

A convolutional neural network with attention mechanism-based malaria detection from blood smear images

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ABSTRACT

With 249 million cases and 608,000 fatalities recorded in 2022, malaria is one of the major worldwide health concerns, particularly in areas with low resources. In this paper, we propose a custom convolutional neural network (CNN) with an integrated attention mechanism to inspect malaria from blood smear images. To improve model robustness, we combined three publicly available datasets from the NIH and Kaggle. The proposed model achieved 98.20% accuracy, 97.85% precision, 98.55% recall, and 98.20% F1-score, outperforming conventional diagnostic methods. In addition, we conduct comparative analyses using two transfer learning models, ResNet50 and DenseNet. ResNet50 attained 95.06% precision, 95.44% recall, with 95.05% F1-score, while DenseNet achieved a precision of 87.96%, recall of 88.33%, and F1-score of 87.90%. For interpretability, Grad-CAM and saliency map visualizations highlighted key image regions, with saliency maps offering finer pixel-level localization. These results highlight the potential of our attention-based CNN as a feasible, interpretable diagnostic tool for malaria, particularly in low-resource settings.

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1. INTRODUCTION

Malaria is a life-risky infectious disease caused by *Plasmodium* parasites along with transmitted through the bites of infected female *Anopheles* mosquitoes. According to the World Health Organization (WHO), malaria remains a major worldwide health factors, with 247 million cases as well as 619,000 deaths in 2021 [1]. The African Region of WHO accounts for 95% of cases with 96% of deaths, with children under five representing about 80% of the fatalities [2]. In addition to Africa, parts of Asia and the Americas also experience high malaria prevalence, often exacerbated by limited healthcare access. Timely diagnosis is inevitable for effective malaria disease and control. Traditional diagnostic methods include microscopic examination of blood smears, rapid diagnostic tests (RDTs), with polymerase chain reaction (PCR) techniques [3]–[5]. How-

ever, these methods face challenges such as dependency on skilled personnel, high cost, or limited accessibility in low-resource settings. To address these limitations, automated diagnostic approaches using machine learning and deep learning have gained traction. Convolutional neural networks (CNNs), in particular, have shown strong potential in analyzing blood smear images to detect malaria-infected cells [6]. Multiple studies have explored this avenue: Yang *et al.* [7] used Faster R-CNN and achieved 91.46% accuracy; Abbas and Dijkstra [8] employed a random forest approach with 93.9% classification accuracy; Liang *et al.* [9] used CNNs and reported 97.5% accuracy on thin smears. Transfer learning has also been explored. Reddy and Juliet [10] utilized ResNet-50 to achieve 97.77% accuracy. Molina *et al.* [11], [12] applied CNNs with accuracies exceeding 97%. Recent works like [13]–[15] further confirm CNNs' effectiveness, with accuracies ranging between 93.89% and 97.81%. Despite high accuracy, most existing CNN models process visual features uniformly and may overlook spatially relevant parasite structures in complex smear backgrounds. To overcome this, we propose a CNN-based model integrated with an attention mechanism that enhances focus on morphologically significant regions including the shape, color, and texture of infected cells—thereby improving interpretability and classification accuracy.

Our proposed model demonstrates superior performance by combining three publicly available datasets, improving robustness across different image distributions. It achieved an overall 98.20% accuracy, 97.85% precision, 98.55% recall, and 98.20% F1-score, outperforming traditional CNN and transfer learning models like ResNet (95.06%) and DenseNet (87.96%).

- A novel attention-augmented CNN model is proposed for malaria detection from blood smear images.
- The model integrates three diverse datasets and achieves an accuracy of 98.20%.
- Comparative analysis with ResNet and DenseNet confirms superior performance.

The remainder of the work is structured as following. Section 2 describes the process. Section 3 summarizes findings and analysis. Section 4 finishes the paper.

2. PROPOSED METHOD

After an extensive analysis of different workflows, we have identified the most effective one for the proposed model. This workflow is designed to deliver our desired outcomes efficiently. The complete process is shown in Figure 1.

