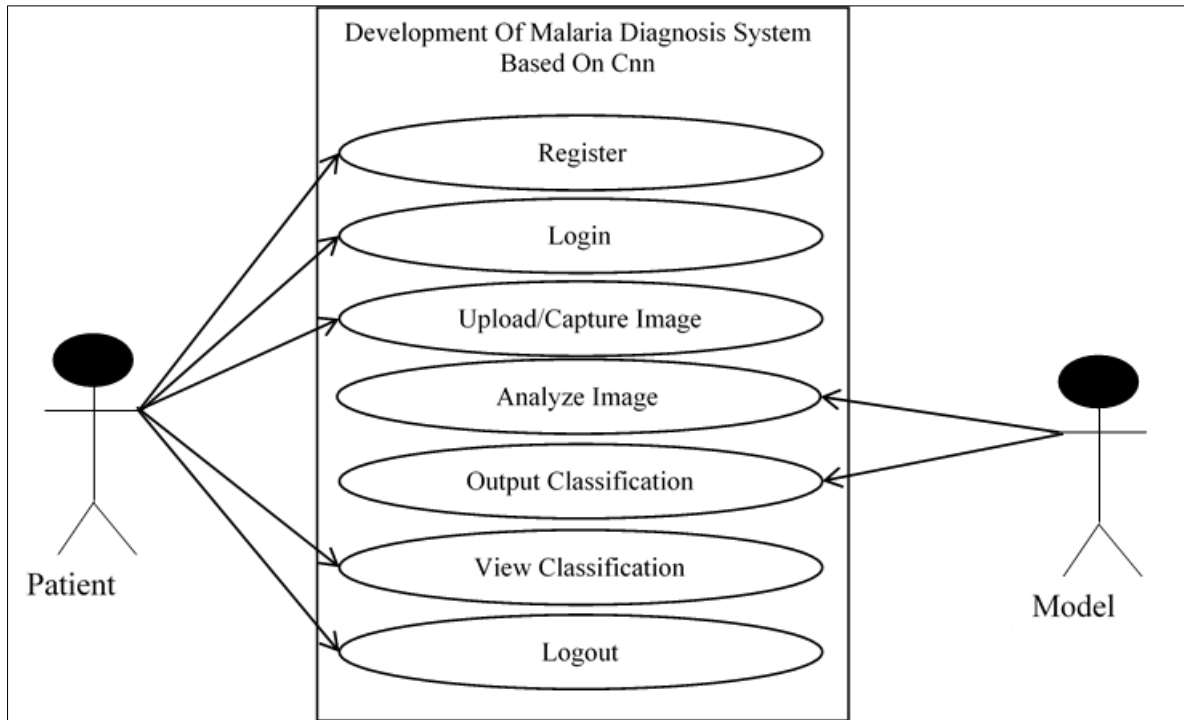
Figure 5 Use Case Diagram of the Proposed System

4. Results

4.1. System Implementation

The proposed framework was implemented using PANDAS, NUMPY, KARAS and TENSORFLOW library. The data for this study was extracted from https://www.kaggle.com/iarunava/cell-images-for-detecting-malaria created by Arunava and used to train the proposed model for Malaria Disease Detection. The model was experimented with CNN algorithm executed on Python version 3.8. All the program codes are implemented in Python programing language via Anaconda distribution (a suitable work environment where python codes can be managed and implemented easily). The distribution comes with enhanced interactive python editors such as Spyder and Jupyter, as well as over hundreds of pre-installed machine learning packages for building high-performance machine learning algorithms.

The TensorFlow and Keras deep learning framework was employed because it is an open-source python software with friendly libraries for image computation that makes machine learning and deep learning implementation easier and faster. It is used in this paper to train CNN model and the CNN model is being deployed on an android application which is been developed on android studio version 4.2.2. The training of the model was carried out on window operating system environment deployed on HP Branded computer system (Laptop), Intel(R) Core (TM) i5-2450M CPU @ 2.50GHz 2.50 GHz processor speed, with 8GB of RAM. All the necessary libraries were installed on anaconda command prompt where the training of the model development is being carried out.

4.1.1. Dataset Description

The dataset used in this research work consists of 27600 cell images, among which 13800 are parasitized while the other 13800 are unparasitized. Figure 6 shows the dataset blood smear images.

4.1.2. Sample Dataset

The dataset was read into python working environment using PANDAS, NUMPY, KARAS and TENSORFLOW library.

