MALARIA DISEASE RECOGNITION THROUGH ADAPTIVE DEEP LEARNING MODELS

Sammy V.Militante

Faculty of College of Engineering and Architecture,
Universityof Antique
Sibalom, Antique,Philippines

sammy.militante@antiquespride.edu.ph

ABSTRACT: Malaria is a disease from blood generated by the Plasmodium parasites spread through the bite of female Anopheles mosquito. Experts usually examine the denseand fineblood slursto diagnose illness and calculate parasitemia. However, their accuracy varieson slurcharacteristics and skill in gradingand counting infected and healthy cells. Such an examination could be laborious for large-scale diagnoses resulting in poor conditions.

Convolutional Neural Network, a divisionof deep learning (DL) models has a superior and scalable result in terms of feature extraction and classification. Automatic screening of malaria with deep learning techniques is a useful diagnostic aid. In this study, the author evaluated the performance of the pre-trained convolutional neural network-based Deep Learning models as feature extractors in classifying infected and uninfected cells to aid in enhancing diseaseexamination. The author experimentally determines the optimal model layers for feature extraction from the underlying data.

KEYWORDS:*malaria, blood smear, deep learning, convolutional neural networks, machine learning*

1.0   INTRODUCTION

Malaria is a severe and deadly disease caused by Plasmodium parasitic infection spreadthrough the bite of a female Anopheles mosquito. Fatal indications and infection in the red blood cells because of these parasites matured in the human liver and are released into the bloodstream. Its estimated death reported by the World Health Organization (WHO) has reached over 435,000 on a global scale [1]. The most vulnerable are the children below five years of age with an estimated death count of 61%. The disease spread has a high occurrence in Africa, South-East Asia, and Eastern Mediterranean regions. It has accounted for an estimated cost of $3.1 billion investment worldwide for malaria control and its eliminationin disease endemic countries [1]. Early identification and treatmentare the best way to avoid and control this type of disease. The most common method to detect the malaria disease is through

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microscopic blood examination [2]. However, labor-intensive diagnosis is a difficult process; theaccuracy of diagnosis is impacted by the accountability enforced by issues including inconsistencyof observation and comprehensivetesting in the disease-endemic countries like the third world countries with limited resources [3].

A study of Poostchi et al. provided a survey on a machine learning algorithm that uses a Computer-aided diagnostic (CADx) tools applied to microscopic blood smear images can lessen the medical burden by assisting with triage and disease analysis. Poostchi et al. [4] delivered a review of such methods. These tools process medical images for usual forms and highlight pathological features to complement clinical decision-making. These tools, CADx has gained popularity in an image-based medical analysis and risk assessment. Yet, this tool used for diagnosing malaria diseases utilized only for an individual dataset and trained for handcrafted feature extraction procedures and trained particularly in resource machinery, position, dimension and region of interest (ROI) [5], [6]. Currently, deep learning (DL) techniques have succeeded in the performance of handcrafted feature extraction mechanisms by self-discovering the features from image data and carrying out extraction features and classification [7]. Convolutional neural networks a divisionof Deep Learning models have proven an encouraging result in image classification, recognition, and localization tasks [8], [9].

Deep learning refers to the use of artificial neural network architectures that contains many processing layers as compared to traditional neural network architectures [7]. Now, computationally possible deep learning models have revolutionized sectors such as image-segmentation,image-recognition, image-detection, classification, voice recognition, and other complicatedmethodsthat deals with the evaluationof important of data [10], [11], [12], [13], [14], [15].

Present studies suggest that the use of a convolutional neural network shows promising results in disease recognition [16] and deep learning algorithms and techniques[16], [17]. An example of a deep neural network that works like the organization of an animal visual cortex. It is intended to routinelyand adaptively extract and learn features from classes of images to perform tasks as such classification [18], [19]. The development of a CNN-based biometric recognition as another example could be done by either modeling-from-scratch or transfer learning [20]. Modeling-from-scratch is a technique in developing a CNN-based biometric that heavily relies on the depth of available datasets through which features of classes will be extracted and learned for recognition. This method of CNN modeling slowly relies on the richness of used datasets and training time for learning new classes [20].

