

An Innovative Deep Learning Method to Diagnose Mosquito-Borne Illnesses in Blood Image Analysis

Shaimaa Saadoon Mahmood ALrfae¹, Doctor Meghdad Aynehband²

¹The computer department of the Islamic Azad University,
Iran

(2) Researcher at the Center for Science and Technology of Architecture and Computer Networks, Faculty of Computer Networks and Communication, Imam Hossein University, Tehran, Iran

and a member of the academic staff of the computer department of the Islamic Azad University, Mahshahr branch - Mahshahr – Iran

Abstract:

Introduction: Malaria, an infectious illness carried by the bite of infected mosquitoes, is a significant public health concern, especially in Africa. The management of mosquito-human contact is crucial to mitigate its transmission. Artificial intelligence, including machine learning and deep learning techniques, is being utilized to enhance the diagnosis and identification of mosquito species. This advancement aims to facilitate the development of more efficient control measures.

Aims and Objective: To analyze the efficiency of three deep learning models in identifying blood-borne diseases by evaluating the macro and micro picture of blood samples.

Method: In this retrospective investigation, three deep learning algorithms, namely Convolutional Neural Networks (CNN), MobileNetV2, and ResNet50, were used to identify mosquito-borne illnesses, focusing on malaria. The research used a dataset of 120 blood samples gathered over one year from the hospital's pathology department. The CNN model streamlines preprocessing with multilayer perceptrons, simplifying malaria component extraction. MobileNetV2, a lightweight network, outperforms others with fewer parameters. Its compact blocks in Dense-MobileNet models minimize constraints and computation expenses. ResNet50 resolves degradation issues with a residual structure, preventing overfitting as hidden layers increase.

Results: The study evaluated three deep learning models (CNN, MobileNetV2, and ResNet50) for medical classification. The study also demonstrated improved True Positive Rates as False Positive Rates increased, indicating better accurate identification while controlling false positives. ResNet50 consistently outperformed the other models, showcasing its superior performance. The study revealed high precision scores for all models, classifying "Uninfected" and "Infected" cases. ResNet50 exhibited slightly higher precision, indicating its precision-based superiority. Overall, all models demonstrated vital accuracy, and ResNet50 showed exceptional performance. The study found that ResNet50 performs better in True Positive and False Positive Rates.

Conclusion: The study has concluded that ResNet50 has shown the best performance in detecting blood-borne diseases.

Keywords: deep learning, blood-borne disease, malaria, blood image analysis.

Introduction

Red blood cells are contaminated by protozoan parasites from the genus *Plasmodium*, which causes malaria. These parasites are dispersed by female *Anopheles* mosquito bites carrying the infection. The majority of child fatalities occur in Africa, where One of the primary root causes for childhood neuro-disability is malaria, which claims a life practically every minute. It is estimated that 3.2 billion individuals in 95 countries and territories might get malaria and develop the disease, of which 1.2 billion are thought to be at high risk (having a probability of more than one in a thousand of contracting malaria in a year), as stated in the World Malaria Report of 2016. In 2016, there were over 438,000 malaria

fatalities and 214 million people with malaria worldwide. The majority of deaths from malaria occurred in children under the age of five, accounting for almost two-thirds of cases, and in the African continent, where an estimated 92%2 all the fatalities from the disease occurred. Malaria typically causes fever, exhaustion, headaches, and, in extreme situations, convulsions and coma that result in death [1].

Reducing mosquito-human interaction can help stop the transmission of malaria-causing viruses (MBDs). As a result, there will be less opportunity for mosquitoes to bite people and transmit infections or parasites. Controlling mosquitoes offers benefits over other methods of reducing illness. First, there may be a resource shortage for medical measures like

West Nile Virus vaccinations. Moreover, MBDs, like drug-resistant malaria, can arise suddenly and adjust to human interventions [2]. The fact that since certain female mosquitoes are known to deposit hundreds of eggs, MBDs have the potential to spread swiftly over a few generations. Increased globalization has the potential to introduce, even when an illness is eliminated locally, new hosts—human and nonhuman—to an area, eventually causing community spread. Instead, a mosquito control method reduces the quantity of disease-carrying mosquitoes. Ideal mosquito management significantly reduces potential transmission routes, even if it cannot ensure the extinction of all MBDs (for example, dengue may be transmitted through human blood transfusions). Even still, many experts concur that current worldwide mosquito control efforts are a "disaster" and that mosquito control measures are still being carried out inadequately [3].

