Malaria Cell Image Classification using Deep Learning

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***Abstract*- In this study we are going to have the deep learning system doing the classifying work for blood slides of cells either infected with malaria or not infected. The foundation of our method involves reflection on the data before processing to enhance quality of images and also in identification of the target cells through extraction of specific features. A model that is fine-tuned to classify blood smears through images with malaria or without is the basis for the early detection. The possibility of this revolutionizes the diagnostics is incredible, especially in conditions of scarcity. With the use of these technologies, we canbe able to turn the diagnosis from long and error-prone diagnostic procedures to faster and precise ones. Such improvement will boost the whole malaria control and the managing health sector. We have developed an approach the goal of which is to be open to innovations with a possibility to update variables to the different settings of health care. With theaim to increase its scalability and useability, we develop an AI- powered deep learning-based diagnosis to popularize its amongpeople. Furthermore, we are still working to make our models much stronger and immune to any forms of errors, thus becoming significant assets in the anti-malaria campaign.**

***Keywords*: Deep Learning, Medical imaging, Malaria cell images, feature extraction, Parasitized and uninfected malaria cell.**

I. INTRODUCTION

Malaria is one of the top world diseases in the tropics, requires precise diagnosis for its treatment. Deep learning which automatically recognizes and classifies with microscope infected cells from blood sample gives a quick result and lessens the burdens of healthcare workers, especially in areas with unavailability of resources, and it a huge help to contribute to improve global health and control of the disease.

The application of deep learning for emulating the method of malarial disease classifications can pave a new way in the field of automated diagnostics. Nonetheless, its expanded usage is tied with some issues like the restricted amount of annotated data sets and high processing time, and generalization issue among others. Finally, the need for clinicians to learn to solve the interpretability barriers raises more questions. This aspect of research is still very basic as it requires in-depth knowledge and understanding to be ableto deploy in clinical settings correctly. Artificial Intelligence (AI) employs deep learning method-based malaria disease classification which provides automatic, fast and accurate detection of infected cells from the microscopic images of blood samples using CNNs. This system produces and enhance the features by automating the process of diagnosis, bringing down the use along with the accuracy. These systems are a promising technology for better carein areas with poor resource availability which would assist to treat and manage malaria globally. To label a slide of blood with deep learning the most critical step is to collect an image base with blood cells annotated into two categories- infected and non-infected separately. Afterward, we optimize the pictures by doing our share of pre-processing. To follow, infected cells are then classified with an accuracy by the CNNs in the subsequent phase. Model performance at last is evaluated using these separate datasets as a check on reliance and thereafter deployment which is considered. The models of artificial intelligence help with computer-aided malaria diagnostic procedures in particular, where healthcare resources are scarce, responding to early diagnosis and disease control on time.

Computer learning algorisms for malaria diagnostics, in resource constrained settings, facilitate and overcome challenges in fully utilizing the diagnostic potential of the conventional methods. They (AI systems) receive the special education after what they are put in use on portable devices and integrated into telemedicine platforms that enable remote diagnosis and consultation. At the same time, data gathering is stagnated and furnishes machine learning designersto optimize their models. These tools contribute to the early diagnosis and consequent treatment which helps to lessen the disease spread and the burden. Besides monetization, they centralize knowledge resources to equip local health workers with skills to improve early detection.

II. LITERATURE REVIEW

Krit Sriporn et.al. [1] proposed a model, which could be used to improve treatment options in decision-making for malaria. The model applied the cross of the image processing and CAD (Computer Aided Diagnostic) system at the level of accuracy. Due to the fact that Xception (Mish Activation + Nadam Optimizer) was more successful in terms of application of CNN Neural Models (CNNs) on a dataset (7000 images), researchers think that it will be appropriate to continue future studies. CNNS detected recall, accuracy, and precision promisingly; as well as, it results in F1 measure accuracy.

