DEEP LEARNING MOBILE APPLICATION TOWARDS MALARIA DIAGNOSIS

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ABSTRACT

The exponential growth in digital technologies characterizing the fourth industrial revolution, such as artificial intelligence, offers an exciting opportunity to save lives threatened by malaria across sub-Saharan Africa. According to WHO 2018, malaria causes over 400,000 deaths each year, mostly children under five years of age, with 90 percent of cases occurring in Sub-Saharan Africa. Malaria mortality can be drastically reduced by ensuring prompt access to diagnosis and treatment. However, the existing traditional methods especially microscopic diagnosis, which is the gold standard, is expensive, experts dependent, time-consuming for a single diagnosis and becomes impractical in areas with a high disease burden. In this paper, we present findings from research using the artificial intelligence technique of computer vision to facilitate a fast diagnosis of malaria, drawing on data from Uganda and Tanzania. The model was integrated and deployed with an Android mobile application. Our results demonstrate that, with regard to time, it took less time to detect and count the plasmodium compared to having a person perform manual counting and diagnosis. This diagnosis technique could be deployed to multiple health facilities and facilitate low-cost universal access to rapid malaria diagnosis.

1 INTRODUCTION

Malaria remains one of the major threats to public health and economic development in Africa. Globally, it is estimated that 216 million cases of malaria occurred in 2017, with Africa bearing the brunt of this burden malaria 2018 report (2018). In Tanzania, malaria is the leading cause of morbidity and mortality, especially in children under 5 years and pregnant women. Malaria kills one child every 30 seconds, about 3000 children every day Report (2018). Malaria is also the leading cause of outpatients, inpatients, and admissions of children less than five years of age at health facilities malaria 2018 report (2018). The most common methods to test for malaria are microscopy and Rapid Diagnostic Tests (RDT) Andrade et al. (2010) Kamel et al. (2016). RDTs are widely used but their chief drawback is that they cannot count the number of parasites. The gold standard for the diagnosis of malaria is therefore microscopy. Evaluation of Giemsa-stained thick blood smears, when performed by expert microscopists, provides an accurate diagnosis of malaria Philip & Rosentha (2012). Nonetheless, there are challenges to this method, it consumes a lot of time to perform a diagnosis, requires experienced technicians which are very few in developing countries, and manually looking at the sample via a microscope is a tedious and eye-straining process.

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Recent years have witnessed an explosive growth of mobile devices. By 2020, there will be 498 million active smartphones in Sub-Saharan Africa, which is a growth of 300 million from the end of 2016 (GSMA notes, 2017). The increasing availability and usage of mobile devices and applications, has presented a unique opportunity for the healthcare sector. Over the last decade, they have been increasingly incorporated into the government health policy and programs across the continent. Yet, to date, the possibilities of combining these mobile devices with Artificial Intelligence has not been adequately explored.

In the area of Artificial Intelligence (AI), several techniques have been adopted to create malaria diagnosis tools that are fast, accurate and require fewer expertsEphraim et al. (2015) Hänscheid (1999). Deep convolutional networks as one of AI techniques have been used for the detection of malaria parasites Hänscheid (1999) S. et al. (2018) Sánchez-Sánchez (2015) W. et al. (2018). In this paper, we aim to show how the existing work applying deep learning to malaria diagnosis can be incorporated into mobile applications to help solve some of the challenges in microscopic diagnosis. To demonstrate the success of this, we use the combined data, Table 1 shows the total number of images used. This data was used to train R-CNN from scratch and quantify parasites in malaria patients, with higher speed and lower dependence on experts compared to existing traditional methods. Our hope is that semi-automation of malaria diagnosis will; (i) reduce the need of an expert to conduct diagnosis, (ii) improve quantification of parasites for clinicians, (iii) fastening the diagnosis process by proving a faster count of parasites in each field view, and (iv) reduce the cost of conducting malaria diagnosis.

2 DATA

The team started working with the public dataset from Makerere University, Uganda .R et al. (2016), to develop a prototype model. Later on, a dataset from Benjamin Mkapa Hospital, Tanzania was added to the training set. Table 1 summarizes the total number of images used. The Tanzanian dataset was collected manually using an Android smartphone camera, whereby the phone camera was mounted on top of the microscope. The images captured were then annotated with bounding boxes by parasitologists and labeled as plasmodium.

