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A Systematic Review of Transfer Learning Approaches for Malaria Diagnosis Using Red Blood Cell Imaging

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ABSTRACT

Malaria remains one of the leading global health burdens, particularly in low-resource regions where access to reliable diagnosis is limited. Conventional microscopy is labor-intensive and dependent on skilled technicians, making it an ideal target for automation. To address this, recent studies have applied deep learning (DL) and transfer learning (TL) techniques to automate malaria diagnosis using red blood cell (RBC) images, achieving remarkable progress in both accuracy and deployment potential. This review consolidates and analyzes 25 peer-reviewed studies that explore various AI-driven malaria detection approaches, focusing on their contributions in model development, data utilization, and performance optimization. It provides a comprehensive synthesis of methods, challenges, and future directions in the field. The analysis employed a structured comparative method by extracting and summarizing key aspects from each study, including datasets, preprocessing techniques, transfer learning strategies, classification models, evaluation metrics, limitations, and recommendations. Tables were constructed to facilitate cross-study comparisons. The results show that most studies achieved high classification accuracy (often above 95%), particularly those using pretrained CNN architectures like VGG16, ResNet, and DenseNet. Several studies extended to species-level or stage-specific classification using multi-class models or transformer-based frameworks. Preprocessing strategies such as color normalization, segmentation, and augmentation were essential for boosting model performance. However, issues like class imbalance, dataset bias, annotation inconsistency, and lack of real-world validation persist across studies. Challenges in generalizability and computational scalability remain key barriers to clinical deployment. Future directions include using GANs for data balancing, adopting domain adaptation and federated learning, and embedding models into mobile or cloud-based diagnostic platforms. In conclusion, while deep learning approaches for malaria detection are technically mature and highly accurate under experimental conditions, broader clinical integration requires robust validation, dataset diversification, and interdisciplinary collaboration.

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1. Introduction

Malaria, an infectious disease caused by the Plasmodium parasite, continues to pose a major global health problem, particularly in tropical and subtropical regions [1]. According to the WHO, the disease results in millions of infections and hundreds of thousands of deaths annually, with the highest concentration of cases occurring in sub-Saharan Africa [2]. Early and precise diagnosis is essential to ensure timely treatment and reduce the risk of severe complications [3]. Traditionally, malaria detection relies on microscopic analysis of blood smears, where laboratory personnel manually examine RBCs for the presence of parasites [4], [5]. However, this manual procedure is labor-intensive, time-consuming, and depends heavily on the skill of the technician, which restricts its scalability, particularly in areas with limited healthcare resources [6]. Recent progress in AI, especially in machine learning and transfer learning, has demonstrated significant potential for improving the accuracy and efficiency of malaria diagnosis [7]-[9]. Transfer learning, which involves adapting a pre-trained model for a new but related task, has emerged as a powerful method for automating image analysis, particularly for detecting malaria parasites in RBC images [10], [11]. This technique is advantageous because it typically requires smaller datasets, addressing one of the main obstacles in medical imaging applications [12]. By utilizing models trained on large-scale datasets, transfer learning can enhance diagnostic accuracy even in conditions where annotated data is scarce, making it highly applicable to medical tasks such as malaria detection [13], [14].

This systematic review aims to critically assess the use of transfer learning approaches in the diagnosis of malaria using RBC images. Through an in-depth analysis of the existing literature, the review evaluates the effectiveness of various transfer learning models, such as CNNs, in detecting malaria parasites and identifies the key challenges, limitations, and future research directions in this field. The primary goal of this review is to provide a comprehensive understanding of how transfer learning can address current diagnostic gaps and its potential for integration into clinical settings, especially in malaria-endemic regions. The review will address several key research questions:

1. How effective are transfer learning models in detecting malaria from RBC images?
2. What are the most successful techniques for applying transfer learning in malaria diagnosis compared to traditional methods?
3. What challenges are encountered in implementing transfer learning for malaria diagnosis, particularly in real-world settings?
4. And how can transfer learning be integrated into diagnostic systems in malaria-endemic areas with limited resources?

Despite the growing body of research on transfer learning for various medical applications, there remain several research gaps that need to be addressed. One major gap is the limited availability of large, diverse datasets for training transfer learning models, which hinders the development of robust and generalized models. Additionally, while laboratory results are promising, real-world validation of these models in clinical settings remains sparse, posing a significant challenge for practical implementation. Furthermore, the quality of RBC images used for training remains inconsistent, and addressing this issue is critical for improving the reliability of transfer learning models in diagnosing malaria. This review is significant because it aims to provide insights into the potential of transfer learning to improve malaria diagnosis and reduce reliance on manual microscopy. By reviewing and analyzing the various transfer learning techniques applied to RBC image analysis, this review seeks to accelerate the adoption of AI technologies in medical practice, particularly in resource-constrained regions that are most affected by malaria. Moreover, the review will highlight important directions for future research, focusing on overcoming the challenges and improving the effectiveness of AI models in clinical environments.

2. Background

2.1. Malaria Diagnostic Methods

Traditionally, malaria detection has depended on microscopic examination of blood smears, in which trained laboratory staff inspect RBCs for the presence of Plasmodium parasites [15], [16]. Microscopy is widely regarded as the "gold standard" for malaria diagnosis because of its high accuracy and capacity to detect parasite forms in the bloodstream [17], [18]. Nevertheless, this method faces several drawbacks, such as the need for highly trained personnel, the lengthy nature of the process, and reliance on the quality of both the microscope and staining techniques [19]. Moreover, microscopy requires substantial time and specialized equipment, which makes it difficult to apply in rural or resource-constrained areas where malaria is highly prevalent [20]. In addition, the approach is susceptible to human error, as technicians must manually examine thousands of RBCs to identify infected cells [21].

As a result, alternative diagnostic methods have been developed to address these shortcomings. Rapid diagnostic tests (RDTs) are now widely used, offering a faster and easier way to detect malaria infection [22], [23]. RDTs detect antigens derived from the Plasmodium parasite, providing results within minutes [24]. However, while RDTs are convenient, they often lack sensitivity, particularly in cases with low parasitemia or early infection [25]. Moreover, they are prone to false-negative results, especially in areas with low-quality testing infrastructure [26]. In response to these limitations, molecular diagnostic methods, such as PCR, have been introduced, which offer greater sensitivity and accuracy by detecting parasite DNA [27]. However, PCR-based methods are expensive, require specialized laboratory facilities, and take longer to provide results [28]. Therefore, despite the advancements in diagnostic technologies, traditional microscopy still plays a central role in malaria diagnosis, especially in clinical settings where rapid results are essential [29].

