

Image Processing for Malaria Detection and Leukocytes Classification in Microscopic Blood Smears

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Abstract:- Malaria is a fatal life-threatening mosquito-borne disease caused by contamination of blood by *Plasmodium* parasites. The conventional and most common way of malaria detection and WBC classification is by visually analysing blood smears through a microscope for infected red blood cells and for specific WBC type manually by trained laboratory technicians, which is time-consuming and leads to potential human errors. The diagnosis and treatment of malaria is highly dependent on the identification of infected red blood cells (RBCs) in microscopic blood smears to monitor patient's health. Thus, an automated image recognition model has to be applied in order to make the detection and classification rapid, easy and accurate with a remarkable practical outcome. Our study explores and make use of various technologies like machine learning, neural networks for automating the leukocytes classification and malaria detection in microscopic blood smear images. A robust model capable of detecting cells and distinguish them as either healthy or unhealthy cells with high accuracy. A large dataset of microscopic blood smears is used to train the model to achieve high performance ratios. This implementation assures timely detection and classification that helps in decision making of patient's health.

Keywords:- Malaria detection, Leukocytes (WBC) classification, Blood Smear, Convolutional Neural Networks (CNN), Machine Learning.

I. INTRODUCTION

Malaria is a critical global health issue caused by *Plasmodium* parasites which is transmitted by the bites of female *Anopheles* mosquitos. The *Plasmodium* parasite has a multistage lifecycle causing a range of symptoms that requires timely treatment to humans affected by malaria. According to the World Malaria Report 2023 published by WHO [1], there were an estimated 249 million malaria cases and 608,000 malaria deaths in 85 countries over the preceding year. Early and accurate diagnosis is mandatory for effective treatment and control of the disease, traditionally achieved through the manual examination of microscopic blood smears that are labour-intensive requiring skilled lab technicians and tends to human error and inconsistencies. WBCs are important components of human immune system. The count of WBCs in the bloodstream can provide a picture of human health. For example, the presence of infections, leukaemia and certain specific types of cancers can be diagnosed based on the classification results and the white blood cell count [2].

Similarly, the classification of white blood cells is vital for diagnosing various haematological disorders and monitoring patient's immune system. Manual WBC classification is also laborious and susceptible to variabilities.

A. Research Background

When an individual is bitten by an infected *Anopheles* mosquito, it initiates a malaria infection by injecting *Plasmodium* parasites in the form of sporozoites. Malaria is the result of infection by a unicellular microorganism belonging to the *Plasmodium* genus, and it can affect humans through five of its species. Amongst these species, *P. falciparum* is more fatal; *P. vivax*, *P. oval*, *P. knowlesi* and *P. malariae* are among the other species [3]. The sporozoites form of *Plasmodium* parasite travel through the liver of an individual and they proliferate asexually in the liver cells for about 7 to 10 days [4]. Once the parasites transform into merozoites, they travel through the bloodstream and settle in the lung capillaries. Subsequently, the merozoites pass through the red blood cells and replicate before causing the cells to rupture. This will become a process of malaria infection from carrier mosquito to another healthy person. The person affected by malaria will suffer and start triggering white blood cells to provide immune against the malaria cells. It causes the symptoms of malaria like high fever, nausea, headache, abdominal pain to happen. White blood cells (WBCs) act as the defense system against disease and produces a variety of antibodies that is used by the body to fight infections, kill harmful disease-causing microorganisms [5]. Different types of WBCs play a various role in the process of fighting against the foreign substances like viruses. Monocytes are immune cells that removes dead or damaged tissue and can destroy cancer cells [6]. Lymphocytes fight against bacteria, viruses. Basophils play a variety of biological responses in the body. Neutrophils repairs damaged tissues and involves in the resolution of infections [7]. Eosinophils fight against infections [8]. Abnormal WBC counts are used to indicate the blood illnesses [9]. WBC discrimination is required to analyze the infections. Thus, the examination of the microscopic blood smear images gives a significant knowledge about the patient's health. This

examination through manual microscopy, hematology analyzers lead to wrong and time-consuming results. Advances in deep learning, specifically convolutional neural networks (CNNs), are beneficial for automating intricate image recognition assignments. By training a CNN on a large dataset of labelled images, this study aims to develop a model that is capable of accurate and consistent classification between parasitized and non-parasitized cells, as well as among various WBC types. This automated approach is meant to support healthcare professionals, reduce diagnostic workload and improve accuracy especially in resource-limited settings.

