INTERNATIONAL JOURNAL OF LATEST TECHNOLOGY IN ENGINEERING, MANAGEMENT & APPLIED SCIENCE (IJLTEMAS)

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XIV, Issue VIII, August 2025

Integrating Explainable AI for Enhanced Dengue Detection from Blood Smears

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DOI: https://doi.org/10.51583/IJLTEMAS.2025.1408000090

Abstract: Dengue fever, a mosquito-borne viral infection caused by the DENV virus, has been spreading rapidly across tropical and subtropical regions, posing a major public health concern and contributing to significant global mortality. Accurate identification of dengue cases remains challenging, making it essential to adopt reliable and efficient diagnostic approaches. This study explores an automated method for detecting dengue from peripheral blood smear (PBS) images using deep learning (DL) techniques, which have gained prominence in computer-assisted diagnosis of various medical conditions. The research utilizes the "Dengue Disease using Blood Smears" dataset and applies multiple classification models, including ResNet50, MobileNets, MobileNetV3-Small, MobileNetV3-Large, and a hybrid ensemble of Xception and MobileNet. For object detection, members of the YOLO family—YOLOV5x6, YOLOV5s6, YOLOV8n, and YOLOV9n—are employed. Experimental results reveal that the Xception–MobileNet ensemble yields the highest classification accuracy, while YOLO-based models effectively localize abnormalities in PBS images. These findings highlight the potential of DL-based approaches to enhance dengue diagnosis, offering a promising direction for improving public health surveillance and outcomes.

"Keywords: Dengue Detection, Blood Smears, Transfer Learning, Ensemble Model, YOLOv9, Explainable AI".

I. Introduction

Dengue, transmitted by *Aedes aegypti* and *Aedes albopictus* mosquitoes, has become a major global health concern since the 1960s. It is widespread in tropical and subtropical regions, with nearly half of the world's population at risk and an estimated 100–400 million infections annually. About 3.9 billion people in over 100 countries remain vulnerable, making dengue one of the fastest-spreading vector-borne diseases . The WHO reports that the Americas, Southeast Asia, and the Western Pacific are most affected, with Asia alone accounting for 70% of global cases. India is among the most severely impacted countries.

Despite extensive research, no fully effective vaccine or antiviral drug exists. While mild dengue causes flu-like symptoms, severe forms lead to plasma leakage, respiratory distress, organ failure, and hemorrhage, contributing to significant morbidity and mortality. With no specific treatment, early detection is vital. Current diagnostics such as NS1 antigen tests and CBC are useful but often limited in accuracy and accessibility, especially in low-resource settings.

Advances in artificial intelligence (AI) and machine learning offer new opportunities for improved detection. Deep learning models analyzing blood smear images can automatically identify key features like platelet and lymphocyte variations, enabling highly accurate diagnosis. Approaches using models such as MobileNetV2 and fuzzy cognitive map–based systems have shown promise in enhancing diagnostic performance and clinical decision-making.

Integrating AI with conventional methods could substantially improve dengue diagnosis, particularly in resource-limited healthcare settings. Machine learning–based image analysis represents a transformative step toward timely and reliable detection.

Related Work

The integration of artificial intelligence (AI) and machine learning in medical diagnostics has gained increasing attention, especially for vector-borne diseases like dengue. Zahiruddin et al. highlighted through a scoping review the growing role of AI in automating dengue detection, reducing manual reliance, and enhancing early diagnosis. Deshpande et al. emphasized AI-driven microscopic analysis of blood smear images, showing how deep learning can improve precision and reduce pathologists' workload.

AI applications in related diseases further demonstrate its potential. Asim et al. used deep learning–based feature fusion for malaria image classification, proving its effectiveness for blood-borne diseases such as dengue. Khan et al. reviewed machine learning–based white blood cell (WBC) analysis, stressing the need for robust architectures and quality datasets to improve automated disease detection.

