

Advancements in Deep Learning for Malaria Detection: A Comprehensive Overview

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Abstract—Malaria remains a critical global health issue, with millions of cases reported annually, particularly in resource-limited regions. Timely and accurate diagnosis is vital to ensure effective treatment, reduce complications, and control transmission. Conventional diagnostic methods, including microscopy and Rapid Diagnostic Tests (RDTs), face considerable limitations such as dependency on skilled personnel, limited sensitivity at low parasitemia levels, and cost constraints. In response, deep learning technologies—especially Convolutional Neural Networks (CNNs)—have emerged as promising tools to overcome these barriers by enabling automated diagnostics based on medical imaging, significantly enhancing precision and scalability. This paper presents a comprehensive review of recent advances in deep learning for malaria diagnosis, highlighting the role of publicly available datasets in driving innovation. It analyzes leading architectures—such as ResNet, VGG, and YOLO—based on their classification performance, including accuracy, sensitivity, and computational efficiency. Furthermore, the review discusses novel directions such as mobile-integrated diagnostics and multi-modal data fusion, which can enhance diagnostic accessibility in low-resource settings. Despite notable progress, challenges remain in terms of dataset imbalance, lack of generalizability, and barriers to clinical deployment. The paper concludes by outlining future research directions and emphasizing the need for robust, adaptable models that can support global malaria control and eradication strategies.

Keywords—Malaria detection; deep learning; Convolutional Neural Networks (CNNs); medical imaging; automated diagnostics

I. INTRODUCTION

Malaria remains one of the most significant global health challenges; this affects millions of individuals annually, particularly in resource-limited regions such as sub-Saharan Africa, Southeast Asia and Latin America. According to the World Health Organization (WHO) over 247 million cases were reported in 2021, with a disproportionate impact on children under five and pregnant women [1]. Early and accurate detection of malaria is critical for effective treatment, prevention of severe complications and reducing transmission rates. The availability of reliable diagnostic tools can directly contribute to reduce the global malaria burden and advance efforts toward its eradication.

Traditional diagnostic methods which include microscopy and Rapid Diagnostic Tests (RDTs) have been widely used for malaria detection. Microscopy, considered the gold standard, involves examining stained blood smears under a microscope to identify malaria parasites [2]. However, this method is labor-intensive, time-consuming and highly dependent on the skill of trained personnel. Similarly, RDTs, although faster and more accessible, often lack sensitivity particularly at low parasite

densities or in mixed infections [3, 4]. Molecular techniques like Polymerase Chain Reaction (PCR) provide higher precision but are costly and require sophisticated infrastructure. This makes them impractical in many malaria-endemic regions [5, 6]. These limitations underscore the need for innovative, automated and scalable diagnostic approaches.

Recent advancements in deep learning have shown transformative potential in malaria detection. Convolutional Neural Networks (CNNs) and other deep learning architectures have demonstrated the ability to analyze blood smear images with accuracies exceeding 95%, achieving performance comparable to or even surpassing traditional diagnostic methods [7, 8]. Furthermore, lightweight and efficient models tailored for mobile applications are expanding access to automated diagnostics in remote and underserved areas [9]. Deep learning enables rapid, accurate and consistent diagnostics. Significantly, it reduces dependence on human expertise and supports large-scale epidemiological monitoring.

This paper provides a comprehensive overview of the advancements in deep learning applied to malaria detection. It explores publicly available datasets, state-of-the-art architectures and their performance metrics. By analyzing the strengths and limitations of various approaches, this review aims to identify key gaps and propose potential future directions. Specifically, this paper seeks to:

- Highlight the significance of publicly available datasets, such as the NIH dataset and Delgado Dataset B and their role in advancing malaria detection research [10, 11].
- Evaluate the performance and applicability of deep learning architectures such as ResNet, VGG, YOLO and hybrid models [12, 13, 14].
- Discuss the challenges faced in deploying these models in real-world scenarios, including resource-limited environments [15, 16].
- Propose strategies to address dataset limitations, model generalization and integration into healthcare systems [17, 14].

This article has been structured to provide a comprehensive overview of advancements in deep learning for malaria detection. Section I introduced the global impact of malaria and the challenges associated with traditional diagnostic methods. Section III presented an overview of publicly available datasets, highlighting their characteristics and limitations. Section IV discussed deep learning architectures and hybrid models, emphasizing their strengths and weaknesses in malaria detection. Section V compared the performance of various

models, with a focus on metrics such as accuracy, sensitivity and computational efficiency, while also analyzing the impact of dataset characteristics. Section VI synthesized the key findings, addressed challenges in scalability and robustness, and proposed future directions. Finally, Section VII concluded the paper by summarizing the key contributions and outlining potential avenues for further research and implementation in real-world healthcare settings.

II. RELATED WORK

Several studies have explored the use of deep learning techniques in the detection and diagnosis of malaria from microscopic blood smear images. This section presents a comparative analysis of prominent contributions in this domain, highlighting the methods used, datasets employed, and performance outcomes.

A. CNN-Based Malaria Detection Approaches

Early works, such as that by Rajaraman et al. [10], utilized convolutional neural networks (CNNs) trained on publicly available thin smear datasets, achieving accuracy levels above 95%. Similarly, Vijayalakshmi and Kanna [18] proposed a transfer learning model based on VGG19-SVM, reporting an accuracy of 93.1%. More recent approaches, including the work of Sriporn et al. [19], integrated state-of-the-art CNN architectures like Xception and ResNet-50, obtaining F1-scores exceeding 98%.

B. Use of Object Detection and Multi-Class Models

In contrast to binary classification models, Manescu et al. [20] developed an end-to-end object detection pipeline for detecting parasites in Thick Blood Films (TBF) using DeepMCNN, which achieved expert-level sensitivity (0.92) and specificity (0.90). This work also provided parasite load estimates, contributing toward WHO-compliant diagnostic standards.

