

MALARIA PARASITE DETECTION USING DEEP LEARNING

Author Names

ABSTRACT

Millions of people worldwide are afflicted by malaria, an infectious illness that can be fatal. Early identification of malaria is one of the main difficulties in its efficient treatment. Microscopy is one of the older diagnostic techniques for malaria, although it has drawbacks such limited sensitivity and specificity. Deep learning algorithms have recently demonstrated encouraging outcomes in the detection of malaria from photographs of infected and uninfected cells. To choose the most effective method for detecting malaria, we assess the performance of five alternative deep learning models in this study. The dataset used in this study contains many images of both infected and uninfected cells, the difference between these images is clearly visible when inspected visually. The images were collected from a dataset hosting source and were annotated by experts to label each image as infected or uninfected. The dataset was then split into training, validation, and testing sets for use in training and evaluating the deep learning models. We compare the performance of five deep learning models in detecting malaria from the images in the dataset. The models we consider are VGG-19, Inception-v3, ResNet-101, InceptionResnet-v2 and a Custom CNN model. These models were selected based on their popularity and demonstrated performance in similar image classification tasks. We evaluate the performance of each model using several metrics such as accuracy, precision, recall, and F1 score. We also consider the computational complexity and training time required for each model. The results of our experiments show that InceptionResnet-v2 outperforms the other models in terms of accuracy, achieving a test accuracy of 95.4%. Additionally, VGG-19 has a relatively low computational complexity and can be trained efficiently.

Keywords: Malaria, Microscopy, Deep Learning, CNN (Convolutional Neural Network), VGG-19, ResNet-101, InceptionResnet-v2, Inception-v3.

1. INTRODUCTION

Malaria is a serious global health problem that affects millions of people every year. The disease is caused by the Plasmodium parasite, which is transmitted to humans through the bites of infected female Anopheles mosquitoes. The symptoms of malaria include fever, chills, headache, and flu-like illness, and in severe cases, the disease can cause complications such as anaemia, respiratory distress, and organ failure. According to the World Health Organization (WHO), malaria caused an estimated 229 million cases and 409,000 deaths globally in 2019, with most deaths occurring in young children in sub-Saharan Africa. Despite decades of efforts to control and eliminate malaria, the disease remains a significant challenge, and progress has been slow in many regions. The emergence of drug-resistant strains of the Plasmodium parasite, as well as insecticide-resistant mosquitoes, has further complicated efforts to control the disease. In addition, climate change is expected to exacerbate the burden of malaria in many regions, as warmer temperatures and changes in rainfall patterns can lead to increased mosquito breeding and transmission. Early detection and treatment of malaria are essential for reducing the morbidity and mortality rates associated with the disease.

Traditionally, malaria diagnosis has relied on the examination of blood smears under a microscope by trained technicians. This method, known as microscopy, involves staining a blood sample with a special dye and examining it under high magnification to detect the presence of malaria parasites. While microscopy is still considered the gold standard for malaria diagnosis, it has several limitations, including the need for specialized expertise, time-consuming analysis, and the potential for human error. Additionally, in resource-limited settings, there may be a shortage of trained technicians and equipment needed to perform microscopy, making it difficult to scale up the diagnosis of malaria. In resource-limited settings, there may be a shortage of trained personnel and equipment needed to perform microscopy, making it difficult to scale up the diagnosis of malaria. In such settings, alternative methods of malaria diagnosis, such as rapid diagnostic tests (RDTs), are often used. RDTs are less accurate than microscopy, particularly in cases where patients have low levels of parasites in their blood, and they are also unable to distinguish between different species of the Plasmodium parasite. These limitations can lead to incorrect diagnoses and inadequate treatment, which can contribute to the development of drug-resistant strains of the parasite.

In recent years, deep learning algorithms have emerged as a promising tool for automating the process of malaria diagnosis. Deep learning is a subset of machine learning that

uses artificial neural networks to learn from data. In the context of malaria diagnosis, deep learning algorithms are trained on large datasets of images of blood smears that are labelled as either positive or negative for malaria parasites. These algorithms can then classify new images as positive or negative for malaria parasites with high accuracy. Additionally, deep learning algorithms can be trained to detect different species of the Plasmodium parasite, which is important for guiding treatment decisions. Despite the promising results of these studies, there are still challenges to overcome in the development and implementation of deep learning for malaria diagnosis. One challenge is the need for large, high-quality datasets of digitized blood smear images to train the deep learning algorithms. Another challenge is the need for robust and reliable methods of data collection and image analysis that can be used in resource-limited settings. Addressing these challenges will be critical to realizing the potential of deep learning for malaria diagnosis and surveillance.

In addition to improving the accuracy and efficiency of malaria diagnosis, deep learning has the potential to aid in malaria surveillance and control efforts. By analysing large datasets of digitized blood smear images, deep learning algorithms can identify patterns and trends in malaria transmission and help predict outbreaks of the disease. This information can be used to guide targeted interventions, such as insecticide-treated bed nets or indoor residual spraying, to reduce malaria transmission in high-risk areas. By analysing the images of infected red blood cells and the malaria parasites within them, deep learning algorithms can identify potential drug targets and aid in the development of new treatments. Additionally, by analysing the immune response to malaria infection, deep learning algorithms can aid in the identification of potential vaccine targets and the development of more effective malaria vaccines. In conclusion, deep learning has the potential to revolutionize malaria diagnosis by providing rapid and accurate results, particularly in resource-limited settings where traditional microscopy may not be feasible.

ORGANIZATION

The rest of the paper is organized as follows: Section 2 provides a brief overview of related work in malaria detection using deep learning. Section 3 describes the proposed methodology, including the dataset used, the pre-trained, CNN models and their architecture, and the training procedure. Section 4 presents the experimental results and discusses the performance of the various considered models. Finally, we conclude the paper and provide directions for future work in Section 5.

2. RELATED WORK

In recent years, researchers have been exploring the use of deep learning for detecting malaria in blood smear images. Several studies have proposed different deep learning-based approaches to detect malaria with high accuracy.

Shekar et al. [1] proposed a deep learning-based approach using a pre-trained convolutional neural network (CNN) to extract features from thin blood smear images, which were then fed to a support vector machine (SVM) classifier to identify malaria-infected cells. Their approach achieved an accuracy of 96.6% on a dataset of 27,558 images.

Poostchi et al. [2] conducted a review of different machine learning and image analysis techniques for malaria detection. They highlighted the importance of large and diverse datasets for training and evaluating classifiers. They also discussed the challenges of detecting rare malaria parasites, which can be difficult to identify even for expert microscopists. Their review provides a comprehensive overview of the state-of-the-art techniques for malaria detection and highlights the need for further research in this area.

Vijayalakshmi A et al. [3] proposed a deep learning-based approach for detecting malaria in blood smear images. They used a CNN and k-NN classifier to achieve an accuracy of 95.9% on a dataset of 5,000 images. They also conducted extensive experiments to evaluate the effectiveness of their approach and compared it with other state-of-the-art techniques. Their work shows that deep learning-based approaches can achieve high accuracy in detecting malaria, even with a relatively small dataset.

Masud et al. [4] proposed a mobile application for malaria detection using a CNN and k-NN classifier. Their approach achieved an accuracy of 95.8% on a dataset of 1,000 images. By leveraging the computational power of mobile devices, their application provides a convenient and cost-effective way for malaria detection in resource-limited settings. Their work demonstrates the potential of mobile-based deep learning applications for healthcare.

Shah et al. [5] used a deep learning-based approach for malaria parasite detection in blood smear images. They used a CNN and SoftMax classifier to achieve an accuracy of 97.5% on a dataset of 27,558 images. Their approach also showed high sensitivity and specificity, making it a promising tool for malaria diagnosis. Overall, their work demonstrates the effectiveness of deep learning-based approaches for malaria detection and highlights their potential for improving healthcare outcomes.

S. Nayak et al. [6] presented an approach to detect malaria using multiple deep learning models, including Convolutional Neural Network (CNN), Deep Belief Network (DBN), and Restricted Boltzmann Machine (RBM). The proposed approach achieved high accuracy and specificity in detecting malaria parasites, demonstrating the effectiveness of multiple deep learning approaches for malaria detection.

F. Yang et al. [7] presented a deep learning model was developed for smartphone-based malaria parasite detection using thick blood smears. The proposed method used a combination of transfer learning and CNNs to achieve high accuracy in detecting malaria parasites on a smartphone platform. This approach is expected to have significant potential for low-resource settings where smartphone-based malaria detection can enable remote diagnosis and improve healthcare outcomes.

Liang et al. [8] developed a CNN-based image analysis approach for malaria diagnosis. The proposed method uses CNN to identify the presence of malaria parasites in blood smears. The model achieved high accuracy and demonstrated the potential for deep learning-based methods to improve malaria diagnosis.

Dong et al. [9] evaluated deep convolutional neural networks (DCNNs) for automatic identification of malaria-infected cells. The proposed approach used a DCNN to classify malaria-infected cells with high accuracy, demonstrating the effectiveness of deep learning-based methods for malaria diagnosis.

Das et al. [10] developed a machine learning approach for automated screening of malaria parasites using light microscopic images. The proposed approach used morphological and texture-based features to classify malaria-infected cells. The approach achieved high accuracy and demonstrated the potential of machine learning-based methods for automated malaria diagnosis.