The dataset was split into three sets namely training, validation, and test sets having a ratio of 80:10:10 respectively.

Table 1: Image datasets used

DATASET	No of patients	No of images	No of parasites
Dataset from Makerere University	N/A	1182	7245
Dataset from Benjamini Mkapa Hospital	28	100	600

3 EXPERIMENT

Our experiment consisted of three parts. First, we developed two deep learning models. We trained an R-CNN algorithmHe et al. (2016) using a publicly available dataset from Makerere University AI Research Lab .R et al. (2016) and a locally collected dataset from Tanzania. We predicted and counted the number of parasites found in an image of a blood smear. Second, we tested and compared each of the two learning models. Finally, we developed an Android mobile application, MalariaChecker, that was integrated with the deep learning model to identify and count malaria parasites. The model is currently locally deployed on the computer server. These three parts are elaborated further below:

3.1 DEVELOPING AND TRAINING THE DEEP LEARNING MODELS

Two custom architectures were designed and trained from scratch, VGG16 and Resnet50. Both VGG16 and Resnet50 were trained from scratch hence no sort of transfer learning was done during

model development. They consisted of a Convolution Neural Network (CNN), Regional Proportional Network (RPN) and a classifier. CNN consisted of a total of 17 layers, with 13 convolution layers, 4 max pool layers. Each of these convolutional blocks is input to an activation function. Here Rectified Linear Units (ReLU) is used as the activation function. The features obtained from CNN are passed through Regional Proportional Network, which consists of 3 convolution layers. RPN returns object proposals. Proposed regions of interest from Regional Proportional Network and features from CNN are passed through Classifier, which classifies the region into respective classes. Figure 1 below summarizes the architecture. Table 2 shows the parameters that were used in the aforementioned architecture to develop the model.

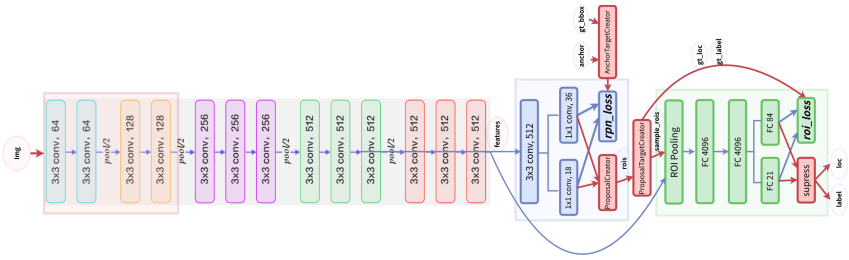

Figure 1: A custom architecture design

Table 2: Summary of the model settings along with the hyper-parameter values

Parameter Name	**Type/Value**
Epochs	1000
Batch Size	32
Optimizer, Learning Rate	Adam, lr = 1e-5
Error Function	Binary cross entropy (RPN loss), categorical cross entropy(classifier loss)
Polling	2 x 2

3.2 Testing the deep learning models

The results from the experiment demonstrated that Resnet50 performed better than VGG16. Table 3, in the results section, summarizes the set of model results obtained from malaria diagnosis experiments.

3.3 Mobile application development

The final step was to develop a mobile application called MalariaChecker used to diagnose malaria. It was developed for Android mobile phones by a team of parasitologists, lab technicians, computer vision researchers and an app developers. The application was developed to test the working of the model in a real-life laboratory diagnosis situation. However, at this stage, we tested the model using existing pictures from the dataset. In the future, we will attach a mobile phone with the app on top of a microscope viewing lens. The mobile phone will then take images of the microscopic field view and then detect the plasmodia, count and localize them from the image. The app will then displays a resulting image with the plasmodia localized with bounding boxes together with the number count of plasmodium present on the field view as shown in figure 2.

