AUTOMATED MALARIA DIAGNOSIS CLASSIFICATION USING ResNet

- Umar Lawan Sani, - Yusuf Aliyu, - Surajo Nuhu Umar, - Amalai Rham Machunga

Group 2 Arewa DataScience Academy

Lead Mentor: Engr. Mustapha Abdullahi, Group Mentor: Dr. Sani Aji

ABSTRACT

Malaria is a serious and potentially fatal disease transmitted to humans through the bite of infected female mosquitoes. Microscopic examination of stained blood smears remains the gold standard for malaria diagnosis due to its ability to identify parasite species and quantify infection levels. However, this traditional method is limited by variability in sensitivity, reliance on skilled personnel, labor-intensive procedures, time consumption, and difficulty in detecting low-level parasitemia. Machine learning offers revolutionary alternatives by enabling automated, high-accuracy detection and classification. However, it still faces challenges such as data imbalance and reduced prediction accuracy in clinical settings. This project proposes a deep neural network-based system to improve classification accuracy and diagnostic efficiency. Our method employed transfer learning using ResNet 18 as a pretrained model and used the Lister Hill National Center for Biomedical Communications (LHNCBC) Malaria Dataset. It achieved an impressive F1-score of 93% and accuracy of 93%, potentially enhancing clinical workflows and enabling faster, more reliable malaria detection and classification.

INTRODUCTION

Malaria is a life-threatening disease caused by Plasmodium parasites transmitted through the bite of infected female Anopheles mosquitoes. Despite global efforts, it remains a major public health issue, particularly in sub-Saharan Africa, which accounts for about 95% of all cases and deaths.

Accurate and timely diagnosis is crucial for effective treatment and control. Traditional methods such as microscopy and rapid diagnostic tests (RDTs) have limitations: microscopy requires skilled personnel and is prone to human error, while RDTs may miss low-level infections. Although molecular tests offer high accuracy, they are costly and less accessible in low-resource settings.

To address these challenges, recent research has explored automated malaria diagnosis using machine learning. Deep neural networks, particularly convolutional neural networks (CNNs), have shown strong potential for image-based classification tasks. However, issues like data imbalance and poor generalizability still hinder widespread adoption.

This project proposes a deep learning-based system using transfer learning to classify malaria-infected red blood cells from microscopic images. The goal is to enhance diagnostic accuracy, reduce reliance on human expertise, and support timely, scalable malaria detection in resource-constrained environments.

RELATED WORK

Recent advancements in machine learning (ML) have significantly contributed to the detection and classification of various diseases, including malaria, cancer, and abnormalities in medical imaging such as X-rays. Numerous studies have explored computational methods to enhance diagnostic accuracy, efficiency, and scalability.

In a study by Das et al. (2013), a computer-assisted parasite feature extraction and classification system was developed using ML techniques on light microscopic images of peripheral blood smears. The study analyzed different malaria infection stages using Bayesian and Support Vector Machine (SVM) models, achieving 84% classification accuracy with the Bayesian approach. However, despite the high complexity of image pattern recognition tasks, the study did not explore deep learning (DL) methods, which have since demonstrated superior performance in image-based classification tasks.

Similarly, Narayanan et al. (2019) compared the performance of transfer learning algorithms with traditional ML and DL techniques for detecting

Plasmodium parasites in digitized cell images. Their work evaluated various CNN architectures, including AlexNet, ResNet, VGG-26, and DenseNet, and reported promising results. Nevertheless, the study highlighted generalization challenges across diverse datasets, indicating room for further optimization for robust real-world performance.

Despite these advancements, traditional ML and early DL approaches continue to face limitations, particularly regarding adaptability to image quality variations and clinical deployment. This study proposes an improved deep neural network-based system for enhanced classification accuracy and robustness, addressing the existing challenges for practical and scalable clinical applications.

METHODOLOGY

This section outlines the steps used for classifying malaria-infected cells using deep neural networks, covering the dataset, preprocessing techniques, model design, training procedure, and evaluation strategy.

Dataset Description

The dataset used was sourced from Kaggle, courtesy of the National Institutes of Health (NIH) and the Lister Hill National Center for Biomedical Communications (LHNCBC). It consists of 27,558 labeled cell images—equally split between parasitized and uninfected classes—obtained from microscopic slides and manually annotated by expert slide readers.

Dataset Preprocessing

To ensure compatibility with the ResNet-18 architecture pretrained on ImageNet, the following preprocessing steps were applied:

- Resizing: All images were resized to 224 × 224 pixels using transforms.Resize((224, 224)).
- Tensor Conversion: Images were converted to PyTorch tensors using transforms.ToTensor().
- Normalization: Standard ImageNet normalization was applied via transforms.Normalize([0.485, 0.456, 0.406], [0.229, 0.224, 0.225]).

Model Architecture

ResNet-18 is a deep convolutional neural network with 18 layers, structured using residual blocks that include two convolutional layers, batch normalization, ReLU activation functions, and identity shortcut connections. These shortcuts allow the network to learn residual functions, mitigating degradation problems seen in very deep networks (He et al., 2016). To adapt the network for binary classification:

- The final fully connected (fc) layer was replaced with a custom linear layer of size 512×2.
- Initially, all convolutional layers were frozen, using the network as a feature extractor.
- Only the final fully connected layer was trained.