B. Research Rationale

From the sayings of Simeon Preston *“The biggest part of our digital transformation is changing the way we think”*. According to Malaria Journal 21 (Article 11, 2022), nearly 60% of the total malaria patients were misdiagnosed on their first visit, and concerning complications affected 18.8% of the patients [10]. The blood film test diagnosis depends on the skill of the individual conducting the test and the level of parasites present. The monotonicity of the test greatly influences the quality of the test [11]. Manual microscopic techniques for malaria detection and WBC classification might lead to incorrect diagnosis if they are influenced by outside parameters or variations in the patient’s physical characteristics [12]. Our implementation includes data preprocessing, model training and validation, making use of techniques like data augmentation and transfer learning to enhance performance of the model. The results demonstrate the potential of deep learning to transform malaria diagnosis and WBC classification, paving the way for integration into clinical practice.

C. Aims and Objectives

Aims:

To provide an automated ML model that is capable of timely detection of malaria and WBC classification to decide about identifying blood ailments. This blood cell recognition depends on the process of segmentation which lead to support the detection of diseases. An enhanced machine learning algorithm is utilized for the classification process to get the ultimate results.

Objectives:

- To create a deep learning model that can automatically detect malaria and classify white blood cells in microscopic blood smears.
- To compile and label a diverse dataset of blood smear images for training and validation.
- To measure the model’s accuracy, sensitivity, and specificity against conventional diagnostic methods.
- To improve diagnostic accuracy and efficiency. Thus, enhancing patient care.
- To design a convolutional neural network (CNN) to accurately identify healthy and infected RBCs and classify different WBC types.
- To explore the deployment of the model in clinical settings to support healthcare professionals, particularly in resource-limited areas.

- To improve patient outcomes and reduce mortality rates by rapid and accurate malaria detection.
- To expand access to quality healthcare.
- To assist medical practitioners in identifying abnormalities of blood and streamlining the diagnostic process.
- To contribute ongoing research and development in the field of medical image analysis with the help of insights generated from these systems.
- To enable a non-medical practitioner to detect malaria and classify WBCs in blood smear images.
- To segment cells accurately using the modern segmentation technology.
- To distinguish between parasitized and non-parasitized malaria cells by an efficient classifying algorithm.
- To reduce delays by decreasing time required for classification and diagnosis.
- To utilize the classification model for clinical purposes.

The remainder of the paper is as follows. Section II proposes literature reviews. Section III presents a detailed description of malaria detection and WBC classification. Section IV shows the results obtained from the model. Finally, concluded the paper in section V with the future direction.

II. LITERATURE SURVEY

Imen Jdey [13] says that diagnosis of a condition like malaria can be done using machine learning and image processing techniques, demonstrating the valuable potential of deep learning for physicians in the field of disease diagnosis. This system is trained using a small set of annotated images which results in less performance when new data from different sources are applied. Thinam Tamang [14] says that with the advancement of deep learning, WBC can be classified in less time with high accuracy. This paper explores various deep learning models such as DenseNet, ResNet, AlexNet, SqueezeNet and VGGNet and their variation based on CNN architecture and concludes that DenseNet-161 demonstrate an exceptional performance with an accuracy of 1.0. Optimization techniques such as normalization, mixed-up augmentation, and label smoothing are also used. This paper less describes the deployment on the client side and how the model is further implemented. Golla Madhu [15] says that an advanced neural network architecture that combines inception-based models with capsule networks, designed for rapid and accurate analysis is made. The diagnostic system combines two types of neural networks: Inception and Imperative Capsule networks. It uses pre-trained Inception model like Inception V3 for obtaining good accuracy. The system couldn't able to recognize parasite species and stages from the images of thin blood smears. Ensaf H. Mohamed [16] says that the proposed hybrid model combines MobileNet-224 for feature extraction and Logistic Regression for classification. The model achieves a rank-1 accuracy of 97.03% by reducing the cost of automating WBC classification. The use of BCCD dataset limits the generalizability of the model to other datasets with different characteristics. The model’s ability to capture domain-

