# A Review Of Dengue & Malaria Detection Systems From Pbs Using Machine Learning

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*Abstract:* Mosquito-borne diseases such as Dengue and Malaria remain major global public health challenges, causing millions of infections and substantial mortality each year, particularly in tropical and subtropical regions. Conventional diagnostic methods for both diseases rely heavily on manual microscopic examination of peripheral blood smears, a process that is labor-intensive, time-consuming, and vulnerable to observer variability. Recent advances in digital pathology and image-processing-based automation offer promising solutions for early, accurate, and cost-effective diagnosis.

In dengue detection, peripheral blood smear (PBS) analysis reveals hallmark changes such as thrombocytopenia and lymphocyte morphological alterations. Machine-learning approaches using morphological and Gray-Level Spatial Dependence Matrix (GLSDM) features extracted from lymphocyte nuclei have demonstrated high diagnostic accuracy, with Support Vector Machine-based models achieving up to 95.74% accuracy in distinguishing dengue-infected samples. Similarly, for malaria diagnosis, automated image analysis systems employing color thresholding, segmentation, blob analysis, watershed techniques, and shape-based classification have shown excellent performance in detecting Plasmodium-infected red blood cells. Systems using texture and intensity features, neural network classifiers, and morphological processing have achieved accuracies ranging from 93% to 99%, significantly reducing dependency on expert microscopists.

This combined study highlights the growing potential of AI-driven digital microscopy for the automated screening of vector-borne diseases. Integrating machine learning, deep learning, and advanced image-processing techniques enables rapid detection of infected cells, accurate parasite quantification, and improved clinical decision-making. Such automated frameworks can provide scalable, low-cost diagnostic support in resource-limited settings, thereby strengthening global disease surveillance and early intervention strategies for both dengue and malaria.

*Index Terms -* Mosquito-borne diseases, Dengue, Malaria, Image-processing, Automation, Machine Learning.

## I INTRODUCTION

Vector-borne diseases continue to pose a significant threat to global health, particularly in tropical and subtropical regions where climatic conditions favor the survival and proliferation of disease-transmitting mosquitoes. Among these diseases, Dengue and Malaria remain two of the most prevalent, life-threatening, and socio-economically burdensome infections. Despite decades of medical advancement, timely diagnosis remains a challenge due to resource constraints, dependence on expert microscopists, and limitations of conventional laboratory techniques. The emergence of digital pathology, medical image processing, and machine learning (ML) offers a transformative opportunity to automate and enhance diagnostic accuracy for both diseases. [1]

Dengue fever, caused by the Dengue virus (DENV) belonging to the Flaviviridae family, infects an estimated 100–400 million individuals annually, with the incidence rising eight-fold over the last two decades. The disease is transmitted to humans primarily through Aedes aegypti mosquitoes. Clinical manifestations range from mild febrile illness to severe and life-threatening conditions characterized by plasma leakage, hemorrhage, and organ impairment. Laboratory investigation plays a key role in early diagnosis, with peripheral blood smear (PBS) examination, complete blood count (CBC) analysis, and NS1 antigen testing being widely used. [11]

In dengue-infected patients, blood smear images often show thrombocytopenia, manifested as a drastic decline in platelet count, and morphological alterations in lymphocytes, such as enlarged and irregular nuclei, increased cytoplasmic volume, and intensified basophilic staining. These features, though clinically well-established, require expert interpretation and are time-consuming to evaluate manually. Recent studies demonstrate that applying machine learning and image-processing techniques—including blob detection for platelet estimation and GLSDM-based texture analysis for lymphocyte classification—achieves diagnostic accuracies above 90%, highlighting the potential of automated dengue detection systems. [2]

Malaria, on the other hand, is caused by protozoan parasites of the genus Plasmodium, transmitted through the bite of infected female Anopheles mosquitoes. It remains a leading cause of morbidity and mortality in low-income regions, with more than 216 million cases reported in 2016 alone. The disease disproportionately affects children, pregnant women, and populations in rural and resource-constrained areas. The gold-standard diagnostic method for malaria is microscopic examination of Giemsa-stained peripheral blood smears, which enables detection of Plasmodium species and estimation of parasitemia—the percentage of infected red blood cells (RBCs). [9] However, manual microscopy is dependent on the skill and experience of trained technicians and is inherently prone to human error. Challenges include differentiating parasites from stain artifacts, distinguishing between overlapping or touching RBCs, and ensuring consistent slide examination. Automated malaria detection systems using image segmentation, morphological analysis, thresholding techniques, watershed transformation, and supervised classification algorithms have shown promising results. Reported accuracies between 93% and 99% indicate that automated microscopy can significantly reduce diagnostic delays and increase reliability in endemic regions. [3]

