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# Malaria Medical Imaging using Deep Learning

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***ABSTRACT***
*Malaria is a blood disease caused by parasites transmitted through the bite of the female Anopheles mosquito. Generally, thick and thin blood smears are examined to diagnose disease and compute parasitemia( the quantitative content of parasites in the blood).However, the accuracy depends on the quality of blood smear and expertise in classifying and counting parasitized and uninfected cells. It's a difficult task for large scale diagnoses which often ends in poor quality.Computer-aided diagnosis and image analysis of these microscopic images of the smears demand expertise in morphological,textural and positional variations of regions of interest for analyzing.Convolution Neural Networks, a class of deep learning models ensures superior results which have better end-to-end feature extraction and classification. Malaria screening using deep learning could serve as an efficient diagnostic aid. A deep learning model is developed to extractfeatures which helps in improved disease screening.*

***KEYWORDS:*** *CNN, Deep Learning.*

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## I. INTRODUCTION

Malaria tends to remain one of the deadly diseases and has a major burden on global human health. It is caused by parasites of the Plasmodium which are carried by the bites of Anopheles mosquitoes. Around 200 million cases and 400,000 deaths have been recorded every year on an average. It is one of the leading causes of neuro-disability in children in Africa. Not only medical research and political efforts but also modern information technology is playing a major role in an attempt to fight the deadly disease. Millions of blood images are examined every year for malaria which involves the laborious task of manual counting of parasites. The accuracy of the parasite counts matters as they are important for measuring drug resistance,drug-effective

One of the challenges has been improper and inadequate malaria diagnosis. Diagnosis can be improved by various image analysis software and machine learning methods. This sober analysis has encouraged the diagnosis of malaria automatically. Thus, the parasite content in the blood (parasitaemia) can be analyzed in a much better way. If the number of infected and uninfected cells is identified, then the computation of parasitaemia is just a mathematical equation. Medical image analysis, medical experts are usually only interested in certain organs visible in the image, which is chiefly why image segmentation is required in almost all medical image related applications at every layer.

## II. Literature review

Bibin D, Nair MS,Punitha P [1] Introduces 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, we extract features from the images and initialize the visible variables of the DBN. A concatenated feature of color and texture is used as a feature vector in this paper. Finally, the DBN is discriminatively fine-tuned using a backpropagation algorithm that computes the probability of class labels.

The optimum size of the DBN architecture used in this paper is 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 The proposed method 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%. This paper is the first application of a DBN for malaria parasite detection in human peripheral blood smear images.

Das DK, Ghosh M, Pal M, Maiti AK, Chakraborty[2] Introduces the development of computer assisted malaria parasite characterization and classification using machine learning approach based on light microscopic images of peripheral blood smears. In doing this, microscopic image acquisition from stained slides, illumination correction and noise reduction, erythrocyte segmentation, feature extraction, feature selection and finally classification of different stages of malaria (Plasmodium vivax and Plasmodium falciparum) have been investigated. The erythrocytes are segmented using marker-controlled watershed transformation and subsequently total ninety-six features describing shape-size and texture of erythrocytes are extracted in respect to the parasitemia infected versus non-infected cells.

Ninety-four features are found to be statistically significant in discriminating against six classes. Here a feature selection-cum-classification scheme has been devised by combining F-statistic, statistical learning techniques i.eBayesian learning and support vector machine (SVM) in order to provide the higher classification accuracy using the best set of discriminating features. Results show that Bayesian approach provides the highest accuracy i.e84% for malaria classification by selecting 19 most significant features while SVM provides highest accuracy i.e.83.5% with 9 most significant features. Finally, the performance of these two classifiers under the feature selection framework has been compared toward malaria parasite classification.

Gopakumar GP, Swetha M, Sai Siva G, Sai Subrahmanyam GRK[3] they studied automatic identification of malaria infected cells using deep learning methods. We used whole slide images of thin blood stains to compile a dataset of malaria-infected red blood cells and non-infected cells, as labeled by a group of four pathologists. We evaluated three types of well-known convolutional neural networks, including the LeNet, AlexNet and GoogLeNet. Simulation results showed that all these deep convolutional neural networks achieved classification accuracies of over 95%, higher than the accuracy of about 92% attainable by using the support vector machine method. Moreover, the deep learning methods have the advantage of being able to automatically learn the features from the input data, thereby requiring minimal inputs from human experts for automated malaria diagnosis.