specific features unique to WBC's is affected due to the reliance on pre-trained models for feature extraction. Muhammad Mujahid [17] says that Efficient Net, a deep learning-based approach for detecting Malaria, is proposed that uses red blood cell images. Furthermore, the proposed approach is validated using k-fold cross-validation to support the results. The experimental findings demonstrate that the approach can accurately detect Malaria from red blood cell images with a 97.57% accuracy rate, making it highly beneficial for medical healthcare professionals in practical applications. The training time is maximum. The model uses the images obtained from cell phones which is often worse than that of digital cameras, thus affecting the accuracy of malaria detection. Wenna Wu [12] says that two aspects, one is quality of extracted features and the other is Radiomic features having greater resolution are integrated. It follows RCTNet based CNN architecture. This paper explores Radiomics-based classification, Deep Learning-based classification, Radiomics and Deep Learning-based classification. This study only focuses on the classification of subset of WBCs and does not consider all classes of WBCs. Prof. Kirti Motwani [18] says that the model uses various segmentation methodologies like edge detection, watershed segmentation and morphological segmentation. The model detects and classify the cells from blood smear image using image processing technique and machine learning using SVM (Support Vector Machine). Process starts with the segmentation of cells, after those infections are segmented. This process is coordinated by the threshold intensity pixel value, by matching the values with the acquired image. By this way, infection is identified. The model is trained with only 110 thin films of blood smear images. Bairaboina Sai Sambasiva Rao [19] says that accuracy and consistency in WBC categorization is improved based on advanced models called MobilenetV3 and ShufflenetV2. The WBC images are segmented using Pyramid Scene Parsing Network (PSPNet), which efficiently isolates the WBCs from the rest of the image. MobilenetV3 is used for extracting features from the segmented images. Artificial Gravitational Cuckoo Search (AGCS) technique helps in selecting the most relevant global and local features. These features are used by the ShufflenetV2 model to classify the WBC images into five different types. The method does not address image noise suppression, which could potentially improve performance. The framework isn't used to test malaria parasite, anemia, leukemia and RBC count to assess its generalizability. Tamal Kumar Kundu [20] says that recent advancements in machine learning techniques for malaria detection and identification in blood smear images is explored, emphasizing challenges associated with image processing. Furthermore, a thorough analysis is conducted to compare different machine learning methods in order to offer a complete summary. Implementing these advanced machine learning and deep learning techniques has the potential to transform the malaria detection and control process. The generalization of these models to diverse populations and different geographic regions may be limited due to variations in the Plasmodium species and staining techniques used in different laboratories. The use of mobile devices and cloud-based solutions for malaria diagnosis raises concerns regarding patient privacy and data security. Ensuring compliance with ethical standards and regulations is crucial for widespread adoption. Rabia Asghar

