RESEARCH PAPER

Predictive Modeling of Malaria Severity Using Clinical and Hematological Data

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ABSTRACT

Malaria is still a serious disease and a global challenge, particularly for developing countries. Traditional diagnostic methods, such as examining blood samples under a microscope, are highly time-consuming and depend heavily on the expertise of the individual performing the analysis, which can lead to errors. But in the era of machine learning a sort of computer technology that can learn patterns and automatically detect malaria from images of blood samples. But too many studies simply check how “accurate” these systems are, and do not always indicate how reliable they can be in real medical conditions. To address this, the paper recommends using multiple ways of evaluating the system other than accuracy. They include monitoring the ability of the system to prevent false alarms (precision), detect the presence of actual malaria cases (recall), maintain a good tradeoff on both (F1-score). (ROC-AUC), determine the cases that were infected and the ones which were not infected. The paper employs a variety of measures to make sure that the malaria detection system is genuinely reliable. The results reveal that CNN models achieve strong accuracy (95.5%) but that additional metrics show deeper indicators of reliability, particularly in terms of false negatives. Our proposed framework allows for a more robust and clinically sound assessment of malaria detection systems.

Keywords: Malaria Detection, Machine Learning, CNN, Multi-Metric Evaluation, Medical Imaging, Reliability.

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1. INTRODUCTION

Every year on April 25, World Malaria Day is observed around the globe. In 2007, it was established by the member states of the World Health Organization at the World Health Assembly [1]. Malaria is not only a serious but often deadly disease, which is spread in humans by the bite of an infected female Anopheles mosquito. The most common early symptoms of Malaria are fever, headache and chills, usually appearing 10–15 days after a person is bitten. In more serious cases of the disease, it can be life-threatening. People might experience extreme fatigue, confusion, recurring seizures, breathing difficulty, dark or blood-tinged urine, yellowing of their skin and eyes (jaundice) and abnormal bleeding. Some types of the disease are particularly dangerous and can be lethal and result in serious complications or death if not treated soon enough. Plasmodium parasites cause malaria and kill millions of people every year in the world. According to the World Malaria Report, there were reportedly 597,000 deaths due to Malaria in 2023, slightly lower than the 600,000 deaths in 2022. By 2030, India is working towards an ambitious target of eradication of Malaria. As a key milestone in the move, the country has set itself the goal of reducing the number of locally transmitted cases to 0 by 2027. Early detection of infection is vital for treatment and morbidity decline. Microscopic examination and other traditional diagnostic methods are labor-intensive and prone to variability. Machine learning and deep learning methods have been proposed as promising methods for automatic malaria detection. Yet most studies focus on accuracy, which may not be adequate in medicine where false negatives may result in critical outcomes. For reliable performance, there is a need for a multi-metric evaluation method. Multiple studies that apply machine learning for identifying malaria are presented in this study. Rajaraman confirmed the detection of malaria parasites using convolutional neural network (CNN) in depth detection model [2]. A. Krizhevsky presented CNN architectures that transformed image classification [3]. Although CNN-based detection of malaria had been reported to have achieved > 97% accuracy, few evaluation metrics have been reported. Recent work stresses the importance of the sensitivity and specificity in medical diagnosis. CNNs (Convolutional Neural Networks) are becoming popular for clinical image analysis methods, especially considering their natural capability to automatically learn features from raw images. While traditional machine learning methods rely on manually manipulated features like shape, texture, or color, the CNNs acquire these features directly from their training. It becomes valuable for such tasks as malaria detection, for which subtle distinctions between parasitized and uninfected red blood cells may be difficult to detect. Previous studies have indicated that CNN-based models can be very effective in classifying cells infected with malaria. For example, Rajaraman et al. [2], have shown that pre-trained CNN models could extract important features from blood smear images, achieving over 95% accuracy on the NIH malaria dataset. Their study also indicated that CNN outperforms traditional classifiers support vector machines (SVM) and K-nearest neighbor (KNN) mainly due to the fact that CNNs do not depend on handcrafted features. Similarly, Bibin et al. [4] have emphasized the benefits of deep learning-based approaches for malaria detection, noting automatic feature extraction increases the consistency and reduces human dependency. Their research verified that deep models cover the variations over image and staining quality. Liang et al. [5] used CNN models with transfer learning to identify infected cells with high sensitivity and specificity. Moreover, Ramos-Briceño et al. [6] successfully trained CNN models to classify all infected and uninfected samples with accuracy nearly 99%. These results show that CNN models are strong and applicable for automated diagnosis of malaria. we concentrate on deep learning models to find and differentiate the infected cells.