C. Dataset Variability and Limitations

Most studies rely on the NIH malaria dataset, which, although accessible, is limited in terms of geographic diversity and class imbalance. Yunda et al. [21] explored detection of *P. vivax* parasites using wavelet-based features and PCA, illustrating the potential for species-specific classification, though with lower true positive rates ($\sim 77\%$).

D. Comparison and Limitations of Prior Work

A comparative analysis of key deep learning-based studies for malaria detection is essential to identify prevailing strengths, methodological trends, and common limitations in the field. Table I summarizes representative works, highlighting the models employed, datasets used, and reported accuracy or sensitivity metrics. This comparison facilitates a critical understanding of performance benchmarks and underscores the need for generalizable and clinically deployable diagnostic models.

TABLE I. SUMMARY OF PRIOR DEEP LEARNING-BASED MALARIA DETECTION STUDIES

Authors	Models/Methods	Datasets	Accuracy (%)
Rajaraman et al. (2018) [10]	Pretrained CNN	NIH Dataset	95.0
Vijayalakshmi et al. (2019) [8]	VGG19 + SVM	Custom Dataset	93.1
Sriporn et al. (2020) [19]	Xception, ResNet	7k Image Set	99.3
Manescu et al. (2020) [20]	DeepMCNN	Clinical TBF Images	92.0 (Sens.)

E. Positioning of the Present Study

While the aforementioned studies demonstrate the utility of CNNs for malaria diagnosis, they often overlook integration with mobile platforms, generalizability across datasets, or WHO-aligned parasitemia estimation. The present study builds upon these foundations by reviewing recent deep learning models in conjunction with dataset limitations, emerging trends in mobile diagnostics, and strategies for real-world deployment.

III. PUBLICLY AVAILABLE DATASETS FOR MALARIA DETECTION

The availability of publicly accessible datasets has been instrumental in advancing deep learning research for malaria detection. They provide a foundation for training, validation and benchmarking of models in diverse diagnostic scenarios.

A. Overview of Datasets

Datasets play a critical role in advancing deep learning applications for malaria detection. Datasets provide the necessary labeled data to train and evaluate models. Publicly available datasets have enabled researchers to benchmark the performance of various architectures and facilitate reproducibility in research. This section provides an overview of four widely used datasets, highlighting their characteristics and significance in the field.

1) *NIH dataset*: The NIH Dataset is one of the most widely used datasets for malaria detection research due to its size and quality. It consists of 27,558 labeled cell images, classified into two categories: parasitized and uninfected cells [7, 11]. The images are derived from thin blood smears and are suitable for training deep learning models for binary classification tasks. This dataset is balanced and well-annotated which supports robust training and evaluation. Its large size and diversity have enabled models such as ResNet and DenseNet to achieve high accuracy, often exceeding 95%. However it primarily focuses on binary classification and does not account for variations in *Plasmodium* species which limits its use for species-specific tasks.

2) *Delgado dataset B*: Delgado Dataset B consists of 331 high-resolution images of Giemsa-stained thin blood smears [3]. This dataset is particularly valuable for fine-grained analysis and morphological studies of malaria parasites. Its high-quality images enable the evaluation of advanced architectures such as ResNet and YOLO which rely on detailed visual features. Although smaller in size compared to the NIH Dataset, Delgado Dataset B provides valuable insights into the

structural characteristics of parasitized cells. Its limited size necessitates the use of data augmentation or transfer learning techniques to achieve robust model performance.

3) *Dijkstra dataset*: The Dijkstra Dataset comprises 883 images of thick and thin blood smears primarily focusing on *Plasmodium falciparum* detection [22]. This dataset offers diversity in smear types and enables researchers to evaluate model performance across different diagnostic settings. The inclusion of both thick and thin smears makes it a unique resource for testing models designed to generalize across various smear preparation techniques. Despite its strengths, the dataset's limited size poses challenges for training deep neural networks without the aid of data augmentation or pre-trained models.

4) *Malaria-LMIC dataset*: The Malaria-LMIC Dataset [23, 16] simulates real-world conditions encountered in low-resource settings with approximately 5,000 images. This dataset is characterized by challenges such as low image quality, diverse environmental conditions and class imbalance. These attributes make it ideal for testing the robustness and adaptability of deep learning models. By replicating real-world scenarios, the dataset emphasizes the importance of lightweight architectures and efficient preprocessing techniques to handle noisy and diverse inputs. It is particularly useful for evaluating the feasibility of deploying models in resource-constrained environments.

Table II summarizes the characteristics of these datasets and provides a quick reference for researchers to identify the most suitable dataset for their specific tasks.

TABLE II. PUBLICLY DATASETS FOR MALARIA DETECTION

Dataset	Size	Key Features
NIH Dataset	27,558	Balanced classes, binary classification, thin smears
Delgado Dataset B	331	High-resolution images, morphological analysis
Dijkstra Dataset	883	Thick and thin smears, <i>P. falciparum</i> focus
Malaria-LMIC Dataset	5,000	Real-world conditions, low image quality, class imbalance

These datasets collectively provide a foundation for advancing deep learning research in malaria detection. Their unique characteristics cater to diverse research needs, ranging from robust binary classification to handling real-world diagnostic challenges.

B. Dataset Characteristics

The quality and characteristics of datasets play a crucial role in determining the effectiveness and reliability of deep learning models for malaria detection. This subsection examines the size, diversity, and class balance of commonly used datasets and analyzes their impact on model performance.

1) *Size, Diversity and Class Balance*: Datasets for malaria detection vary significantly in terms of size, diversity and class distribution which directly influence the robustness and generalizability of trained models. Larger datasets, such as the NIH dataset containing over 27,000 labeled cell images, provide extensive training opportunities, enabling models to learn complex patterns and achieve better generalization [11].

However, smaller datasets like the Delgado Dataset B (331 images) often require augmentation or transfer learning techniques to compensate for their limited size [14].