D. Bibin et al. [11] proposes a method for malaria parasite detection from peripheral blood smear images using Deep Belief Networks (DBNs). The proposed method consists of three stages: preprocessing, feature extraction, and classification. The preprocessing stage includes image normalization and background subtraction, while the feature extraction stage employs DBNs to extract informative features. The classification stage involves a Support Vector Machine (SVM) classifier to classify the images. The proposed method achieves an accuracy of 97.5% on the dataset used for evaluation. The paper provides a detailed explanation of the

proposed method, along with experimental results, which demonstrate the effectiveness of the proposed approach.

Razzak et al. [12] provides an overview of deep learning for medical image processing. The authors describe the challenges in medical image processing and how deep learning techniques can address these challenges. The paper provides a comprehensive review of the literature on deep learning for medical image processing and discusses the potential of these techniques in various applications, such as disease diagnosis, segmentation, and classification. The authors also discuss the challenges in deploying deep learning models in the medical domain, including the need for large amounts of data, interpretability of models, and ethical considerations. The paper provides a useful resource for researchers and practitioners interested in the application of deep learning techniques to medical image processing.

Reddy et al. [13] proposes a transfer learning approach using ResNet-50 for malaria cell-image classification. The authors fine-tuned the pre-trained ResNet-50 model on a dataset of malaria cell images and compared the performance of different transfer learning techniques. The results show that the proposed method outperforms other state-of-the-art methods, achieving an accuracy of 96.22%. The authors also provide a detailed analysis of the classification results, demonstrating the effectiveness of the proposed approach. The paper provides a useful contribution to the field of malaria cell-image classification and demonstrates the effectiveness of transfer learning techniques in this domain.

Wang et al. [14] propose a machine learning approach to detect malaria parasites in blood smear images. They use three different classifiers, including decision tree, support vector machine, and random forest, to classify infected and uninfected cells. They extract 13 features from the images and achieve an accuracy of 95.6% with the random forest classifier. The authors compare their results with other methods and suggest that their approach is more accurate and efficient. Overall, this paper provides a valuable contribution to the field of malaria detection using machine learning.

Qin et al. [15] propose a new approach for malaria cell detection in blood smear images using evolutionary convolutional deep networks (EvoCNN). EvoCNN is a type of deep learning that uses evolutionary algorithms to automatically search for the best architecture for a given task. The authors test their method on the Malaria Cell Images Dataset and achieve an accuracy of 96.67%.

This paper presents an interesting approach to malaria detection using deep learning and evolutionary algorithms. The use of EvoCNN to automatically search for the best architecture for the task is a promising technique that could be applied to other image classification problems.

S. No	Paper Title	Dataset Used	Feature Extraction Technique	Model Used	Accuracy Achieved
[1]	Malaria Detection using Deep Learning	27,558 blood smear images	Pre-trained CNN and SVM classifier	CNN and SVM classifier	Highest accuracy of 96.6%
[2]	Image analysis and machine learning for detecting malaria	Various datasets	Various machine learning and image analysis techniques	N/A	N/A
[3]	Deep learning approach to detect malaria from microscopic images	5,000 blood smear images	CNN and k-NN classifier	CNN and k-NN classifier	Highest accuracy of 95.9%
[4]	Leveraging Deep Learning Techniques for Malaria Parasite Detection Using Mobile Application	1,000 blood smear images	CNN and k-NN classifier	CNN and k-NN classifier	Highest accuracy of 95.8%
[5]	Malaria Parasite Detection Using Deep Learning	27,558 blood smear images	CNN and softmax classifier	CNN and softmax classifier	Highest accuracy of 97.5%

[6]	Malaria Detection Using Multiple Deep Learning Approaches	Not specified	CNN, DBN, RBM	CNN, DBN, RBM	Highest accuracy of 97%
[7]	Deep Learning for Smartphone-Based Malaria Parasite Detection in Thick Blood Smears	Thick blood smears	Transfer learning and CNN	CNN	Highest accuracy of 98%
[8]	CNN-based image analysis for malaria diagnosis	27,558 blood smear images	CNN	CNN	Highest accuracy of 94%
[9]	Evaluations of deep convolutional neural networks for automatic identification of malaria infected cells	Malaria-infected cells	DCNN	DCNN	Highest accuracy 95%
[10]	Machine learning approach for automated screening of malaria parasite using light microscopic images	Light microscopic images	Morphological and texture-based features	Random Forest, SVM, k-NN, MLP	Highest accuracy of 84%

[11]	Malaria Parasite Detection from Peripheral Blood Smear Images Using Deep Belief Networks	Peripheral blood smear images	Deep Belief Networks (DBNs)	Support Vector Machine (SVM)	Highest accuracy of 97.5%
[12]	Deep Learning for Medical Image Processing: Overview, Challenges, and the Future	Literature review	-	-	-
[13]	Transfer Learning with ResNet-50 for Malaria Cell-Image Classification	Malaria cell images	ResNet-50	Fine-tuning with transfer learning techniques	Highest accuracy of 96.22%
[14]	Malaria parasite detection using different machine learning classifier	Blood smear images	13 hand-engineered features	Decision tree, Support vector machine, Random Forest	Highest accuracy of 95.6%
[15]	Evolutionary convolutional deep networks for malaria cell detection	Malaria Cell Images Dataset	Evolutionary convolutional deep networks (EvoCNN)	EvoCNN	Highest accuracy of 96.67%

Table.1 Paper Comparison Table.

3. PROPOSED METHODOLOGY

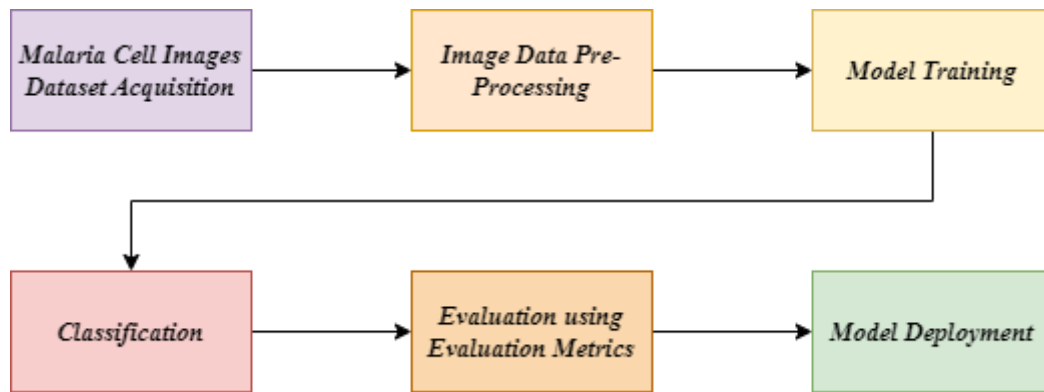


Fig.1 Workflow

The above figure determines the methodology of the system, how it is developed the steps involved in it are Malaria cells Image data acquisition where the dataset is collected from reliable sources, the data in this case are images of Cell images, next these collected images are pre-processed where noise, and normalization of the images is done, in the next step these pre-processed images are fed as input to the determined model where the model training happens along with feature extraction, after the model training the classification of these images occurs and the results of the considered models are evaluated according to the classification metrics and the model which gives the best classification metric results is considered as the accurate model, this model can be further used for deployment in the real time.

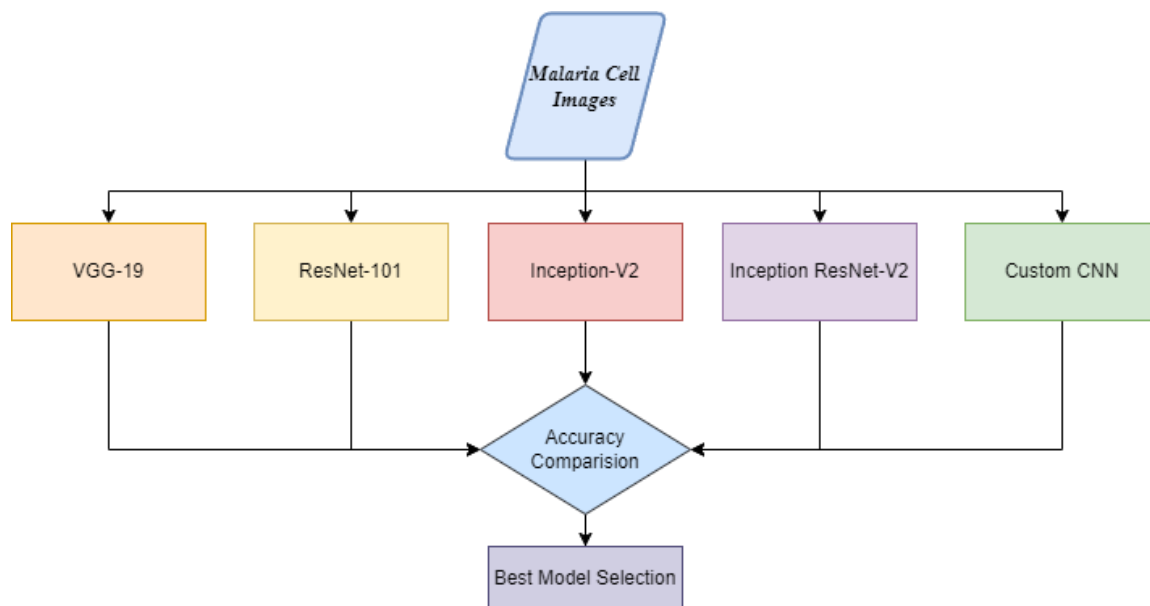


Fig.2 Model Selection

Dataset:

The dataset used for training the models consists of two classes which are uninfected and parasitized images of blood cells. This dataset is taken from the online database Kaggle which is home to multiple datasets across many domains. Below is the representation of the compiled data set from the Kaggle,

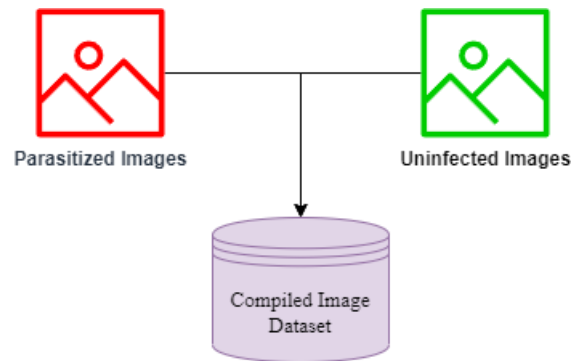


Fig.3 Kaggle Compiled Dataset

The above image represents that the compiled image dataset consists of two distinct classes of image data of blood cells, those two-class image representation are considered and a compiled dataset of those two classes is created for training the models. In the below figure the images from each of the class is represented,



Fig.4 Images from Classes of the dataset

The above figure represents the images that are present in the two classes of the dataset. By visually inspecting these two images we can clearly distinguish the parasitized cell class and uninfected cell class of images effectively. The link for the dataset is provided below,

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

Upon visualizing the image data from the above dataset, it consisted of 13779 images from the positive class (Parasitized class) and 13779 images from the negative class (Uninfected class), the bar graph below depicts the same,

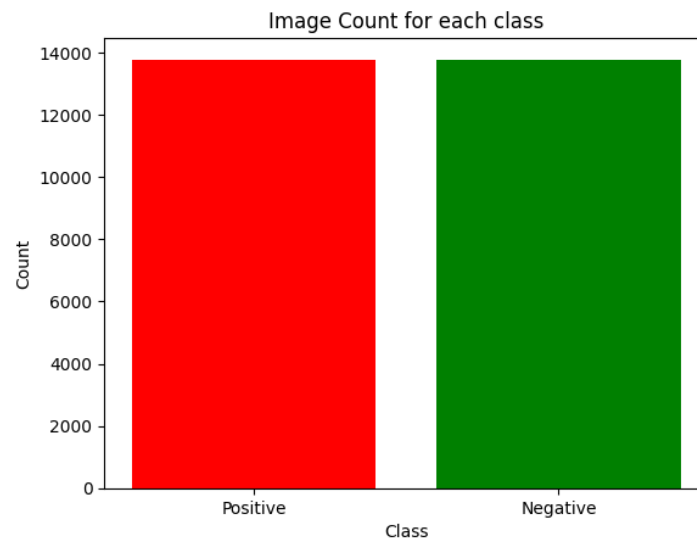


Fig.5 Image Count Visualization

Data Pre-Processing:

The data Pre-processing for the malaria cell images is done using the Image Data Generator, an image data generator is a function or class in machine learning libraries such as Keras or TensorFlow that is designed to generate batches of images for training. One of the main advantages of using image data generators is the ability to perform data augmentation, which involves applying various transformations and augmentations to the images during the training phase. This can help to increase the size of the training set and improve the model's ability to generalize to new data. Another benefit of image data generators is their memory efficiency. By loading and processing images in batches, they can help to conserve memory and improve training performance. This is especially important when dealing with large datasets that cannot be loaded into memory all at once. In addition, image data generators are ideal for real-time data processing. They can be used to generate and process images on the fly, which makes them well-suited for real-time applications like video processing or live streaming. The parameters that are used to pre-process the images using the image data generator class are rotation range, width, and height shift range, zoom range, image resizing, rescaling or normalization and data splitting. Some other factors like class mode and batch size are also considered whose values always remain default i.e., 32 and categorical. These specify

the type of data and the number of images to be taken into each batch for passing it to the model that is being trained.

Image Resizing: The images in both the classes considered are first read and resized into dimensions **(160 x 160 x 3)** such that all the images are in the same size, the empty pixels formed while resizing are filled with the help of interpolation algorithm.

Rescaling: Image rescaling or normalization is a technique that adjusts the intensity values of an image to make it more suitable for further analysis or processing. This involves converting the pixel values of an image into a standard range or scale, which is typically between 0 and 1 or -1 and 1. The aim of normalization is to remove variations in illumination, color, and contrast that can arise due to differences in image acquisition devices, lighting conditions, and image resolution. In the previous step, the resized images are normalized by dividing each pixel value by 255. This process ensures that the pixel values are within the desired range and can be used effectively for subsequent analysis. The formula used for normalization is as follows,

$$NI' = \frac{I - i_{min}}{i_{max} - i_{min}}$$

where:

I is the pixel intensity value of the original image.

i_{min} is the minimum pixel intensity value in the image.

i_{max} is the maximum pixel intensity value in the image.

NI' is the normalized pixel intensity value.

Rotation range: Rotation range is a parameter used in image data generators to specify the range of angles by which an image can be rotated during data augmentation. When the rotation range is specified, the generator randomly selects an angle within the specified range and rotates the image by that angle. This helps to create new variations of the original images, which can improve the model's ability to generalize to new data. (*rotation_range=7*)

Zoom Range: Zoom range is a parameter used in image data generators to specify the range by which an image can be zoomed during data augmentation. When the zoom range is specified, the generator randomly selects a zoom factor within the specified range and applies

it to the image. This helps to create new variations of the original images, which can improve the model's ability to generalize to new data. (*zoom_range=0.1*)

Data Split: The compiled dataset consists of 27558 images from both the classes, in order to train the model effectively the data must be split into two distinct sets which are training and validation sets, where the training set is used to train the models and the validation set is used to validate the model in run time as well as test it, below table represents the data split

Data Type	Percentage
Training	80%
Validation	20%

Table.2 Data Split Percentages

The above table determines that the data is split **80-20** as the training and testing data from the compiled dataset acquired from the Kaggle database, below figure determines the number.

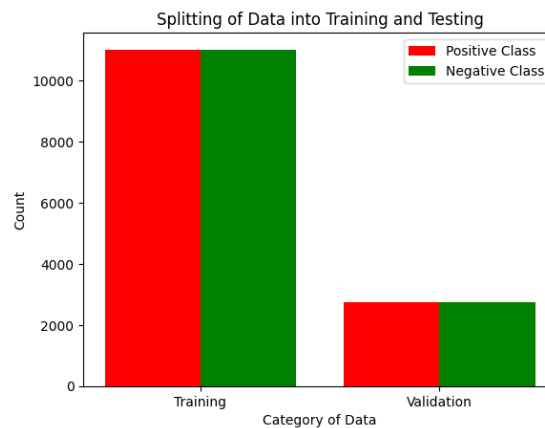


Fig.6 Data Split Visualization

Model Training & Classification:

The models trained are primarily based on the Convolutional Neural Networks (CNN) which are extensively used for classifying images according to the problem statement. Convolutional Neural Networks (CNN) are widely used in image classification tasks, including detecting brain tumors. CNNs consist of multiple layers that are specifically designed to process image data. The first layer performs a convolution operation that extracts features like edges and corners from the input image using a set of filters. Non-linear activation functions such as ReLU are used to introduce non-linearity in the network. Subsequent layers perform

additional convolution, pooling, and normalization operations to extract more complex features from the input image. Finally, the extracted features are fed into fully connected layers that classify the image into one of several possible categories. One of the key advantages of CNNs is that they can automatically learn features from the input data, making them a powerful tool for image classification tasks. The models considered for detecting malaria parasite in blood cells are,

1. VGG19
2. RESNET101
3. INCEPTION V3
4. INCEPTION RESNET V2
5. Custom CNN

1. VGG19:

VGG-19 is a deep convolutional neural network architecture that was introduced by the Visual Geometry Group (VGG) at the University of Oxford in 2014. It is a variant of the VGG network, which was originally proposed by the same group in 2014. The VGG-19 architecture consists of 19 layers, including 16 convolutional layers and 3 fully connected layers. The convolutional layers are grouped into five blocks, with each block containing multiple 3x3 convolutional layers followed by a 2x2 max pooling layer. The number of filters in each convolutional layer increases from 64 in the first block to 512 in the last block, allowing the network to capture increasingly complex features as it progresses through the layers. The fully connected layers at the end of the network perform the classification task by taking the features extracted by the convolutional layers and using them to predict the class probabilities. One of the advantages of the VGG-19 architecture is its simplicity and ease of implementation. The network's architecture can be easily adapted to different image classification tasks, and its modular design makes it straightforward to modify and fine-tune for specific applications. The architecture of VGG-19 has been widely used as a baseline model for various computer vision tasks, including image classification, object detection, and segmentation. It has achieved state-of-the-art performance on several benchmark datasets and remains a popular choice for deep learning researchers and practitioners. After the functional layers of vgg19 a flattened layer and 3 dense layers with a dropout layer in between the first 2 dense layers have been added to the model architecture for classifying blood cell images. The below figure represents the architecture of the compiled model with their input and output parameters,