2.Related Work.

Deep learning techniques have become more common in recent years to ensure medical decision-making in clinical practice. Blood smear images are photographs of blood samples taken under a microscope, through which we spread out a thin smear on a slide so that doctors can see diseases such as malaria and other blood disorders. Charles Louis Alphonse Laveran was the first to observe malaria parasites in human blood under the microscope in year 1880. This set the scene for more traditional diagnostic methods relying on manual examination. F. B. Tek was one of the first to bring forth one of the early machine learning-based methods with image processing and classification as part of the process to automate the detection of malaria, in 2010. In 2016 Liang et al. introduced CNNs, allowing more accurate and timely identification via automatic feature extraction from blood smear images. Rajaraman et al. employed pre-trained models such as VGG16 and ResNet for malaria-targeted discrimination. Their method increased overall performance however, it also struggled with overfitting. Most recently, more sophisticated malaria detection models, including attention -based mechanisms as core concept of deep learning. Although these methods obtain high accuracy, often 97-99%, they have limited generalization and reliable performance in practical clinical real-life case studies. The different methods used to process the dataset and their dependent results are shown in Table 1.

3. Methodology

There are multiple aspects comprising the method such as data collection, preprocessing, model building, training, and evaluation

3.1 Dataset: The dataset used in this study is the NIH Malaria Dataset, a publicly available on National Institutes of Health website. It has 27558 microscopic images of red blood cells with a parasitized type (infected) and an uninfected type (healthy) classification. For this research, a curated version of the dataset was extracted by manual inspection. A total of 10620 good quality images were chosen to get reliable model for training. Among these, 5780 images are refined, are in the parasitized class of images, and 4840 in the uninfected class. This procedure of careful data selection and preprocessing significantly improves the overall quality of the dataset, enabling the model to learn more effectively from clean and representative examples. Several preprocessing steps were performed for efficient model training and to improve generalization.

Table.1 Comparative Analysis of Existing Studies

Year	Approach	Dataset	Accuracy	Observations	Authors	Ref.
2010	Image Processing + ML	Blood Smear	~90%	Early automated detection approach	Tek et al.	[7]
2013	SVM, RF	Blood Smear	94%	ML baseline models	Das et al.	[8]
2014	ML + Image Processing	Blood Smear	93%	Early ML pipeline	Oliveira et al.	[9]
2016	Custom CNN	Thin Smear	97.37%	CNN outperformed traditional ML	Liang et al.	[5]
2017	Deep CNN	NIH Dataset	98%	High classification accuracy	Dong et al.	[10]
2017	CNN + Feature Extraction	Blood Smear	96%	Reduced manual effort	Bibin et al.	[4]
2018	Transfer Learning (VGG16, ResNet)	NIH Dataset	91–95%	Pre-trained models effective	Rajaraman et al.	[2]
2018	DL Review	Multiple	—	DL widely applied in healthcare	Razzak et al.	[11]
2018	DL Survey	NIH Dataset	—	Overview of ML/DL methods	Poostchi et al.	[12]
2018	CNN	Blood Smear	95%	Improved detection accuracy	Sivaramakrishnan et al.	[13]
2018	Deep CNN	Microscopy Images	97%	High sensitivity	Gopakumar et al.	[14]
2019	CNN, SVM	NIH Dataset	97.77%	Augmentation improves results	Rahman et al.	[15]
2019	CNN	Microscopy Images	96%	Reliable classification	Militante et al.,	[16]

2019	CNN	NIH Dataset	98%	High performance model	Reddy et al.	[17]
2020	ACDN (Attention CNN)	NIH Dataset	97.47%	Better convergence & precision	Quan et al.	[18]
2020	CNN + Screening	Thick Smear	97%	Mobile-based detection	Yang et al.	[19]
2020	Capsule Network	NIH Dataset	98%	Captures spatial features	Khan et al.	[20]
2020	CNN + SVM	NIH Dataset	96%	Hybrid improves accuracy	Sharma et al.	[21]
2021	CNN	Blood Smear	97%	Good generalization	Singh et al.	[22]
2022	Hybrid DL	NIH Dataset	99%	Very high accuracy	Patel et al.	[23]

3.2 Data Cleaning

In the Malaria cell image dataset, data cleaning leads to higher-quality input data and, consequently, better performance of the CNN model. We verified the integrity of all images and removed corrupted or unreadable files to maintain the overall quality of the dataset. Duplicate data was also identified and eliminated to prevent bias, as repeated samples can cause the model to overfit to specific patterns.

