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Enhancing An Image Blood Staining Malaria Diagnosis Using Convolution Neural Network On Raspberry Pi

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Abstract: Malaria is a common disease in Sub-Saharan Africa, the disease is caused by a class of parasites called protozoan, and it is transmitted by female Anopheles mosquitoes to humans. Plasmodium ovale, plasmodium vivax, plasmodium knowlesi, plasmodium falciparum, and plasmodiummalariae. The five known plasmodium species that cause malaria in humans. The microscopic diagnosis has always been a gold standard but today, computational tools like deep learning are used in malaria prediction. The deep learning model use images to diagnose infection. The model was trained using the Kaggle dataset with 27,560 images with equal instances of primary images,used to validate primary images from the microscope were annotated using Roboflow. A total of 27 primary images were collected. The model gave accuracy and precision of 85% and Recall of 96% both on the personal computer and Raspberry Pi 4. This research provides a prototype for enhancing malaria diagnosis from images by deploying a deep learning model - a convolution neural network, on a Raspberry Pi. This research has proven the possibility of classifying malaria images as parasitized or unparasitized by deploying a deep-learning model on the Raspberry Pi. This study demonstrates that Raspberry Pi can be utilized for diagnosis and overcome the constraint of requiring high computer hardware specifications to operate a deep learning model. The result obtained 90% accuracy in the detection of parasites in the Red Blood Smear.

Keyword: Raspberry Pi; Malaria; deep learning;Red Blood Smear; Convolution Neural Network

Nomenclature

Abbreviation	Expansion
MRDT	Malaria Rapid Diagnostic Tests
ML	Machine Learning
DL	Deep Learning
WHO	World Health Organization
CNN	Convolution Neural Network
ANN	Artificial Neural Networks
DNN	Deep Neural Networks
YOLO	You Only Look Once
PPV	Positive Predictive Value
Mask-R-CNN	Mask Regional-Convolution Neural Network
DCNN	Deep Convolution Neural Network
RBS	Red Blood Smear
ReLU	Rectified Linear Unit
USB	Universal Serial Bus
ROM	Read Only Memory
PC	Personal Computer
LBP	Local Binary Pattern
DLNM	Distributed Lag Nonlinear Model
JPEG	Joint Pixel Expert Group
RBC	Red Blood Cells
FC	Fully Connected

1. Introduction

Nigeria has a large malaria burden with 25% of malaria illnesses globally.This leads to pressure on laboratory technicians who give false results on malaria diagnoses [11]. The adoption of MDT in Nigeria

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has been fraught with challenges as most healthcare personnel in Nigeria judged MRDT results to be erroneous. Conversely, most healthcare practitioners have a preference for microscopy over MRDTs for malaria diagnosis in Nigeria [11]. The microscopic diagnosis has always been a gold standard. According to [12], sensitivity and specificity are usually greater than those of MRDT in the diagnosis of malaria.Despite this evidence, results obtained from microscopic diagnoses can be subjective as they are influenced by the expertise of the laboratory technician. This is why automatic image recognition technologies based on ML have been proposed and applied to malaria blood smears for diagnosis previously. However, the practical performance of these efforts has not been sufficient so far, resulting in continuing research into the application of ML and model optimization for malaria detection. This study therefore investigated how DL can be used in automatic image recognition technology for malaria diagnosis.

Malaria is a widely spread disease which is caused by a protozoan that is one of the main causes of death globally [10]. Sub-Saharan Africa is a hotspot for malaria illness. Malaria is estimated to afflict 216 million people worldwide, with 445,000 deaths occurring each year [10]. The five Plasmodium species that induce malaria are *Plasmodium ovale*, *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium malaria*, and *Plasmodium knowlesi*. These all cause malaria in humans with Plasmodium vivax and Plasmodium falciparum are said to be the deadliest of them all, and renowned for their resistance-developing abilities against most available anti-malaria, including the most recent antimalarial artemisinin-based combination therapy [13]. For hundreds of years, scientists and physicians have worked to prevent and treat malaria parasites (Plasmodium). Plasmodium parasites have traveled to every continent of the world excluding Antarctica [9].