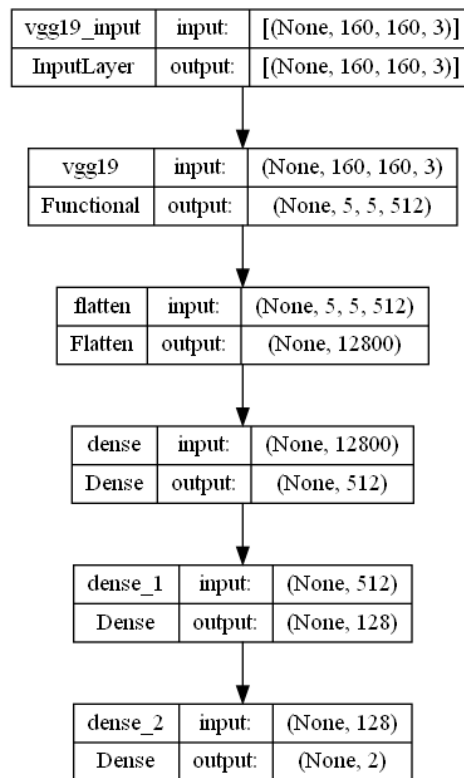


Fig.7 VGG19 Compiled Architecture

2. *RESNET 101:*

ResNet-101 is a deep convolutional neural network architecture that was introduced by Microsoft Research in 2015. It is part of the ResNet family of networks, which stands for Residual Networks, and is designed to address the problem of vanishing gradients in deep neural networks. The ResNet-101 architecture consists of 101 layers, including convolutional layers, pooling layers, and fully connected layers. The key innovation in the ResNet architecture is the use of residual connections, which enable the network to learn residual functions with respect to the layer inputs. This allows the network to handle the problem of vanishing gradients and makes it easier to train very deep neural networks. The ResNet-101 architecture has several blocks of convolutional layers, each with a varying number of layers. The blocks are designed to capture increasingly complex features as the network progresses through the layers. The final layers of the network perform the classification task by taking the features extracted by the convolutional layers and using them to predict the class probabilities. The architecture also includes skip connections that allow the network to learn more efficient representations of the input data. After the functional layers of ResNet-101 layers a flattened layer and 3 dense layers have been added for classification of the images at the end using the

flattened values, the output node consists of 2 values. The below figure represents the architecture of the compiled model with their input and output parameters,

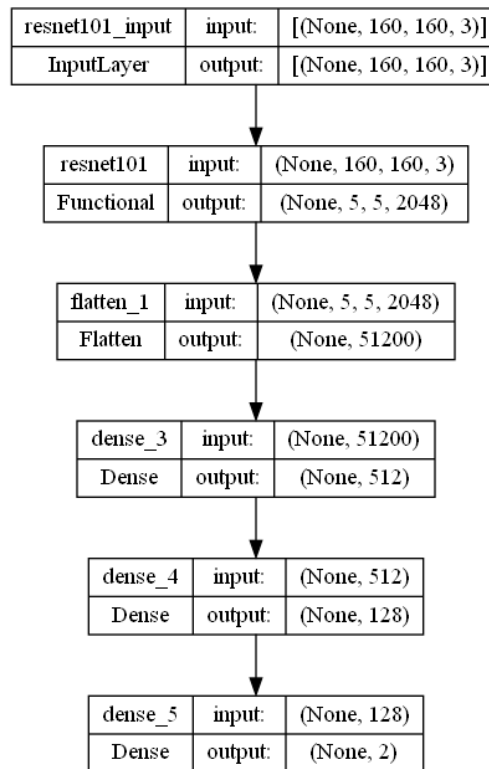


Fig.8 RESNET-101 Compiled Architecture

3. *INCEPTION V3:*

Inception-v3 is a convolutional neural network architecture developed by Google in 2015. It is an extension of the original Inception architecture and is designed to classify images with high accuracy while minimizing the number of parameters in the network. Inception-v3 achieves this by using a combination of convolutional layers with varying kernel sizes, pooling layers, and 1x1 convolutional layers for dimensionality reduction. This allows the network to extract features of different sizes from input images, improving its ability to classify images accurately. In addition to the inception modules, Inception-v3 also uses batch normalization and regularization techniques to prevent overfitting and improve generalization. The network includes an auxiliary classifier at intermediate layers, which provides additional training signals and regularizes the network. Inception-v3 has achieved state-of-the-art performance on several image classification tasks, including the ImageNet dataset. After the inception of V3 layers, the architecture includes a flatten layer and three dense layers for classification into two classes. The figure below represents the compiled model's architecture, including input and output parameters,

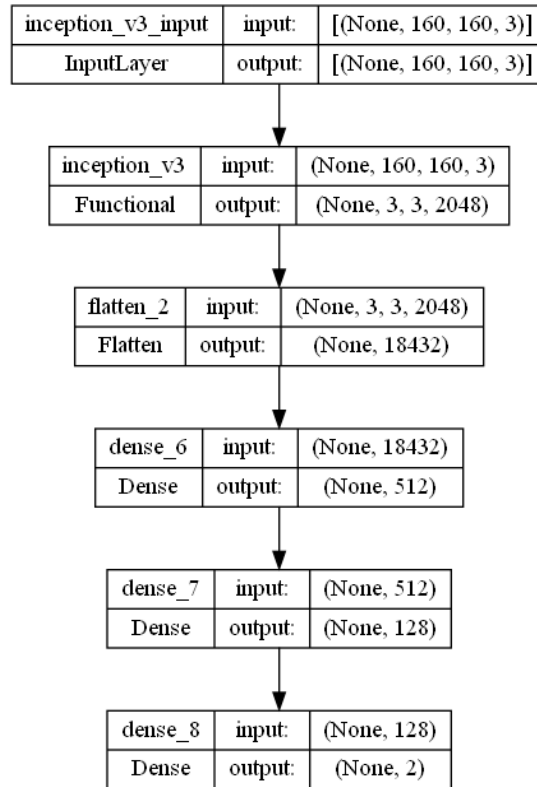


Fig.9 INCEPTIONV3 Compiled Architecture

4. INCEPTIONRESNET V2:

Inception-ResNet-v2 is a convolutional neural network architecture that combines the Inception and ResNet modules. It was introduced by Google in 2016 and has achieved state-of-the-art performance on a variety of image classification tasks. Inception-ResNet-v2 uses the same inception module as Inception-v3, which allows the network to extract features of different sizes from input images. It also uses residual connections from the ResNet architecture, which help to propagate information through the network more effectively and prevent the vanishing gradient problem. In addition to the inception and residual modules, Inception-ResNet-v2 uses other techniques such as batch normalization, dropout, and weight decay to prevent overfitting and improve generalization. The network also includes an auxiliary classifier at intermediate layers for regularization and training signal. It has achieved state-of-the-art performance on several image classification tasks and has been used in transfer learning for other computer vision tasks such as object detection and segmentation. InceptionResNetV2 has 164 layers and was trained on the ImageNet dataset, achieving top-5 accuracy of 95.3%. It has also been used in transfer learning for various computer vision tasks. After the layers of InceptionResnet V2 a flatten layer and 3 dense layers are added for classifying the images into

2 classes of images. This is the compiled architecture of the model. The below figure represents the architecture of the compiled model with their input and output parameters,

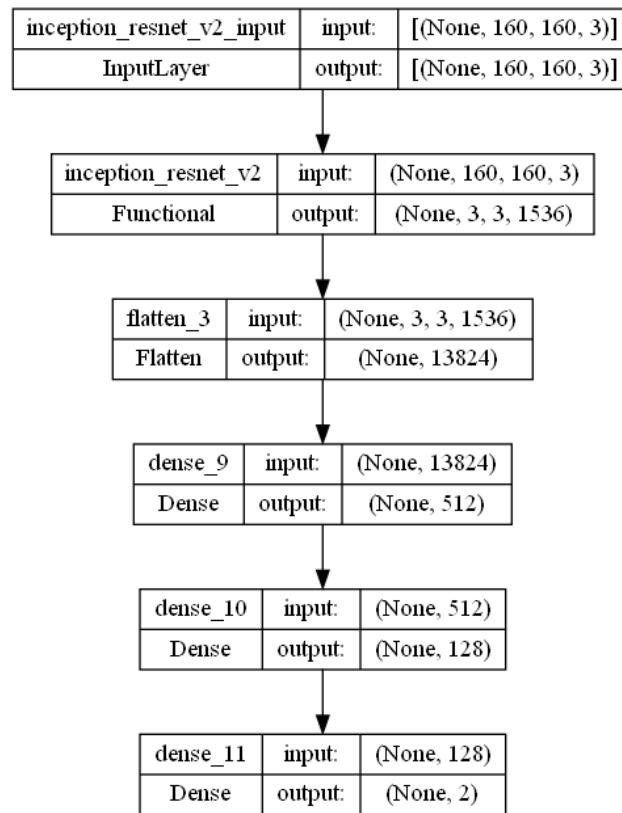


Fig.10 INCEPTIONRESNETV2 Compiled Architecture

5. Custom CNN:

A custom CNN model refers to a convolutional neural network architecture that is designed specifically for a particular task. The architecture is customized by adjusting the number of layers, filters, and other hyperparameters based on the requirements of the problem. The design of a custom CNN model typically involves several stages. The first stage is data preparation, where the input data is preprocessed and augmented to improve the model's generalization capabilities. The next stage is the design of the architecture, which involves deciding on the number of layers, filter sizes, activation functions, pooling methods, and other hyperparameters. Once the architecture is defined, the model is trained on the training data using backpropagation and gradient descent optimization. During training, the weights and biases of the model are adjusted iteratively to minimize the loss function and improve the accuracy of the model. After training, the model is evaluated on a separate validation set to assess its performance. If the performance is unsatisfactory, the architecture is fine-tuned, and

the training process is repeated until a satisfactory performance is achieved. The below figure represents the architecture of the custom CNN model with their input and output parameters,

