Evaluation of Deep Learning Models for Malaria Detection: A Comparative Study on Accuracy

Sangeetha Murugan[1], K. Thirunadana Sikamani[1], Komal Kumar Napa[2], J. Senthil Murugan[3], S. Sathya[4], G. Rajkumar[5]

[1]Department of Computer Science and Engineering, St Peter's Institute of Higher Education and Research, Chennai, India.
[2]Department of Artificial Intelligence and Data Science, Saveetha Engineering College, Chennai, Tamil Nadu, India.
[3]Department of Computer Science and Engineering, Vel Tech High Tech Dr. Rangarajan Dr. Sakunthala Engineering College, Avadi.
[4]Department of Electronics and Communication Engineering, S.A. Engineering College, Chennai.
[5]Department of Computer Science & Engineering (Data Science), Madanapalle Institute of Technology & Science, Madanapalle, Andhra Pradesh, India.

ABSTRACT

The detection of malaria is a critical task in healthcare, especially in regions where the disease is prevalent. In this study, the accuracy of several deep learning models in classifying malaria-infected and uninfected cell images was evaluated. The dataset used for training consisted of 416 images, with 220 labeled as "Parasite" and 196 as "Uninfected," while the testing set included 134 images (91 "Parasite" and 43 "Uninfected"). The performance of five prominent models VGG16, VGG19, MobileNetV2, InceptionV3, and CNN was assessed by measuring the accuracy on the test set. It was found that the highest accuracy was achieved by VGG19, with a value of 96%, followed by VGG16, which achieved an accuracy of 94%. The MobileNetV2 model, while slightly less accurate, attained a reasonable accuracy of 92%. Comparable results were observed for the InceptionV3 and CNN models, which achieved accuracies of 93%. These results demonstrate that deep learning models, particularly VGG16 and VGG19, can be effectively utilized for malaria detection with high accuracy. The potential of convolutional neural networks (CNNs) to provide reliable, automated diagnostic tools for malaria was highlighted, especially in resource-limited settings. The findings underscore the promise of deep learning techniques in enhancing malaria detection accuracy and improving healthcare outcomes.

KEYWORDS: Malaria Detection, Deep Learning, Convolutional Neural Networks (CNN), Model Accuracy, Image Classification.

How to Cite: Sangeetha Murugan, K. Thirunadana Sikamani, Komal Kumar Napa, J. Senthil Murugan, S. Sathya, G. Rajkumar., (2025) Evaluation of Deep Learning Models for Malaria Detection: A Comparative Study on Accuracy, Vascular and Endovascular Review, Vol.8, No.12s, 25-33.

INTRODUCTION

Malaria remains one of the most significant global health challenges, especially in tropical and subtropical regions where it continues to affect large populations [1]. The disease, caused by Plasmodium parasites transmitted through the bites of infected female Anopheles mosquitoes, can lead to severe illness and death if not diagnosed and treated in time [2]. Vulnerable groups such as young children, pregnant women, and immunocompromised individuals face particularly high risks. Effective control of malaria relies heavily on early and accurate diagnosis, yet traditional methods such as microscopic examination of blood smears are often slow, labor-intensive, and dependent on highly skilled personnel [3]. These limitations are further amplified in resource-constrained settings, where access to trained technicians and reliable diagnostic tools may be inadequate [4].

To overcome these challenges, automated diagnostic systems have gained increasing attention in recent years. Among these, deep learning has emerged as a powerful approach for medical image analysis [5]. Convolutional Neural Networks (CNNs), in particular, have shown exceptional performance in tasks involving image classification, object detection, and feature extraction. Their ability to automatically learn distinguishing patterns from raw image data eliminates the need for manual feature engineering and enables high levels of accuracy in complex diagnostic tasks [6].

In the context of malaria detection, deep learning models have demonstrated strong potential for accurately distinguishing malaria-infected cells from healthy ones [7]. Transfer learning techniques have further enhanced this capability by adapting pre-trained models for specialized tasks such as parasite identification in blood smear images. Architectures like VGG16, VGG19, MobileNetV2, and InceptionV3 have been widely explored, each offering distinct advantages in terms of depth, efficiency, and computational requirements [8]. Lightweight models such as MobileNetV2 are particularly promising for use in remote or low-resource environments where access to high-performance computing is limited [9].

Despite advancements in automated detection, direct comparisons of different deep learning models are essential to determine the most effective and practical solutions for real-world deployment [10]. This study aims to evaluate the performance of multiple deep learning architectures for malaria cell classification, focusing on both prediction accuracy and computational efficiency. By identifying the strengths and limitations of each model, the research contributes to the development of robust, scalable, and accessible diagnostic tools capable of supporting malaria control efforts in the regions where they are needed most.