[21] says that Machine Learning and Deep Learning models are reviewed for WBC classification, highlighting their contribution to medical image analysis. The methodology also provides a detailed analysis of Transfer Machine Learning (TML) technique for WBC classification and it include their application in medical diagnosis. It considers the challenges like dataset availability and suggests future directions using advanced DL networks. While ML and DL have been used for white blood cell classification, there's a gap in utilizing the latest advancements like transfer learning and meta-learning processes. There's a scarcity of publicly accessible, high-quality datasets for medical image analysis. Srishti Srivastava [22] says that the model identifies malarial infection using the smart phones. It uses a pre-trained CNN for detection of malarial parasite. The obtained RGB image is stained into grayscale, gaussian blur to reduce noise and edge. After staining, ring structure is formed with the visible cytoplasm for an infected cell whereas no such rings are formed in the uninfected person's blood cell. This uses a small camera-equipped computing device attached to a magnifying device for image magnification which require various staining techniques. Sami H. Ismael [23] says that the cell images are segmented in order to isolate each WBC. Then, each segmented image is scanned to prepare a dataset. Later, shape and texture features are extracted from the scanned images. Finally, various machine learning algorithms (like K* classifier, Additive Regression, Bagging, Input Mapped Classifier, and Decision Table) are applied separately to these features to classify the WBCs. The results from each algorithm are compared to determine which one performs best based on different criteria. The nature of cell images is complex, making segmentation and classification is challenging. The system's effectiveness in other types of medical image classification beyond white blood cells is not discussed. Usha Kumari [11] says that a computer-based approach for automatically detecting malaria parasite through Image Processing and Machine Learning (ML) techniques is developed. The outcome of malaria cell images, whether parasitic or non-parasitic, has been determined using various features and a machine learning model. The accuracy of the trained model is 97.93%. The computational requirements for training and deploying advanced machine learning models can be prohibitive, particularly in low-resource settings where malaria is most prevalent. Implementation in remote areas is hindered by infrastructure and technological limitations, such as internet connectivity and access to high-quality imaging devices. Changhun Jung [24] says that research on W-Net based CNN model is proposed. It describes the benefits of using pre-trained W-Net model in a transfer learning context. This experiment compares the original WBC images with synthetic WBC images and resulted in high degree similarity. This evaluates the classification with AlexNet, VGGNet, ResNet and RNN. This paper concludes that W-Net performs well than other CNN- and RNN- based model architectures. The dataset used for training the W-Net model which is taken from The Catholic University of Korea may have an imbalance in the distribution of the five WBC types, which can affect the model's performance. Collins M. Morang'a [25] says that the machine learning model is trained with hematological data of 2207 participants. Binary classifier is implemented to identify the parameter that can classify uncomplicated malaria, severe malaria using ANN –

Artificial Neural Network. As a result, the model gives mean blood platelet and cell volume using random forest technique. It is used only for the classification. Only focuses on clinical decision support. Sai Srinivas Vellela [26] says that the effectiveness of combining Recurrent Neural Networks (RNN) and Convolutional Neural Networks (CNN) to classify different types of white blood cells (WBCs) is evaluated. It is developed for automating blood test analyses and diagnosing blood-related diseases to benefit the pharmaceutical and healthcare industries. The performance of the CNN-RNN model is heavily reliant on the dataset used for training. A dataset with limited diversity or size may not provide a comprehensive understanding of blood cell subtypes. The hybrid CNN-RNN architecture is more complex than a single model approach, potentially leading to longer training times and the need for more computational resources.

III. PROPOSED SYSTEM

A. Overview

The conventional malaria detection and WBC classification methods helped medical practitioners to know about the presence of cell or the type of it with some possibilities of human error in a longer period of time, whereas malaria detection and WBC classification by image processing gives the high accurate result in a less time. Table 1 depicts the comparison between the classical and the modern techniques for malaria detection and leukocytes classification.

Aspect	Conventional System	Proposed System
Diagnosis Method	Manual microscopic examination	Automated image processing and ML
Efficiency	Time-consuming and labor-intensive	Fast and efficient
Accuracy	Variable; depends on technician skill	High; consistent performance across samples
Resource Requirement	Requires skilled technicians and microscopes	Requires high-resolution images and computational power
Accessibility	Limited to locations with skilled personnel	Broad; can be deployed in remote or resource-limited settings
Training & Expertise	Extensive training needed for technicians	Initial setup and occasional maintenance
Subjectivity	High; prone to human error	Low; objective and consistent
Scalability	Limited; increases resource demand	High; easily scalable with additional hardware

