Avalokiteshvara Journal of Artificial Intelligence

http://hcapit.org/ajai.html

ISSN – 3049-3889

Research Article

Deep Learning-Based Malaria Detection: A Comparative Study of CNN Architectures

Shweta Kharat[1]

[1]Independent Researcher, Mumbai, MS, India.

shwetakharat413@gmail.com

Corresponding Author Email: shwetakharat413@gmail.com

Abstract

Malaria continues to pose a significant global health challenge, necessitating accurate and timely diagnostic methods to enhance patient outcomes. Traditional microscopic techniques, though effective, are labor-intensive and reliant on expert interpretation. This study investigates the potential of deep learning-based approaches for automated malaria detection, evaluating the performance of MobileNetV2, NASNetMobile, Xception, and InceptionResNetV2. Comparative analysis reveals that Xception outperformed the other models, offering an optimal balance of accuracy and efficiency. This study provides a robust foundation for selecting the most suitable deep learning models for malaria diagnosis, particularly in resource-limited settings.

Keywords: Deep Learning, CNN, Malaria Detection, MobileNetV2, NASNetMobile, Xception, InceptionResNetV2, Automated Diagnosis

1. Introduction

Malaria continues to be one of the deadliest diseases impacting millions of people globally. Early and accurate detection is crucial for effective treatment and the prevention of further complications. Conventional diagnostic methods rely on microscopic examination of blood smears, which are often time-consuming and require skilled medical professionals. Automated analysis using Artificial Intelligence has proven to reduce time while ensuring accuracy.

https://doi.org/10.63820/3049-3889.vol.1.issue.01.005

Deep learning has revolutionized the medical field particularly medical imaging, by providing solutions for disease diagnosis, detection and classification. Convolutional Neural Networks (CNNs) have demonstrated higher accuracy in detecting malaria-infected cells from microscopic images. However, selection of deep learning models often requires comprehensive evaluation of different architectures and is a time-consuming task.

This study conducts a comparative analysis of deep learning models including MobileNetV2, NASNet, Xception, and InceptionResNetV2, for classifying malaria- infected and healthy cells. The evaluation focuses on their performance in terms of accuracy and computational efficiency.

The remainder of this paper is structured as follows: Section 2 provides a comprehensive review of related work. Section 3 details the proposed methodology. Section 4 presents the results and comparative performance evaluation. Finally, Section 5 concludes the study.

2. Related Work

EfficientNet-Based Approach for Malaria Detection [3] Mujahid et al. (2024) proposed an EfficientNet-based malaria detection model, achieving 97.57% accuracy and an AUC score of 99.21%, outperformed other pre-trained deep learning models in terms of accuracy and computational efficiency. Their study reinforced the effectiveness of CNN-based architectures in malaria diagnosis.

Sukumaran et al. (2023) [4] proposed an optimized YOLOv4 model for malaria detection, replacing the CSP-DarkNet53 backbone with ResNet50 and pruning residual blocks. Their modified YOLOv4-RC3_4 model achieved a mean average precision (mAP) of 90.70%, surpassing the original YOLOv4 by over 9%. This model also demonstrated improved computational efficiency, making it more viable for real-time applications.

Boit and Patil (2024) [5] introduced a novel hybrid model, EDRI, which integrates EfficientNetB2 with DenseNet, ResNet, and Inception blocks for malaria parasite detection. Trained on the NIH Malaria dataset containing 27,558 labeled microscopic red blood cell images, the EDRI model achieved an accuracy of 97.8% and an AUC score of 99.76%, highlighting its robust performance in automated malaria screening

These studies underscore the efficacy of various CNN architectures in automating malaria diagnosis. However, there is still a need for a broader comparative analysis of different deep learning models to assess their accuracy, computational efficiency, and real-world applicability in healthcare settings. This research aims to bridge this gap by evaluating multiple architectures for malaria detection.

