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Automating Malaria Diagnosis from Blood Smear Images Using Deep Transfer Learning

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Abstract:

Malaria is a disease that is found all throughout the world, primarily in tropical places. When a human is bitten by an infected female Anopheles mosquito, parasites enter the bloodstream and kill red blood cells (RBCs), which transport oxygen. The flu was the first symptom of malaria. After a few days/weeks, the symptoms generally arise. A lethal parasite may live in a person's body for nearly a year without generating any symptoms. As a result, postponing treatment might lead to complications and, in the worst-case scenario, death. As a result, early detection of malaria can save a lot of lives. In practise, radiologists look at a blood smear (thin/thick) to identify the disease and calculate parasitemia to diagnose malaria. One of the most effective methods for diagnosing malaria is microscopy. The microscope was often used since it was affordable yet time consuming. Quality blood smears and the presence of a trained expert in the differentiation between parasitized and non-parasitized blood cells are crucial for an accurate diagnosis. To automate the detection of malaria parasites in blood smear microscopy pictures, we employed Transfer learning, a deep learning approach, on pre-trained VGG16, VGG19, and ResNet50 models.

Keywords: *CNN, KNN, classifier; malaria; detection; blood smear microscopic images; transfer learning; deep learning; VGG16; VGG19; ResNet50.*

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1. INTRODUCTION:

Malaria [1] parasitic disease produced by Plasmodium parasite and carried through mosquitos. Malaria is the disease that is prevalent around globe, mostly in tropical areas. The distribution of malaria around the earth is seen in Figure 1. Parasites enters blood that whenever a human is struck by an infectious female Anopheles mosquito then tend to destroy Red blood cells (RBCs), that transport oxygen. The flu was initial sign of malaria [2]. The symptoms usually appears after a few days/weeks. Significantly, fatal parasite may survive in a person's body for almost a year without causing any symptoms. As a result, delaying treatment might result in complications and even death. As a result, early malaria identification can save countless lives. Malaria disease affects around half the population of globe and responsible for more than 400,000 deaths per year.

In practice, radiologists examine blood (thin/thick) smear to diagnose the disease and parasitemia calculation to diagnose malaria. Microscopy is one of the best alternatives for diagnosing malaria [3,4], as it can detect parasite in the blood drops in thicker blood smear. Thiner blood smear, on the other hand, are utilized to differentiate parasite species and progression of malaria stage. The use of the microscope was frequent since it was inexpensive yet time taking. Accuracy of the examination is dependent on quality of the blood smears and the presence of the qualified individual, a knowledgeable in categorization and evaluation of parasitized and uninfected blood cell.

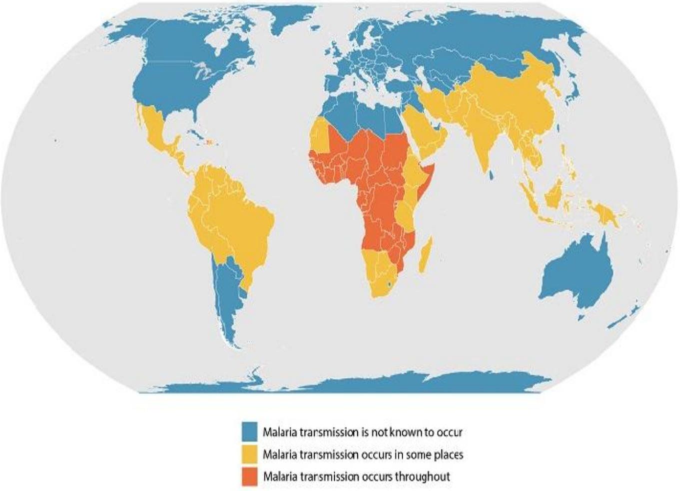


Figure 1. The estimated areas of malaria transmission around the globe are depicted on this map. (Image source: [5])

2. LITERATURE SURVEY

Unsupervised machine learning (ML) methods using a stacked autoencoder to learn characteristics from images of healthy and diseased cells were proposed in [6,7]. The deep learning models to classify malaria cells in red blood smear was proposed by authors in [8]. The model uses a 16-layer CNN model, which beats transfer learning-based models which employ AlexNet [9].