Diversity is another critical factor, as datasets should encompass images from different populations, geographical regions and imaging conditions. Datasets such as the Malaria-LMIC dataset attempt to replicate real-world variability by including low-quality and diverse smear images, simulating the challenges encountered in resource-constrained environments [23].

Class balance also plays a vital role in model performance. Many datasets exhibit imbalanced distributions, with a significantly higher number of uninfected cells compared to parasitized ones. This imbalance can lead to biased models that perform poorly on minority classes, such as parasitized cell detection. Addressing this imbalance through data augmentation or synthetic oversampling is essential for improving model fairness and reliability.

Table III summarizes the key characteristics of commonly used datasets for malaria detection.

TABLE III. CHARACTERISTICS OF COMMON MALARIA DETECTION DATASETS

Dataset	Size	Diversity	Class Balance
NIH Dataset	27,558 images	High	Balanced
Delgado Dataset B	331 images	Low	Imbalanced
Dijkstra Dataset	883 images	Medium	Balanced
Malaria-LMIC Dataset	5,000 images	High	Imbalanced

2) *Impact on model performance*: Dataset characteristics have a profound impact on the performance of deep learning models. Larger datasets, such as the NIH dataset, contribute to higher model accuracy and generalizability due to their extensive data coverage [7]. In contrast, models trained on smaller datasets, like Delgado Dataset B, often exhibit overfitting and reduced robustness unless enhanced by transfer learning or data augmentation techniques [12].

Diverse datasets are crucial for ensuring that models can generalize across varied clinical settings and imaging conditions. For instance, the Malaria-LMIC dataset, despite its smaller size, provides valuable insights into real-world scenarios by incorporating low-quality images which helps evaluate the robustness of models under challenging conditions [23]. Class imbalance, if not addressed, can significantly impact performance metrics such as sensitivity and specificity, particularly in detecting parasitized cells.

The importance of dataset characteristics is visually represented in Fig. 1 and Fig. 2. Fig. 1 highlights the disparity in dataset sizes, while Fig. 2 emphasizes the relative importance of key attributes, such as image quality, size, diversity and class balance, in determining model effectiveness.

Understanding and addressing these dataset characteristics is essential for building robust, scalable and clinically viable deep learning models for malaria detection.

C. Challenges with Existing Datasets

The effectiveness of deep learning models in malaria detection largely depends on the quality, diversity and represen-

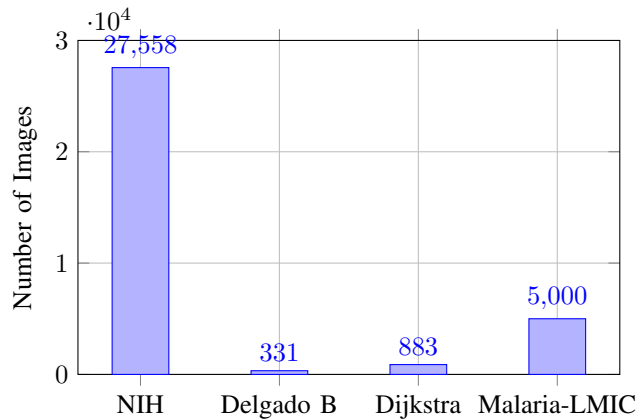


Fig. 1. Dataset sizes for malaria detection.

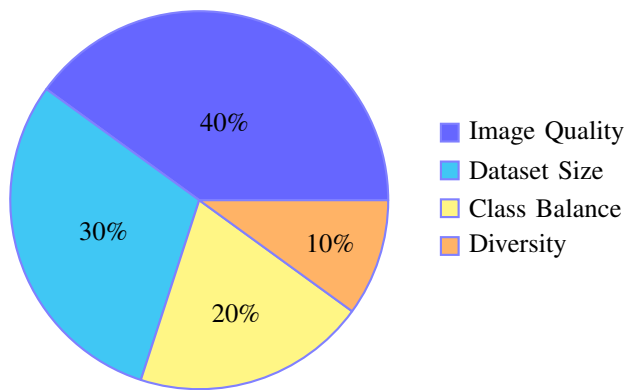


Fig. 2. Dataset characteristics.

tativeness of the datasets used during training and evaluation. However, existing datasets face several challenges that limit their applicability and generalization to real-world scenarios.

The statistics depicted in Fig. 2 highlight the relative importance of various dataset characteristics in determining the performance of deep learning models for malaria detection. Image quality accounts for 40% of the impact, emphasizing the significance of high-resolution, well-annotated images for extracting meaningful features. Dataset size contributes 30%, underlining the importance of large datasets to ensure robust learning and generalization. Class balance, representing 20%, addresses the need to mitigate biases caused by imbalanced datasets which can lead to skewed predictions. Finally, diversity constitutes 10% and reflects the role of heterogeneous imaging conditions and geographic variations in enhancing model adaptability and robustness across real-world settings.

1) *Limited diversity and annotation quality*: Most publicly available datasets, such as the NIH dataset [7], consist of images collected under controlled conditions with limited geographical and environmental diversity. These datasets often fail to capture the variations in blood smear preparation, staining techniques and imaging equipment prevalent across different regions. As a result, models trained on such datasets may exhibit reduced performance when applied to samples from diverse clinical settings.

Annotation quality is another critical issue. The process of labeling blood smear images requires significant domain expertise, especially for identifying parasitized cells and distinguishing between different *Plasmodium* species. Errors or inconsistencies in annotations can introduce biases, leading to inaccurate predictions and reduced model reliability [14].

To illustrate the distribution of dataset diversity and quality challenges, Table IV summarizes the characteristics of major malaria detection datasets, while Fig. 3 highlights the importance of key dataset attributes such as diversity, quality and size.

2) *Class imbalance and its implications*: Class imbalance is a prevalent issue in malaria datasets, where the number of uninfected cell images often exceeds that of parasitized cell images. This imbalance can lead to biased models that are overly sensitive to the majority class, reducing sensitivity and recall for detecting infected cells [23]. Addressing this imbalance is crucial, as it directly impacts the ability of models to accurately diagnose malaria, particularly in low-parasitemia samples.