Control tactics and control strategies are the two halves of mosquito control. Mosquito control measures define the optimal interaction between mosquitoes, people, and the environment. Costs, the health of the environment, human health, and supply are their limitations. They also depend on imprecise data on mosquito numbers at the moment and exhibit significant variation due to environmental factors [4]. Thus, issues like "Should we eliminate any mosquitoes of their function as pollinators, instead of just some species?" are addressed by mosquito management tactics. Strategies for controlling mosquitoes can also aid in optimal resource allocation in lessening the detrimental effects of MBDs. Techniques for controlling mosquitoes, such as prevention, modification, and eradication, are informed by mosquito control methods [5]. First, methods of pure prevention involve clearing areas where mosquitoes may develop and establishing environments that are unfriendly to them. Insect repellents and mosquito nets are two prevention strategies designed for human interactions. Secondly, modification methods, including introducing *Wolbachia* infections, aim to alter the features of mosquitoes. Ultimately, pesticides, larvacide, and bug traps are examples of eradication methods. These methods can be applied at macro-scales to cities and regions or micro-scales to people and neighborhoods [6].

Advances in the application of artificial intelligence (AI) have enabled faster and more accurate sample analysis than is possible with the human eye. For instance, a machine learning (ML) approach can achieve an overall accuracy of up to 90%. Medical image classification makes extensive use of machine learning (ML) along with advanced learning (DL) techniques [7]. DL techniques are beginning to be used in medical equipment. Similar DL techniques and microscopy pictures are used to detect parasites from malaria in blood

cells. Imagegraphs from minor or thick blood stains are typically used to make these pictures [8]. Vast areas are, therefore, more susceptible to parasite infestation due to the thick covering of the red blood cells. As a result, comprehensive smear methods can more precisely identify malaria parasites throughout blood cells. The streaks are thin, revealing a tiny coating of blood. Physicians often employ them to differentiate between the different stages of malaria. Accurate cancer diagnosis depends on human expertise and the quality of smears. However, DL-based algorithms have shown that it is possible to effectively use both thick and thin spots to detect malaria [9].

It has proven possible to recognize mosquitoes and stop the transmission of illnesses carried by vectors by using machine learning along with deep understanding. Park et al. employed By using mosquito population data from a digital mosquito monitoring system (DMS), a faster region-convolutional neural network (R-CNN) based on ResNet was developed for investigating *Culex pipiens pallens* Coquillett, 1898 (*Cx. pip*), *Aedes albopictus* Skuse, 1895 (*Ae. albo*), *Anopheles* spp., as well as various other flying insects [10]. To identify different species of dengue by leveraging the sounds of their wings, studies have suggested species classification models composed of machine learning classifiers utilizing wavelet analysis and the collected acoustic details from mosquito wings. Oodwin et al. developed an algorithm for recognizing unlearned species using the Xception model. Siddiqui et al. detected dengue using quicker R-CNN and Inception V2 [11]. An insect classification and identification system was created via AlexNet utilizing a support vector machine and SVM to distinguish between *Aedes albopictus* and *Aedes aegypti* Linnaeus, 1762. The characteristics of each body component were retrieved. Although several mosquito recognition and categorization models have been developed, most have focused more on picture classification than object identification or have yet to provide results for comparable species. Because previous research uses mosquito carcasses, it is deemed inappropriate for real-world applications. There are, nonetheless, a few investigations on extant and closely related species [12]. This current study obtained 120 blood samples, conducted diagnostic tests under the three deep learning models (Convolutional Neural Networks, MobileNetV2, and ResNet50), and analyzed their accuracy, precision, and ROC.

