

Full Length Article

A novel attention-enhanced hybrid deep learning approach for malaria diagnosis in microscopic cell images

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ARTICLE INFO

Keywords:

Malaria
Microscopy
Deep learning
Attention mechanism
Medical image classification
Diagnosis

ABSTRACT

Background: Malaria remains a major global public health challenge, transmitted through the bites of infected female mosquitoes. Despite progress in prevention and treatment, the disease continues to cause significant morbidity and mortality, especially among children and pregnant women. Conventional diagnostic methods relying on microscopic examination are time-consuming, dependent on skilled personnel, and prone to human error. Existing deep learning models for malaria detection often show limited performance and overfitting.

Methods: A hybrid deep learning model was developed by combining EfficientNetB0 with a custom convolutional neural network (CNN) enhanced by attention mechanisms to classify malaria-infected and uninfected red blood cell images. EfficientNetB0 provided pre-trained global feature extraction, while the custom CNN captured domain-specific features. The model was trained and evaluated using a publicly available malaria dataset.

Findings: The proposed hybrid model achieved a classification accuracy of 96.53%, precision of 94.80%, recall of 98.22%, F1-score of 95.95%, and an AUC of 99.12%. Attention maps offered interpretability by highlighting biologically relevant regions within cell images. Comparative experiments showed that the hybrid model outperformed standalone EfficientNetB0 and CNN architectures.

Interpretation: Integrating global and domain-specific feature representations significantly improves malaria image classification performance. The proposed hybrid model demonstrates strong potential for use in automated malaria diagnosis systems, supporting early detection and timely treatment.

1. Introduction

Malaria is a life-threatening disease caused by *plasmodium* parasites and transmitted to humans by certain infected mosquitoes, primarily prevalent in tropical regions. It is both preventable and treatable.¹ The latest World Malaria Report, according to the World Health Organisation (WHO), highlights an increase in malaria cases, rising to 263 million in 2023 from 252 million in 2022 across 83 countries. Meanwhile, malaria-related deaths slightly declined to 597,000 in 2023 from 600,000 in 2022. Vulnerable groups, such as pregnant women and children under five, face a higher risk of malaria, underscoring the need for prompt and precise diagnosis. A timely and accurate diagnosis is crucial to prevent complications and reduce transmission. Malaria screening involves analysing blood slides under a microscope to identify infected red blood cells, a process that can be time-intensive and laborious.² In addition, these traditional diagnostic methods, such as microscopy and Rapid Diagnostic Tests (RDTs), often face limitations like dependence on skilled personnel, susceptibility to human

error, and variable sensitivity, particularly in cases of low parasite-density infections.^{3,4} Malaria-infected blood smears are often dense and complex, with overlapping cells.⁵ As the infection advances, cell textures evolve, complicating the distinction between healthy and infected samples. This complexity can reduce the accuracy and efficiency of pathologists' visual analysis of blood smears.⁶ Rapid Diagnostic Tests (RDTs) have emerged as alternatives, offering faster results and easier field deployment. However, RDTs also exhibit limitations, including reduced sensitivity in low-transmission settings and potential for false-negative results, particularly with certain *Plasmodium* species.⁷

These challenges highlight the urgent need for innovative diagnostic methods that ensure accuracy, speed, and accessibility, particularly in resource-limited settings.⁸ Artificial Intelligence (AI) have demonstrated remarkable potential in addressing challenges in the healthcare industry.⁹ Early machine learning approaches in malaria detection relied on traditional methods such as rule-based systems

Peer review under the responsibility of Editorial Office of Informatics and Health.

