**CHAPTER FIVE**

**SUMMARY AND CONCLUSION**

**5.1 Summary**

Malaria is the leading cause of morbidity and mortality in tropical and subtropical countries. WHO estimates the number of malaria deaths at 435,000 for 2018. Machine learning has great potential to lighten the burden of malaria in temperate regions around the world where mosquitoes thrive especially in remote sub-Saharan Africa. However, the accuracy of the manual method of malaria diagnosis using microscopy depends on the human expert. However, it is prone to some shortcomings which include time consumption and excessive workload for the pathologists. We propose an automated diagnostic system that can exclude the human expert from the process or serve as an aid for an expert to lower workload and improve accuracy. The ultimate goal of this work was to develop a system for detecting malaria using microscopic images of stained blood samples.

Thus in the process of this work, an accurate, speedy and affordable system of malaria detection using stained blood smear images was developed. The method is based on supervised machine learning using deep learning algorithms which involves training a convolutional neural network and using it to test for the presence of malaria parasites in blood smear images. Images of infected and non-infected blood samples were given to the convolutional neural network as training data and relevant features were extracted from them and eventually further classification can be made by the network based on the features extracted from the images. The classification entailed the detection of malaria parasites. The algorithm successfully trained on 1,000 images with a training and validation accuracy of 100.00% respectively and it was tested on the images of four blood samples that it had not seen before and further classified them as infected or uninfected with a 100% accuracy. The battle against the devastating burden of malaria will continue. Early and accurate diagnosis is one of the keystones in the fight against this. This project work can be described as a required component in the development of a tool that will bring a healthy and malaria-free world one step closer to reality.

**5.5 Conclusion**

The detection of Malaria parasites is done by pathologists manually using Microscopes. So, the chances of false detection due to human error is present, which in turn can result into fatal conditions. This work curbs the human error while detecting the presence of malaria parasites in the blood sample by using a convolutional neural network. The system is well trained in a robust manner and achieved a high percentage of accurate prediction and no false-positives as at this time. This goes to show that neural networks can learn how to process different staining and lighting variations if only enough training data are being presented to the network.

**5.4 Recommendations**

A convolutional neural network for detecting malarial parasites in images of blood samples is developed, and its capabilities and limitations are characterized. Although the neural network exhibits basic functionality and a high-level of accuracy on test images, further training is necessary in order to improve robustness to the point where it can be usefully applied to a wide variety of images and then deployed for commercial use in hospitals, clinics, etc. A number of areas of potential improvement were identified, and will provide guidance as development continues. The current system provides a useful framework which can be refined and extended in order to improve accuracy, tolerance of image noise, and further capabilities.

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**Appendix A:** Project Source Code

The Training Code:

%Load the input images for training from the datastore

*imagepath = fullfile('myImages');*

*imds = imageDatastore(imagepath, 'IncludeSubfolders',true,'LabelSource','FolderNames');*

%Split inputs into training and validation sets(70% and 30% respectively)

*[trainDS,valDS] = splitEachLabel(imds,0.7,0.3, 'randomized');*

%Specify the training parameters like learnrate, batchsize, e.t.c.

*opts = trainingOptions('sgdm', 'InitialLearnRate', 0.001,...*

*'ValidationData', valDS,...*

*'Plots','training-progress',...*

*'MiniBatchSize', 24,...*

*'ValidationPatience', 3, 'ExecutionEnvironment','cpu');*

%Train the network

*nnet = trainNetwork(trainDS, cnnmalaria, opts);*

The Implementation Code:

%%%

% Create the figure window. First, resize the window to have twice the

% width, and create two subplots.

*h = figure;*

*h.Position(3) = 2\*h.Position(3);*

*ax1 = subplot(1,2,1);*

*ax2 = subplot(1,2,2);*

%%%

% In the left subplot, display the image and classification together.

*load cnnmalaria1000;*

*im = imread('t1.jpg'); %Read the image*

* *imshow(im);*

*image(ax1,im)*

*im = imresize(im,[200,200]);*

*[label,score] = classify(nnet,im);*

*title(ax1,{'CNN prediction = ' char(label)});*

%%%

% Select the top two predictions by selecting the classes with the highest

% scores.

*[~,idx] = sort(score,'descend');*

*idx = idx(2:-1:1);*

*classes = nnet.Layers(end).Classes;*

*classNamesTop = string(classes(idx));*

*scoreTop = score(idx);*

%%%

% Display the top two predictions as a histogram.

*bar3(ax2,scoreTop)*

*xlim(ax2,[0 1])*

*title(ax2,'Prediction Probability')*

*xlabel(ax2,'Probability for the two classes')*

*yticklabels(ax2,classNamesTop)*

*ax2.YAxisLocation = 'right';*

**Appendix B:** User Guide

Step 1: Start the MATLAB application

Step 2: Place the images of the blood samples in the MATLAB workspace

Step 3: Launch the MATLAB script to check the images of the blood samples

Step 4: The convolutional neural network issues a prediction and plots a bar chart to show the estimated prediction probability.

Step 5: The user can choose to mail, print or save the resulting output.