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Deep Learning Model for Improved Malaria Prediction and Severity Classification

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Abstract

Malaria remains a major health problem worldwide, especially in poor countries where quick and accurate diagnosis can save lives. This study presents a deep learning approach to improve how we detect malaria and measure how serious the infection is. We used a type of artificial intelligence called Convolutional Neural Networks (CNNs) to look at images of blood cells taken from microscopes and identify malaria parasites in them. Our model can not only tell if a cell is infected or not; it can also figure out how severe the infection is by counting how many parasites are present. To make the model work better, we applied a preprocessing technique called Gaussian blur, which helps reduce noise in the images and makes important features clearer. We tested the model using different training-to-testing splits (90:10, 80:20, 70:30, 60:40 and 50:50) and compared its performance with and without Gaussian blur. The CNN model with Gaussian blur achieved the best accuracy of 94.97% on the 90:10 data split. When we compared the CNN with other common machine learning models; Random Forest, Decision Tree and Logistic Regression; the CNN performed far better, showing that deep learning is a powerful tool for malaria diagnosis. The model also successfully classified infection severity as mild, moderate, or severe based on parasitemia levels (the percentage of infected red blood cells). These results suggest that CNN-based systems could provide fast, reliable and affordable malaria diagnosis in places where expert microscopists are scarce. Future work should focus on testing the model with larger and more diverse datasets and deploying it on mobile or web platforms for real-world use.

Keywords: Convolutional neural networks; Malaria detection; Severity classification; Gaussian blur; Deep learning; Medical image analysis; Parasitemia

Abbreviations: The following abbreviations are used in this manuscript:

Convolutional Neural Network (CNN), Deep Learning (DL), Machine Learning (ML), Artificial Intelligence (AI), Rapid Diagnostic Test (RDT), World Health Organization (WHO), Centers for Disease Control and Prevention (CDC), Red Blood Cell (RBC), True Positive (TP), True Negative (TN), False Positive (FP), False Negative (FN), Rectified Linear Unit (RLU), Random Forest (RF), Decision Tree (DT), Logistic Regression (LR)

Introduction

Malaria is one of the deadliest diseases in the world. According to the World Health Organization, there were about 249 million cases of malaria worldwide in 2022, resulting in over 600,000 deaths. Nigeria bears the heaviest burden, accounting for nearly 31% of all malaria deaths globally. The disease is caused by a parasite called plasmodium, which is spread through the bites of infected mosquitoes. When a person gets malaria, the parasites infect their red blood cells and the severity of the illness depends on how many cells are infected; a measure called parasitemia.

Traditionally, doctors diagnose malaria by looking at blood samples under a microscope. A trained technician examines the blood smear and counts how many cells contain parasites. This method works, but it has several problems. First, it requires skilled people who may not be available in rural or

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poor areas. Second, it is slow and tiring, especially when many samples need to be checked. Third, it can miss infections when the number of parasites is very low (low parasitemia). Rapid Diagnostic Tests (RDTs) are another option; they are faster and easier to use, but they are less sensitive and can give wrong results.

In recent years, deep learning; a branch of artificial intelligence has shown great promise in analyzing medical images. Deep learning models, especially Convolutional Neural Networks (CNNs), can learn to recognize patterns in images automatically, without needing a human to tell them what features to look for [1]. CNNs have been used successfully to detect diseases like cancer, tuberculosis and diabetic retinopathy from medical images.

Several researchers have applied deep learning to malaria detection. For example, Esraa et al. developed a Malaria CNN (MCNN) that achieved about 99.29% accuracy in identifying infected versus uninfected cells using transfer learning [2]. Sumit et al. built a lightweight CNN that achieved 95.4% accuracy, designed to work on mobile devices [3]. Hemachandran et al. compared different deep learning architectures and found that ResNet50 achieved 99.23% accuracy [4]. Wojciech et al. used semantic segmentation to reach 99.68% accuracy [5].

However, most of these studies focus only on telling whether a cell is infected or not; a binary classification problem. They do not address the question of how severe the infection is. Knowing the severity of malaria is important because it helps doctors decide what treatment to give and whether the patient needs immediate care. Mild malaria can be treated with oral medication at home, but severe malaria requires hospital care and injectable drugs.

This study aims to fill that gap. We developed a CNN model that not only detects malaria parasites in blood smear images but also classifies the severity of the infection based on parasitemia levels. We also tested how Gaussian blur; a preprocessing technique that smooths images; affects the model's performance. By doing this, we hope to create a tool that can provide both diagnosis and severity assessment in one step, making it useful for clinics and hospitals in resource; limited settings.

Materials and Methods

Dataset description

We used a publicly available dataset from Kaggle called the malaria cell image dataset. The original dataset contains 27,558 labeled images of red blood cells, divided into two groups: parasitized *i.e.* cells containing malaria parasites and uninfected *i.e.* healthy cells. However, due to limits in our computer processing power, we used a subset of 4,000 images; 2,000 parasitized and 2,000 uninfected. Each image was resized to 64×64 pixels and normalized so that all pixel values were on a similar scale, which helps the model learn faster and more reliably.