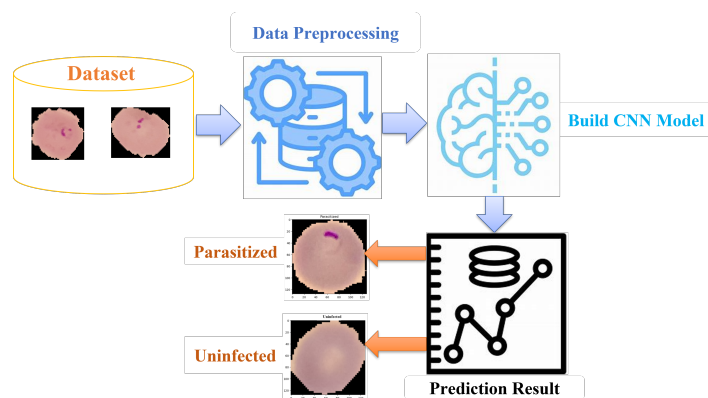


Figure 1. Proposed methodology

2.1. Dataset description and splitting

To achieve accurate classification of malaria-parasitized and uninfected cells, our study merged three distinct datasets, evaluating their results individually. This multi-dataset approach enhances model robustness and ensures performance across varied image sets. The first dataset, from Kaggle [16], contains 27,558 thin blood smear images with diverse magnifications along with lighting. The second dataset, sourced from the National Institute of Health (NIH) [17], includes 1,141 high-resolution thick blood smear images of white blood cells. The third dataset, also from NIH [18], consists of 1,883 white blood cell smear images. Figure 2 shows sample images from the datasets, where Figure 2(a) presents a thin infected blood cell, Figure 2(b) shows an infected thick white blood cell, and Figure 2(c) illustrates an uninfected thick white blood cell.

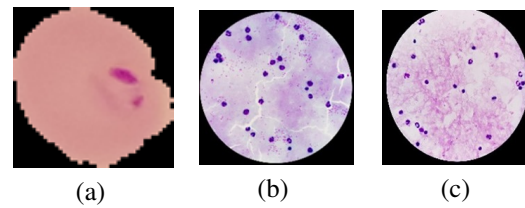


Figure 2. Sample images from the datasets: (a) thin infected blood cell, (b) infected thick white blood cell, and (c) uninfected thick white blood cell

2.2. Data preprocessing

Data preprocessing is vital in deep learning for effective learning from raw data. All RGB images, originally ranging from 76×68 to 152×141 , are resized to $64 \times 64 \times 3$ for uniformity. Rotation, flipping, cropping, as well as noise addition are applied to expand the dataset and enhance generalization. The dataset is divided into 70% training, 15% validation, as well as 15% testing sets to evaluate performance and reduce overfitting. Image distribution across these sets is displayed in Table 1.

Table 1. Optimal dataset division for training and testing

Label	Training	Validation	Test	Total
Parasitized	10683	2304	2304	15291
Uninfected	10683	2304	2304	15291
Total	21366	4608	4608	30582

2.3. Building a CNN model for malaria detection

CNNs are widely used in image classification [19]–[21] researches for their ability to learn hierarchical features directly from raw input data. They are composed of convolutional, pooling, and fully connected layers. These layers extract spatial patterns such as shape, color, and texture—critical for analyzing medical images like blood smears.

To detect malaria parasites effectively, we designed a lightweight CNN model trained from scratch. This customized architecture includes smaller convolutional and pooling layers for computational efficiency, dropout layers to prevent overfitting, and a softmax output layer for multi-classification. The proposed model achieved an accuracy of 98.20%, outdoing pre-trained alternatives and proving its suitability for specialized medical image analysis. The architecture is summarized in Table 2.

Table 2. Architecture summary

Layer description	Output dimensions	Parameter
Conv2D	(None, 64, 64, 16)	448
Conv2D	(None, 64, 64, 16)	2320
Maxpooling2D	(None, 32, 32, 16)	0
Conv2D	(None, 32, 32, 32)	4640
Conv2D	(None, 32, 32, 32)	9248
Attention block	(None, 32, 32, 32)	292
Maxpooling 2D	(None, 16, 16, 32)	0
Conv2D	(None, 16, 16, 64)	18496
Conv2D	(None, 16, 16, 64)	36928
Maxpooling 2D	(None, 8, 8, 64)	0
conv2d.6	(None, 8, 8, 128)	73856
conv2d.7	(None, 8, 8, 128)	147584
Maxpooling 2D	(None, 4, 4, 128)	0
Dropout	(None, 4, 4, 128)	0
Flatten	(None, 2048)	0
Dense	(None, 256)	524544
Dropout	(None, 256)	0
Dense	(None, 2)	514
Total parameter: 818,578		
Trainable parameter: 818,578		
Non-trainable parameter:0		

3. EXPERIMENTAL PREPARATION AND ASSESSMENT

The architecture is implemented and trained using Google Colab with a Tesla T4 GPU (16 GB) and Python 3.10.12. Accuracy, recall, precision, and the F1-score are used to evaluate the model's performance. Accuracy reflects the proportion of correct predictions. However, in imbalanced datasets, it may not provide a complete picture. Hence, we also refer to the confusion matrix components: true positives (TP), false positives (FP), and false negatives (FN), and true negatives (TN). Precision quantifies the ratio of correctly predicted positive observations to total predicted positives, while recall or sensitivity measures the ability to detect actual positives. F1-score, the harmonic mean of precision with recall, provides a regular assessment in the class disparity.