2.2. The Concept of Transfer Learning

Transfer learning is an advanced machine learning method that utilizes knowledge gained from one task to enhance performance on another related task [30]-[32]. For malaria diagnosis, this approach employs pre-trained models built on large and diverse datasets to identify parasites in RBC images, even when only a limited amount of annotated data is available [33], [34]. This technique is particularly advantageous in medical fields because collecting large, high-quality labeled datasets for training deep learning models is often a difficult and resource-intensive process [35]. Transfer learning generally involves two main stages: feature extraction and fine-tuning [36], [37]. In the feature extraction stage, a model pre-trained on a large dataset (such as ImageNet for image classification) is used to obtain relevant features from the input images [38]. These extracted features are then applied to classify data for the new task, in this case, malaria detection [39]. Fine-tuning, on the other hand, consists of retraining a pre-trained model with a smaller, task-specific dataset to adjust its weights for the new task [40]-[42]. This strategy allows the model to reach high levels of accuracy even when trained with relatively small datasets, making it highly valuable in medical contexts where annotated data is often limited [43], [44].

Transfer learning has shown remarkable success in various fields, including image recognition and medical image analysis [45]-[47]. It has been used in numerous studies for automated malaria detection, where models like CNNs are trained using pre-existing image datasets [48]-[50]. By utilizing transfer learning, researchers have successfully developed models that can analyze RBC images and identify malaria-infected cells with high accuracy, thereby reducing the need for manual inspection by human technicians. These models offer several advantages, such as increased speed, accuracy, and scalability, making them highly suitable for malaria diagnosis, particularly in low-resource settings. The next section provides a literature review highlighting various transfer learning approaches used in malaria detection.

3. Methodology

3.1. Search Strategy

The Search Strategy for investigating transfer learning approaches for malaria diagnosis using red blood cell (RBC) imaging (Fig. 1) is designed to retrieve relevant literature from ScienceDirect, IEEE Xplore, and Nature databases. A single, complex search query is formulated to ensure that the search captures a comprehensive range of articles focused on both AI-driven diagnostic techniques and RBC image analysis for malaria detection. The query integrates keywords related to transfer learning, deep learning, artificial intelligence, and RBC imaging, enabling the identification of relevant studies that explore innovative approaches in malaria diagnosis. By focusing on these key elements, the search will cover cutting-edge advancements and their practical applications in detecting malaria from RBC images. The chosen search query is ("malaria diagnosis" OR "malaria detection") AND ("transfer learning" OR "deep learning" OR "artificial intelligence") AND ("RBC" OR "red blood cell" OR "blood smear"). This query is structured to encompass a broad range of studies. It combines the terms "malaria diagnosis" and "malaria detection" with AI-based techniques like transfer learning, deep learning, and artificial intelligence. The search specifically targets studies related to RBC imaging or red blood cell imaging, ensuring that the results are focused on the use of AI for detecting malaria through RBC image analysis. To refine the results, filters will be applied to include only peer-reviewed research articles published within the last 10 years (2015–2024). This will help in capturing the most recent and relevant studies that align with the goal of understanding the role of transfer learning in improving malaria diagnosis. By using this single, unified search query across the three databases, the strategy ensures consistent and comprehensive retrieval of literature that contributes to the ongoing development of AI-based diagnostic methods for malaria.

3.2. Eligibility Criteria

To guarantee that only relevant and high-quality studies are considered, specific eligibility criteria were defined for this systematic review on transfer learning approaches for malaria detection using RBC imaging. These criteria will guide the selection of studies that contribute valuable insights into the application of transfer learning, deep learning, and artificial intelligence (AI) in the diagnosis of malaria, specifically focusing on RBC imaging. The following are the inclusion criteria used.

1. Peer-reviewed research articles focusing on transfer learning or AI-based models for malaria diagnosis through RBC images.
2. Studies published in English.
3. Studies published between 2015 and 2024.
4. Studies with experimental methodology and performance metrics like accuracy, sensitivity, and specificity.

3.3. Study Selection

For the selection of studies related to transfer learning approaches for malaria diagnosis using RBC imaging, we followed a structured and systematic process to ensure that only relevant, high-quality studies were included in the review. The goal was to identify studies specifically focused on the application of AI-based techniques, particularly transfer learning, in the context of malaria diagnosis through RBC image analysis. To manage the article selection process efficiently, we used the Rayyan web-based tool, which helped remove duplicate records and enabled the creation of a unique, comprehensive database of references. The study selection process consisted of three phases:

1. Assessing the Title. In this first phase, the titles of the articles were screened to identify studies directly related to malaria diagnosis using AI techniques such as transfer learning or deep learning applied to RBC imaging. Articles unrelated to this specific focus, such as those discussing other diseases or non-AI-based diagnostic methods, were excluded at this stage.

2. Reviewing the Abstract and Keywords. After the initial title screening, we reviewed the abstracts and keywords of the remaining studies to further assess their relevance. We focused on studies that specifically explored the application of transfer learning and deep learning techniques for malaria detection through RBC imaging. Studies that met these criteria were selected for full-text evaluation.
3. Analyzing the Full Text. In the final phase, the full texts of the selected articles were thoroughly reviewed. The studies were assessed based on the eligibility criteria, including the relevance of the diagnostic methods discussed, the application of transfer learning techniques, and the quality of the data and methodology. Articles that met the inclusion criteria and adhered to high methodological standards were included in the final review.

This structured, multi-step selection process ensured that only the most pertinent and scientifically robust studies, aligned with the inclusion criteria, were included in the review. By following this rigorous approach, we were able to compile a comprehensive collection of studies that explore the integration of transfer learning with malaria diagnosis using RBC imaging, focusing on both traditional and AI-enhanced diagnostic methods.

