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Intelligent Multi-Stage Malaria Detection and Life-Stage Classification Using Deep Learning

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Abstract

The labor-intensive nature of blood smear testing for the presence of malaria in humans requires a trained individual in order to yield accurate test results so to reduce the lengthy testing process, we propose a two-tiered deep learning method for both diagnosing individuals for the presence of malaria and classifying their infection(s) by the stage of the parasite (i.e. ring, trophozoite, schizont, or gametocyte). The first tier will utilize a convolutional neural network (CNN) to make the determination of whether an image has evidence of a malaria infection. The second tier will classify those images that contain malaria parasites based on the parasite life stage. To improve the interpretability of the results, we will use Gradient-weighted Class Activation Mapping algorithm (Grad-CAM) allowing for more accurate visualization of the reasoning behind the way the model classified each image and establish a confidence threshold so that experts may investigate the classification for confirmation. We have conducted preliminary testing on the system for its ability to detect malaria and the preliminary results have been favorable but the development work needed to classify the different life stages of the malaria parasite is still underway. This system provides the ability to rapidly, accurately and interpetably identify malaria. In addition to providing a quick method for diagnosing malaria, this system may be applied to low-resource settings depending on available resources. Lastly, the implementation of data augmentation and preprocessing techniques will increase the performance of the model. Taking into consideration that the design of the system is modular, there are no limitations in developing additional models for future integration into this system. This research highlights the capabilities of integrating deep learning with explainability techniques to better inform the physician or clinician based on medical images.

Keywords; Medical Image Analysis, Malaria Detection, Convolutional Neural Network (CNN), Multi-stage Classification, Transfer Learning.

INTRODUCTION

Malaria remains an important global health issue, causing significant morbidity and mortality, mainly in tropical and subtropical regions. The World Health Organization (WHO) estimates millions of cases of malaria are reported every year, with the majority from developing countries [1]. Accurate and timely diagnosis is critical to preventing malaria expansion and controlling malaria spread. Currently, visual inspection of microscopic blood smear images by professionals trained in malaria diagnosis is the established method for diagnosing malaria; however, this method is laborious, time-consuming, and prone to inconsistencies.

Over the last few years, advances in deep learning, particularly convolutional neural networks (CNNs), have demonstrated the ability to improve medical imaging. Several authors have examined the use of CNNs for automatic malaria detection. M. Mujahid et al., for example, created an effective deep learning framework to detect malaria in red blood cell images with high accuracy [2]. Similarly, Q. A. Arshad et al. developed a standardized dataset and method for the classification of the life cycle of malaria parasites, with an emphasis on multi-class stage classification [3]. Finally, transfer learning techniques were discussed in several studies (e.g., R. Sivaramakrishnan et al.) for classifying red blood cells as either infected or uninfected on publicly available datasets [4].

While these have made progress in malaria diagnosis, most systems are limited to binary classification (infected or not infected) and do not assess parasite life-cycle stages, which are essential for disease monitoring and treatment. Moreover, existing systems often act as "black boxes" which hinder their clinical uptake due to a lack of explainability.

This paper presents a two-stage deep learning approach for malaria diagnosis to overcome these challenges. The initial stage detects the presence of infection, and the second stage categories infected images according to the parasite life cycle stages (ring, trophozoite, schizont, or gametocyte). Moreover, to improve interpretability, this paper uses Gradient-weighted Class Activation Mapping (Grad-CAM) to generate visual explanations. Moreover, a thresholding approach based on prediction confidence is proposed to flag uncertain cases, facilitating human-in-the-loop verification.

The proposed model seeks to combine accuracy and explainability in automated malaria diagnosis, thus making it better fit for clinical practice, particularly in resource-constrained environments.

RELATED WORK

Our work extends advancements in three key areas: deep learning for medical image analysis, malaria detection, and explainable artificial intelligence (XAI). Here, we highlight some of the seminal research that inspired this work.

*A. **Deep Learning for Medical Image Analysis***

Deep learning has revolutionised medical image analysis by facilitating automated feature learning and accurate classification. Convolutional Neural Networks (CNNs) have gained popularity in medical diagnosis applications for their capacity to learn increasingly abstract features from images. Recent research, including H.Yang et al. [7] proved the success of deep CNN models in medical imaging tasks including classification and detection. Similarly, J.Liang et al. [11] demonstrated the feasibility of deep learning techniques for high accuracy biomedical image classification, further establishing the potential for clinical applications.

This progress has inspired the use of deep learning in microscopic image analysis for disease diagnosis, such as malaria.

*B. **Automated Malaria Detection Systems***

An extensive amount of research has been conducted on how to automate malaria diagnosis from blood smear microscope photographs. T.Rahaman et al.[8], through their application of transfer learning and a pre-trained CNN for infected and non-infected cell identification, demonstrated improved performance regarding traditional machine learning techniques. K.Bibin et al.[9], using deep learning performed feature extraction from their all samples of parasites, were able show some advantages of using deep models to find the more difficult-to-detect fine detail patterns.