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<https://doi.org/10.1016/j.infoh.2025.11.004>

Received 13 June 2025; Received in revised form 14 November 2025; Accepted 24 November 2025

Available online 3 March 2026

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and conventional statistical techniques, which proved insufficient for handling the complexity and variability inherent in microscopic image quality.^{10,11} Support Vector Machines (SVMs) and random forests brought improvements in classifying malaria-infected cells but struggled with high-dimensional data and complex patterns typical of medical images.¹² These traditional ML approaches faced significant limitations in generalisation across diverse populations and varying imaging conditions.¹³

The emergence of deep learning revolutionised medical imaging by providing end-to-end learning capabilities from extensive datasets.¹⁴ Deep neural networks, particularly CNNs, significantly enhanced malaria detection accuracy through automatic feature extraction and adaptation to new data.¹⁵ However, deep learning techniques present their own challenges, including requirements for large amounts of labelled training data and criticism regarding the lack of interpretability.^{16,17}

Due to this advancement, several researchers have used deep learning approaches to diagnose malaria. Shah et al.¹⁸ proposed a custom CNN for the classification of healthy and infected blood samples. The architecture comprises three convolutional layers followed by fully connected layers. The network employs a cascade of convolutional layers with multiple filters per layer. The model achieved 95% accuracy. Using the transfer learning approach, Vijayalakshmi and Rajesh Kanna¹⁹ utilised VGG for feature extraction and SVM to diagnose malaria infection in a malaria digital corpus. The model has an accuracy of 93.3%. Similarly, Gill et al.²⁰ used VGG19 and achieved over 90% accuracy. On the other hand, Prasher et al.¹ evaluated custom CNN and three different pretrained models, including InceptionNet, ResNet, and VGG19. InceptionNet performed best with an accuracy of 94.5%.

Kumar et al.²¹ explored the effectiveness of deep CNNs in malaria detection, highlighting the models' ability to learn intricate characteristics from image data that traditional methods often overlook. Oktovianus et al.²² conducted comprehensive benchmarking of CNN models specifically for malaria cell detection, providing crucial insights into model selection and performance optimisation. Their results confirmed the superiority of deeper architectures, such as ResNet, in capturing complex visual patterns compared to simpler models. Additionally, Kafaf et al.²³ analysed the predictive capabilities of CNNs for malaria disease detection, further contributing to the evidence supporting deep learning methodologies in epidemiological contexts.

Attention mechanisms have emerged as fundamental components in deep learning, particularly for image-based tasks, offering significant advantages in medical imaging and pattern recognition.²⁴ These mechanisms enable models to prioritise specific features or regions within images, enhancing their ability to discern relevant information from complex datasets. The integration of attention mechanisms allows for more refined analysis results, essential for accurate evaluations in clinical contexts.²⁵

Recent studies have demonstrated the transformative effects of attention mechanisms in medical image analysis. Papanastasiou et al.²⁶ examined the essential role of attention in medical image analysis, suggesting that while attention mechanisms are powerful, their effectiveness varies according to context and specific tasks. Lin et al.²⁷ discussed incorporating multiple attention mechanisms in convolutional neural networks to enhance MRI classification, further affirming the versatility of this approach.

Hybrid deep learning architectures have gained prominence by combining different types of neural networks to leverage their respective strengths, improving feature extraction and modelling capabilities.²⁸ These architectures effectively process various data modalities, such as integrating medical data and radiographic images to develop robust disease classification frameworks.^{29,30} In respiratory disease contexts, hybrid models have offered innovative solutions, with CNN-GRU combinations showing particular promise for disease detection and classification.³¹

Despite significant advancements in malaria diagnosis using deep learning, current models face several persistent limitations. Some studies are prone to overfitting and rely exclusively on either a pre-trained model (transfer learning) or a custom CNN, but rarely combine both. Most approaches lack interpretability, making it difficult for clinicians to trust or validate model decision-making processes. Additionally, many models do not effectively leverage spatial and contextual relationships in cell images, limiting diagnostic accuracy.

This study proposed a hybrid framework that balances the broad generalisation capabilities of a pre-trained model with the domain-specific feature learning of a custom CNN. Moreover, an attention mechanism is integrated into the hybrid architecture to enhance the model's ability to focus on malaria-infected regions, thereby capturing both global and malaria-specific features. The outcomes of this research will contribute to the development of practical, AI-driven diagnostic tools that can support early malaria detection and reduce the burden on healthcare systems in endemic regions. Its design aims to deliver superior classification performance compared to standard deep learning approaches.