The Faster R-CNN, a CNN-based object identification model, was presented by the authors in [10]. Imagenet [11] is used to initialize the model, and then their dataset is used for fine-tuning. Another model employing deep relative attributes (DRA) [13] was proposed by [12]. The authors employ CNN to identify epileptic seizures [14]. [15] Suggested an automated technique that takes into account both the segmentation and categorization of malaria parasites. The segmentation system is based on a deep CNN [16], while the classification system is based over an Extreme learning machine (ELM) [17].

The study [18] use a “computer aided diagnostic (CAD)” tool which incorporates the ML technique to aid medical practitioners in analyzing disorders using blood smear pictures. The CAD technology was able to extract pathological traits from scans and aid specialists in their decision-making. Through the refining of feature extraction algorithms, CAD has attracted attention in image-based clinical testing, and this technology is utilized to diagnose malaria infections [19,20].

The authors presented a mobile phone RDT scanner platform which can function with the a variety of “lateral flow immuno chromatographic tests” and other test. [26] Small and inexpensive digital RDT scanner connects to a phone's existing cameras unit, where RDTs may be placed and scanned. Raw pictures of such RDTs then are electronically processed by a software programme running on the smartphone to validate the RDT and interpret diagnostic results automatically. Furthermore, smart RDT scanner that runs on smartphones actually gives spatiotemporal information for the presence of major contagious diseases, allowing epidemics to be tracked.

The researchers evaluated the diagnostic effectiveness of a device for automatic RDT interpretation that employs smartphone technology and picture processing software. [23] The device's diagnosis performance is equivalent to visual analysis of RDTs. In additional to virtually actual case report and quality monitoring, providing standardised automatic translation of RDTs in distant locations will considerably improve huge adoption of RDT-based malaria diagnosis programmes.

The researchers in this article developed a smartphone app that counts malaria parasites in images of stained blood smear films using the Giemsa method. [21,24,25] They used marker control watersheds for thinner blood smears to accurately detect and segment individual red blood cells, separate contacting cells, and meet the need for real processing. In order to identify individual cells, they apply a multi-scale

Laplacian of Gaussian filter to the green channel of the RGB color slide images. Estimated centroids of single cell which would act as approximation centroid to marker-control watersheds segmentation process are indicated by the local edges of Laplacian of Gaussian response. Otsu thresholding is used to calculate the cell foreground masks, cell borders were retrieved by calculating gradient magnitudes across lower values of blue-green channels. Watershed transform is then applied to edge, foreground mask, cell marker in the segmentation stage for segmenting and segregate contacting cells. To categorize cells, they employed a DL technique using CNN to distinguish infected cells from uninfected ones. [21,25]

The authors explain a smartphone application for Android smartphones which uses Giemsa-stained blood smear film pictures to detect malaria. [22] The major image component comprises of complex morphologic processes capable of detecting red and white blood cells as well as identifying parasite in infected cell. Programme identifies various parasite life stage and estimates parasitemia. The programme provides a diagnostic in less than 60 seconds and it had been tested, confirmed on many versions of tablets and android smart phones.

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

DL mimics operation of human brain, that is made up of a massive number of neuron that are regulated by the central nervous system. DL, like machine learning, is made up of a large number of neural network (NN), where every neuron presented as the single node, overall activity managed by CPU [7]. Deep learning models have revolutionized a variety of fields, including voice recognition, classification, image detection, identification, segmentation and other complex operations which need large amounts of data analysis [32][33][34].

Deep learning, like machine learning, includes reinforced, semi-supervised, unsupervised, supersized methods. Tasks such as object detection, image classification, and image segmentation were all completed using supervised models. Main benefit of DL is the automated extraction of characteristics in raw information. Design of every model differs depending on the amount of layers and varied functionalities. The CNN became an interesting field for machine vision scientists as the foundation of any DL model to image processing techniques. CNN executes several phases of execution via distinct layers. Generic CNN architecture is illustrated in Figure 2.

CNN is the supervise DL approach that had a transformative impact on many image based and machine vision applications. CNN were widely utilized in domains such as face recognition, object detection, picture categorization, and so forth. As illustrated in Figure 2, CNN model elements includes "Convolutional layers, pooling layers, fully connected layers, activation functions", and so forth.