Malaria preventive efforts began in Massachusetts in 1896. An epidemic in Uxbridge spurred health official, Dr. Leonard White, to report the incident to the State Board of Health, which resulted in research on mosquito-malaria relationships and the first malaria preventive measures. Giovanni Battista Grassi, Rome University professor of Comparative Anatomy and Italian scientist, indicated that plasmodium can only be transmitted by Anopheles [12]. According to the WHO, nineteen countries in Africa contribute over 80 percent of the world's malaria burden and over 90% of deaths globally [10]. Malaria symptoms appear within 360 hours (15 days) of infection and if not treated can lead to severe illness within the next 24 hours (1 day). DL has been applied in malaria diagnosis. The application of ML is useful in biological applications with impacts that can be divided into three broad categories: (1) Computer-aided diagnosis to assist physicians in making more accurate and timely diagnoses, with better harmonization and fewer contradictory diagnoses. (2) Improving patient medical care with better therapies.(3) Improving human well-being by studying diseases, and how environmental variables influence dissemination and behavioral patterns [2].

This study investigated the enhancement of an image of blood staining malaria diagnosis using a CNN. This study demonstrates that Raspberry Pi can be utilized for remote malaria diagnosis and overcome the constraint of requiring high computer hardware specifications to operate a DL model as well as confirmatory test thereby eliminating erroneous results of laboratory technicians who give false results on malaria diagnoses.

The paper is organized as follows: Section 2 explains the Literature review, Section 3 provides the methodology, Section 4 mentions the Comparative analysis of PC and Raspberry Pi methodology, Section 5 explains the System requirement of Raspberry Pi, Section 6 provides Procedures for Raspberry Pi configuration, Sections 7 mentions Configuration of accessing Raspberry Pi,Section 8 explains the result and discussion, Section 9 represent the advantages and disadvantages, Section 10 concludes the paper.

2. Literature

2.1 Literature Review

Deep Learning in Malaria Diagnosis

DL has been used in the medical industry to handle a variety of issues, including facial recognition, effective categorization of skin burns, cancer diagnosis, malaria detection, and financial fraud detection [9]. Millions of blood smears are examined yearly using a microscope to determine the presence of the Plasmodium parasite in the cell.To identify whether the person is infected or not, CNN set hidden layers are put together to determine images and if a cell is infected or not. Currently, there is a lot of available data on DL both biological and chemical data which requires the use of computational tools [17]. The microscopic diagnosis has always been a gold standard. ANN was first discovered in 1943 [4]. The degree of complexity of Neural Networks (NNs) and the number of hidden layers separate from conventional ANN to DL. It makes use of a large number of hidden layers and traditional CNN makes use of a couple of hidden layers, this is the reason behind the hindrance of hardware in the olden days. The emergence of

immensely influential CPUs and GPU hardware is the reason DL can make use of many more nodes in each layer [4]. DL relies on ANN. These neural networks, known as DNNs, include numerous layers and a high number of neurons DNNs [18]. DL is significant in picture mining and recognition, which may be used to forecast malaria [1]. The microscopic diagnosis has always been a gold *Plasmodium vivax* and *Plasmodium falciparum*infection.It works by extracting hidden and important features of an image. A total of twelve journals were considered while 3 that are loosely related were benchmarked.

The use of a microscope for malaria diagnostics has become the global standard for malaria detection. The DL method is used in image recognition and categorization is now frequently used in medicine. A CNN is a kind of DL that is commonly used by computational biologists. The Giemsa stained dataset is used as an illustration of a CNN dataset. Thick blood stains were taken with a Smartphone camera through the ocular of a microscope at 100 magnification ACNN is needed to group red blood cells into infected and uninfected cells[19].

The algorithm finds candidate objects using a model that segments traditional feature extraction with the use of CNN [1]. The features extracted include rectangular Haar features, texture, morphology, and color. The algorithm is trained using trained and test data called Plasmodium falciparum and negative samples of Plasmodium falciparum. This algorithm was tested on Plasmodium vivax patients. however, the result only applies to Plasmodium falciparum patients [20].

The performance of three popular CNNs, LeNet-5, AlexNet, and GoogLeNet, was evaluated. [21] assessed the performances of AlexNet, VGG-16, ResNet-50, Xception, DenseNet-121, and their custom-built model to discover the ideal layer of a pre-trained model to extract characteristics from underlying malaria parasite data.