The common barrier in traditional diagnostic workflows for both dengue and malaria is the dependence on manual visual interpretation of blood smear images. This approach is slow, labor-intensive, and subject to inter-observer variability. Furthermore, rural or under-resourced health centers often face shortages of trained laboratory personnel. Image-processing techniques address these issues by enabling automated feature extraction from digital blood smear images. For dengue, features such as platelet count, lymphocyte nuclear area, perimeter, circularity, eccentricity, and GLSDM-derived texture properties allow classifiers to distinguish between normal and infected samples. [10]

For malaria, intensity-based segmentation, color thresholding, morphological operations, and shape descriptors help identify infected RBCs and quantify parasitemia with high precision. These automated methods not only reduce the workload of pathologists but also standardize diagnostic procedures and improve reproducibility. [4] Another key advancement is the integration of machine learning (ML) and deep learning (DL) models into diagnostic frameworks. Classical ML algorithms—such as Support Vector Machines (SVM), Decision Trees (DT), Naïve Bayes, and K-Nearest Neighbors (KNN)—have been successfully applied in both dengue and malaria image analysis. [14]

In dengue detection, SVM models using morphological and GLSDM features of lymphocyte nuclei have achieved accuracies up to 95.74%. In malaria detection, neural networks, local binary patterns (LBP), co-occurrence matrices, and template-based approaches have achieved high sensitivity and specificity in parasite identification. Deep learning models, including MobileNetV2, AlexNet, ResNet, and custom CNN architectures, further enhance performance by learning complex patterns without manual feature engineering. These models demonstrate robustness against variations in staining, illumination, microscope quality, and morphological diversity. [5]

Digital pathology, combined with AI-driven microscopy, has thus emerged as a transformative diagnostic tool. It enables rapid scanning of entire slides, automated identification of regions of interest, and consistent extraction of clinically relevant features. Importantly, these technologies have the potential to be implemented in low-cost computing environments such as Raspberry Pi-based digital microscopes and

cloud-connected mobile diagnostic systems. Such innovations are especially valuable in underserved communities, where early detection and timely intervention are critical to preventing disease progression and reducing mortality. [6]

Despite promising advancements, challenges remain. Variations in slide preparation, staining inconsistencies, imaging artifacts, noise, and overlapping cells can affect algorithm performance. The need for large, annotated datasets is another limiting factor, particularly for training deep neural networks. Nevertheless, the growing availability of open-source medical image databases, combined with increasing computational power and optimized algorithms, continues to accelerate progress in automated disease detection. [7]

