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Malarial Cell Classification Using Deep Learning

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**Abstract:** Malaria, which is caused by Plasmodium parasites, is a blood disease spread by the bite of a female Anopheles mosquito. There are almost 240 million instances in the United States. Each year, the illness affects roughly 40% of the population. A third of the world's population is in jeopardy. Macroscopic examinations generally take a long time. Examine thick and thin blood smears to diagnose a sickness or a condition's cause and discover what makes people vulnerable. Nonetheless, the accuracy of a smear depends on the quality of the smear and the knowledge of the situation. Parasite and non-parasite cells are classified and counted. The gold standard for diagnosis is manual assessment. It needs several actions to be completed. Furthermore, this procedure is used even when it comes to analysis, and it leads to erroneous and late conclusions. In the hands of professionals, our project's goal is to reduce human dependency, and the model is responsive. Malaria analysis is carried out automatically. A deep learning subcategory Convolutional Neural Networks (CNNs) are a kind of model that guarantees end-to-end results that are exceptionally adaptable and sophisticated in the extraction and classification of attributes. The accuracy and the techniques used have unwavering quality, speed, and affordability. Examinations are crucial to the disease's treatment and prevention, utter annihilation. We compared the overall results of this research. The performance of a CNN-based DL model that has been pre-trained as distinct extractors gets us closer to categorizing parasites and non-parasite cells to help in the detection of advanced illness. The best model layers for extracting attributes from the experimentally underlying records are determined. The information included in the dataset contains a wide range of parasitic and non-parasite blood image samples. To achieve a precise result, we've used Size, color, form, and cell size are all dominant traits. Count the number of photos to aid in the categorization process. CNN's that have been pre-trained are being utilized as a potential technique for the output of attribute extraction, which may be used to determine this. It has statistical support. As a result of these changes, automation in the pursuit of a cure, microscopy might be a huge help as a low-cost, simple, and reliable approach for identifying malaria. With the help of CNN, our model can recognize the image model and conclude whether it’s malarial affected or not. Our model provided 96 percent accuracy and 97 percent validation accuracy. VGG-19 has a training accuracy of 96% and a validation accuracy of 97%, with a 10% train loss and a 9% validation loss.

**Keywords:** Deep learning; malaria; vgg19; accuracy; dataset.

**1 Introduction**

Malaria is a potentially fatal disease caused by a parasite that infects a specific type of mosquito that feeds on humans. Malaria typically causes severe illness, including high fevers, shaking chills, and flu-like symptoms. Malaria is a potentially fatal disease, but illness and death can usually be avoided. Five species of Plasmodium (single-celled parasites) can infect humans and cause illness: Plasmodium falciparum (or P. falciparum), Plasmodium malariae (or P. malariae), Plasmodium vivax (or P. vivax), Plasmodium ovale (or P. ovale) and Plasmodium knowlesi (or P. knowlesi). Malaria caused by the falciparum parasite may be fatal. Severe falciparum malaria patients may have liver and renal failure, seizures, and comas. Infections with P. vivax and P. ovale, although rarely severe, usually result in less serious sickness. However, the parasites may stay latent in the liver for months, causing symptoms to resurface months or even years later.

Malaria is an old illness; allusions to what was almost certainly malaria can be found in Chinese documents from about 2700 BC, Mesopotamian clay tablets from 2000 BC, Egyptian papyri from 1570 BC, and Hindu scriptures from the sixth century BC. Such historical documents must be treated with care, but as we get into the twentieth century, we are starting to tread on more solid footing. Early Greeks, such as Homer (about 850 BC), Empedocles of Agrigentum (around 550 BC), and Hippocrates (circa 400 BC), we're well aware of the distinctive ill health, malarial fevers, and enlarged spleens found in people living in swampy areas. For over 2500 years, malaria fevers were thought to be caused by miasmas rising from marshes, and it is usually assumed that the name malaria originates from the Italian mal'aria, which means spoiled air, but this has been questioned. The World Health Organization predicts that 229 million clinical cases of malaria occurred globally in 2019, with 409,000 people dying from the disease, the majority of whom were children in Africa. Malaria is a major economic burden on many countries because it causes so much sickness and death. Because many malaria-affected countries are already impoverished, the illness perpetuates a vicious cycle of sickness and poverty.