Ahmet Çinar et.al. [2] discussed about the creating process of an aid which is able to perform the down study of the malaria virus images but also it allowed the usage of the CNN (convolutional neural network) classification technique of the healthy and the parasitized images through a medium filter and the Gaussian filter because it is to go on with the finality of the high parity of the parasite identification and annihilation. Ultimately, we are able to fine-tune this Dense Net system down to the smallest nerve fiber in this in-depth analysis. These are what we mean with a photo, with the combination of an ultra-mega resolution image, and the way to do algorithm in image processing, using MATLAB, as a tool.

Suresh Chandra Satapathy et.al.[3] proposed a malaria detection solution with a DCNN "Falcon" model and used the real time image data. The "Falcon" model aims to detect the parasitic cells in the blood smears of the malaria screener dataset and performs precision on the sample consistency levels. The experimental output shows no overcoming and no class inequity so that the evaluation is a comparatively trustworthy classification report like modern CNN as of malaria-infected blood smear using the CNN model that predicts the bio-images of the trained medical staff for standardizing the conventional manual malaria diagnosis. The dimensions of the CNN design are intensified through the ten-folding process of ten-folds cross-validating of 27,558 individual blood smears. We compare three CNN models: The three main imitations that we will focus on include Basic, Frozen, and Fine Tuned. Now the most suitable model is chosen/ The best model is selected.

K. Hemachandran et.al.[5] looked into the application of deep learning techniques in the realm of Malaria Diagnosis. Use our AI to write for you about: Biomedical research: Deep learning and Malaria Diagnosis. The main mandate is to build on the optical techniques that are currently available for diagnostics. The article is on Neural Network models such as CNN, MobileNetValue and ResNet50 so the dataset provided by the National Institutes of Health (NIH) will be used. The goal of the article is to develop a technology which will enhance the Malaria surveillance system with the automatic image detection devices.

R Sreemathy et.al.[6] focused on machine learning technique with deep learning involving an implication of convolutional neural networks (CNN), that might be applied to identify malaria parasites in a fast and accurate way. As it is, some predefined computer vision models such as Alex Net, ResNet50, and VGG19 to be used as feature extraction models with respect to both infected and uninfected cells are analyzed. This paper will investigate if transfer learning is a way to raise malaria parasite detecting performance.

Militante, S.V. et.al.[7] claims a cutting-edge approach to diagnose malaria, with the aid of CNNs (Convolutional Neural Networks). This method seeks to overcome the limit of the standard blood smear tests and increase the accuracy of the cell identification and effectively classifying them. Experimental work shows that ResNet, Google Net, and VGGNet are impeccable models for extraction of features from cells using CNN. The use of high-resolution microscopy is a novel approach which might completely change the way malaria diagnostics is taken. Inaccuracy as well as big-scale screening campaigns will be improved.

Suraksha, S., et.al.[8] invented a new technique by means of convolutional neural network to recognize red blood cells infected by women are normal and uninfected one in blood smear images. The network of Convolutional Neural Networks (VGG) which have been trained previously was employed to extract features from both healthy and infected cells automatically. As the simplified method has demonstrated by having applied test on the available dataset of the blood cells images which contains properly labelled cells with and without parasites, it works accurately with performance in the same line with the previous Support Vector Machines popularly used method.

Gill, K.S., et.al.[9]. Discuses The main concept in this is the computer learning algorithms, through which the images of large volumes are passed. Then, there is easy identification of patterns which are true for malaria infection determination. We intend to have a model trained image classification that is an auto-recognizer and is powered by deep learning to detect malaria accurately and benefit from the already pre-retained knowledge. Starting with our strategy development the key component is commitment of the individual.

Kassim, et.al.[10] focuses on the recent achievements that are being implemented in separate convolutional neural networks (CNN), for instance for red blood cell recognition. Multiple research studies have done with convolutional neural network (CNN) models so as to extract RBC from holographic images and microscopic images; this process of prediction of pixels-wise is frequent, and that is why at times, it is very time consuming. In such case, other methods that acquire images of minuscule size are also put into involved by the other methods which often includes the process of segmentation and classification. The consultant explains all the difficulties mentioned of the mentioned strategies and utilize a hybrid deep learning approaches of U-Net and Faster R-CNN for higher detection accuracy and efficient in microscopy regarding large-scale above.

