

Adaptive Marine Predators Algorithm for Optimizing CNNs in Malaria Detection [†]

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Abstract

Malaria remains a major global health burden, requiring rapid and reliable diagnostic tools to complement or replace labor-intensive manual microscopy. Although deep learning methods have demonstrated strong potential for automated malaria diagnosis, many existing approaches depend on computationally expensive transfer learning architectures or exhibit sensitivity to suboptimal hyperparameter configurations. This study proposes a lightweight automated framework for binary classification of malaria cell images using a custom Convolutional Neural Network (CNN) optimized by a novel Adaptive Marine Predators Algorithm (AMPA). The proposed AMPA integrates a state-aware adaptive control factor that dynamically adjusts step size based on population loss, thereby improving search efficiency and reducing susceptibility to local optima. The framework was evaluated on the NIH Malaria Cell Image Dataset containing 27,558 single-cell images. Experimental results show that the AMPA-optimized CNN achieves a testing accuracy of 95.00% and an Area Under the Curve of 0.986. Comparative experiments indicate that the proposed model outperforms several reported lightweight architectures, including MobileNetV2 (92.00%) and YOLO-based detectors (94.07%), while achieving performance comparable to deeper networks such as VGG-16 (94.88%), with substantially lower computational complexity. The model further attains high sensitivity (0.94) and precision (0.96), supporting its suitability as a robust and resource-efficient approach for automated malaria screening research.

Keywords: malaria detection; Convolutional Neural Networks (CNNs); hyperparameter optimization; Marine Predators Algorithm (MPA); adaptive step-size; multi-objective optimization



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1. Introduction

Malaria remains a persistent global public health challenge, particularly in tropical and subtropical regions. According to the World Health Organization (2022) (<https://www.who.int/teams/global-malaria-programme/reports/world-malaria-report-2022> accessed

on 29 December 2025), millions of cases are reported annually, with children less than five years of age and pregnant women representing the most vulnerable populations. Accurate and timely detection of *Plasmodium* infections is critical for effective disease management [1]. Currently, microscopic examination of Giemsa-stained thin blood smears serves as the diagnostic gold standard. While reliable when conducted by trained personnel, this approach is labor-intensive, time-consuming, and prone to inter-observer variability [2]. In resource-constrained settings, shortages of skilled microscopists further limit diagnostic capacity, motivating the development of automated and scalable detection tools.

Deep learning, particularly Convolutional Neural Networks (CNNs), has transformed biomedical image analysis by enabling automated extraction of hierarchical features from high-resolution microscopy images [3,4]. CNN-based approaches have demonstrated potential for malaria parasite detection, improving throughput and consistency relative to manual microscopy [5–7]. Nevertheless, practical deployment remains constrained by the trade-off between diagnostic accuracy and computational efficiency [8]. High-capacity models can achieve strong performance but require substantial memory and computational resources, limiting their suitability for low-resource or edge-based environments. Conversely, lightweight models and optimized network architectures can reduce computational demands but often struggle with fine-grained single-cell discrimination.

To address these challenges, this study proposes a lightweight CNN for malaria cell classification optimized via an Adaptive Marine Predators Algorithm (AMPA). The adaptive optimization incorporates a State-Aware Control Factor that monitors population-level loss to adjust step size, promoting exploration and improving convergence stability. This approach systematically identifies well-conditioned network configurations while maintaining computational efficiency.

The main contributions of this work are:

- Development of an adaptive variant of the Marine Predators Algorithm that adjusts step size based on population loss dynamics, enhancing convergence stability during CNN hyperparameter optimization.
- Design and optimization of a task-specific lightweight CNN for malaria cell classification, avoiding reliance on large pre-trained backbones.
- Quantitative evaluation of the proposed framework on a standard malaria dataset compared against representative lightweight CNNs and detection-based approaches.