3.3 Image Resizing

The dataset contains images with varied dimensions; therefore, all images were resized to a uniform size to ensure consistency in input for the model. Each image was resized to 120 × 120 × 3, which represents the standard structure of input data before it is fed into the CNN model. Since every image has the same height and width of 120 pixels, the inputs remain consistent across the dataset.Each image consists of three color channels—red, green, and blue (RGB). Maintaining a uniform image size helps the model learn patterns more effectively, while the color channels provide important visual variations in the cells that assist in classifying whether a cell is infected or not in Malaria detection.

3.4. Normalization

Normalization in convolutional neural networks (CNNs) is an essential part of preprocessing for image-based machine learning models. In the Malaria dataset, each image consists of pixel values ranging from 0 to 255, as they are RGB images. Directly using these values can lead to unstable training and slower convergence. Therefore, normalization is applied to rescale the values, typically to a range between 0 and 1. This ensures that all pixel values are on a consistent scale, helping the model learn more effectively and improving convergence during training.

$$.Normalized\ Pixel\ Value = \frac{Pixel\ value}{255} \qquad \text{Eq.1}$$

Pixel intensity values were scaled to the range [0, 1] by dividing them by 255, which helps achieve faster convergence during training and stabilizes the learning process. To reduce overfitting and improve model robustness, augmentation techniques were applied, including: rotation, horizontal - vertical flipping, Zooming and shifting. Fig. 1 represents the CNN for analysis of malaria cell. It starts with an input image 120 × 120 × 3 a micro-color blood cell image that is a coloured microorganism. This image is transformed to a set of convolutional layers, ReLU- activation functions, and varied filters are used to derive important features, such as edges, textures, parasite patterns. As they delve into the network the convolutional layers can learn more complex and higher-level representations of the cell structures. Pooling operations (implicit in the algorithm) are implemented to reduce the spatial dimensions of the feature maps while preserving the most important features which achieves better computational efficiency and decreases overfitting. The acquired feature maps are flattened into a 1D vector from the extracted model (top layer) that is used as input to the fully connected (dense) one. This layer provides high dimensional reasoning, integrating all features learned to produce an image decision. A dropout layer is added to randomly switch off some neurons during training to prevent overfitting and to improve the generalization capability of the model. Finally, the output layer implements a sigmoid activation function that generates a probability score to give an output that serves to classify the image to parasitized (infected) or uninfected (infected). Therefore, the CNN can learn hierarchical features in complex and accurate classification of malaria-infected cells. Linearity turns 2D feature maps into a 1D vector. The class distribution of the malaria dataset employed in this study is shown in Figure 2, which indicates the number of images in each category. From the data set 5,780 infected (parasitized) cells, 4,840 healthy (uninfected) cells can be seen. That means that the data contains some imbalance on the data set more infected samples than healthy ones. Consideration of such a distribution is critical during the model training process since this imbalance will affect model learning and can make biased predictions toward the majority. But the spread over the two classes is not too great, so it is easy to use the dataset as a baseline for the good training of machine learning and deep learning models.

4 Result and Discussion.

In Figure 3, the Malaria dataset contains samples of both parasitized (infected) and uninfected (healthy) red blood cells. Parasitized cells also have visible abnormalities, such as dark purple spot or irregular shape with red blood cells containing malaria parasite microbe. The uninfected cells, meanwhile, are of a fairly uniform shape and colour with no interesting internal artifacts or parasite formation. These observed visual characteristics underpin classification and enable the CNN model to understand and distinguish between healthy and infected cells. This comparison illustrates that the small differences in texture, intensity of colors, as well as differences in shapes are important for the model's effective malaria detection. Figure 4 depicts the performance of the CNN model in training and validating accuracy over multiple epochs. The training accuracy initially starts at a lower value (about 72%), indicating that the model is still only in the early learning stage and has not had a chance to pick up upon any underlying patterns in the data in its training input. But after the first epoch, a sharp increase in accuracy gradually develops, which is to say that the model quickly learns important features from input images. The training validation accuracies both increase and converge over time to about 95–96% at the last epochs of training. The accuracy obtained during validation follows the accuracy achieved during training period, which means a model generalizes well to some of unseen data and has not significantly overfitted. The small difference between the two curves indicates effective learning and good model performance. The graph shows that the CNN model is highly accurate and provides consistent and reliable training and validation results for a Malaria cell classification task.The confusion Matrix of the CNN model is shown in this figure 5 to evaluate the accuracy of CNN on malaria cell images. The map provides a comparison between the actual labels and predicted labels of two groups: infected and uninfected cells. When examining the matrix, 1094 parasitized cells are classified correctly as parasitized (true positives) and 64 parasitized are misclassified as uninfected (false negatives). Similarly, 932 uninfected cells are accurate in identifying them as uninfected (true negatives) whereas 34 of the uninfected cells are incorrectly classified as parasitized (false positives). These results demonstrate the model performs very well in differentiating between infected and normal cells, with relatively high accuracy and few misclassifications. The smaller false positive(s)and false negative(s) number indicate that the model holds on to a good equilibrium of sensitivity and specificity. The confusion matrix indicates that the CNN model is very good and reliable for detecting malaria from both classes of classifiers.