The LBP approach was particularly successful in classifying blood smears as thin or thick. To determine the intensity patterns inside the cells and count infected cells, K-means clustering algorithms and morphological procedures were applied. Using segmentation and morphological approaches, standard datasets were utilized to assess thick and thin blood smear pictures. Specificity and sensitivity were used to compare the results [22].

Deep learning algorithms were employed by [15] in the diagnosis of malaria, which was accomplished by establishing an effective mobile system that delivers solutions by giving mobile healthcare to patients. They discussed in the research how DL architecture (for example, CNN) was utilized in malaria diagnosis to obtain high accuracy, achieving 97.30% accuracy with the input photos. [23] worked on the modification of YOLOV3.This was done to be able to handle small-size object detection. The neural network was applied to a total of two datasets with a total image of 2703 from a total of 133 people. The patch level is the only level evaluation that was done. Think blood smear and thin blood smear were prepared and studied under the microscope.The thin and thick blood smear extraction of parasites was performed with the two distinguished based on histogram type (bimodal vs. unimodal). After the picture recognition, each kind of design was completed for different pipeline phases, with each design based on (1) adaptive thresholding, (2) color space conversions, and connecting components. They analyzed 87 thick blood smear pictures, and 30 photos of thin blood smears, and displayed parasitic tally findings on a patch level [5].

[13] found that Otsu's thresholding and morphological filtering may be utilized to distinguish erythrocyte regions from additional blood components detected in smears. The separation is accomplished by the utilization of an intrinsic geometrical attribute of the clump's concavity point detection.Nonetheless, the geometrical deformation is unaffected. According to their findings, erythrocyte segmentation accuracy was 97.95 percent, with an 8.76 percent increase. [16] conducted their study using thin blood smear images from digital microscopic. As a result, they recorded that sensitivity was 91.6 percent and the PPV)was 89.1 percent, showing that the parasite detection performance is trustworthy and may be employed in hospitals. Utilized 27,558 pictures from the National Institute of Health, 13,779 of which were normal and 13,779 of which were malaria-infected. Although the photographs ranged in size and had different components, they were all resized to 22,224 to suit the input form of the VGG16 pre-trained framework used. In addition, as part of the data preparation before training, the data were divided into three groups: 70% of the data for each class were labeled as training data., validation data 30% of the time, and testing data 10% of the time. The training data was further reduced to 60% of its original size. Two tests were performed: one with conventional training pieces and one with oppositional training 9 pieces. During regular training, original photographs were used, and unfriendly images were presented or placed in a test image throughout testing and afterward [7].

The author [26] think smear images obtained from a microscope view were taken with a smartphone.The research aimed to detect if a patient was infected or not infected with the Plasmodium parasite and if the patient was infected it was due to *Plasmodium falciparum* or *Plasmodium vivax*, other Plasmodium species were not taken into consideration for this study. Plasmodium VF-Net first detected the presence of plasmodium then Mask R-CNN was used to filter out false-positive results. An overall 90% accuracy was achieved in this framework on patient level and images. [3] detected malaria

using real-time images. In the journal "Falcon" a type of DCNN was introduced, which was used on blood smear slide images of a malaria screening tool to detect malaria. An accuracy of 95.2% was obtained from malaria detection when compared with existing CNN models. A DNN was employed with machine learning algorithms including the ensemble method, which was used to identify plasmodium infection from RBS images, other algorithms used include cyclical, constant learning, and transfer learning. A total of 27558 images were classified using the ImageNet database with a mixture of the ML algorithm. A total of 80% of the images were for training, and 10% each for testing and validation.