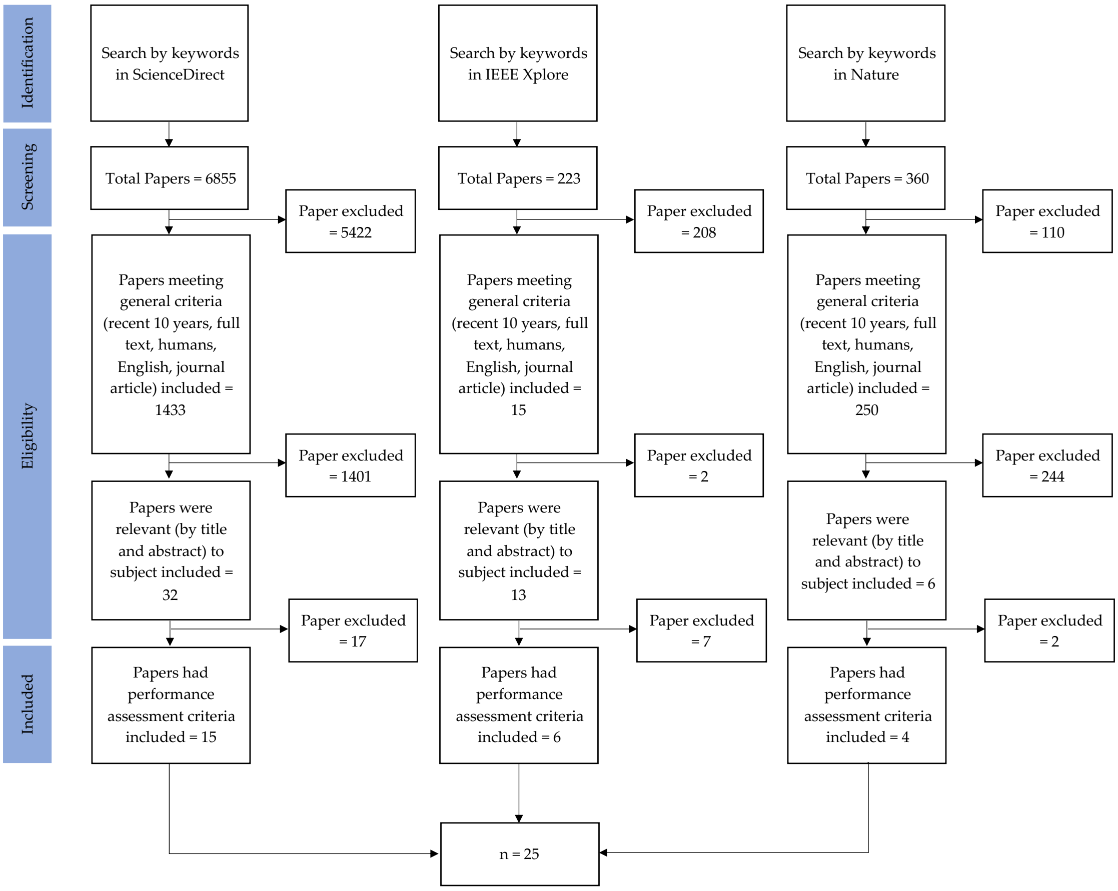

Fig. 1. PRISMA process for data collection

3.4. Quality Assessment

The quality assessment for the selected studies on transfer learning approaches for malaria diagnosis using RBC imaging was conducted to ensure that only high-quality and reliable research contributed to the findings of this systematic review. To evaluate the methodological rigor of each study, we used established quality assessment tools suitable for evaluating AI-based medical research. This involved assessing the clarity of the study design, the appropriateness of methods used (such as model selection, data preprocessing, and training procedures), and the reliability of results, including performance metrics such as accuracy, sensitivity, specificity, and precision. Studies with clear methodologies, robust statistical analyses, and transparency in data reporting were considered of higher quality and were included in the final review. Additionally, the studies were evaluated for their clinical relevance and real-world applicability. This involved determining whether the research provided practical insights into the real-world use of AI and transfer learning in malaria diagnosis, particularly in low-resource settings where traditional diagnostic methods may be limited. Studies that demonstrated the practical deployment of AI models for malaria diagnosis or showcased strong validation of the models in real clinical environments were given priority. This ensured that the review reflects not only strong methodological soundness but also real-world applicability, providing insights into how AI and transfer learning are being integrated into malaria diagnostics.

The final quality assessment also emphasized the transparency of data reporting and comprehensiveness of model validation across different datasets. Only studies that provided detailed descriptions of the datasets used, model architectures, and evaluation metrics were included, ensuring that the results were reproducible, reliable, and comparable. By following this rigorous process, the review was able to compile a comprehensive collection of studies that both adhered to high methodological standards and contributed valuable insights into the integration of transfer learning in malaria diagnosis using RBC imaging.

4. Transfer Learning Approaches for Malaria Diagnosis

This systematic review explores 25 studies published between 2015 and 2024 on transfer learning approaches for malaria diagnosis using red blood cell imaging, as summarized in Table 1. Key aspects analyzed include the contributing authors and publication years, the variety of preprocessing techniques, the specific transfer learning models utilized, and the performance metrics reported.

Table 1. Summary of Studies on the Application of Transfer Learning for RBC-Based Malaria Detection

Ref	Authors & Year	Preprocessing Techniques	Transfer Learning Approach	Performance Metrics
[51]	Rahman et al., 2021	Resizing, Normalization, Class balancing via GANs, Threshold adjustment	Pretrained on ImageNet, TL-NIH on Malaria dataset (27,558 samples)	TL-NIH: Accuracy = 99.35%, F1 = 96.85%, Sensitivity = 92.31%, Specificity = 99.76%.
[52]	Loh et al., 2021	Image contrast enhancement, Thresholding, Morphological operations	Pretrained on COCO dataset, Mask R-CNN	Detection Accuracy = 94.57%, mAP = 0.731.
[53]	Liu et al., 2023	Patch generation, Multiscale extraction, Heatmap generation	Transformer-based architecture	Cell-level: Accuracy = 98.62%, AUC = 99.92%. Image-level: Accuracy = 97%, AUC = 98.84%.
[54]	Diker, 2022	Image resizing, Feature extraction from CNN, Dimensionality reduction (NCA)	Custom model	Accuracy = 99.90%, Sensitivity = 99.98%, Specificity = 87.50%.
[55]	Bhuiyan et al., 2023	Resizing, Normalization, Data Augmentation (Rotation, Zoom, Flip)	Pretrained: VGG16(R), VGG19(R), DenseNet201(R)	VGG16(R): Accuracy = 97.52%. Ensemble: Accuracy = 97.92%, F1 = 97.92%.
[56]	Qadri et al., 2023	Train-test split, K-fold cross-validation, Feature extraction	Pretrained NASNet model	Accuracy = 99%, Precision/Recall/F1 = 0.99.
[57]	Molina et al., 2021	Image enhancement, Median filtering, Data augmentation	Pretrained VGG-16, fine-tuned	Accuracy = 99.5%, Sensitivity = 99.2%, F1 = 97.4%.
[58]	Alnussairi et al., 2022	Resizing, Encoding, Data augmentation (Rotation, Flip, Zoom)	Pretrained: VGG-19, ResNet-50, MobileNetV2, fine-tuned	Accuracy = 100%, Precision = 100%, Recall = 100%, F1 = 100%.
[59]	Acherar et al., 2022	Resizing, Watershed segmentation, Expert labeling, Data augmentation	Pretrained VGG-19, ResNet-50, EfficientNet-B7	VGG-19-NRC: Accuracy = 99.7%, F1 = 97.1%,