In this context, the present research aims to integrate advanced image-processing techniques with machine learning frameworks to develop a robust, automated diagnostic system for both malaria and dengue using digital microscope images. By leveraging platelet and lymphocyte characteristics for dengue detection, and RBC morphology and parasite identification for malaria detection, the system seeks to provide a comprehensive diagnostic solution that is accurate, fast, and scalable. Such a system holds significant potential for deployment in primary healthcare centers, community clinics, and field-level screening programs, thereby contributing to early intervention and improved disease management. [8]
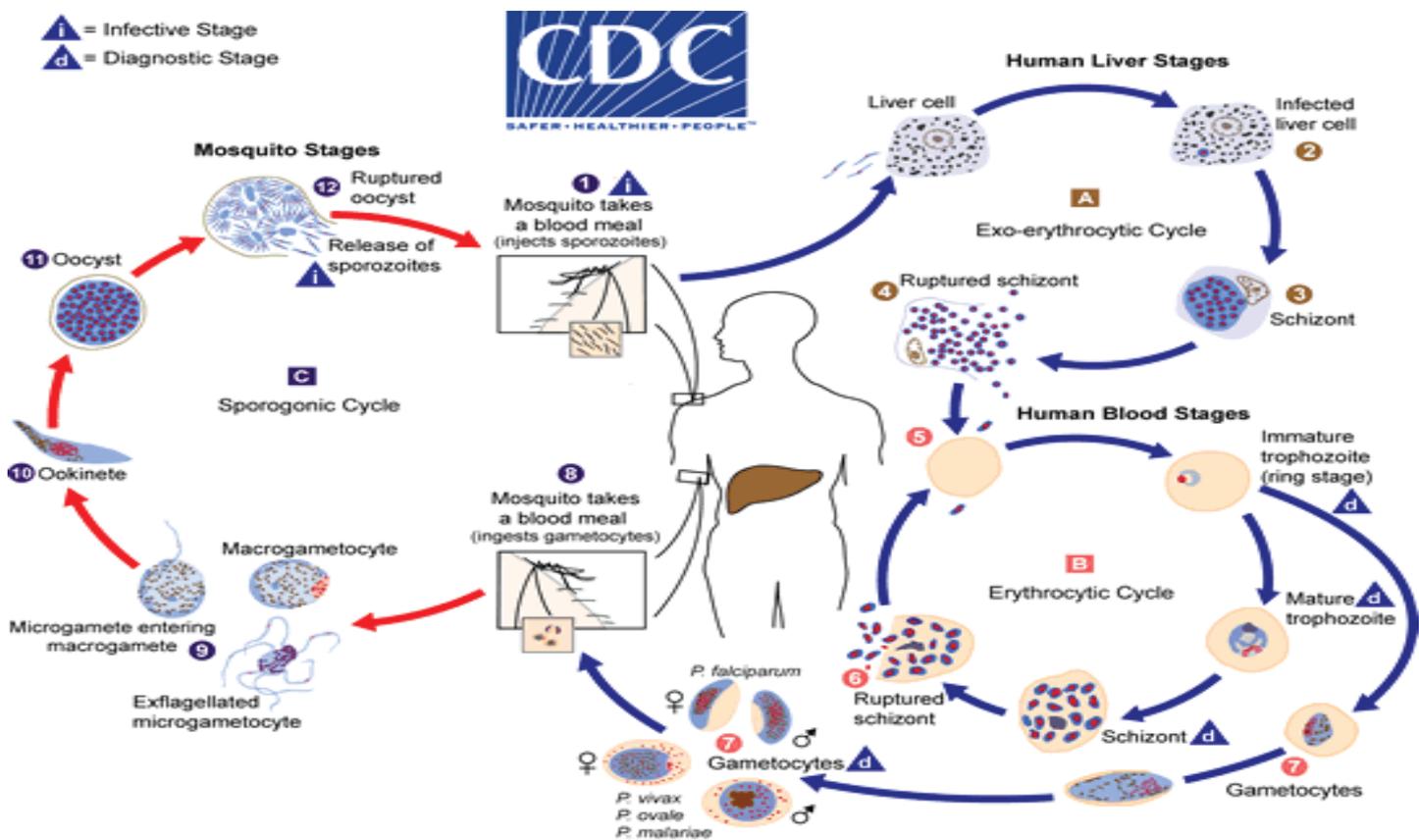


**STAGES OF MALARIA PARASITIC INFECTION IN RBCS**

## II LITERATURE REVIEW

Vector-borne diseases such as Dengue and Malaria have received significant global attention due to their high morbidity and mortality rates. Conventional microscopic screening of peripheral blood smears remains the clinical gold standard for both diseases; however, it is time-consuming, labor-intensive, and prone to human errors. In the last two decades, advancements in digital pathology, image processing, and machine learning have revolutionized automated diagnostic systems. This section reviews the existing research on image-based detection of Dengue and Malaria, with emphasis on feature extraction techniques, segmentation approaches, classification frameworks, and performance outcomes.

## 1. LITERATURE REVIEW ON DENGUE DETECTION

Dengue virus infection induces identifiable hematological abnormalities such as thrombocytopenia and lymphocyte morphological changes, motivating researchers to explore automated microscopic analysis for dengue diagnosis.

