Explainable CNN for Malaria Cell Detection

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***Abstract*— Malaria is an infectious disease caused by *Plasmodium* parasites, transmitted through mosquito bites. Symptoms include fever, headache, and vomiting, and in severe cases, seizures and coma. The World Health Organization reports that there were 228 million cases and 405,000 deaths in 2018, with Africa representing 93% of total cases and 94% of total deaths. Rapid diagnosis and subsequent treatment are the most effective means to mitigate the progression into serious symptoms. However, many fatal cases have been attributed to poor access to healthcare resources for malaria screenings. In these low-resource settings, the use of light microscopy on a thin blood smear with Giemsa stain is used to examine the severity of infection, requiring tedious and manual counting by a trained technician. To address the malaria endemic in Africa and its coexisting socioeconomic constraints, I propose an automated, web app - based screening process that takes advantage of already existing resources.**

***Keywords*— Malaria, Neural networks, Machine learning, Infectious disease, Red blood cell, Public health, Global health, Data science, Deep learning, Epidemiology**

I. Introduction

Malaria can be diagnosed based on clinical symptoms, although the Center for Disease Control (CDC) always recommends confirming the diagnosis with a laboratory test (CDC, 2020). Laboratory tests can include the use of PCR to identify the specific strain of *Plasmodium* in a confirmed malaria case (Hong et al., 2013), antigen detection kits to detect *Plasmodium*-derived antigens (Polpanich et al., 2007; Khan et al., 2010), and serology tests such as ELISA to detect antibodies targeting malaria parasites (Murungi et al., 2019). These methods are expensive and often infeasible to implement in low-resource settings due to the required equipment and use of trained technicians (CDC, 2020). In low-resource settings, the use of light microscopy on a thin or thick blood smear with Giemsa stain is often used to confirm the presence of malaria parasites (Charpentier et al., 2020). Infection severity is frequently measured through the percentage of red blood cells infected with malaria parasites, also known as percent parasitemia or parasitemia burden. However, the diagnostic accuracy of using Giemsa-strained thin blood smears depends heavily on the level of expertise in the technician, who must manually classify and count the number of malaria-infected red blood cells. This results in significant inter-observer variability due to the different levels of expertise in technicians in low-resource settings, who often have to learn other tasks and cannot be adequately trained for this specific task as a result (Billo et al., 2013; Bowers et al., 2009). For example, one study in Nigeria found that while both health providers and community members are familiar with malaria tests, there has been significant concern with the reliability of test results due to technician incompetency (Ezeoke et al., 2012). Meanwhile, microscopy-based diagnosis of malaria at primary health care facilities in Tanzania had a sensitivity of 74.5% and specificity of 59.0%, also indicating that technicians may not have proper training (Ngasala et al., 2012). A study in Angola also made similar conclusions that there is inadequate training for technicians involved in microscopy-based diagnosis of malaria (Nazar-Pembele, Rojas & ngel Nez, 2016).

The use of machine learning methods, particularly neural networks, is rapidly growing in many areas of clinical application. The two primary applications are involved with either segmentation or classification in clinical images (Shen, Wu & Suk, 2017; Anwar et al., 2018; Litjens et al., 2017) or histological images (Kan, 2017; Wang et al., 2019). In particular, the use of machine learning to diagnose malaria is of interest, where various classification models were developed by several groups to determine whether a red blood cell is infected or uninfected, as shown in Table 1.

TABLE I
PREVIOUS ATTEMPTS BY OTHER RESEARCH GROUPS TO CLASSIFY INFECTED RED BLOOD CELLS.

A SIGNIFICANT NUMBER OF GROUPS USED THEIR OWN DATASETS, WHILE OTHER GROUPS USED THE NIH DATASET.