Ref	Authors & Year	Preprocessing Techniques	Transfer Learning Approach	Performance Metrics
				Sensitivity = 100%, Specificity = 50%.
[60]	Zedda et al., 2024	Data augmentation (rotation, Gaussian noise, HSV shifts)	Pretrained on COCO2017, YOLOv5 backbone	mAP = 99.1%.
[61]	Singla et al., 2020	Phase unwrapping, RBC patch extraction, Morphological operations, Data augmentation	Pretrained on ImageNet: AlexNet, VGG16, ResNet50, GoogLeNet	Accuracy = 97%, Sensitivity = 97%, AROC = 0.99.
[62]	Ilyas et al., 2024	Label conversion, Data augmentation	Unsupervised Domain Adaptation (F2DA, Adversarial training)	mAP improved from 31.3% to 55.19%, mPQ = 78.78%.
[63]	Nugroho et al., 2023	Green channel extraction, Contrast stretching, SMOTE for class balancing	Pretrained DenseNet121, MobileNet V2, MnasNet	F1-score = 0.91, Sensitivity = 99.6%.
[64]	Hassan et al., 2022	Image resizing, Data augmentation, Normalization	Pretrained: InceptionV3, ResNet50, VGG19	Accuracy = 98.90%, F1 = 98.94%, Sensitivity = 99.29%, MCC = 97.80%.
[65]	Amin et al. 2023	Image resizing, Segmentation, Data splitting	VGG16 pretrained on ImageNet	Accuracy = 96.6%, Precision = 95.53%, F1 = 96.33%, AUC-ROC = 0.98.
[66]	Chen et al., 2023	Color enhancement, Data augmentation, Normalization	Pretrained MobileNet V1	Segmentation: Accuracy = 98.47%. Classification: Accuracy = 98%.
[67]	Sukumarran et al., 2024	Data augmentation, Normalization, Cropping infected cells	Pretrained: DenseNet-121, ResNet-50, VGG-16, AlexNet, MobileNetv2, EfficientNet	YOLOv5: mAP = 96% (MP-IDB). DenseNet-121: Accuracy = 95.5%.
[68]	Koirala et al., 2022	Ground truth correction, Re-annotation, Data formatting	Pretrained COCO weights for YOLOv4	YOLOv4: mAP = 93.99%, mAP = 94.07%.
[69]	Zhong et al., 2023	Fuzzy Inference, Clustering, Morphological operations, Histogram equalization	Pretrained models: VGG-16, VGG-19, AlexNet, GoogLeNet, ResNet-50, ResNet-101	VGG-19: Accuracy = 97.98%. AlexNet: Accuracy >92.44%.
[70]	Özbilge et al., 2024	Image resizing, Annotation, no augmentation or hyperparameter tuning	Pretrained weights on COCO, fine-tuned for malaria parasite detection	YOLOv8s: F1 = 0.8646, mAP = 0.9031. Ensemble: F1 = 0.8972, mAP = 0.6214.
[71]	Gupta et al., 2022	Channel selection, Patch extraction, Class balancing	Pretrained ResNet-18 on ImageNet, SimCLR and supervised contrastive learning phases	AUC = SimSearch (200 samples) = 0.93, Semantic Segmentation = 0.85.
[72]	Kanakasabapathy et al., 2021	Image resizing, Augmentation (flip, rotation), SIFT feature extraction	Unsupervised domain adaptation using adversarial learning, frozen pretrained weights with pseudo-labeling	MD3: Accuracy = 90%. MD2: Accuracy = 90%. MD1_t: Accuracy = 95%.
[73]	Kittichai et al., 2021	RBC cropping using YOLOv3, Data augmentation, Class balancing	Pretrained on ImageNet: Darknet variants, Densenet201	Darknet: Accuracy = 99.2%, Sensitivity = 99.2%, AUC = 0.986–1.000.
[74]	Tan et al., 2023	One-hot encoding, Data augmentation, WGAN-GP for synthetic images	Pretrained Swin Transformer, MobileViT	Swin Transformer: Accuracy = 99.885%, F1-score = 99.599%. MobileViT: slightly lower accuracy but more efficient.
[75]	Mujahid et al., 2024	Image resizing, Class balancing, Batch normalization	EfficientNet-B2 pretrained, fine-tuned on malaria dataset	Accuracy = 97.57%, Precision = 96.59%, F1-score = 97.55%, AUC = 99.21%

Recent advances in malaria detection using transfer learning have revealed consistent improvements in diagnostic performance, particularly when coupled with thoughtful preprocessing strategies. Many studies begin by employing standard techniques such as image resizing, normalization, and color correction to ensure data consistency. For instance, Rahman et al. [51] applied color constancy normalization and GAN-based synthetic data to balance the dataset, yielding a high classification accuracy of 99.35% using a domain-specific transfer learning model (TL-NIH). Their results demonstrated the benefit of leveraging pretraining on a medically relevant dataset compared to generic ImageNet weights, especially when tested on the independent MP-IDB dataset. Similarly, Bhuiyan et al. [55] enhanced their models with rotation, zoom, and flipping, achieving 97.92% accuracy through an ensemble of VGG16, VGG19, and DenseNet201, all fine-tuned from ImageNet. Beyond basic preprocessing, some researchers implemented specialized techniques to enhance morphological features or augment data with limited annotations. Loh et al. [52] relied on manual polygon-based annotations and applied contrast enhancement with morphological operations to improve segmentation in stage-specific classification using Mask R-CNN. Liu et al. [53] developed a novel transformer-based model with patch extraction from YOLOv5, multi-scale heatmaps, and positional encoding, achieving 98.62% cell-level accuracy and 98.84% AUC on image-level analysis. Notably, their approach did not depend on conventional pretrained weights, marking a shift toward more task-tailored self-supervised learning in medical imaging.

Other studies focused on optimizing transfer learning pipelines through deeper architectures and fine-tuned layers. Molina et al. [57] retrained all layers of a VGG-16 model originally pretrained on ImageNet after image enhancement steps such as green channel selection and Otsu segmentation. Their smear-level diagnosis attained perfect sensitivity, while image-level classification yielded 99.5% accuracy. In contrast, Alnussairi et al. [58] and Acherar et al. [59] reported nearly perfect results (100% accuracy) using VGG-19, ResNet-50, and MobileNetV2, but concerns about overfitting or dataset simplicity remain. In parallel, Qadri et al. [56] showcased that NASNet-extracted features classified with SVM or logistic regression reached 99% accuracy in a highly efficient manner, reinforcing the advantage of feature-level transfer learning. Interestingly, not all studies relied on pretrained weights. Diker [54] introduced a custom CNN without external initialization, instead applying NCA for dimensionality reduction and Bayesian optimization for classification. This model achieved 99.9% accuracy and an MCC of 99.81%, challenging the assumption that pretrained networks are always necessary for high performance. Conversely, models that did leverage pretrained architectures often required substantial adaptation to generalize across domains. Ilyas et al. [62] addressed domain shifts using Fourier-based unsupervised adaptation (F2DA), improving object detection mAP from 31.3% to 55.19% and segmentation quality in cross-magnification conditions, validating the importance of domain alignment.