Malaria is spread by mosquito bites from infected female Anopheles mosquitos. Only Anopheles mosquitoes may spread malaria, and they must have been infected with a blood meal from an infected human before. When a mosquito bites an infected individual, a minute quantity of blood is drawn, which includes minuscule malaria parasites. When the mosquito takes its next blood meal, about a week later, these parasites mix with the insect's saliva and are injected into the person who has been bitten. Because the malaria parasite is located in an infected person's red blood cells, malaria may also be transferred by blood transfusion, organ transplant, or the shared use of blood-contaminated needles or syringes. Malaria may also be passed from a woman to her unborn child before or after birth (this is known as "congenital" malaria). Plasmodium falciparum is the most prevalent kind of malaria that causes severe and life-threatening illness; it is found in many African nations south of the Sahara Desert. People who are often bitten by P. falciparum-infected mosquitos are at the greatest risk of contracting malaria. Malaria is more likely to kill those who have little or no immunity to it, such as small children, pregnant women, and travelers from malaria-free areas. This illness is more likely to strike poor people in rural regions that lack access to health care. As a consequence of all of these circumstances, an estimated 90% of malaria fatalities occur in Africa south of the Sahara, with the majority of these deaths occurring in children under the age of five. Malaria may be treated with medication. You may also take medication to reduce your chances of contracting the condition.

If someone has the malaria virus within them, then they have to do a blood test in the hospital. To detect malaria, the doctor has to see a smear image of the blood to determine whether the blood is affected by malaria or not. If it is affected, then he is malaria positive, and if not, he is negative. But the maximum time between the images of a healthy blood smear image and an affected blood smear image is very much the same. It’s hard to identify the malaria virus from the image it produces in the naked eye. For that, the patient has to test his blood multiple times to see if he has malaria or go home knowing that he is not affected, but the reality is the opposite. Sometimes the malaria virus can be found in a very minor position. So, it’s not possible to detect many times. If it remains undetected, then it can spread and people can die.

Using computing algorithms for cost-effective solutions to support interoperable healthcare [1] in lowering diseases has been a major focus of research in recent decades. Neto et al. [2], for example, suggested a simulator for replicating epidemiological events in real-time. For malaria identification and classification, Kaewkamnerd et al. [3] presented a five-phase image analysis approach. Anggraini et al. [4] created a program that uses image segmentation techniques to separate blood cells from their surroundings. In addition, Rajaraman et al. [5] created feature extractors for uninfected and parasitized blood cell categorization using pre-trained CNN-based deep learning models to aid illness detection. Using the underlying data, the researchers employed an experimental technique to find the best model layers. Two fully connected dense layers and three convolutional layers make up the CNN model. The performance is tested by extracting features from uninfected and parasitized blood cells using VGG-16, AlexNet, Xception, DenseNet-121, and ResNet-50. [6] and Liang et al. [7] both offer exclusively CNN-based malaria classifiers, in contrast to [8].

MOMALA [9] is a smartphone and microscope-based application designed to swiftly and inexpensively detect malaria. On a standard blood-smeared slide, the MOMALA app can detect the presence of malaria parasites. The blood smear is photographed using a phone camera mounted to the microscope's ocular, which is subsequently analyzed. Currently, the application is heavily reliant on microscopes that are large, bulky, and difficult to carry.

[10] developed a mobile app that captures photographs of blood samples and detects malaria almost instantly. We can evaluate blood samples without consulting microscope technicians by using a smartphone app. The program works by clamping a smartphone to the eyepiece of a microscope, then analyzing blood sample photographs and painting a red circle around malaria parasites A lab worker examines the case afterward. The extraction of meaningful features is critical to the efficiency of any machine learning approach. The bulk of computer-assisted diagnostic systems that use machine learning models for image analysis generate choices based on manually developed characteristics [11]– [12]. The approach also needs computer vision ability to assess the variation in picture size, color, background, angle, and location of interest. Deep learning algorithms may be effectively employed to overcome the limitations of a hand-engineered feature extraction technique [13]. To uncover hierarchical feature relations in raw picture data, deep learning models use a sequence of successive layers with hidden nonlinear processing units. Nonlinear decision-making, learning difficulty, feature extraction, and classification are all aided by low-level features abstracted from higher-level traits [14]. Furthermore, when dealing with large volumes of data and processing resources, deep learning models outperform kernel-based approaches like Support Vector Machines (SVMs), making them extremely scalable [15].