2. Related Work

Deep learning, particularly CNNs, has been widely applied for automated malaria parasite detection to overcome manual microscopy limitations, including labor intensity and inter-observer variability [9]. High-capacity architectures such as VGG-16, VGG-19, ResNet-50, and DenseNet-121 achieve strong performance but are computationally expensive and typically trained using transfer learning from natural images, limiting suitability in low-resource settings [10].

Lightweight CNNs, including MobileNetV2, EfficientNet-B0, ShuffleNet, and SqueezeNet, reduce memory and inference time, while YOLO-based detection frameworks offer object-level classification [11]. However, both approaches can struggle with fine-grained single-cell discrimination when parasitic features are subtle or overlapping [12]. Attention mechanisms and multi-scale feature extraction have been used to enhance sensitivity without substantially increasing complexity [13].

Efficient hyperparameter selection is critical for lightweight CNNs. Exhaustive grid search is computationally prohibitive, motivating metaheuristic algorithms such as Genetic Algorithms, Particle Swarm Optimization, Whale Optimization, and Marine Predators Algorithm [14–16].

Knowledge distillation has also been employed to transfer representational knowledge from large teacher networks to compact student models, enabling efficient deployment while maintaining accuracy [17]. More recently, Vision–Language Models (VLMs) have been introduced in medical image analysis to integrate visual features with clinical text, supporting multimodal reasoning and generalization [18]. Despite their effectiveness in complex diagnostic settings, VLMs require large-scale pre-training, multimodal annotations, and substantial computational resources, which limit their applicability to single-cell malaria classification and low-resource deployment scenarios.

In contrast to approaches relying on large pre-trained backbones, multimodal foundation models, or post hoc compression, the present work focuses on task-coupled optimization of a lightweight CNN using an adaptive metaheuristic strategy. This design emphasizes alignment between optimization dynamics, model capacity, and task-specific constraints.

3. Materials and Methods

This study proposes an automated framework for the classification of malaria-infected erythrocytes using a custom Convolutional Neural Network (CNN) [19]. To reduce dependence on manual hyperparameter tuning and to improve the reliability of the classification process, both architectural and training hyperparameters of the CNN are optimized using a novel Adaptive Marine Predators Algorithm (AMPA). The Marine Predators Algorithm (MPA), originally introduced by [20] as a nature-inspired metaheuristic based on predator–prey foraging strategies, has demonstrated effectiveness in solving complex global optimization problems. Nevertheless, when applied to high-dimensional and multimodal search spaces such as those encountered in deep neural network optimization, the standard MPA may suffer from premature convergence and reduced exploration capability.

In this study, the original MPA is systematically adapted and extended to address these limitations. The proposed AMPA incorporates a State-Aware Adaptive Control mechanism that monitors population-level loss behavior and dynamically adjusts the search step size. This modification is intended to enhance exploration during stagnation phases and to improve convergence stability, thereby making the algorithm more suitable for CNN hyperparameter optimization in medical image classification tasks.

The overall methodology is structured into three main phases: (i) dataset preprocessing and normalization, (ii) task-specific CNN modeling, and (iii) bio-inspired hyperparameter optimization using AMPA, followed by controlled retraining and comprehensive performance evaluation.

3.1. Dataset Acquisition and Preprocessing

Experiments were conducted using the NIH Malaria Cell Image Dataset (https://data.lhncbc.nlm.nih.gov/public/Malaria/cell_images.zip) (accessed on 12 January 2026), a widely used benchmark in medical image analysis [5]. The dataset contains 27,558 segmented erythrocyte images per class (Parasitized and Uninfected). All images were resized to a fixed spatial resolution of 64×64 pixels with three color channels (RGB) to standardize network input. Pixel intensities were normalized to the range $[0, 1]$ as:

$$x'_{ij} = \frac{x_{ij}}{255}$$

The dataset was partitioned into training (80%) and validation (20%) subsets using a directory-level split. To support reproducibility, random seeds were fixed for NumPy and TensorFlow during data loading and model initialization.