3.1. Convolutional Layer

This layer takes RGB picture as input/the result from some other layer for some further process. The optimization function's focus is to achieve kernels which accurately reflect the data. This layer includes a series of statistical methods for extracting feature maps for input picture [16].

3.2. Activation Layer

Nonlinearity increase power of the neural network. Following each convolutional layer, a non-linear activation layer were added. Each convolutional layer that makes up this layer does, in fact, have a non-linear ReLU (Rectified Linear Unit) that is continuously delivered.

3.3. Pooling Layer

After the activation layer, a down-sampling layer will be used for lowering spatial dimension. Typically, a 2x2 filter is used on input for generating the output dependent on kind of pooling. Pooling layer prevents overfitting by reducing computation rate, training time, amount of features and feature maps dimension [20].

When a model achieves 99 or 100 percent accuracy on train set and only 50% accuracy on testing data, it is said to be overfitted, and it solved by adding dropout layer, which drop out the random selection of activation by decreasing the cost to zero. Dropout is the generalization function which learns the representation of diverse patterns. Then, to construct a smaller dimensional feature map, Rectified linear and max pooling are utilized [21].

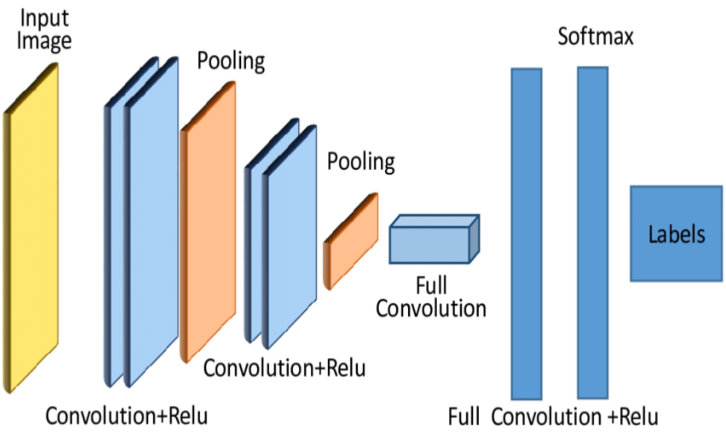


Figure 2. Generic CNN architecture (Image source : [27])

3.4. Fully-Connected Layer (FC)

This layer finds extremely higher level feature which are strongly related to the class or object. Inputs to the FC layer was the set of characteristics to categorizing pictures without taking into account spatial structure of images. The FC layer's output is the result of flattening the pooling layer's output, a process that converts a three-dimensional vector into a one-dimensional vector[42][43][44][45].

Convolutional Neural Networks showed promising results in disease identification experiments with effectiveness and accuracy [16], [17] [18], [19]. Disease recognition CNN based methods which may be built from scratch or through TL [20]. Developing a model from scratch is a time-consuming and inefficient method that relies solely on the size of the dataset required for learning and retrieving identification features [21], [22].

4. METHODOLOGY

CNN-based image categorization has shown relatively good performance. The purpose of this research is to categorize malaria blood smear microscopic images using Transfer learning, a deep learning technique using pre-trained VGG16, VGG19, and ResNet50 models. Proposed system overview is shown in figure 3.