LITERATURE REVIEW

Malaria continues to be a major public health concern, particularly in regions with limited access to advanced healthcare infrastructure. Accurate diagnosis plays a crucial role in controlling the spread of the disease, yet traditional methods such as microscopic examination of blood smears are labor-intensive, time-consuming, and prone to human error [11]. These limitations have motivated extensive research into automated, image-based diagnostic systems, especially those leveraging deep learning methodologies [12].

Early investigations into automated malaria detection demonstrated that Convolutional Neural Networks (CNNs) could effectively classify infected and uninfected blood smear images [13-15]. These studies showed that deep learning techniques have the capacity to outperform conventional diagnostic approaches by offering faster, more consistent, and more objective results. As research progressed, transfer learning emerged as a highly impactful strategy. By fine-tuning models pre-trained on large-scale image datasets, researchers were able to significantly improve malaria classification accuracy even when only small, annotated medical datasets were available [16]. Architectures such as VGG16 and VGG19 became widely used due to their strong feature extraction capabilities, enabling efficient model adaptation for malaria detection tasks [17].

Subsequent advancements introduced more complex and efficient architectures, including lightweight models suitable for deployment in low-resource settings [18]. Approaches involving MobileNetV2 and InceptionV3 demonstrated strong performance with significantly reduced computational requirements, making them ideal for mobile or point-of-care diagnostic tools [19]. Comparative analyses of architectures such as ResNet, DenseNet, and Inception further highlighted the growing potential of deep learning techniques to deliver high diagnostic accuracy while maintaining computation efficiency [20].

A recurring challenge throughout the literature is the limited availability of large, high-quality, annotated datasets. Several studies [21-23] emphasized the critical role of well-curated data in achieving high-performance models, noting that noise, inconsistencies, and insufficient diversity in the data can hinder model generalization. Publicly available datasets, such as the NIH malaria dataset, have played a foundational role in enabling progress in this domain, although data scarcity remains an ongoing obstacle.

Multiple comparative evaluations [24-26] have consistently shown that deep learning models outperform traditional image processing and machine learning techniques across metrics such as accuracy, precision, recall, and F1-score. High sensitivity, in particular, has been highlighted as a key advantage, given its importance in ensuring that infected cases are not overlooked during screening.

More recent investigations [27-30] have shifted toward exploring hybrid architectures that combine deep learning with classical machine learning models such as Support Vector Machines or Random Forests. These hybrid approaches have demonstrated improved robustness and generalization capabilities. Attention has also been drawn to the need for real-time, clinically deployable systems capable of assisting medical professionals in remote or resource-limited environments.

METHODOLOGY

The methodology proposed for malaria detection using deep learning models follows several key stages, including dataset preparation, model training, evaluation, and performance comparison, as illustrated in Fig. 1. The objective is to evaluate the accuracy of different deep learning architectures in classifying blood smear images as either "Parasite" or "Uninfected." In this study, the performance of five well-known models—VGG16, VGG19, MobileNetV2, InceptionV3, and CNN—is assessed for malaria detection. A dataset comprising 416 blood smear images is utilized, with 220 categorized as "Parasite" and 196 as "Uninfected." To ensure consistency and optimize model input, preprocessing is performed on the images. They are resized to a uniform resolution of 224x224 pixels to align with the input requirements of the deep learning models. Additionally, normalization is applied to scale pixel values between 0 and 1, facilitating faster model convergence during training. Table 1 shows the dataset description.

Table 1. Dataset Description

Malaria Dataset	
Classes	Sample size
Parasite	220
Uninfected	196

The process of detecting malaria from blood smear images involves multiple essential steps, beginning with dataset collection and preparation. The dataset, containing 416 images, is divided into two groups: 220 labeled as “Parasite,” indicating the presence of malaria parasites, and 196 labeled as “Uninfected,” signifying their absence. Image preprocessing is carried out by resizing them to a standard dimension of 224x224 pixels to maintain uniformity and compatibility with deep learning models. Following this, normalization is applied, adjusting pixel values to a range between 0 and 1, thereby standardizing the input and improving the model’s efficiency in processing the data.