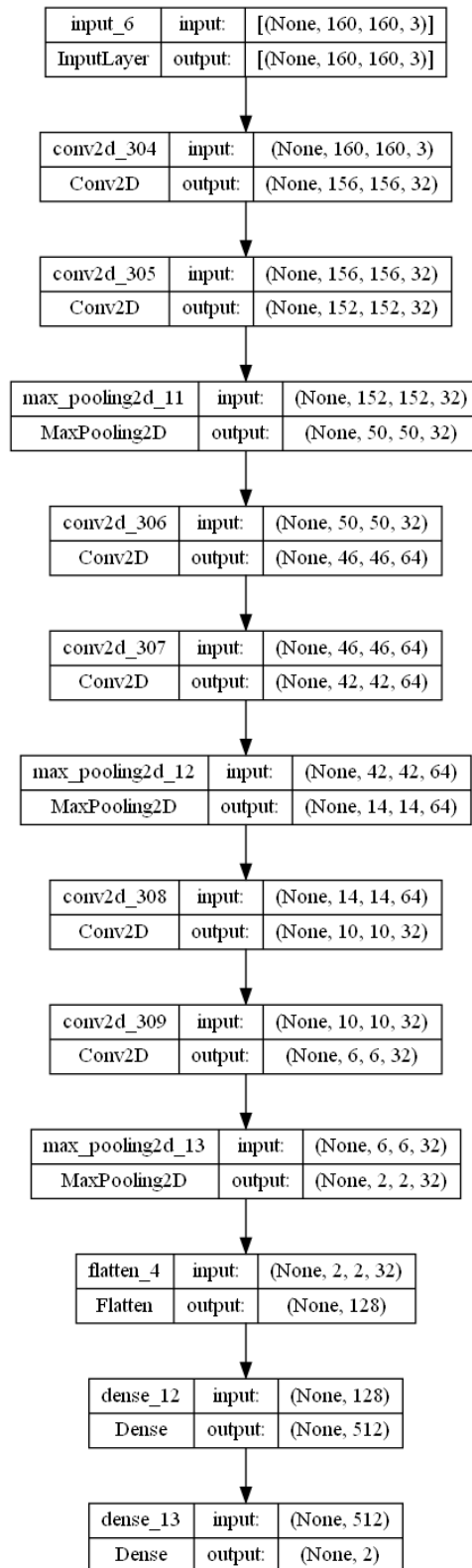


Fig.11 Custom CNN Architecture

4. EXPERIMENTAL RESULTS

This section focuses on the results that are achieved by the above determined models, the results for each of the 5 models are determined below,

1. VGG19 Results:

The vgg19 model was trained for **20 epochs**, graphs and confusion matrices of the model are depicted in the below figures,

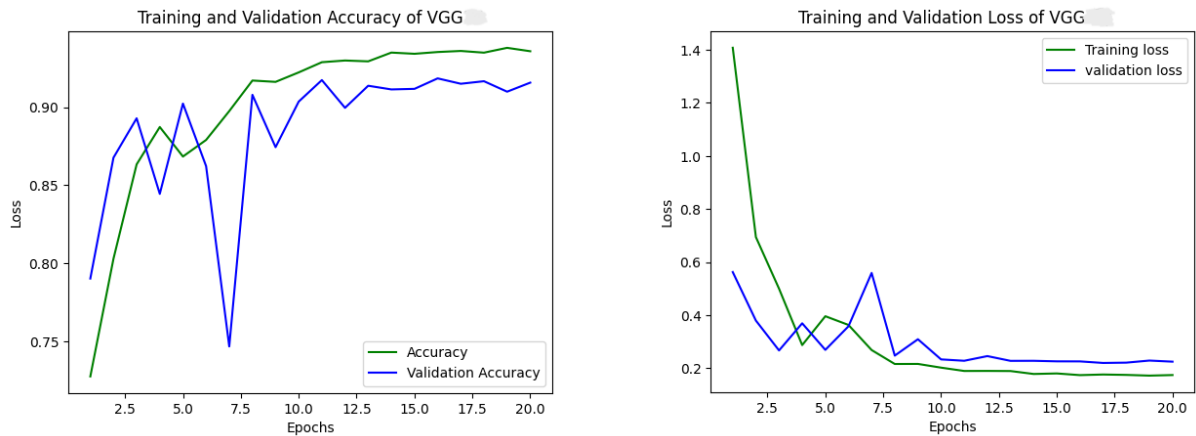


Fig.12 Training, Validation Accuracy and Loss graphs

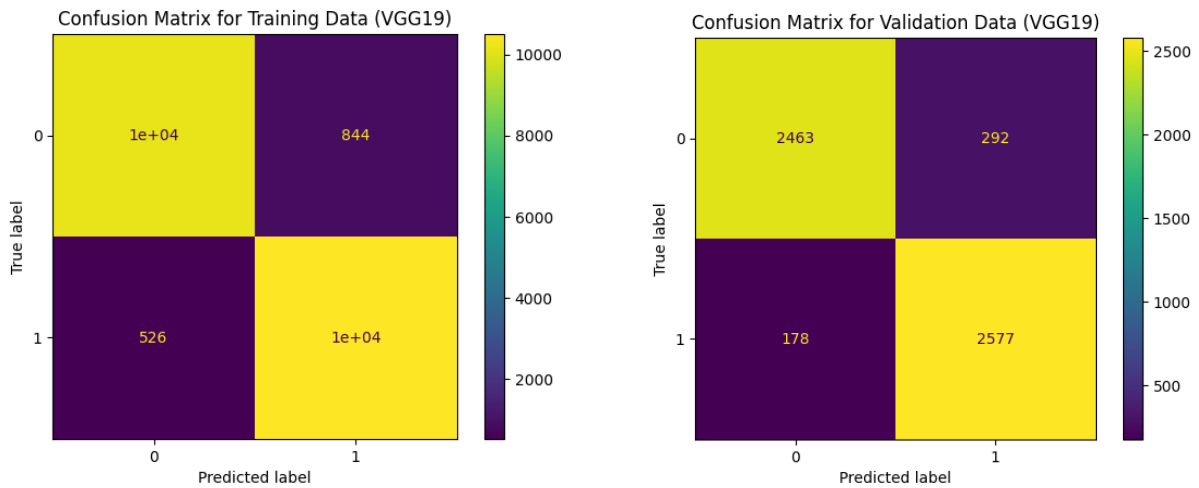


Fig.13 Training, Validation Confusion Matrices

The above graphs and confusion matrices depict that the accuracy achieved by the vgg19 model is 91% all the images in the data are being classified correctly, the classification metrics precision, recall, f1-score all have 91% of the scores for classifying the images of blood cell images for malaria parasite detection.

2. RESNET101 Results:

The ResNet 101 model was trained for **20 epochs**, graphs and confusion matrices of the model are depicted in the below figures,