To improve generalization and reduce overfitting during final model training, real-time data augmentation was applied to the training set. Augmentation operations included

random rotations within $\pm 20^\circ$, zoom transformations up to 15%, and horizontal flipping. No augmentation was applied during the optimization phase to preserve fitness stability and reduce computational cost.

3.2. Convolutional Neural Network Formulation

The baseline classifier is a sequential convolutional neural network designed to extract hierarchical spatial features from erythrocyte images. The architecture consists of two convolutional blocks followed by a dense classification head. The convolutional feature extraction process is modeled as:

$$h_k^{(l)} = \text{ReLU}\left(\sum_c W_{k,c}^{(l)} * x_c^{(l-1)} + b_k^{(l)}\right) \quad (1)$$

where $h_k^{(l)}$ denotes the k -th feature map at layer, and represent learnable filters and biases, respectively, and $*$ denotes the convolution operator. The activation function is defined as:

$$\text{ReLU}(z) = \max(0, z) \quad (2)$$

Following spatial downsampling through max pooling, the resulting feature maps are flattened and passed to a dense layer with dropout regularization. The final prediction is produced using a sigmoid-activated neuron:

$$\hat{y} = \frac{1}{1 + e^{-(w_d \cdot h_{\text{flat}} + b_d)}} \quad (3)$$

The network is trained using the binary cross-entropy loss function:

$$\mathcal{L} = -\frac{1}{N} \sum_{i=1}^N [y_i \log(\hat{y}_i) + (1 - y_i) \log(1 - \hat{y}_i)] \quad (4)$$

Hyperparameters optimized by the Adaptive Marine Predators Algorithm include the number of convolutional filters, the number of dense neurons, the dropout rate, and the learning rate. The search bounds are defined as follows:

$$\begin{aligned} \text{Filters}_1 &\in [16, 64] \\ \text{Filters}_2 &\in [32, 128] \\ \text{Dense Neurons} &\in [64, 256] \\ \text{Dropout Rate} &\in [0.1, 0.5] \\ \text{Learning Rate} &\in [10^{-4}, 10^{-2}] \end{aligned}$$

3.3. Proposed Adaptive Marine Predators Algorithm (AMPA)

CNN hyperparameters are optimized using an Adaptive Marine Predators Algorithm. The standard Marine Predators Algorithm (MPA) simulates the foraging behavior of marine predators through Brownian motion and Lévy flight strategies. However, its fixed step-size decay can lead to premature stagnation when applied to high-dimensional and non-convex search spaces such as those encountered in CNN hyperparameter optimization.

The Adaptive Marine Predators Algorithm (AMPA) is introduced as a task-coupled optimization strategy that directly facilitates the design of an effective lightweight CNN for malaria cell classification. In this task, discriminative visual cues are subtle and the performance of lightweight models is highly sensitive to the interaction between network capacity and training hyperparameters. AMPA addresses this sensitivity by adaptively optimizing both architectural and training parameters using a state-aware control mechanism guided by population-level validation loss. This coupling stabilizes convergence and

reduces stagnation in the non-convex hyperparameter space, enabling the CNN to learn task-aligned representations from erythrocyte imagery while maintaining computational efficiency suitable for resource-constrained medical settings.

To mitigate premature stagnation, a state-aware adaptive control factor $CF(t)$ is introduced to regulate exploration pressure based on the population's average validation loss.

$$CF(t) = (1 - \frac{t}{T})(2\frac{t}{T}) \times \alpha(t) \quad (5)$$

where t denotes the current iteration and T is the maximum number of iterations. The adaptive coefficient $\alpha(t)$ is defined as:

$$\alpha(t) = \begin{cases} 1.2, & \text{if } t > 0 \text{ and } \bar{L}_t > \delta \\ 1.0, & \text{otherwise} \end{cases} \quad (6)$$

Here, $\bar{L}_t$ represents the average validation loss of the population at iteration t , and the stagnation threshold is fixed as $\delta = 0.85$.