Author	Methodology	Advantages	Disadvantages
[9]	DLNM	• Good performance for short-term prediction. • Flexible statistical approach	Did not provide details on the potential assumptions or limitations of the model itself.
[7]	CNN	• Improved Robustness and accuracy in classification. • Efficient and fast method for generating adversarial images,	A comparison of the model is not provided.
[19]	CNN	• Higher accuracy. • Outperforms a transfer learning model in various performance indicators such as sensitivity, specificity, precision, F1 score, and Matthews correlation coefficient. • Robustness and effectiveness in malaria diagnosis.	More complex CNN architecture may require more powerful computing resources,
[20]	DL	• Providing an automated solution for the diagnosis and quantitation of malaria. • Patient-level performance metrics are used for evaluating the automated diagnosis methods, providing a comprehensive assessment of the system's effectiveness	Multiple field evaluation is not possible.
[22]	(LBP)	• Reducing the need for manual diagnosis and the associated time and errors. • Provide accurate identification of infected cells	May be sensitive to variations in image quality, such as noise and low contrast, which can affect the accuracy of parasite detection
[23]	YOLOv3 detection algorithm	Offers a low-cost alternative for rapid malaria screening in low-resource settings, potentially reducing the dependence on manual microscopic examination.	This method required a skilled expert to identify the exert result.
[5]	unsupervised learning technique	• Capture of microscopic fields of thin and thick blood smears from different patient slides. • Use of JPEG format to reduce the space complexity of the algorithm. • Evaluation of the proposed algorithm through experimental results.	Relied completely on unsupervised learning for the detection of infected RBCs. which may result in false positives or false negatives.
[16]	Adaptive thresholding	• Efficient, contributing to better system performance and eliminating objects that may interfere with the detection process. • Easily accessible and can be processed efficiently,	Need more images for the process.

3. Methodology

1. Machine Learning

The libraries imported for this model include Pandas, cv2, numpy, pandas, matplotlib,seaborn, and Keras. The CNN was used to identify infected and uninfected blood cells. The model has a total of seventeen layers, the steps involved in the CNN model are:

i. Convolution Layer
ii. PoolingLayer
iii. Activation Function
iv. Full connection 16
v. Loss function

a. Convolution Layer in CNN architecture

The convolution layer is a highly significant component. It is composed of many convolution filters known as kernels. The input convolves the image using these filters to produce the output feature map, which is represented as N-dimensional metrics. The convolution Layer entails the following steps: There are steps involved in Convolution layer namely:

i. **Input image**: It is placed over the input image, starting from the top-left corner and working your way down within the borders,and then check how many cells in the input image match the feature detector's results. The number of matched cells is then placed in the feature map's top-left cell [24]. In the Kaggle dataset, 27,560 cell pictures with an equivalent amount of parasitized and uninfected cells are used.

ii**. Feature detector:** The feature detector is subsequently shifted to the right one cell after another and the process is repeated. The stride is the name given to this action of one pixel. Feature detection is often referred to as Kernel. The kernel is described as a matrix of discrete integers or values. Each number is referred to as the kernel weight. Random values are set as kernel weights at the start of the training procedure for CNN. Furthermore, several approaches are utilized to establish the weights. Following that, these weights are altered during the individual training period, allowing the kernel to learn to obtain significant characteristics [24].

iii. **Feature map:** The feature map cells can represent any integer, not just 1s and 0s.The fundamental computations are performed at each phase of the convolution layer [24].

b. ReLU:

ReLU is not a different step in the creation of CNN. It is an extra step to the convolution technique. This is the most used algorithm in the CNN context. It translates the complete numbers of the given positive integers. ReLU's main benefit above all others is its decreased computational load. Its numerical representation is:

$$f(x)ReLU = max(0, x) \tag{1}$$

While using ReLU, several significant challenges may occur concurrently. Assume you have an erroneous back-propagation technique with a larger gradient. Whenever the gradient is sent via the ReLU function, the values are changed so that the neuron is never activated again. This is known as "Dying ReLU," and there are certain ReLU solutions that can aid with such issues. Rather than ReLU downscaling negative values, this activation function guarantees they are not discarded. It is used to address the issue of Dying ReLU.

