

Malaria parasite cell identification in blood smear microscopic images using Deep Learning

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Abstract

Deep learning (DL) is very useful in biology and medicine because it can be applied to massive volumes of data. DL has emerged as an important new technique for interpreting unique elements of cell-biological activities at different sizes. Malaria is a mosquito-borne parasitic illness caused by the Plasmodium parasite. Malaria is the most frequent illness globally, mostly in tropical regions. Symptoms often appear after one or two weeks. A dangerous parasite can live unnoticed in a person's body for up to a year. Delaying treatment may result in complications and even death. As a result, early malaria detection can save many lives. In practise, radiologists detect the condition using parasitemia estimates and blood (thin/thick) smear testing. Microscopy is the greatest choice for identifying malaria since it may detect parasites in blood drops in thicker blood smears. A microscope was frequently utilized since it was inexpensive yet time-consuming. The accuracy of the examination is dependent on the quality of the blood smears and the availability of a competent expert who is proficient in identifying and assessing parasitized and uninfected blood cells. The primary goal of this study is to use deep learning techniques to detect malaria parasites at early stage in microscopic images.

Nimmagadda Muralikrishna

Keywords: Deep learning, Microscopic Images, Parasitemia, malaria, CNN;

1. Introduction

Deep learning (DL), can be particularly helpful in the fields of biology and medicine since it can be applied to vast amounts of data. Several variables, such as the following, have contributed to the rapid expansion of DL in biomedical imaging:

(a) the accumulation of massive amounts of data produced by digital imaging tools, such as microscopes;

(b) the accessibility of robust yet reasonably priced hardware and software computational tools that can be used to process data; and

(c) the capacity to make use of information from various microscopy sources by improving imaging resolution. Due to the interaction of these elements, DL has emerged as a crucial new tool for deciphering novel aspects of cell-biological events on various scales. [1]

1.1 Malaria

Malaria [2] is a parasitic disease by mosquito and infected by the Plasmodium parasite. The disease that is most common worldwide, mostly from tropical region, is malaria. Figure 1 depicts how malaria is transmitted around world. When an “infected female Anopheles” mosquito bites the person, parasite enters into circulation and starts to kill RBCs, which carries oxygen.

Malaria first appeared as the flu [3]. Usually, the symptoms start to show after one or two weeks. Deadly parasite will remain undetected in a person's body for up to a year. Delaying treatment might therefore lead to problems and even death. Early malaria detection can therefore save a great deal of lives. Around half of global population was afflicted by malaria, which causes more than 400,000 deaths annually.

In real life, radiologists use parasitemia calculations and blood (thin/thick) smear examination to identify the disease. The best alternative for detecting malaria is microscopy because it can find parasite in blood drops in thicker blood smears [4,5]. On the other hand, thinner blood smears are used to distinguish parasite species and the advancement of malaria stage.

Since using a microscope was affordable yet time-consuming, it was often used. The quality of the blood smears and the availability of a qualified individual who is skilled in classifying and evaluating parasitized and uninfected blood cells are both necessary for the examination to be accurate.

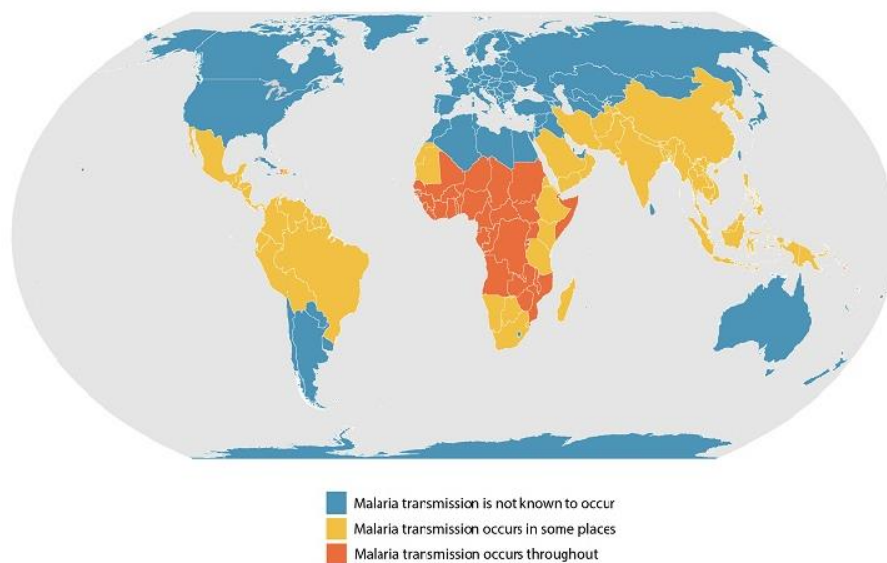


Figure 1. The estimated areas of malaria transmission around the globe are depicted on this map. (Image source: [6])

The main aim of this research work is to detect malaria in microscopic images using deep learning techniques.