Alnussairi, et.al.[11] Introduces a new paradigm of using deep convolutional neural network approach as an alternative way of diagnosis which is able to identify and detect parasites in blood from microscopic images of red blood cell smears. Transfer learning strategy is implemented using pre-trained CNN models (VGG19, ResNet50, and MobileNetV2) whereas two steps of detection and classification of malaria are undertaken. Modeling is presented that studies the effects of data preprocessing, the feature extraction techniques and classification algorithms, and data augmentation techniques for the improvement of the model performance. This research maintains that convolutional neural network-based deep learning algorithms are competent in automating the diagnosis of malaria based on blood cell photos which is a highlighting feature in medical image classification that helps in disease diagnosis.

Delgado-Ortet, et.al.[12] focuses on the impute statistics information gathering that involves d such features as scanning, segmentation, attributes feature extraction, and classification. Unlike the something-type algorithms, the approach proposed will be using DL networks, to avoid the pre-processing stages and completing manual feature extraction. A range of tools were tested which included, thresholding and morphological operations, which were investigated as part of the research. The trials illustrated the division method to be very accurate to RBCs with high blood between these two classes. The methodology includes data processing, feature finding, and network training with the particularuse of identifying red blood cells and masking the students in order to be the main input layer for the proposed CNN system.

Nayak, et.al.[13] the most common Malaria diagnosis method is looking at thick and thin blood films by microscope; thick film reveals parasites, whereas in thin film we know what kind of species it is. Through image processing, many automated systems have been developed alongside distinctive machine learning approaches that strengthen this identification and which are operated faster. For example, DL has been a useful tool in examinations of medical imaging with an expected improvement of diagnosis quality in different imaging domain domains, in which DL have already shown outstanding results. We will also evaluate Optimal feature extraction methods until we establish the effectiveness of DL models at categorizing cells belonging to a parasite and other non- parasite classes for this paper. Automation systems were earlier recognized as a great contributor towards better management and treatment of malaria in that they identified the disease additionally in the early stages of the process.

Silka, et.al. [14] presents the state-of-the-art CNN model for malaria diagnosis test and with more accuracy and more time-awareness as other similar existing methods. The model turns out to be the one that achieved the highest sensitivity and specificity rates for nonspecific and specific blood sample classification due to the use of the batch normalization algorithm. As well, the work of evaluate of other malaria miscellaneous performance's deep learning model is analyzed to show how Deep Learning may assist in the diagnosingof infectious diseases.

Vijayalakshmi, A, et.al. [15] focuses on the deep learning models that are used for malaria detection in microscopic images, such as VGG16, VGG19, LeNet-5, and Alex Net and they vary greatly in accuracy. Malaria Detection Using Various Types of Deep Learning Models Such as Vgg16, Vgg19, Lenet-5, And Alex net models S. Revathy et.al.[4] proposed an automatic detection model Has Led Toresults that were classified as either low or medium as well as high accuracy levels were achieved using the combinations of VGG networks and Support Vector Machines (SVM) techniques for classification, Malaria detection has largely relied on models such as LeNet-5 and Alex Net but there are efforts aimed at enhancing their accuracy.

This paper will focus on increasing the effectiveness of deep learning models in categorizing malaria-infected cells by deployingstrategies of transfer learning. It is equally important to note that these methods enhance the training course, thus providing more effective diagnostic of malaria. This form of approach therefore goes a long way in enhancing the diagnosis and classification of malaria more than the previous forms of research.