Method

Research Design

This retrospective study has obtained a dataset from the hospital pathology laboratory to experiment with the trained modules of the algorithms. The study used three algorithms,

Convolutional Neural Networks (CNN), MobileNetV2, and ResNet50 (Figure 1), and discussed various technical aspects such as dataset definition, the proposed architecture, and its components. This study used these deep learning algorithms to diagnose a mosquito-borne disease. In this study, we have considered malaria as the identifying disease and used the three deep learning models by feeding data in terms of macro and micro images of blood, either infected or not infected. This dataset consisted of 120 samples and was taken from our hospital's pathology department, and it was completed from September 2022 to August 2023. The effectiveness of the CNN model is that it supports deep learning that employs a variant of the multilayer perceptron to reach the essential minimum preprocessing. CNN is a feed-forward artificial neural network that can simplify setting effective component extraction and type of malaria, which needs parts of expertise. It includes various processing layers that can be used in image analysis.

On the other hand, this study used the MobileNetV2 Model, which has a compact and light deep neural network with fewer parameters and higher performance than other deep neural networks. This model can minimize the number of network parameters and increase the accuracy of variety. MobileNet model is commonly used as compact blocks in Dense-MobileNet models. It is the close interconnections that are completed within the blocks. The model can further reduce constraints and computation expenses by selecting a small growth rate.

Moreover, the ResNet50 model helped our team resolve the degradation problems of various neural network architectures. The hidden layer increases when the training error also grows. To solve this issue, this team has offered the residual structure.

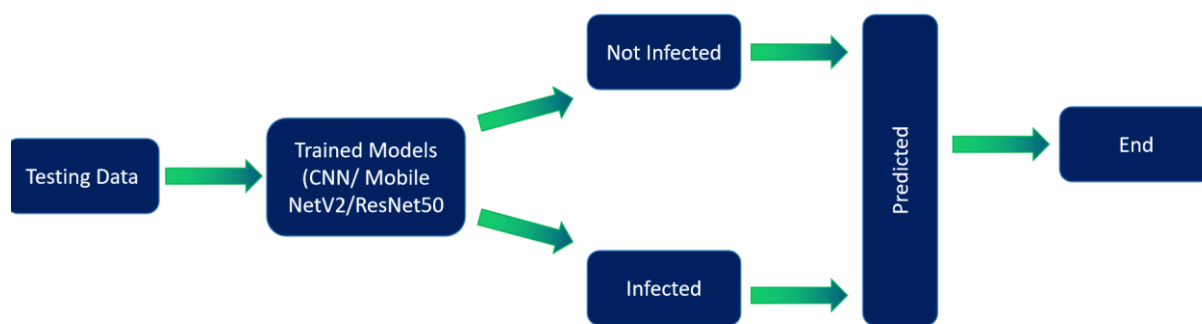


Figure 1: Schematic representation of the trained models

Results

Table 1 presents the training and validation accuracy of three deep learning models (CNN, MobileNetV2, and ResNet50) across different numbers of epochs. At 0 generations, the CNN model has a training accuracy of 0.68 and a validation accuracy of 0.98, while the MobileNetV2 and ResNet50

models start at 0.96 for both training and validation accuracy. As the number of epochs increases, all models improve training and validation accuracy. By 25 generations, the CNN model achieves a training accuracy of 0.95 and a validation accuracy of 0.95. The MobileNetV2 and ResNet50 models reach a perfect training accuracy of 1 and maintain high validation accuracies of 0.97 and 0.95, respectively.

Table 1: Training and Validation accuracy of each deep learning model

Number of Epochs	CNN Model		MobileNetV2 Model		ResNet50	
	Training Accuracy	Validation Accuracy	Training Accuracy	Validation Accuracy	Training Accuracy	Validation Accuracy
0 Epochs	0	0.68	0	0.98	0.96	0.96
5 Epochs	0.83	0.94	0.97	0.96	0.97	0.94
10 Epochs	0.9	0.91	0.96	0.96	0.98	0.96
15 Epochs	0.92	0.94	0.98	0.97	0.99	0.97