In the cognitive computing discipline, a comparable body of work has made a similar contribution. According to Zhang et al. [16], an interactive robot might be used as a security mechanism for authentication and access control while regulating access to private data stored in the cloud. In a second attempt [17], they presented a breakthrough cognitive IoT paradigm based on cognitive computing technologies. A group of researchers also suggested using Mech-RL as an agent-based literary consultant and a new channel of the meta-path learning technique [18]. Furthermore, there is a slew of research aimed at developing frameworks on mobile edge to deliver a variety of related services such as secure in-home IoT therapy, content recommendations, and position-based services for network amenities, similar to our battery-operated mobile-based malaria detection application that can be easily deployed to edge and IoT devices.

Relevant work in the literature generally used several pre-trained CNN variants for malaria diagnosis in blood smear pictures, such as AlexNet, VGG-16, ResNet-50, Xception, DenseNet-121, and customized CNN models, and produced relatively better results than using a bespoke CNN architecture, such as AlexNet, VGG-16, ResNet-50, Xception, DenseNet-121, and customized CNN models, and produced relatively better results than using a bespoke CNN architecture. These findings, on the other hand, were obtained by feature extraction and subsequent training, which took a long time in some instances, up to 24 hours in certain circumstances. Additionally, due to their size and complexity, these models are not suited for use with battery-powered mobile devices. In contrast, we developed a simpler and more computationally efficient CNN model with fewer trainable parameters (discussed in the Model Configuration section), which produced comparable or better results, keeping in mind that our model would be deployed on the battery-powered edge and IoT devices such as smartphones. Furthermore, most approaches in the literature use a de facto SGD optimizer with a range of learning rate schedules, including adaptive learning rates, which are susceptible to saddle point or local minima difficulties. We were able to obtain quicker model convergence with fewer trials and hyperparameter adjustments by using an SGD optimizer with a cyclical learning rate schedule and an automated optimum learning rate finder. Finally, image augmentation is used in most cutting-edge models to enhance model generalizability at the expense of greater training time. Our model without data augmentation shows quicker convergence and generalizability to unseen data by appropriately adjusting hyperparameters such as learning rate, regularization by batch normalization, and moderate dropouts in convolutional and dense layers.

The models presented based on custom CNN and its pre-trained variations seem to be the closest to our model among the analyzed malaria detection methods in the literature. As a result, we ran a state-of-the-art comparison with these models to show that our model may be used in a mobile-based system, particularly in distant disaster survival zones. The problems associated with manual diagnosis argue in favor of automating the malaria diagnosis process. The automation of the diagnosis process will ensure accurate disease diagnosis and, as a result, holds the promise of delivering dependable health care to resource-limited areas. As a result, rural areas that lack specialized infrastructure and trained personnel can greatly benefit from automated diagnosis. Automating malaria diagnosis entails adapting conventional microscopy methods, expertise, practices, and knowledge to a computerized system structure. Malaria detection at an early stage is critical for ensuring proper diagnosis and increasing the chances of cure.

Due to the severity and number of fatalities claimed by this disease, it is reasonable to accept the possibility of minor implementation errors introduced by an automated system. An automated system consists of streamlined image processing techniques for initial filtering and segmentation, as well as a pattern recognition suite. Previous research has found that the degree of agreement between clinicians on the severity of the disease in a given patent sample is very low. As a result, a computer-assisted system as a decision support system can be critical to a faster and more reliable diagnosis. It can help provide a benchmark and a standardized method of measuring the disease's level of infection. There isn't a large enough, high-quality image dataset of pathologically annotated cell images to fully train multiple-layer neural networks. As a result, we collaborated with a pathology team to create a dataset. After preprocessing the data, we randomly selected a large number of cell images and sent them to pathologists at the University of Alabama at Birmingham. The entire dataset of slide images has been evenly divided into four segments. Each pathologist is assigned two segments, ensuring that each cell image is viewed and labeled by at least two experienced pathologists. One cell image can only be considered infected and included in our final dataset if all of the reviewers mark it positively; otherwise, it is excluded.