Liang Z, Powell A, Ersoy I, Poostchi M, Silamut K, Palaniappan K, Guo P, Hossain MA, Sameer A, Maude RJ, Huang JX, Jaeger S, Thoma G[4] Malaria is a major global health threat. The standard way of diagnosing

malaria is by visually examining blood smears for parasite-infected red blood cells under the microscope by qualified technicians. This method is inefficient and the diagnosis depends on the experience and the knowledge of the person doing the examination. Automatic image recognition technologies based on machine learning have been applied to malaria blood smears for diagnosis before. However, the practical performance has not been sufficient so far.This study proposes a new and robust machine learning model based on convolutional neural network (CNN) to automatically classify single cells in thin blood smears on standard microscope slides as either infected or uninfected. In a ten-fold cross-validation based on 27,578 single cell images, the average accuracy of our new 16-layer CNN model is 97.37%. A transfer learning model only achieves 91.99% on the same images. The CNN model shows superiority over the transfer learning model in all performance indicators such as sensitivity (96.99% vs 89.00%), specificity (97.75% vs 94.98%), precision (97.73% vs 95.12%), F1 score (97.36% vs 90.24%), and Matthews correlation coefficient (94.75% vs 85.25%). The architecture of a CNN will largely determine the final net performance after training. The basic mechanism of deep learning is to apply a multi-layer network to map the input space
by transforming it at the hidden nodes. Using a series of propagations transformations,the network tries to learn the optimal mapping of the input data through a process called back-propagation.

## III. PROPOSED SYSTEM

Comprehensively, our proposed framework mainly involves the following way
1. Image Pre-processing .
2. Splitting the data to train and test
3. Building the model Convolution Neural Network
4.Training the model

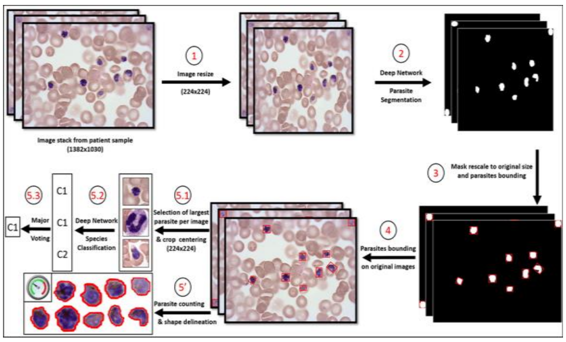


Fig: Malaria image categorization

### 3.1 Image Pre-processing

Image pre-processing is the term for operations on images at the lowest level of abstraction. These operations do not increase image information content but they decrease it if entropy is an information measure.

The aim of pre-processing is an improvement of the image data that suppresses undesired distortions or enhances some image features relevant for further processing and analysis tasks.

**3.2 Splitting the data to train and test**

The procedure involves taking a dataset and dividing it into two subsets. The first subset is used to fit the model and is referred to as the training dataset. The second subset is not used to train the model; instead, the input element of the dataset is provided to the model, then predictions are made and compared to the expected values. This second dataset is referred to as the test dataset.

- **Train Dataset**: Used to fit the machine learning model.
- **Test Dataset**: Used to evaluate the fit machine learning model.

**3.3 Building the model Convolution Neural**

Manual diagnosis of blood smears is an intensive manual process that requires expertise in classifying and counting parasitized and uninfected cells. This process may not scale well, especially in regions where the right expertise is hard to find.Some advancements have been made in leveraging state-of-the-art image processing and analysis techniques to extract hand-engineered features and build machine learning-based classification models. However, these models are not scalable with more data being available for training and given the fact that hand-engineered features take a lot of time.Deep learning models, or more specifically

convolutional neural networks (CNNs), have proven very effective in a wide variety of computer vision tasks.Convolution layers learn spatial hierarchical patterns from data, which are also translation-invariant, so they are able to learn different aspects of images. For example, the first convolution layer will learn small and local patterns, such as edges and corners, a second convolution layer will learn larger patterns based on the features from the first layers, and so on. This allows CNNs to automate feature engineering and learn effective features that generalize well on new data points. Pooling layers helps with dimension reduction.Thus, CNNs help with automated and scalable feature engineering. Also,plugging in dense layers at the end of the model enables us to perform tasks like image classification.

**3.4 Training the model**

To find the optimum and efficient model, different approaches were investigated. Among the series of experiments, feature extractions and classification using convolutional neural networks (CNNs) along with augmentation and without augmentation is discussed under General training procedure.To develop an efficient and highly accurate model for the detection of the malaria parasite from segmented cell images, a series of experiments involving both machine learning and deep learning techniques were performed.

## IV. RESULTS AND DISCUSSION:

**CNN:**

A Convolutional Neural Network (CNN) is a type of Deep Learning architecture commonly used for image classification and recognition tasks. It consists of multiple layers, including Convolutional layers, Pooling layers, and fully connected layers. The Convolutional layer applies filters to the input image to extract features, the Pooling layer downsamples the image to reduce computation, and the fully connected layer makes the final prediction. The network learns the optimal filters through backpropagation and gradient descent.

It is assumed that the reader knows the concept of Neural networks. When it comes to Machine Learning, Artificial Neural Network_ perform really well. Artificial Neural Networks are used in various classification tasks like image, audio, words. Different types of Neural Networks are used for different purposes, for example for predicting the sequence of words we use Recurrent Neural Networks more precisely an LSTM, similarly for image classification we use Convolution Neural networks. In this blog, we are going to build a basic building block for CNN. Before diving into the Convolution Neural Network, let us first revisit some concepts of Neural Network.

In a regular Neural Network there are three types of layers:

1.**Input Layers:** It's the layer in which we give input to our model. The number of neurons in this layer is equal to the total number of features in our data (number of pixels in the case of an image).