The main goals of this paper can be summarized as follows:
• Identify the best CNN model for malaria disease detection through adaptive deep learning methods.

• Compare each deep convolutional neural network architecture used in malaria disease detection in terms of accuracy performance.

2.0   CONVOLUTIONAL NEURAL NETWORK

Deep Learning is a subsectionof machine learning that is a subsectionof artificial intelligence that plays a vital role in developing human intelligible and independent systems. Deep Learning imitates the functionality of the human brain, which consists of an enormous number of neurons controlled by a central nervous system. Similarly, deep learning also composed of several numbers of neural networks, where each neuron is represented as a single node, and the entire activity is controlled by the computer's processor.

The architecture of each model varies from one another based on the number of layers and various functions. The base part of every deep learning model for computer vision and image processing applications is the Convolutional Neural Network (CNN). Components of a CNN model includes convolutional layers, pooling layers, fully connected layers, activation functions, etc. as shown in figure 1.
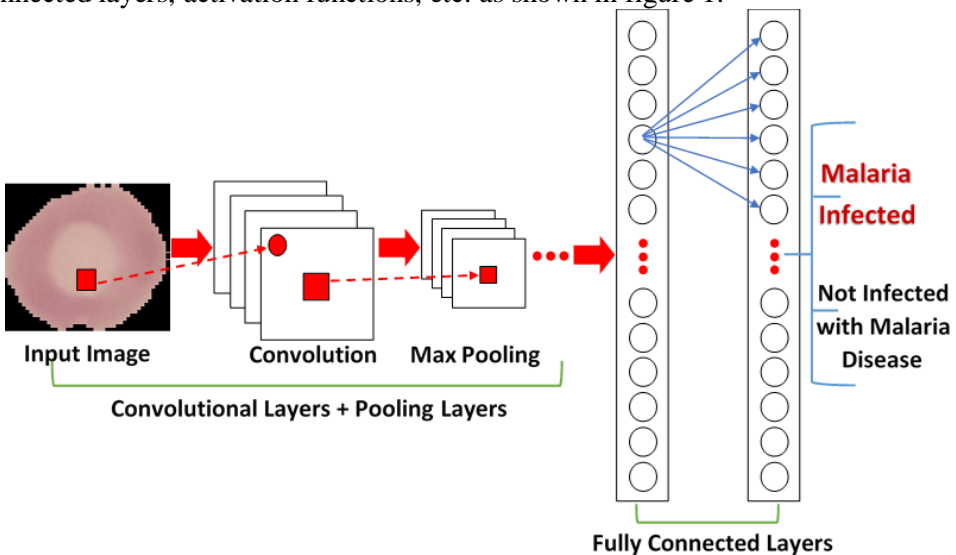

Figure1:Aflow chartof thefeature selection heuristic

2.1   Convolution Layer

The layer receives as input an RGB image or an output of another layer for further processing. Input received is read as pixel values to produce feature maps representing low-level features such as edgingsand curves. Higher-level unique features can be identified through a series of additional layers of convolution.

2.2   Activation Layer

Non-linearity makes a neural network more powerful. A non-linear activation layer is applied immediately after each convolution layer.

2.3   Pooling Layer

A downsampling layer applied after the activation layer to reduce the spatial dimension with no change in depth. Usually, a filter of size 2x2 is applied to the input to produce an output based on the type of pooling. Pooling can be either max pooling or average pooling where either the maximum value or the average value from every sub-region bounded by the filter is taken. Pooling has no parameters.

Overfitting is a situation where the model achieves 100% or 99% on the training set but an average of 50% on the test data. This can be overcome by introducing dropout layers where a random collection of activations is dropped out by setting the value to 0. Dropout is a function that improves generalization by learning several different representations of patterns. Later, ReLU and max pooling are applied to get a reduced dimension feature map.