More recent studies have seen M.Mujahid et al. [2] developed a lightweight CNN model for efficient detection of malaria-infected red blood cells with high accuracy. Further-more, Q.A.Arshad et al. [3] proposed a benchmark data set for malaria parasite life-cycle classification, highlighting the need for multi-stage classification rather than a binary approach. Other research has explored the use of lightweight CNNs and hybrid approaches to optimize performance, reduce computational costs, and allow deployment on resource-limited platforms.

While these works have made valuable contributions, the majority focus on binary classification and fail to address the classification of parasite life-cycle stages, which is required for complete diagnosis.

C. Multi-Stage Classification and Dataset Advancements

There has been growing interest in the finer classification of malaria parasites based on their life cycle. Researchers have developed multi-class classification systems to identify ring, trophozoite, schizont and gametocyte stages of the parasite, which help to understand the severity of disease [3]. Novel models such as attention-based CNNs and ensemble learning have been developed to enhance stagespecific classification [13].

But such systems are sometimes plagued by problems such as class imbalance, small training data, and poor performance on complex stages of parasites. Moreover, the absence of largescale benchmark datasets impacts model generalisation. While benchmark datasets have improved consistency and evaluation, there is still a need for further improvements to enable real-world deployment.

*D. **Explainability in Medical AI Systems***

A major obstacle to implementing Deep Learning technology in healthcare is the difficulty of interpreting the outcome of a model. Clinicians frequently have great difficulty interpreting the predictions generated by these

models because they function as “black boxes.” To remedy this issue, researchers have developed Explainable AI (XAI) solutions.

The use of Gradient-weighted Class Activation Mapping (Grad-CAM) as a visual explanation of prediction has become very widespread following its introduction by R. R. Selvaraju and colleagues [15]. Grad-CAM pinpoints image regions that are significant contributors to specific prediction outcomes. As noted by N. Srivastava et al. [14], the use of Grad-CAM significantly contributes to interpretability of malaria diagnostic models.

In addition, confidence-based predictions and uncertainty models have been developed to identify uncertain prediction cases to help facilitate human-in-the-loop verification and therefore make AI technology more trustworthy for clinical applications [16].

METHODOLOGY

A. *System Overview*

To develop a diagnostic system for malaria from blood smear images, a two-stage deep learning process is used. The system consists of four main components: stage 1 (infection classifier), stage 2 (life-stage classifier), a Grad-CAM explainability module, and a confidence-based decision system. Together, these modules make accurate, explainable, and robust predictions.

B. *Dataset and Preprocessing*

1) *Dataset Description and Splitting*

The model uses publicly available datasets of malaria-infected and uninfected red blood cells in order to train the deep learning algorithm. The datasets are split into training, validation, and test sets, with the proportion of 70% for training, 15% for validation, and 15% for testing.

In the second stage of classification, only infected samples are retained; these samples will then be classified as ring, trophozoite, schizont, or gametocyte.

2) *Preprocessing Pipeline*

Each image undergoes the following preprocessing steps:

- Resizing to a fixed dimension (e.g., 224 × 224 pixels)
- Pixel normalization to the range [0,1]
- Noise reduction and contrast enhancement (if required)

3) *Data Augmentation*

To improve model robustness and prevent overfitting, data augmentation techniques are applied:

- Rotation, flipping, and zooming
- Brightness and contrast adjustment
- Random cropping and scaling

C. *Model Architecture*

The two primary components which are an explainable and reliable aspect to the proposed approach, are two stages, along with Stage 1 detecting parasitic infection, and Stage 2 classifying samples that contain infected cells based on the various stages of the parasite’s lifecycle.

To achieve visual explanation of the prediction of infected, Grad-CAM will be used, and to ensure reliable prediction from the trained model, the use of a confidence basis (using the predicted class’s probability) will be employed.

1) *Stage 1: Infection Detection Model*

Stage 1 uses a Convolutional Neural Network (CNN) to label the input image as:

- Infected
- Uninfected

Transfer learning is applied by pretraining the model with weights from an existing model and then finetuning with the malaria dataset to enhance the model performance and training speed.

2) *Stage 2: Life-Stage Classification Model*

The second stage model is only invoked if the image is identified as infected. This model classifies into:

- Ring stage
- Trophozoite
- Schizont
- Gametocyte

A deep CNN is employed to capture subtle features of different parasite stages. Imbalanced classes are addressed through weighted loss functions or augmentation.

3) *Explainability Module (Grad-CAM)*

To increase the explainability, Gradient-weighted Class Activation Mapping (Grad-CAM) is incorporated in both

stages. This visualisation helps by producing a heatmap of the parts of the image that are most important for the model's decision.