20 Epochs	0.98	0.94	0.99	0.96	1	0.94
25 Epochs	0.95	0.95	1	0.97	1	0.95

Table 2 provides the training and validation loss values for the same three deep learning models across different numbers of epochs. At 0 generations, the CNN model has a training loss of 1.7 and a validation loss of 0.63. The MobileNetV2 and ResNet50 models start with lower losses, at 0.2 for training and 0.11 for validation. As the epochs progress, all

models demonstrate a consistent decrease in both training and validation losses. By 25 epochs, the CNN model reaches a stable training loss of 0.2 and a validation loss of 0.21. The MobileNetV2 and ResNet50 models also maintain low losses, with values ranging from 0.15 to 0.01, indicating effective learning and generalization.

Table 2: Training and Validation accuracy of each deep learning model

Number of Epochs	CNN Model		MobileNetV2 Model		ResNet50	
	Training Loss	Validation Loss	Training Loss	Validation Loss	Training Loss	Validation Loss
0 Epochs	1.7	0.63	0.2	0.11	0.1	0.1
5 Epochs	0.4	0.2	0.11	0.5	0.03	0.19
10 Epochs	0.2	0.19	0.8	0.9	0.25	0.01
15 Epochs	0.31	0.2	1	0.7	0.17	0.01
20 Epochs	0.2	0.21	0.3	0.6	0.16	0.01
25 Epochs	0.2	0.21	0.11	0.5	0.15	0.01

Figure 2 provides the True Positive Rate (Sensitivity) and False Positive Rate (1 - Specificity) for three different deep learning models (CNN, MobileNetV2, and ResNet50) at various False Positive Rate (FPR) thresholds. At an FPR of 0, all models start with a True Positive Rate of 0, indicating that they do not make optimistic predictions at this threshold. As the FPR threshold increases, all models improve their True Positive Rate, meaning better performance in correctly identifying true positives while controlling the false positive rate.

At an FPR of 0.01, the models exhibit True Positive Rates ranging from 0.79 to 0.85, showing their ability to correctly identify positive cases while maintaining a low false positive rate. This trend continues as the FPR threshold increases. At higher FPR thresholds, all models support high True Positive Rates, indicating robust performance in correctly identifying positive cases even when the false positive rate is higher. ResNet50 consistently demonstrates the highest True Positive Rates across various FPR thresholds, followed by MobileNetV2 and CNN, indicating its superior performance in this evaluation.