2. Literature survey

The study describes an Android smartphone software that uses images of blood smear films stained with Giemsa to identify malaria. [7] Primary imaging component contains, intricate morphologic processes which would recognize parasites inside infected cells as well as detects white and red blood cells. The programme calculates parasitemia and recognizes different stages of parasite life. Immediately after 60 seconds, the application offers the diagnosis, and it was tried out and verified on various Android tablets and smart phones.

The researchers assessed the diagnostic efficacy of an automated RDT interpretation system that makes use of image processing algorithms and mobile technologies. [8] Device's diagnosis performance is on par with RDT visual analysis. RDT-based malaria diagnosis programmes will be used much more widely if standardized automatic translation of RDTs is made available in remote regions. This is in addition to practically real case reports and quality monitoring.

The authors demonstrated a platform for a mobile phone RDT scanner which works with a range of "lateral flow immuno chromatographic tests" and other testing. [9] RDTs may be put and scanned using a small, low-cost digital RDT scanner that attaches to a phone's existing camera unit. A smartphone app then electronically processes the raw images of these RDTs to validate the RDT and automatically interpret the diagnostic data. Furthermore, a smartphone-based smart RDT scanner really provides spatiotemporal information about the occurrence of key infectious illnesses, enabling the tracking of epidemics.

A "computer assisted diagnostic (CAD)" application that uses the ML approach is used in the study [10] to assist medical professionals in evaluating illnesses using blood smear images. From scans, the CAD technology was able to identify pathological characteristics that helped professionals make decisions. The development of feature extraction algorithms has brought CAD to the forefront of image-based clinical testing, where it is used to detect malaria infections [11,12].

The authors of [13] introduced the Faster R-CNN, a CNN-based object detection model. The model is developed using their dataset after being fine-tuned using Imagenet [14]. Deep relative attributes (DRA) are used in yet another paradigm that was put out by [15]. CNN is used by the authors to recognize epileptic seizures [16]. The segmentation and classification of malaria parasites are both taken into consideration by the automated method that was proposed in [17]. While the classification system is based on an "Extreme learning machine (ELM)" [18], segmentation method is based on a deep CNN [19].

Unsupervised machine learning (ML) methods using stacked autoencoder to extract characteristics from images of infected and non-infected cells were put forth in the literature in [20,21]. Authors in [22] presented deep learning algorithms to categorize malaria cells in red blood cells. The approach uses a 16-layer CNN model to beat transfer learning-based models that rely on AlexNet [23].

3. Deep learning (DL), Convolutional neural network (CNN) and Transfer learning (TL)

The way the human brain functions, which is composed of a large number of neurons under the authority of Central nervous system, is mimicked by DL[37]. Similar to machine learning, DL have various neural networks (NN), here every neuron will be represented as the separate node, with CPU controlling overall activities [21]. Voice recognition, classification, image detection, identification, segmentation, and other complicated processes requiring extensive data processing have all been transformed by deep learning models [24-26].

DL uses reinforced, semi-supervised, unsupervised, and supervised techniques. For completing tasks like object identification, image classification, and image segmentation, supervised models were employed[37]. The automatic extraction of characteristics from raw data is the primary advantage of DL. Every model has a different design depending on the number of layers and the various features. As base of any DL model to image processing techniques, CNN became an intriguing subject for machine vision specialists. CNN uses many layers to carry out various execution steps. Figure 2 presents an illustration of a generic CNN architecture [36].

Numerous image-based and machine vision applications have undergone radical change as a result of CNN, a supervised DL method [38]. In areas like face recognition, object identification, image classification, and others, CNN was often used. CNN components are "Convolutional layers, pooling layers, fully connected layers, activation functions," and so on, as shown in Figure 2.

3.1. Convolutional Layer

This layer receives RGB image as input/output of another layer to process. Goal of the optimization function is to produce kernels that faithfully represent the data[39]. A number of statistical techniques are used in this layer to extract feature maps from input image [19][45].