Noisy ReLU: To make ReLU noisy, the function applies a Gaussian distribution. It is mathematically represented as

$$f(x)NoisyReLU = max(x + Y), with\ Y \sim N(0, \sigma(x)) \tag{2}$$

c.The pooling layer: The fundamental role of the pooling layer is to subsample the image features. These maps are created using convolution techniques. This method alternatively reduces detailed feature maps to lower feature maps. At the same time, it retains the majority of the dominant information (or characteristics) throughout the pooling process. The stride and kernel are both size-assigned before the pooling process in the same way that the convolution operation is. Diverse pooling strategies are available for usage at varying pooling levels.

d. Activation Function: The major reason for activation functions in every level of neural networks is to connect both input and output. The weight is accumulated by the neuron input and it is used to input with the help of its bias. To put it simply, activation functions select if or if not in the stimulation of a neuron in response to a given input data by producing the appropriate output [24].

e. Fully Connected Layer: The layer is frequently found after individual CNN designs. Individual neuron in this layer is interconnected to every previous layer, using the so-called FC technique. It serves as the CNN classifier. As a feed-forward ANN, it follows the fundamental method of the standard various-layer perception neural network. The prior pooling or convolution layer supplies 19 inputs to the FC layer. This input is a vector that is formed after padding the feature maps. The FC layer output reflects the final CNN output.

f. Loss Functions: The last layer of CNN architecture is the output layer.It is in charge of the final categorization. In the CNN model, in the output layer, various loss functions are utilized to determine the anticipated inaccuracy generated over the training data. This mistake displays the difference

between the output as planned and the actual output.The CNN learning procedure will then be used to optimize it.The loss function, likewise, two parameters are used for error detection. The CNN estimated output is the first parameter(also known as prediction). The second disagreement is the actual output (also known as the label).

g. Convolution Neural Network Regularization: The main issue in getting well-behaved generalizations in CNN models is over-fitting. When a model is effective with training fails on test data (unseen data), it is said to be overfitted. The inverse is an under-fitted model, which arises when the model doesn't learn enough from the training data. If the system works well on both the training set and testing data, it is considered successful. It is said to be "just-fitted."

h. Batch Normalization: The following are the benefits of using batch normalization:
i. It prevents the vanishing gradient issue from occurring.
ii. It is capable of successfully controlling the poor weight initialization.
iii. It considerably minimizes the amount of time needed for network convergence (for large-scale datasets).
iv. It has a difficult time reducing training reliance across hyper-parameters

2. Acquisition of Secondary data methodology

Secondary data was acquired from Kaggle.The Kaggle malaria dataset had 27,560 malaria cell images,with an equal instant of both parasitized and unparasitized cell images the dataset was obtained from the Kaggle website.

3. Primary data collection

Primary data was gathered from Covenant University Hospital, with 50 images collected, An Olympus microscope was used to view the microscope slides at Covenant University Medical Center. 15 The staining procedures are listed below:
1. In a staining jar, prepare freshly worked Giemsa stain.
2. 40 ml of Giemsa working buffer should be added to a second staining jar. Add 2 drops of Triton X-100 to 20 l. Convert volume to jar size.
3. Slides should be exposed for 45–60 minutes to the working Giemsa stain (2.5%).
4. Slides with thin smears should be removed and rinsed in the Giemsa buffer three to four times. Five minutes should be given to thick streaks in the buffer.
5. Slides should be dried vertically on a rack[14]. The images were collected using a mobile camera and viewed under the microscope at 100x resolution. After the image collection from the microscope using an iPhone X mobile phone camera, the images were, renamed and resized to 148 by 148 pixels and annotated on Roboflow individually and saved.
CNN is built on three levels:

(i) the convolution layer,
(ii) (ii) the pooling layer, and
(iii) (iii) the complete connection layer

The images were then used to run the model. The step for Primary image annotation follows:

1. Create an account on Roboflow
2. Select a name for the image project
3. Upload images
4. Annotate images individually
5. Label individual image source
6. Preprocessing
7. Generate annotated images.
4. Step-by-Step Algorithm of the Model Algorithm.