2.4   Fully Connected Layer

This layer identifies very high-level features that greatly correlate to an object or class. Input to a fully connected layer is a set of features for classifying images without considering the spatial structure of the images. Most of the models use two fully connected layers. The output of a fully connected layer is a 1D vector obtained by flattening the output of the final pooling layer. Flattening is a process of arranging 3D volume into a 1D vector.

3.0   METHODOLOGY

In this section, malaria images collection and data preprocessing are described. This is followed by the discussion of used CNN architectures. Latter subsections discuss the details of the used method in each step of the study framework as shown in figure 2.

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┌─────────────────────┐        ┌─────────────────────┐
│                     │        │ Malaria image pre-  │
│ Malaria infected and│        │ processing          │
│ uninfected image    │──────▶ │ Cropping            │
│ database            │        │ Resizing            │
│                     │        │ Histogram           │
│                     │        │ Data Augmentation   │
└─────────────────────┘        └─────────────────────┘
                                          │
                                          ▼
┌─────────────────────┐        ┌─────────────────────┐
│                     │        │ Training            │
│ Testing and         │◀────── │ Feature Extraction  │
│ Validation          │        │ Fine-Tuning         │
│                     │        │                     │
└─────────────────────┘        └─────────────────────┘
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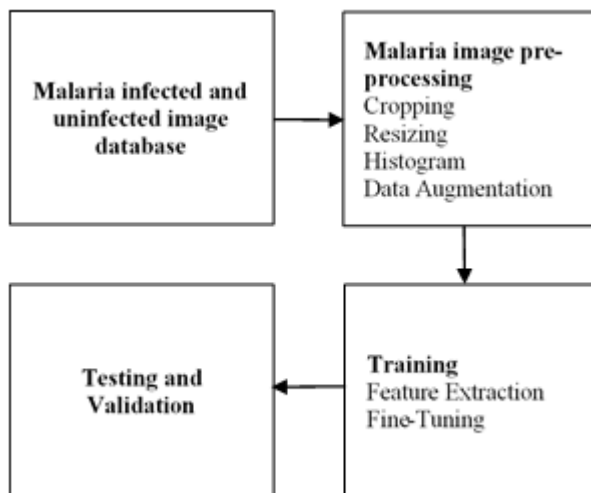
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Figure2:Malaria Disease Detection Framework

3.1   Image Dataset Acquisition

The first step is the collection of images of blood slur consisting of infected with malaria diseases and not infected with malaria diseases is used in the framework for this study. The dataset used in this study was collected from the National Library of Medicine (NLM) which comprisesof a total 27,558 cell images of malaria-infected diseases and not infected with malaria diseases.

3.2   Preprocessing of Images

Preprocessing of images is the second step in the used malaria detection framework of the study. Every malaria-infected and not infected diseased images are manually cropped to produce a set of images with different square dimensions. However, to satisfy the input requirement of the used CNN architectures, cropped images are resized to 96x96 square pixels. To avoid overfitting and remembering the precise details of each image by CNN architectures, each image is automatically resized to 32x32 pixels. As preparation for transfer learning, 80% of the preprocessed images are assigned for the training while the remaining 20% is kept for testing and validation of each CNN. There are no other methods applied aside from the processes stated above. Figure 3 and figure 4 shows the sample of collected and preprocessed images with malaria-infected and not infected diseases.
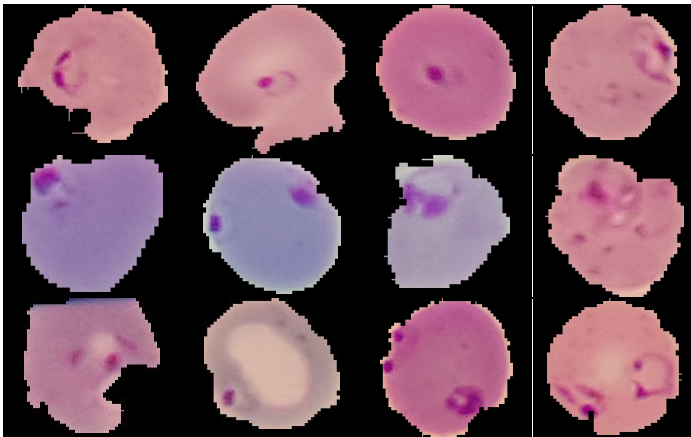