Stage-aware detection was another focus in several works. Singla et al. [61] developed a two-level model to classify both infection presence and trophozoite stage using customized CNNs and ImageNet-based models like VGG16 and ResNet50, achieving up to 97% accuracy. Nugroho et al. [63] built on this by comparing lightweight and deep pretrained models such as DenseNet121 and ShuffleNet, where DenseNet outperformed YOLOv5 and Faster R-CNN with 99.6% sensitivity and 0.91 F1-score. Likewise, Hassan et al. [64] tested InceptionV3, ResNet50, and VGG19 with categorical cross-entropy, with VGG19 achieving 98.9% accuracy and an MCC of 97.8%. Data scarcity and class imbalance were also addressed creatively. Amin et al. [65] used level-set segmentation and labeled only a fraction of training data. Still, their VGG16-based model reached 96.6% accuracy and 0.98 AUC. Chen et al. [66] leveraged MobileNetV1 with automatic color enhancement and reported 98% classification accuracy alongside strong segmentation performance (DICE = 95.28%). Sukumarran et al. [67] explored multi-architecture comparisons on YOLOv4-cropped images and found DenseNet-121 to provide the highest macro-averaged accuracy (95.5%), though YOLOv5's performance dropped during cross-validation, indicating potential overfitting risks.

Speed and efficiency were emphasized in models targeting deployment. Koirala et al. [68] optimized YOLOv4 variants for speed and precision using refined annotations. Their YOLO-mp-4l model achieved 94.07% mAP with a 93ms inference time, far outperforming full YOLOv4 in speed.

Zhong et al. [69] applied a fuzzy inference system for deblurring and segmented parasites via clustering methods. Their VGG-19 model reached 97.98% accuracy, while also estimating white blood cells with an R^2 of 0.98, enabling extended diagnostic capabilities. Some of the most sophisticated architectures came from real-time and edge-computing studies. Özbilge et al. [70] utilized YOLOv8 variants trained on COCO and VOC datasets without data augmentation, achieving mAP@[0.5:0.95] of 0.6214 through ensemble learning. Gupta et al. [71] introduced SimSearch, a semi-supervised ResNet-18-based system incorporating contrastive learning and user-guided patch selection, which reached AUC PR values up to 0.93 with high segmentation accuracy. In similar low-resource or domain-shifted contexts, Kanakasabapathy et al. [72] applied no-source adversarial adaptation using MD-nets, outperforming traditional TL frameworks with 90% accuracy and AUC of 0.952 even without access to source data.

Expanding the scope of AI detection beyond humans, Kittichai et al. [73] addressed avian malaria with a hybrid two-stage model based on YOLOv3 and Darknet. Their approach achieved 99.2% accuracy, sensitivity, and specificity, highlighting the model's generalizability across species. Cutting-edge architectures were also explored by Tan et al. [74], who integrated WGAN-GP synthetic augmentation with transformer-based models. Swin Transformer achieved 99.89% accuracy and 99.60% F1-score, while MobileViT offered faster inference suitable for smartphones. Lastly, Mujahid et al. [75] used EfficientNet-B2 with dropout and batch normalization, achieving a balanced performance of 97.57% accuracy and 99.21% AUC, validating its readiness for deployment in clinical or edge settings.

5. Datasets for Malaria Diagnosis

The reviewed studies, summarized in Table 2, utilize a wide variety of datasets to develop and evaluate AI models for malaria diagnosis from RBC images. Most of them employ either publicly available datasets such as the NIH Malaria Dataset or curated datasets from clinical sources. For example, the transformed BBBC041v1 dataset [51] contains over 63,000 single-cell RBC images, split into binary classes (infected vs uninfected), with a highly imbalanced yet realistic sample distribution. Similarly, the P. falciparum 3D7 dataset [52] includes training, validation, and test splits for four classes: uninfected reticulocytes, ring forms, trophozoites, and schizonts, and is used for both segmentation (via Mask R-CNN) and multi-class stage-specific classification. Studies such as [53] and [54] utilize smartphone-captured or RGB-stained RBC images, with the SmartMalariaNET dataset [53] comprising 1,822 thin blood smear images across 140 patients. This dataset enables binary classification (infected vs uninfected) using mobile-acquired images, which mirrors low-resource diagnostic scenarios. The widely used NIH Malaria Dataset [54], [55], [58], [64], [65], and [75] appears in multiple studies, offering 27,558 balanced RGB-stained single RBC images (13,779 infected and 13,779 uninfected). These studies typically frame the task as a binary classification problem and serve as a benchmark for model comparison.

Several datasets go beyond binary classification by incorporating additional classes or morphological labels. The segmented RBC dataset [57] includes morphological features (RGB-based) and is labeled with six classes: normal RBCs, malaria-infected cells, Howell-Jolly (HJ) bodies, platelet (PLT) fragments, basophilic stippling (BS), and Pappenheimer (PP) bodies. Likewise, the MP-IDB dataset [60], [66], and [67] offers high-resolution thin blood smear images annotated by Plasmodium species and stages (e.g., P. vivax, P. malariae, P. falciparum, P. ovale), allowing for multiclass classification tasks. Study [63] also provides multi-stage and multi-species annotations from the PlasmoID Dataset, comprising 468 RGB microscopy images annotated with 691 malaria parasites. In terms of data volume and diversity, the NRC Dataset [59] is particularly rich, containing 68,485 cell images from 202 patients. It includes both infected and uninfected RBCs extracted from Giemsa-stained thin smears, offering a large and diverse pool for model training and validation. Additionally, some datasets incorporate phase-based imaging [61] or focus on nuclei detection via bounding boxes, as in the M5 Dataset [62] with over 20,000 labeled nuclei. These provide opportunities for more granular classification and segmentation tasks, including instance-level detection and healthy-vs-infected differentiation under various optical modalities.

Several datasets focus on augmenting and preprocessing for model generalizability. For example, the mixed dataset in [69] combines NIH and Sudan-sourced images, featuring over 46,000 samples including both malaria parasites and white blood cells (WBCs), using 64×64-pixel RGB patches. Dataset [74] also scales up its size via augmentation, creating 14,400 synthetic images and mixing 64,800 for broader generalization across devices and conditions. Similarly, the dataset in [68] provides bounding box annotations for 2,703 training and 1,182 test images, allowing object detection models to localize parasites within images. Other notable datasets include [70], which contains 1,081 thin blood smear images annotated with bounding boxes for Plasmodium stages, and [71], which focuses on high-resolution microscopy patches with 607 labeled trophozoites. Datasets [72] and [73] further refine RBC-level annotations, with [73] involving a two-stage setup: first for RBC detection (432 images), and second for stage classification (12,761 cropped RBCs). These are particularly useful for models requiring multi-stage pipelines or hierarchical classification strategies. In summary, the datasets employed across these 25 studies vary in size, resolution, imaging modality, and label structure. Most studies target binary classification (infected vs uninfected), while others expand to multi-class or species-stage classification. The diversity in data sources (ranging from standard laboratory images to smartphone microscopy) enables the development of robust, scalable, and real-world applicable AI systems for malaria diagnosis.