3. Methodology

3.1 Dataset

The dataset used in this study is the Cell Images for Detecting Malaria, sourced from the NIH and available on Kaggle [1][2]. It includes 27,560 images of red blood cells, split into two categories: 13,780 infected with malaria parasites and 13,780 uninfected. The original images, with varying dimensions, were resized to 128x128 pixels to ensure consistency and compatibility with the CNN models used in this research.

3.2 Data Preprocessing

Data preprocessing was performed using the ImageDataGenerator class from TensorFlow Keras. The images were rescaled to the range [0, 1] by dividing the pixel values by 255, which is a crucial step for normalizing the data. This rescaling ensures that the pixel values are within a range that facilitates faster convergence during the training of deep learning models.

3.3 Data Splitting

The dataset was split into two main subsets, with 80% allocated for training the models and the remaining 20% used for validation to evaluate the model's performance. Both the training and validation datasets were resized to 128x128 pixels, and the pixel values were rescaled as part of the preprocessing.

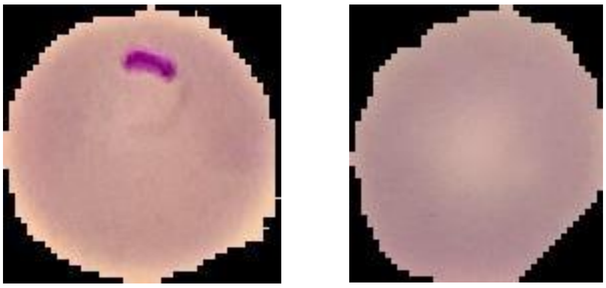

Figure 1: The image on the left shows a parasitized cell, while the one on the right shows an uninfected cell.

4. Results and Discussion

4. 1 Model Performance

This section presents the performance evaluation of the selected deep learning models: MobileNetV2, NASNetMobile, Xception, and InceptionResNetV2. The models were assessed based on accuracy, loss, inference time, and classification metrics.

4.1.1 Evaluation Metrics

The primary evaluation metric used in this study was accuracy, calculated using the formula:

$$\text{Accuracy} = \frac{\text{Number of Correct Predictions}}{\text{Total Number of Predictions}}$$

Accuracy provides a clear measure of the model's effectiveness in correctly classifying images. During the training process, accuracy was computed at each epoch to assess the model's performance on the validation dataset, ensuring continuous improvement throughout the training process.

The models were trained for 5 epochs, with a step size of 300 steps per epoch and 100 validation steps. This setup allowed for thorough evaluation of the model at each stage of training. The models were trained and evaluated on Google Colab's CPU, utilizing Python 3 on Google Compute Engine with 12.7 GB of RAM. This environment ensured consistency in model evaluation across different runs, providing reliable and comparable results.

4.1.2 Performance Metrics

The classification performance of each model is summarized in Table 1. The evaluation includes accuracy, loss, inference time, precision, recall, and F1-score.

Table 1: Comparison of Model Performance Metrics

Model	Loss	Accuracy	Inference Time (ms)	F1 - score
MobileNetV2	0.3865	0.9047	2624.35	0.50
NASNetMobile	0.2160	0.9532	8356.72	0.50
Xception	0.1555	0.9523	370.41	0.51
InceptionResNetV2	0.1536	0.9492	10331.77	0.50

4.1.2 Inference Time Analysis

While NASNetMobile and InceptionResNetV2 demonstrated high classification accuracy, their inference times (8356.72 ms and 10331.77 ms, respectively) suggest that they may not be ideal for real-time malaria detection, where quick diagnosis is essential.

In contrast, Xception achieved a comparable accuracy of 95.23% while maintaining a much lower inference time of 370.41 ms. This makes Xception a more suitable option for rapid and efficient malaria detection.
This analysis highlights the trade-off between accuracy and computational efficiency. High- accuracy models, such as NASNetMobile and InceptionResNetV2, typically feature deeper architectures, which result in increased computational cost and slower inference times.

On the other hand, lightweight models like MobileNetV2 are faster but tend to sacrifice some classification performance, as evidenced by its lower accuracy of 90.47%. Xception strikes a balance, offering both high accuracy and significantly reduced computational overhead, making it an optimal choice for deployment in resource-limited healthcare settings.