With the help of deep learning, our model can detect the malaria virus from the blood smear image very precisely. Our model can analyze and identify which blood reports are affected and which are not. So, it will be very easy to detect, and many people’s lives can be saved by this deep learning model.

Our project is for the common people. This system can detect malaria in cells very accurately and quickly. So, because of this, many people’s lives can be saved. They can get proper treatment. With the output of the project, our expected result will be to get the highest accuracy of any existing similar system. The majority of studies achieved an accuracy level of around 90%. In contrast, some pre-trained models were used in the current paper study. VGG16 had a training accuracy of 96% and a validation accuracy of 97%. The accuracy percentage of the models used in this study is higher than that of previous studies, making the models in this study more reliable. Multiple model comparisons have confirmed their robustness, and the scheme can be drawn using study analysis. An introduction has been presented in section 1, a methodology in section 2, results and analysis in section 3, and a conclusion in section 4. Then we have given the references from which we have collected some information regarding this topic.

**2 Methodology**

From a series of experiments, we selected our best model in terms of both performance and effectiveness, which is discussed in the proposed model architecture subsections. The training details subsections go over experimental details and experimental settings. The training of the models is discussed in three sections: general training procedure, distillation training procedure, and autoencoder training procedure. Details can be found in the appropriate subsections. There are 13780 parasitic and 13780 healthy data points in the data set. The CNN methods, which have become increasingly popular in recent years, were used to classify malaria images. The application was created in MATLAB and used the models Alex Net, ResNet50, DenseNet201, Vgg19, Google Net, and Inceptionv3. The original data was first classified into six different architectures, after which the Gauss and Median filters were applied to the data set. This is a CNN model created by Oxford University's Visual Geometry Group (VGG) for large-scale image recognition. The VGG model is one of the most prominent models in the ILSVRC-2014 competition, achieving 92.7 percent accuracy on ImageNet testing data. It comes in two varieties: VGG16 and VGG19. The former has 16 layers, 5 max-pooling layers, and 5 blocks of convolutional layers, with two or more convolutional layers in each block. The VGG16 outperformed the previous models in the ILSVRC-2012 and ILSVRC-2013 competitions. The VGG19 has 19 layers, including 5 max-pooling layers and 5 convolutional layer blocks. The only difference between VGG19 and VGG16 is in the last three convolution blocks, which have four convolutional layers in VGG19 and three in VGG16.

***2.1 Materials and Tools:***

Anaconda and Jupyter Notebook will be used in this project. Python will be our preferred programming language. The Anaconda Navigator can look up packages on Anaconda.org or in a local Anaconda Repository. It works with Windows, macOS, and Linux. The Jupyter Notebook is a free and open-source web application that allows you to create and share documents with live code, equations, visualizations, and narrative text. Data cleaning and transformation, numerical simulation, statistical modeling, data visualization, machine learning, and lots of other applications are possible.  A level-set-based algorithm for detecting and segmenting red blood cells is also presented. An expert slide reader at the Mahidol-Oxford Tropical Medicine Research Unit manually annotated all of these images. The dataset includes 27,560 cell images with equal numbers of parasitized and uninfected cells. Figures 1 and 2 show images of parasitized and uninfected cells, respectively. We randomly divided the dataset into 80 percent training samples and 20% testing samples for each class. We further divide the (randomly chosen) training dataset into 90% and 10% groups for training and validation purposes.

***2.2 Dataset Description:***

Data for this paper was obtained from the Kaggle dataset. Data classes are classified into two types. This information is used to diagnose malaria. The data in the first class is non-parasitic, while the data in the second class is parasitic. The techniques for data collection and preprocessing are covered in the subsections that follow. The data used to support the research outcome are freely available at

<https://www.kaggle.com/itsdaniyal/malerial-cell-classification-dataset>

***2.3 Block Diagram:***

Deep learning is the ability of computers to process and learn from data. The main difference between deep learning models and traditional neural networks is that deep learning models have multiple layers. In 2012, deep learning was put on hold. Deep learning's popularity skyrocketed after the Deep Learning model won the ImageNet competition in 2012. One of the reasons that deep learning has recently gained popularity is the development of cards with faster processing speeds. As data volumes increased, so did the proclivity for deep learning.