4.1 Proposed CNN Model Flowchart

This flowchart summarizes an algorithm: Input Image → Preprocessing → Feature Extraction → Classification — Output. The CNN model is trained to extract and learn features progressively in blood smear images and is illustrated in Fig 3. Resizing (120 × 120 × 3), normalization, and data cleaning enhance model consistency and training stability. This eliminates noise and boosts feature intelligibility. Initially, the convolutional layers learn basic visual patterns (edges, textures.) The deeper the network goes, the more and more complex features it learns which helps in distinguishing between infected and uninfected cells. Hierarchical features using multiple convolutional layers is well-suited to the CNN model and the pooling reduces the complexity significantly. The dense layer gives a good learning capability and dropout helps stop overfitting, which makes the model applicable for accurate malaria classification. Pooling layer reduces cost of computation so that training takes less time and memory is less. Automated learning reduces, human mistakes, subjective interpretation and improves reliability in medical image analysis. The image is treated as a 3D Tensor, height(H), Width(W) And channel(C). An image is a structured numerical data cube:

Spatial info → H, W, Color/depth info → C

Image→Conv→ReLU→Pool→FC→Softmax

$input = HxWxC$, for VGG16 224 x 224 x 3

$y(i,j,k) = \sum_m \sum_n \sum_c x(i+m, j+n, c).w(m,n,c,k) + b_k$

Convolution operation is input image-filter/kernel and b is bias, VGG16 uses 3x3 filter stride = 1, padding = 1

ReLU removes negative values, adds non linearity $f(x) = \max(0, x)$

$y(i,j) = max_{(m,n)\in R}\, x(i+m, j+n)$ VGG16 uses downsampling (2x2, stride 2) and size reduces 224 → 112 → 56 → 28 → 14 → 7

Dense Layer converts feature maps into classification scores $y = Wx + b$ **I**mageNet is a large-scale image dataset used to train and evaluate deep learning models, especially CNNs like VGG16.

SoftMax converts raw scores into probabilities (0 to 1) so that the network can decide the most likely class.

