

Leveraging Deep Learning for Malaria Cell Classification Using CNN, Resnet50 and VGG19

Abstract:

This report provides a detailed account of our approach to malaria cell classification using deep learning techniques. We outline the challenges encountered during the model development process and the strategies employed to overcome them. Additionally, we present key findings from our experimentation process, highlighting the effectiveness of our approach in addressing these challenges.

1. Introduction:

Malaria remains a significant global health challenge, necessitating accurate and efficient diagnostic methods. Automated classification of malaria-infected cells using deep learning models offers a promising solution to this problem. In this section, we introduce our methodology and motivation for the study.

2. Dataset Preprocessing:

We describe the challenges faced during dataset preprocessing, including the large size of the dataset and computational constraints. To address these challenges, we implemented techniques such as resizing images and early stopping to enhance model generalization and improve performance on unseen data.

3. Model Selection and Architecture:

We outline the challenges encountered in selecting the appropriate deep learning architecture for malaria cell classification. Computational limitations and model complexity were significant hurdles. Despite these challenges, we rationalized our choice of convolutional neural networks (CNNs) which has the accuracy of about 92.19% as the primary model architecture, as they offered a balance between computational efficiency and model performance.

Additionally, we attempted to compare the performance of CNN, VGG19 (90% accuracy), and ResNet50(92.80% accuracy) architectures. Although both VGG19 and ResNet50 has been trained in the first attempt which took hours to train and we have got the accuracy for VGG19 (90%), and for ResNet50(92.80%). However, due to computational resource limitations and the extended time required to retrain VGG19 and ResNet50 models, we

prioritized the CNN architecture for our study. Although ResNet50 has showed us high accuracy in comparison with the CNN but when I saved the model in my next attempt size of the model increased and hence, I switched to CNN for further process.

4. Training Optimization:

We address the challenges encountered during the training process, including long training times and memory constraints. To optimize training, we implemented strategies such as reducing image size, batch size, and epoch count and early stopping. These optimizations significantly improved computational efficiency without sacrificing model performance.

5. Model Saving Challenges:

An additional challenge arose during the process of saving the trained model. The size of the saved model exceeded the desired threshold i.e. 25mb (Github maximum limit for uploading any document), posing difficulties in deployment and storage. To overcome this challenge, we explored quantization techniques and compression methods to reduce the model size while maintaining performance.

6. Experimental Results:

Results from our experimentation process are presented, demonstrating the effectiveness of our approach in overcoming the challenges faced. Despite initial setbacks, our optimized CNN model achieved competitive accuracy metrics while significantly reducing training time and computational resources.

7. Discussion:

We discuss the challenges encountered during the model development process and the strategies employed to overcome them. Our approach highlights the importance of balancing computational constraints with model performance in resource-limited settings.

8. Conclusion:

We conclude the report with a summary of our key findings and insights. Our approach demonstrates the feasibility of using deep learning techniques for malaria cell classification in resource-constrained environments.