Data augmentation techniques, such as synthetic data generation, flipping and rotation, have been employed to mitigate class imbalance. However, these approaches often fall short of replicating the complexity and variability of real-world data. Fig. 3 visually represents the impact of class imbalance and dataset characteristics on model performance.

TABLE IV. CHARACTERISTICS OF MAJOR DATASETS FOR MALARIA DETECTION

Dataset	Image Type	Size	Key Features
NIH Dataset	Cell images	27,558	Parasitized/Uninfected, Thin Smears
Delgado Dataset B	Thin smears	331	High-Resolution, Giemsa-Stained
Dijkstra Dataset	Thick and Thin Smears	883	Focus on <i>Plasmodium falciparum</i>
Malaria-LMIC	Real-world images	5,000	Diverse, Low-Quality Challenges

IV. DEEP LEARNING ARCHITECTURES FOR MALARIA DETECTION

The rapid advancements in deep learning have revolutionized the field of medical imaging and offer innovative solutions for automated malaria detection by leveraging powerful CNNs and other state-of-the-art architectures.

A. Convolutional Neural Networks (CNNs)

CNNs are fundamental in applying deep learning to malaria detection, excelling in automatically extracting hierarchical features from medical images. This subsection reviews key CNN architectures—ResNet [24], VGG [8], YOLO [25], MobileNet [15], and DenseNet [13]—highlighting their advantages and drawbacks in malaria diagnostics. ResNet’s residual learning enables very deep models but may be computationally heavy. VGG offers simplicity and strong feature extraction at a high resource cost. YOLO is valued for real-time detection, ideal for field diagnostics. MobileNet provides efficient lightweight performance for mobile platforms. DenseNet enhances feature reuse and accuracy but requires significant computation.

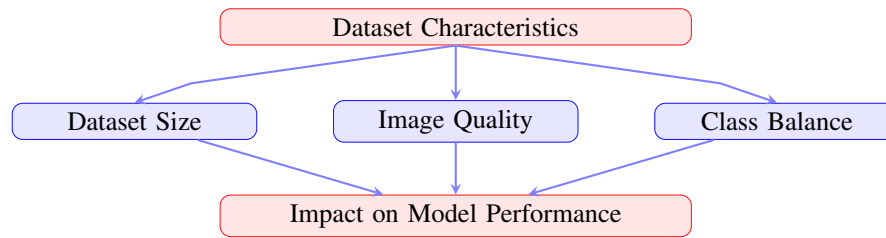


Fig. 3. Dataset characteristics on model performance.

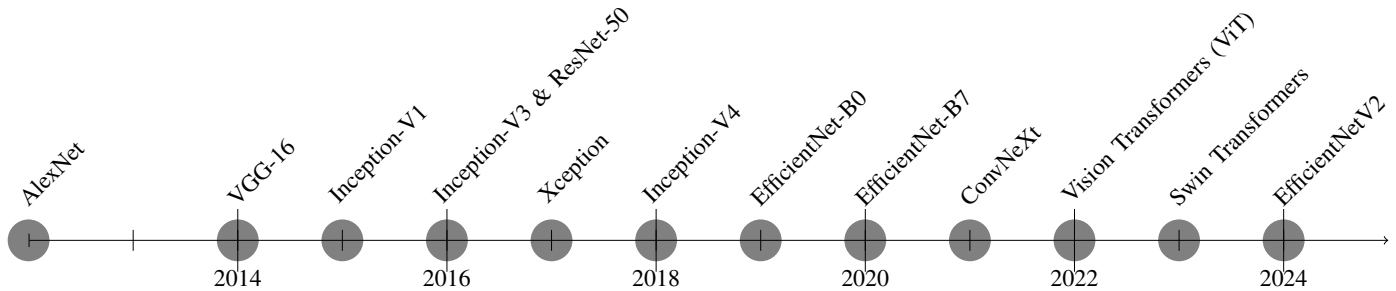


Fig. 4. CNN Architectures timeline (2012-2024).

Fig. 4 illustrates the evolution of CNNs from AlexNet to EfficientNetV2, marking key milestones in image analysis.

1) *AlexNet*: AlexNet [26] was the first deep CNN to achieve groundbreaking image classification results by deepening network capacity and applying optimization strategies.

2) *ResNet*: ResNet introduces skip connections to tackle vanishing gradients, allowing deeper networks like ResNet-50 to perform well. It achieves up to 97% accuracy on datasets such as NIH [11, 8], though its resource demands may limit use in low-resource settings [24].

3) *VGG*: VGG16/VGG19 [27] feature stacked convolutional layers, offering high accuracy and implementation simplicity but with high memory requirements, limiting mobile diagnostic deployment.

4) *YOLO*: YOLO [28, 25] detects objects in real time by predicting bounding boxes in a grid. Effective for fast malaria detection, but less accurate for small objects [2].

5) *MobileNet*: MobileNet [15, 29] uses depthwise separable convolutions to reduce computations, suitable for mobile deployment despite slight accuracy trade-offs [20].

6) *DenseNet*: DenseNet [30, 27] connects each layer to all previous ones, improving gradient flow and reducing parameters. It excels with small or imbalanced datasets but demands high computation [13, 31].

B. Transfer Learning Models

Transfer learning has emerged as a powerful approach in deep learning, particularly advantageous in scenarios where the availability of large, labeled datasets is limited—a common challenge in medical imaging, including malaria detection. By leveraging pre-trained models, transfer learning enables the adaptation of existing architectures trained on extensive

datasets to specific tasks, significantly reducing the need for domain-specific annotated data.