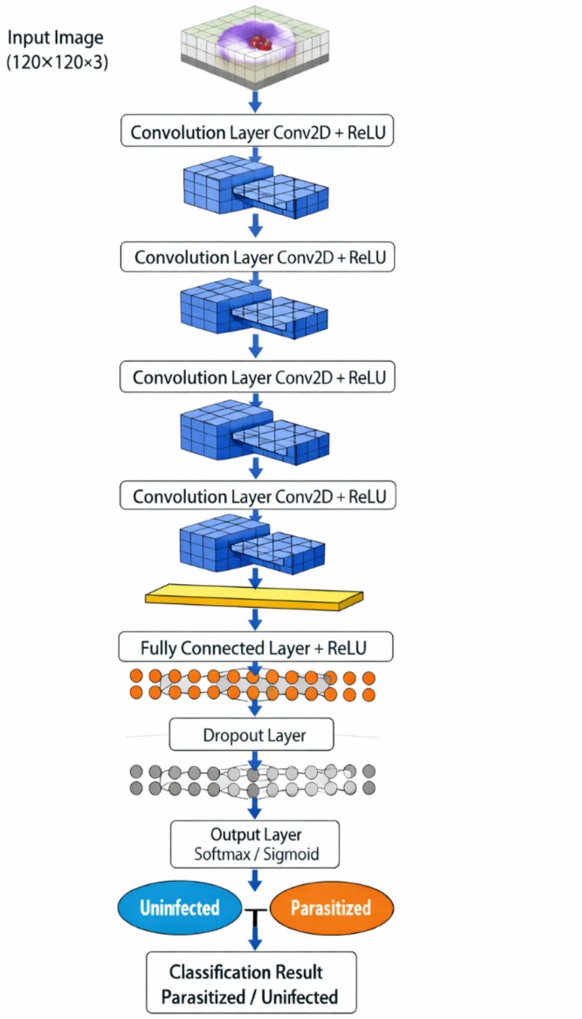


Fig.1 Architecture of a Convolutional Neural Network

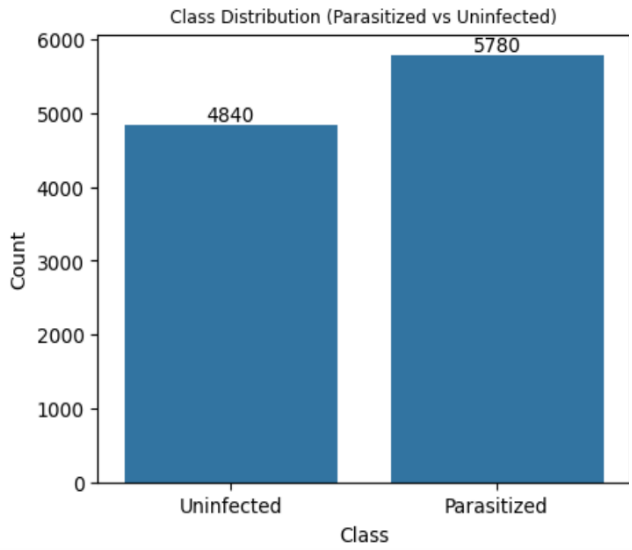


Fig.2 Architecture of a Convolutional Neural Network

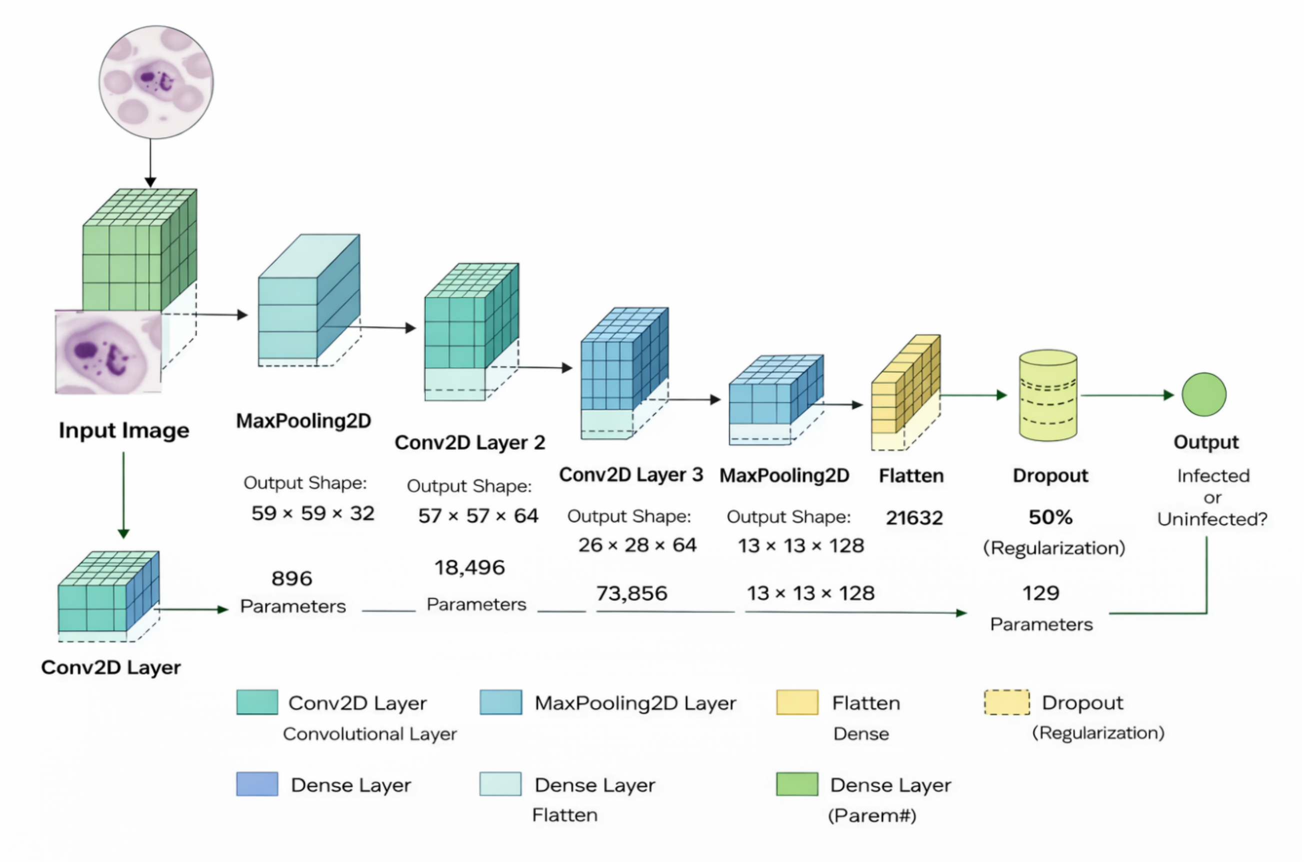
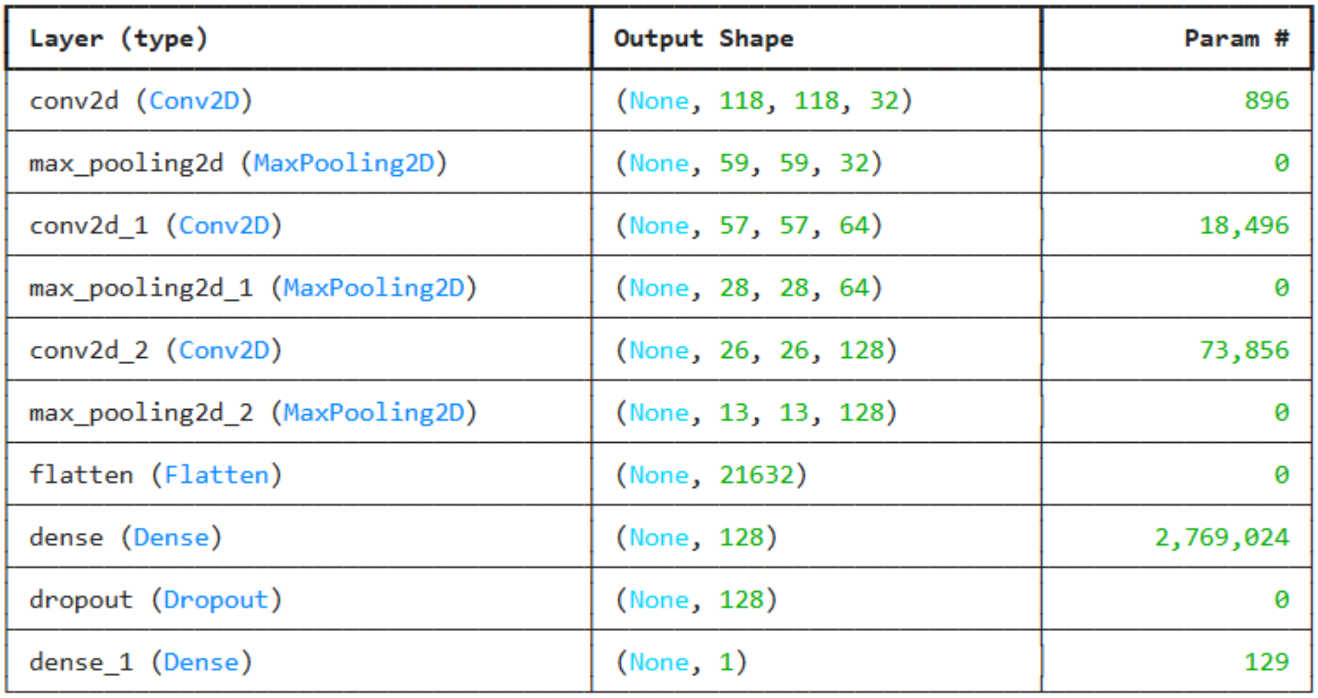


Fig3. Flowchart of Proposed CNN Model for Malaria Detection

Table.2 Layer-wise Description of the CNN Model



Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 118, 118, 32)	896
max_pooling2d (MaxPooling2D)	(None, 59, 59, 32)	0
conv2d_1 (Conv2D)	(None, 57, 57, 64)	18,496
max_pooling2d_1 (MaxPooling2D)	(None, 28, 28, 64)	0
conv2d_2 (Conv2D)	(None, 26, 26, 128)	73,856
max_pooling2d_2 (MaxPooling2D)	(None, 13, 13, 128)	0
flatten (Flatten)	(None, 21632)	0
dense (Dense)	(None, 128)	2,769,024
dropout (Dropout)	(None, 128)	0
dense_1 (Dense)	(None, 1)	129