The hyperparameters of the Adaptive Marine Predators Algorithm (AMPA) were selected based on preliminary empirical evaluation and computational constraints. Different population sizes were examined in pilot experiments, and a population of 20 provided a suitable balance between solution diversity and optimization cost, given that each fitness evaluation requires partial CNN training. Smaller populations exhibited reduced convergence stability, whereas larger populations increased runtime without yielding consistent performance improvements.

The adaptive control threshold δ was set to 0.85 to regulate the sensitivity of the state-aware step-size adjustment. Values in the range $[0.8, 0.9]$ were evaluated, and $\delta = 0.85$ consistently detected stagnation in population-level validation loss without inducing premature or excessive adaptation. This setting enabled responsive yet stable regulation of the exploration–exploitation balance during optimization.

3.4. Optimization Phases

Let P denote the prey population and E the elite solution. Position updates follow three behavioral phases.

Phase 1: Exploration ($t < T/3$)

During early iterations, prey move faster than predators, enabling global exploration through Brownian motion:

$$P_{\text{new}} = P_{\text{old}} + 0.5 \cdot R_B \otimes CF(t) \otimes (P_{\text{old}} - E) \quad (7)$$

where R_B is a vector of normally distributed random variables.

Phase 2: Transition ($T/3 < t < 2T/3$)

The population is divided into two subgroups. One continues Brownian exploration, while the other applies Levy-based exploitation. The Levy flight is defined as:

$$\text{Levy}(\beta) = \frac{u}{|v|^{1/\beta}}, u \sim \mathcal{N}(0, \sigma^2), v \sim \mathcal{N}(0, 1) \quad (8)$$

The corresponding position update is given by:

$$P_{\text{new}} = E + 0.5 \cdot \text{Levy}(\beta) \otimes CF(t) \otimes (E - P_{\text{old}}) \quad (9)$$

Phase 3: Exploitation ($t > 2T/3$)

In the final phase, population dynamics are dominated by Levy-driven exploitation with adaptive scaling to accelerate convergence. After each update, all hyperparameters are clipped to their predefined bounds to ensure feasibility.

3.5. Computational Cost and Efficiency Considerations

The primary computational cost of the proposed framework arises from the population-based hyperparameter optimization performed by the Adaptive Marine Predators Algorithm (AMPA). To reduce overhead, each candidate CNN configuration is evaluated using single-epoch training to obtain a proxy validation loss, which preserves the relative ranking of solutions while limiting training cost. Efficiency is further enhanced through the use of a lightweight CNN with a constrained parameter space and a fixed AMPA population of 20, resulting in a compact model of 1,625,281 parameters.

After hyperparameter selection, the final CNN is retrained with early stopping based on validation loss, ensuring convergence without unnecessary computation. AMPA is applied only during the offline optimization stage and incurs no inference-time cost. Deployment evaluation on the target dataset demonstrates favorable efficiency, with an average inference latency of 92.23 ms per image, indicating suitability for rapid malaria detection in resource-constrained environments.

3.6. Experimental Setup and Evaluation Protocol

AMPA is executed with a population size of 20 over 8 iterations. Each candidate solution is evaluated using a proxy fitness function obtained by training the CNN for one epoch with limited steps per epoch. This strategy reduces computational cost while preserving discriminatory power.

The fitness function is defined as:

$$\text{Fitness} = 0.7 \cdot \text{ValAcc} - 0.3 \cdot \text{ValLoss}$$

The elite hyperparameter configuration identified by AMPA is used to train a final CNN model with early stopping and model checkpointing. Training employs the Adam optimizer, a batch size of 32, and a maximum of 10 epochs.

The final CNN model was trained for a maximum of 10 epochs with early stopping based on validation loss. This upper bound was selected based on observed convergence behavior, as both training and validation losses stabilized within the early epochs. Early stopping prevented unnecessary training once no further improvement was observed, reducing the risk of overfitting while ensuring adequate model convergence. The close agreement between training and validation performance indicates that the selected training duration was sufficient and does not result in underfitting. A link to the full implementation is provided in the Supplementary Materials Section.