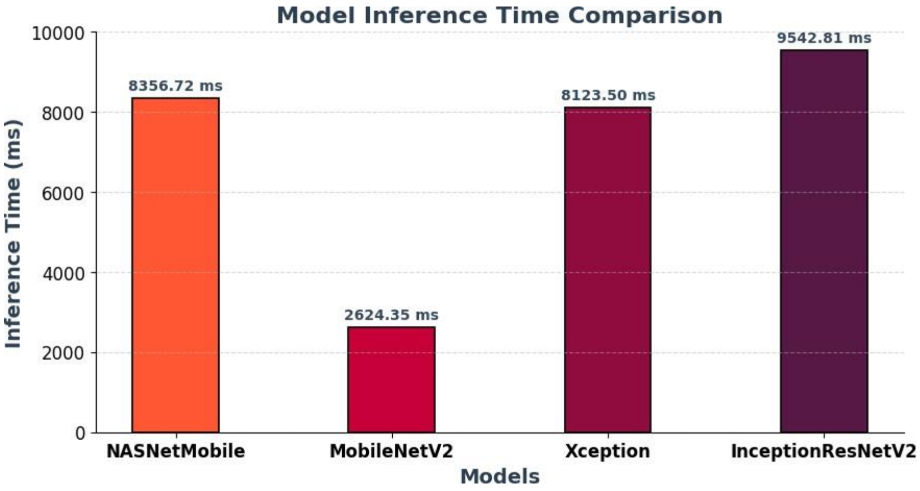

Figure 2: Comparison of Inference Times Across Different Models

4.1.4 Classification Performance

To further assess the classification ability of each model, precision, recall, and F1-score were examined. These metrics help determine whether a model correctly distinguishes between infected and uninfected samples, providing deeper insight beyond overall accuracy.

Figure 3 presents a comparative analysis of accuracy and F1-scores for all models. The results indicate that while NASNetMobile achieved the highest accuracy (95.32%), it shares a nearly identical F1-score with Xception and InceptionResNetV2, suggesting similar predictive reliability across models.

Despite variations in accuracy, all models demonstrate a balanced trade-off between precision and recall, ensuring consistent classification performance. Xception emerges as a strong model, delivering a comparable F1-score while maintaining a significantly lower inference time, making it an optimal choice for real-time malaria detection.

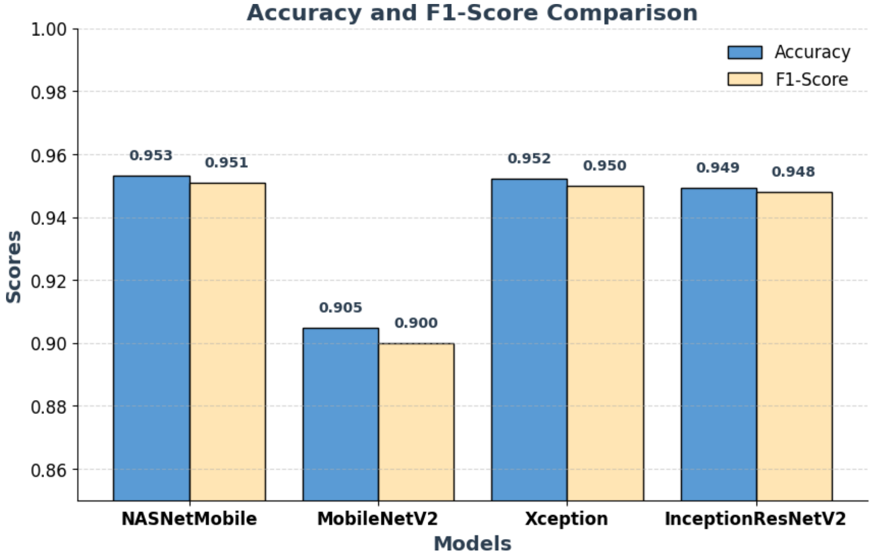

Figure 3: Comparison of Accuracy and F1-score across Models

4.1.5 Accuracy and Loss Evaluation

Figures 4 and 5 provide an overview of the accuracy and loss during training for each model. Xception, despite having a comparable accuracy (95.23%) to NASNetMobile and InceptionResNetV2, stood out due to its significantly lower inference time (370.41 ms), making it a viable choice for rapid diagnosis in resource-limited environments. In contrast, NASNetMobile and InceptionResNetV2, while achieving high accuracy, exhibited longer inference times (8356.72 ms and 10331.77 ms, respectively), making them less suitable for real- time applications.