This paper is presented in the idea to employ deep learning technology for malaria cell image classification. Thus, the utilization of deep learning algorithms to distinguish infected cells marks the idea behind this paper as a promising method to diagnose and treat malaria, especially in the limited resources of the regions affected by this disease. Moreover, emphasis on the design of AI-based deep learning diagnosis systems in the context of the specified paper makes it appear progressive and dedicated to the enhancement of health care breakthrough, which can transform the diagnostic and control strategies to combat malaria.

III. DATASET DESCRIPTION

There are the Malaria dataset belonging to cellular images that contain 27,558 balanced pictures which are as much parasitic as uninfected half of them also complaining typically infected with Plasmodium Parasite while the other half of them is uninfected. JPEG images contribute a lot to the training of machine learning models which are developed to automatically identify malaria parasites and for the creation of the image processing technologies for the commend of blood smears.

https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria

Sample images from dataset:

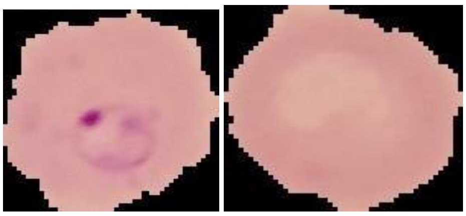

Fig.1 Parasitized and uninfected malaria cell

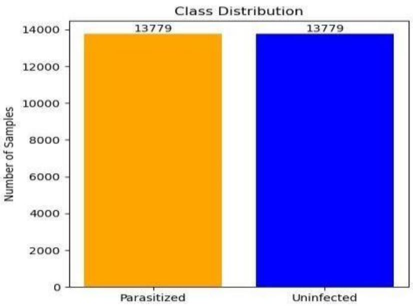

Fig.2 no. of samples in parasitized and unparasitized

IV. METHODOLOGY

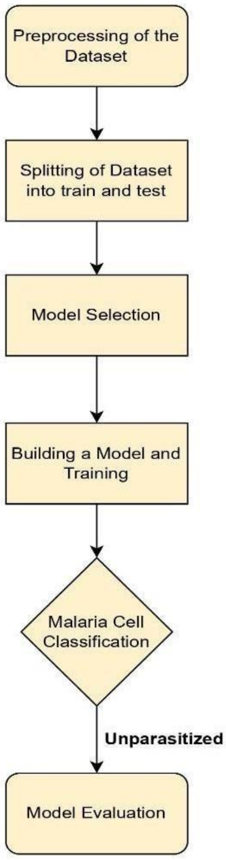

Fig.3 Flowchart diagram for malaria cell classification

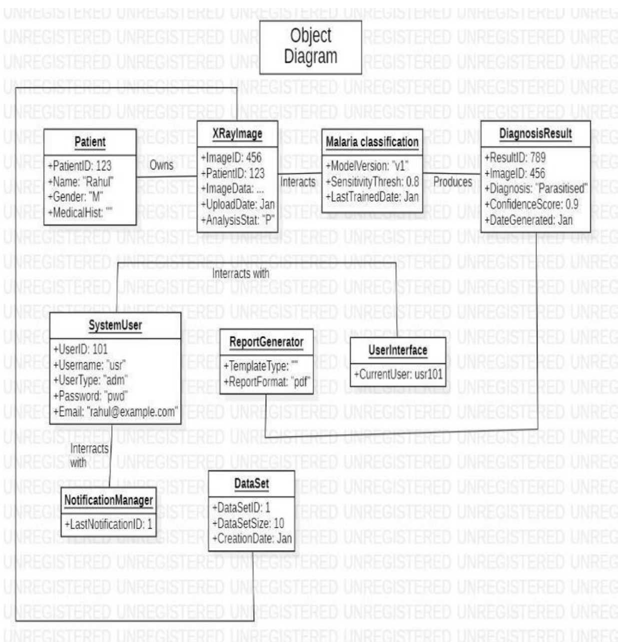

Fig.4 A black and white object diagram of a medical image analysis

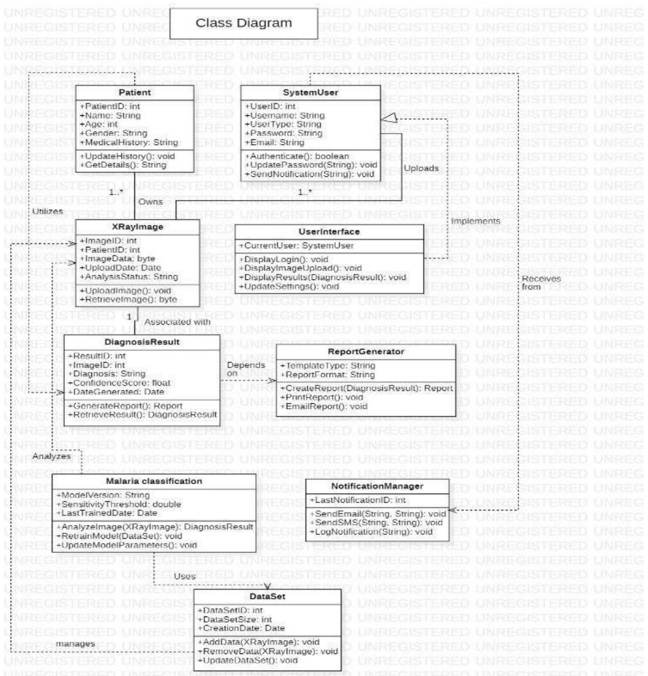

Fig.5 Class diagram of a medical image analysis system for diagnosis

The methodology follows a streamlined process and it goes as follow:

A. Data Preprocessing:

Firstly, when the data is sent into the model's phase a few of expectation factors are prepared. The next step we make is to convert already normalize the pixels values within the range of 0-1. We use now step by step methods and it is very fast and stable for preforming trainers' activity. The subsequent action is to employ data balancing techniques to constrain class imbalance where data is of such nature it inclines towards certain types of cells. In addition to this, the number of cells from both classes, i. e., infected and non-infected, will be decent and accommodative. Data augmentation techniques are also commonly used to bring the crease of diversity to the dataset and especially stop the situation of overfitting, the constants are as following: rotation, flipping, zooming, move around etc.