Source	Accuracy	Sensitivity	Specificity
Ross et al. (2006)	73.0	85.0	NR
Das et al. (2013)	93.2	94.0	87.9
Liang et al. (2017)	97.3	96.9	97.8
Rajaraman et al. (2018)	98.6	98.1	99.2
Rahman et al. (2019)	97.7	97.4	97.9
Rajaraman, Jaeger and Antani (2019)	99.5	NR	NR

II. Dataset

NIH Gov's Official Malaria dataset is used in this research work. The dataset contains a total of 27558 images of Malaria infected and Non-infected cells. The images are RGB images varying in sizes from 76 x 68 to 152 x 141. For standardized research purpose, all images were resized to 64x64x3 dimension. As the number of images were sufficient for training a CNN model and enough to prevent overfitting, no data augmentation was done on the images. The results obtained outperformed all the existing methods, so there was no need of applying data augmentation to improve the results.

Fig. 1 shows a glimpse of resized images belonging to both the classes from the dataset. Dataset was first split into a Training set and Testing set in the ratio 70:30. To observe how the trained model performs on unseen images, we should have a good number of images in the test set which is why we allotted 30% of the dataset for testing purpose.

The Training set was further divided into Training and Validation set in the ratio 90:10.

So, the final Image wise split was:

- Train: 17361
- Val: 1929
- Test: 8268

III. Custom Convolutional Neural Network

In my experiments I trained the custom CNN using RMSProp as the optimization algorithm with the Adam Optimizer and binary crossentropy as the loss algorithm. The learning rate was set at 0.00001.

TABLE III
THIS TABLE SHOWS THE STRUCTURE OF MY CUSTOM CONVOLUTIONAL NEURAL NETWORK

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 148, 148, 32)	896
max_pooling2d (MaxPooling2D)	(None, 74, 74, 32)	0
conv2d_1 (Conv2D)	(None, 72, 72, 64)	18496
max_pooling2d_1 (MaxPooling2)	(None, 36, 36, 64)	0
conv2d_2 (Conv2D)	(None, 34, 34, 128)	73856
max_pooling2d_2 (MaxPooling2)	(None, 17, 17, 128)	0
conv2d_3 (Conv2D)	(None, 15, 15, 128)	147584
max_pooling2d_3 (MaxPooling2)	(None, 7, 7, 128)	0
flatten (Flatten)	(None, 6272)	0
dropout (Dropout)	(None, 6272)	0
dense (Dense)	(None, 512)	3211776
dense_1 (Dense)	(None, 2)	1026

My CNN model has three convolution and pooling layers followed by dropout for regularization two dense layers.

IV. Explaining the CNN

To make our model explainable, we have implemented the Grad-CAM technique. Using this technique, we can determine what part of the input affects the output.

Gradient-weighted Class Activation Mapping (Grad-CAM), uses the gradients of any target concept, flowing into the final convolutional layer to produce a coarse localization map highlighting important regions in the image for predicting the concept. Grad-CAM is applicable to a wide variety of CNN model-families: (1) CNNs with fully connected layers, (2) CNNs used for structured outputs, (3) CNNs used in tasks with multimodal inputs or reinforcement learning, without any architectural changes or re-training. We combine Grad-CAM with fine-grained visualizations to create a high-resolution class-discriminative visualization and apply it to off-the-shelf image classification, captioning, and visual question answering (VQA) models, including ResNet-based architectures. In the context of image classification models, our visualizations (a) lend insights into their failure modes, (b) are robust to adversarial images, (c) outperform previous methods on localization, (d) are more faithful to the underlying model and (e) help achieve generalization by identifying dataset bias.

This can be especially helpful if we want to find the exact area in which the parasite is present.

V. Results

We get a ***validation accuracy*** of **95.46%** which is pretty good, and a ***training accuracy*** of **95.12%** after 20 epochs. We can get a clear perspective on this by plotting the training and validation accuracy and loss curves.