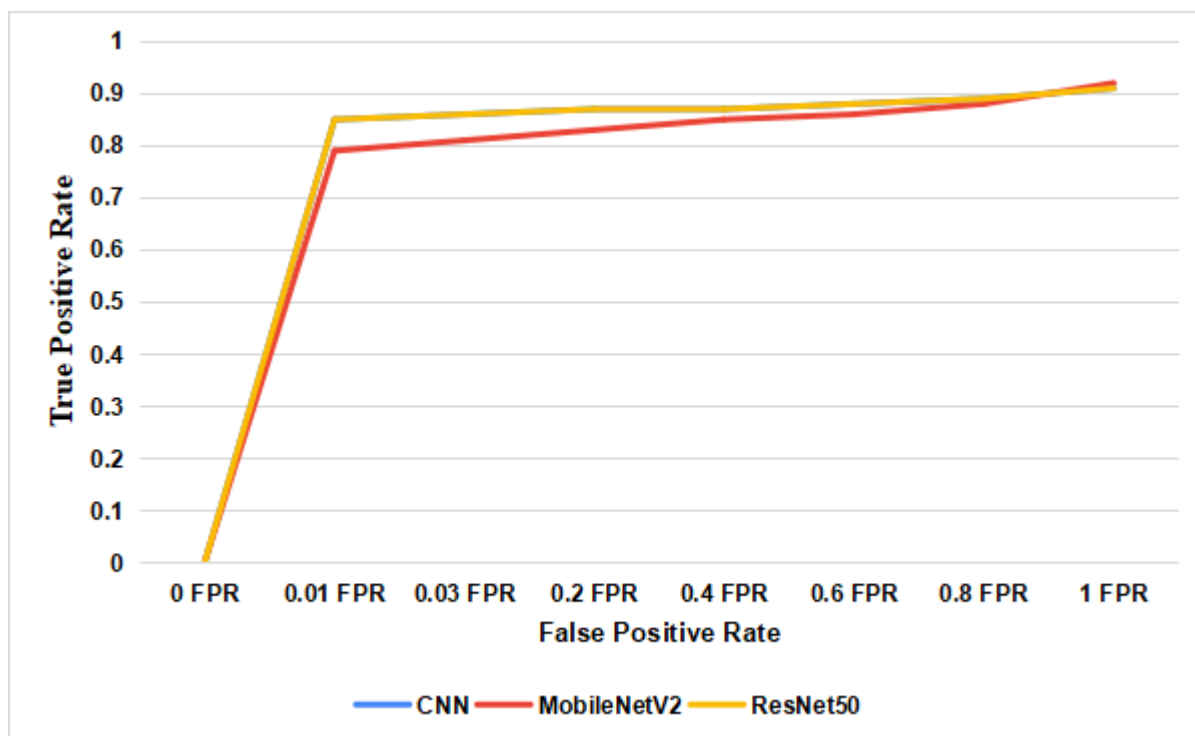


Figure 2: ROC of three models

Figure 3 displays the precision scores for three different deep learning models (CNN, MobileNetV2, and ResNet50) in classifying two categories: "Uninfected" and "Infected". For the "Uninfected" class, the models perform pretty well. CNN achieves a precision of 0.94, meaning that out of all the instances it predicted as "Uninfected," 94% were correct. MobileNetV2 and ResNet50 perform even slightly better, with both achieving a precision of 0.968, indicating a very high level of accuracy in identifying uninfected cases. In the "Infected" class, all three models demonstrate excellent precision scores. CNN has a precision of 0.958, and MobileNetV2 and ResNet50 achieve an accuracy 0.964. This signifies that these models are highly accurate in correctly identifying infected cases. Looking at the "Macro average"

and "Weighted average," we get an overall assessment. The "Macro average" takes the average precision for each class without considering class imbalance.

In contrast, "Weighted average" considers class imbalance by weighting the average based on the number of samples in each class. In this case, all models show high precision scores across macro and weighted averages. The models demonstrate consistent and excellent performance in accurately identifying both "Uninfected" and "Infected" cases, with minimal misclassifications. ResNet50 has slightly higher precision in most categories, indicating its superior performance in precision-based evaluation.