4.1.3. Preprocessing of Data

The data was fine-tuned to remove all the outliers from the dataset to get a clean dataset for the experimentation of this research work, the steps taken to fine-tune the dataset includes the identification and handling of the missing values, splitting the dataset into training and test data and feature scaling.
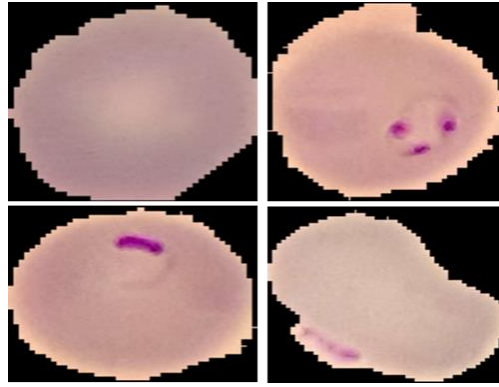
Figure 6 Dataset Blood Smear Images

4.1.4. Splitting of Dataset into Training and Test Set

The dataset was split into training and testing set as 70% of the entire data was apportioned for training and 30% for testing. The number of instances for training data and test data set is as shown in Table 1

Table 1 Data Split

Dataset	# image
Training	19320
Test	8280
Total	27600

4.1.5. Classification

After obtaining clean dataset, the training data and it corresponding labels were fed into the classification model. This research employed CNN for the classification task. CNN is a type of Neural Network model which allows the extraction of higher representations of image content. Unlike the classical image recognition where image features are defined manually, CNN takes the image's raw pixel data, trains the model, then extracts the features automatically for better classification. This is implemented on Keras framework built on tensorflow (backend) used to design the proposed model framework. The parameters for the implementation are:

- Learning rate = 0.1
- Activation function = Relu
- Batch size = 32
- Epoch = 50

All these parameters were passed to achieve an accuracy of 97%.

4.1.6. Model Prediction and Performance Metrics

The trained model, fine-tuned and evaluated on test data, gives the following metrics (tables 2 and 3) and proves to have better accuracy than other systems reviewed in the research.

Table 2 Model Prediction Accuracy

Model	Accuracy
Development of malaria diagnosis system based on CNN	97.00%

Table 3 Comparing Model Performances

Model Description	Accuracy	Sources
Malaria Disease Detection System Based On Convolutional Neural Network (CNN)	97.00%	The Proposed Model
Automated image processing method for the diagnosis and classification of malaria on thin blood smears	85.00%	Nicholas E. R. et al., (2006)
Feature extraction and classification for detection malaria parasites in thin blood smear	90.8%	Hanung A. N. et. al. (2015)

4.1.7. CNN Learning Curves

This subsection discusses the outcome of the CNN learning process during training. Figure 7 shows the learning curve. This was carried out for each category or parameter over 50 epochs.
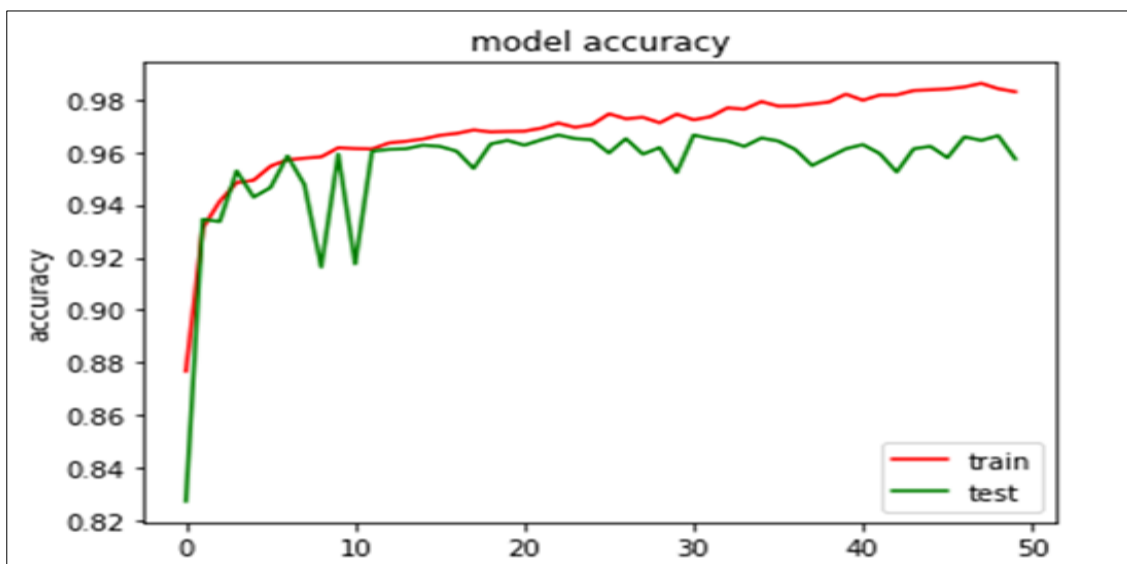