Beyond diagnostics, Riswantini and Nugraheni discussed AI's role in epidemic management, highlighting its ability to process large-scale medical data for outbreak prediction and early diagnosis. Sangameswaran introduced MAIScope, a portable vision AI microscope enabling low-cost, real-time blood-borne disease detection in rural settings.

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Broader AI applications also provide insights. Almotairi et al. examined AI's role in COVID-19 management, particularly in medical imaging and data-driven diagnostics, which can be adapted for dengue detection. Similarly, Ayalew et al. proposed an IoT-based smart malaria classification system, illustrating how AI-integrated IoT models can support real-time disease tracking.

II. Materials And Methods

The proposed system employs an AI-based model for automated dengue detection using peripheral blood smear (PBS) images. Deep learning architectures such as CNN, MobileNetV2, Xception, NASNet, and YOLO are applied to extract and classify lymphocyte nucleus features, enhancing diagnostic accuracy. Feature extraction and classification are performed through deep learning–based image processing, with ensemble learning integrated to further improve predictive performance. The dataset includes both dengue-infected and normal blood smear samples. This AI-driven approach minimizes reliance on manual microscopic examination and offers an efficient solution for early detection in clinical and remote healthcare settings.

System Workflow:

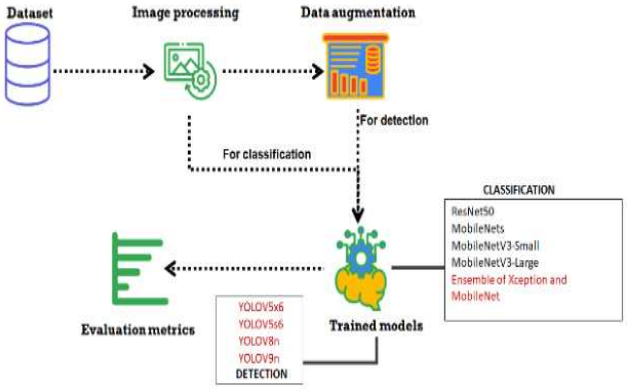


Fig.1 Proposed Architecture

The proposed system (Fig. 1) automatically detects dengue from peripheral blood smear (PBS) images using Explainable AI and transfer learning. Images are preprocessed, augmented, and analyzed using YOLO for detection, while ResNet50, MobileNet variants, and ensembles are used for classification. Model performance is evaluated with standard metrics to ensure accurate and interpretable diagnosis.

i) Dataset Collection:

The dataset comprises dengue-infected and normal PBS images collected from medical repositories and diagnostic centers. High-quality labeled data undergo preprocessing (noise removal, contrast enhancement, normalization) and augmentation to improve model robustness. This dataset forms the basis for training deep learning models in automated dengue diagnosis.

ii) Image Processing:

Images are normalized (pixel values scaled 0–1) for uniformity. To improve generalization, training images undergo augmentation (shear, zoom, flipping, orientation changes), while test images are only normalized to preserve evaluation integrity. These steps enhance feature extraction, reduce overfitting, and improve classification accuracy

iii) Data Augmentation*:*

To improve model generalization, data augmentation is applied to blood smear images by introducing transformations such as shear, zoom, and controlled flipping. These variations provide diverse perspectives without altering essential features, helping the model reduce overfitting and perform better on unseen data. Augmentation is applied only to the training set, while the test set remains unchanged to ensure unbiased evaluation. This approach strengthens the model's ability to accurately detect dengue-infected cells.

iii) Algorithms:

A)Classification:

- **ResNet50:** Employs residual learning for robust feature extraction, improving accuracy in classifying infected vs. healthy samples.
- **MobileNet:** Lightweight CNN optimized for efficiency, suitable for real-time use in resource-constrained settings.
- **MobileNetV3-Small:** Fast, efficient, with attention modules for rapid clinical diagnostics.
- **MobileNetV3-Large:** Balances computational efficiency with enhanced feature extraction.

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• **Xception + MobileNet Ensemble:** Combines depthwise convolutions and efficiency for improved detection.