### 1.1 Platelet Detection and Thrombocytopenia Analysis

| Sr No | Author | Title | Research Area | Identified Research Gaps |
|---|---|---|---|---|
| 1 | *Cruz et al. (2018)* | A Raspberry-Pi based detection system for platelet counting using HSV color space and connected-component analysis | Their method demonstrated the feasibility of deploying cost-effective embedded systems for blood smear interpretation. | Lack of unified diagnostic frameworks for detecting multiple blood-borne diseases using common image-processing pipelines. |
| 2 | Evangeline et al. (2019) | Contrast stretching and Otsu thresholding for platelet segmentation followed by edge detection | Their approach highlighted the importance of preprocessing to enhance platelet visibility against red blood cells. | Insufficient large-scale annotated datasets, especially for dengue lymphocyte images. |
| 3 | Meimban et al. (2020) | Python OpenCV's blob detection technique to detect platelets from 100× microscopic images | The use of blob features, area, inertia, and convexity filters, demonstrated high robustness in detecting small circular structures like platelets. | Variability in staining, slide preparation, and illumination affecting segmentation consistency. |
| 4 | Mahanta et al. (2021) | L*a*b color space segmentation combined with morphological filtering to isolate platelets | These studies collectively establish blob detection and color segmentation as reliable techniques for automated thrombocytopenia screening. | Limited research on combining handcrafted and deep features in an ensemble framework for dual-disease diagnosis. |

### 1.2 Lymphocyte Morphology-Based Dengue Detection

| Sr No | Author | Title | Research Area | Identified Research Gaps |
|---|---|---|---|---|
| 1 | Manik et al. (2017) | Segmentation of white blood cell nuclei and extraction of geometric features | A framework that segments white blood cell (WBC) nuclei and extracts geometric features for classification using neural networks | Lack of unified diagnostic frameworks for detecting multiple blood-borne diseases using common image-processing pipelines. |
| 2 | Mayrose et al. (2023) | Segmentation of lymphocyte nuclei using Otsu thresholding after contrast enhancement. | This study establishes lymphocyte-based ML classification as a strong approach for dengue diagnosis | Insufficient large-scale annotated datasets, especially for dengue lymphocyte images. |

### 1.3 Deep Learning Approaches

Deep learning-based digital pathology has gained momentum. Transfer learning models such as MobileNetV2, ResNet, and CNN architectures have been explored for nucleus-based dengue detection. Deep features from pre-trained CNN models improve classification accuracy by capturing higher-order texture patterns that handcrafted features cannot represent. ReliefF and other feature-selection techniques further enhance classifier performance by selecting the most discriminative features.

Overall, literature shows strong support for combining cell morphology, textural descriptors, and deep learning for robust dengue diagnostics from blood smears.

## 2. LITERATURE REVIEW ON MALARIA DETECTION THROUGH IMAGE PROCESSING

Malaria researchers have widely explored image-based automated detection of Plasmodium parasites in Giemsa-stained thin blood smears.

| Sr No | Auther | Title | Research Area | Identified Research Gaps |
|---|---|---|---|---|
| 1 | Tek et al. (2006, 2009) | Identifying Plasmodium parasites by using color and texture features. | Their methods involved preprocessing, color normalization, morphological feature extraction, and statistical classification, demonstrating the potential of automation for malaria screening. | Limited research on combining handcrafted and deep features in an ensemble framework for dual-disease diagnosis. |
| 2 | Savkare and Narote (2009) | edge detection, morphological processing, and segmentation to estimate parasitemia levels. | Their approach emphasized the importance of eliminating central pallor artifacts in RBCs to avoid misclassification. | Computational challenges in deploying deep learning models on low-cost hardware for rural clinical settings. |
| 3 | Pallavi Suradkar (2013) | a multi-step system including thresholding, edge detection, binarization, RBC counting, and parasite extraction. | Their two-stage classifier combining color intensity selection with morphological analysis achieved promising results. | Lack of unified diagnostic frameworks for detecting multiple blood-borne diseases using common image-processing pipelines. |
| 4 | Ghanmode & Paikrao (2018) | a system for calculating parasitemia | They used grayscale conversion, segmentation using region-based thresholding, and morphological shape analysis. | Variability in staining, slide preparation, and illumination affecting segmentation consistency. |

## 2.1 RBC Segmentation and Feature Extraction Techniques

Detection accuracy greatly depends on precise identification of RBC boundaries and infected cells. Various segmentation methods have been proposed:

- **Thresholding (Global/Adaptive/Otsu)**
  Converts images to binary form based on pixel intensities.
- **Color channel selection (Red, Green, YIQ, HSV)**
  Used to isolate parasites which stain distinctly from RBC cytoplasm.
- **Watershed segmentation**
  Adopted for separating overlapping or touching RBCs; however, prone to over-segmentation unless minima suppression is applied.
- **Morphological operations**
  Applied to refine cell boundaries, fill central pallor regions, and remove noise.