Figure 3: Sample images of Malaria infected disease

Figure 4: Sample images of uninfected with malaria diseases

3.3   Feature Extraction

The convolutional layers extract features from the resized images. The third step of the study includes feature extraction and fine-tuning which are the core methods in training and modeling of the study. The sub-section below discusses the used CNN architectures for modeling malaria disease detection. Earlier layers of each architecture are used as a feature extractor.

3.3.1 GoogLeNet

GoogLeNet is a small CNN that is very close to human-level performance with its exploitation of multiple layers of convolution or inception modules in parallel and bottleneck strategy to control overfitting and parameter explosion. On architectural-level performance, GoogLeNet uses small convolutions, batch normalization, and factorization and because it uses smaller convolutions, parameters are drastically reduced within the network. GoogLeNet's parameter is approximately 4 million which is 15-times smaller than AlexNet.

3.3.2 ResNet

ResNet architecture can manage the degradation of image classification accuracy on a deeper layer of convolutions. ResNet introduces the use of residual blocks for learning. On the architectural view, ResNet is composed of combined multiple sized convolution filters that can manage accuracy degradation and reduces training time. In this paper, ResNet-18 is used. ResNet-18 is a version of ResNet that has 2 layers of convolution in a residual block and is 18 layers deep for a total depth of 75 layers.

3.3.3 AlexNet

AlexNet is considered as the first state-of-the-art deep learning approach after it outperformed traditional computer vision methods in terms of accuracy and recognition rates. It is the most well-studied CNN architecture due to its impact on most image classification tasks. The architecture and network design of AlexNet are composed of 8 sequential layers with approximately 60 million parameters for a total

of 25 layers.

3.3.4 VGGNet

VGG network architecture consists of 16 convolutional layers and this network is characterized by its simplicity, using only 3×3 convolutional layers stacked on top of each other in increasing depth. Reducing volume size is handled by max pooling. Two fully connected layers, each with 4,096 nodes are then followed by a softmax classifier. VGGNet consists of 138 million parameters and it is the most used image recognition architectures.

3.4 Fine Tuning

Fine-tuning is the final method used in the study, earlier layers of each CNN architectures are used for feature extraction while the last 2-3 layers are for learning. To let each architecture, learn classes of malaria-infected disease and not infected with the disease, the last 2-3 layers of each architecture are replaced with layers of the same kind but of different parameters.

Each model is architected to learn classes of malaria-infected disease and not infected with the disease with a weight rate and neuron bias rate of 20 on both the fully connected layers and softmax or activation to further accelerate the process of learning on new layers. Fully connected, softmax and classification layers are replaced in each architecture.

4.0 EXPERIMENTAL SETTINGS

Automatic data augmentation procedures have been used to increase the dataset by randomly rotating the images by a small amount of 25 degrees, horizontal flipping, vertical, and horizontal shifting of images. The optimization was carried out using Adam optimizer with categorical cross-entropy as the loss function. A batch size of 64 has been used, and the model has been trained for 100 epochs. The initial learning rate has been set to 0.01. Early stopping has also been used to monitor the validation loss and stop the training process once it increases. All the experiments were performed on ASUS laptop computer with 8th generation Intel Core i7 processor,16 GB memory and 4GB video graphics card.