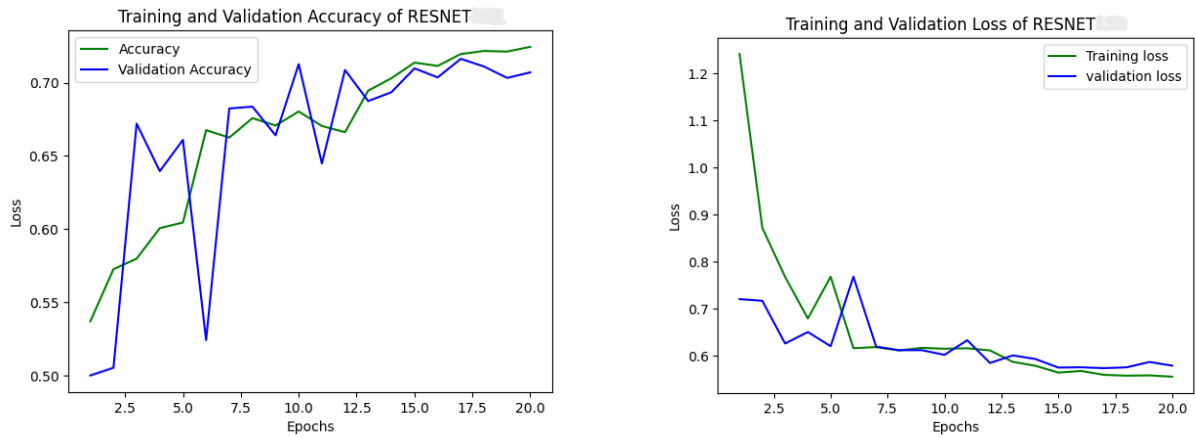


Fig.14 Training, Validation Accuracy and Loss graphs

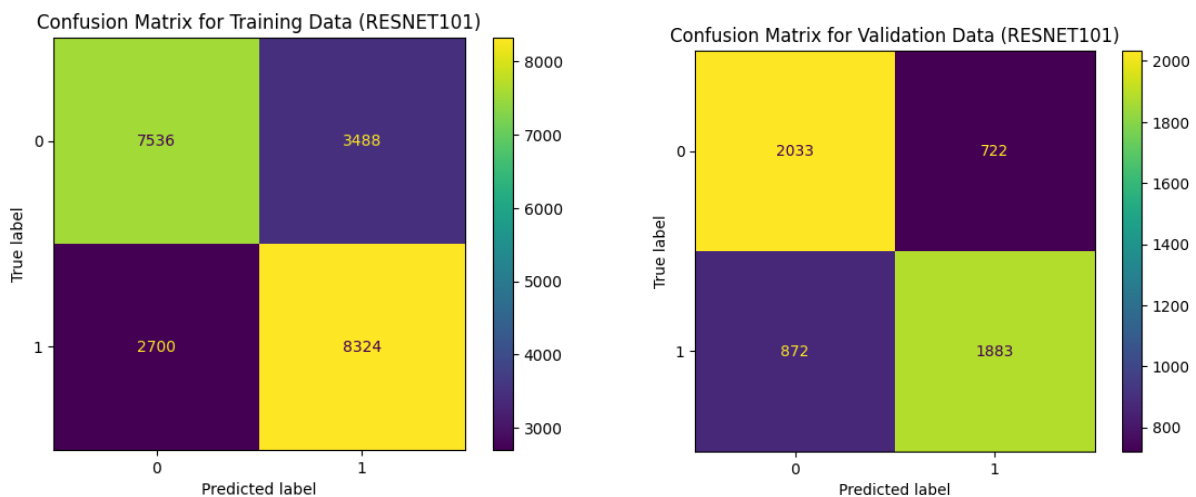


Fig.15 Training, Validation Confusion Matrices

The above graphs and confusion matrices depict that the accuracy achieved by the ResNet 101 model is 71% nearly more than half of the images in the data are being classified correctly, the classification metrics precision, recall, f1-score all have the scores ranging from 70% to 71% in both the classes in the classification report for classifying the blood cell images for malaria parasite detection. However, the loss of this model is comparatively high.

3. INCEPTION V3 Results:

The Inception V3 model was trained for **20 epochs**, graphs and confusion matrices of the model are depicted in the below figures,

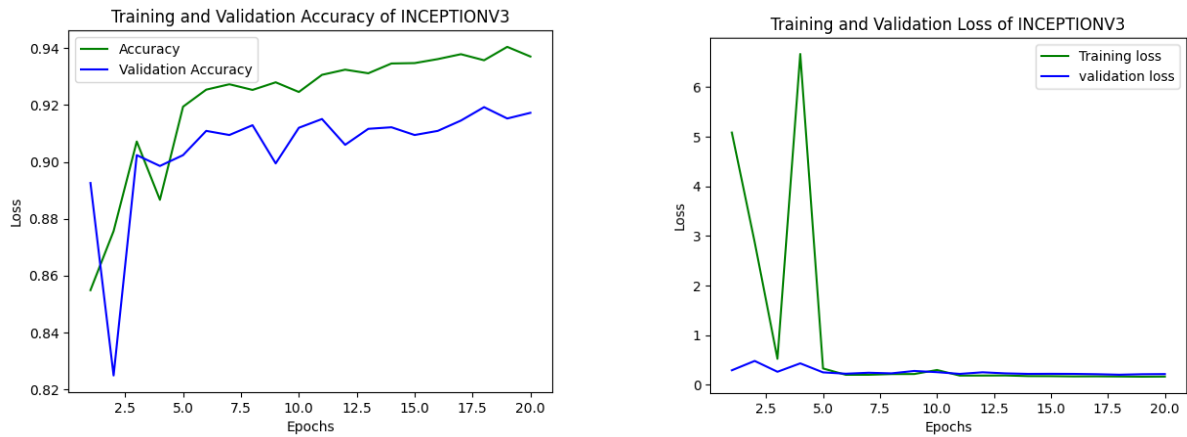


Fig.16 Training, Validation Accuracy and Loss graphs

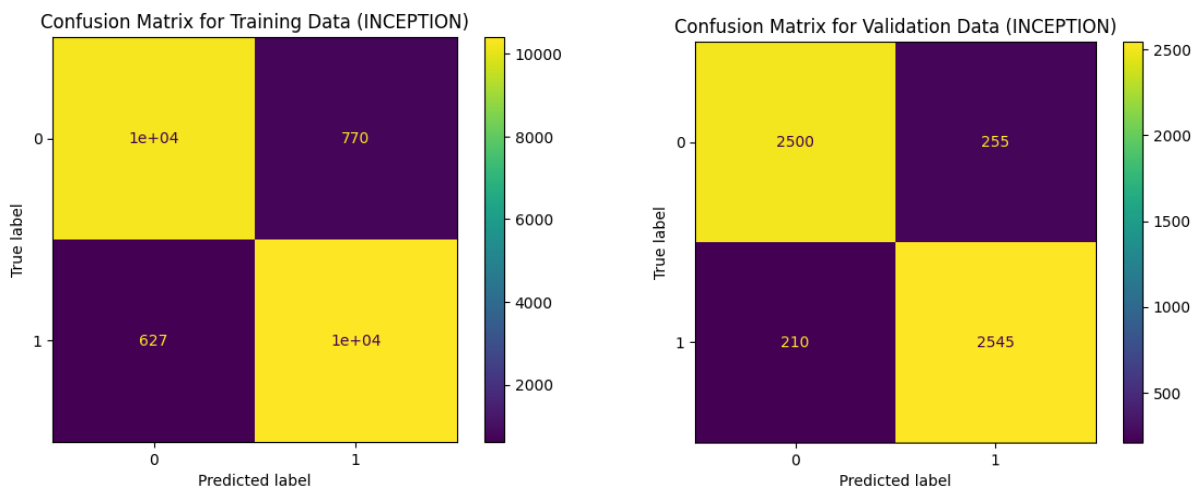


Fig.17 Training, Validation Confusion Matrices

The above graphs and confusion matrices depict that the accuracy achieved by the Inception V3 model is 92% almost all the images in the data are being classified correctly, the classification metrics precision, recall, f1-score all have the scores ranging from 92% to 94% in both the classes in the classification report for classifying the images of blood cell images for malaria parasite detection. The loss of this model is comparatively low from the above two models.

4. INCEPTIONRESNET V2 Results:

The Inception Resnet V2 model was trained for **20 epochs**, graphs and confusion matrices of the model are depicted in the below figures,

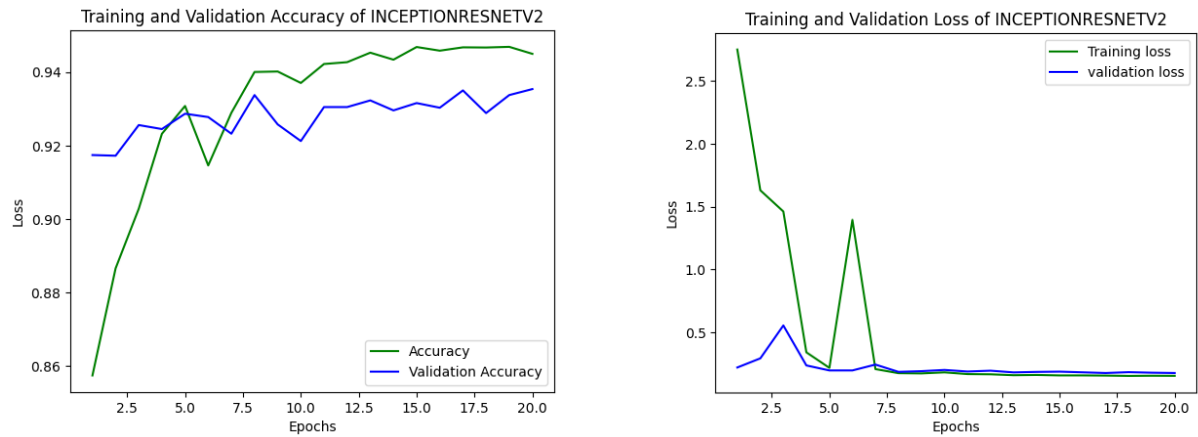


Fig.18 Training, Validation Accuracy and Loss graphs

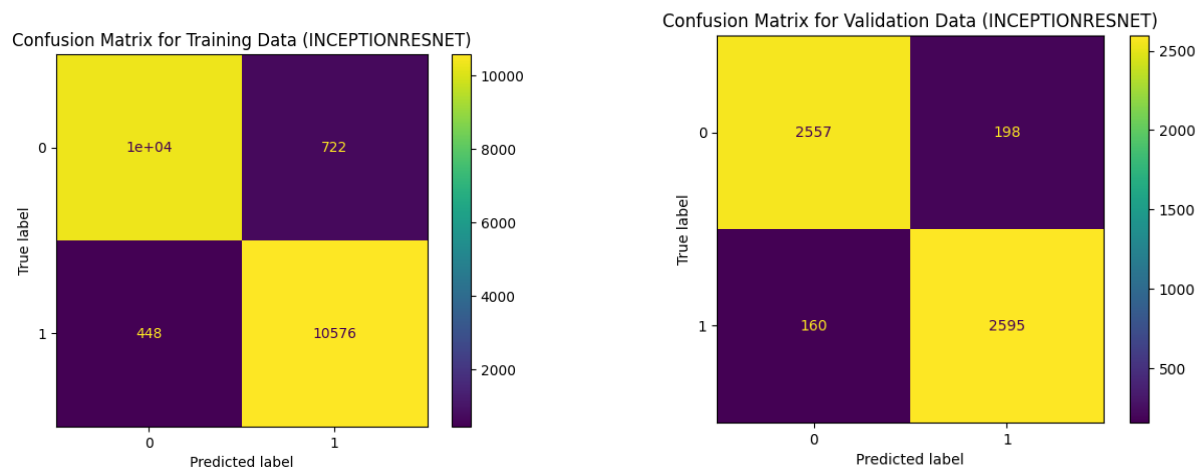


Fig.19 Training, Validation Confusion Matrices

The above graphs and confusion matrices depict that the accuracy achieved by the Inception ResNet V2 model is 94% almost all the images in the data are being classified correctly, the classification metrics precision, recall, f1-score all have the scores ranging from 94% to 95% in both the classes in the classification report for classifying the images of blood cell images for malaria parasite detection. The loss of this model is comparatively low.