Table 3.1

B. Dependencies

Software Requirements:

- Python
- Anaconda Navigator

Frameworks used:

- numpy
- pandas
- matplotlib
- streamlit
- tensorflow

C. Workflow

A diverse dataset of blood smear images containing both infected and uninfected white blood cells (WBCs) is acquired. The images are pre-processed by resizing, normalizing, and augmenting to enhance model performance. A deep learning architecture like CNN is selected and transfer learning for feature extraction is employed. The dataset is split into training, validation, and test sets. The model is trained using the training set and is optimized for accuracy and F1 score. The model's performance is validated on the validation set, adjusting hyperparameters as necessary. The model is evaluated on the test set to assess generalization ability and quantify classification performance. The trained model is integrated into a deployable system with user-friendly interfaces for image input and result display. Backend infrastructure is implemented for efficient inference and scalability. Ethical considerations regarding patient privacy, data security, and regulatory compliance are ensured throughout the system's lifecycle.

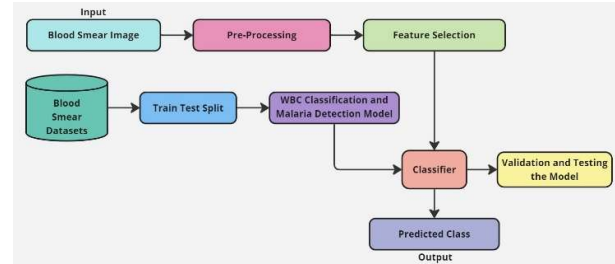


Fig 3.1 Block Diagram

Data Collection:

In the context of automating the finding of infected white blood cells using multi-level thresholding, the input stage involves acquiring digital images of blood samples containing white blood cells. These images serve as the primary source of data for the automated classifying system. The input images may be obtained through microscopy or other imaging techniques and are typically captured using specialized equipment to ensure high resolution and clarity. The quality and consistency of the input images play a crucial role in the accuracy and reliability of the classifying process, making proper image acquisition techniques essential for the success of the system.

Pre-processing:

Pre-processing of the input images is necessary to enhance their quality and prepare them for subsequent analysis. This stage involves a series of image processing techniques aimed at removing noise, correcting distortions, and enhancing contrast and sharpness. Common pre-processing steps may include filtering, histogram equalization, and morphological operations. By applying these pre-processing techniques, the input images are optimized for feature extraction, improving the accuracy and robustness of the classifying algorithm.

Feature Extraction:

Feature extraction is a critical step in the automatic classifying of infected white blood cells, where relevant information or characteristics of the cells are identified and extracted from the pre-processed images. In this context, features such as shape, texture, and intensity are extracted from the white blood cells to differentiate between infected and uninfected cells. Multi-level thresholding techniques are employed to segment the cells from the background and isolate regions of interest. These extracted features serve as input to the classifying algorithm, enabling the system to accurately quantify the number of infected white blood cells present in the sample.

Database:

The database serves as a repository for storing and organizing the extracted features and corresponding cell classifies from the input images. Each entry in the database typically includes information such as the image identifier, extracted features, and the corresponding cell classification. This database plays a crucial role in training and evaluating the performance of the classifying algorithm. Additionally, it provides a valuable resource for data analysis and quality control, allowing researchers to track and compare cell classifies across different samples and experiments.

CNN (Convolutional Neural Network):

CNNs belong to a category of deep learning models that are specifically created for tasks related to analysing images. In the context of automatic classifying of infected white blood cells, CNNs can be employed to further refine the feature extraction process and improve the accuracy of cell classification. By training a CNN on a large dataset of annotated images, the model can learn to automatically identify and classify white blood cells based on their visual characteristics. This enables the system to achieve higher accuracy and efficiency in classifying infected cells, also reducing the reliance on manual intervention and subjective interpretation.