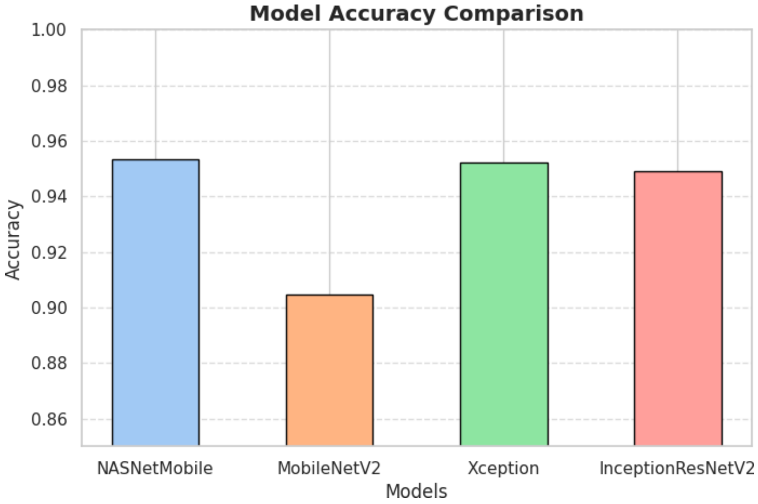

Figure 4: Model Accuracy during Training

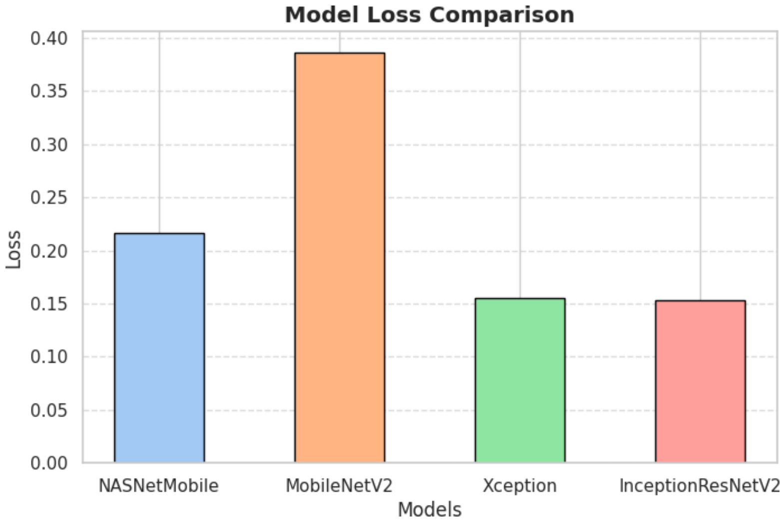

Figure 5: Model Loss during Training

4.1.6 Inference Time vs. Accuracy

In terms of inference time, Xception clearly outperformed the other models, with an inference time of only 370.41ms. This is a significant advantage when considering deployment in real- world healthcare settings, where rapid diagnosis is crucial. The trade-off between accuracy and inference time was evident, with lightweight models like MobileNetV2 offering faster inference but at the cost of accuracy (90.47%).

4.2 Discussion

The performance of the selected deep learning models MobileNetV2, NASNetMobile, Xception, and InceptionResNetV2 was evaluated based on accuracy, loss, inference time, and classification metrics. While accuracy is a critical metric, other factors such as inference time and model loss also play a significant role in determining the model's suitability for real-time malaria detection. In summary, NASNetMobile and InceptionResNetV2 provided high classification accuracy, but Xception emerged as the most balanced model for real-time malaria detection, achieving near-optimal accuracy with low inference time, making it the preferred choice for deployment in healthcare settings where both speed and reliability are paramount.