Table 2. Summary of Datasets for Malaria Diagnosis

Ref	Dataset	Training & Testing Details	Features & Classification
[51]	BBBC041v1 (transformed)	▪ 63,645 total samples ▪ 56,149 uninfected, 2,099 infected (train) ▪ 5,098 uninfected, 299 infected (test)	▪ Feature: single-cell RBC images ▪ Classification: Binary (infected vs uninfected)
[52]	P. falciparum 3D7 dataset	▪ 173 train, 64 val, 60 test ▪ 4 classes: uninfected reticulocytes, ring, trophozoite, schizont	▪ Mask R-CNN for segmentation ▪ Classification: Multi-class (stage-specific classification)
[53]	SmartMalariaNET dataset	▪ 1,822 thin-blood-smear images (from 140 patients) ▪ 297 train, 99 val, 100 test	▪ Smartphone-captured Giemsa-stained smears ▪ Classification: Binary (infected vs uninfected)
[54]	NIH Malaria Dataset	▪ 27,558 cell images total (13,779 infected, 13,779 uninfected)	▪ RGB-stained single RBC images ▪ Classification: Binary (infected vs uninfected)
[55]	NIH Malaria Dataset (LHNCBC, NLM)	▪ 27,558 images (13,779 parasitized, 13,779 uninfected) ▪ Captured via Android smartphone	▪ RGB microscopic images of RBCs ▪ Classification: Binary (infected vs uninfected)
[56]	Malaria RBC dataset from Kaggle (BioImage Informatics II)	▪ 27,601 images	▪ Spatial features from images, probability-based features ▪ Classification: Binary (infected vs uninfected)
[57]	Segmented RBC images	▪ 6,415 RBC images for training ▪ 23 new smears for testing	▪ Morphological image data (RGB-based) ▪ Classification: Multi-class (normal, malaria, HJ, PP, BS, PLT)
[58]	NIH Malaria Dataset	▪ 27,557 images (13,778 parasitized, 13,779 uninfected)	▪ RGB microscopic images of RBCs ▪ Classification: Binary (infected vs uninfected)
[59]	NRC Dataset	▪ 68,485 cell images (14,752 infected RBCs, 53,733 uninfected components) from 202 patients	▪ RGB images of Giemsa-stained thin blood smears ▪ Classification: Binary (infected vs uninfected)
[60]	MP-IDB	▪ 210 images of 4 species (104 Pf, 37 Pm, 29 Po, 40 Pv)	▪ RGB images of thin blood smear at high resolution ▪ Classification: Multi-class (species classification)
[61]	RBC phase images	▪ 5,400 images for training & validation	▪ Phase images per RGB wavelength

Ref	Dataset	Training & Testing Details	Features & Classification
		▪ Test set: 350 images	▪ Classification: Binary (healthy vs infected)
[62]	M5 Dataset	▪ 7,543 images with 20,331 labeled nuclei	▪ Red blood cell microscopy images, annotated with bounding boxes ▪ Classification: Binary (infected vs uninfected)
[63]	PlasmoID Dataset	▪ 468 microscopy images ▪ 691 labeled malaria parasites	▪ RGB color images (1600x1200) ▪ Classification: Multi-class (species and stages)
[64]	NIH Malaria Dataset via Kaggle	▪ 27,558 images	▪ RGB images (224×224) ▪ Classification: Binary (infected vs uninfected)
[65]	NIH Malaria Dataset (thin blood smear images)	▪ 2,500 used (1,250 infected, 1,250 uninfected)	▪ RGB images (128×128) ▪ Classification: Binary (infected vs uninfected)
[66]	MP-IDB Dataset	▪ 229 thin blood smear images ▪ Image size: 2592×1944 pixels	▪ Plasmodium species and life stages (16 classes) ▪ Classification: Multi-class (species and stages)
[67]	MP-IDB & MRC-UNIMAS datasets	▪ 446 images for Stage 1; further augmented and split into train/validation/test	▪ Giemsa-stained thin blood smears ▪ Classification: Multi-class (species and stages)
[68]	Malaria dataset	▪ 2703 images for training, 1182 for testing	▪ RGB images, bounding box annotations for parasites ▪ Classification: Binary (parasites present vs absent)
[69]	NIH dataset	▪ Mixed dataset (NIH + Sudan) ▪ 23,398 infected + 23,398 healthy images ▪ Classification: Binary (infected vs uninfected)	▪ RGB images (patches 64×64 px), containing malaria parasites and WBCs ▪ Classification: Binary (infected vs uninfected)
[70]	Thin blood smear images	▪ 1,081 images ▪ Annotated bounding boxes for parasites	▪ Image pixels, annotated bounding boxes ▪ Classification: Multi-class (stages of Plasmodium)
[71]	BBBC041v1 dataset	▪ 258 microscopy images ▪ 607 annotated trophozoites	▪ RGB microscopy patches of blood smear images ▪ Classification: Binary (infected vs uninfected)
[72]	Malaria dataset	▪ 27,558 labeled RBC images	▪ Red blood cell images, with or without parasites ▪ Classification: Binary (infected vs uninfected)
[73]	Microscopic images of RBC	▪ Stage 1: 432 images for RBC detection ▪ Stage 2: 12,761 cropped single RBC images	▪ Single-cell blood smear images ▪ Classification: Multi-class (stages of Plasmodium)
[74]	Original RBC images	▪ 2,061 images from 100 patients ▪ Augmented: 14,400 images ▪ Mixed: 64,800 images	▪ Various microscopy images ▪ Classification: Multi-class (species and stages)
[75]	NIH Malaria Dataset	▪ 27,558 cell images	▪ Microscopic RGB images of RBCs ▪ Classification: Binary (infected vs uninfected)

6. Main Findings and Contributions

Recent developments in malaria diagnosis powered by artificial intelligence (AI) have shown remarkable improvements, especially with the implementation of deep learning and transfer learning approaches. Multiple investigations have reported that pre-trained models trained on medical-specific datasets (e.g., TL-NIH) deliver superior accuracy and reliability compared to traditional ImageNet-based models [51]. For instance, VGG-19 consistently achieved superior classification results, and synthetic data was found to improve sensitivity despite introducing some false positives [51]. These models support computer-aided diagnosis (CADx) tools, which are especially critical in low-resource settings where trained microscopists are limited. Additionally, the use of Mask R-CNN and ensemble learning approaches further boosted detection performance and efficiency [52], [55]. Notably, automated diagnosis systems were reported to be up to 15 times faster than manual examination [52], making them practical for large-scale deployment in endemic areas. Smartphone-compatible tools like AIDMAN have also shown clinical-grade performance, handling dye impurities and cell overlap effectively [53].