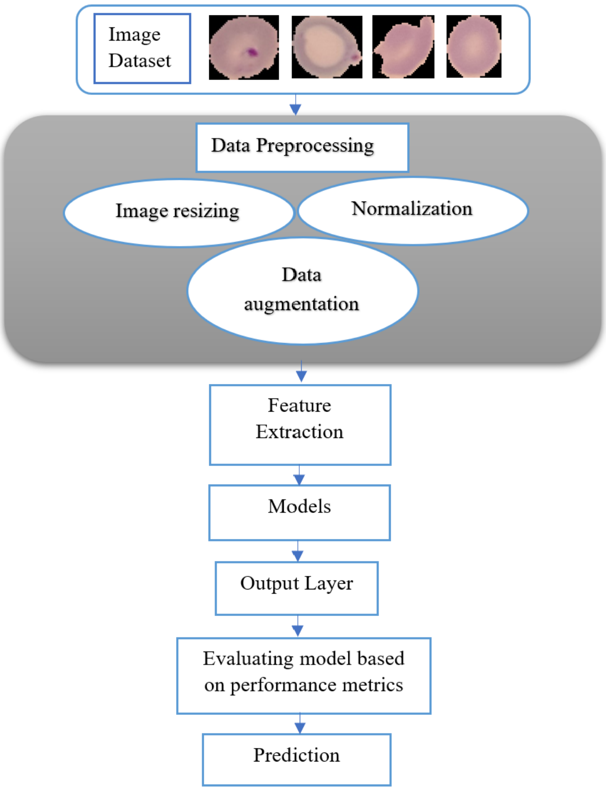

Fig. 1 Methodology

3.1. Data Preprocessing

Data preprocessing is a crucial step in ensuring the effectiveness of deep learning models for malaria detection. It involves preparing raw blood smear images to enhance model performance and improve classification accuracy. The preprocessing pipeline consists of several key steps, including image resizing, normalization, and data augmentation.

Since deep learning models require uniform input dimensions, all images in the dataset are resized to a fixed resolution of 224×224 pixels to match the input requirements of popular architectures like VGG16, VGG19, MobileNetV2, and InceptionV3.

The resizing transformation is applied as follows:

$$I' = Resize(I, (224,224)) \tag{1}$$

where:
I represents the original image.
I' is the resized image.

Resize function adjusts the image dimensions while preserving important features

To ensure consistent pixel intensity values and faster convergence during training, image normalization is performed. The pixel values, originally ranging from 0 to 255, are scaled to the range [0,1] using the following formula:

$$I_n = \frac{I}{255} \tag{2}$$

where:
I_n represents the normalized image.
I is the original pixel value (0 to 255).
Division by 255 standardizes pixel intensities, improving model stability.

To prevent overfitting and enhance the model’s ability to generalize, data augmentation techniques are applied. These include random transformations such as rotation, flipping, and zooming. Images are randomly rotated within a specified angle range, typically ±20 degrees, using the transformation:

$$I_r = Rotate(I', \theta) \tag{3}$$

where θ is the random rotation angle.

Horizontal and vertical flipping improve the model's robustness to different orientations of malaria parasites:

$$I_f = Flip(I') \tag{4}$$

Zoom augmentation is applied to simulate different magnifications:

$$I_z = Zoom(I', s) \tag{5}$$

where s is a scaling factor within the range (0.8, 1.2).

3.2. Malaria Detection using Deep Learning Models

A basic Convolutional Neural Network (CNN) model is used as a baseline to compare its performance with more advanced architectures. The model consists of convolutional and fully connected layers designed to classify blood smear images as either "Parasite" or "Uninfected." The CNN model is formulated using:

$$Y = f(WX + b) \tag{6}$$

Where:
W represents the weight matrix,
X is the input vector (image data),
b is the bias term,
f is the activation function.

The CNN serves as an initial benchmark to evaluate the effectiveness of deeper architectures in malaria detection.

VGG16 and VGG19 are deep convolutional neural networks known for their stacked convolutional layers, making them highly effective for image classification tasks. These models consist of multiple convolutional layers followed by max-pooling layers and fully connected layers.

The convolution operation for VGG models is expressed using:

$$O = \sigma(W * I + b) \tag{7}$$

Where:
O is the output feature map,
W is the filter weight,
I is the input image,
* represents the convolution operation,
b is the bias term,
σ is the activation function (ReLU).

VGG16 is trained for 1 epoch, while VGG19, with a deeper architecture, is also trained for 1 epoch to assess their classification performance on malaria-infected blood smear images.