3.2. Activation Layer

The neural network's power is increased by nonlinearity. Non-linear activation layer was added after every convolutional. This layer's convolutional layers all have non-linear Rectified Linear Units (ReLUs) that are assigned constants [35].

3.3. Pooling Layer

To minimize spatial dimension, downsampling layer will be added after activation layer. A 2x2 filter is typically used on input to generate the output based on the kind of pooling[37]. By lowering computation rate, training duration, number of features, and size of feature maps, pooling layer reduces overfitting [27].

A model is considered to be overfitted when it achieves 99 or 100 percent accuracy on train set but only 50% accuracy on testing data [34]. The problem is resolved with, adding a dropout layer, which eliminates the random selection of activation by reducing the cost to 0[40][44]. The generalization function known as Dropout learns how to represent various patterns. Then, max pooling and rectified linear are used to create a lower dimensional feature map [28][43].

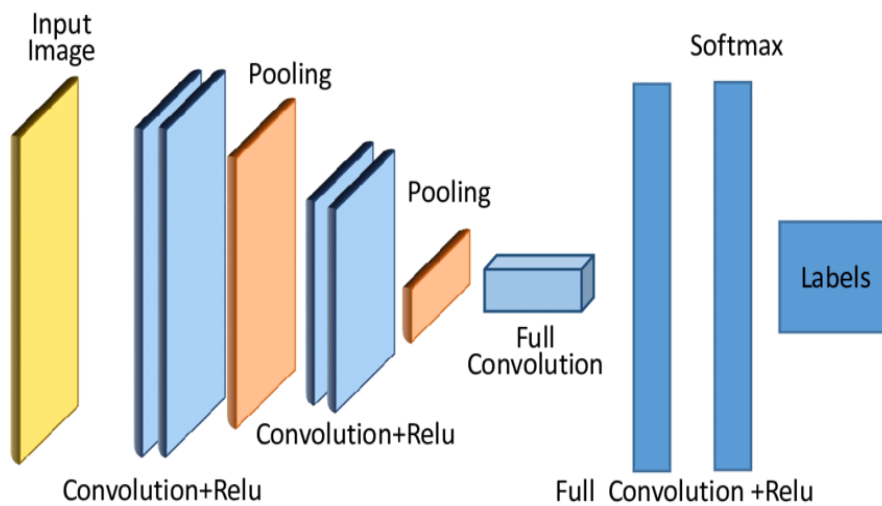


Figure 2. Generic CNN architecture (Image source : [29])

3.4. Fully-Connected Layer (FC)

FC identify extremely higher level features which have a close relationship to the class or object. Without taking into consideration of images spatial structure, a set of attributes were used as inputs to the FC layer. The pooling layer's output is flattened in order to produce the FC layer's results, which is how a three-dimensional vector is converted into a one-dimensional vector[41][42].

Convolutional Neural Networks demonstrated effective and accurate illness diagnosis in tests [18,19]. CNN-based algorithms for disease identification that may be created from scratch or through TL [27]. The method of starting from scratch relies only on the amount of data required to learn and retrieve attributes for identification, and training the model requires a lot of computing time [28], [7].

4. Methodology

CNN-based image classification has performed rather well. This study uses transfer learning, a deep learning approach, to classify microscopic pictures of malaria blood smears. Transfer learning uses pre-trained VGG16, and ResNet50 models. Figure 3 displays an overview of the proposed system.