5.0 RESULTS AND ANALYSIS

The results show that the model performs well on the dataset and can be used as a means for classification of classes of malaria-infected disease and not infected with the. Figure 5 illustrates the validation accuracy and loss using the ResNet model. Figure 6 displays the validation accuracy and loss using the VGG model. Figure 7 and figure 8 show the validation accuracy and loss using GoogleNet and AlexNet model respectively. Figure 9 illustrates the prediction model of malaria disease infected image using different deep learning models. All models achieved an accuracy rate of 100% in predicting a malaria disease based on the image. Figure 10 displays the

prediction model of an image not infected with malaria disease using different deep learning models. In this sample image, all the models achieved an accuracy rate of 100%.
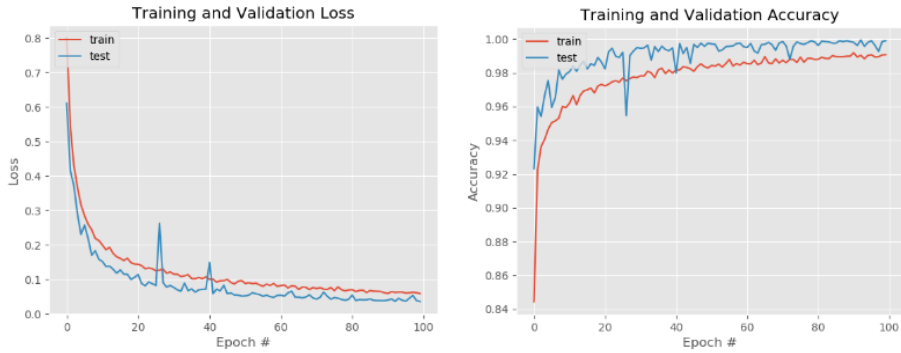

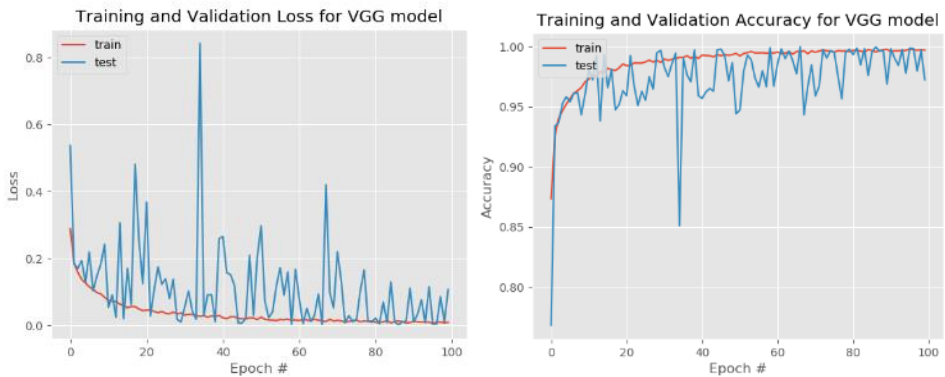Figure 5: Plots of accuracy and loss against epochs using ResNet model

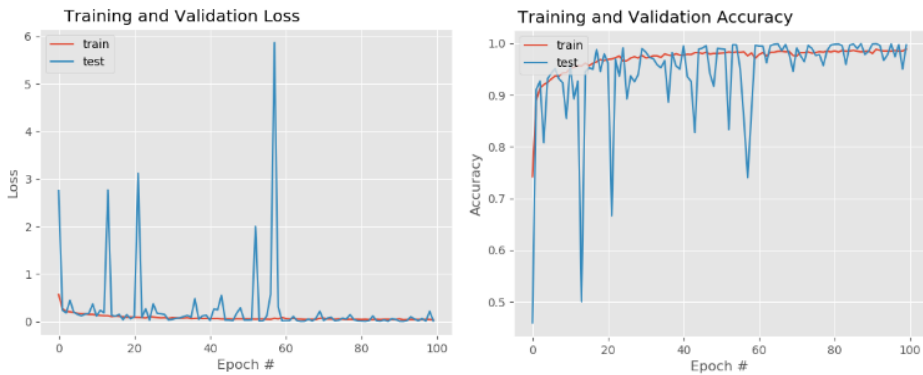Figure6: Plots of accuracy and loss against epochs using the VGG model