To assess generalization, the model was tested on a held-out test set. Table 3 presents a comparative analysis of our CNN with ResNet and DenseNet. The proposed model achieves a balance between accuracy as well as training efficiency, with lower training time than ResNet but slightly higher than DenseNet. Figure 3 demonstrates stable learning without signs of overfitting or underfitting, with Figure 3(a) showing the accuracy trend and Figure 3(b) showing the loss trend. This validates the model's generalization capability to unseen data.

Table 3. Performance comparison on test set

Metric	ResNet	DenseNet	Proposed CNN
Test accuracy (%)	95.06	87.96	98.20
Precision (%)	94.67	87.48	97.85
Recall (%)	95.44	88.33	98.55
F1-score (%)	95.05	87.90	98.20
Training time (s)	2038.2	1840.6	2008.93

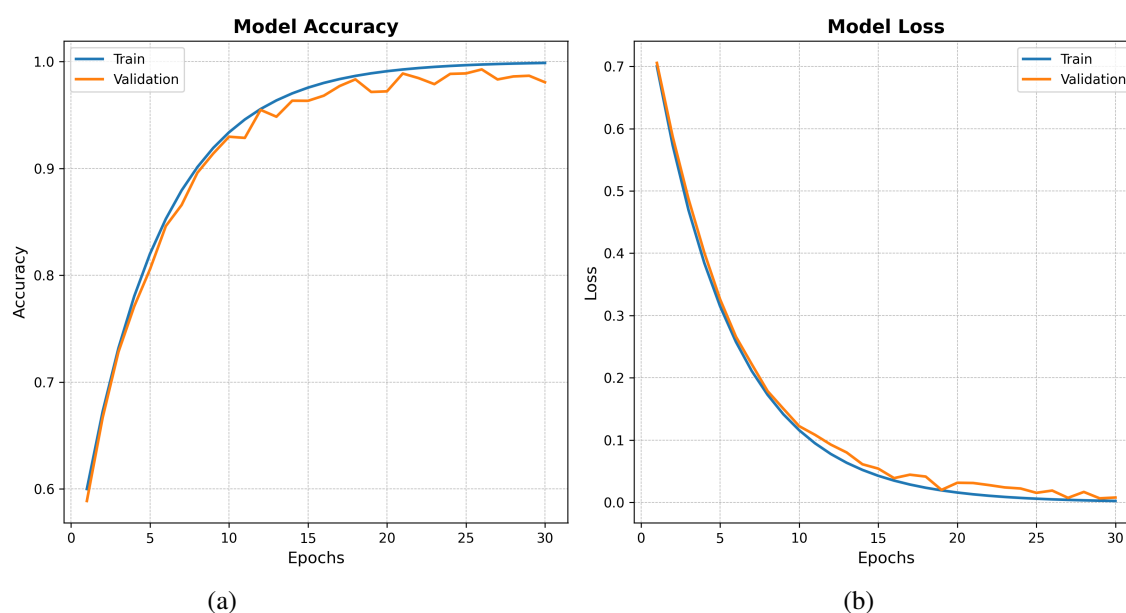


Figure 3. Trends of the proposed model: (a) accuracy and (b) loss

To improve interpretability for clinical users, we used Grad-CAM and saliency maps. As illustrated in Figures 4 and 5, Grad-CAM highlights broad attention regions, which may limit precision. Saliency maps, offering pixel-level gradients, provide more accurate localization of infected areas, enhancing clinical relevance and trust. Extensive experiments confirmed the proposed model's superior accuracy, interpretability, and efficiency. Its ability to generalize across diverse test samples marks its potential as a reliable method for malaria diagnosis in real-world clinical settings.