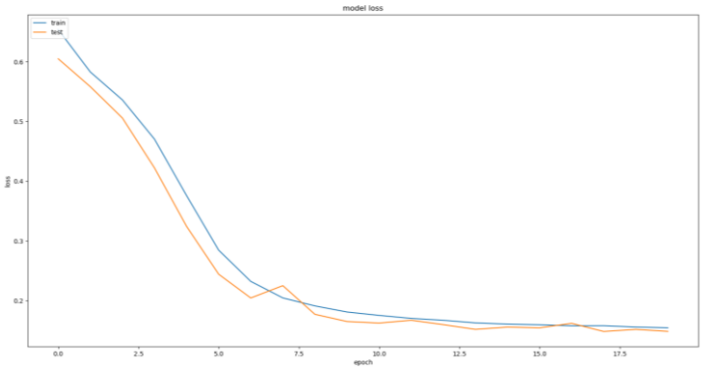

Figure 1 Loss Curve for the Custom CNN

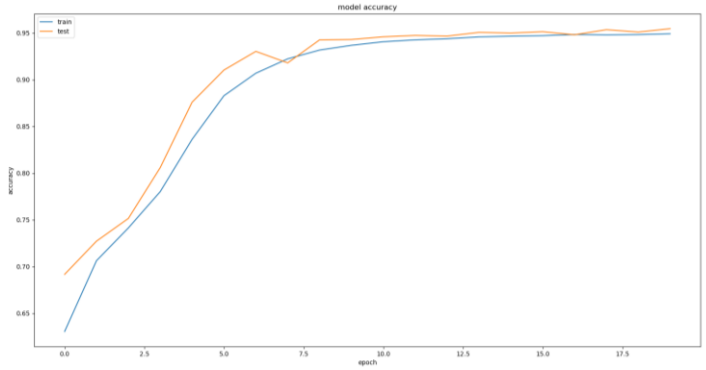

Figure 2 Accuracy Curve for the Custom CNN

As we see, there is not a considerable amount of progress after the 6th epoch, but I was able to achieve a ***validation accuracy*** of **95.12%.**

The custom convolutional neural net was able to produce satisfactory results:

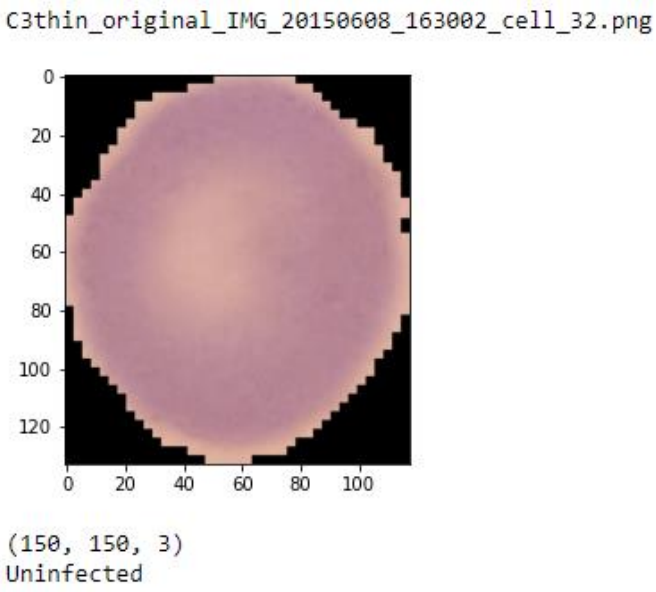

Figure 3 Prediction of an unseen Uninfected Cell

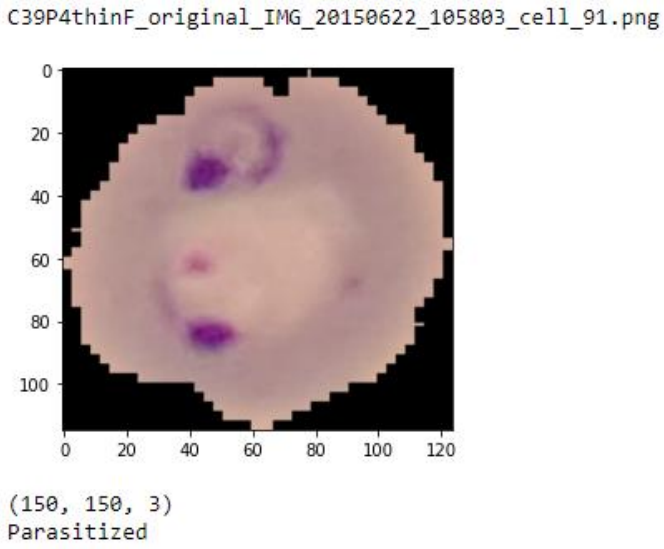

Figure 4 Prediction of an unseen Parisitized Cell

Using the Grad-CAM technique, I was able to determine which part of the image influenced the prediction the most. This can be especially useful to detect the parasite present in the given RBC image. The output given by this technique was a heatmap:

The output below shows the heatmap of a parasitized cell. As we can see the model is heavily influenced by the part which contains the parasite.