4 Results and discussion

4.1 Model selection

In the study of malaria diagnosis using computational techniques, several models are used. However, Resnet50 and VGG16 are the commonly used models that have performed well in different object

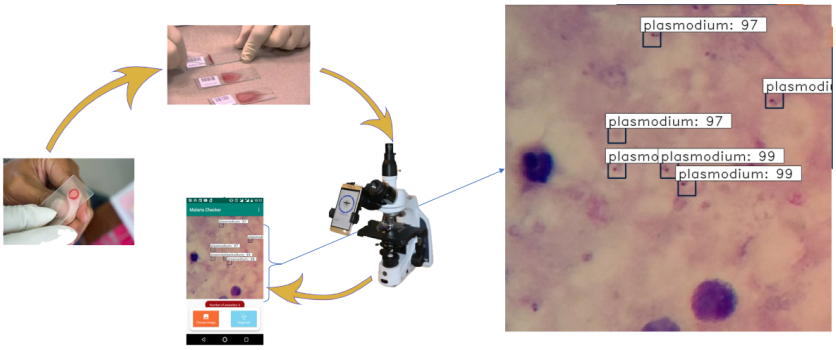

Figure 2: Diagnosis Workflow consisting of app screenshot

detection tasks Q. et al. (2019). Therefore, out of two models we had two choose the model that performed best. We used F1 measure [16] as an evaluation metric on the selection between the two models. F1 measure is widely used for binary classification when one class is not well represented such as plasmodium class in our study. 80 percent of the entire data set were used to train the two models, and 10 percent of the data set were used to finetune them to get the best version. Afterwards, the remaining 10 percent was used to evaluate the performance of these two models. Resnet50 performed better than VGG16 in terms of F1 Score as indicated on Table 3. Therefore Resnet50 was integrated with our mobile application.

Table 3: F1 Scores for Resnet50 and VGG16

Model	**F1 Score**
Resnet50	0.882
VGG16	0.821

4.2 Practicality of the Application

In regard to practicality, we measured the time spent in single diagnosis using manual microscopic examination versas using our mobile application (MalariaChecker). We collected responses from two lab technicians who used our MalariaChecker mobile application. Manual count and identification of parasites by a well trained expert takes 12 seconds i.e 10 seconds to examine a single region under the microscope and 2 seconds to write down the count. WHO recommends for a single diagnosis a lab technician to examine 100 regions making a complete single diagnosis to take 15 to 20 minutes. With our mobile checker a single examination of a region under a less trained expert took 5 seconds making a complete diagnosis of 100 regions to be between 8 to 9 minutes. Hence, it took less time to detect and count the plasmodium compared to having a person perform manual counting.

4.3 Ethical Issues

The data was collected from patients with suspected cases of malaria who willingly went to hospital for diagnosis and treatment. We took images of what the lab technician was examining under the microscope. To avoid privacy violation of patients, no details about the patient were taken for this research rather than the images of their stained blood samples.

4.4 Drawbacks and Future Study

It came to our notice that different lab technicians had different labels on a single image. Therefore, the use of a single lab technician as we did in this study may lead to labelling errors. In future, as we continue with the study we will focus on having more than one expert (lab technicians) to

label a single image during the data labeling process and then compute the average. Future work could also better utilize transfer learning and see how the model will perform compared to training the models from scratch. In addition, understanding why the model made certain predictions such as false positive and false negative could also be valuable to improve the model performance. We lastly purport that training of a smaller network that can easily be deployed in a limited resource area such as a mobile phone will eliminate the need to deploy the model in a computer server. This will increase its applicability in places with little or no access to the internet such as rural areas.

5 CONCLUSION

The results confirmed that the model's performance surpassed that of the medical experts in terms of time spent to perform diagnosis. Improved accuracy of malaria diagnosis with the correct count of parasites, will assist health care systems to improve patient treatment. It may also help them identify patients' progress or reaction towards a specific drug treatment hence good record on drug resistance. The model performed well when challenged with data from multiple institutions, suggesting that with a sufficiently large training set, we might be able to deploy the model to many institutions. In this feasibility study, we found that the compliance of malaria diagnosis application with manual procedurals was satisfactory in the clinical setting. However, improvements in the work process policy is suggested for improving timeliness and efficiency. The dataset used is set free and open for public use and we hope this work will inspire others to build AI-based tools for critical disease in areas with high disease burden and limited resources of experts and equipment.

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