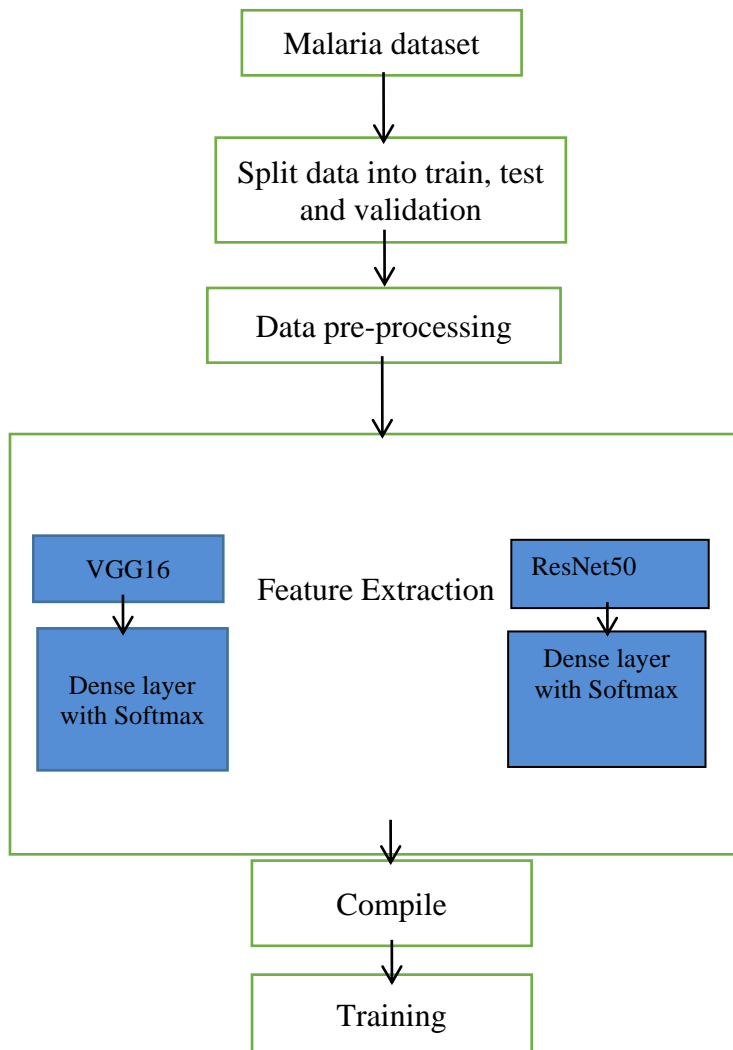


Figure 3: Proposed Deep-Architecture

4.1 Data Collection and Data pre-processing

The Malaria dataset was taken from [31]'s kaggle, which was sourced from [30]. We divided the 550 blood smear images from the original dataset into 416 images for train and 134 images for test to form malaria dataset for suggested model. Samples of infected and uninfected blood smears are shown in Figures 4, 5, respectively. Images in the dataset are downsized to 224x224 pixels.



Figure 4: Samples of malaria Parasite

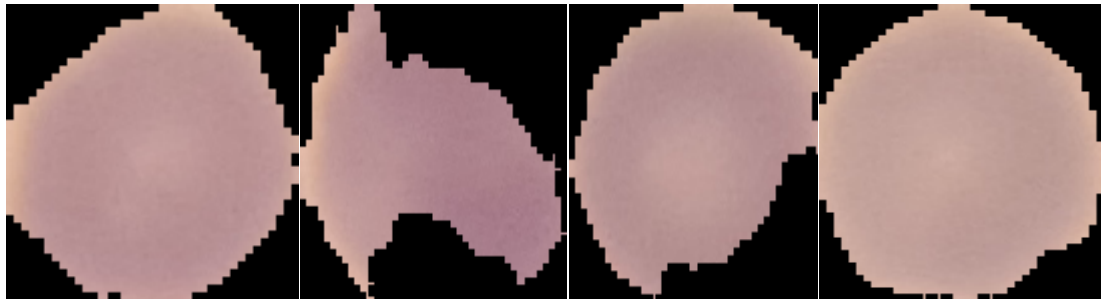


Figure 5: Samples of Uninfected

4.2 Feature Extraction

Convolutional layers were utilized to extract data in scaled photos. Next Stage of research concentrates on feature extraction, fine-tune the model to train., and CNN design for malaria disease detection system modelling.

4.2.1 Transfer learning (TL)

Underlying network learns base datasets, and then initial features were used to train another network on malaria dataset. Pre-train models used on comparative data gave good outcomes for tasks involving image classification. Just a few companies have created models which take months to train with current technology, like VGG by Oxford[29], Inception model by Google [31]. ResNet by Microsoft [32]. Those models were free to download and can be paired with much more contemporary models which use photos as inputs to provide more accurate data. Malaria dataset is trained on pre-trained VGG16 and ResNet50 models to detect malaria disease.

4.2.2 VGG

VGG ranked first in image localization and 2nd in image classification challenge at the 2014 “Image Net Large Scale Visual Recognition Competition (ILSVRC)”. Oxford academics created VGG and released weights and design online. The design shown in Figure 6 was created using only 3*3 convolution layers, 2*2 maximum pooling layers, and fully connected layers at the bottom. Size of received picture must be 224*224*3. (RGB image). The VGG16 (figure 6) is being used to detect malaria infection.