This study addresses the following research question: *How can a hybrid deep learning approach, enhanced with attention mechanisms, improve the classification accuracy and interpretability of malaria-infected versus uninfected red blood cell images?* To answer this question, the study sets out to achieve the following objectives:

1. To develop a hybrid deep learning architecture combining EfficientNetB0 and a custom CNN for improved feature representation.
2. To integrate an attention mechanism to enhance model interpretability and focus on diagnostically relevant regions.
3. To evaluate the model's performance using standard classification metrics and compare it with baseline models.
4. To assess the model's potential for deployment in resource-limited settings through interpretability and efficiency analysis.

The remainder of the paper is structured as follows: Section 2 describes the proposed hybrid model and attention mechanism. Section 3 outlines the experimental setup and evaluation metrics. Section 4 presents and discusses the results. Finally, Section 5 concludes the paper and suggests directions for future work.

2. Materials and methods

This study focuses on the automated diagnosis of malaria from cell images using a novel hybrid deep learning model that combines EfficientNetB0 and a custom CNN, augmented with an attention mechanism. This section presents the dataset used, the preprocessing steps, and the methodology employed in model design and training.

2.1. Dataset description and preprocessing

The dataset comprises Giemsa-stained thick blood smear slides from *Plasmodium vivax*-infected patients and uninfected patients obtained from sourced from the U.S. National Library of Medicine (NLM).³² It contains 27,558 Red blood cells (RBCs) from Giemsa-stained thin blood slides of the image. It entails infected cells and an equal number of uninfected cell images, thereby providing a balanced and diverse dataset for model training and evaluation. It is important to note that While malaria infections can be caused by five different Plasmodium species with distinct clinical presentations and treatment requirements, the current dataset does not differentiate between species. To ensure uniformity and compatibility with the model's input requirements, all images were resized to dimensions of 200 × 200 pixels. Pixel values were normalised to the [0,1] range through rescaling by dividing by 255. This improves training stability and convergence speed by ensuring that input features (pixel intensities) are within a range conducive to gradient-based optimisation. The dataset was divided into