The Deep Learning Algorithm

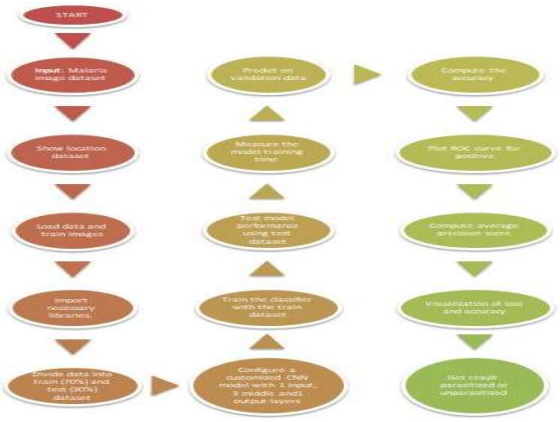


Fig. 1. *Flow process of the DL algorithm*

4. Comparative analysis of PC and Raspberry Pi methodology

The Raspberry Pi is a little replica of a modern computing device capable of doing complex tasks. The module makes use of a variety of as a result.It can only run open-source operating systems and programs on it. Raspberry Pi also allows the user to browse the internet and send email. Raspberry Pi supports a variety of programming languages including Python, C, C++, Perl, Ruby, and BASIC. Raspberry Pi previously had its operating system, known as Raspbian, which is centered on Linux. Raspberry Pi has been used majorly in facial detection through the process of extracting certain features such as nose, eye, and mouth, but in this research,Raspberry Pi was used to run a deep learning model for malaria diagnosis. Raspberry Pi operates on the Raspberry operating system (OS). The model was run on Thonnypython.The most recent Raspberry Pi 4 Model B. FCC ID:2ABCB-RPI4B was used.

5. System Requirement of Raspberry Pi

The required materials for this research are:

1. Raspberry Pi (2GB): The Raspberry Pi 4(Model B. FCC ID:2ABCB-RPI4B) is the most recent Raspberry Pi mode., It was ordered from E-commerce (Jumia). The technical specifications of the device are listed:
   - i. Processor: Broadcom BCM2711, Quad-core
   - ii. Cortex-A72 (ARM v8) 64-bit quad-core SoC @ 1.5GHz
   - iii. RAM: 2GB LPDDR4 RAM
   - iv. Bluetooth: Bluetooth 5.0
   - v. Wi-Fi: 5.15 GHz to 5.25 GHz IEEE 802.11ac
   - vi. Wireless USB: 2 USB 3.0 ports; 2 USB 2.0 ports
   - vii. Ethernet: Gigabit Ethernet viii. HDMI: 2 × micro-HDMI ports (up to 4kp60 supported)
   - ix. Storage: MicroSD Card Slot (32 gb) x. Power Supply: 5V/3A USB Type C Power
   - xi. Dimensions: 85.6mm × 56.5mm
2. Power bank (40000 mAh): The power bank serves and is the power source of the Raspberry Pi.It was connected to the Raspberry Pi using a Type C USB cable. The power bank brand used for this research is Aukey Power Bank.
3. Memory card (64 GB): The memory card used for this project was made by SanDisk, the importance of the memory card is to serve as the ROM for the Raspberry Pi.

6. Procedures for Raspberry Pi configuration

The Raspberry Pi has to be configured before the model can run on the Raspberry Pi and then compare results with a Personal Computer. Raspberry Pi configuration steps:

1. Insert memory card to laptop through SD card reader.
2. Download the SD card formatted for Windows on www.sdcardformater
3. Download Raspberry Pi OS
4. Download and install Win32 Disk Manager.
5. Copy the path of Raspberry OS to Win32 Disk manager and click write

6. Download Putty and install
7. Download Xming and install
8. Eject the SD card and put in Raspberry Pi
9. Download and install VNC Viewer on a laptop

After the configuration process, a setup command line is done

i. Download and install VNC Viewer
ii. Execute sudo apt-get install python- matplotlib
iii. Type sudo apt-get install python-NumPy to install python
iv. Execute sudo apt-get install python- Scipy
vi. Type sudo apt-get install python-imaging to install python This was done to enable the running of codes on the Raspberry Pi.

7. Configuration of accessing Raspberry Pi

The following steps show how Raspberry Pi was configured to run remotely. Figure 3 visually represents the configuration of Raspberry Pi.