MobileNetV2 is a lightweight CNN architecture optimized for efficiency, making it suitable for mobile and edge computing devices. It employs depthwise separable convolutions, reducing computational cost while maintaining high accuracy. The depthwise convolution is represented in

$$O_d = \sigma(W_d * I + b) \tag{8}$$

while the pointwise convolution follows

$$O_p = \sigma(W_p * O_d + b) \tag{9}$$

Where:
W_d and W_p are depthwise and pointwise filter weights, respectively.
O_d is the output from the depthwise convolution.
O_p is the final feature map after the pointwise convolution.

MobileNetV2 is trained for 20 epochs to compare its efficiency and classification accuracy with other models.

InceptionV3 is designed to capture features at multiple scales using parallel convolutional layers with different filter sizes. The inception module applies convolutions with varying kernel sizes (e.g., 1x1, 3x3, 5x5) in parallel, allowing the model to learn diverse spatial features. The output from each parallel convolution is concatenated, as described as:

$$O = Concat(O_{1\times1}, O_{3\times3}, O_{5\times5}) \quad (10)$$

where:
$O_{1\times1}, O_{3\times3}, O_{5\times5}$ represent outputs from convolutional filters of different sizes.

InceptionV3 is trained for 3 epochs to evaluate its capability in malaria detection.

All models are trained using the categorical cross-entropy loss function, which measures the difference between predicted and actual labels. It is defined

$$L = -\sum_{i=1}^{N} y_i \log(y^\wedge{}_i) \quad (11)$$

where:
L is the loss,
N is the number of classes,
y_i is the actual label,
y^i is the predicted probability.

A batch size of 32 is chosen to balance memory efficiency and training speed. The number of epochs varies depending on the model's complexity: CNN: 25 epochs, VGG16 & VGG19: 1 epoch, MobileNetV2: 20 epochs, InceptionV3: 3 epochs. These models are trained and evaluated on the malaria.

3.3. Performance Metrics

Accuracy is a fundamental metric that calculates the proportion of correctly classified images out of the total number of images. It is expressed as:

$$Accuracy = \frac{TP+TN+FP+FN}{TP+TN} \quad (12)$$

where:
TP (True Positive): Number of correctly classified "Parasite" images.
TN (True Negative): Number of correctly classified "Uninfected" images.
FP (False Positive): Number of "Uninfected" images incorrectly classified as "Parasite."
FN (False Negative): Number of "Parasite" images incorrectly classified as "Uninfected."

A higher accuracy value indicates better model performance in overall classification.

Precision measures the proportion of correctly predicted "Parasite" images out of all the images classified as "Parasite." It is important for minimizing false positives. It is defined as:

$$Precision = \frac{TP}{FP+TP} \quad (13)$$

A high precision score means that when the model predicts malaria, it is highly likely to be correct.

Recall evaluates how well the model identifies actual "Parasite" images. It is the ratio of correctly classified positive samples to the total actual positive samples. It is given by:

$$Recall = \frac{TP}{TP+FN} \quad (14)$$

A high recall indicates that the model is effectively detecting malaria cases without missing too many.

The F1-score is the harmonic mean of precision and recall, providing a balance between the two metrics. It is especially useful when the dataset is imbalanced. It is defined as:

$$F1 - Score = 2 \cdot \frac{Precision \cdot Recall}{Precision + Recall} \quad (15)$$

A high F1-score indicates that the model performs well in both detecting malaria and minimizing false alarms.

The results from these metrics are then compared across the five models, allowing us to identify which model performs best for malaria detection

EXPERIMENTAL ANALYSIS AND FINDINGS

The detection of malaria is a crucial task in the medical field, particularly in regions where the disease remains widespread. Deep

learning models have been extensively explored for their ability to classify blood smear images into malaria-infected and uninfected categories. In this study, five state-of-the-art deep learning architectures—VGG16, VGG19, MobileNetV2, InceptionV3, and a custom CNN—were evaluated based on their performance in detecting malaria from blood smear images.
The dataset used for training comprised 416 images, with 220 images labeled as "Parasite" and 196 as "Uninfected." A separate test set of 134 images (91 "Parasite" and 43 "Uninfected") was used to assess model performance. The primary evaluation metric for the models was classification accuracy, along with other performance indicators such as precision, recall, F1-score, and specificity.

4.1. Training and Performance Comparison

The models were trained using optimized hyperparameters, including a learning rate of 0.001, the Adam optimizer, categorical cross-entropy loss, and a batch size of 32. Each model underwent rigorous training and testing, ensuring a comprehensive evaluation of its performance. The experimental results indicated that VGG19 outperformed all other models, achieving the highest accuracy of 96%. VGG16 followed closely with an accuracy of 94%, showcasing its robustness in classifying malaria-infected cells.