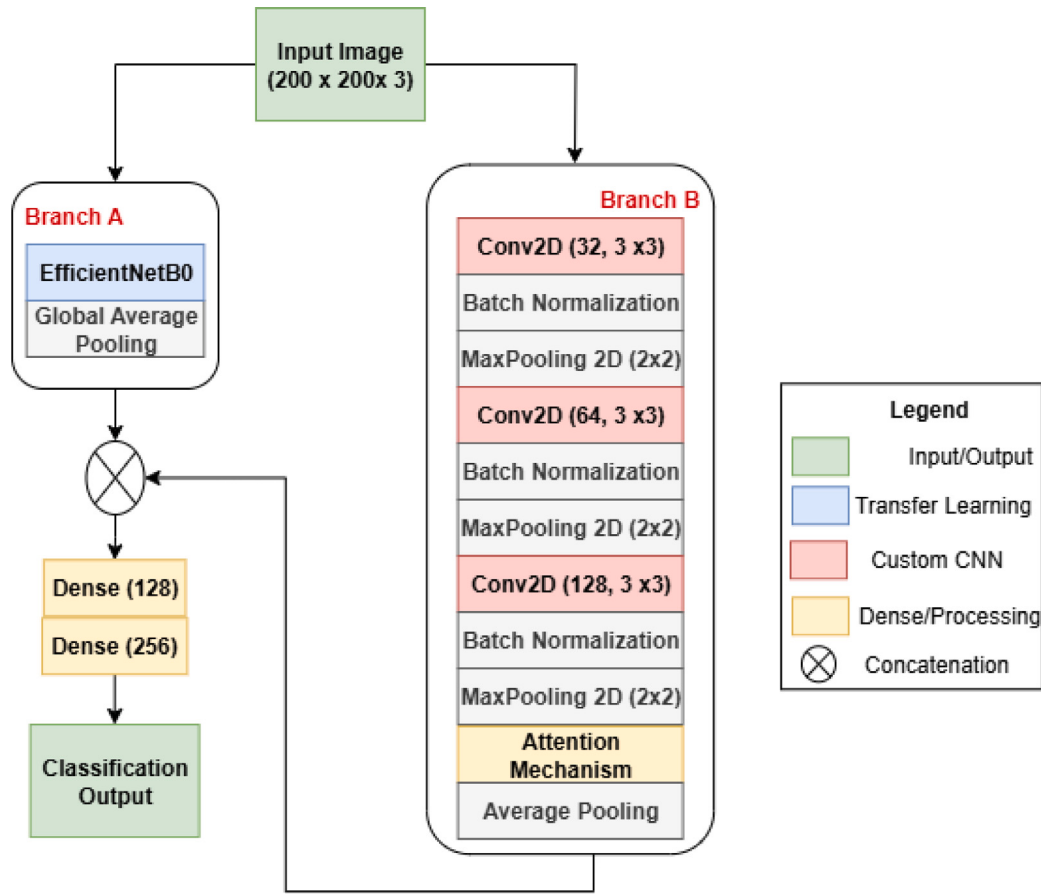


Fig. 1. The Hybrid Model Architecture for Malaria Diagnosis.

80% training and 20% testing to evaluate the model, as done by existing works.^{18,19} Stratified splitting was used to maintain equal class distribution across training, validation, and test sets, ensuring reliable performance metrics.

2.2. The developed attention-enhanced model

The developed model combines transfer learning with a custom-designed feature extraction pathway specifically tailored for malaria parasite detection, as shown in Fig. 1. The architecture consists of two parallel branches: a pre-trained EfficientNetB0 base model that leverages general visual features learned from the ImageNet dataset, and a custom CNN branch designed to capture malaria-specific features. The first branch (Branch A) of the architecture incorporates EfficientNetB0 pre-trained on ImageNet, as shown in Fig. 1. All weights in the branch were frozen to prevent large gradient updates that could destroy the useful representations already learned. Features extracted from the EfficientNetB0 model were processed through a global average pooling layer to reduce dimensionality while preserving spatial information. EfficientNetB0 was chosen due to its superior parameter efficiency (fewer parameters for comparable performance), compound scaling method that balances network depth, width, and resolution and lower computational cost.³³

The second branch (Branch B) consists of a specialised CNN designed to detect features unique to malaria parasites. The branch includes three convolutional blocks, each containing a 2D convolutional layer with increasing filter sizes (32, 64, and 128) and Max pooling for down-sampling. An attention mechanism was incorporated after the final convolutional block to help the model focus on regions of interest that are most relevant to parasite detection.³⁴ The model training entails a two-phase approach: In the first phase, only the

custom CNN branch was trained and the classification head, while keeping the EfficientNetB0 weights frozen. This allowed the model to learn malaria-specific features without disrupting the pre-trained general features. In the second phase, we unfreeze the EfficientNetB0 base model. In addition, it allowed for minor adjustments to the pre-trained weights, adapting them to the specific characteristics of malaria cell images. Mathematically, the proposed model is formulated as:

2.2.1. Mathematical formulation of the proposed model

Let $D = \{x_i, y_i\}_{i=1}^N$ denote the dataset, where each $x_i \in \mathbb{R}^{H \times W \times C}$ represents a microscopic image of a red blood cell with height, width, and colour channels (RGB). The corresponding label $y_i \in \{0, 1\}$ indicates whether the cell is uninfected (0) or infected with malaria parasites (1).

The goal is to learn a function $f : \mathbb{R}^{H \times W \times C} \rightarrow [0, 1]$ that maps each input image to a probability score, indicating the likelihood of infection.

The proposed model consists of two parallel feature extractors:

1. **EfficientNetB0 Backbone:** A pre-trained EfficientNetB0 model extracts high-level semantic features from the input image. This produces a feature vector $z^{(e)} \in \mathbb{R}^{d_e}$.
2. **Custom CNN Module:** A lightweight CNN, designed specifically for this task, is used to extract localised and domain-specific features from the same input image. This yields a second feature vector $z^{(c)} \in \mathbb{R}^{d_c}$.