B) Detection:

• **YOLOV5x6:** High-resolution real-time detection for accurate localization of dengue abnormalities.

• **YOLOV5s6:** Compact and efficient, optimized for low-resource environments.

• **YOLOV8n:** Improves speed and generalization across diverse blood smear samples.

• **YOLOV9n:** Latest variant offering higher accuracy and optimized real-time detection.

III. Results & Discussion

Accuracy: Accuracy measures a model's ability to correctly classify positive and negative cases. It is defined as:

$$Accuracy = \frac{\mathrm{TP} + \mathrm{TN}}{\mathrm{TP} + \mathrm{FP} + \mathrm{TN} + \mathrm{FN}} (1)$$

Precision: Precision evaluates the proportion of correctly classified positive cases among all predicted positives:

$$Precision = \frac{\text{True Positive}}{\text{True Positive } + \text{False Positive}} (2)$$

Recall: Recall measures the ability of a model to capture all actual positives:

$$Recall = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}} (3)$$

F1-Score: The F1-score combines precision and recall, offering a balanced measure of accuracy:

$$F1\ Score = 2 * \frac{Recall\ \mathrm{X}\ Precision}{Recall + Precision} * 100 (1)$$

mAP: mAP evaluates ranking quality by averaging precision across all queries:$mAP = \frac{1}{n}\sum_{k=1}^{k=n} AP_k$ (5)

Table (1): Presents performance metrics (Accuracy, Precision, Recall, F1-Score) for each algorithm. The Ensemble model consistently achieves the highest values across all metrics, with comparative results shown for other models..

Table (2): Shows detection metrics (Precision, Recall, mAP). YOLOv9 outperforms all other algorithms across these measures, with comparisons provided for the remaining models.

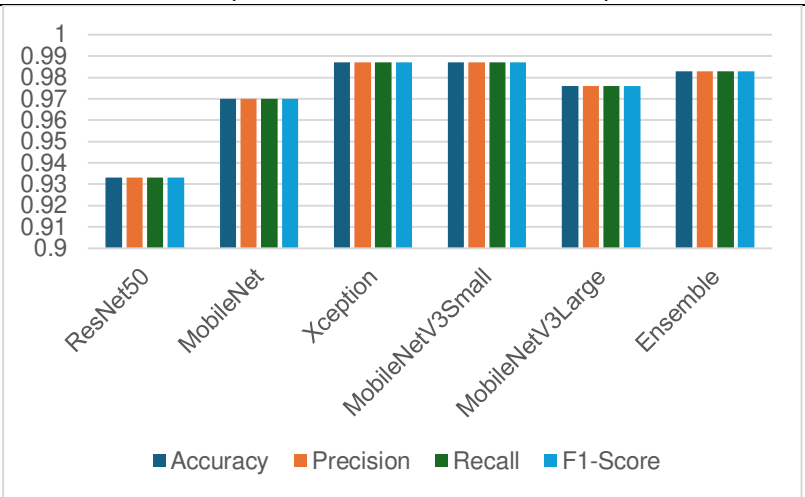
Table.1 Performance Evaluation Table for Classification

ML Model	Accuracy	Precision	Recall	F1-Score
ResNet50	0.933	0.933	0.933	0.933
MobileNet	0.970	0.970	0.970	0.970
Xception	0.987	0.987	0.987	0.987
MobileNetV3Small	0.987	0.987	0.987	0.987
MobileNetV3Large	0.976	0.976	0.976	0.976
Ensemble	0.983	0.983	0.983	0.983