Pre-trained models such as InceptionV3 and Xception have shown remarkable success in malaria detection tasks. As noted by Rajaraman et al. (2019) [7], InceptionV3, known for its efficient inception modules, is particularly effective at learning complex spatial hierarchies in blood smear images. This model has demonstrated accuracy levels exceeding 95% when fine-tuned on malaria datasets, such as the NIH dataset. Similarly, Sriporn et al. (2020) [19] highlight that Xception, which employs depthwise separable convolutions, achieves superior feature extraction with reduced computational costs. These attributes make it highly suitable for malaria detection, especially in resource-constrained settings.

The primary benefit of transfer learning lies in its ability to address the challenges of data scarcity. In medical imaging, obtaining large-scale, high-quality labeled datasets often requires significant expertise and resources, which may not be feasible in low-resource regions. Transfer learning alleviates this issue by reusing knowledge from models pre-trained on general-purpose image datasets, such as ImageNet, and adapting them to malaria detection. This approach not only reduces the computational burden but also enhances the performance of models on smaller, specialized datasets.

Additionally, Masud et al. (2020) [16] explain that transfer learning facilitates faster convergence during training, as the initial layers of the pre-trained model already contain well-established feature extraction capabilities. This enables researchers to focus on fine-tuning the higher-level layers to capture task-specific patterns, such as the morphological differences between parasitized and uninfected blood cells. The use of pre-trained architectures like InceptionV3 and Xception thus provides a robust foundation for achieving high diagnostic accuracy in malaria detection without the extensive computational resources typically required for training models

from scratch.

C. Hybrid and Ensemble Learning Approaches

Hybrid and ensemble learning approaches have emerged as effective strategies to enhance the accuracy and robustness of malaria detection systems. These methods combine the strengths of CNNs with traditional machine learning classifiers or integrate multiple deep learning models to address limitations such as overfitting, class imbalance and dataset variability [18]. By leveraging ensemble methods like VGG-19 combined with SqueezeNet or ResNet with Gradient Boosting, researchers have achieved significant improvements in sensitivity and specificity for malaria classification tasks [24]. These techniques also mitigate the impact of dataset variability, particularly in real-world applications where diverse and unbalanced data present substantial challenges [15, 8].

One prominent hybrid approach as shown in Fig. 5 involves using CNNs for feature extraction followed by classification using traditional machine learning algorithms, such as Support Vector Machines (SVMs).

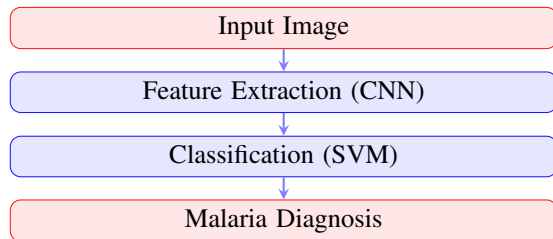


Fig. 5. CNN-SVM Hybrid approach for malaria detection.

TABLE V. TIMELINE OF CNN-SVM HYBRID MODELS DEVELOPMENT (2012-2023)

Year	Development and contribution	References
2012	Yunda et al. proposed hybrid CNNs with feature extraction for malaria detection.	[21]
2015	Gu et al. highlighted the integration of CNNs with classifiers like SVM for robust feature-based tasks.	[30]
2017	Srinivas et al. emphasized using hybrid CNN-SVM approaches for specific computer vision problems.	[32]
2019	Vijayalakshmi and Kanna developed VGG-SVM hybrids for malaria detection with improved accuracy.	[18]
2020	Yang et al. utilized CNN-SVM combinations to enhance mobile malaria detection systems.	[15]
2021	Nakasi et al. integrated CNN-SVM models for thick blood smear malaria detection and smartphone deployment.	[24]
2023	Jiang et al. explored advanced SVM integration for generalization in medical imaging.	[33]

Table V shows the evolution of CNN-SVM hybrid models from their early applications in malaria detection and general computer vision tasks to their refinement for medical imaging and real-world deployment. It highlights significant studies and innovations in using SVM to enhance CNN-based feature extraction and classification.

For example, Fuhad et al. (2020) demonstrated a CNN-SVM hybrid model that achieved an accuracy of 95.8% on a

dataset of thin blood smear images [17]. In this framework, the CNN layers extract complex spatial features from the images which are then fed into an SVM for classification. This combination leverages the feature extraction capabilities of CNNs while benefiting from the robust decision boundaries provided by SVMs.

This hybrid approach is particularly advantageous in scenarios with limited datasets or class imbalance, where traditional deep learning classifiers might struggle to achieve high generalization.

Ensemble learning combines predictions from multiple models to improve diagnostic robustness and reduce variance. Rajaraman et al. (2019) developed an ensemble of VGG-19 and SqueezeNet architectures, achieving sensitivity and specificity values of 97.3% and 96.8%, respectively [7]. By leveraging the diverse strengths of individual models, ensemble methods effectively address variability in image quality and dataset characteristics.

Table VI shows the performance of key ensemble learning methods for malaria detection, highlighting their strengths in handling diverse data.

TABLE VI. PERFORMANCE OF ENSEMBLE LEARNING METHODS FOR MALARIA DETECTION

Ensemble Method	Accuracy (%)	Key Insights
VGG-19 + SqueezeNet [8]	97.3	High sensitivity and specificity
Inception-v3 + MobileNet [15]	98.5	Enhanced recall, ideal for field settings
ResNet + Gradient Boosting [24]	98.2	Robust feature extraction for complex data
EfficientNet + XG-Boost [34]	98.8	Superior performance on imbalanced datasets
Xception + Random Forest [19]	97.9	Improved computational efficiency and accuracy
DenseNet + Logistic Regression [16]	98.1	Effective in reducing false negatives in parasite detection

V. PERFORMANCE ANALYSIS OF DEEP LEARNING MODELS

This section evaluates the performance of deep learning models for malaria detection, focusing on standard metrics like accuracy, sensitivity, specificity and computational efficiency. It emphasizes the impact of dataset diversity, quality and size on model robustness and clinical applicability.

A. Comparison of Model Performance

The performance of deep learning models in malaria detection has been extensively evaluated using standard metrics such as accuracy, sensitivity, specificity and computational efficiency. These metrics provide insights into the robustness, reliability and applicability of different architectures under various scenarios.