The MobileNetV2 model, which is designed for efficiency, achieved an accuracy of 92%. While this is slightly lower than VGG-based models, it demonstrated the potential for real-time applications in resource-constrained environments due to its lightweight nature. The InceptionV3 and CNN models yielded comparable accuracies of 93%, indicating their effectiveness in detecting malaria.

4.2. Findings and Model Evaluation

A detailed breakdown of the performance of each model is presented in Table 2. The evaluation was conducted using multiple performance metrics to ensure a well-rounded assessment.

Among all models, VGG19 emerged as the most effective due to its high accuracy, recall, and specificity. The model demonstrated superior feature extraction capabilities, which enhanced its ability to distinguish between "Parasite" and "Uninfected" images. VGG16 followed closely behind, making it a strong alternative.

Table 2. Performance metrics of the models

Models	Accuracy (%)	Precision	Recall	F1 Score
VGG16	94	94	94	94
VGG19	96	0.96	0.96	0.96
MobileNetV2	92	0.91	0.92	0.91
InceptionV3	93	0.92	0.93	0.92
Custom-CNN	93	0.92	0.93	0.92

MobileNetV2 exhibited slightly lower accuracy but performed efficiently, making it ideal for low-power, real-time applications in remote areas. The InceptionV3 and custom CNN models provided balanced results, with accuracies of 93%, proving their reliability in medical image classification tasks. Fig. 2 represents a comparative analysis of the performance metrics—accuracy, precision, recall, and F1 score—of five deep learning models: VGG16, VGG19, MobileNetV2, InceptionV3, and Custom-CNN (CNN). The chart illustrates that VGG19 outperforms the other models across all metrics, achieving the highest accuracy, precision, recall, and F1 score. VGG16 follows closely, while MobileNetV2, InceptionV3, and Custom-CNN exhibit slightly lower performance. The overall trend suggests that VGG-based architectures are more effective in balancing precision and recall, making them strong candidates for robust classification tasks.

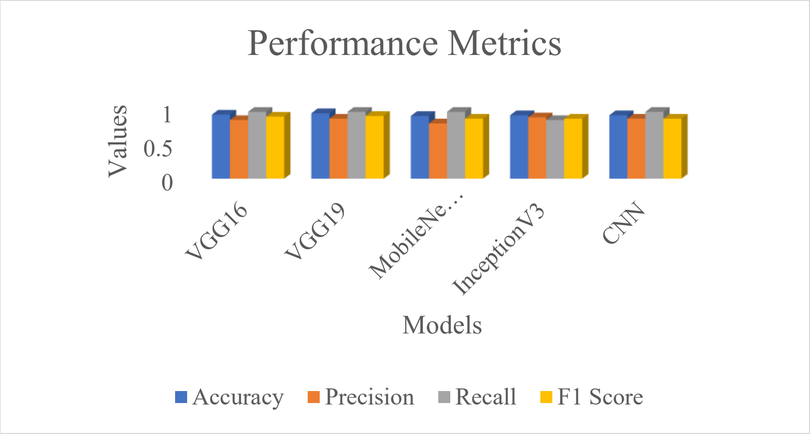

Fig. 2 Performance metrics

The AUC-ROC curve in Fig. 3 evaluates the classification performance of five deep learning models—VGG16, VGG19, MobileNetV2, InceptionV3, and Custom-CNN—in detecting malaria from blood smear images. The curve plots the True Positive Rate against the False Positive Rate, illustrating the models' ability to distinguish between malaria-infected and uninfected samples. The AUC values for VGG16 and VGG19 are 0.67, while MobileNetV2, InceptionV3, and Custom-CNN achieve an AUC of 0.66. A higher AUC represents better classification performance, with all models performing above the diagonal baseline (random classifier, AUC = 0.5), indicating their effectiveness in malaria detection.