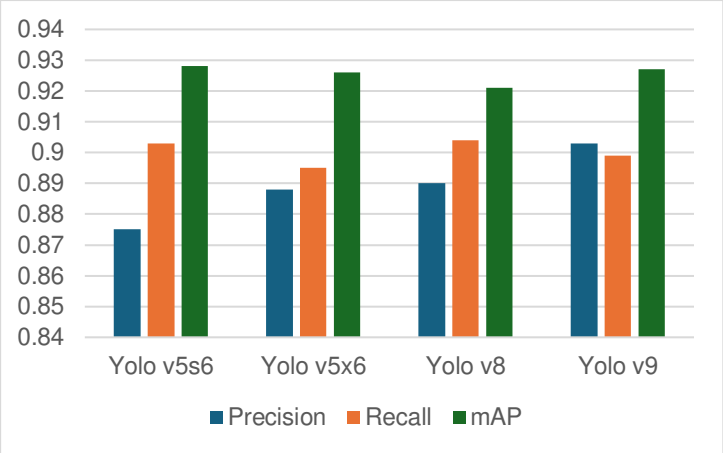
Table.2 Performance Evaluation Table for Detection

ML Model	Precision	Recall	mAP
Yolo v5s6	0.875	0.903	0.928
Yolo v5x6	0.888	0.895	0.926
Yolo v8	0.890	0.904	0.921
Yolo v9	0.903	0.899	0.927

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Graph.1 Comparison Graphs for Classification

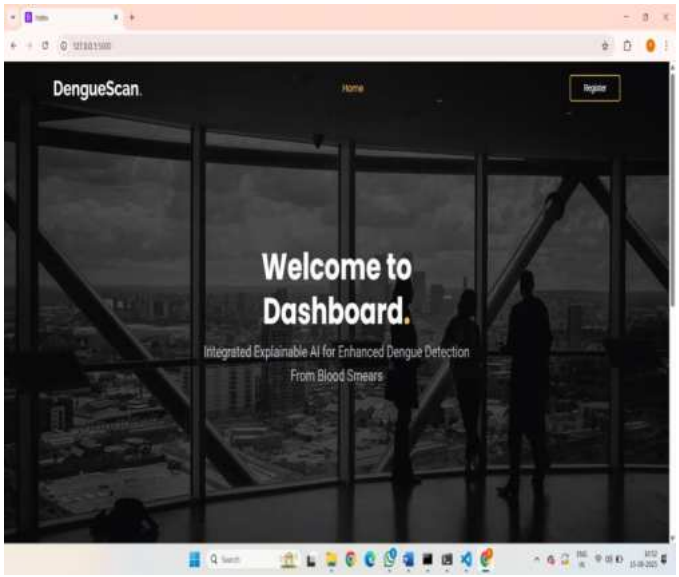


Graph.2 Comparison Graphs for Detection

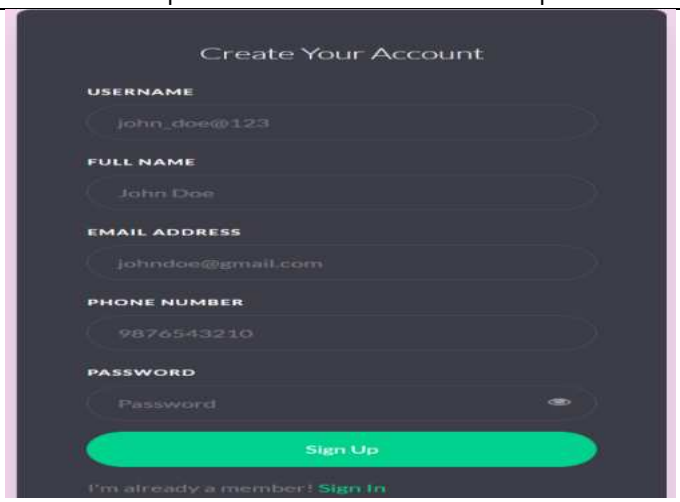
Graph 1: Accuracy (blue), Precision (orange), Recall (green), and F1-Score (sky blue) are compared across models. The Ensemble model demonstrates superior performance, achieving the highest values on all metrics.