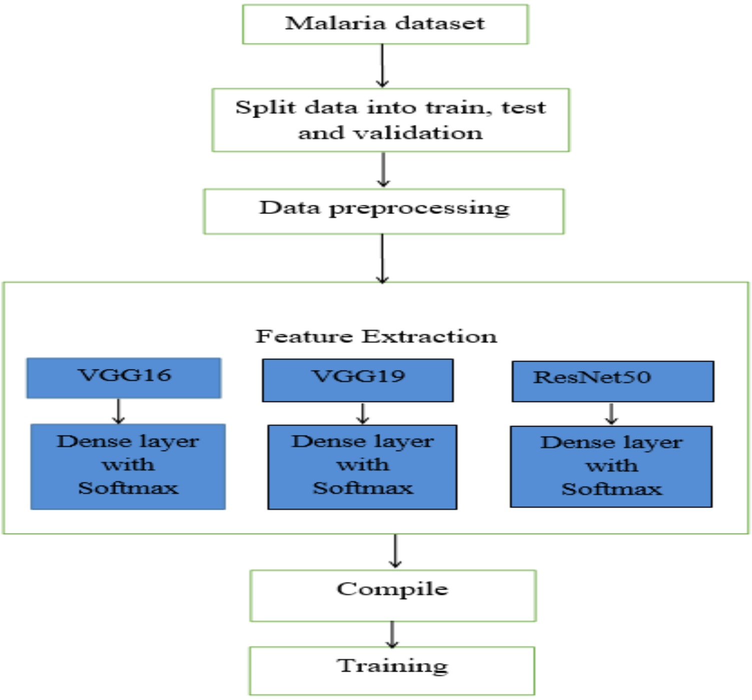


Figure 3: Proposed Deep-Architecture

4.1 Data Collection and Data Preprocessing

The Malaria dataset was obtained from kaggle at [28], which was obtained from [29]. To create the malaria dataset for the proposed model, we took 550 blood smear pictures from the original dataset and split them into 416 photos for training and 134 images for testing. Figure 4, 5 show samples of parasite and uninfected blood smear instances. The dataset's images were all resized to 224x224 pixels.

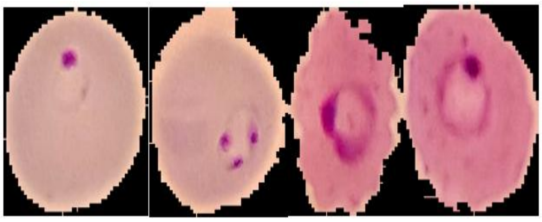


Figure 4: Samples of malaria Parasite

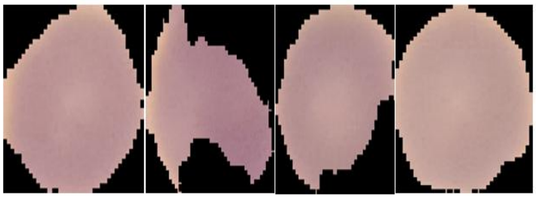


Figure 5: Samples of Uninfected

4.2 Feature Extraction

Convolutional layers were utilized for extracting information from scaled pictures. Next stage of the research will involve feature-extraction, fine tuning the model to train, as well as usage of CNN design for modelling malaria disease detection system.

4.2.1 Transfer learning (TL)

The base network is trained with base datasets, then features learned in first step were reused for the other network to train on the malaria dataset. In image classification tasks, the employment of pre-train model on comparable data gave positive result. Few companies have created models that takes months for training on modern technology, such as the Microsoft ResNet Model [29], the Google Inception Model [28], and the Oxford VGG Model [27]. Those model's could be downloaded and used in conjunction with newer model that use photographs as input to offer more accurate result. Malaria dataset will be trained on Pretrained VGG16, VGG19, ResNet50 models in order to detect malaria disease detection[36][37].

4.2.2 VGG

VGG, received second place in the image classification challenge and first place in the image localization test at the "Image Net Large Scale Visual Recognition Challenge (ILSVRC)" in 2014. An Oxford members of academics created VGG and made weights, structure available online. Figure 6 illustrates, structure and it was created using only 3*3 convolution layers, 2*2 max pooling layers, and fully linked layers at end. The size of incoming image should be 224*224*3. (RGB image). We are using both VGG16 (figure 6) and VGG19 (figure 7) models to detect malaria disease[38][39].

