

Malaria detection in red blood cells through feature extraction using CNN

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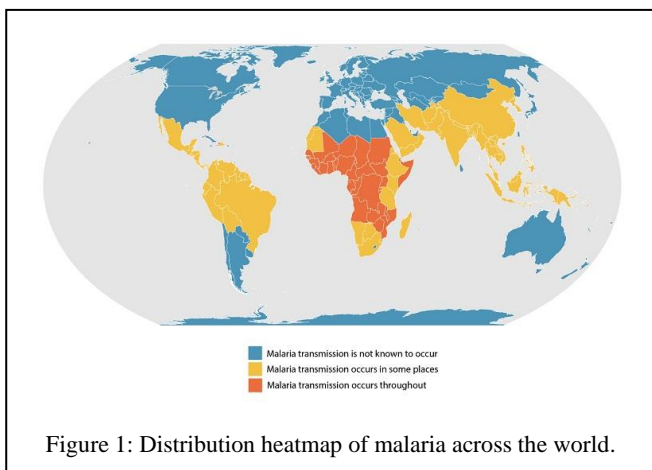
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Abstract – Traditionally diagnosis of malaria is done using manual diagnosis of blood smears in some regions. This, however is an intensive manual process that requires expertise in classifying and counting parasitized and uninfected cells. This process may not scale well, especially in regions where the right expertise is hard to find. Deep learning models, or more specifically convolutional neural networks (CNNs), have proven very effective in a wide variety of computer vision tasks. Furthermore, once trained and deployed, they are also highly scalable. This paper is an attempt at training an ideal CNN to enable automation of detecting the parasites in a red blood cell. The problem is approached as a binary classification problem and cross entropy loss is used as the loss function.

Keywords - Deep learning, Convolutional Neural Network, Classification, Malaria diagnosis.

I. INTRODUCTION

Malaria is a deadly, infectious, mosquito-borne disease caused by Plasmodium parasites that are transmitted by the bites of infected female Anopheles mosquitoes. Malaria is prevalent across the globe especially in tropical regions. Nearly half the world's population is at risk from malaria and there are over 200 million malaria cases and approximately 400,000 deaths due to malaria every year. This is a motivating factor to make malaria detection and diagnosis fast, easy and effective.

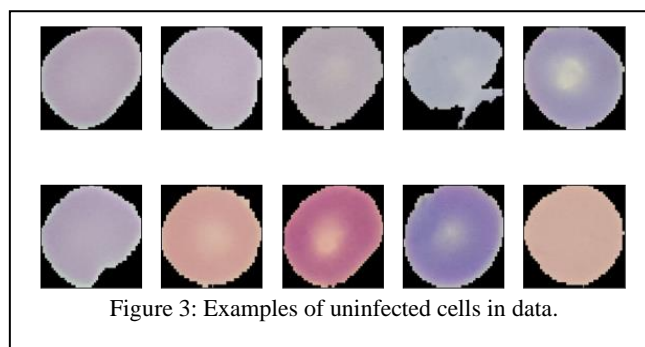
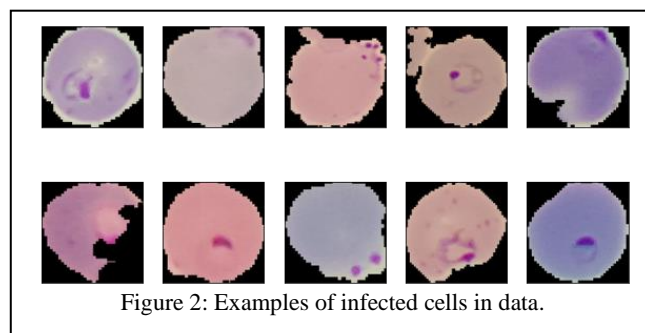


There are several methods that can be used for malaria detection and diagnosis. Some methods include rapid diagnostic tests (RDT) and polymerase chain reaction (PCR) both of which are manual processes and are typically used where high-quality microscopy services are not readily available. Based on the guidelines from the WHO protocol, this procedure involves intensive examination of the blood

smear at a 100X magnification, where people manually count red blood cells that contain parasites out of 5000 cells.

With regular manual diagnosis of blood smears, it is an intensive manual process requiring proper expertise in classifying and counting the parasitized and uninfected cells. Typically this may not scale well and might cause problems if we do not have the right expertise in specific regions around the world. Deep Learning models, or to be more specific, Convolutional Neural Networks (CNNs) have proven to be really effective in a wide variety of computer vision tasks.

Dataset contains images that belong to two classes – Parasitized and Uninfected. Dataset is balanced with 13779 examples of cells labeled Parasitized and Uninfected. To ensure a proper generalization of the model once trained, this dataset is split as 0.72 training, 0.18 validation and 0.1 testing sets.



