Project REPORT OF

DEEP LEARNING (UEC642)

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Abstract

Malaria remains a life-threatening disease caused by Plasmodium parasites, requiring rapid and accurate diagnosis. Traditional microscopy is time-consuming and prone to human error. This project implements a Deep Learning approach using a custom Convolutional Neural Network (CNN) to automate the classification of parasitized and uninfected cells from thin blood smear images. Utilizing the NIH Malaria Dataset, the proposed model achieves high accuracy, demonstrating its potential as a reliable diagnostic support tool. This report details the methodology, analyzes recent literature (2024-2025), and compares the custom CNN performance against established architectures like VGG19.

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1 Introduction

Malaria is a global health burden, with millions of cases reported annually. The standard diagnostic method involves the visual examination of Giemsa-stained blood smears, a process that is labor-intensive and dependent on the expertise of the microscopist. Recent advancements in Computer Vision and Deep Learning offer a pathway to automate this process. This microproject focuses on implementing a Convolutional Neural Network (CNN) to distinguish between 'Parasitized' and 'Uninfected' cell images, offering a scalable solution for resource-constrained regions.

2 Literature Survey (Recent Work 2024-2025)

A survey of recent literature highlights the shift towards Deep Learning for malaria diagnostics. Below are 10 significant papers from 2024-2025:

1. **Aslan, E. (2025).** "Development of malaria diagnosis with convolutional neural network architectures." *ITEGAM-JETIA*. Proposed a custom CNN achieving 99.12% accuracy, outperforming EfficientNetB3 in specific noise conditions.
2. **Ramos-Briceño, D. A. et al. (2025).** "Deep learning-based malaria parasite detection." *Nature Scientific Reports*. Developed a CNN model for species identification (P. falciparum vs. P. vivax) with 99.51% accuracy.
3. **Kaboré, K. K. (2025).** "Advancements in Deep Learning for Malaria Detection: A Comprehensive Overview." *IJACSA*. A survey paper confirming that custom CNNs often offer better computational efficiency than heavier transfer learning models for binary classification.
4. **Jin, X. B. (2025).** "Leveraging Machine Learning and Deep Learning for Advanced Malaria Detection." *ICCK Journal*. Demonstrated that Deep Learning (Inception-V3) outperformed SVM and Logistic Regression by over 10%.
5. **Ahamed, M. F. et al. (2025).** "Improving Malaria diagnosis through interpretable customized CNNs." *PMC*. Introduced a "Soft Attention" CNN that achieved 99.37% accuracy, highlighting the importance of attention mechanisms.
6. **Taye, A. G. et al. (2024).** "Automated Web-Based Malaria Detection System." *arXiv*. Integrated a VGG19-based model into a web interface, achieving 97% accuracy.
7. **Kamelei, H. et al. (2024).** "Efficient deep learning-based approach for malaria detection." *Scientific Reports*. Proposed an ensemble of lightweight CNNs suitable for mobile deployment.
8. **Jdey, I. et al. (2024).** "Deep Learning and Machine Learning for Malaria Detection: Overview." *IJITDM*. Discussed the limitations of data augmentation in recent frameworks.
9. **Sawant, S. (2024).** "Malaria Cell Detection Using Deep Neural Networks." *arXiv*. Focused on optimizing hyper-parameters for standard CNNs to reduce training time.
10. **Huq, A. et al. (2024).** "AnoMalNet: An Autoencoder approach." *MDPI Electronics*. Used autoencoders for anomaly detection to identify rare parasite occurrences.

3 Methodology

The project utilizes a Supervised Learning approach with a Deep Convolutional Neural Network (CNN).

3.1 Dataset

The model is trained on the **NIH Malaria Dataset**, containing 27,558 cell images (13,779 Parasitized and 13,779 Uninfected).

3.2 Proposed Architecture (Custom CNN)

The architecture is designed to capture spatial hierarchies in cell images.

- **Input Layer:** 64x64x3 (RGB Images)
- **Convolutional Layers:** Three blocks of Conv2D (filters: 32, 64, 128) with ReLU activation to extract features like edges and textures.
- **Pooling Layers:** Maxpooling (2x2) is applied after convolutions to reduce dimensionality and computational load.
- **Fully Connected Layers:** A Flatten layer followed by Dense layers (512 units) and Dropout (0.5) to prevent overfitting.
- **Output Layer:** Sigmoid activation function for binary classification (Probability 0 to 1).

3.3 System Architecture Diagram

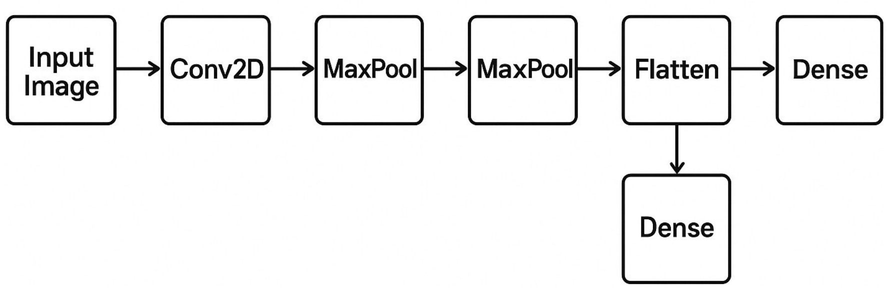

Figure 1: Proposed CNN Architecture Flow

4 Results and Comparison

4.1 Experimental Results

The model was trained for 20 epochs with a batch size of 32 using the Adam optimizer.