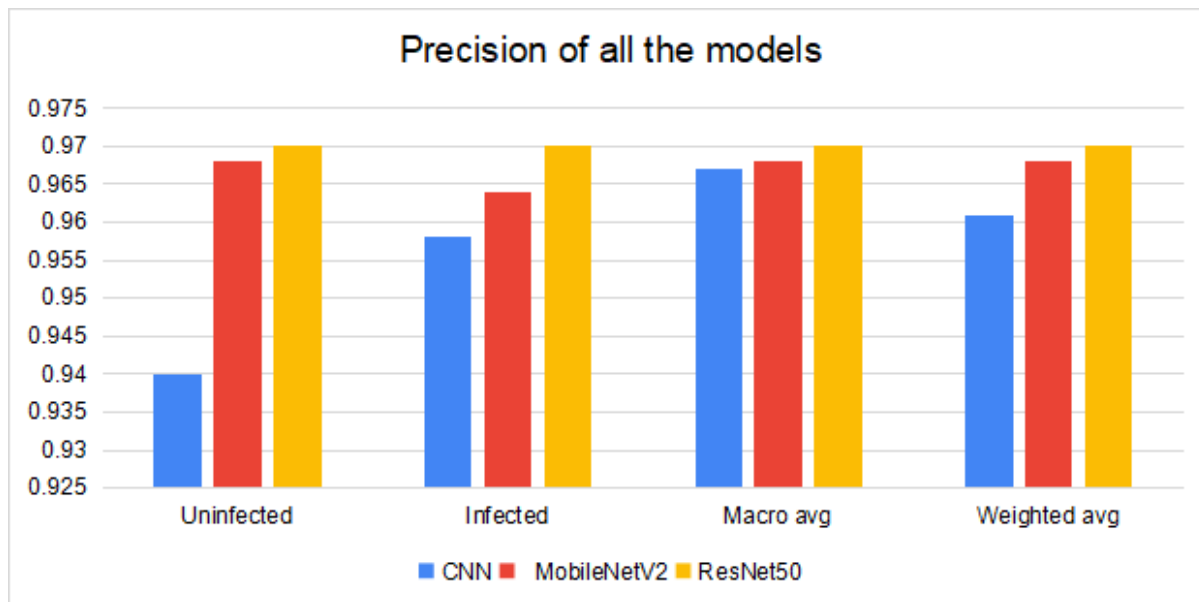


Figure 3: Precision of the three deep learning models

Table 3 provides a detailed breakdown of the model predictions for three different models, CNN, MobileNetV2, and ResNet50, at varying False Positive Rate (FPR) levels. At a False Positive Rate of 0, which means no uninfected cases were incorrectly classified as infected, all models performed flawlessly distinguishing between infected and uninfected patients, resulting in zero false positives.

As the False Positive Rate increases, indicating a higher likelihood of incorrectly classifying uninfected cases, we observe corresponding increases in the predicted number of infected and uninfected patients. Interestingly, all three

models show consistent trends in their predictions across different FPR levels. For instance, at an FPR of 0.4, all models predict 104 infected cases, with MobileNetV2 and ResNet50 also mispredicting 48 uninfected points. This suggests a similar pattern of performance among the three models. Overall, this table provides valuable insights into the models' predictive abilities at different levels of False Positive Rate, demonstrating their respective strengths and weaknesses in classifying infected and uninfected cases. These results can be crucial for evaluating the models' reliability and suitability for practical applications in disease classification.

Table 3: Training and Validation accuracy of each deep learning model

FPR	CNN		MobileNetV2		ResNet50	
	Infected	Uninfected	Infected	Uninfected	Infected	Uninfected
0FPR	0	0	0	0	0	0
0.01 FPR	102	1	95	1	102	1
0.03 FPR	103	3	97	3	103	3
0.2 FPR	104	24	98	24	104	24
0.4 FPR	104	48	100	48	104	48
0.6 FPR	105	72	103	72	105	72
0.8 FPR	106	96	105	96	106	96
1 FPR	109	120	110	120	109	120

Discussion

Contagious illness: More than 500,000 individuals worldwide lose their lives to the deadly viral illness malaria each year. Misdiagnosis or delayed diagnosis accounts for the

majority of these fatalities. Currently, For recognizing malaria, an operating microscope is considered the most effective equipment. However, it takes time and is prone to human mistakes. The evaluation procedure has to be automated since it is a primary worldwide health concern.

This article aims to convince readers that the diagnosing process should be automated to eliminate the necessity for human intervention [13].

Using deep-learning technologies like image processing and convolutional neural networks (CNNs), parasitemia on microscopic blood slides is assessed to improve diagnostic precision. The method is predicated on the known variability in erythrocyte intensity and Plasmodium parasite intensity features [14]. The CNN frameworks ResNet50, ResNet34, VGG-16, and VGG-19 are fed images of fed and noninfected erythrocytes. These models have all been trained on the same dataset. The fine-tuning and transfer learning methods are applied, and the results are compared. Among the models that were assessed, the VGG-19 model performed the best overall when considering the parameters and dataset [15].

Since 2000, malaria, a disease spread by mosquitoes, is thought to have killed half a million people globally. Comprehensive testing in laboratories for malaria can be expensive and time-consuming, and it also needs skilled laboratory staff. Furthermore, human analysis could be better. Diagnosis performance can be improved by combining picture segmentation and denoising techniques via Generative Adversarial Networks (GANs) as a data augmentation tool. Several deep learning models, including CNN, ResNet50, & VGG19, have been employed to recognize the Plasmodium infection in pictures of thick blood smears. Compared to other methods, the experimental findings indicate that the model based on VGG19 performed the best, attaining 98.46%. This study shows how artificial intelligence may increase pathogen detection speed and accuracy, which is more efficient than manual analysis [16].