Fig.4 Dataset cell Images: Parasitized and Uninfected

4.2 Comparison of CNN and VGG16 Model

The VGG model, developed by Oxford University's Visual Geometry Group (VGG), is a well-known convolutional neural network designed for large-scale image recognition tasks. It is introduced in ILSVRC 2014 (ImageNet Large Scale Visual Recognition Challenge), Known for its simplicity and depth, achieved top performance in image classification tasks. It consists of 16 convolutional layers, along with three fully connected layers and five max-pooling layers, making it a deep and powerful model for image classification. Fig.6 shows CNN Model Performance. The graph compares the performance of a custom CNN model and the VGG16 model for malaria detection across multiple training epochs. It shows that VGG16 starts with a higher accuracy (around 0.938) compared to CNN (around 0.918), indicating the advantage of transfer learning with pretrained features. While the CNN model improves rapidly and reaches about 0.954 accuracy within a few epochs, VGG16 increases more gradually but achieves a slightly higher peak accuracy of around 0.957–0.958. Moreover, VGG16 exhibits greater stability in performance over time, but has a slight decrease after subsequent epochs that may indicate overfitting. VGG16 provides generally better accuracy and reliability for malaria classification, while on the other hand CNN provides faster, less complex learning in general and lower computational complexity for resource-constrained scenarios. With steady improvement, the CNN model achieves accuracy of nearly 95.4% at epoch 4, which is showing that it works well. The confusion matrix indicates that the model has a very good separating performance parasitized infection-mediated infections from uninfected strains of the cells. Of all actual parasitized cases, 1094 were correctly identified and 64 cases incorrectly described as uninfected, i.e., a slight number of missed infections. Similarly, 932 of the uninfected samples were well predicted with a mere 34 incorrectly classified as parasitized. But there are some false negatives too — that's telling that some parasitized cases remain being missed; it may matter to medical applications, in which not detecting an infection is worse than a false alarm. Because with ImageNet training, we trained the model to learn generic visual patterns like edges, textures, and shapes. These learned representations can be molded into recognizing the vital characters in medical images, such as major aspects found in medical images and distinguish infected from uninfected cells. .

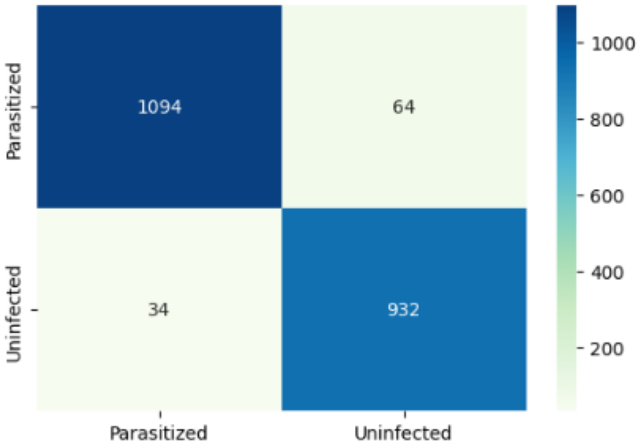


Fig.5 confusion matrix

Figure 7 shows easily identifiable cells, suggesting that the model accurately differentiates between parasitized and uninfected cells when visual features are clear and well-defined.. In general, correctly classified parasitized cells generally show more accurate visual characteristics like clear purple spots or ring-shaped structures, whereas uninfected cells show more uniform color. The findings indicated significant dependence of that model on these visual cues for decision-making.