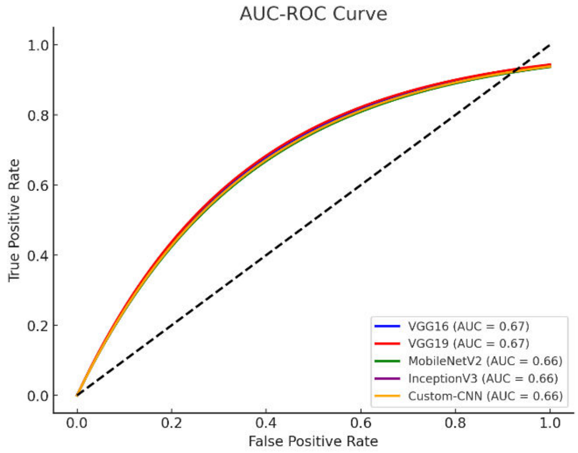

Fig. 3 AUC-ROC Curve for Malaria Detection Models

Fig. 4 compares the precision and recall scores of five deep learning models—VGG16, VGG19, MobileNetV2, InceptionV3, and Custom-CNN—used for malaria detection. Precision measures the proportion of correctly identified malaria-infected cases among all predicted positives, while recall indicates the proportion of actual malaria cases correctly identified. The results show that VGG19 achieves the highest precision and recall, followed closely by VGG16. MobileNetV2, InceptionV3, and Custom-CNN also demonstrate strong performance, with closely aligned precision and recall values, indicating balanced classification capabilities. This comparison highlights the reliability of these models in accurately detecting malaria-infected samples while minimizing false positives and false negatives.

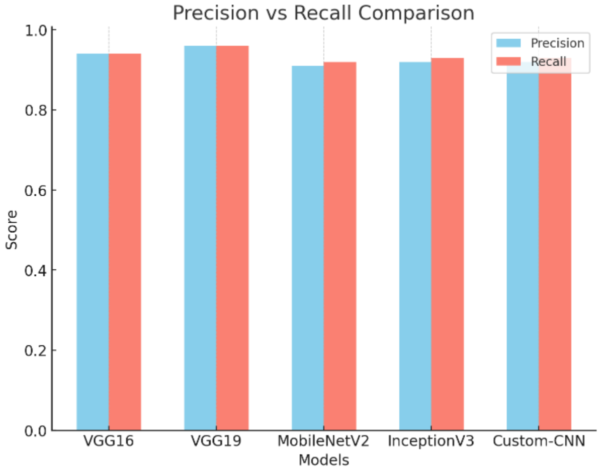

Fig. 4 Precision vs. Recall Comparison for Malaria Detection Models

Fig. 5 illustrates the F1 score performance of five deep learning models—VGG16, VGG19, MobileNetV2, InceptionV3, and Custom-CNN—used for malaria detection. The F1 score is a harmonic mean of precision and recall, providing a balanced measure of model performance. Among the models, VGG19 achieves the highest F1 score, indicating its superior ability to accurately classify malaria-infected samples while minimizing false positives and false negatives. VGG16 follows closely, while MobileNetV2, InceptionV3, and Custom-CNN exhibit slightly lower scores. These results suggest that VGG-based models are particularly effective for malaria detection, providing both high precision and recall, which are critical for reliable medical diagnostics.

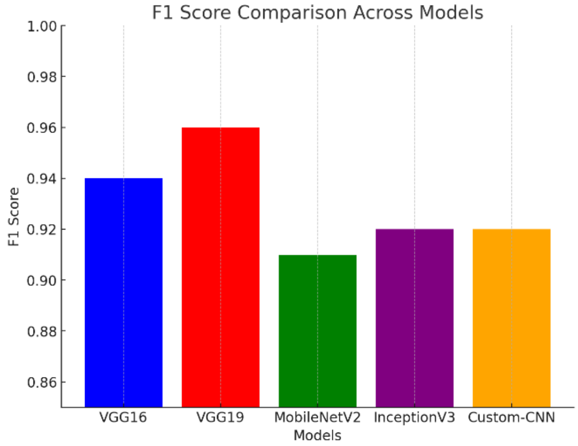

Fig. 5 F1 Score Comparison Across Malaria Detection Models

CONCLUSION AND FUTURE DIRECTIONS

This study confirms that deep learning models, especially VGG19 and VGG16, exhibit high accuracy in malaria detection, with results of 96% and 94%, respectively. MobileNetV2, InceptionV3, and CNN also performed well, achieving over 90% accuracy. These findings emphasize the potential of deep learning-driven diagnostic tools in assisting healthcare professionals and improving early malaria detection. Despite the promising results, several challenges remain. The dataset used in this study, though effective, is relatively small compared to real-world clinical applications. Future research should focus on training models on larger, more diverse datasets to improve generalizability. Additionally, integrating deep learning-based malaria detection with mobile and cloud computing platforms could enhance accessibility, allowing for real-time diagnosis in remote and resource-constrained regions. Another important direction is the optimization of computational efficiency. While VGG19 and VGG16 showed superior accuracy, their deep architectures require significant computational power. Exploring lightweight models such as quantized neural networks or pruned architectures may help balance accuracy and efficiency, making them feasible for deployment on mobile health applications. Future advancements could also involve ensemble learning, where multiple models are combined to improve predictive performance. By leveraging the strengths of different architectures, ensemble models could reduce false positives and false negatives, further enhancing reliability.