In many parts of the world, bites from female Anopheles mosquitoes can result in malaria, a potentially fatal illness. We present a sophisticated convolutional neural network (CNN) that improves the precision of malaria detection by using patches divided from microscopic images of red blood cell smears [17]. In Giemsa-stained spots, we generate the automatic parasite detection using three CNN pre-trained models: VGG19, ResNet50, and MobileNetV2. We provide the transfer learning strategy since short datasets perform poorly for CNNs. Transfer learning is solving problems with small datasets and extracting visual characteristics from big general datasets. We employ three CNN-trained CNN-trained models to identify and categorize malaria parasites as a transfer learning strategy

We experimentally assessed the suggested CNN models using the malaria dataset from the National Institute of Health (NIH). The correctness of our proposed model is around 100% [18].

One of the worst insects that harms people worldwide is the mosquito. Forecasting and proactive prevention are crucial for preventing illnesses spread by mosquitoes. Unfortunately, most mosquito identification is done by hand, costing time and leading to human mistakes. In this work, we used a deep learning-based recognition of items strategy to construct an autonomous image analysis system for species identification of mosquitoes [19]. A bite capture device was utilized to get color and fluorescence photos of live mosquitoes, which were then used to create an object identification model based on deep learning. With a 91.7% F1 score, combining a quicker region-convolutional neural network design and a swine transformer showed the most outstanding performance among the object identification models based on deep learning. This suggests that the automatic identification technique may be quickly implemented to effectively investigate vector-borne mosquito species and populations with less field labor [20].

Conclusion

The study has concluded that ResNet50 has shown the best performance in detecting the blood-borne disease. The findings of this current study indicate that all three deep learning models (CNN, MobileNetV2, and ResNet50) perform exceptionally well in classifying "Uninfected" and "Infected" cases. All models demonstrate high precision for the "Uninfected" class, with MobileNetV2 and ResNet50 slightly outperforming CNN. In the "Infected" category, all models exhibit excellent precision, further emphasizing their accuracy in identifying infected cases. Both macro and weighted averages affirm the consistent high performance across classes. ResNet50 consistently outshines the other models, particularly in precision-based evaluation.

Additionally, the models demonstrate effective learning and generalization over epochs, as indicated by the decreasing training and validation losses. These results collectively highlight the effectiveness of deep learning models, particularly ResNet50, in accurately classifying medical cases, providing valuable insights for clinical applications. The developed models have been extensively analyzed, and statistical analysis showed that the ResNet50 model was better in accuracy, precision, and ROC. The findings were validated and compared. In this age, diagnostic methods need to be emphasized the most, and detection of malaria or other mosquito-borne diseases will contribute to early and accurate diagnosis, which may reduce the infection and economic burden on society. Incorporating technologies like deep learning, machine learning, and artificial intelligence in disease diagnosis will increase the accuracy of healthcare and promptness of healthcare services. However, these technologies must be validated more on a broader population

and in different cases. There is a need to conduct similar studies on various communities and individuals with various underlying conditions.