B. Design and Developing DL Model:

We apply the most recent version of DenseNet201, VGG16, Efficient Net or Inception models, a type of deep learning architectures implemented for pre-training. Through time, they have designed performant solutions for one of the most severe images-classification challenges. Subsequently, models get trained by taking the transfer learning approach. This is done by pairing the toplayers as they serve to make the models adaptable to the malaria celltask. Lastly, the total number of classes in last layers is tuned to be two classes as elicited by the infected and non-infected cells.

C. Model Training and Evaluating Models:

The sample will be divided into three parts, i. e., train set, validation set, and test set. It is also regarded as train set and validation set with each getting 2 parts, and the remaining part is used as a test set. The training set (here everything about model initialization) and training (here the initial losses and the resulting optimizers such as the Adam) can be seen as the initialization and training process itself. Models are also determined to set aside their own time for the mindful state of mind to have a chance to make mistakes on their own and avoid inflating their results. And, hyperparams are altered to fine-tune the model once the validation is done on the training set. Following the training and test dataset completion we should know the performance metrics performance metrics such as specificity, precision, recall accuracy, and their-score–F1.

D. Hyper parameter Tuning:

Experimented on the variising different hyperparameters. Strategies the move according to (learning rate, batch size, and optimizer) to advance the performance. By means of the metaheuristics, like grid search or random search, the area of the hyperparameter space can be more or less efficiently explored.

E. Analyzing the Results:

Evaluation metrics is applied to assess performance of the models after the evaluation process. The confusion matrix is a visualization tool that helps in establishing where models could be making mistakes. Learning curves plots are helpful in finding when model is overfitting as well as underfitting the data. Those models rendering the best results are filtered down for deployment.