Image preprocessing

Before feeding the images into the model, we applied several preprocessing steps:

Normalization: We scaled the pixel values so they had an average of zero and a standard deviation of one. This helps the model train more smoothly.

Gaussian blur: We applied a smoothing filter called Gaussian blur to reduce noise and soften the edges in the images. We used a 3×3 kernel size, which means each pixel's new value is calculated by averaging it with its eight neighboring pixels, weighted by a Gaussian (bell-shaped) curve. The purpose of this step is to remove small distracting details and help the model focus on the bigger, more important structures in the cells.

Segmentation: We used simple image processing techniques to separate the cells from the background, so the model could focus on the cells themselves rather than irrelevant empty space.

Parasitemia computation

To measure how severe a malaria infection is, we calculated parasitemia; the percentage of red blood cells that are infected. The formula is:

$$Parasitemia = \frac{Number\ of\ infected\ RBCs}{Total\ number\ of\ RBCd} X100$$

Based on the parasitemia percentage, the infection was classified into three categories. An infection was considered mild (negative) when less than 1% of the cells were infected. It was classified as moderate when the percentage of infected cells ranged from 1% to 10%. Infections with more than 10% infected cells were classified as severe.

CNN model architecture

We built a Convolutional Neural Network (CNN) using TensorFlow/Keras. A CNN works by passing the image through several layers that gradually learn to detect features; starting from simple ones like edges and colors and building up to more complex ones like shapes and patterns specific to malaria parasites.

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The basic building block of a CNN is the convolution operation. If we have an input image XX and a filter (also called a kernel) WW, the convolution operation produces a feature map FF:

F(i,j)=(X∗W)(i,j)=∑m∑nX(i+m,j+n)·W(m,n)F(i,j)=(X∗W)(i, j)=m∑n∑

X(i+m,j+n)·W(m,n)

F(i, j)\): The value of the feature map at position \((i, j)\),

W(m, n)\): The value of the filter/kernel at position \((m, n)\),

After each convolution layer, we applied an activation function called ReLU (Rectified Linear Unit), which introduces non-linearity:

ReLU(x)=max(0,x)ReLU(x)=max(0,x)

We also used max pooling layers to reduce the size of the feature maps, keeping only the most important information. At the end of the network, we added fully connected layers that combine all the features to make a final prediction whether the cell is infected or not and how severe the infection is.

Experimental Design

We designed our experiments to test three things:

- How well the CNN performs at different training/testing data splits
- Whether Gaussian blur improves the model's performance
- How the CNN compares with traditional machine learning models

We split the data into five different training-to-testing ratios: 90:10, 80:20, 70:30, 60:40 and 50:50. For each split, we trained the model twice; once with original images and once with images that had Gaussian blur applied. We also trained three other models (random forest, decision tree and logistic regression) for comparison.

Evaluation Metrics

We measured the model's performance using several metrics:

- **Accuracy:** The percentage of all predictions that were correct
- **Precision:** Of all the cells the model said were infected, how many were actually infected
- **Recall:** Of all the actually infected cells, how many did the model correctly identify
- **F1-Score:** A balanced average of precision and recall
- **Confusion Matrix:** A table showing true positives, true negatives, false positives and false negatives

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

$$Precision = \frac{TP}{TP + FP}$$

$$Recall = \frac{TP}{TP + FN}$$

$$F1 - Score = 2\frac{X(Precision\ X\ Recall)}{Precision + Recall}$$

Results

CNN performance with gaussian blur

The CNN model with Gaussian blur preprocessing achieved consistently high performance across all data splits. As shown in **Table 1**, the best accuracy was 94.97% on the 90:10 split. Performance remained strong even as the data split became more balanced, with the 50:50 split still achieving 92.9% accuracy.

Table 1: CNN with Gaussian blur performance across different data split.

Split Ratio	Accuracy	Precision	F1-Score	Recall
90:10	0.9497	0.94	0.94	0.94
80:20	0.9495	0.94	0.94	0.94
70:30	0.9249	0.94	0.94	0.94
60:40	0.9138	0.92	0.93	0.93
50:50	0.929	0.93	0.93	0.93

CNN performance without gaussian blur

Without Gaussian blur, the CNN still performed well, but slightly lower. The best accuracy was 94.25% on the 90:10 split and performance declined more noticeably as the data split became more balanced, reaching 92.17% on the 50:50 split (**Table 2**).

Table 2: CNN without Gaussian blur performance across different data splits.

Split Ratio	Accuracy	Precision	F1-Score	Recall
90:10	0.9425	0.94	0.94	0.94
80:20	0.9387	0.94	0.94	0.94
70:30	0.9341	0.93	0.93	0.93
60:40	0.9268	0.93	0.93	0.93
50:50	0.9217	0.92	0.92	0.92

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Comparison of all models

When we compared the CNN with traditional machine learning models on the 90:10 split (**Table 3**), the CNN outperformed all others by a large margin. The CNN with blur achieved 94.9% accuracy, while the next best model; Random Forest with blur only reached 79.5%. Decision Tree and Logistic Regression performed much worse, at 67.1% and 62.5% respectively.