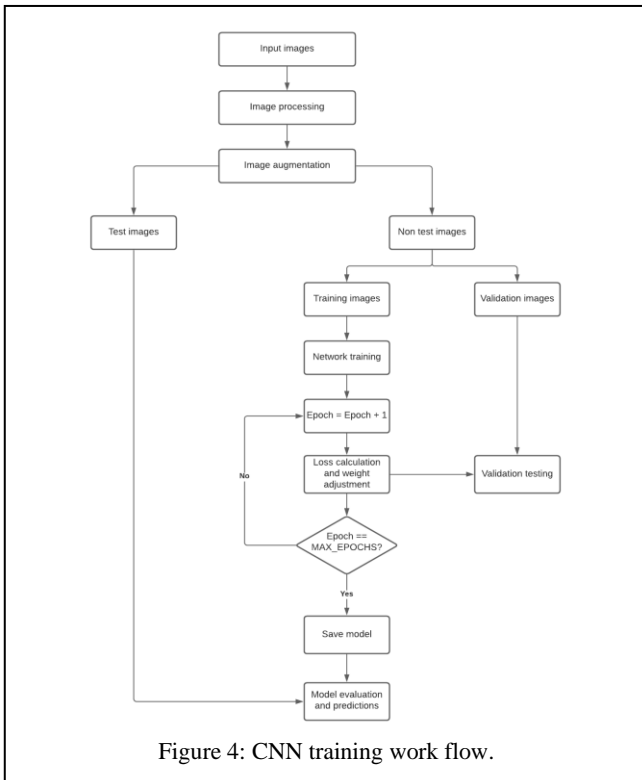
II. RELATED WORK

The paper “Pre-trained convolutional neural networks as feature extractors toward improved parasite detection in thin blood smear images” leverages a total of six pre-trained

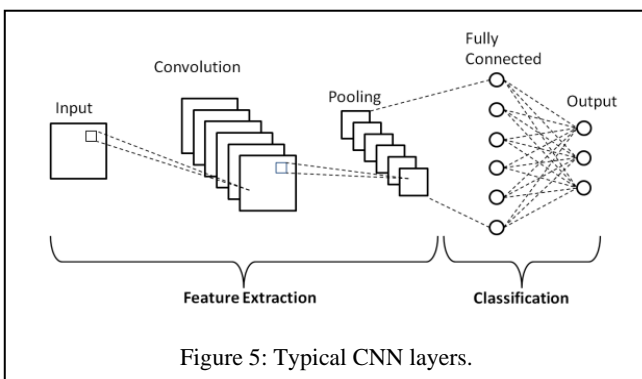
models on the data mentioned in their paper to obtain an impressive accuracy of 95.9% using transfer learning from VGG16 in detecting malaria vs. non-infected samples. This paper attempts to achieve a similar accuracy on unseen test data with CNN defined from scratch.

III. ARCHITECTURE

Training workflow involves pre-processing of the input images to ensure that they are all of same dimensions i.e. 120x120x3 and a real time augmentation of images using TensorFlow is performed to increase the training examples and also to ensure that the final trained model generalizes well.



The key layers in a CNN model include convolution and pooling layers. Convolution layers learn spatial hierarchical patterns from the data, which are also translation invariant. Hence, they are able to learn different aspects of images. This allows CNNs to automate feature engineering and learn effective features which generalize well on new data points.



Pooling layers help with down-sampling and dimension reduction.

The CNN that was selected consists of 3 blocks of [CONV+POOL] where CONV refers to 2D convolution layer and POOL here refers to 2d max pooling layer and 3 fully connected layers with ReLU activation units. This CNN uses dropout regularization and early stopping with threshold at 97% to avoid overfitting on the training set. ReLU function is given by:

$$R(z) = \begin{cases} z & z > 0 \\ 0 & z \leq 0 \end{cases}$$

Model accepts inputs of dimensions 120x120x3 which refers to width, height and the number of channels of the image and a single output which is a sigmoid unit at the end of 2 fully connected layers. Sigmoid function is given by:

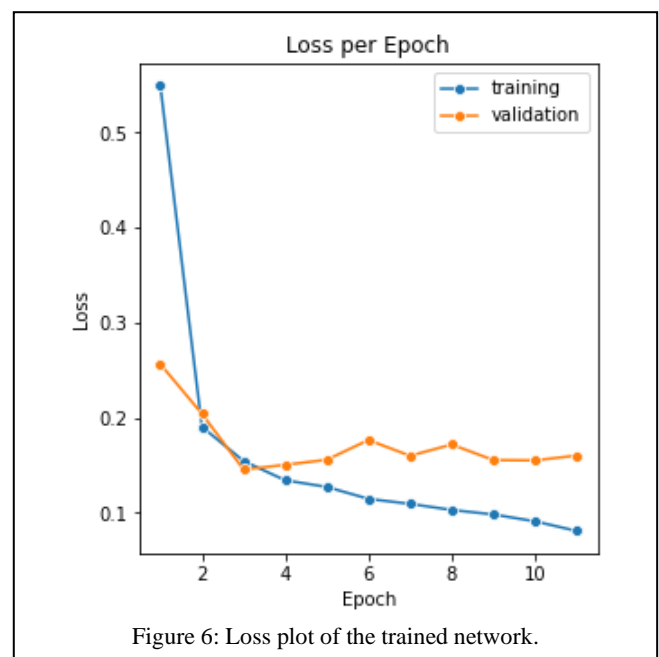
$$S(x) = \frac{1}{1 + e^{-x}}$$

Adaptive moment estimation or Adam is used as the optimization algorithm. Adam combines the advantages of two other extensions of stochastic gradient descent – Adaptive Gradient Algorithm (AdaGrad) and Root Mean Square Propagation (RMSProp). Specifically, the algorithm calculates an exponential moving average of the gradient and the squared gradient, and the parameters β_1 and β_2 control the decay rates of these moving averages.

IV. RESULT ANALYSIS

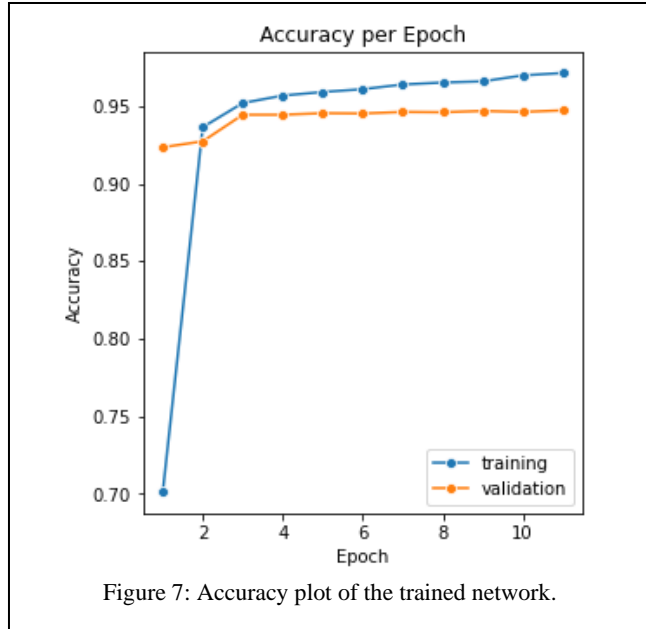
Loss function selected to train and evaluate the model is the categorical cross entropy loss which works well for classification tasks in machine learning.

$$L = -\frac{1}{m} \sum_{i=1}^m y_i \cdot \log(\hat{y}_i)$$

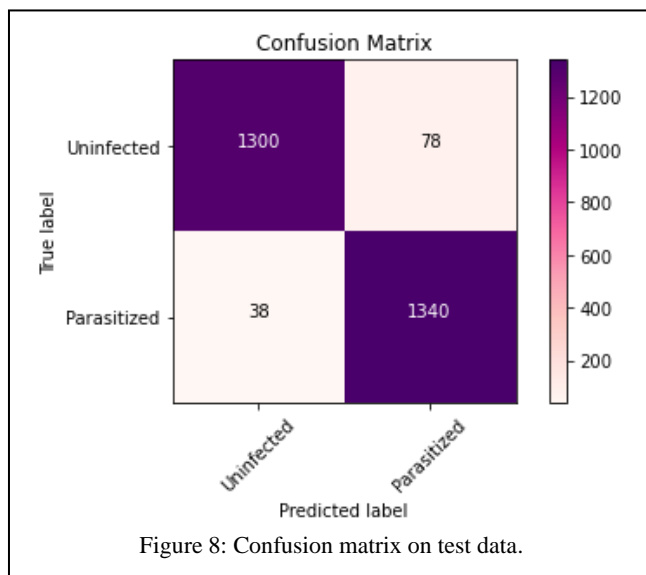


Loss plot of the model shows a downward trend while the accuracy plot shows an upward trend indicating a successful convergence of the model.

To avoid overfitting, a callback function was used to stop the training at 97% of accuracy. Final loss on training set was 0.0867 and Accuracy on training set was 0.9711.



Accuracy achieved on unseen test set is 95.8% with a loss of 0.1386. Confusion matrix shows only 38 false positives and 78 false negatives out of 2756 total test images.



V. CONCLUSION

In this paper, an interesting real-world medical imaging case study of malaria detection has been examined. Malaria detection by itself isn't an easy procedure and the lack of availability of personnel in some areas across the globe

makes it even more of a serious concern. By deploying well trained models like the one described in this paper to the cloud, this diagnosis process can be easily automated and scaled with reliable accuracy. This is one of the many fields in healthcare which can benefit from capabilities of AI and make it more accessible to everyone.

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