Final model performance is evaluated using accuracy, sensitivity, specificity, precision, recall, F1-score, and the area under the ROC curve. All experiments are implemented in Python 3.10 using TensorFlow/Keras and executed on an NVIDIA T4 GPU.

4. Results

4.1. Classification Performance on the Independent Test Set

The AMPA-optimized CNN was evaluated on an independent held-out test set comprising 5510 images, evenly distributed between the Parasitized (2755) and Uninfected (2755) classes. This test set was excluded from both the hyperparameter optimization phase and the model training phase.

The model achieved an overall classification accuracy of 95.00% on the test set. Table 1 reports the class-wise precision, recall, F1-score, and support. For the Parasitized class,

precision was 0.96, recall was 0.94, and the F1-score was 0.95. For the Uninfected class, precision was 0.94, recall was 0.96, and the F1-score was 0.95. The macro-averaged and weighted-averaged precision, recall, and F1-scores were all 0.95.

Table 1. Classification report on the independent test set.

Class	Precision	Recall	F1-Score	Support
Parasitized	0.96	0.94	0.95	2755
Uninfected	0.94	0.96	0.95	2755
Accuracy			0.95	5510
Macro Avg	0.95	0.95	0.95	5510
Weighted Avg	0.95	0.95	0.95	5510

The confusion matrix corresponding to these results is presented in Figure 1, showing the distribution of correct and incorrect predictions for both classes. The receiver operating characteristic (ROC) curve obtained on the test set is also shown in Figure 1. The area under the ROC curve (AUC) was 0.986.

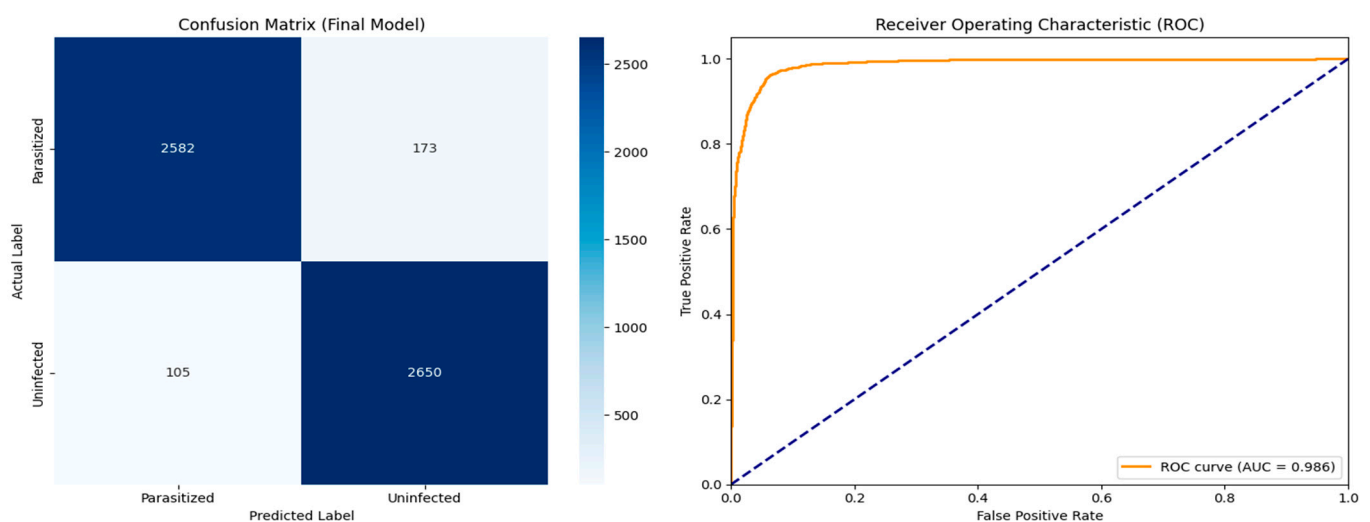


Figure 1. Confusion matrix and ROC curve of the final AMPA-optimized CNN on the independent test set.