The two feature vectors are concatenated to form a unified feature representation:

$$z = [z^{(e)}, z^{(c)}] \in \mathbb{R}^d \quad (1)$$

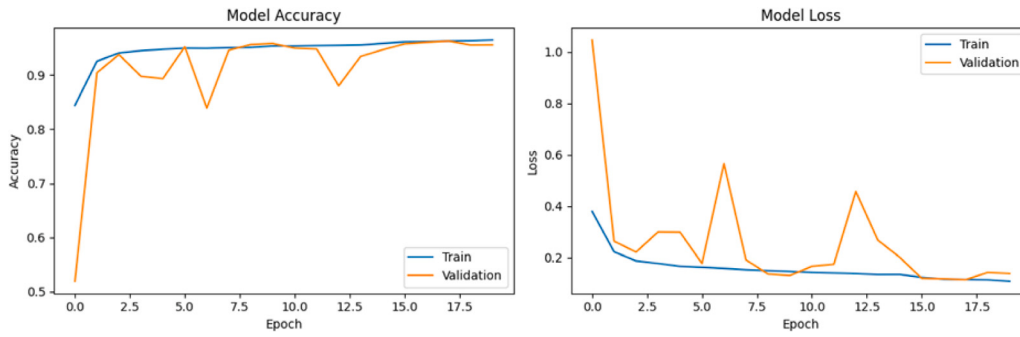


Fig. 2. The training and testing loss and accuracy of the model.

, where $d = d_e + d_c$. An attention mechanism is applied to the concatenated vector to enhance the model's focus on diagnostically relevant features. Let $\alpha \in \mathbb{R}^d$ denote the attention weight vector, computed as

$$\alpha = \text{softmax}(W_a) \cdot \tanh(W_z z + b_z) \quad (2)$$

where W_z , W_a and b_z are trainable parameters. The element-wise product between α and z produces the attention-weighted feature vector:

$$\hat{z} = \alpha \odot z \quad (3)$$

The resulting vector $\hat{z}$ from Eq. (3) is passed through a fully connected layer with a sigmoid activation to obtain the final prediction:

$$\hat{y} = \sigma(W_o \hat{z} + b_o) \quad (4)$$

Where W_o and b_o are trainable weights and biases, and denotes the sigmoid function, ensuring $\hat{y} \in [0, 1]$. The model is trained using the binary cross-entropy loss function:

$$L = -\frac{1}{N} \sum_{i=1}^N [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)] \quad (5)$$

The objective is to optimise all model parameters θ , including those of EfficientNetB0, the custom CNN, and the attention module, by minimising the loss:

$$\theta \leftarrow \argmin_{\theta} L(\theta) \quad (6)$$

This formulation enables the model to learn a robust combination of global and local features while using attention to enhance interpretability and focus on critical image regions for accurate malaria diagnosis.

2.3. Model explainability and interpretability

Here, visual explanation mechanisms addressed the critical need for transparency in medical AI systems. Interpretability is particularly important in malaria diagnosis, where clinicians must understand the basis for model predictions to establish trust and enable integration into clinical workflows. Gradient-weighted Class Activation Mapping (Grad-CAM) was implemented to visualise the regions of input images that most influenced the model's classification decisions. This technique generates heatmaps highlighting areas that strongly activate the network when making specific predictions, providing critical insight into the model's decision-making process.³⁵ The integration of attention mechanisms enhances the proposed model's diagnostic performance and improves transparency by highlighting clinically relevant regions within cell images. The effectiveness of this approach is evaluated through extensive experiments, as detailed in the following section.

3. Results

This section presents the performance evaluation of the proposed hybrid deep learning model for malaria diagnosis in cell images. The

Table 1
Summary of the model performance.