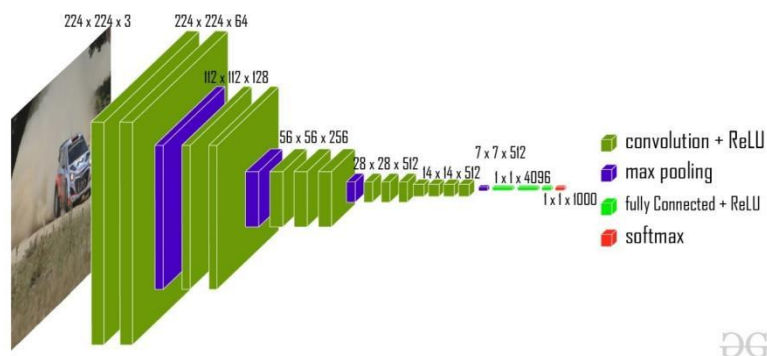


Figure 6: VGG16 Architecture (Image source: [33])

4.2.3 ResNet

The ResNet design can manage an accuracy decrease in image classification on deep convolutional layers [33]. In the past, NN learned by stacking convolutional layers; the more depth a model has, the more it will learn. In contrast, as network depth increases, accuracy reaches saturation and deteriorates. ResNet proposes residual block learning as the remedy. ResNet is built using varied size convolutional filters to

help control accuracy loss and shorten training times. To detect malaria, ResNet50 is being used for experiment.

5. Experimental results and analysis

Photos of parasite and uninfected blood smears in the malaria dataset have all been scaled to 224x224 pixels. There were 134 pictures in test set and 416 images in train and validation sets. The experiment was run in Google Collab, and a free GPU was used to train the model.

The images will be input into pre-trained ResNet50, VGG16 models, which will include ImageNet pre-trained weights. Final layer is going to be fully connected dense layer with softmax activation. To learn input data, pre-trained weights would be employed, and single learning layer would be intensively activated using softmax function, which is effective for category categorization. Loss was determined during compilation using categorical crossentropy and the 'adam' optimizer. In furthermore, model is trained over 100 epochs with 32 batch size. Accuracy and loss of the model are used to assess models efficacy.

Categorical crossentropy loss is calculated as,

$$\text{Loss} = - \sum_{i=1}^{\text{output size}} y(i) * \log \sim y(i) \tag{1}$$

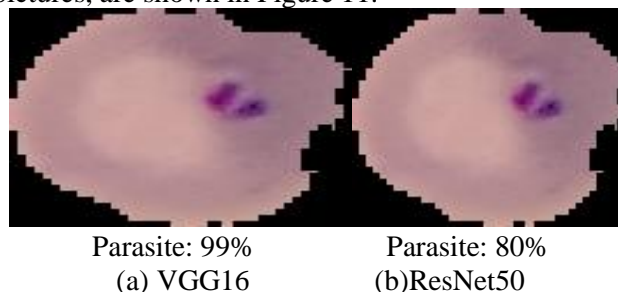
Where,

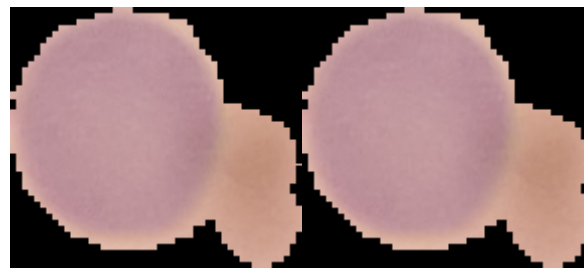
- Output size : scalar value count in model output
- $y(i)$: corresponding target value
- $\sim y(i)$: i-th scalar value in model output

The accuracy is determined as follows, which used to determine the model's correctness.

$$\text{Accuracy} = \frac{\text{True Negatives} + \text{True positive}}{\text{True Positive} + \text{False positive} + \text{True Negative} + \text{False Negative}} \tag{2}$$

Figure 7 displays train and validation loss for VGG16 model, while Figure 8 displays its accuracy. Figure 9 displays train and validation loss for ResNet50 model, while Figure 10 displays its accuracy. Table 1 displays quantifiable findings for the performance of all three models. As a result of the short dataset and higher validation accuracy than other models, VGG16 produced superior results. The qualitative findings from the proposed approach, which accurately identified the malaria parasite and uninfected cells from blood smear microscopic pictures, are shown in Figure 11.