## 2.2 Parasite Detection and Classification Approaches

Malaria parasite detection relies on distinguishing infected from non-infected RBCs using:
- **Color intensity variations** (parasites appear violet/blue)
- **Circularity and shape deformities inside RBCs**
- **Texture descriptors** for trophozoites, schizonts, and gametocytes

Approaches include:
- **Euclidean classifier vs. SVM:** SVM achieved 93.33% accuracy compared to 80% for Euclidean classification, highlighting the importance of ML-based approaches.
- **Neural networks:** Backpropagation-trained ANN achieved 99.68% accuracy on extracted features.

- **Variance-based detection and color co-occurrence matrices:** Effective for identifying parasite presence in low contrast images.

## 2.3 Deep Learning Contributions

CNN models have been widely applied to malaria datasets such as the NIH Malaria Database. These networks automate feature extraction and offer superior performance, with accuracies exceeding 95% on large datasets.

Techniques include:
- **Patch-based CNN classification**
- **Transfer learning using AlexNet/ResNet**
- **Encoder–decoder segmentation networks**

These works reflect a clear trend toward deep learning dominance in malaria diagnostics.

## 3. COMPARATIVE ANALYSIS OF DENGUE AND MALARIA IMAGE-PROCESSING LITERATURE

| Parameter | Dengue Studies | Malaria Studies |
|---|---|---|
| **Primary ROI** | Platelets, lymphocytes | RBCs, parasites |
| **Segmentation Techniques** | Otsu, K-means, contrast stretching | Watershed, Otsu, region-based, color threshold |
| **Feature Types** | Morphology + GLSDM + Deep Features | Intensity, texture, shape, morphology |
| **Best Classifier** | SVM (93.62–95.74%) | ANN/SVM (93–99%) |
| **Key Challenge** | Differentiating reactive lymphocytes | Identifying parasite structures within RBCs |
| **Common Issues** | Slide variation, nucleus overlap | Overlapping RBCs, stain artifacts |

The literature clearly demonstrates that image processing combined with machine learning provides highly accurate diagnostic support for both diseases. Dengue research focuses on lymphocyte texture and platelet counting, while malaria research centers on parasitized RBC recognition and parasitemia estimation. Both fields increasingly rely on deep learning for enhanced accuracy and automated feature learning.

## 4. SUMMARY OF LITERATURE GAPS

Despite the significant progress, key research gaps remain:

- Lack of unified diagnostic frameworks for detecting multiple blood-borne diseases using common image-processing pipelines.

- Insufficient large-scale annotated datasets, especially for dengue lymphocyte images.

- Variability in staining, slide preparation, and illumination affecting segmentation consistency.

- Computational challenges in deploying deep learning models on low-cost hardware for rural clinical settings.

- Limited research on combining handcrafted and deep features in an ensemble framework for dual-disease diagnosis.

These gaps motivate the development of an integrated, automated system capable of diagnosing both dengue and malaria using advanced image-processing and machine learning techniques.

## III PROPOSED METHODOLOGY

The proposed methodology aims to design an integrated image-processing and machine-learning-based diagnostic system capable of detecting Dengue (through platelet and lymphocyte analysis) and Malaria (through infected red blood cell classification) using microscopic peripheral blood smear (PBS) images. The workflow consists of the following major stages:

1. IMAGE ACQUISITION

2. PREPROCESSING

3. SEGMENTATION

4. FEATURE EXTRACTION

5. CLASSIFICATION

6. PERFORMANCE EVALUATION

Each component is described in detail below.

### 1. IMAGE ACQUISITION

Peripheral Blood Smear (PBS) images are collected using a 100× oil-immersion optical microscope equipped with a digital camera. Two types of slides are used:

- Giemsa-stained thin blood smear images (for malaria)
- Wright/Giemsa-stained PBS images (for dengue lymphocyte and platelet analysis)

The images are captured under uniform illumination and saved in RGB format with resolutions ranging from 1280×960 to 2048×1536 pixels. To ensure generalizability, images are collected from:

- Publicly available datasets
- Hospital laboratory microscope systems
- Research publications acknowledged dataset samples

All images are manually annotated by experienced laboratory technicians for ground truth.