Accuracy is a primary metric for assessing the overall correctness of model predictions, reflecting its ability to classify parasitized and uninfected cells correctly. Sensitivity (or recall) measures the model's capacity to detect parasitized cells accurately, while specificity evaluates the model's ability to correctly identify uninfected cells. High sensitivity is critical

for minimizing false negatives which can lead to untreated infections, whereas high specificity ensures a low rate of false positives, reducing unnecessary treatments. As shown in Fig. 6, deep learning models such as ResNet-50 and DenseNet achieve exceptionally high accuracy, sensitivity and specificity making them reliable for clinical applications. YOLO models, optimized for real-time detection, also demonstrate robust performance, particularly in scenarios requiring rapid diagnostics.

Computational efficiency is a critical factor, especially in resource-constrained settings. Models like MobileNet are optimized for lightweight deployment, achieving inference times of less than one second on smartphones [9]. YOLOv4, designed for real-time object detection, balances speed and accuracy. It is suitable for large-scale diagnostic initiatives. On the other hand, deeper architectures such as ResNet-50 and DenseNet require more computational resources and longer training times but provide higher accuracy and robustness.

The comparison of deep learning models highlights a trade-off between computational efficiency and diagnostic performance. Models like ResNet-50 and DenseNet are well-suited for high-resource settings due to their superior accuracy, while MobileNet and YOLOv4 cater to real-time and mobile-based diagnostics in resource-limited environments. These results emphasize the importance of selecting appropriate models based on the specific requirements of the diagnostic context.

B. Impact of Dataset Characteristics

The characteristics of datasets used for training deep learning models play a pivotal role in determining their performance in malaria detection tasks. Factors such as image quality, dataset size and diversity significantly influence the robustness and accuracy of these models. This section explores how these attributes impact the effectiveness of deep learning-based malaria diagnostics.

High-resolution and well-annotated images are critical for enabling models to extract meaningful features and distinguish between parasitized and uninfected cells. For example, Rajaraman et al. (2019) [7] and Dong et al. (2019) [11] highlighted that datasets like the NIH dataset, which contains high-quality thin blood smear images, have been instrumental in achieving diagnostic accuracies exceeding 95%. Conversely, Poostchi et al. (2018) [14] demonstrated that datasets with poor-quality images, such as those affected by staining artifacts or low resolution, often lead to reduced model performance and increased false negatives, particularly in detecting low-parasitemia cases.

The size of a dataset determines the extent to which a model can generalize to unseen data. Larger datasets, such as the NIH dataset with 27,558 labeled images, allow for more robust feature learning and better performance across diverse diagnostic scenarios (Dong et al., 2019) [11]. However, as Masud et al. (2020) [16] note, many malaria datasets suffer from class imbalance, with a disproportionate number of uninfected images compared to parasitized ones. This imbalance can bias models towards over-predicting the majority class, leading to suboptimal sensitivity in identifying infected cells. Additionally, strategies to address class imbalance, as discussed by Jiang et al. (2021) [33], such as focal loss, can help mitigate this issue and improve model robustness.

Dataset diversity, encompassing variations in staining methods, imaging equipment, and geographic representation, enhances the robustness of models across different environments. For instance, Yang et al. (2019) [9] highlight how the Malaria-LMIC dataset introduces real-world challenges such as low-quality imaging and environmental noise, helping to evaluate model adaptability. Similarly, Poostchi et al. (2018) [14] emphasize that models trained on geographically diverse datasets are more likely to perform well in real-world deployments, where variability in imaging conditions is inevitable.

Fig. 7 illustrates how dataset characteristics—image quality, size, class balance and diversity—significantly influence the performance and robustness of deep learning models for malaria detection.

C. Applications and Limitations

Deep learning models have demonstrated significant potential in enhancing malaria diagnostics, particularly in automating the detection process and reducing dependency on skilled personnel. These models excel in various real-world applications but also face challenges that hinder their widespread adoption and efficacy.

1) Applications in real-world scenarios:

a) *Automated blood smear analysis:* CNNs have achieved diagnostic accuracies exceeding 95% in the detection of parasitized and uninfected cells in blood smear images, as demonstrated by models such as ResNet-50 and DenseNet (Rajaraman et al., 2019 [7]; Vijayalakshmi et al., 2020 [8]). These advancements enable rapid and consistent analysis, significantly reducing the time required for diagnosis compared to traditional microscopy.

b) *Mobile-based diagnostics:* Lightweight architectures like MobileNet have been integrated into smartphone-based diagnostic platforms. They provide accessible and cost-effective solutions for remote and resource-constrained regions (Yang et al., 2019 [9]; Masud et al., 2020 [16]). These platforms facilitate real-time malaria detection, empowering healthcare workers with portable diagnostic tools.

c) *Large-scale screening and epidemiological monitoring:* Deep learning models, such as YOLOv4, have demonstrated high efficiency in processing large volumes of data for malaria screening (Chibuta et al., 2020 [2]). These models are particularly useful in public health initiatives, where rapid identification of malaria hotspots can guide targeted interventions.

d) *Cross-species detection and mixed infections:* Advanced models like DeepMCNN have shown promise in detecting different species of *Plasmodium* parasites and addressing the challenges of mixed infections, which are often missed by traditional RDTs (Masud et al., 2020 [16]).

2) Limitations and challenges:

a) *Dataset limitations:* Many publicly available datasets, such as the NIH dataset, lack diversity in imaging conditions, staining methods, and geographical representation, as noted by Poostchi et al. (2018) [14] and Rajaraman et al. (2018) [10]. This restricts the generalizability of models trained on such datasets to varied real-world scenarios.