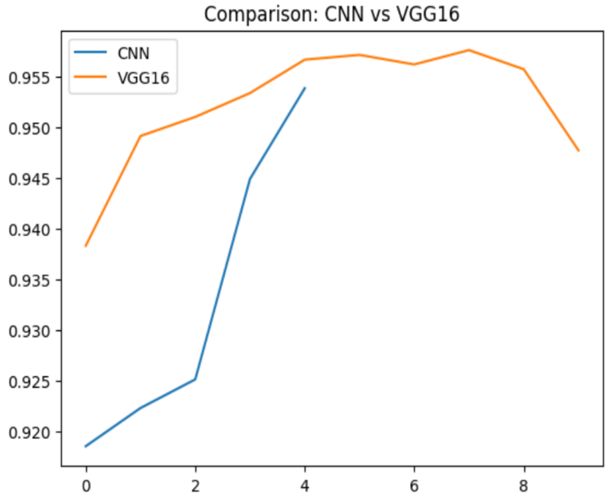


Fig.6 Performance Comparison of CNN and VGG16

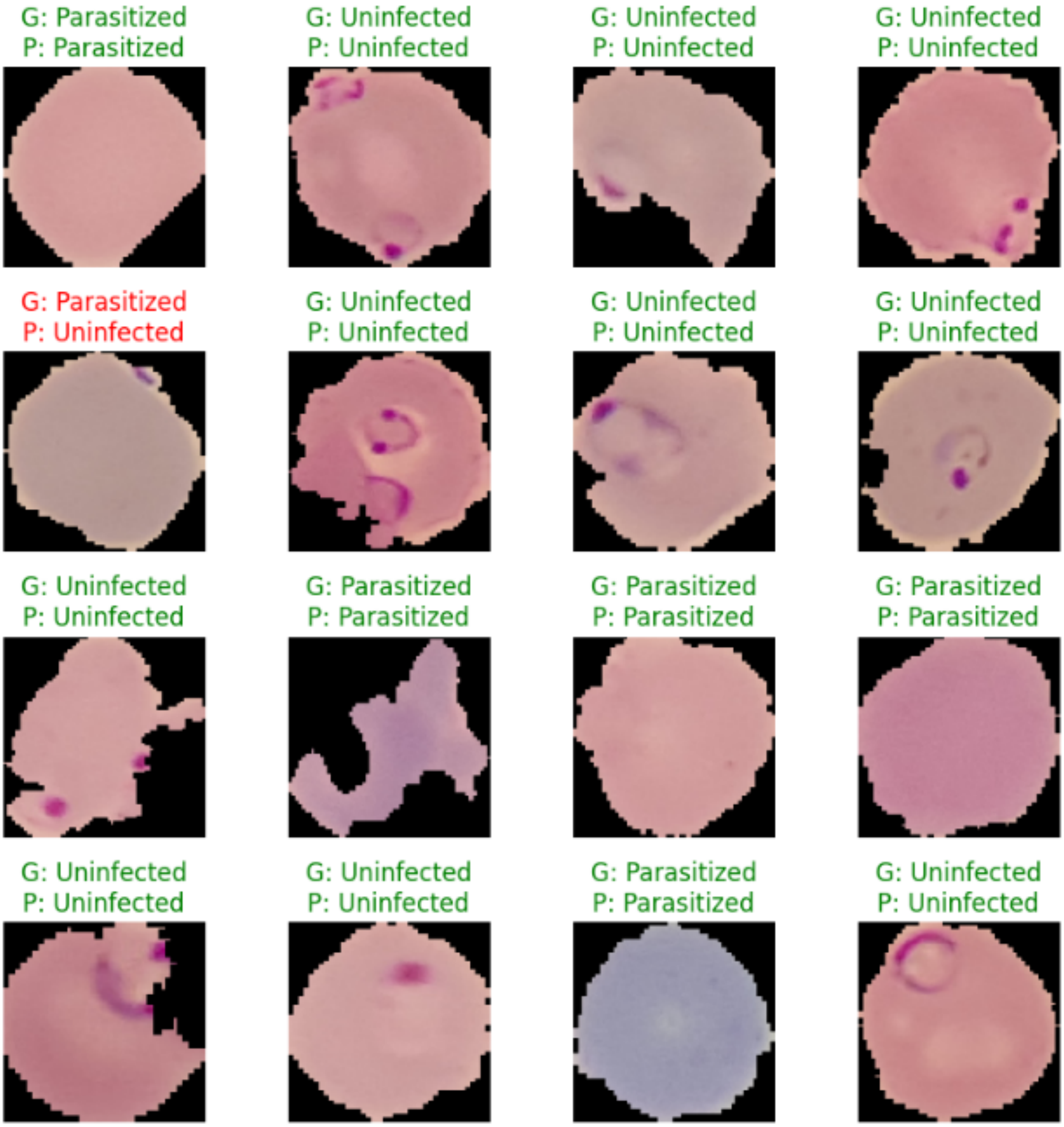


Fig.7 Image Classification Performance Analysis

5.CONCLUSION

This study emphasizes accuracy and evaluation analysis on multiple metrics, such as precision, recall, and F1-score, to obtain reliable performance in real-world scenarios. Data augmentation and correct preprocessing techniques are used to improve the robustness of the model. This study highlights improvements of early malaria detection based on the analysis of thick red blood cell images based on a recently developed CNN architecture that yields good results.

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