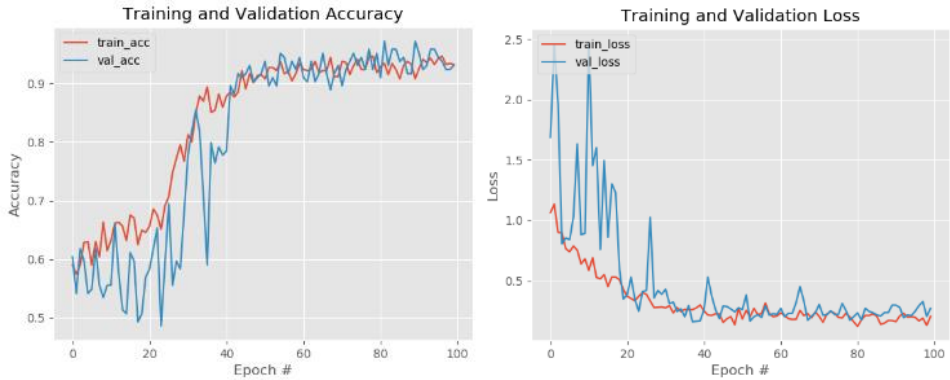Figure 7: Plots of accuracy and loss against epochs using the GoogleNet model

Figure 8: Plots of accuracy and loss against epochs using AlexNet model
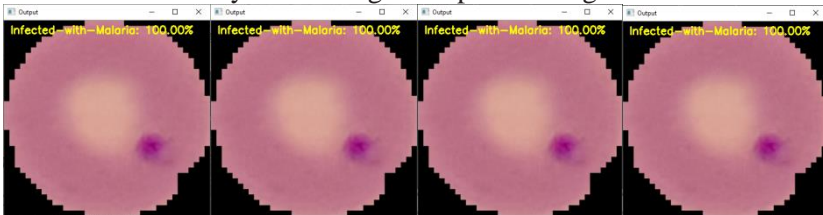

Figure 9: Shows the models of GoogleNet (far left image), VGGNet (left image), ResNet (right image) and AlexNet (far right image) predicted the image is infected with malaria disease.
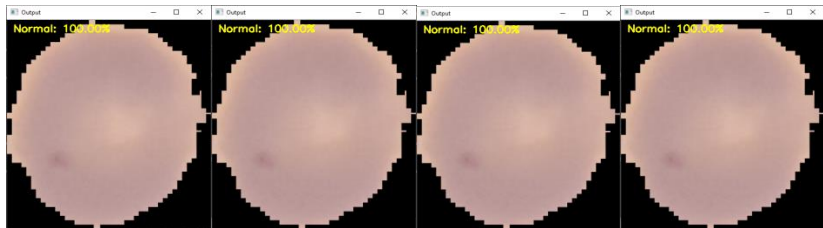

Figure 10: Shows the models of GoogleNet (far left image), VGGNet (left image), ResNet (right image) and AlexNet (far right image) predicted the image is NOT infected with malaria disease.

6.0   CONCLUSION AND RECOMMENDATION

This paper explores the adaptive deep learning using malaria detection through computer vision using 4 convolutional neural network models namely: AlexNet, GoogleNet, ResNet and VGGNet. The malaria-infected diseases and uninfected diseases dataset are acquired from the National Library of Medicine (NLM) database. 80% of acquired images are used as training data while the remaining 20% is used for testing and validation. Performance results of each generated malaria detection model

are compared in the context of their training time, learned features, accuracy, and losses in recognizing the images. It is identified that the ResNet, AlexNet, GoogleNet, and VGGNet are the best CNN models for malaria disease detection in adaptive deep learning.

For future studies, an adaptation of other convolutional neural network architectures like Inception-v3, shuffle Net, MobileNet-v2 and handcrafted CNN architectures for malaria disease detection should be performed using standard training configuration. Adaptation of methods used in this study to other disease detection and recognition should be employed to provide better references to the deep learning studies.

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