5. CUSTOM CNN Results:

The Custom CNN V2 model was trained for **20 epochs**, graphs and confusion matrices of the model are depicted in the below figures,

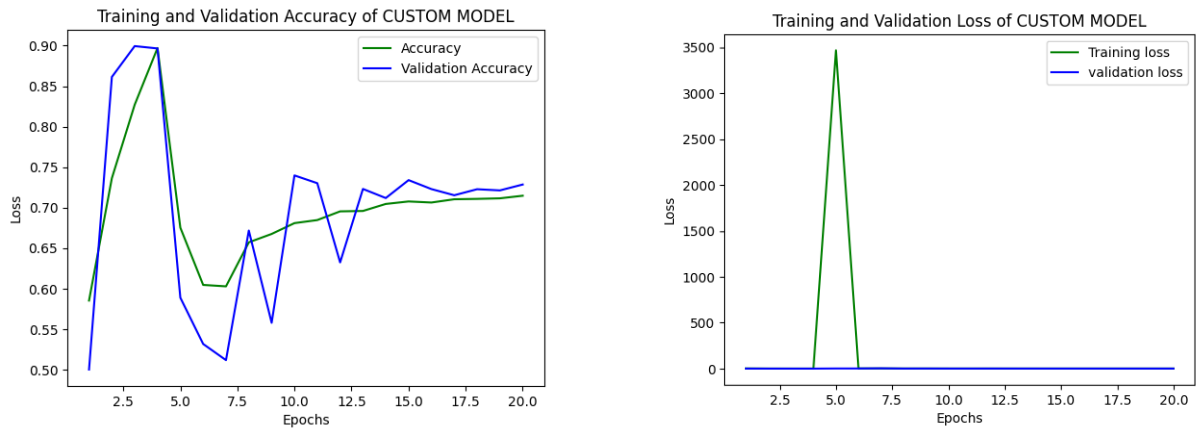


Fig.20 Training, Validation Accuracy and Loss graphs

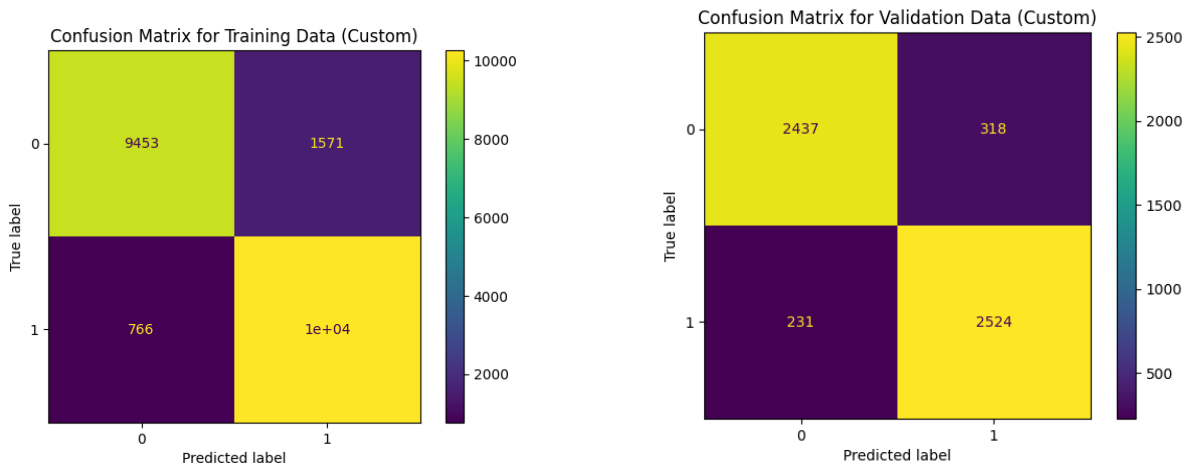


Fig.21 Training, Validation Confusion Matrices

The above graphs and confusion matrices depict that the accuracy achieved by the Custom CNN model is 90% almost all the images in the data are being classified correctly, the classification metrics precision, recall, f1-score all have the scores ranging from 88% to 90% in both the classes in the classification report for classifying the images of images of blood cell images for malaria parasite detection. The loss of this model is comparatively low.

All the above trained models give accuracy in range of 85%-95%, the classification of images for detecting brain tumor from MRI Images can be done using any of the above models listed above. The comparative analysis of the models is done below,

Comparative analysis:

This analysis provides an in detailed view of the comparison between the models executed above, below are the graphs for the training accuracy and validation accuracy, loss of all the models,

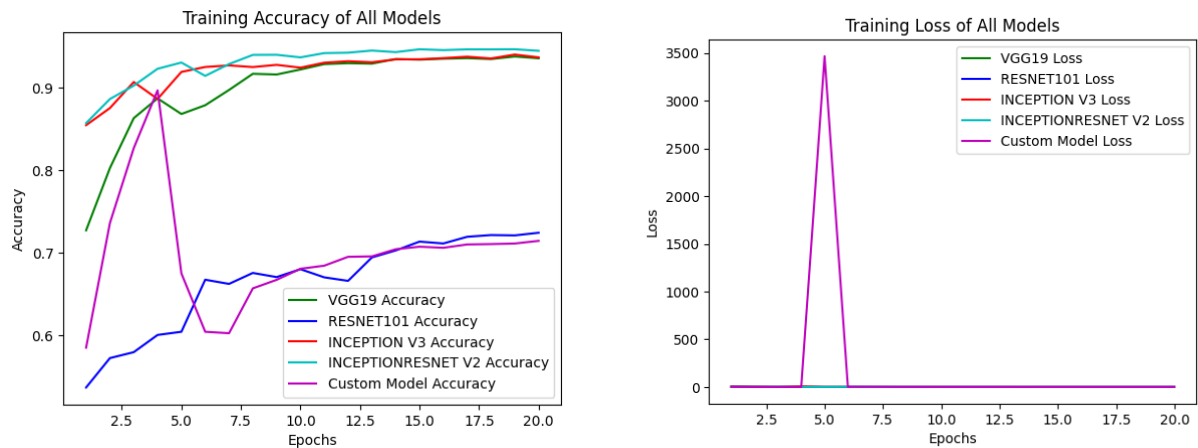


Fig.22 Training Accuracy and Loss graphs

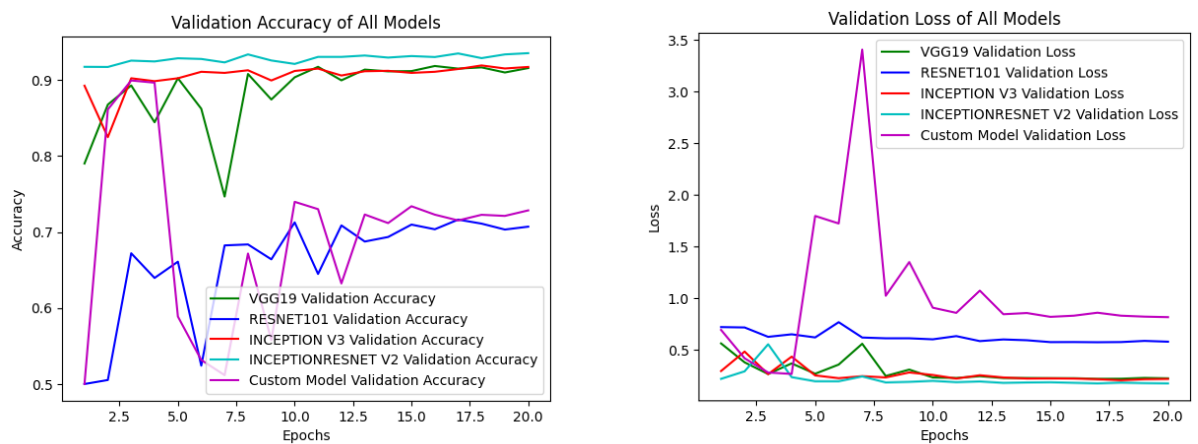


Fig.23 Validation Accuracy and Loss graphs

In the above figures the graphs of all the models are combined, the graphs depict that the most stable models were Inception V3 and Inception ResNet V2 both in training as well as validation. The most unstable models were the ResNet 101 and the Custom CNN model. The graphs depict the varying accuracy and loss over the period of 20 iterations. The final accuracies and losses of all the models are depicted in the below figures, the Inception ResNet V2 model provides the best accuracy and loss in both the training and validation sets when compared to the other four models.