### 2. PREPROCESSING

Preprocessing enhances image quality, removes noise, and improves segmentation accuracy. It includes the following steps:

### 2.1 Noise Reduction

Gaussian blur and median filters are applied to remove salt-and-pepper noise, staining artifacts, and illumination irregularities.

### 2.2 Color Space Transformation

The RGB images are converted to alternative color spaces for better isolation of diagnostic features:

- HSV for platelet color enhancement
- LAB for nucleus–cytoplasm contrast
- YCbCr for parasite differentiation in malaria images

## 2.3 Histogram Equalization

Contrast Limited Adaptive Histogram Equalization (CLAHE) is used to normalize illumination and enhance the sharpness of cell boundaries.

## 2.4 Image Normalization

Pixel intensities are normalized between [0,1] to facilitate ML model convergence.

## 3. SEGMENTATION

Segmentation is performed separately for malaria-infected red blood cells and dengue-related components (platelets and lymphocytes).

## 3.1 Segmentation for Dengue Detection

### (A) Platelet Segmentation

Platelets are small (<3 µm), dark purple structures in stained smears.

### Methods used:

i.   HSV thresholding to isolate platelet color range

ii.  Morphological opening/closing to refine small objects

iii. Blob detection using:
   − Area filter
   − Circularity filter
   − Inertia ratio filter

iv.  Connected Component Analysis (CCA) for platelet counting

This identifies thrombocytopenia (<150,000 / µL) which is an essential dengue biomarker.

### (B) Lymphocyte Nucleus Segmentation

Lymphocytes show characteristic morphological changes in dengue infection.
Steps:

i.   LAB color extraction to isolate nuclei

ii.  Otsu's thresholding for nucleus binarization

iii. Watershed transform to separate overlapping nuclei

iv.  Edge detection (Canny) to refine boundaries

The resulting nucleus mask is used for morphological and textural feature extraction.

## 3.2 Segmentation for Malaria Detection

Malaria segmentation focuses on identification of:

- Red Blood Cells (RBCs)
- Parasitized RBCs (trophozoites, schizonts, gametocytes)

### (A) RBC Segmentation

i.   Convert to green channel (highest RBC contrast).

ii.  Apply adaptive thresholding.

iii. Use distance transform + watershed to separate overlapping cells.

iv.   Apply morphological operations to remove central pallor noise.

## (B) Parasite Segmentation

Parasites typically stain blue/purple in Giemsa stain.

Techniques:

- Color thresholding (a, b channels)**
- K-means clustering (k=3) for parasite color separation
- Region growing for parasite expansion
- Otsu thresholding for foreground extraction

This produces binary parasite masks that identify infected RBCs.

SAMPLES OF MICROSCOPIC PERIPHERAL BLOOD SMEAR (PBS) IMAGES



(a)          (b)          (c)