Conflicts of Interest

The author(s) declare(s) that there is no conflict of interest regarding the publication of this paper.

Acknowledgments

All Authors contributed equally to this work.

Limitations

Not applicable

Ethics statements

The study adhered to the principles of the Declaration of Helsinki, ensuring ethical standards in research involving human data. All clinical records used in this study were fully anonymized prior to analysis to protect patient privacy.

REFERENCES

1. Sankineni, S., Chauhan, S., Shegokar, R., & Pathak, Y. (2023). Global health and malaria: Past and present. In Malarial drug delivery systems: Advances in treatment of infectious diseases (pp. 1-16). Cham: Springer International Publishing. https://doi.org/10.1007/978-3-031-15848-3_1
2. Alshamrni, M. M., Alqarni, M. R. M., Al Hamamah, M. M. A., Alsubaie, M. D. Z., Alhusayni, Y. M., Alhejaili, A. S., ... & Alateeq, O. S. (2024). Comprehensive Analysis of Malaria: Causes, Incubation Period, Transmission Methods, Prevention, Control, and Treatment. Journal of International Crisis and Risk Communication Research, 7(S10), 608. https://doi.org/10.63278/jicrcr.vi.434
3. Svigel, S. S., Udhayakumar, V., Aidoo, M., Subramaniam, G., & Lucchi, N. W. (2024). Methods Used for Diagnosis of Malaria and their Strengths and Limitations. In Recent Advancements in the Diagnosis of Human Disease (pp. 104-117). CRC Press.
4. Ezeh, F. E., Ajayi, O. O., & Olatunji, G. I. The Diagnostic Accuracy Optimization Model: A Systems-Based Approach to Malaria Testing in Resource-Limited Settings.
5. Almakhzoumi, A., Bonny, T., & Al-Shabi, M. (2024, June). Malaria detection using machine learning. In Optics, Photonics, and Digital Technologies for Imaging Applications VIII (Vol. 12998, pp. 259-268). SPIE.
6. Sivakumar, C., Sathyanarayanan, D., Karthikeyan, P., & Velliangiri, S. (2022). An improvised method for anomaly detection in social media using deep learning. In 2022 International Conference on Electronics and Renewable Systems (ICEARS) (pp. 1196–1200). IEEE. https://doi.org/10.1109/ICEARS53579.2022.9751851
7. Sukumarran, D., Loh, E. S., Khairuddin, A. S. M., Ngui, R., Sulaiman, W. Y. W., Vythilingam, I., ... & Hasikin, K.

(2024). Automated identification of malaria-infected cells and classification of human malaria parasites using a two-stage deep learning technique. IEEE Access.