Metrics	Hybrid Model	EfficientNet Two-phase	EfficientNet Single-phase	Custom CNN+ATT	Custom CNN
Accuracy (%)	96.53	96.08	60.33	96.42	96.01
Precision (%)	94.80	94.55	71.41	94.34	94.34
Recall (%)	98.22	97.52	30.08	98.50	97.61
F1-Score (%)	95.95	96.01	42.33	96.38	95.95
AUC (%)	99.12	99.19	68.63	99.24	99.23

training dataset was allocated for model training, while the testing set was utilised for validation. The model's performance was assessed using accuracy, precision, recall, and area under the receiver operating characteristic curve (AUC) as evaluation metrics. Adam optimiser with an initial learning rate of 0.001 was used. The hybrid model demonstrated superior classification performance across all evaluation metrics compared to baseline models. Table 1 summarises the results on the test dataset.

The proposed hybrid model achieved the highest overall classification performance with an accuracy of 96.53%, a high recall of 98.22%, and a robust AUC of 99.12%, indicating its ability to reliably distinguish between infected and uninfected cell images. Although the EfficientNetB0 with two-phase training demonstrated comparable performance, it slightly lagged in recall and accuracy. Conversely, the EfficientNetB0 single-phase training model significantly underperformed, with an accuracy of only 60.33% and a recall of 30.08%, highlighting the importance of gradual fine-tuning in transfer learning. The custom CNN model with attention achieved performance close to the hybrid model, indicating the value of attention mechanisms. However, the hybrid approach's ability to balance global and domain-specific feature learning led to marginally better outcomes. The hybrid model demonstrated strong diagnostic performance; its high recall is clinically critical as it minimises false negatives. Moreover, these results show promise for meeting WHO standards for malaria diagnostics, where a sensitivity of >95% is recommended, though clinical validation is required to confirm real-world performance.

The learning curve of the model is shown in Fig. 2. Demonstrates stable convergence over the 20 epochs. The loss curves indicate a rapid reduction in error within the initial epochs, suggesting effective feature learning. Occasional spikes in validation loss are smoothed out in later epochs, affirming the robustness of the model.

Fig. 3. showcases the confusion matrix which further affirms the model's strong classification performance.

Based on the confusion matrix, the model exhibits minimal misclassification errors indicating high reliability for malaria parasite detection in cell images. The effectiveness of the hybrid model is further validated using Grad-CAM as shown in Fig. 4. These Grad-CAM visualisations highlight biologically relevant areas in the uninfected cell images, providing insight into the model's decision-making process. The heatmaps demonstrate that the model consistently focuses on critical

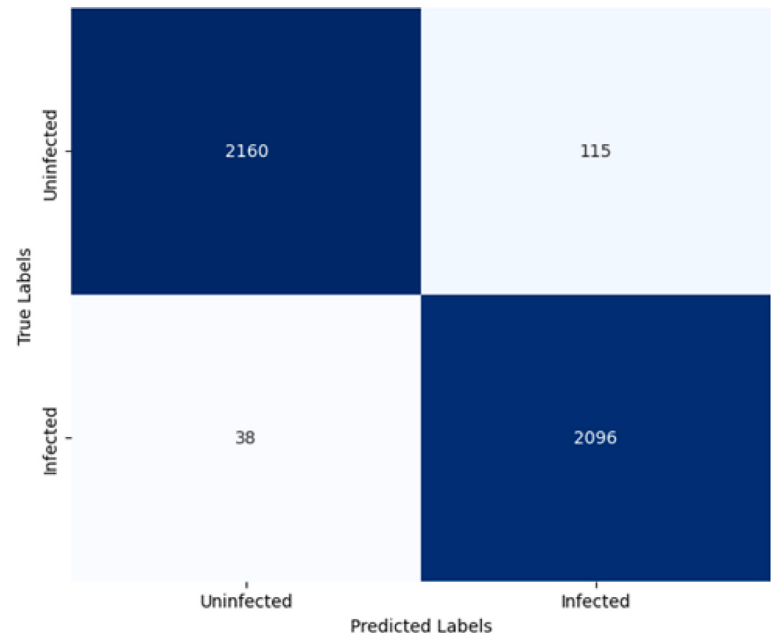


Fig. 3. Confusion Matrix Visualisation of the model on the testing set.