4.2. Training Dynamics and Convergence

Figure 2 presents the training and validation accuracy and loss curves. Training accuracy increased across epochs and stabilized in later epochs. Validation accuracy followed a similar pattern and remained close to the training accuracy.

Training loss decreased steadily throughout training. Validation loss decreased during the early epochs and remained within a narrow range thereafter. Early stopping terminated training at the epoch corresponding to the minimum validation loss.

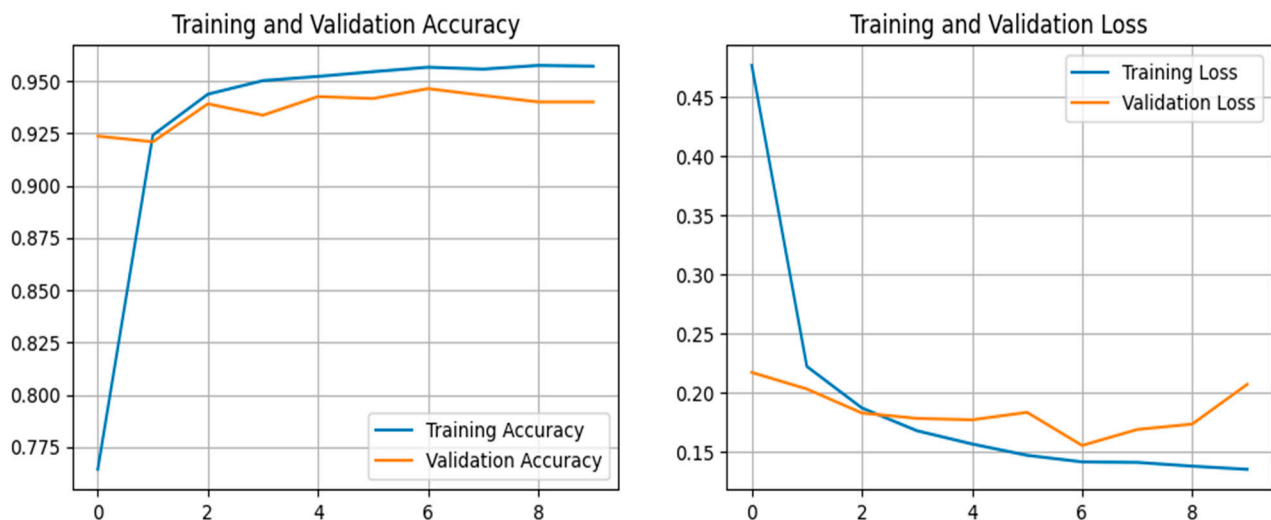


Figure 2. Training and validation accuracy and loss curves of the final model.

4.3. Comparative Results with Existing Studies

Table 2 summarizes classification accuracies reported in selected recent studies on malaria cell image classification using the same dataset, together with the accuracy obtained by the proposed AMPA-optimized CNN. The reported values were taken directly from the respective publications. The proposed AMPA-optimized CNN achieved a test accuracy of 95.00%. The comparative accuracies of transfer learning, custom CNN, and detection-based approaches are listed in Table 2.

Table 2. Comparison with reported results in the literature.

Reference	Methodology	Reported Accuracy
[5]	MobileNetV2 (transfer learning)	92.00%
[21]	YOLO-mp-3l	96.88%
[5]	VGG-16 (transfer learning)	94.00%
[5]	Custom-CNN	93.00%
[5]	VGG-19	96.00%
[6]	VGG-19 (transfer learning)	97.00%
[22]	VGG-16	86.00%
[22]	Custom-CNN	83.00%
Proposed method	AMPA-optimized CNN	95.00%

5. Discussion

The experimental results indicate that the proposed AMPA-optimized CNN achieves consistent classification performance on the malaria cell image dataset. This behavior is associated with the combined effects of task-specific architectural design, adaptive hyperparameter optimization, and controlled training procedures. Accordingly, this section discusses how these methodological components relate to the observed behavior of the model.