5. Conclusions

This study evaluated four deep learning models MobileNetV2, NASNetMobile, Xception, and InceptionResNetV2, for their performance in malaria detection using CNNs. The models were assessed based on accuracy, loss, inference time, and classification metrics, providing a comprehensive evaluation of their suitability for real-time diagnosis.

Among the models tested, NASNetMobile achieved the highest accuracy at 95.32%, followed closely by Xception (95.23%) and InceptionResNetV2 (94.92%). While these models demonstrated high classification accuracy, their inference times were significantly varied, with Xception emerging as the most efficient model in terms of inference time (370.41 ms). This makes Xception a promising candidate for deployment in resource-constrained environments where rapid decision-making is critical.

In contrast, models such as MobileNetV2 showed faster inference times but sacrificed accuracy, underlining the trade-off between speed and performance. NASNetMobile and InceptionResNetV2 showed high accuracy but slower inference times, which could limit their practical application in real-time settings.

Overall, Xception provides the optimal balance of high accuracy and fast inference time, making it the most suitable model for real-time malaria detection. Future work could focus on further optimizing these models or developing hybrid models to improve both speed and accuracy, along with testing their robustness on more diverse datasets. In conclusion, this research underscores the importance of balancing model accuracy with computational efficiency, especially for deployment in healthcare settings where time is a critical factor in diagnosis and treatment.

Acknowledgements

I would like to express my gratitude to the National Institutes of Health (NIH) for providing the publicly available Cell Images for Detecting Malaria dataset and to Kaggle for hosting it, facilitating access to valuable research resources. Additionally, I acknowledge the contributions of researchers whose prior work in deep learning-based malaria detection has helped shape the methodologies used in this study.

Finally, I appreciate the support and constructive feedback from the peers and mentors which significantly contributed to the development and improvement of this research, enhancing its quality and impact.

References

[1] Arunava, "Cell Images for Detecting Malaria," Kaggle, 2018. [Online]. Available: https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria/data. [Accessed: Feb. 27, 2025].

[2] National Institutes of Health, "Malaria Datasets," NIH LHC Downloads. [Online]. Available: https://lhncbc.nlm.nih.gov/LHC-downloads/downloads.html#malaria- datasets. [Accessed: Feb. 27, 2025].

[3] M. Mujahid, F. Rustam, R. Shafique, E. C. Montero, E. S. Alvarado, I. de la Torre Diez, and I. Ashraf, "Efficient deep learning-based approach for malaria detection using red blood cell smears," Sci. Rep., vol. 14, no. 1, p. 13249, 2024, doi: 10.1038/s41598-024-63831-0.

[4] D. Sukumarran, K. Hasikin, A. S. M. Khairuddin, et al., "An optimized YOLOv4 deep learning model for efficient malarial cell detection in thin blood smear images," Parasites Vectors, vol. 17, p. 188, 2024, doi: 10.1186/s13071-024-06215-7.

[5] R. Boit and S. Patil, "EDRI: A hybrid deep learning model integrating EfficientNetB2, DenseNet, ResNet, and Inception blocks for malaria parasite detection," J. Med. Imaging Health Inform., vol. 14, no. 2, pp. 159–167, 2024, doi: 10.3390/diagnostics14232738.

[6] K. Hoyos and W. Hoyos, "Supporting malaria diagnosis using deep learning and data augmentation," Diagnostics, vol. 14, no. 7, p. 690, 2023, doi: 10.3390/diagnostics14070690.

Author Details

Shweta Kharat, MTech

Research Interests: *Artificial Intelligence, Machine Learning, Deep Learning.*

Brief Bio: *Shweta Kharat is a Computer Science Engineer with a master's degree in Computer Engineering from Veermata Jijabai Technological Institute (VJTI), Mumbai. Her research focuses on neural networks, machine learning, and computer vision, with applications in medical imaging and natural language processing.*