2**.Hidden Layer:** The input from the Input layer is then feed into the hidden layer. There can be many hidden layers depending upon our model and data size. Each hidden layer can have different numbers of neurons which are generally greater than the number of features. The output from each layer is computed by matrix multiplication of output of the previous layer with learnable weights of that layer and then by the addition of learnable biases followed by activation function which makes the network nonlinear.

3**.Output Layer:** The output from the hidden layer is then fed into a logistic function like sigmoid or softmax which converts the output of each class into the probability score of each class. The data is then fed into the model and output from each layer is obtained. This step is called feedforward, we then calculate the error using an error function, some common error functions are cross-entropy, square loss error, etc. After that, we backpropagate into the model by calculating the derivatives. This step is called Backpropagation which basically is used to minimize the loss.

**RESULT SCREENSHOTS:**

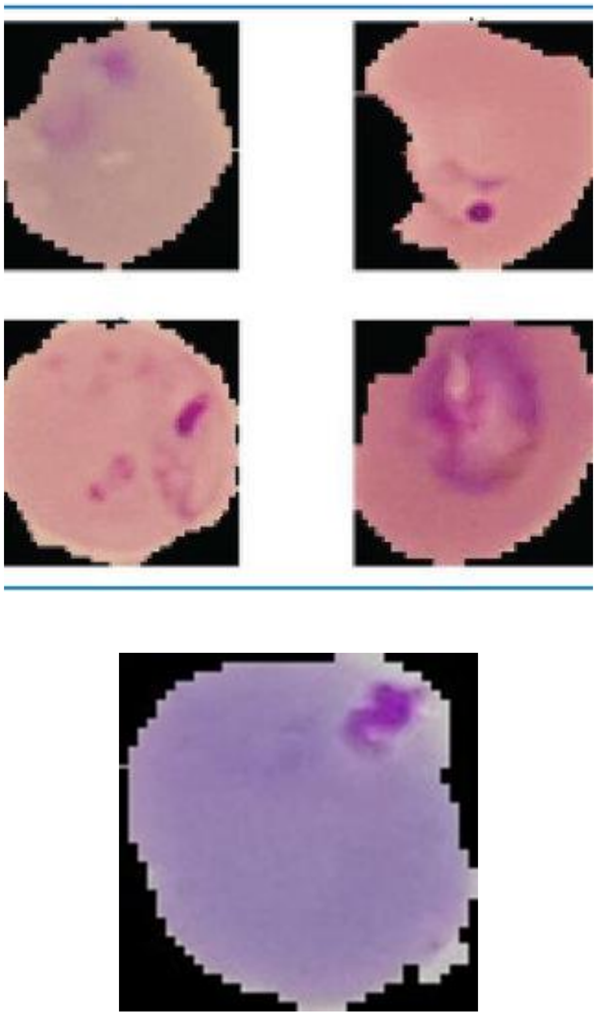

**Fig-1:**Parasitized Image

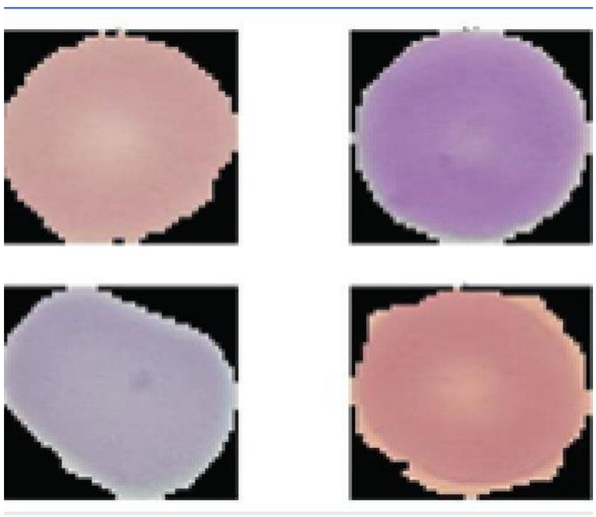

**Fig-2:** Unaffected Image


**Fig-3:**Testing an unaffected image


**Fig-4:**Result as Unaffected

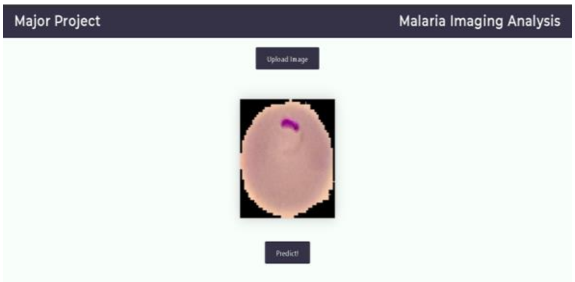


**Fig-5:**Testing a parasitised image


**Fig:6:** Result as parasitized

## CONCLUSION

To have more accurate results three stages are used: Image enhancement, segmentation, feature extraction stage. The CNN algorithm gives more accuracy (84.55%)

## FUTURE EFFECTS

This application is supportive for the identification of malaria for grown-up malaria pictures. It gives the paired organized outcome i.e.., whether the individual is influenced or not influenced. In future expansion to this application can be completed for kids. Which likewise needs some extra smoothing procedures.

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