Uninfected: 99%

(c) VGG16

Uninfected: 99%

(d) ResNet50

Figure 11: Qualitative results achieved by the proposed deep architectures

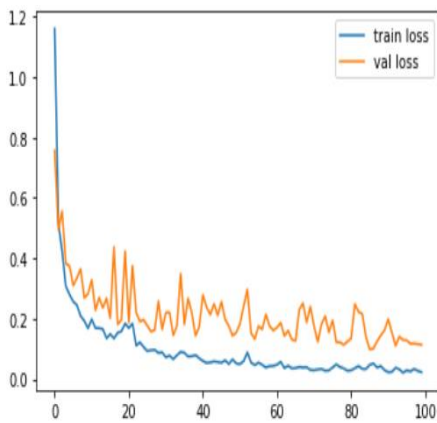


Figure 7: VGG16 train and Validation loss

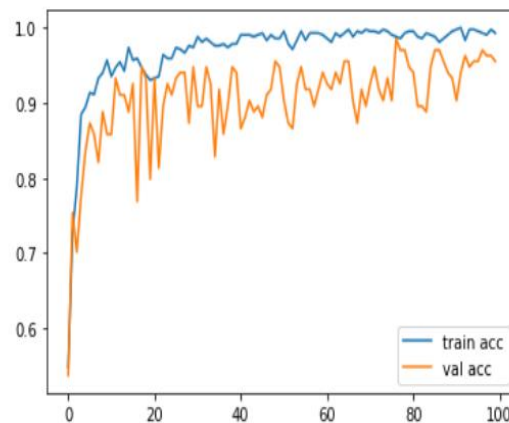


Figure 8: VGG16 train and Validation accuracy

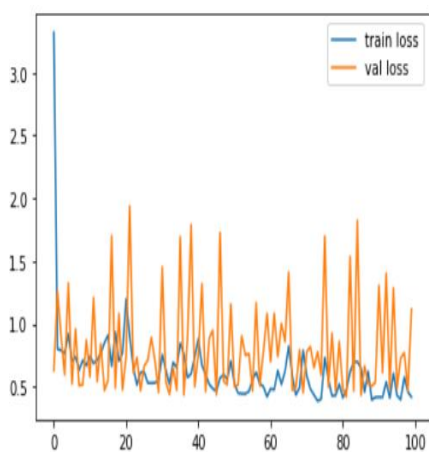


Figure 9: ResNet50 train, Validation loss

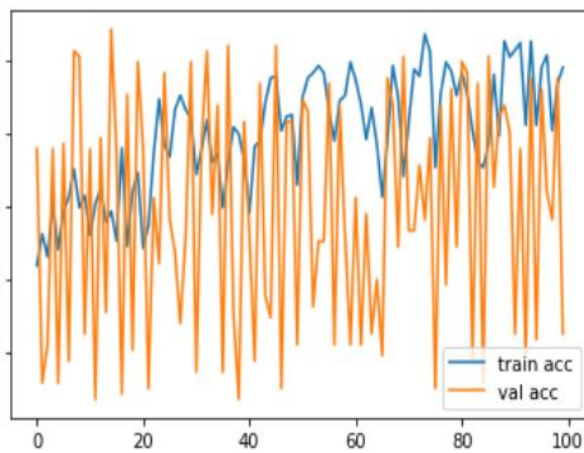


Figure 10: ResNet50 train, Validation accuracy

Table 1: Quantitative results achieved by VGG16, ResNet50 on malaria dataset

Models	Train Accuracy	Validation Accuracy	Validation Loss	Train Loss
VGG16	99	97	0.1	0.02
ResNet50	80	61	0.7	0.3

6. Conclusion

Microscopy is one of the most effective methods for diagnosing malaria. The microscope was often used since it was affordable yet time consuming. The examination's accuracy is determined on the quality of the blood smears and the presence of a trained expert who is educated in the categorization and assessment of parasitized and uninfected blood cells. Therefore we used Transfer learning, a deep learning approach on pre-trained VGG16, and ResNet50 models, to detect malaria parasites in blood smear microscopic images. The dataset is divided into two parts: 80 percent for training and validation and 20 percent for testing. The original images are scaled to 224x224 before being fed to pretrained deep models. VGG16 outperformed ResNet50, achieving 97 percent validation accuracy and a loss of 0.02.

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