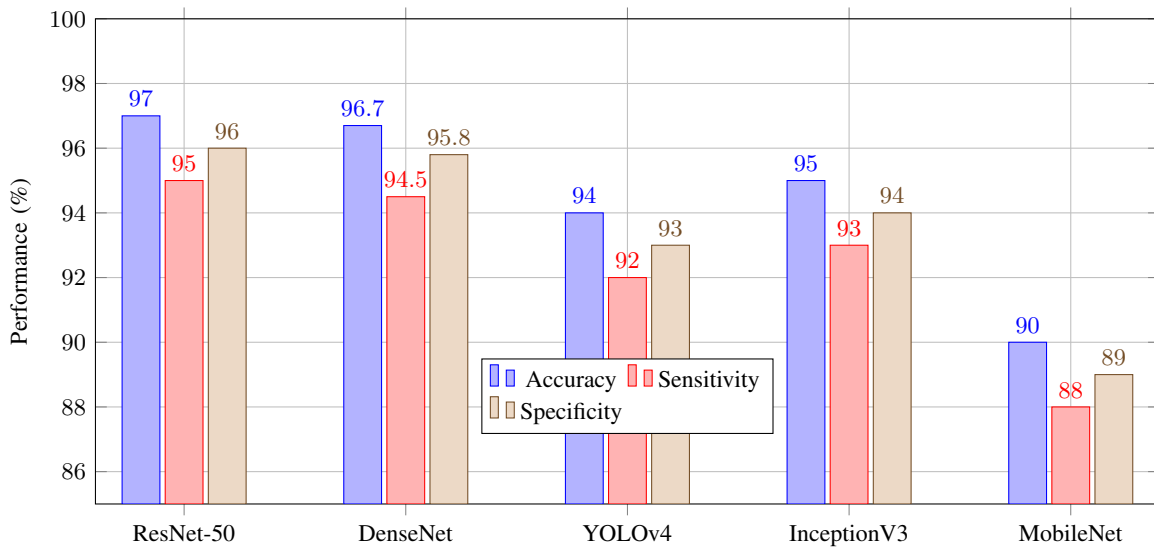


Fig. 6. Comparison of model performance metrics [7, 11, 9, 16].

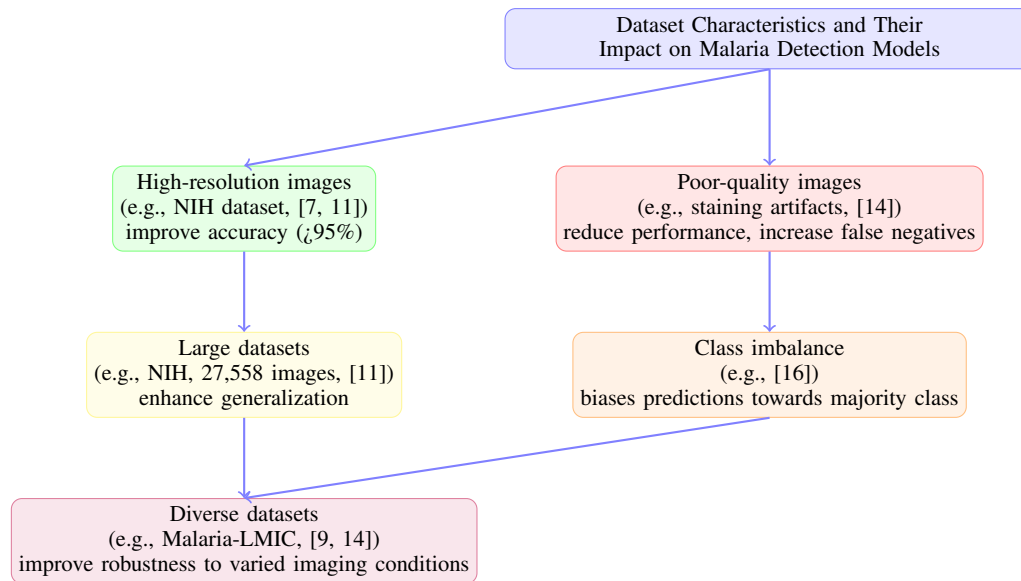


Fig. 7. Impact of dataset characteristics on malaria detection performance.

b) Variability in imaging conditions: Differences in blood smear preparation, staining protocols, and imaging equipment across laboratories introduce variability that can adversely affect model performance when deployed in new environments, as highlighted by Yang et al. (2019) [23].

c) Interpretability concerns: While deep learning models offer high accuracy, their “black-box” nature limits interpretability, raising concerns among clinicians about the reliability of automated decisions. Yang et al. (2020) [15] discuss emerging solutions, such as saliency maps and Grad-CAM, though their adoption in clinical practice remains limited.

d) Resource requirements: Deep learning models like ResNet-50 and DenseNet require high computational power for training and deployment, which can be prohibitive in resource-constrained settings, as observed by Dong et al. (2019) [11]

and Fuhad et al. (2020) [17]. Although lightweight models like MobileNet address some of these concerns, they often involve trade-offs in accuracy.

e) Regulatory and ethical challenges: The integration of deep learning into clinical workflows is subject to regulatory scrutiny, particularly concerning data privacy and the ethical implications of automated diagnostics. Chibuta et al. (2020) [2] emphasize the importance of ensuring compliance with international standards for broader adoption.

VI. DISCUSSION

The analysis presented in this paper highlights the transformative potential of deep learning for malaria detection, as well as the challenges and opportunities that lie ahead. This discussion section synthesizes the key takeaways, addresses

critical challenges and suggests pathways for future research and implementation.

A. Key takeaways from the analysis

The application of deep learning in malaria detection has shown significant advancements:

a) High diagnostic accuracy: Models such as ResNet-50 and DenseNet have achieved diagnostic accuracies exceeding 95%, showcasing their effectiveness in identifying malaria-infected cells (Rajaraman et al., 2019 [7]; Dong et al., 2019 [11]). These accuracies are comparable to and in some cases surpass traditional methods like microscopy and RDTs.

b) Publicly available datasets: The availability of datasets such as the NIH dataset and Delgado Dataset B has been instrumental in training and validating these models (Rajaraman et al., 2018 [10]). These datasets provide a standardized benchmark for assessing model performance.

c) Emerging architectures and trends: Lightweight architectures like MobileNet and real-time detection models such as YOLOv4 have made it possible to deploy these systems in resource-limited settings (Yang et al., 2019 [9]; Chibuta et al., 2020 [2]).

d) Potential for integration: The integration of deep learning into mobile and telehealth platforms offers a promising avenue for improving malaria diagnostics in underserved regions (Masud et al., 2020 [16]; Yang et al., 2019 [23]).