1. Ensure Raspberry Pi is powered either to an electric socket or power bank
2. Raspberry Pi OS has been installed on the Memory card of the Raspberry Pi.
3. The Raspberry Pi is connected to WiFi
4. Download and install Putty on your PC.
5. Input the IP address of Raspberry Pi in Putty
6. Log in to Raspberry Pi with username and password
7. Input sudo apt-get install xrdp and click enter
8. Open Remote desktop connection input Raspberry Pi IP address

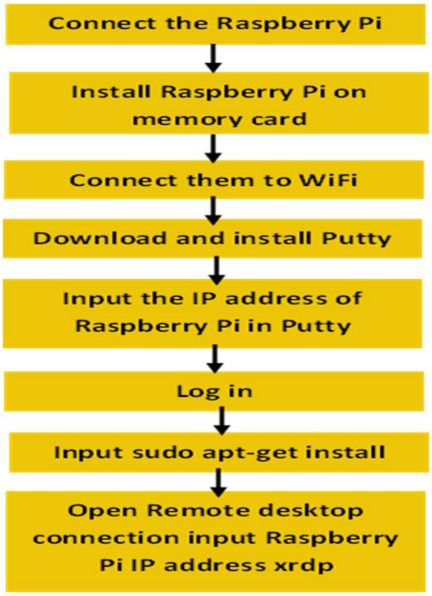


Fig. 2. *Flow Chat on Raspberry Pi*

8. Result and discussion

This session provides an overview of the results of the research objectives and a discussion of the results.

1.Acquisition of primary data and secondary data Kaggle

The malaria cell image dataset had 27560 images with an equal instance of parasitized and unparasitized cell images used for this research.The dataset was obtained from the Kaggle website. The 27 primary data images were obtained. Table 1 shows the result for the Acquisition of secondary data Class of Malaria cell images and Table 2 shows the result for acquired primary image data.

Table 1: *Result for Acquisition of secondary data Class of Malaria cell images*

Class of Malaria cell images	Number of Malaria cell images
Parasitized Malaria Cell images	13,780
Unparasitized Malaria Cell images	13,780

Table 2: *Result for acquired primary image data.*

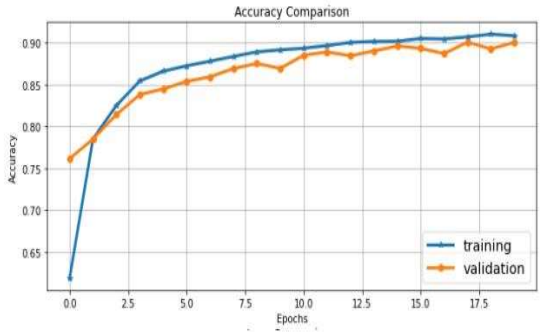
Class of Malaria cell images	
Parasitized Malaria Cell images	21
Unparasitized Malaria Cell images	6

2. Design and training of the model using acquired secondary image data and primary blood stain images for validation: The model was designed to operate remotely over the internet.This is to enable easy access to the Raspberry Pi DL model irrespective of location or time. The Raspberry Pi 27 however has to be connected to a power supply such as a power bank and connected to the internet. Table 3 explains the comparative result of personal computers and Rasberry Pi.

Table 3: *Comparative result of Model on Personal Computer and Raspberry Pi.*

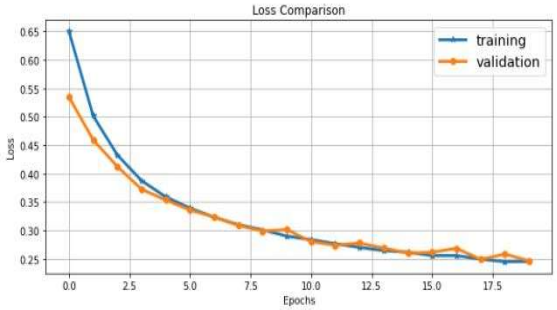
Personal Computer				Raspberry Pi			
Precision	Recall	Accuracy	Loss	Precision	Recall	Accuracy	Loss
0.8504	0.9694	0.8504	0.248	0.8504	0.9694	0.8504	0.248

According to[25] an Area Under ROC Curve (AUC) of 0.5 indicates no discrimination (i.e., the capacity to diagnose people with and without the disease or condition based on the test), 0.7 to 0.8 is regarded as good, 0.8 to 0.9 is considered excellent, and greater than 0.9 is considered remarkable. Fig 3 represents the ROC curve for calculating accuracy through training and validation. The ROC Curve as the epoch increases the loss function 29 reduces and accuracy increases as the epoch increases. It is represented in Fig 4. The datasets were also run on Raspberry Pi and the results of the DL and Raspberry Pi are considerably the same. Table 2 shows the DL model with the seventeen layers.