In terms of real-world applicability, several studies focused on developing lightweight and efficient models suitable for mobile or point-of-care use. Approaches such as NASNet-based feature extraction [56], ensemble CNNs [55], and customized YOLO architectures [60] showed promising results in both early and mature parasite detection. These tools are designed for integration with portable devices like smartphones and compact microscopes, making them ideal for field diagnostics. One noteworthy system, AIDMAN, demonstrated robustness even under challenging imaging conditions such as staining impurities and cell overlaps [53]. Meanwhile, TL-SGAN achieved high accuracy with minimal labeled data, offering a semi-supervised solution to the problem of limited ground truth annotations in medical images [65]. These innovations significantly contribute to the democratization of malaria diagnostics, extending accessibility to underdeveloped regions [54], [57], [58].

Another significant development lies in enhancing diagnostic precision and generalization across domains. Advanced segmentation methods such as pixel-level localization (as seen in FARS) and attention-based deep networks have enabled models to maintain high performance across varying microscope types and magnification levels [62]. These approaches help in detecting not only malaria-infected cells but also other inclusions such as Howell-Jolly bodies or platelets [57], thereby increasing clinical utility. Simultaneously, data augmentation and domain adaptation strategies have played crucial roles in reducing overfitting and ensuring the model's applicability to diverse datasets [64]. Studies combining classical image processing with deep learning further improved region-of-interest extraction and classification accuracy, particularly in local and rural settings such as Indonesia [63]. These studies underscore the importance of adaptable and interpretable AI models that can seamlessly integrate into existing laboratory workflows or function independently in decentralized settings [59], [61].

Some of the most innovative studies also explored the integration of AI diagnostics with broader computational infrastructures. For instance, the implementation of edge–cloud architectures and blockchain technologies has allowed for secure, traceable, and scalable diagnostic systems [66]. These systems ensure that patient data remains protected while supporting rapid remote analysis. In addition, models like YOLOv4 and DenseNet-121 were successfully utilized for species-level malaria classification, enhancing the specificity of diagnosis, which is crucial for appropriate treatment planning [67]. The development of compact and efficient models, such as YOLO-mp and EfficientNet-B2, offers high performance with reduced memory and computational requirements, allowing deployment even on low-end devices [68], [75]. Ensemble techniques and anchor-free object detectors such as YOLOv8 have also shown superior performance for detecting small parasites in thin blood smears [70].

Furthermore, novel diagnostic frameworks like SimSearch and MD-nets enable fast malaria detection even in domain-shifted or low-quality image conditions, without requiring source data access [71], [72]. These systems are highly valuable for applications in rural clinics and mobile health units. Importantly, AI has also been extended to veterinary medicine, with models like Darknet classifying stages of Plasmodium gallinaceum in poultry [73]. Additionally, transformer-based models like Swin Transformer and MobileViT have emerged as top-performing architectures, supporting multiclass classification and efficient deployment on edge devices such as smartphones or IoT-based diagnostic systems [74]. In summary, the collective findings from these studies highlight how transfer learning, ensemble modeling, segmentation, and deployment-focused architecture design are revolutionizing malaria diagnostics. These AI-driven tools offer high diagnostic accuracy, reduced dependency on human experts, and the flexibility to operate in both clinical and remote settings. Their contributions are vital not only for accelerating malaria detection and treatment but also for strengthening global health systems, particularly in regions with limited resources and high disease burden. Through continuous innovation, these AI models are paving the way for scalable, accessible, and equitable solutions in infectious disease management.

7. Challenges and Future Recommendations

7.1. Challenges and Limitations

Although deep learning and transfer learning have brought notable progress in malaria detection, numerous studies have highlighted critical obstacles that hinder the broader applicability and clinical implementation of these models. A predominant issue across multiple studies is class imbalance. Rahman et al. [51] highlighted a severe imbalance of 1:26 between infected and uninfected samples, which complicates classification and often leads to bias toward the dominant class. Similarly, Kittichai et al. [73] faced an extreme scarcity of gametocyte images in avian malaria datasets, leading to classification bias and increased dependency on technician oversight to reduce false positives. The imbalance also impairs model sensitivity for underrepresented classes, as noted by Gupta et al. [71], whose performance on trophozoite detection dropped significantly due to rarity in training samples. Another major concern involves data labeling and annotation quality. Several studies reported errors and ambiguity in ground truth data, which subsequently affected model accuracy. Loh et al. [52] pointed to difficulties in labeling transitional parasite stages and unannotated normocytes, which resulted in estimation errors and threshold sensitivity. Similarly, Koirala et al. [68] described inconsistencies in public datasets, such as off-center, blank, or mislabeled bounding boxes, which introduced false negatives. The reliance on manually labeled or pseudo-labeled data using weak supervision also introduces noise, as Ilyas et al. [62] observed when synthetic segmentation labels reduced accuracy under certain evaluation conditions.

A critical limitation mentioned by many researchers is dataset size and diversity. Liu et al. [53] and Tan et al. [74] both emphasized that their datasets were drawn from a relatively small number of patients, raising concerns about generalizability across populations and settings. This limitation was echoed by Nugroho et al. [63] and Özbilge et al. [70], who noted that limited datasets, along with hardware constraints, prevented evaluation on larger or multiclass benchmarks. Furthermore, Mujahid et al. [75] and Amin et al. [65] restricted their experiments to binary classification (infected vs. uninfected) and acknowledged that this limitation hinders their models' applicability to real-world diagnostics, which often require species- or stage-specific detection. Hardware and computational constraints also emerged as recurring themes. Diker [54] conducted training on a low-end GPU with limited VRAM, which constrained the complexity of models and experimentation scope. Molina et al. [57] and Singla et al. [61] both mentioned the need for standardized or automated image acquisition systems, as performance variability increases when input images differ in resolution or microscope setup. Similarly, high computational cost and memory requirements were cited as barriers to deployment by Alnussairi et al. [58], Hassan et al. [64], and Zhong et al. [69], with some noting that memory-intensive models such as VGG or ResNet may be impractical for low-resource settings.

Cross-dataset generalization remains an unsolved issue in the field. Zedda et al. [60] and Acherar et al. [59] reported decreased performance when models trained on NIH or NRC data were tested on new datasets or external patients. In the case of Zedda et al. [60], the YOLO-based model struggled to detect Plasmodium vivax due to its small parasite size and low prevalence, and even generated false positives on white blood cell nuclei. Chen et al. [66] and Sukumarran et al. [67] also struggled with generalization due to limited class samples or imbalance, especially for P. malariae and P. ovale. In addition, several works revealed that model architecture choices and evaluation settings can influence interpretability and accuracy. Qadri et al. [56] noted that CNN-based features yielded poor performance (~61%) compared to transfer-based ones, and NASNet suffered from validation accuracy fluctuations. Kanakasabapathy et al. [72] pointed out that domain-adapted models still rely on pretrained weights, which may carry biased feature representations from unrelated tasks. They also emphasized the challenge of validating models with minimal labeled data, particularly in settings with poor image quality.