Fully Connected

AlexNet

Vgg19

Inceptionv3

GoogleNet

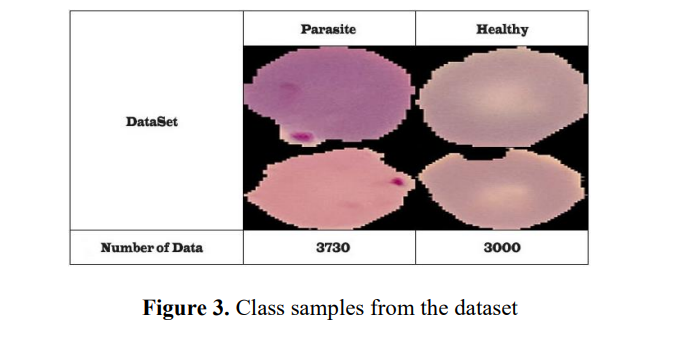
ResNet50

SoftMax

DenseNet201

Classification

Parasite



+

+

Dataset

Healthy

[19]

Fig 1: Classifications with original data with CNN architecture

CNN is mostly trained on network data. When images are fed into the network, they go through multiple layers to complete the learning process. Figure 1 depicts the classification of the original data. Individual images are processed using the DenseNet201, ResNet50, Alexnet, Vgg19, GoogleNet, and Inceptionv3 architectures before being classified as parasitic or healthy. Then, the Median Filter and the Gaussian Filter were applied separately to all of the data in the dataset. The data obtained is classified using the structure depicted in Figure 2.

Fully Connected

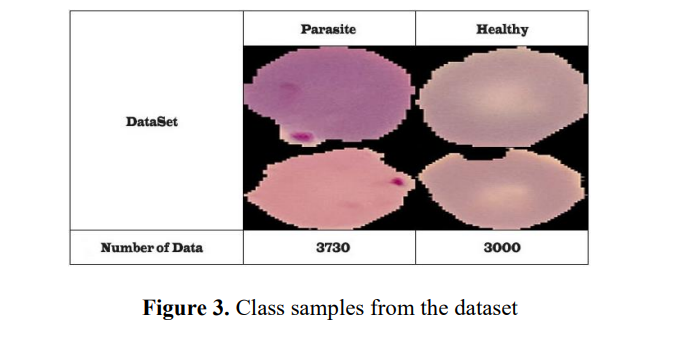
AlexNet

SoftMax

DenseNet201

Classification

ResNet50



+

+

Pre-processing

Dataset

Vgg19

GoogleNet

Parasite

Inceptionv3

Healthy

[19]

Fig 2: Classifications with data after filters with CNN architecture

Classification Layer

SoftMax Layer

Fully Connected Layer

Convolutional Layers 1-6

Color

Constancy

Input

Image

Resample to

50 x 50

Parasitized

Uninfected

[20]

Fig 3: Fast CNN architecture

Convolutional neural networks are used in this paper. CNNs are one of the most popular deep learning networks for image classification and other computer vision applications. CNN networks are made up of several layers. The Convolution Layer, Fully Connected Layer, Pooling Layer, Rectified Linear Unit (Relu) Layer, Dropout Layer, Normalization Layer, and Softmax Layer are the different types of layers.

***2.4. System Architecture:***

Healthy

Deep Learning

Input

Output

Affected People

**Figure 4:** System Architecture

***2.4.1 Convolutional Layer:***

The convolution layer is the primary building block of a CNN. It is in charge of the vast majority of the network's computational load. This layer performs a dot product on two matrices, one of which is a set of learnable parameters known as a kernel and the other being the restricted section of the receptive field. The kernel is smaller than a picture but has more depth. This means that if the image has three (RGB) channels, the kernel height and width will be small, but the depth will be large. Images with more pixels have a higher resolution. The network will display a square table of pixels or continuous pixels in digital images, computer graphics images, or bitmap images. Pixels are only one of the tiniest points in digital images like display papers or other multimedia. Each pixel will be assigned its own space based on its coordinates. In a color image system, the intensity of each pixel varies. Color intensity is shown for each color, such as red, green, blue, yellow, and black. The flattened convolutional layer's function is to transform a multidimensional vector into a one-dimensional vector.