Y= Accuracy
X= Epoch

Fig.3. *ROC Curve for Accuracy Comparison of Model*



Y= Accuracy
X= Epoch

Fig. 4. *ROC Curve for Loss Comparison of Model*

Table 2: *The DL model with seventeen layers.*

Layer (type)	Output Shape	Param #
input_1 (InputLayer)	[(None, 98, 98, 3)]	0
block1_conv1 (Conv2D)	(None, 98, 98, 64)	1792
block1_conv2 (Conv2D)	(None, 98, 98, 64)	36928
block1_pool (MaxPooling2D)	(None, 49, 49, 64)	0
block2_conv1 (Conv2D)	(None, 49, 49, 128)	73856
block2_conv2 (Conv2D)	(None, 49, 49, 128)	147584
block2_pool (MaxPooling2D)	(None, 24, 24, 128)	0
block3_conv1 (Conv2D)	(None, 24, 24, 256)	295168
block3_conv2 (Conv2D)	(None, 24, 24, 256)	590080
block3_conv3 (Conv2D)	(None, 24, 24, 256)	590080
block3_conv4 (Conv2D)	(None, 24, 24, 256)	590080
block3_pool (MaxPooling2D)	(None, 12, 12, 256)	0
block4_conv1 (Conv2D)	(None, 12, 12, 512)	1180160
block4_conv2 (Conv2D)	(None, 12, 12, 512)	2359808
block4_conv3 (Conv2D)	(None, 12, 12, 512)	2359808
block4_conv4 (Conv2D)	(None, 12, 12, 512)	2359808
block4_pool (MaxPooling2D)	(None, 6, 6, 512)	0
block5_conv1 (Conv2D)	(None, 6, 6, 512)	2359808
block5_conv2 (Conv2D)	(None, 6, 6, 512)	2359808
block5_conv3 (Conv2D)	(None, 6, 6, 512)	2359808
block5_conv4 (Conv2D)	(None, 6, 6, 512)	2359808
block5_pool (MaxPooling2D)	(None, 3, 3, 512)	0
flatten (Flatten)	(None, 4608)	0
dense (Dense)	(None, 1)	4609

Total params: 20,028,993
Trainable params: 4,609
Non-trainable params: 20,024,384

9. Advantages and Disadvantages

Advantage

- This method can operate on low-specification hardware to operate a DL model and Raspberry Pi for remote malaria diagnosis.
- The CNN model allows for a more comprehensive analysis of infected and uninfected blood cells.
- This method provides insights into the ideal layer of a pre-trained model for extracting characteristics from malaria parasite data
- This method offers improved accuracy in malaria diagnosis and insights into optimizing CNN models for malaria detection.
- This method increases the detection processing speed.

Disadvantage

- While training, it required sufficient data for CNN and it is a time-consuming process.
- In CNN models, medical image processing and analysis is crucial for large image dataset to obtain reliable results.

10. Conclusion

The DL model can classify images as parasitized and unparasitized with an accuracy of 90%. Furthermore, as the epoch of the ROC Curve increases, the loss function reduces, while accuracy increases as the epoch increases. The Raspberry Pi is also capable of malaria diagnosis using deep learning. Its results are comparable with those achieved on a personal computer. This research additionally proves that Raspberry Pi can be used for malaria diagnostics remotely, and also helps to circumvent the limitation of high computer hardware specifications needed to run a deep learning model. This research provides a prototype for enhancing malaria detection from images by deploying a deep learning model – a convolution neural network, on a Raspberry Pi. This research also makes available fifty primary malaria image datasets. This research is recommended as a confirmatory test, as the model can classify images obtained from the laboratory as parasitized or unparasitized. The disadvantage of this model is that images have to be labeled to identify which image belongs to a patient as images are analyzed randomly which can be tiring.

Compliance with Ethical Standards

Conflicts of interest: Authors declared that they have no conflict of interest.

Human participants: The conducted research follows the ethical standards and the authors ensured that they have not conducted any studies with human participants or animals.

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