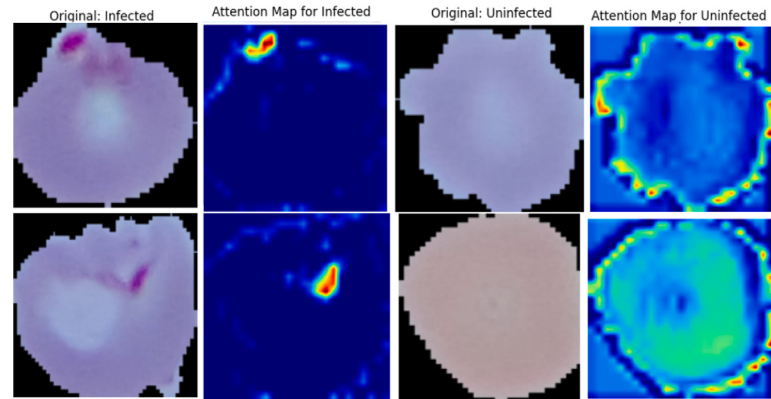


Fig. 4. Grad-CAM heatmap visualisations for infected and uninfected malaria cell image samples.

Table 2
Comparison of the proposed model with existing state-of-the-art studies.

Reference	Method	Accuracy	F1-Score	Precision	Recall
Delgado-Ortet et al. ³⁶	CNN	93.72	–	–	–
Irmak ³⁷	CNN	95.28	–	95.1	95.5
Negi et al. ³⁸	CNN	95.70	96	96	96
Vijayalakshmi and Rajesh Kanna ¹⁹	VGG19+SVM	93.1	91.66	89.95	93.44
Prasher et al. ¹	Inception	94.5	–	–	–
This study	Hybrid	96.53	94.80	98.22	95.95

cellular structures associated with infection status, thereby enhancing interpretability and trustworthiness. This ability to localise meaningful features without explicit pixel-level annotations underscores the advantage of incorporating Grad-CAM for explainability in medical image classification tasks.

Based on the visualisation pattern in Fig. 4, for infected cells, there is high attention at the cell periphery where parasites can be located and for uninfected cells, the attention is more distributed or focused on specific internal features.

The results of the proposed approach are compared with those of previously published studies on malaria detection that utilised the same dataset. Table 2. Showcases the results of the comparison.

4. Discussion

Malaria remains a critical global health threat, with severe complications arising from delayed or inaccurate diagnosis. If left untreated, it can result in severe complications, including organ failure, anaemia, hypoglycaemia, respiratory distress, coma, and potentially death.³⁹ This study introduced a hybrid deep learning model integrating EfficientNetB0 and a custom CNN architecture, enhanced with an attention mechanism, to address the challenges of malaria detection from microscopic cell images. The proposed model achieved an accuracy of 96.53%, outperforming individual baseline models and demonstrating

the benefits of two-phase fine-tuning in transfer learning. Attention-based visualisation using Grad-CAM confirmed the model's ability to highlight biologically meaningful regions without manual annotation, thus improving both interpretability and trustworthiness. Compared to existing models, the proposed approach achieves higher diagnostic accuracy with greater computational efficiency, meeting WHO diagnostic standards and making it suitable for low-resource environments. Nevertheless, while the results are promising, real-world clinical validation remains necessary to fully assess the model's deployment feasibility.

4.1. Theoretical contributions

This study advances the theoretical understanding of how hybrid deep learning architectures, integrating both pre-trained global feature extractors and custom domain-specific models, can enhance malaria diagnosis in microscopic imaging. By demonstrating that attention mechanisms can be effectively employed to highlight biologically relevant regions without explicit annotations, the findings support the growing theoretical emphasis on interpretable AI in medical imaging. The results also contribute to the theory that lightweight, efficient models can achieve state-of-the-art performance without requiring prohibitively large computational resources, thereby challenging the traditional reliance on excessively deep or complex architectures for medical diagnostics.