Fully Connected Layer

Input

Convolution Layer

Pooling Layer

Output

ReLU Layer

Figure 4: Architecture of a CNN

If we have an input of size W x W x D and a given number of kernels with a spatial size of F, stride S, and amount of padding P, we can calculate the size of the output volume using the following formula:

= (1)

***2.4.2 Pooling Layer:***

The pooling layer is one of the concepts used for extracting important features from convolutional neural networks in order to reduce the dimensions of the data by combining the outputs of neuron clusters at one layer into a single neuron in the next layer, which reduces the repeatability of neural network features while preserving information about the key features via this algorithm. It can also increase its network instruction cycle and avoid overfitting in the analysis of high-complexity problems. The maximum pooling method, the average pooling method, and the Gaussian pooling method are all common pooling layer calculation methods, with the latter being the most widely used and representing the largest pooling method. The following is a detailed description of its distinctions.

**3 Results and Analysis**

After training with the trained generator, validation generator, step-per epoch equal to 8, and 10 epochs, our model provided 96 percent accuracy and 97 percent validation accuracy in the 10th epoch. The training accuracy was quite low in the first few epochs, starting at 91% and rising to 96 percent after the tenth. The validation accuracy began at 95% and ended at 0.9716 after the tenth epoch. VGG-19 has a training accuracy of 96% and a validation accuracy of 97%, with a 10% train loss and a 9% validation loss.

***3.1 Model Accuracy:***

The accuracy plot shows that the train's accuracy increased rapidly after each epoch. The accuracy was 91% in the first epoch and increased with each subsequent epoch. The model's validation accuracy was 95 percent and increased until the last epoch. The model accuracy plot shows that an increasing line has been drawn for training accuracy and a line that is around 95 percent–97 percent accuracy all the time during the epoch for test accuracy. Model accuracy and model loss are depicted in Figs. 5 (a), 5 (b), and 5 (c), respectively.

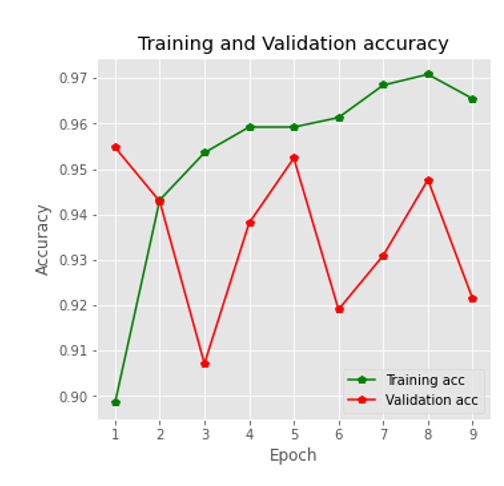


Figure 5: (a) Model accuracy

Our model was trained for a total of 10 epochs, as shown here. There are no signs of over- or under-fitting on the model. The ResNet architecture, Keras, and Tensor Flow were used to create this deep learning medical imaging "malaria classifier" model. The design requirements chosen are successfully tested. Our accuracy and loss plots for the malaria classifier model training and validation show that we achieved high accuracy and low loss.

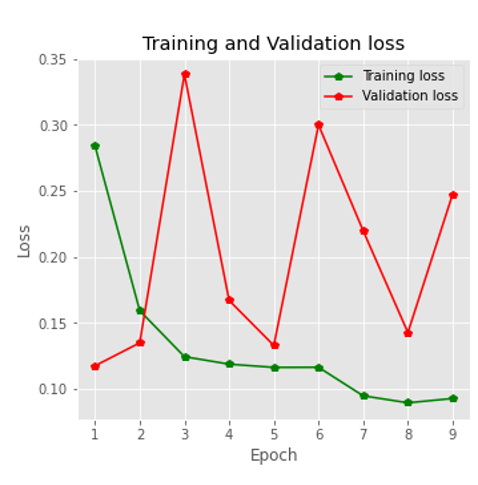


Figure 5:(b) Model loss

The loss plot shows that the train's loss decreased rapidly after each epoch. The loss was 22% in the first epoch and decreased with each subsequent epoch. The model's validation loss was 12 percent and increased until the last epoch. The model loss plot shows that a decreasing line has been drawn for training loss and a line that is around 12 percent–8 percent loss all the time during the epoch for test loss.