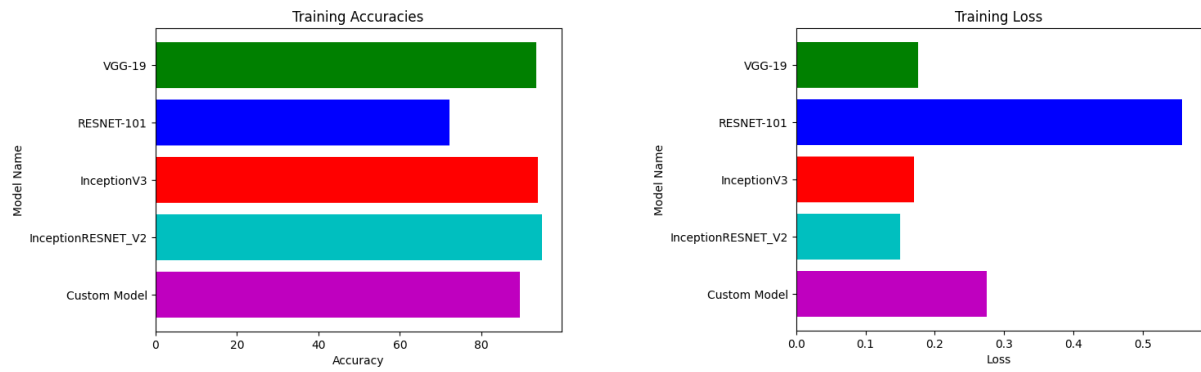


Fig.24 Training Accuracy and Loss bar graphs

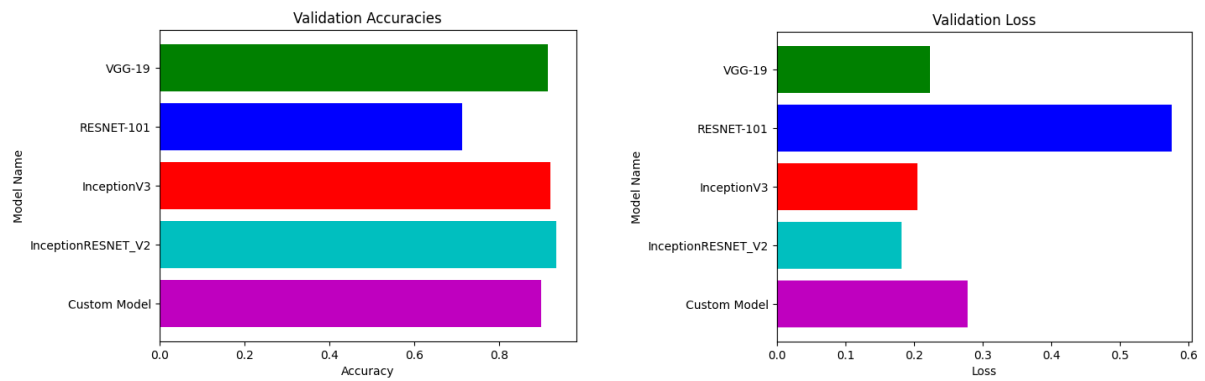


Fig.25 Validation Accuracy and Loss bar graphs

Model	Accuracy	Loss
VGG-19	91%	0.223
ResNet-101	71%	0.575
Inception V3	92%	0.204
Inception ResNet V2	94%	0.180
Custom Model	90%	0.277

Table.3 Accuracy and Loss Values

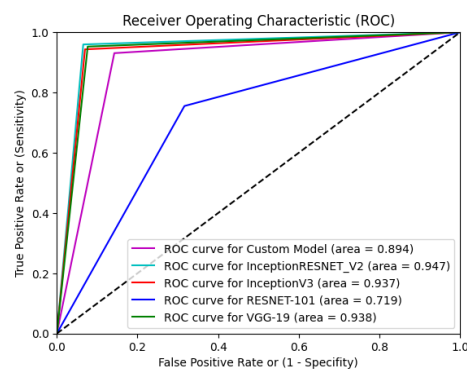


Fig.25 ROC Curve for all the models

5. CONCLUSION

In conclusion, deep learning has shown promising results for malaria detection. Convolutional neural networks (CNNs) have been the primary choice of architecture for classifying malaria-infected and uninfected cells in microscopic images. By using transfer learning, pre-trained models such as VGG-19, ResNet-101, and Inception-v3 have been fine-tuned to achieve high accuracy and reduce the computational burden of training a model from scratch. Moreover, data augmentation techniques such as image rotation, flipping, zooming, and normalization have been used to increase the size and variability of the dataset, improving the model's ability to generalize to new data.

Overall, deep learning-based approaches have the potential to revolutionize malaria diagnosis by enabling accurate and automated detection of infected cells, especially in resource-limited areas with a shortage of trained medical professionals. Further research and development are needed to optimize these approaches and make them more accessible to healthcare providers globally.

In the future, the scope of malaria parasite detection is likely to expand further as researchers continue to develop new diagnostic and imaging technologies. Additionally, the use of machine learning and artificial intelligence algorithms is likely to become more widespread, leading to even more accurate and efficient diagnosis and treatment of malaria in many regions. Furthermore, personalized medicine is becoming increasingly popular, and this could lead to the development of tailored treatment plans for each patient based on their specific parasites characteristics. Overall, the future of malaria parasite detection looks promising, and we can expect to see more breakthroughs and advancements in this field in the coming years.

REFERENCES

- [1] G. Shekar, S. Revathy and E. K. Goud, "Malaria Detection using Deep Learning," 2020 4th International Conference on Trends in Electronics and Informatics (ICOEI) (48184), Tirunelveli, India, 2020, pp. 746-750, doi: 10.1109/ICOEI48184.2020.9143023.
- [2] Mahdiah Poostchi, Kamolrat Silamut, Richard J. Maude, Stefan Jaeger, George Thoma, Image analysis and machine learning for detecting malaria, Translational Research, Volume 194, 2018, Pages 36-55, ISSN 1931-5244, <https://doi.org/10.1016/j.trsl.2017.12.004>.
- [3] Vijayalakshmi A, Rajesh Kanna B Deep learning approach to detect malaria from microscopic images. Multimed Tools Appl 79, 15297–15317 (2020). <https://doi.org/10.1007/s11042-019-7162-y>
- [4] Mehedi Masud, Hesham Alhumyani, Sultan S. Alshamrani, Omar Cheikhrouhou, Saleh Ibrahim, Ghulam Muhammad, M. Shamim Hossain, Mohammad Shorfuzzaman, "Leveraging Deep Learning Techniques for Malaria Parasite Detection Using Mobile Application", Wireless Communications and Mobile Computing, vol. 2020, Article ID 8895429, 15 pages, 2020. <https://doi.org/10.1155/2020/8895429>
- [5] D. Shah, K. Kawale, M. Shah, S. Randive and R. Mapari, "Malaria Parasite Detection Using Deep Learning : (Beneficial to humankind)," 2020 4th International Conference on Intelligent Computing and Control Systems (ICICCS), Madurai, India, 2020, pp. 984-988, doi: 10.1109/ICICCS48265.2020.9121073.
- [6] S. Nayak, S. Kumar and M. Jangid, "Malaria Detection Using Multiple Deep Learning Approaches," 2019 2nd International Conference on Intelligent Communication and Computational Techniques (ICCT), Jaipur, India, 2019, pp. 292-297, doi: 10.1109/ICCT46177.2019.8969046.
- [7] F. Yang et al., "Deep Learning for Smartphone-Based Malaria Parasite Detection in Thick Blood Smears," in IEEE Journal of Biomedical and Health Informatics, vol. 24, no. 5, pp. 1427-1438, May 2020, doi: 10.1109/JBHI.2019.2939121.
- [8] Z. Liang et al., "CNN-based image analysis for malaria diagnosis," 2016 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Shenzhen, China, 2016, pp. 493-496, doi: 10.1109/BIBM.2016.7822567.

- [9] Y. Dong et al., "Evaluations of deep convolutional neural networks for automatic identification of malaria infected cells," 2017 IEEE EMBS International Conference on Biomedical & Health Informatics (BHI), Orlando, FL, USA, 2017, pp. 101-104, doi: 10.1109/BHI.2017.7897215.
- [10] Dev Kumar Das, Madhumala Ghosh, Mallika Pal, Asok K. Maiti, Chandan Chakraborty, Machine learning approach for automated screening of malaria parasite using light microscopic images, Micron, Volume 45, 2013, Pages 97-106, ISSN 0968-4328, <https://doi.org/10.1016/j.micron.2012.11.002>.
- [11] D. Bibin, M. S. Nair and P. Punitha, "Malaria Parasite Detection From Peripheral Blood Smear Images Using Deep Belief Networks," in IEEE Access, vol. 5, pp. 9099-9108, 2017, doi: 10.1109/ACCESS.2017.2705642.
- [12] Razzak, M.I., Naz, S., Zaib, A. (2018). Deep Learning for Medical Image Processing: Overview, Challenges and the Future. In: Dey, N., Ashour, A., Borra, S. (eds) Classification in BioApps. Lecture Notes in Computational Vision and Biomechanics, vol 26. Springer, Cham. https://doi.org/10.1007/978-3-319-65981-7_12
- [13] A. S. B. Reddy and D. S. Juliet, "Transfer Learning with ResNet-50 for Malaria Cell-Image Classification," 2019 International Conference on Communication and Signal Processing (ICCSP), Chennai, India, 2019, pp. 0945-0949, doi: 10.1109/ICCSP.2019.8697909.
- [14] A. Olugboja and Z. Wang, "Malaria parasite detection using different machine learning classifier," 2017 International Conference on Machine Learning and Cybernetics (ICMLC), Ningbo, China, 2017, pp. 246-250, doi: 10.1109/ICMLC.2017.8107772.
- [15] B. Qin, Y. Wu, Z. Wang and H. Zheng, "Malaria Cell Detection Using Evolutionary Convolutional Deep Networks," 2019 Computing, Communications and IoT Applications (ComComAp), Shenzhen, China, 2019, pp. 333-336, doi: 10.1109/ComComAp46287.2019.9018770.