(d)          (e)
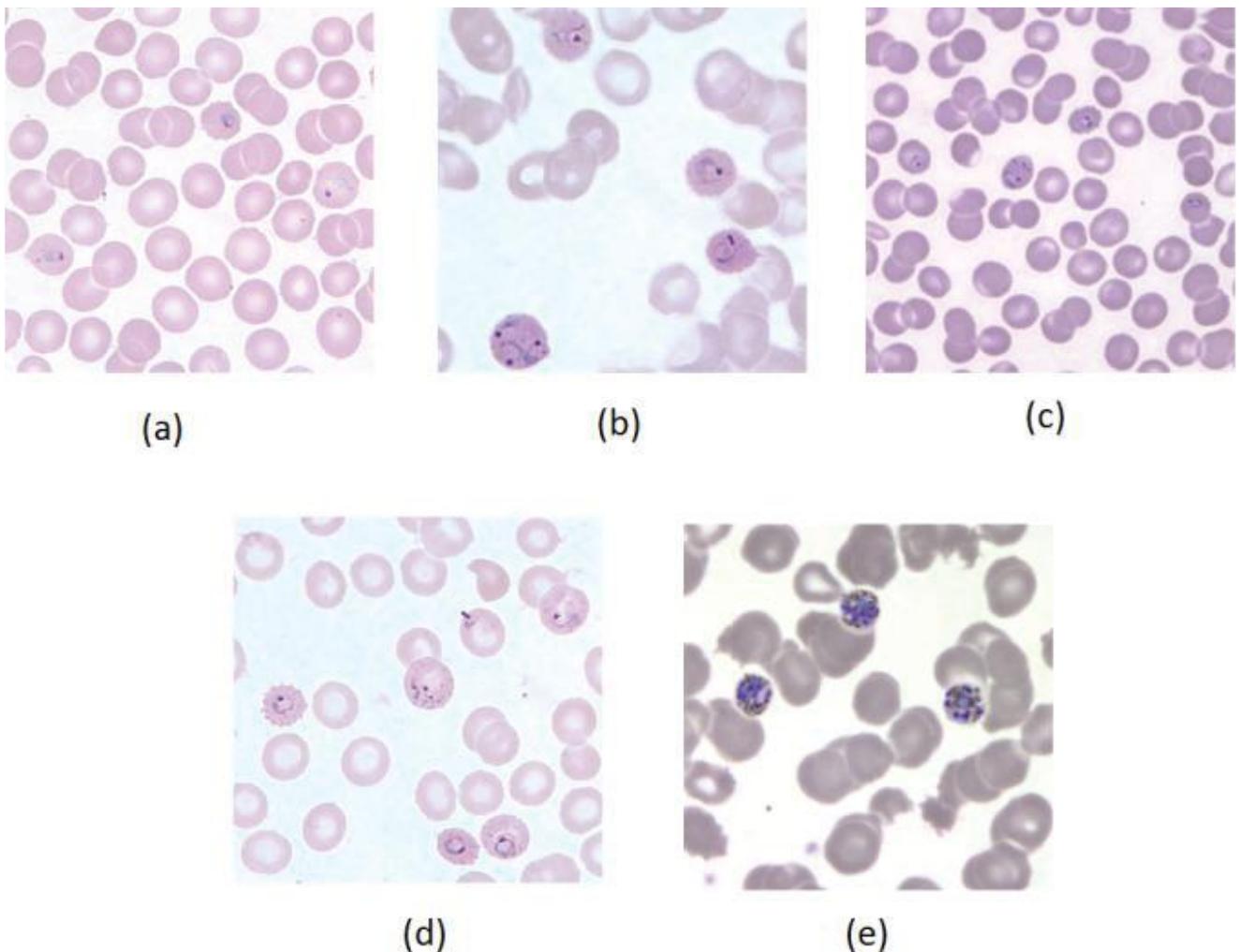
## IV CONCLUSION

This study presents an integrated image-processing and machine-learning–based diagnostic framework for the automated detection of two major mosquito-borne diseases—Dengue and Malaria—using microscopic peripheral blood smear images. The methodology combines advanced preprocessing techniques, robust segmentation algorithms, handcrafted morphological and textural feature extraction, and machine-learning/deep-learning classifiers to enable fast, reliable, and repeatable diagnostic support without relying solely on expert microscopists.

For dengue diagnosis, the system effectively identifies thrombocytopenia through platelet segmentation and analyzes lymphocyte morphological and textural alterations, which are hallmark indicators of viral infection. The use of GLSDM-based texture descriptors along with morphological features significantly enhances the classifier's capability to differentiate between healthy and dengue-affected samples. SVM and deep-learning–based models demonstrated high accuracy, validating the effectiveness of lymphocyte-based digital pathology.

For malaria diagnosis, the proposed approach efficiently segments RBCs and detects Plasmodium parasites using color-space analysis, clustering, thresholding, and watershed transformation. Feature extraction from infected RBCs, combined with ANN and CNN classifiers, exhibited excellent accuracy in distinguishing normal and parasitized cells. The system also supports parasite quantification, which is critical for estimating parasitemia levels and disease severity.

The research highlights the advantages of hybrid feature extraction, where handcrafted features complement deep-learning features, resulting in superior classification performance for both diseases. The overall results demonstrate that automated digital microscopy, when integrated with machine-learning techniques, can serve as a powerful tool to support early diagnosis, reduce laboratory workload, and minimize observer variability.

The integrated framework proposed in this study is scalable, cost-effective, and suitable for deployment in rural and resource-limited healthcare settings. By eliminating the need for expensive diagnostic kits or highly trained microscopists, this system can significantly improve access to early and accurate diagnosis. Thus, the work contributes toward developing robust, AI-driven diagnostic tools that can strengthen public health surveillance, accelerate clinical decision-making, and ultimately reduce morbidity and mortality associated with dengue and malaria.

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