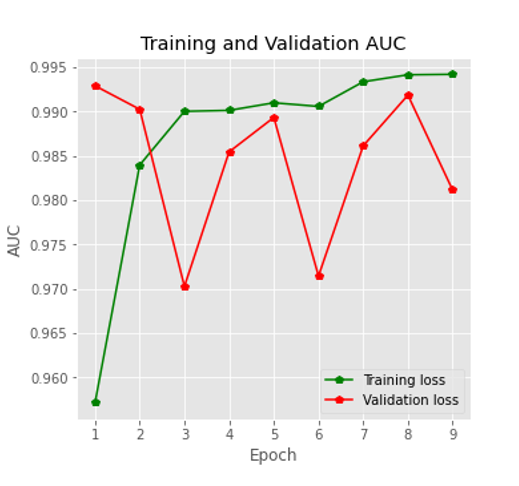


Figure 5:(c) Model AUC

It can be assumed from the model loss plot that both the lines of training loss and test loss have gradually decreased. The training loss was 20 percent after the first epoch and 10 percent after ten epochs. After the first epoch, the validation loss was 12%, and after 10 epochs, it was 8%. Figure 5 depicts a plot of the model loss.

***3.2 Model Comparison:***

In this study, the DenseNet201, ResNet50, AlexNet, Vgg19, GoogleNet, and Inceptionv3 pretrained models were compared to various previous models. In this study, InceptionV3, DenseNet201, AlexNet, GoogleNet and VGG19 produced better results in accuracy and efficiency than the models used in previous studies. The accuracy of the pretrained models improved noticeably. Table 1 shows a comparison of various models and data sets.

**Table 1:** Model Comparison

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  |  |  | | --- | --- | --- | --- | |  | | | | | This paper (model name) | Accuracy (%) | Reference paper (model name) | Accuracy (%) | |  | | | | | VGG-19 | 97.16 | Ref [19] (VGG-19) | 85.6 | | Inceptionv3 | 96.92 | (Inception V3) | 93.3 | | ResNet50 | 91.95 | (ResNet50) | 92.8 | | GoogleNet | 95.00 | (GoogleNet) | 92.5 | | AlexNet | 90.45 | (AlexNet) | 87.3 | | DenseNet201 | 96.11 | (DenseNet201) | 94.3 | |  | | | | |  | | | | |

Except for ResNet50, all of the models in Table 1 are extremely accurate. Out of all the pretrained models, DenseNet201, ResNet50, AlexNet, Vgg19, GoogleNet, and Inceptionv3 have consistently produced smooth results from the start and have nearly the highest accuracy of all the other research.

**4 Conclusion**

Malaria is a global disease that has claimed the lives of millions of people. We briefly described the workflow for classifying red blood cell images and went over the data augmentation methods we proposed to address the problem of training deep convolutional neural networks with a small dataset. Our model is based on the VGG. VGG19 is overly complex for the task; a simplified version works better in this application and avoids overfitting. The classification accuracy associated with training, validating, and testing with various combinations of the original dataset and significantly augmented datasets were then compared. Our observations show that deep learning can be used effectively to detect malaria parasites on thin blood smears. The proposed model outperforms or is comparable to previous research. We demonstrated that it is not necessary to use very deep neural networks to achieve high accuracy and that shallower versions may be preferable. We relabeled incorrectly classified images in the dataset. More work is needed to create a deep learning model capable of distinguishing between true parasites, impurities, and artifacts in the same way that a human expert would. However, the presented model correctly identifies the majority of cases. A well-executed system would require several factors to communicate with one another. This entails the characteristics of the microscope, the type of staining used, the slide preparation mechanism, as well as image exploration and machine learning software. The use of images with varying characteristics in each piece of research increases the difficulty in determining which method is best to use. This implies that the method proposed in this field of study is highly dependent on the image's characteristics. Because deep learning has gained widespread acceptance, a gigantic amount of support has taken the lead in data acquisition efforts. In addition, annotated data image repositories for preparation are now widely understood.

**Data Availability Statement:**

The data used to support the research outcome are freely available at

<https://www.kaggle.com/itsdaniyal/malerial-cell-classification-dataset>

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**Conflicts of Interest:** The authors would like to simply state that there are no conflicts of interest in this study.

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