Lastly, a number of studies flagged real-world deployment limitations, including image variability, standardization of acquisition protocols, and the lack of testing in diverse geographic or clinical contexts. Bhuiyan et al. [55] and Liu et al. [53] admitted that their models were trained on well-structured datasets and have not been fully validated in operational field conditions. Several others such as SmartMalariaNet [53] and Gupta et al. [71] stressed the need for robust pipelines that can handle rare cases, noisy patches, or input images captured in uncontrolled environments. In summary, while the reviewed studies demonstrate high accuracy under controlled conditions, their limitations converge on three core issues: (1) limited dataset diversity and labeling inconsistencies, (2) class imbalance and performance degradation for rare classes, and (3) computational constraints and domain transferability challenges. Addressing these limitations is essential to ensure that malaria detection models can evolve from promising research tools into reliable, deployable diagnostic systems across real-world healthcare settings.

7.2. Future Recommendations

A significant number of future directions proposed by the studies revolve around improving dataset quality, diversity, and annotation. Many authors emphasized the importance of expanding datasets to include more parasite species, life stages, and image sources. Rahman et al. [51] recommended the use of synthetic data generation, particularly via GANs, to balance rare classes and simulate diverse parasite morphologies. Similarly, Loh et al. [52] and Kittichai et al. [73] suggested increasing the number of annotated gametocytes and incorporating fine-grained labels for transitional stages to enhance model granularity and real-world reliability. This aligns with the call from Liu et al. [53] to collect data from multiple countries and adopt thick-smear imaging for broader diagnostic application, including co-infections such as Trypanosoma or Microfilaria. Others, like Nugroho et al. [63], proposed developing adaptive thresholding methods to mitigate luminance variation and enrich the dataset with greater generalization potential. Beyond data enrichment, many studies highlighted the need for architectural improvements and model adaptation to real-world scenarios. Diker [54] and Bhuiyan et al. [55] proposed evaluating novel network architectures and extending existing binary classifiers into multi-class systems for species- and stage-specific classification. Researchers also noted that existing backbones like VGG16 could be replaced with newer and more efficient models such as DenseNet or ResNet to increase classification performance and reduce computational cost [65], [69]. Moreover, Qadri et al. [56] advocated for the use of more advanced pretrained models and the development of a web-based tool to enable real-time malaria monitoring and public health integration.

The theme of deployment and real-time implementation was prevalent across several recommendations. Authors proposed embedding diagnostic models into portable and mobile devices to enable use in field settings. For instance, Molina et al. [57] and Sukumarran et al. [67] encouraged integration into real-time mobile applications, while Diker [54] and Singh et al. [64] envisioned mobile-compatible CNN tools optimized for species detection. To enable such deployment, the use of lightweight models and segmentation techniques suited for edge devices was stressed by Chen et al. [66], who also proposed optimizing the system for other infectious diseases beyond malaria. Özbilge et al. [70] highlighted the need for longer training epochs and more robust ensembling strategies to refine model performance in embedded systems. Some studies proposed extending AI diagnostic frameworks to other diseases or modalities. For example, Alnussairi et al. [58] and Ilyas et al. [62] envisioned applying their methodologies to different medical imaging domains, while Zhong et al. [69] recommended exploring Vision Transformers (ViT) to improve generalization, especially in blurred or low-quality images. Singh et al. [61] even suggested incorporating spectral response modeling to adapt detection to other red blood cell disorders such as sickle cell anemia or diabetes-related changes.

Equally important, several authors emphasized improving interoperability and collaborative development. Kanakasabapathy et al. [72] proposed extending their MD-net framework to federated learning across medical institutions and enhancing model interpretability through multimodal data integration. Koirala et al. [68] called for standardized data labeling practices and interdisciplinary collaboration between machine learning experts and clinicians. Likewise, Tan et al. [74] and Mujahid et al. [75] suggested incorporating metadata such as climate, demographics, and geography into prediction models for improved performance across environmental conditions. Lastly, the studies acknowledged the importance of rigorous validation and clinical translation. Multiple authors (including SmartMalariaNet [53], Molina et al. [57], and Kittichai et al. [73]) recommended conducting clinical proof-of-concept studies, inter-/intra-observer validation, and external testing on independent, multicenter datasets. These steps are necessary to move AI-based malaria detection from the research lab to frontline diagnostic use, especially in resource-limited areas where malaria remains a significant health threat.

8. Conclusion

Over the past few years, the application of deep learning and transfer learning has significantly advanced automated malaria detection, offering high levels of accuracy, speed, and scalability. The reviewed studies demonstrated that convolutional neural networks (CNNs), especially those pretrained on ImageNet (such as VGG16, VGG19, ResNet, DenseNet), consistently perform well in binary classification tasks (infected vs. uninfected), with many models reaching accuracy above 95%, and in some cases even achieving near-perfect scores under controlled conditions. More advanced models, including transformers, ensemble techniques, and domain-adaptive networks, further improved classification and segmentation precision, particularly when fine-tuned using medically relevant datasets like NIH or NRC. Effective preprocessing methods (such as color normalization, patch extraction, and image augmentation) were found to be critical in enhancing model performance. Moreover, transfer learning approaches that reused features from pretrained weights provided strong baselines and helped overcome the challenge of limited labeled medical data. However, model performance often varied depending on data source, image modality (e.g., thin vs. thick smears), and labeling quality.

Despite these strengths, several key limitations remain. Class imbalance, especially in detecting rare parasite stages or species like P. ovale or gametocytes, continues to hamper sensitivity and generalizability. Inconsistent annotations, limited dataset diversity, and reliance on data from a single geographic or institutional source limit the robustness of many models when applied to new clinical settings. Moreover, the heavy computational requirements of deep models and insufficient real-world testing restrict their feasibility in low-resource areas most affected by malaria. To address these challenges, future research should prioritize data enrichment (e.g., via GANs, diffusion models, and international data pooling), model optimization for multiclass and multi-stage classification, and real-world validation including federated learning and mobile deployment. Clinical proof-of-concept trials, cross-institutional collaborations, and open benchmarking standards will be essential to ensure reproducibility and global impact. In conclusion, while current AI-based systems for malaria detection show high promise and technical feasibility, transitioning from research prototypes to reliable clinical tools requires overcoming challenges in data quality, model robustness, and deployment constraints. Future innovations must emphasize equity, interpretability, and integration with healthcare infrastructures to realize AI's full potential in global malaria control and eradication efforts.

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