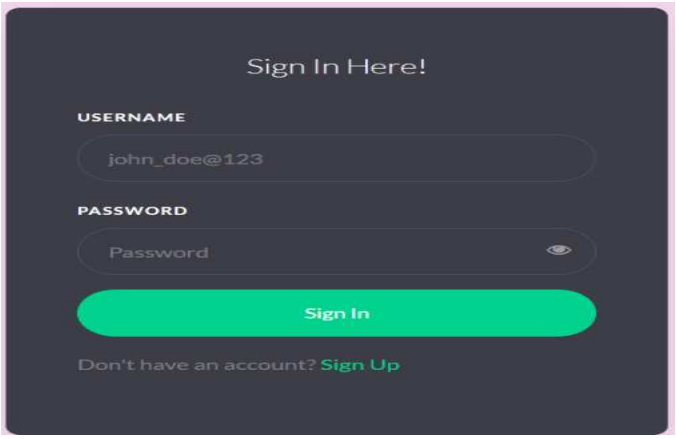
Graph 2: Precision (blue), Recall (orange), and mAP (green) are compared for detection models. YOLOv9 consistently outperforms others, showing the best performance across all metrics.

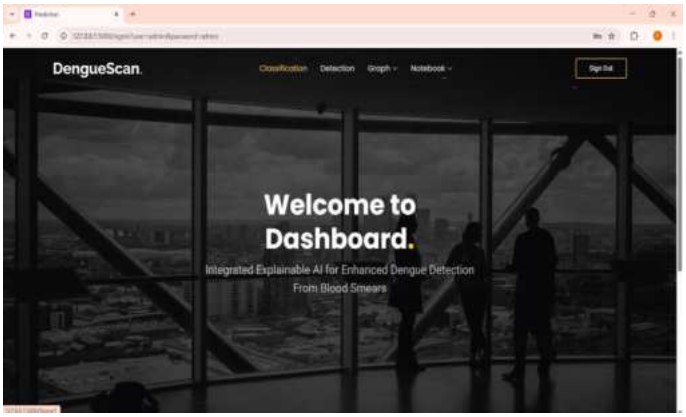
5. Screens:

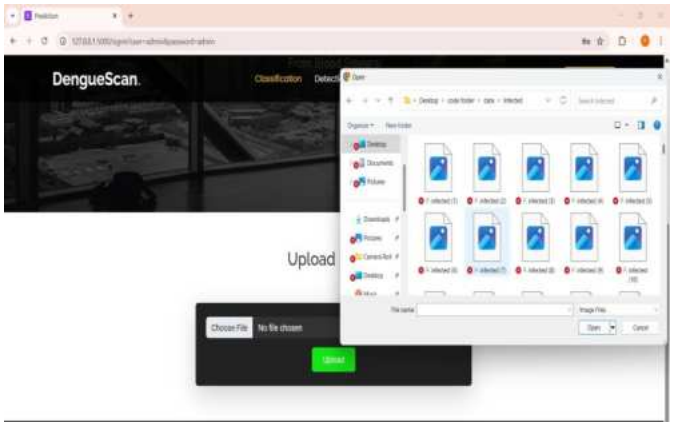


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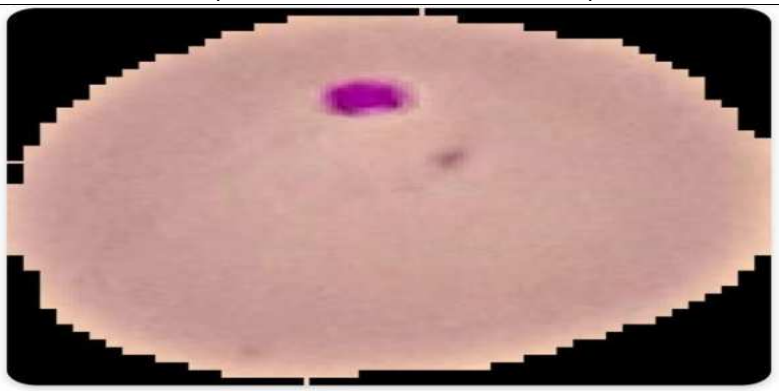