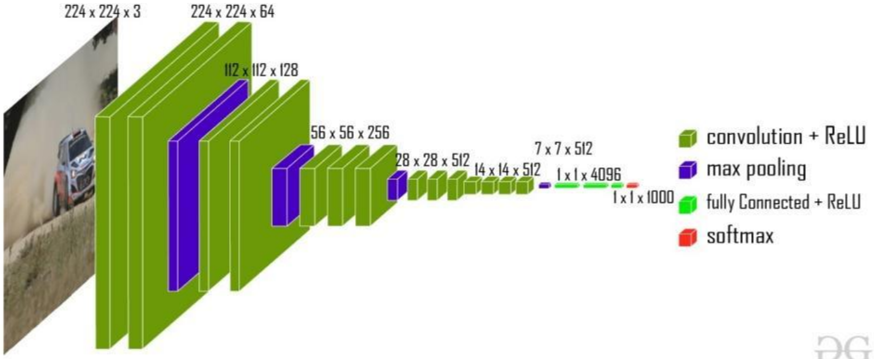
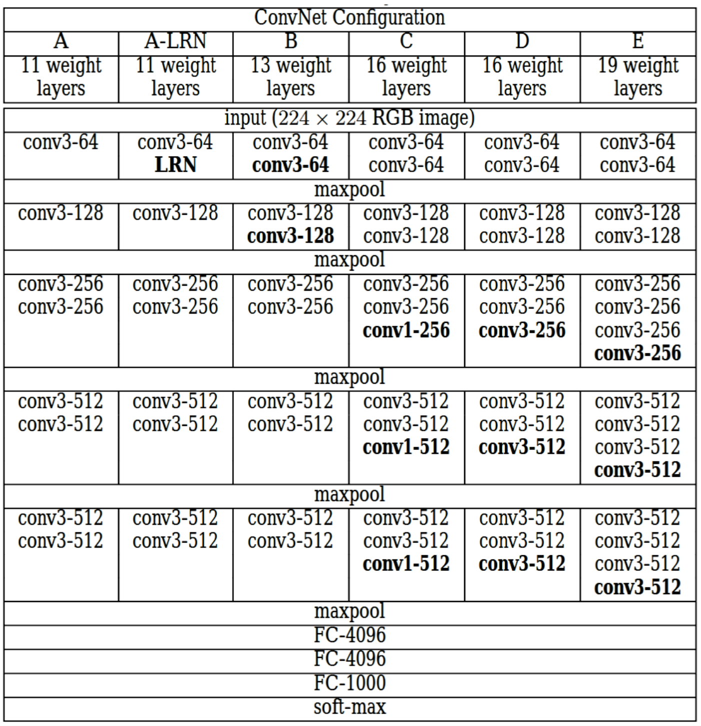


Figure 6: VGG16 Architecture (Image source: [30])



ConvNet Configuration					
A	A-LRN	B	C	D	E
11 weight layers	11 weight layers	13 weight layers	16 weight layers	16 weight layers	19 weight layers
input (224 × 224 RGB image)					
conv3-64	conv3-64 **LRN**	conv3-64 **conv3-64**	conv3-64 conv3-64	conv3-64 conv3-64	conv3-64 conv3-64
maxpool					
conv3-128	conv3-128	conv3-128 **conv3-128**	conv3-128 conv3-128	conv3-128 conv3-128	conv3-128 conv3-128
maxpool					
conv3-256 conv3-256	conv3-256 conv3-256	conv3-256 conv3-256	conv3-256 conv3-256 **conv1-256**	conv3-256 conv3-256 **conv3-256**	conv3-256 conv3-256 conv3-256 **conv3-256**
maxpool					
conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512 **conv1-512**	conv3-512 conv3-512 **conv3-512**	conv3-512 conv3-512 conv3-512 **conv3-512**
maxpool					
conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512 **conv1-512**	conv3-512 conv3-512 **conv3-512**	conv3-512 conv3-512 conv3-512 **conv3-512**
maxpool					
FC-4096					
FC-4096					
FC-1000					
soft-max					

Figure 7: VGG19 Architecture (Image source: [31])

4.2.3 ResNet

The ResNet design can handle image categorization accuracy loss on deep layers of convolutional [30]. Traditionally, NN learnt by stacking convolutional layer; more depth provided the model, more it will learn. Whereas, network depth rises, accuracy becomes saturated and degrades[40][41]. As the solution, ResNet offers usage of residual block to learn. ResNet architecturally constructed with different size convolutional filter which may regulate accuracy deterioration, minimize train time. For the experimentation, we are considering ResNet50 model.

5. EXPERIMENTAL RESULTS AND ANALYSIS

Images of both infected and uninfected blood smears were included in the malaria dataset, and all were scaled down to a uniform 224 by 224 pixels. A total of 416 images were used for the training and validation phases, but only 134 were used for the testing phase. A free GPU was used to train the model throughout the experiment, which was run on Google Collab.