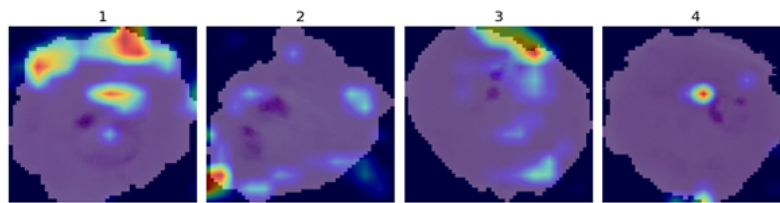


Figure 4. Model attention visualization using Grad-CAM

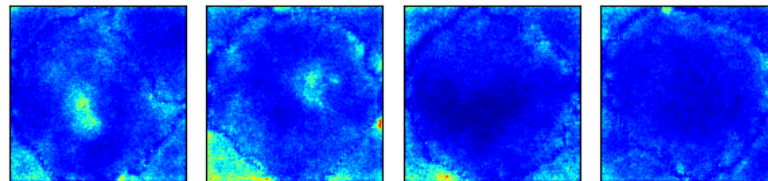


Figure 5. Model attention visualization using saliency maps

Table 4 illustrates the existing works with our work. From all of these papers, the proposed model provided the highest results. The scalability of our model in resource-constrained environments may be hampered by its reliance on high-quality RGB photos and significant processing resources. Optimizing the model with lower-resolution photos, edge computing, or lighter architectures may increase its viability in such contexts.

Table 4. Summary of related work in malaria detection using ML techniques

Sources	Dataset type	Method used	Performance
[7]	Smartphone images (thick smear)	Faster R-CNN	Acc: 91.46%, Sens: 90.16%, Spec: 92.75%
[8]	2000 thin smear images	Random Forest	Acc: 96.8%, Class. Acc: 93.9% (4-stage)
[22]	27,558 thick smear images	RF, SVM, ANN, KNN	Acc: 97.8%, Sens: 98.7%, Spec: 96.9%
[11]	1500 auto microscope images	Sequential categorization method	Acc: 98.5%, Class. Acc: 97.9%
[9]	Thin smear images	CNN	Acc: 97.5%
[23]	Blood cell images	CNN	Acc: 96.5%
[24]	13,272 peripheral smear images	Deep Belief Networks	Acc: 96.9%, Sens: 98.2%
[25]	2267 images	CNN for CBC and malaria detection	RBC: 97.34%, WBC: 95.68%, Malaria: 95.29%
[12]	Blood smear images	CNN	Acc: 97.2%, F1: 0.75 (malaria), Acc: 96.5%, F1: 0.71 (other)
[10]	Thin smear images	Transfer learning	Acc: 97.77%, Sens: 97.75%, Spec: 97.80%
[14]	LHNCB thick smear dataset	Pretrained CNN	Acc: 93.89%
[13]	NIH microscopy images	CNN	Acc: 97.81%
[26]	Blood smear images	CNN	Acc: 95.73%
[15]	Blood smear images	CNN	Acc: 94%
Proposed model	NIH microscopy images	Customized CNN	Acc: 98.2%, Precision 97.85%, Recall 98.55%, F1-score 98.20%

4. CONCLUSION

This study introduced a tailored CNN model with an integrated attention mechanism for classifying malaria using blood smear images. The proposed method achieved a 98.20% accuracy, surpassing baseline methods. It also demonstrated strong performance in other metrics, achieving a 97.85% precision, 98.55% recall, and 98.20% F1-score, indicating robust identification of malaria-positive cases. We compared our model against ResNet50 and DenseNet to evaluate its effectiveness. ResNet50 achieved 95.06% accuracy, 94.67% precision, 95.44% recall, along with an F1-score of 95.05%. DenseNet obtained 87.96% accuracy, 87.48% precision, 88.33% recall, and 87.90% F1-score. These comparisons confirm the strength of the proposed architecture in malaria detection. In addition to improved performance, the model offers practical advantages by potentially easing the diagnostic burden on medical staff, especially in low-resource environments where

conventional methods are still prevalent. Despite the promising outcomes, there remain challenges in distinguishing various parasite types and developmental stages. Future work will aim to address these issues and refine the model for broader clinical deployment.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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Shahina Haque	✓	✓			✓	✓			✓	✓				
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C : Conceptualization

M : Methodology

So : Software

Va : Validation

Fo : Formal Analysis

I : Investigation

R : Resources

D : Data Curation

O : Writing - Original Draft

E : Writing - Review & Editing

Vi : Visualization

Su : Supervision

P : Project Administration

Fu : Funding Acquisition

CONFLICT OF INTEREST STATEMENT

The authors declare that they have no conflict of interest.

DATA AVAILABILITY

The supporting data of this study are open available in the Kaggle at <https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria>, reference [16]; and NIH-NLM platform at <https://data.lhncbc.nlm.nih.gov/public/Malaria/NIH-NLM-ThickBloodSmearsU/NIH-NLM-ThickBloodSmearsU.zip>, reference [17] and https://data.lhncbc.nlm.nih.gov/public/Malaria/Thick_Smears_150/index.html, reference [18].

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