IV. RESULT AND ANALYSIS

This section contains the complete experiments on the WBC images obtained from the Kaggle dataset. The Core i3 8th generation computer is used operating with Windows 10 64-bit, and 4GB of RAM. We used a batch size of 32-bit and 30 epochs.

The following Fig 4.1 shows the model training:

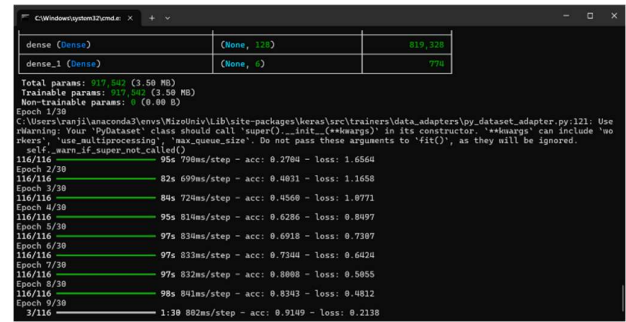


Fig 4.1 Model Training

The following Fig 4.2 shows the graph obtained at the end of model training:

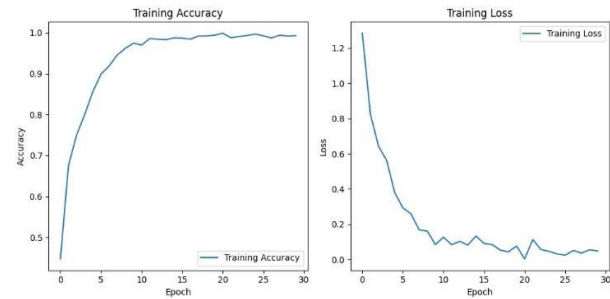


Fig 4.2 Training Graph

The following Fig 4.3 and Fig 4.4 shows the Confusion Matrices:

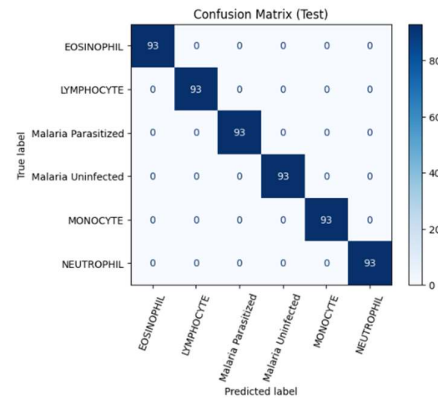


Fig 4.3 Test Confusion Matrix

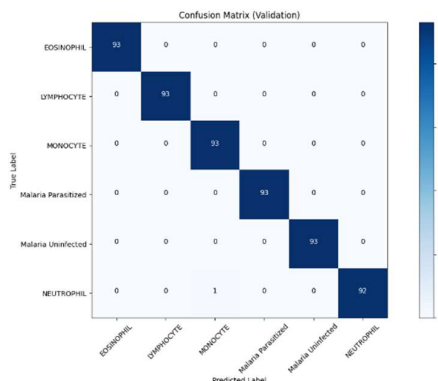


Fig 4.4 Validation Confusion Matrix

The following Fig 4.5 and Fig 4.6 shows the Output of the Model:

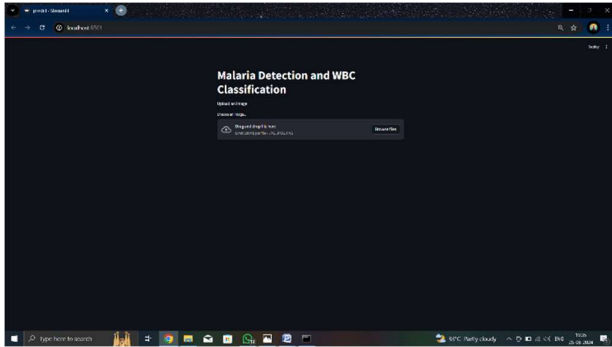


Fig 4.5 Output Webpage

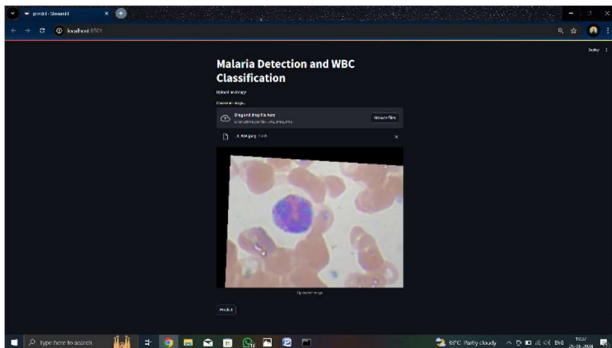


Fig 4.6 Uploading of Blood Smear Image

The following Fig 4.7 and Fig 4.8 shows the results obtained to malaria infected and uninfected blood smear image:

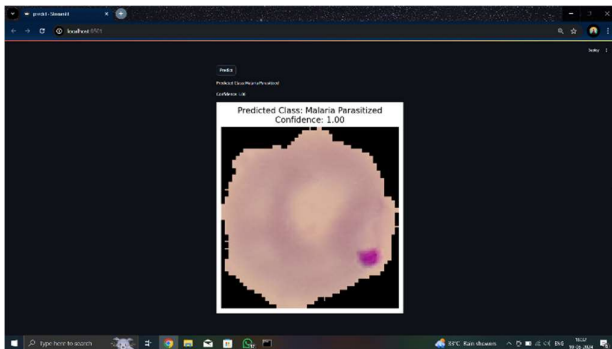


Fig 4.7 Malaria Infected

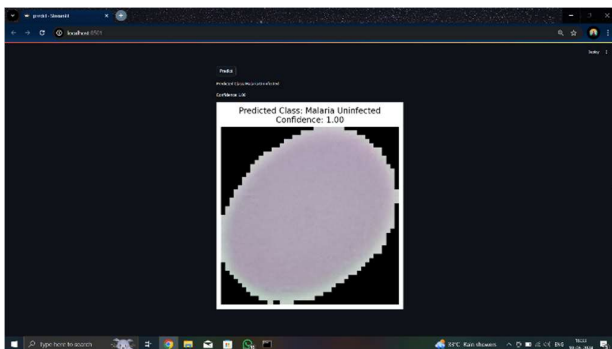


Fig 4.8 Malaria Uninfected

The following Fig 4.9, Fig 4.10, Fig 4.11 and Fig 4.12 shows the results obtained to each WBC types:

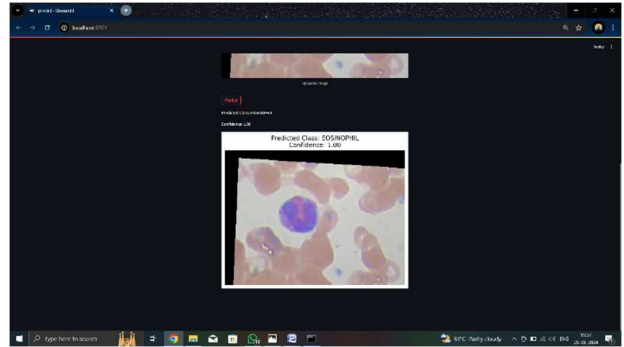


Fig 4.9 Eosinophil

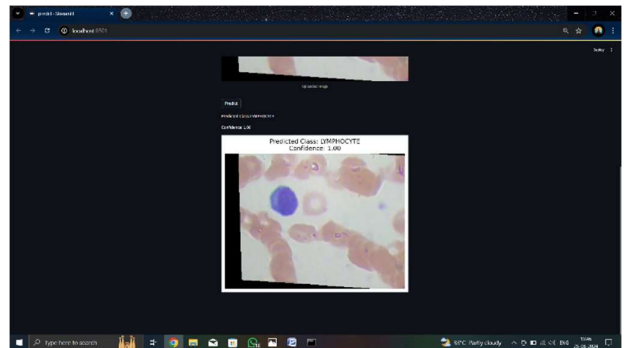


Fig 4.10 Lymphocyte

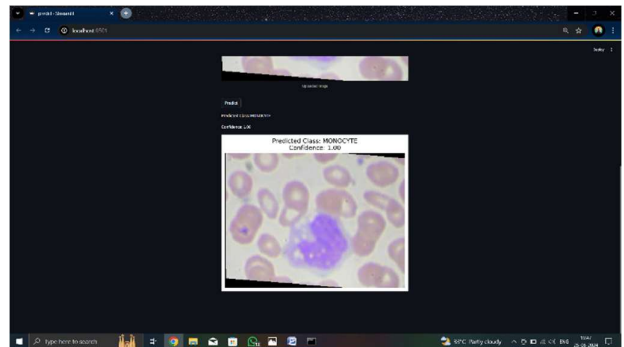


Fig 4.11 Monocyte

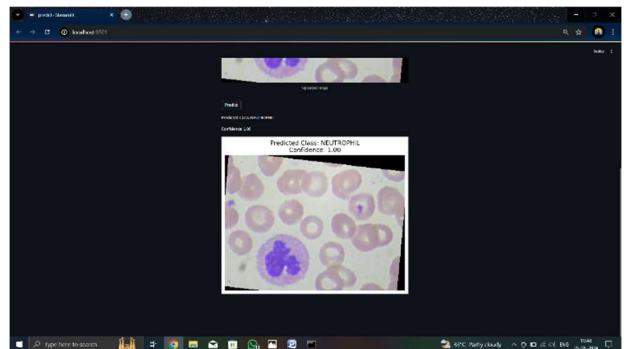


Fig 4.12 Neutrophil

The following table 4.1 shows the accuracy and averages:

Attributes	Precision	Recall	F1-Score	Support
Accuracy			1.00	558
Macro Average	1.00	1.00	1.00	558
Weighted Average	1.00	1.00	1.00	558

Table 4.1

The following table 4.2 depicts the classification report of malaria detection and WBC classification:

Classes	Precision	Recall	F1-Score	Support
Eosinophil	1.00	1.00	1.00	93
Lymphocyte	1.00	1.00	1.00	93
Monocyte	0.99	1.00	0.99	93
Neutrophil	1.00	0.99	0.99	93
Malaria Infected	1.00	1.00	1.00	93
Malaria Uninfected	1.00	1.00	1.00	93

Table 4.2

IV. CONCLUSION

In conclusion, the development of a deep learning system for WBC and malaria classification presents a promising approach for enhancing diagnostic capabilities in malaria-endemic regions. Through the utilization of convolutional neural networks (CNNs) and extensive data preprocessing, our model demonstrates robust performance in accurately distinguishing between infected and uninfected WBCs in blood smear images. The system's high accuracy and efficiency hold significant potential for aiding healthcare professionals in timely malaria diagnosis and treatment, thereby contributing to improved patient outcomes and public health efforts. The model's performance undergoes continuous refinement and validation to guarantee its reliability in actual clinical environments. It is crucial to prioritize ethical considerations like patient privacy and regulatory compliance when deploying and implementing AI-driven diagnostic tools in healthcare settings.

Future works:

Continual learning: Implementing strategies for continual learning would allow the model to adapt and improve over time as new data becomes available, ensuring its relevance in dynamic healthcare environments.

Transferability to other diseases: Expanding the scope of the model to classify WBC abnormalities associated with other diseases beyond malaria, such as leukaemia or dengue fever, would broaden its utility in clinical practice.

Deployment in resource-constrained settings: Optimizing the model for deployment on low-resource devices or in offline settings would facilitate its usage in remote or underserved areas where access to healthcare infrastructure is limited.

Integration with telemedicine platforms: Integrating the model into telemedicine platforms could enable remote diagnosis and consultation, facilitating timely interventions and improving patient access to healthcare services.

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