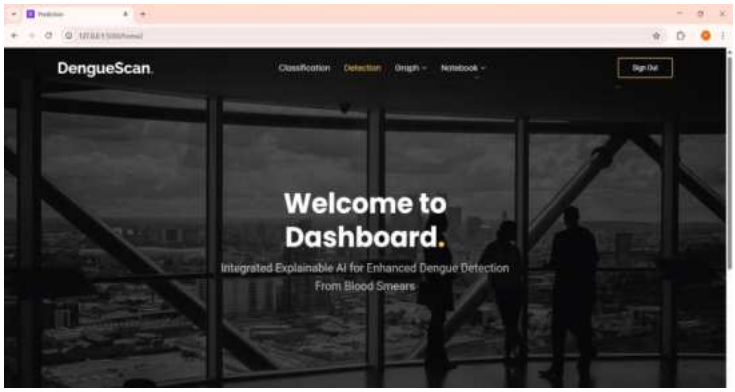


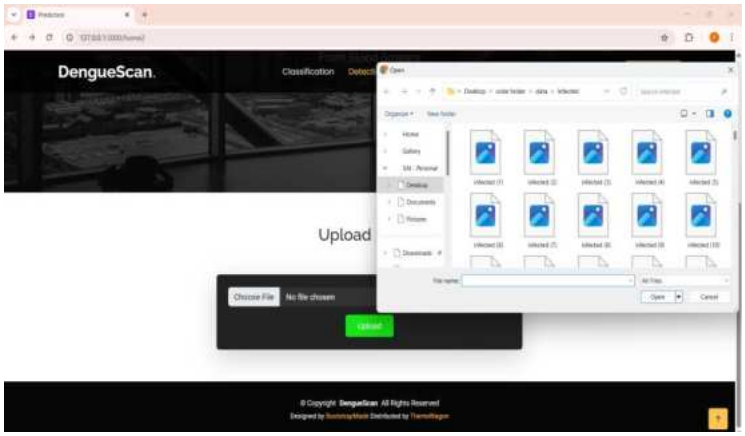
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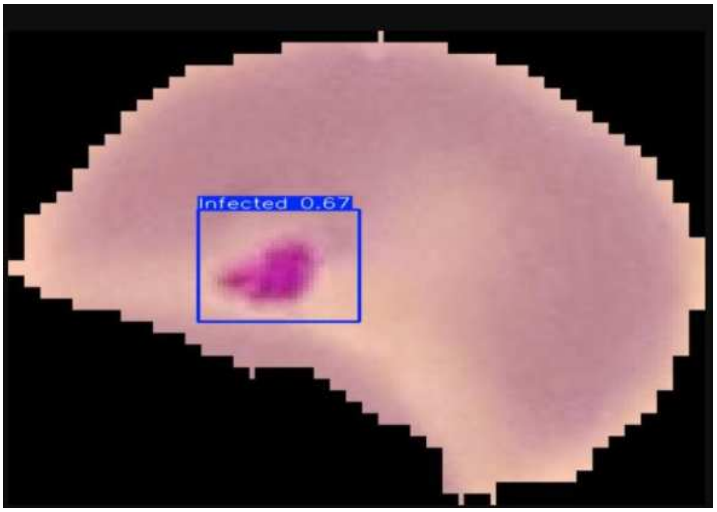


The Prediction is:

Infected







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IV. Conclusion

Peripheral blood smear (PBS) analysis, when combined with tests like Complete Blood Count and NS1 antigen capture, significantly improves dengue detection, especially in low-resource settings. Deep learning with transfer learning further enhances reliability, with the ensemble classification model achieving **98.3% accuracy** and YOLOv9 reaching a **90.3% detection rate** for infected regions. The use of explainable AI increases transparency and trust, providing an efficient and accurate alternative to manual microscopy while reducing diagnostic errors. This system supports early diagnosis, better disease management, and improved patient outcomes.

Future work may focus on integrating multi-modal data (clinical records, genetic markers) to improve accuracy, extending the model to other blood-borne diseases, and enabling real-time deployment via mobile or cloud platforms. Federated learning can also enhance generalization while preserving data privacy across institutions.

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