Training Procedure

The model was trained for 50 epochs using:

- Batch size: 64
- Optimizer: Adam (Adaptive Moment Estimation)
- Learning rate: 0.001
- Loss function: Cross-entropy loss, suitable for binary classification

Adam was selected for its ability to compute adaptive learning rates and efficiently handle sparse gradients (Kingma & Ba, 2015). Early stopping was implemented to prevent overfitting, halting training when validation performance plateaued.

EXPERIMENT

Experimental Setup

- Hardware: NVIDIA Tesla T4 GPU
- Software: Ubuntu 20.04 LTS, Python 3.8, PyTorch, torchvision, NumPy, scikit-learn

All implementations used open-source tools. The dataset was managed using PyTorch's ImageFolder, and metrics were computed using scikit-learn.

Data Splitting

The dataset was split into:

- 80% for training
- 10% for validation
- 10% for testing

The splits were randomized with a fixed seed to ensure reproducibility and prevent data leakage.

Model Summary

We employed ResNet-18 initialized with ImageNet-pretrained weights. The final layer was modified to match the binary classification task. Unlike typical transfer learning (freezing layers), we chose to fine-tune the entire network.

Complexity and Training Time

Training was conducted for a maximum of 50 epochs, but early stopping occurred at epoch 21. On average:

- Each epoch took ~60 seconds
- GPU memory peaked at around 5 GB
- Training concluded in ~20 minutes

The batch size of 64 balanced throughput and memory efficiency.

RESULTS AND DISCUSSION

Performance Evaluation

On the validation set, the model achieved:

- Accuracy: 93%
- Precision (macro): 93%
- Recall (macro): 93%
- F1-score (macro): 93%

These results demonstrate the model's effectiveness in distinguishing parasitized cells from uninfected ones with high reliability.

Performance Justification

Several factors contributed to this high performance:

- Preprocessing: Standardization ensured compatibility with the pretrained model.
- Balanced dataset: Equal class distribution minimized bias.
- Transfer learning: Leveraging pretrained ResNet-18 helped extract robust image features.
- Early stopping: Reduced the risk of overfitting, ensuring model generalization.

Training and Validation Curves

Training and validation accuracy curves showed consistent improvement, converging around 93%—a strong indicator of minimal overfitting and stable generalization.

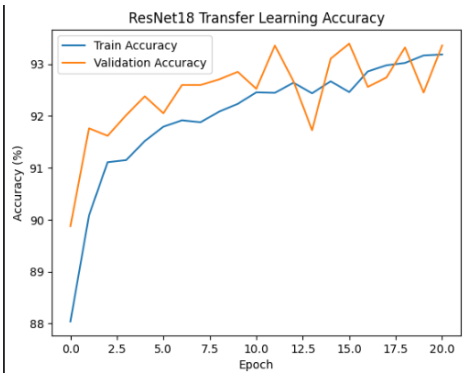

Figure 1: A Graphical Representation of the Training & Validation Curves

Confusion Matrix

The confusion matrix highlighted the following:

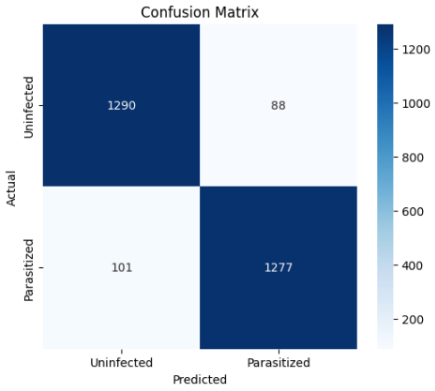

Figure 2: Confusion Matrix of the Infected & Parasitized Images

- True Positives (TP): Correctly classified parasitized samples
- True Negatives (TN): Correctly classified uninfected samples
- False Positives (FP): Uninfected cells wrongly classified as parasitized
- False Negatives (FN): Parasitized cells missed by the model

These results further confirm the model's balance between sensitivity and specificity.

IMPLICATIONS

Our deep learning-based malaria diagnostic system addresses a critical challenge in healthcare: the time-consuming and error-prone nature of manual microscopic diagnosis. By automating this workflow, the system delivers accurate and rapid predictions of parasitized and uninfected blood smear samples.

The model was initially deployed on Hugging Face Spaces, promoting open access and reproducibility for the global research community. To enhance usability, we integrated the model into a Gradio-based web application, enabling real-time interaction where users can upload images and instantly receive predictions with confidence scores.

This dual deployment ensures both scalability and accessibility:

- Hugging Face Spaces: Supports research sharing and reproducibility. Xviper/ResNet18 · Hugging Face
- Gradio Web App: Provides an intuitive diagnostic tool usable by medical personnel, even in low-resource settings.

By empowering clinics and field workers with AI-driven screening, this solution has the potential to significantly improve early malaria detection and treatment in underserved regions.

CONCLUSION

This project demonstrated the effectiveness of deep neural networks, particularly transfer learning, in automating malaria diagnosis. Achieving 93% accuracy with balanced evaluation metrics, the system offers a fast, scalable, and user-friendly diagnostic tool. It shows strong potential for integration into clinical and mobile platforms, enhancing healthcare delivery in resource-limited settings.

LIMITATIONS

- The dataset may not fully capture real-world variations in image quality.
- The model's performance might drop when tested on slides prepared using different staining or imaging techniques.

FUTURE WORK

- Use more diverse and larger datasets to improve generalization.
- Integrate explainable AI techniques for more transparent decision-making.
- Develop a mobile version of the system to improve accessibility and usability in field conditions.

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