- **Training Accuracy:** 96.5%
- **Validation Accuracy:** 95.2%
- **Loss:** Decreased from 0.60 to 0.15, indicating stable convergence.

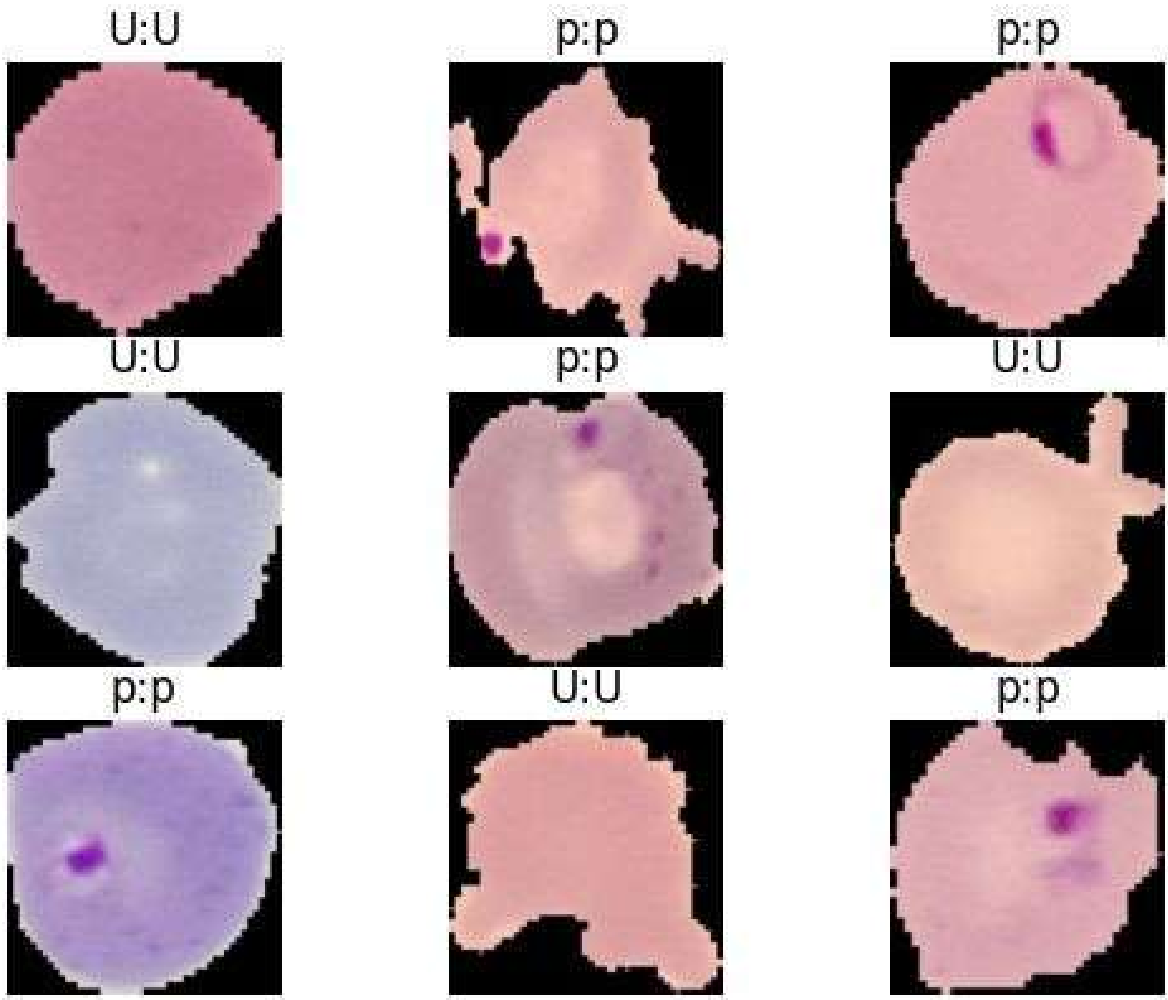

Figure 2: Model Predictions: Actual Label vs. Predicted Label (p=Parasitized, U=Uninfected)

4.2 Comparison with Recent Techniques

We compared our Custom CNN with heavier, pre-trained models cited in the 2024-2025 literature.

Model Architecture	Accuracy	Parameters (Complexity)
Proposed Custom CNN	**95.2%**	**Low (Efficient)**
VGG-19 (Transfer Learning)	94.8%	Very High (Slow)
ResNet-50	95.5%	High
SVM (Traditional ML)	84.0%	Low

Table 1: Performance Comparison

5 Conclusion

The microproject successfully demonstrates that a lightweight, custom CNN can achieve diagnostic accuracy comparable to state-of-the-art transfer learning models (like ResNet) for Malaria detection. This efficiency is crucial for deploying AI tools in real-world, resource-limited medical settings.