References

- [1] Poostchi M, Silamut K, Maude RJ, Jaeger S, Thoma G. Image analysis and machine learning for detecting malaria. *Transl Res.* 2018 Apr;194:36-55. Doi: 10.1016/j.trsl.2017.12.004. Epub 2018 Jan 12. PMID: 29360430; PMCID: PMC5840030.
- [2] S. Abas, M. Zukhairin, A. Jaya, A. Rahman, Z. Abal Mosquito Larvae Detection using Deep Learning *International Journal of Innovative Technology and Exploring Engineering (IJTITEE)*, 8 (12) (2019), pp. 804-809
- [3] Emily S. Acheson, Andrew A. Plowright, Jeremy T. Kerr: Where have all the mosquito nets gone? Spatial modeling reveals mosquito net distributions across Tanzania do not target optimal *Anopheles* mosquito habitats in *Malar. J.*, 14 (322) (2015), pp. 1-14, [10.1186/s12936-015-0841-x](https://doi.org/10.1186/s12936-015-0841-x) **RESEARCH**
- [4] Hammad Ahmad, Asad Ali, Syeda Hira Fatima, Farrah Zaidi, Muhammad Khisroon, Syed Basit Rasheed, Ihsan Ullah, Saleem Ullah, Muhammad Shakir Spatial modeling of Dengue prevalence and kriging prediction of Dengue outbreak in Khyber Pakhtunkhwa (Pakistan) using presence only data *Stoch. Env. Res. Risk A.*, 34 (7) (2020), pp. 1023-1036, [10.1007/s00477-020-01818-9](https://doi.org/10.1007/s00477-020-01818-9)
- [5] IkeOluwapo Ajayi, Romeo Bellini, Pascal Boireau, Steven Bradbury, Salome A. Bukachi, LeeChing Ng, Fang Jing, Pattamaporn Kittayapong, Pablo Liedo, Kenneth Linthicum Guidance framework for testing the sterile insect technique as a vector control tool against *Aedes*-borne diseases *World Health Organization* (2020)
- [6] N.J. Vickers [Animal communication: when i'm calling you, will you answer too?](https://doi.org/10.1093/cbb/cba011) *Curr Biol* (2017)
- [7] M.S. Mahdi, "Proposed Secure Internet of Everything (IoE) in Health Care,"..
- [8] K. Chakradeo, S. Titarenko, M.J. Delves, and M. Delves, "Malaria parasite detection using deep learning methods". *New...*
- [9] A. Kadhim *et al.* Proposal of new keys generator for DES algorithms depending on multi techniques *Eng Technol J* (2014)
- [10] Lee S, Kim H, Cho BK. Deep Learning-Based Image Classification for Major Mosquito Species Inhabiting Korea. *Insects.* 2023 Jun 5;14(6):526. doi: 10.3390/insects14060526. PMID: 37367342; PMCID: PMC10299581.
- [11] Jameela T, Athotha K, Singh N, Gunjan VK, Kahali S. Deep Learning and Transfer Learning for Malaria Detection. *Comput Intell Neurosci.* 2022 Jun 29;2022:2221728. doi: 10.1155/2022/2221728. PMID: 35814548; PMCID: PMC9259269.
- [12] A. Rahman *et al.*, "Improving Malaria Parasite Detection from Red Blood Cell using Deep Convolutional Neural Networks," pp. 1-33, 2019,
- [13] L. Approach, "diagnostics Analyzing Malaria Disease Using Effective Deep Learning Approach," pp. 1-22.
- [14] M.S. Mahdi *et al.* A Novel Aided diagnosis schema for covid 19 using convolution neural network *IOP Conf Ser: Mater Sci Eng* (2021)
- [15] M.S. Mahdi *et al.* An improved chacha algorithm for securing data on IoT devices *SN Appl Sci* (2021)
- [16] Semwal A., Melvin L.M.J., Mohan R.E., Ramalingam B., Pathmakumar T. AI-Enabled Mosquito Surveillance and Population Mapping Using Dragonfly Robot. *Sensors.* 2022;22:4921. doi: 10.3390/s22134921.
- [17] Cotar A.I., Falcuta E., Prioteasa L.F., Dinu S., Ceianu C.S., Paz S. Transmission dynamics of the West Nile virus in mosquito vector populations under the influence of weather factors in the Danube Delta, Romania. *EcoHealth.* 2016;13:796-807. doi: 10.1007/s10393-016-1176-y.
- [18] Kim S.-R. A study on the possibility and risk of dengue fever in Korea due to climate change and the main contents and improvement measures of the [Infectious DiseaseControl and Prevention Act *Leg. Theory Pract. Rev.* 2020;8:131-149. doi: 10.30833/LTPR.2020.08.8.3.131.
- [19] Japanese Encephalitis Alert Issued Confirmed 85.7% of Vector-Borne Mosquitoes in Busan. [(accessed on 4 November 2021)].
- [20] Bhargavi B.S., Moa A. Global outbreaks of zika infection by epidemic observatory (EpiWATCH), 2016-2019. *Glob. Biosecur.* 2020;2:1. doi: 10.31646/gbio.83.