Figure 7 Model Training Accuracy

4.1.8. Evaluation and Results

The performance metric applied include accuracy, precision, recall and f1-score whose parameters were obtained from confusion matrix computation. The four components of the confusion metrics are as follows:

- True Positive (TP): Intruder's activity that is successfully classified as attacks.
- True Negative (TN): Classify the normal activities are as normal.
- False-Positive (FP): Wrongly classify the normal activity as an attack.
- False Negative (FN): Classify the intrusive activities as normal activity.

The expression of the metrics from the confusion matrix is described as an equation from (1) to (4).

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots(1)$$

$$\text{Precision} = \frac{TP}{TP + FP} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (2)$$

$$\text{Recall} = \frac{TP}{TP + FN} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (3)$$

$$\text{F1-score} = 2 * \frac{precision * recall}{precision + Recall} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (4)$$

Table 4 Confusion Matrix

Total Number of Predication		Predicted Class	
		0	**1**
Actual Class	0	*TN*	*FP*
	1	*FN*	*TP*

A confusion matrix in Table 4 summarizes the prediction results on a classification model of a malaria dataset. The number of correct and incorrect predictions is summarized with count values and broken down by each class as shown in Figure.
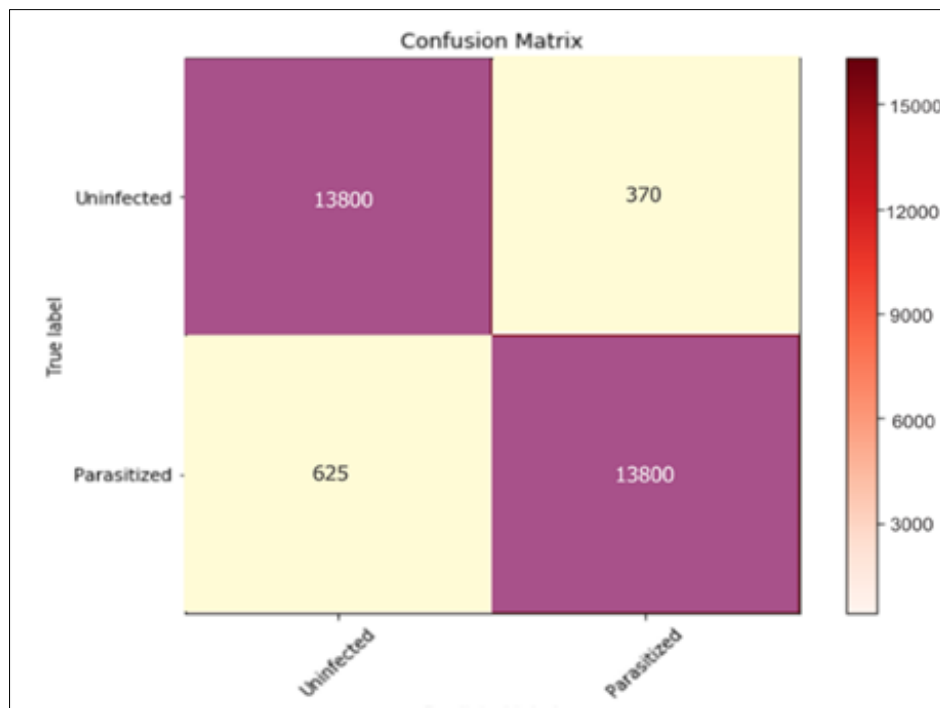

Figure 8 Confusion Matrix Prediction

5. Discussions

This section summarizes the results obtained through the model presented in the aforementioned sections. The data used for this research was fine-tuned to remove all the outliers from the dataset to get a clean dataset for the experimentation of this research work. After obtaining clean dataset, the training data and it corresponding labels were fed into the classification model. The model achieved the accuracy of 0.97 (97.00%), precision of 0.96 (96.00%) recall 0.94 (94.00%) and F1-score of 0.97 (97.00%).