F. Model Evaluation and Deployment:

In the last metric the system uses to pick the best-performing model is relied on. The model is run and deployed on the appropriate environment, whether that's TensorFlow serving, flask Rest API, or docker containers. In this context, the counts of deployed model's performance in real-world environment is tracked, and the upgrades are done as needed to keep the system at its peak performance level.

V. RESULTS

The result section covering the evaluation, the four architecture is used to assess the metrics which translate into doing the three evaluations. Between the two models both are built with the same synaptic populations yet the layers get universal training. In this instance, we use loss, precision, recall, accuracy and F1 score depending performance model as the metrics. In here, the accuracy of five deep learning algorithms' Models for semantic class malaria cell image is evaluated that include InceptionV3, MobileNetV2, EfficientNet-B3, ResNet50 and DenseNet201. All models are performed to the same dataset and based on how well these models can get the topmost of precision, recall and F1 scores. These statistics demonstrated that our best ResNet50 performed brilliantly, and the Efficient Net B3 and DenseNet201 followed closely and targeted the same piece as well. On the other hand, we also found that the Inception-V3 architecture was highly accurate while the particular performance metrics of the MobileNet-V2 were almost the same as the average of all the other networks. This situation points at the functional architecture layers' ability for the classification of fish cells. Literature-wise, these benchmarks can beconsidered as these.