B. Challenges in Scalability, Resource Efficiency and Robustness

Despite these advancements, several challenges remain that hinder the scalability and robustness of deep learning-based malaria detection systems:

1) Scalability: Deploying deep learning models in real-world scenarios requires scalable solutions that can handle variations in imaging conditions, equipment, and geographical settings. The generalization of models across diverse populations remains a critical issue, as highlighted by Poostchi et al. (2018) [14] and Yang et al. (2020) [15].

2) Resource efficiency: While models like MobileNet have demonstrated low computational requirements, others such as ResNet and DenseNet necessitate high-end GPUs, limiting their deployment in resource-constrained environments, as discussed by Yang et al. (2019) [9].

3) Robustness and bias: Dataset limitations, including imbalanced class distributions and lack of diversity, can introduce biases, affecting the reliability of these models in different contexts. Rajaraman et al. (2018) [10] and Poostchi et al. (2018) [14] emphasize the importance of addressing these challenges. Fig. 3 illustrates the impact of dataset characteristics on model performance.

4) Interpretability: The lack of interpretability in model predictions remains a barrier to clinical adoption. Clinicians require insights into the decision-making process of these systems to trust their outputs, as noted by Yang et al. (2020) [15].

C. Future Directions for Addressing Challenges

To address the identified challenges, future research should focus on:

1) Dataset enhancement: Collaborations across institutions to create diverse, high-quality datasets that represent a wide range of imaging conditions, geographical locations, and patient demographics have been highlighted by Masud et al. (2020) [16], Nakasi et al. (2020) [29], Yang et al. (2020) [15], and Khosla and Saini (2020) [35].

2) Model optimization: Development of lightweight and computationally efficient models that can operate on low-resource devices without compromising accuracy has been extensively discussed by Yang et al. (2019) [9], Yang et al. (2020) [15], Abdurahman et al. (2020) [25], and Nakasi et al. (2021) [24].

3) Explainable AI (XAI): Integration of explainability techniques like Grad-CAM and saliency maps to enhance model transparency and build trust among clinicians has been emphasized by Yang et al. (2020) [15], Masud et al. (2020) [16], Molina et al. (2021) [27], and Manescu et al. (2020) [20].

4) System integration: Embedding AI models into telehealth and mobile platforms to facilitate real-time diagnostics and improve accessibility has been proposed by Masud et al. (2020) [16], Yang et al. (2020) [15], Nakasi et al. (2020) [29], and Nakasi et al. (2021) [24].

VII. CONCLUSION AND FUTURE WORKS

The application of deep learning in malaria detection has emerged as a transformative approach, addressing the critical need for accurate and timely diagnostics in resource-limited settings. This paper has presented a comprehensive overview of the advancements in this field, highlighting the potential of deep learning architectures to automate malaria detection with accuracy comparable to traditional methods. Models such as ResNet-50, DenseNet, and YOLO have demonstrated remarkable diagnostic performance, achieving accuracy levels exceeding 95% in various studies [7, 8]. Moreover, lightweight architectures like MobileNet are facilitating the integration of these technologies into mobile and telehealth platforms and expanding their accessibility to underserved regions [9].

Publicly available datasets, including the NIH dataset and Delgado Dataset B, have played a pivotal role in training and validating these models. However, challenges such as dataset bias, limited diversity, and class imbalance remain significant, necessitating the development of more comprehensive and representative datasets [14, 10]. Additionally, emerging trends in multi-modal data integration, combining clinical, genomic, and imaging data, offer promising avenues for enhancing diagnostic accuracy and robustness [16].

Despite notable progress, this study has several limitations that should be acknowledged. The absence of a concrete experimental validation restricts the ability to empirically assess the effectiveness of the reviewed models in a real-world or simulated deployment. Furthermore, while the paper provides an overview of various deep learning models, it lacks a detailed comparative analysis, both qualitative and quantitative, against similar contemporary approaches. These limitations

underscore the need for more rigorous empirical benchmarking and validation in future work.

Looking forward, future research should prioritize the following directions:

1) *Improving dataset quality and diversity*: Developing large-scale, geographically diverse, and well-annotated datasets is essential for training models that generalize well across different populations and imaging conditions. Data augmentation techniques and synthetic data generation can also be explored to address class imbalance and enhance model robustness [17, 14].

2) *Advancing lightweight models*: Designing lightweight and computationally efficient models, such as optimized versions of MobileNet and YOLO, is critical for enabling real-time diagnostics on mobile devices. These models must balance accuracy with resource constraints to ensure their feasibility in low-resource settings [9].

3) *Integration into health systems*: Embedding deep learning-based diagnostic systems into existing healthcare infrastructures, particularly in malaria-endemic regions, can enhance accessibility and scalability. Mobile applications and telehealth platforms should be leveraged to provide real-time, on-the-spot diagnostics for healthcare workers [16, 15].

4) *Enhancing explainability and trust*: Integrating explainable AI (XAI) techniques, such as saliency maps and Grad-CAM, will make model predictions more interpretable and clinically reliable. Ensuring transparency in decision-making processes is vital for building trust among healthcare professionals and stakeholders [7].

5) *Incorporating experimental validation and benchmarking*: Future studies should include empirical validation of proposed methods using independent test datasets or clinical data to strengthen their practical credibility. Additionally, comparative analyses with other state-of-the-art techniques will enable a clearer assessment of relative strengths, limitations, and application domains.

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