Table 3: Model comparison on 90:10 split.

Model	Accuracy	Precision	F1-Score	Recall
CNN blurred	0.949	0.94	0.94	0.94
CNN	0.938	0.94	0.94	0.94
RF blurred	0.795	0.79	0.79	0.79
RF	0.786	0.79	0.79	0.79
DT blurred	0.671	0.68	0.67	0.68
DT	0.665	0.66	0.66	0.67
LR blurred	0.625	0.63	0.62	0.63
LR	0.591	0.59	0.59	0.59

Severity classification results

We tested the model's ability to compute malaria severity using sample images. The CNN model's predictions matched the actual microscopic examination results with 94.97% similarity.

The random forest model achieved 79.75% similarity, while decision tree and logistic regression scored 68.72% and 65.10% respectively.

For example, on one test image, the model predicted a parasitemia level of 0.88%, classifying it as negative (mild). On another image, it predicted 87.00% parasitemia, classifying it as severe. These results demonstrate that the model can not only detect malaria but also provide a meaningful assessment of how serious the infection is.

Discussion

Our results show that CNN models are highly effective for both malaria detection and severity classification. The model achieved its best performance (94.97% accuracy) with the 90:10 data split and when Gaussian blur was applied.

This makes sense because more training data helps the model learn better and Gaussian blur helps remove noise that could confuse the model.

The finding that Gaussian blur improves performance is important. In real-world settings, microscope images are not always perfect; they can be blurry, poorly lit, or have other quality issues. By training the model with blurred images, we make it more robust and better able to handle imperfect real-world images. This finding is consistent with previous research by Yoshihara et al., who showed that training CNNs with blurred images makes them more resilient to image quality variations [6].

The CNN's superior performance compared to traditional models (random forest, decision tree, logistic regression) is expected. CNNs are designed specifically for image data they can automatically learn spatial patterns and hierarchies of features, whereas traditional models require features to be manually extracted and may miss important information.

Our comparison with prior work shows that our results are competitive. While Esraa et al. achieved 99.29% accuracy using transfer learning with pre-trained networks [2], our simpler CNN architecture achieved 94.97% while also providing severity classification; something their model did not directly address. Similarly, Sumit et al. achieved 95.4% with a lightweight CNN [3] and our results (94.97%) are in a similar range.

One limitation of our study is the dataset size. Due to computational constraints, we used only 4,000 out of the 27,558 available images. A larger dataset would likely improve the model's accuracy and generalizability. Additionally, the dataset comes from a public repository and may not fully represent the diversity of malaria parasite strains found in different regions, such as Nigeria.

Another limitation is that our severity classification is based purely on parasitemia levels measured from images. In clinical practice, doctors consider many other factors; such as the patient's symptoms, age, hemoglobin levels and other laboratory tests; when determining severity and treatment.

Conclusions

This study successfully demonstrated that Convolutional Neural Networks (CNNs) can be used not only to detect malaria parasites in blood smear images but also to classify the severity of the infection. Our main findings are:

- The CNN model with Gaussian blur preprocessing achieved the highest accuracy of 94.97%, outperforming traditional machine learning models by a significant margin.
- Gaussian blur preprocessing improved the model's performance, making it more robust and better able to handle image noise.

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- The model successfully computed parasitemia levels and classified infections as mild, moderate, or severe, bridging the gap between simple detection and clinically meaningful diagnosis.
- CNNs consistently outperformed random forest, decision tree and logistic regression models across all testing scenarios.

These findings suggest that deep learning-based systems could play an important role in malaria diagnosis, especially in resource limited settings where access to expert microscopists is limited. By providing both detection and severity assessment in a single automated step, such systems could help healthcare workers make faster and more informed treatment decisions.

Future research should focus on:

- **Dataset expansion:** Training on larger and more diverse datasets that include images from different countries and microscope types
- **Transfer learning:** Using pre-trained models to potentially improve accuracy further
- **Real-world deployment:** Testing the model on mobile or web platforms for use in clinics and field settings
- **Multi-class classification:** Extending the model to identify different Plasmodium species
- **Clinical validation:** Testing the system in actual healthcare settings to evaluate its real-world performance and impact

Author Contributions

Conceptualization, S.L.T., A.I. and S.A.B.; methodology, S.L.T. and A.D.B.; software, S.L.T.; validation, S.L.T., A.I., S.A.B. and A.D.B; formal analysis, S.L.T.; investigation, S.L.T.; resources, S.L.T., A.I. and S.A.B.; data curation, S.L.T.; writing; original draft preparation, S.L.T.; writing; review and editing, S.L.T., A.I. and S.A.B.; visualization, S.L.T.; supervision, A.I. and S.A.B.; project administration, S.L.T. All authors have read and agreed to the published version of the manuscript.

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