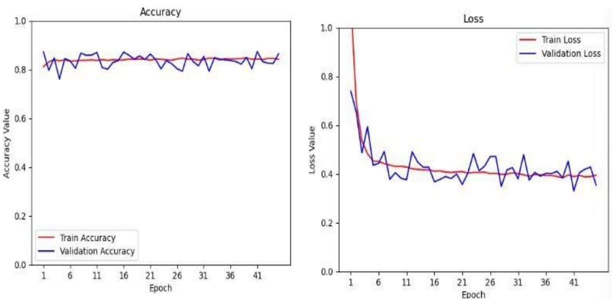

Fig.6: Accuracy and loss plots for InceptionV3 model

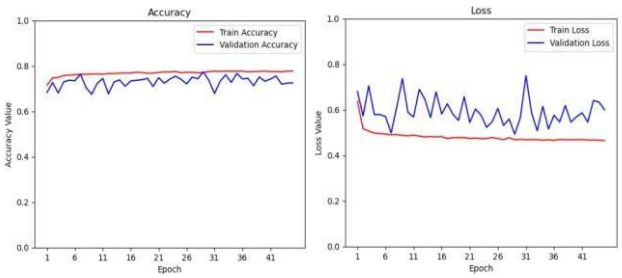

Fig.7: Accuracy and loss plots for MobilenetV2 model

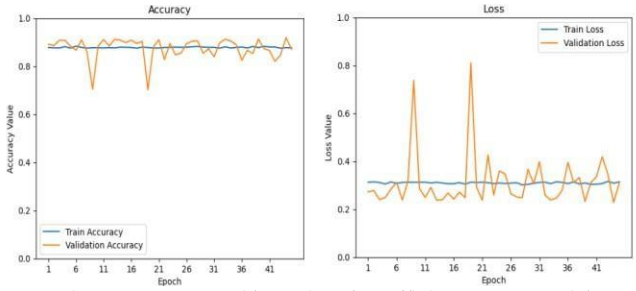

Fig.8: Accuracy and loss plots for EfficientNetB3 model

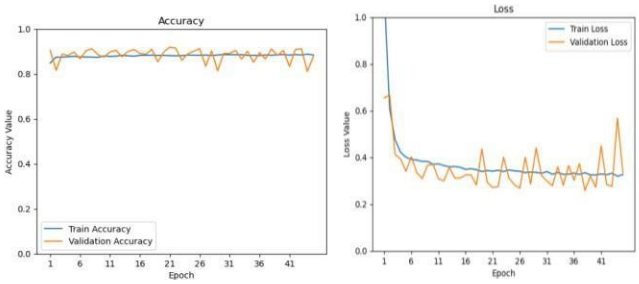

Fig.9: Accuracy and loss plots for RESNET50 model

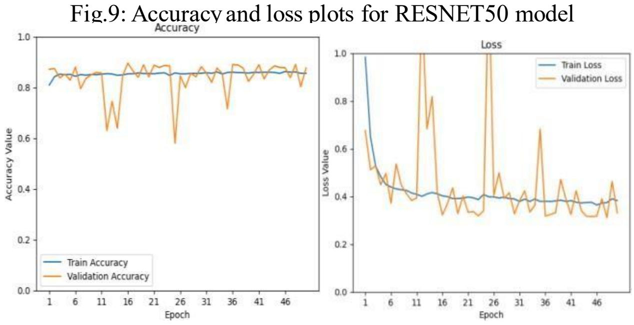

Fig.10: Accuracy and loss plots for DenseNet201 model

Fig.6, Fig.7, Fig.8, Fig.9, Fig.10 displays display four metrices Train accuracy, Validation accuracy, Train loss, Validation loss. This provides an overall understanding of the model's performance.

Table 1: Performance of the Models

Models	Metrices			
	Accuracy	Precision	Recall	F1_Score
InceptionV3	0.86	0.875	0.865	0.865
MobileNetv2	0.73	0.775	0.73	0.715
Efficient net B3	0.87	0.89	0.87	0.87
RESNET50	0.88	0.89	0.88	0.875
DenseNet201	0.88	0.88	0.875	0.875

Table 1 compares the performance of the five models for malaria disease classification. Metrics such as accuracy, precision, recall, and F1 score are evaluated. Based on these metrics it is clear that Dense201, Resnet50 appears to be the best-performing model among all the models.

Table 2: Metrics for training, validation, testing

	Accuracy		
Models	training	validation	testing
InceptionV3	0.8413	0.8354	0.86
MobileNetv2	0.7711	0.7299	0.73
Efficient net B3	0.8784	0.8827	0.87
RESNET50	0.8844	0.8865	0.88
DenseNet201	0.8503	0.8358	0.88

Table 2 compares the accuracy metrics performance for the five models for malaria disease classification. Metrics such as training accuracy, validation accuracy and testing accuracy are evaluated. Based on this metrics it is clear that Dense201, Resnet201 are the best-performing model among all the models.

Table 3: Loss Metrics for training, validation, testing

	Loss		
Models	training	validation	testing
InceptionV3	0.3872	0.3413	0.35429
MobileNetv2	0.4889	0.6801	0.6001
Efficient net B3	0.3114	0.2707	0.31006
RESNET50	0.3152	0.3357	0.33398
DenseNet201	0.4013	0.3724	0.33096

Table 3 compares the Loss metrics performance for the five models for malaria disease classification. Metrics such as training loss, validation loss and testing loss are evaluated. Based on this metrics it is clear that Mobile net has highest loss and it is inefficient. The most efficient model is Densenet201.

VI. CONCLUSION

To sum up, malaria is highly threatening disease for the people life. In this Various deep learning models have been used on cell images for diagnosing malaria and the models under consideration herein include InceptionV3, MobileNetV2, Efficient Net B3, ResNet50 and DenseNet201. The same test data was employed in the training process and then the performances of the models were determined by the measures such as precision, recall, F measure, accuracy, and loss. Overall, ResNet50 yielded the satisfactory prediction result, which were similar to Efficient Net B3 and DenseNet201. Out of all networks used, InceptionVN3 and MobileNetV2 did well though MobileNetV2 was slightly better than the rest in most cases. The paper has suggested ResNet50 and Efficient Net B3 for this task predetermining them for accurate detection of malaria cells. This paper may face several limitations in terms of transferring the same to different population groups, presence of some biases in the training data, detailed discussion on resources for model deployment and handling of such models, Model interpretability and proposing ethical consideration and probable bias which can occur in AI-controlled diagnostic systems that can be researched further and might need attention for implementation in practical medical applications for practical use.

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