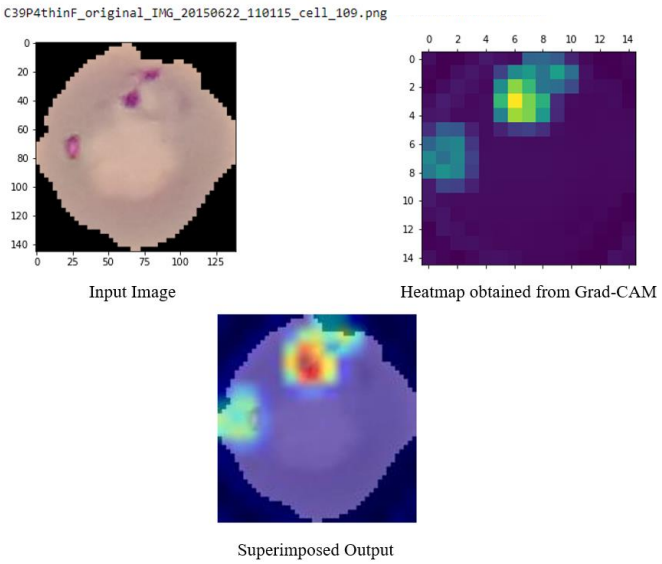

Figure 5 Grad-CAM on a Parasitized Cell

Meanwhile, in an uninfected cell, the whole cell influences the prediction made by the model.

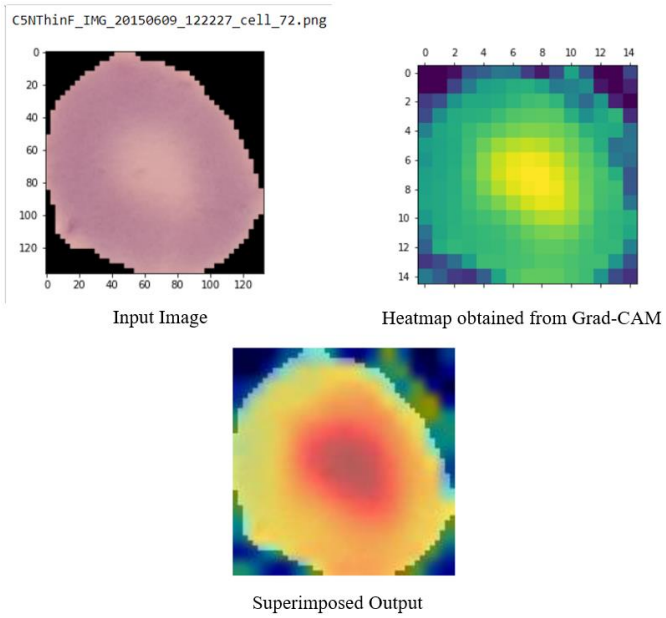

Figure 6 Grad-CAM on an Uninfected Cell

VI. Conclusions

Malaria, being a life-threatening disease, its early diagnosis can save a lot of lives. The accuracy of diagnosing malaria from blood smears relies on the efficiency of medical professionals and the quality of instruments used in the diagnostic process. This leads to a heavy strain on medical professionals in rural areas with less medical facilities. Deep learning methods with high accuracy in diagnosing the disease can alleviate this strain on health care system and make the diagnostic process easier and faster. The proposed method can prove to be an effective medical diagnosis aid following its

near negligible wrong predictions and high classification accuracy. Also, the fact that such a superior performance is achieved even after using a small neural network architecture, reduces the computational time, additionally giving my method an edge over existing methods that use heavy CNN models.

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