5.1. Program Main Menu

The program main menu depicts the various links a user will encounter upon launching the system that points to other areas of interest. Figure 9, 10 and 11 show the program main menu for each role in the system.
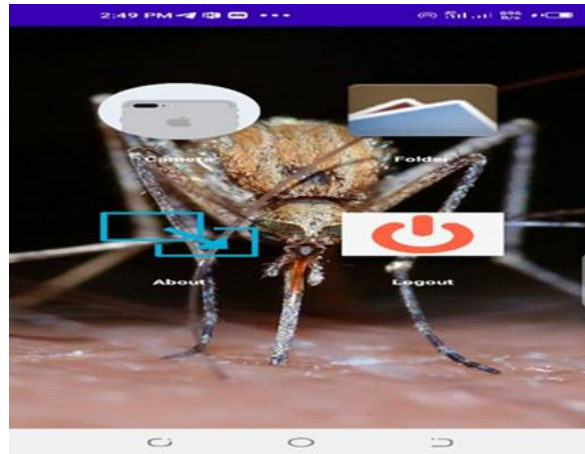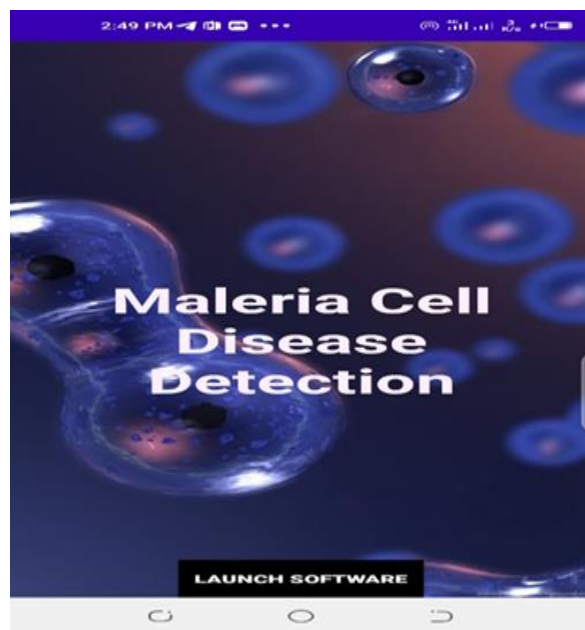
Figure 9 Program Main Menu
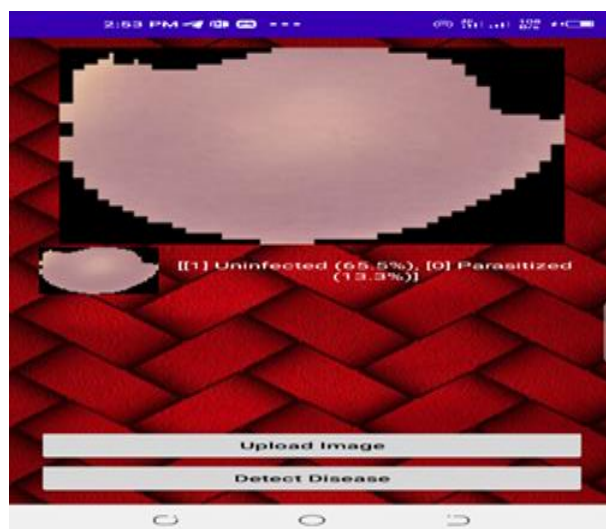

Figure 10 Program Splash Screen

Figure 11 Program Module Displaying Cell Classification

6. Conclusion

The prospects of automating malaria diagnosis with its obvious advantages have attracted many researchers, especially in the last decade. Hundreds of millions of blood films are examined every year for malaria, which involves manual counting of parasites and infected red blood cells by a trained microscopist. Deep learning which is a subset of artificial intelligence have provided many algorithms for the classification of various Based on the outcome during the testing phase of the developed software, the system aids in increasing the convenience of diagnosing malaria disease from blood smears using a mobile device. Also, it will aid in curtailing the cost of paying for a microscopic diagnosis by patients.

Recommendation

Based on the research carried out, it is recommended for each and every individual wanting to further research in this regard and to all medical laboratory scientist, to lessen the vigorous and time-consuming task of getting the diagnosis of a diseased malaria blood cell.

Future work

This research work is limited to the detection of malaria cell disease on a blood cell only. Further research for improvement and enhancement can be made whereby a system that will not just carry out malaria cell detection but also be able to save the diagnosis as an image on the user's device.

Compliance with ethical standards

Disclosure of conflict of interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

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