The images will be fed into pre-trained VGG16, VGG19, ResNet50 models, which will incorporate imagenet pre-train weights, and final layer will be the fully connected dense layer with softmax activation. Input data will be learnt using pre-train weights, and single learning layer will be dense using the softmax activation function, which performs well with categorical categorization. To calculate loss during compilation, categorical crossentropy is used and the 'adam' optimizier were employed. The batch size for this model's training is 32, and it was given 100 epochs of data. The model's efficiency is evaluated in terms of both accuracy and loss. The below shows the Python code used to compile the model.

```
model.compile(
loss='categorical_crossentropy',
optimizer='adam',
metrics=['accuracy']
)
```

Categorical crossentrophy loss is calculated as,

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

Where,

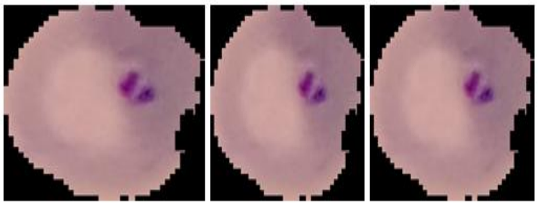
Output size : number of scalar values in the model output
y(i) : corresponding target value
~y(i) : i-th scalar value in the model output

Accuracy is calculated as below: Equation (2) is the general formula, whereas equation (3) is the detailed one, to calculate the accuracy of the model.

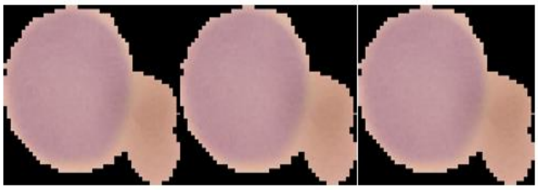
$$\text{Accuracy} = \frac{\text{Number of correct predictions}}{\text{Total number of predictions}} \rightarrow (2)$$

$$\text{Accuracy} = \frac{\text{True Negatives} + \text{True positive}}{\text{True Positive} + \text{False positive} + \text{True Negative} + \text{False Negative}} \rightarrow (3)$$

The VGG16 model's accuracy is depicted in Figure 9, while its train and validation loss are depicted in Figure 8. The VGG19 model's accuracy is depicted in Figure 11, and its train and validation loss are displayed in Figure 10. The ResNet50 model's accuracy is depicted in Figure 13, while its train and validation loss are depicted in Figure 12. All the three models performance quantitative results is shown in table 1. Among other models VGG16 model has achieved higher validation accuracy, as the dataset is small VGG16 gave better results. Figure 14 represents the qualitative results given by the proposed system and correctly able to classify the malaria parasite and uninfected cells from blood smear microscopic images.