A central factor contributing to the reported performance is the design of a CNN architecture tailored specifically to binary malaria cell classification. Unlike very deep transfer learning architectures such as VGG-16 and VGG-19, which were originally developed for large-scale natural image recognition, the proposed network was configured directly for microscopic erythrocyte imagery. The constrained depth and reduced parameter space promote focused feature extraction and limit unnecessary representational complexity. This

alignment between model capacity and task structure supports the learning of discriminative morphological and textural patterns associated with parasitized and uninfected cells.

The performance of the proposed framework is further attributable to the methodological coupling between the lightweight CNN and the Adaptive Marine Predators Algorithm. Rather than functioning as an external tuning procedure, AMPA facilitates learning by guiding the CNN toward stable and discriminative configurations adapted to malaria-specific visual characteristics. By incorporating a state-aware control factor driven by population-level validation loss, the optimization process adaptively modifies its exploration dynamics in response to stagnation and convergence instability. This mechanism enables systematic traversal of the hyperparameter space without reliance on a fixed decay schedule, resulting in stable convergence and balanced class-wise performance.

Relative to lightweight transfer learning approaches such as MobileNetV2, the proposed framework performs feature learning entirely within the target domain. Pre-trained models encode representations derived from large natural image corpora, which may not adequately reflect the microstructural characteristics of hematological imagery. Training the network from scratch under AMPA-guided hyperparameter selection allows features to be learned directly from erythrocyte morphology and staining patterns present in the dataset, providing a methodological explanation for the observed performance differences.

Detection-based approaches such as YOLO-mp-3l reformulate malaria diagnosis as an object localization problem. In contrast, the present work treats the task strictly as binary image classification. This formulation removes the requirement for spatial localization and concentrates model capacity on appearance-based cues. The reported outcomes indicate that, for the NIH malaria dataset, a classification-centered framework is sufficient to capture discriminative infection-related patterns.

Although VGG-19-based methods report higher accuracies, these results are obtained using substantially deeper architectures with large parameter counts and extensive reliance on pre-trained weights. The proposed AMPA-optimized CNN attains comparable performance using a more compact architecture combined with an adaptive optimization strategy. This observation highlights the importance of methodological alignment between architecture, optimization dynamics, and task requirements rather than architectural scale alone.

Despite these findings, several limitations must be acknowledged. First, all experiments were conducted on a single public dataset, which restricts conclusions regarding cross-dataset generalization. Second, the study addresses only binary classification and does not consider parasite life-cycle staging or mixed infection scenarios. Third, the meta-heuristic optimization procedure introduces additional computational cost, which may affect scalability when extended to deeper models or higher-resolution imagery.

Future work should therefore investigate the transferability of the proposed framework to independent malaria datasets and other hematological imaging tasks. Extensions to multiclass classification, efficiency-aware optimization, and integration with clinical screening workflows also represent relevant directions for further study.

6. Conclusions

This study proposed an AMPA-optimized Convolutional Neural Network for binary classification of malaria cell images. The framework integrates a task-specific CNN architecture with an adaptive bio-inspired hyperparameter optimization strategy.

The proposed model achieved high classification accuracy with balanced precision, recall, and F1-scores across both classes. Comparative evaluation shows that the method outperforms several lightweight and detection-based models and attains performance comparable to deeper transfer learning architectures, despite lower architectural complexity.

These findings indicate that aligning model architecture and optimization strategy with task requirements can produce competitive performance without reliance on very deep pre-trained networks. Future work will focus on multiclass extension, cross-dataset evaluation, and integration of interpretability techniques.

Supplementary Materials: The code is available at https://github.com/bbash/bbash/blob/main/conference_review.ipynb (accessed 16 January 2026).

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