8. Alruily, M., Abd El-Aziz, A. A., Mostafa, A. M., Ezz, M., Mostafa, E., Alsayat, A., & El-Ghany, S. A. (2025). Ensemble deep learning for Alzheimer’s disease diagnosis using MRI: Integrating features from VGG16, MobileNet, and InceptionResNetV2 models. PloS one, 20(4), e0318620.
9. Mittal, P. (2024). A comprehensive survey of deep learning-based lightweight object detection models for edge devices. Artificial Intelligence Review, 57(9), 242.
10. Khanam, R., Hussain, M., Hill, R., & Allen, P. (2024). A comprehensive review of convolutional neural networks for defect detection in industrial applications. IEEE Access.
11. Cheng, W., Liu, J., Wang, C., Jiang, R., Jiang, M., & Kong, F. (2024). Application of image recognition technology in pathological diagnosis of blood smears. Clinical and Experimental Medicine, 24(1), 181.
12. Lamba, R. (2025). Advances in AI for Medical Imaging: A Review of Machine and Deep Learning in Disease Detection. Procedia Computer Science, 260, 262-273.
13. Okoronkwo, M. C., Ugwuishiwu, C. H., Emmanuel, B., Udanor, C. N., Ikerionwu, C., Oguikel, O. E., ... & Ike, A. C. (2025). A Comparative Study of Convolutional Neural Networks (CNN) Architectures on Microscopic Blood Film Images for Malaria Diagnosis. Journal of Image and Graphics, 13(4).
14. Kundu, T. K., Das, S., & Nidhya, R. (2025). Detection of Peripheral Blood Smear Malarial Parasitic Microscopic Images Utilizing Convolutional Neural Network. Generative Artificial Intelligence: Concepts and Applications, 121-142.
15. Mujahid, M., Rustam, F., Shafique, R., Montero, E. C., Alvarado, E. S., de la Torre Diez, I., & Ashraf, I. (2024). Efficient deep learning-based approach for malaria detection using red blood cell smears. Scientific Reports, 14(1), 13249.
16. Reddy C, K. K., PR, A., Almushharaf, A., Talla, R., Baili, J., Cho, Y., & Nam, Y. (2025). An Optimized Transfer Learning Approach Integrat-ing Deep Convolutional Feature Extractors for Malaria Parasite Classification in Erythrocyte Microscopy. Frontiers in Medicine, 12, 1684973.
17. Kafaf, D. A., Thamir, N. N., & AL-Hadithy, S. S. (2024). Malaria disease prediction based on convolutional neural networks. Journal of Applied Engineering and Technological Science (JAETS), 5(2), 1165-1181.
18. Xu, M., Cai, D., Yin, W., Wang, S., Jin, X., & Liu, X. (2025). Resource-efficient algorithms and systems of foundation models: A survey. ACM Computing Surveys, 57(5), 1-39.
19. Han, G. R., Goncharov, A., Eryilmaz, M., Ye, S., Palanisamy, B., Ghosh, R., ... & Ozcan, A. (2025). Machine learning in point-of-care testing: Innovations, challenges, and opportunities. Nature Communications, 16(1), 3165.
20. Kumar, C. M., & Sankar, J. S. (2024, June). Comparative Analysis of Convolutional Neural Networks for Brain Tumor Detection: A Study of VGG16, ResNet, Inception, and DenseNet Models. In 2024 3rd International Conference on Applied Artificial Intelligence and Computing (ICAAIC) (pp. 41-46). IEEE.
21. Thakuria, T., Rahman, T., Mahanta, D. R., Khataniar, S. K., Goswami, R. D., Rahman, T., & Mahanta, L. B. (2024). Deep learning for early diagnosis of oral cancer via smartphone and DSLR image analysis: a systematic review. Expert Review of Medical Devices, 21(12), 1189-1204.
22. Mohite, R. V., & Kakade, S. V. (2024). Leveraging Big Data Analytics and Artificial Intelligence for Early Detection and Diagnosis of Alzheimer's Disease. Frontiers in Health Informatics, 13(3).
23. Kumar, N. K., Vigneswari, D., Kavya, M., Ramya, K., & Druthi, T. L. (2018). Predicting non-small cell lung cancer: a machine learning paradigm. Journal of Computational and Theoretical Nanoscience, 15(6-7), 2055-2058.
24. Benachour, Y., Flitti, F., & Khalid, H. M. (2025). Enhancing Malaria Detection Through Deep Learning: A Comparative Study of Convolutional Neural Networks. IEEE Access.
25. Shahin, O. R., Alshammari, H. H., Alabdali, R. N., Salaheldin, A. M., & Saleh, N. (2025). Automated multi-model framework for malaria detection using deep learning and feature fusion. Scientific Reports, 15(1), 25672.
26. Swaathi, V. E., & Marndi, A. (2024, October). Comparative Analysis of Different Deep Learning Models for Malaria Detection. In International Conference on Sustainable and Innovative Solutions for Current Challenges in Engineering & Technology (pp. 193-203). Singapore: Springer Nature Singapore.
27. Ahmed, W. A., Mohammed, B. N., & Ibrahim, A. K. (2025). A Hybrid Approach for Malaria Classification using CNN-Based Feature Extraction and Traditional Machine Learning Classifiers. Science Journal of University of Zakho, 13(3), 342-347.
28. Folorunsho, O., Faboya, O. O., Mogaji, S. A., Willie, E., & Ochidi, I. (2025). Optimising Malaria Prediction from Cell Images Using Forward Selection and Support Vector Machine Classifier. University of Ibadan Journal of Science and Logics in ICT Research, 13(1), 109-117.
29. Saha, M., Bhaumik, R., Ranganath, A., Basu, M. T., & Pagadala, P. K. (2024, October). A Comprehensive Survey of Deep Learning Techniques in Malaria Diagnosi. In 2024 IEEE 6th International Conference on Cybernetics, Cognition and Machine Learning Applications (ICCCMLA) (pp. 61-66). IEEE.
30. Kumar, N. K., & Sikamani, K. T. (2021, March). Malarial Epidemic Resurge in India and its Future Implication. In 2021 7th International Conference on Advanced Computing and Communication Systems (ICACCS) (Vol. 1, pp. 193-198). IEEE.