Parasite: 99% Parasite: 99% Parasite: 80%
(a) VGG16 (b)VGG19 (c) ResNet50



Uninfected: 99% Uninfected: 99% Uninfected: 99%
(d) VGG16 (e)VGG19 (f) ResNet50

Figure 14: Qualitative results achieved by the proposed deep architectures

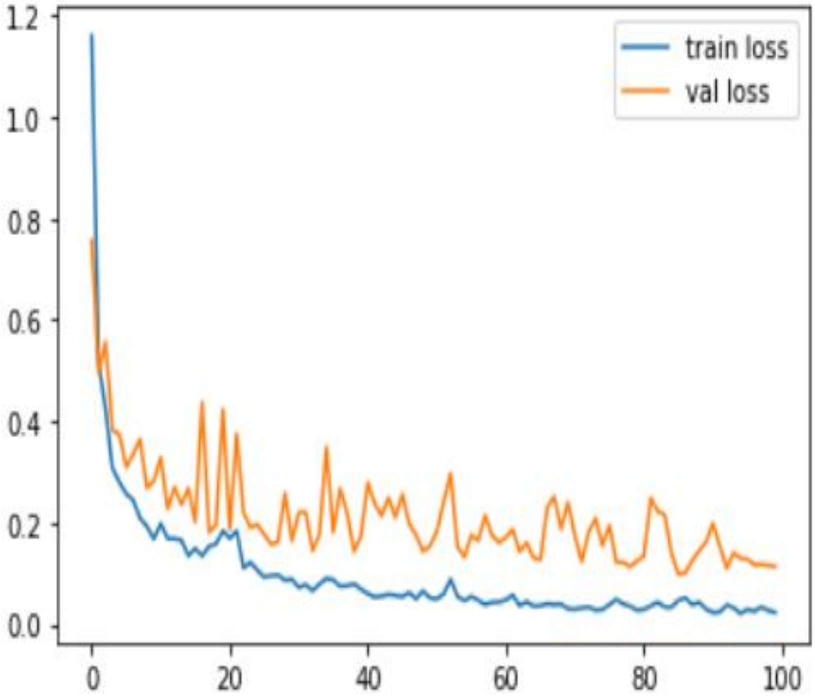


Figure 8: VGG16 train and Validation loss

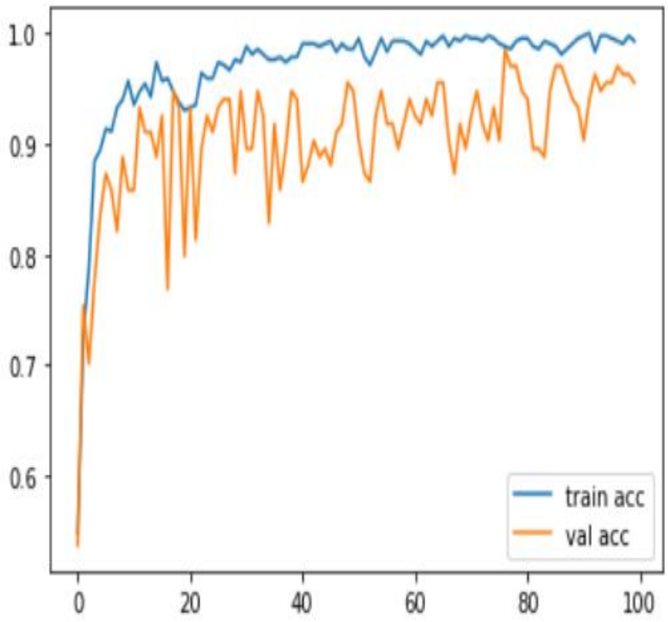


Figure 9: VGG16 train and Validation accuracy

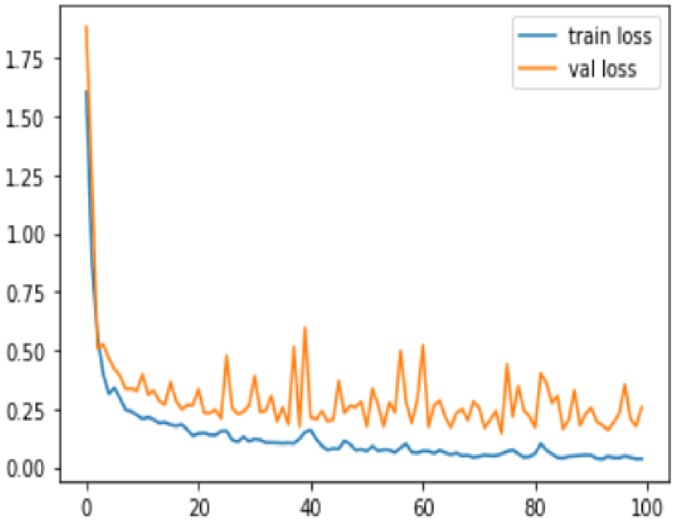


Figure 10: VGG19 train and Validation loss

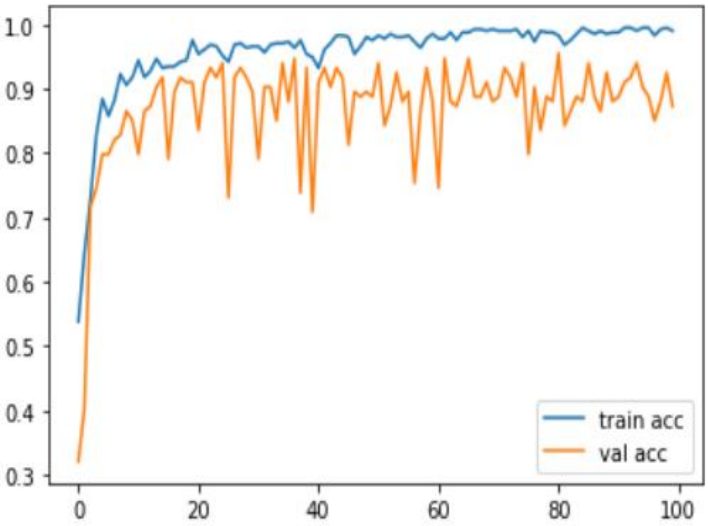


Figure 11: VGG19 train and Validation accuracy

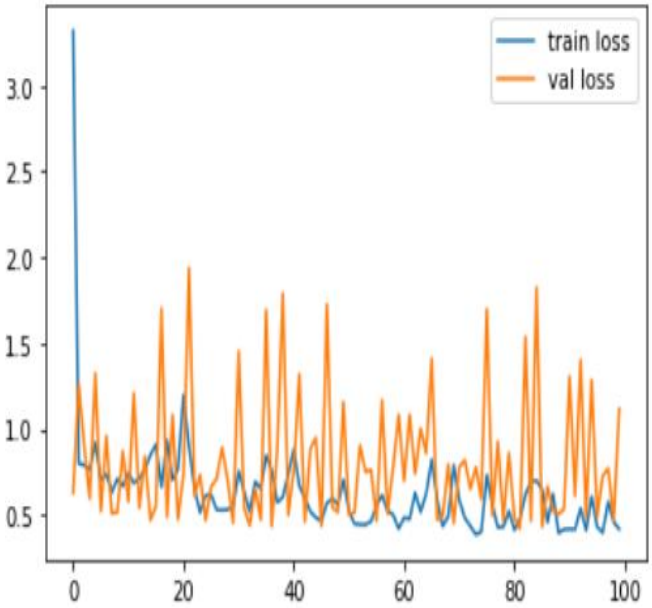


Figure 12: ResNet50 train, Validation loss

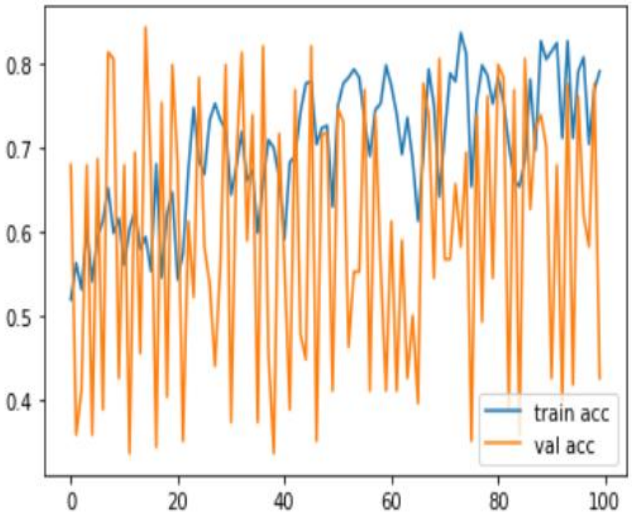


Figure 13: ResNet50 train, Validation accuracy

Table 1: Quantitative results achieved by VGG16, VGG19, ResNet50 on malaria dataset

Models	Train Accuracy	Validation Accuracy	Validation Loss	Train Loss
VGG16	99	97	0.1	0.02
VGG19	99	93	0.15	0.03
ResNet50	80	61	0.7	0.3

6. **CONCLUSION**

Malaria is the disease that is prevalent around globe, mostly in tropical areas. Parasites enters blood that whenever a human is struck by an infectious female Anopheles mosquito then tend to destroy Red blood cells (RBCs), that transport oxygen. The flu was initial sign of malaria. The symptoms usually appears after a few days/weeks. Significantly, fatal parasite may survive in a person's body for almost a year without causing any symptoms. As a result, delaying treatment might result in complications and even death. As a result, early malaria identification can save countless lives. In practice, radiologists examine blood (thin/thick) smear to diagnose the disease and parasitemia calculation to diagnose malaria. Microscopy is one of the best alternatives for diagnosing malaria. The use of the microscope was frequent since it was inexpensive yet time taking. Accuracy of the examination is dependent on quality of the blood smears and the presence of the qualified individual, a knowledgeable in categorization and evaluation of parasitized and uninfected blood cell. So we automated to detect malaria parasite from blood smear microscopic images using Transfer learning, a deep learning technique on pre-trained VGG16, VGG19, and ResNet50 models. Dataset is splitted into 80 percent for train and validation and 20 percent for test set. Image resizing is done on original images and resized to 224x224 and then gave to pretrained deep models. VGG16 has out performed compared to VGG19 and ResNet50, achieved an validation accuracy 97 Percent and loss as 0.02.

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