4.2. Methodological contributions

Methodologically, this study introduces a hybrid attention-enhanced deep learning pipeline that strategically combines EfficientNetB0's global feature extraction capabilities with a lightweight, task-specific CNN. The two-phase fine-tuning approach ensures better model adaptation to the malaria domain compared to single-phase transfer learning, which underperformed significantly. In addition, the integration of Grad-CAM for attention validation provides a novel way to quantitatively and qualitatively assess model interpretability, offering an important methodological contribution for future AI-based diagnostic research.

4.3. Managerial and practical implications

From a practical perspective, the hybrid model's high sensitivity and computational efficiency suggest it is well-suited for deployment in resource-constrained healthcare settings, where access to expert microscopists is limited. The ability to achieve WHO-compliant diagnostic performance while requiring lower hardware specifications opens opportunities for integration into automated microscopy systems, mobile health units, and point-of-care diagnostic tools. In addition, the enhanced interpretability facilitated by attention mechanisms and Grad-CAM visualisations can foster greater trust among healthcare providers, potentially accelerating the adoption of AI-based diagnostics in clinical practice.

4.4. Limitations, future directions and implementation considerations

Despite the promising results, the study has certain limitations. The model has not yet been validated using prospective clinical data, and its performance has only been assessed on publicly available datasets. Future work will focus on prospective clinical trials to validate the model's performance in live diagnostic settings. Furthermore, extending the current binary classification framework to a multi-class system capable of distinguishing between different malaria stages could provide more granular diagnostic support, aiding targeted treatment strategies. Additionally, the proposed model addresses the fundamental challenge of detecting malaria infection presence but does not differentiate between *Plasmodium* species. In clinical practice, species identification is

critical as *P. falciparum* infections require urgent treatment due to potential for severe complications, while *P. vivax* infections may require different treatment protocols including liver-stage elimination therapy. The future study will look into species infection classification. As AI technologies become increasingly integrated into healthcare diagnostics, ethical considerations must be addressed. Ensuring transparency, minimising algorithmic bias, and maintaining clinician oversight are essential for responsible deployment. Also, protecting patient data privacy and maintaining equitable access to diagnostic technologies are critical challenges that must be addressed in future deployment efforts.

5. Conclusions

This study introduced a hybrid deep learning model combining EfficientNetB0 and a custom CNN, augmented with attention mechanisms, for automated malaria diagnosis. The two-phase transfer learning strategy enabled effective adaptation of pre-trained features to the malaria imaging domain, resulting in consistent performance improvements over individual baseline models. The proposed hybrid architecture achieved superior accuracy, recall, and AUC while maintaining model interpretability through attention-based visualisations, thereby reinforcing the value of combining pre-trained networks with domain-specific feature extractors. Nevertheless, the study has certain limitations. Validation was performed exclusively on retrospective data, and prospective clinical evaluation is required to fully assess the model's real-world applicability. Furthermore, the binary classification framework limits clinical utility compared to multi-class approaches capable of staging infections or differentiating between parasite species. Despite these limitations, the proposed system demonstrates potential for deployment in resource-constrained healthcare environments where rapid and accurate malaria diagnosis is critical. Future research will aim to extend the model to multi-class classification tasks, conduct clinical trials in operational settings, and explore lightweight, mobile-compatible implementations integrated with clinical decision support systems to enhance accessibility and impact.

Ethics statement

As this research involved only secondary analysis of anonymized, pre-existing images and did not involve direct interaction with human participants, animals, or sensitive personal data, ethical approval and informed consent were not required for this specific study.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

CRediT authorship contribution statement

Oladosu Oyebisi Oladimeji: Writing – review & editing, Writing – original draft, Visualization, Methodology, Investigation, Conceptualization. **Ayodeji Olusegun Ibitoye:** Writing – review & editing, Writing – original draft, Supervision, Investigation.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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