This allows:

- Visualization of parasite-infected regions
- Verification of model decision-making
- Increased trust for clinical use

4) Confidence-Based Decision Module

A confidence thresholding strategy is applied to enhance accuracy. Below a certain confidence threshold the predictions are reported as:

- Uncertain cases (sent for expert review)

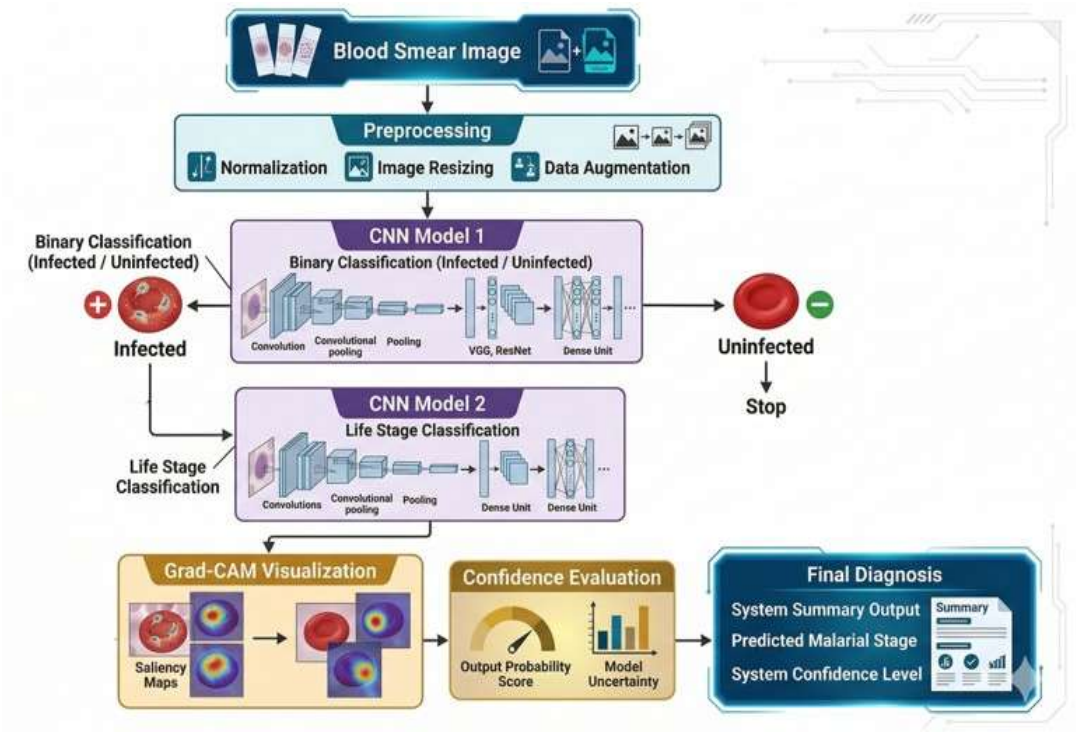

Fig. 1: Proposed two-stage malaria detection framework. The system performs infection detection (Stage 1), followed by life-cycle classification (Stage 2). Grad-CAM provides interpretability, and a confidence-based mechanism ensures reliable predictions.

D. Loss Function and Training Strategy

Training is performed using a combination of typical loss functions:

- Binary Cross-Entropy Loss of 1st Stage
- Categorical Cross-Entropy Loss of 2nd Stage
  The overall loss function is defined as:

$$L = \alpha L_{stage1} + \beta L_{stage1}$$

where L_{stage1} represents infection classification loss, L_{stage2} represents life-stage classification loss, and α, β are weighting coefficients.

Adam optimizer is used to optimize the model with a learning rate of 1×10^{-4} and a batch size of 32 is used.

E. Training Procedure

The training process follows a structured pipeline:

- Train VGG Stage 1 model with all images (infected vs. uninfected)
- Select infected samples and train Stage 2 model
- Add Grad-CAM for visualization
- Use thresholding to validate model predictions
- Test models on independent dataset
- Select top models based on validation accuracy

F. Evaluation Metrics

The performance of the system is evaluated using the following:

- Accuracy
- Precision, Recall, and F1-Score
- Confusion Matrix
- ROC-AUC Curve (for Stage 1) Additionally:
- Grad-CAM visualizations are used for qualitative analysis
- Confidence scores are used for uncertainty estimation

G. *Workflow Summary*

The overall workflow of the system is as follows:

1) Input blood smear image
2) Stage 1: Detect infection
3) Stage 2: Classify life stage (if infected)
4) Generate Grad-CAM heatmap
5) Apply confidence threshold
6) Output prediction with explanation

EXPERIMENTAL RESULTS

In this section, we provide a detailed explanation of the performance of the proposed two-stage malaria detection system. The system's performance is evaluated through interpretation using a confusion matrix, quantitative measures, qualitative analysis and reliability analysis. This includes the detection of infection (Stage 1), classification of life-cycle (Stage 2), interpretability through Grad-CAM, and prediction analysis.

A. *Stage 1: Infection Detection Performance*

Stage 1 of the framework is a binary classification of infected and uninfected blood smear images. The model exhibits high accuracy and reliability with a few misclassifications.

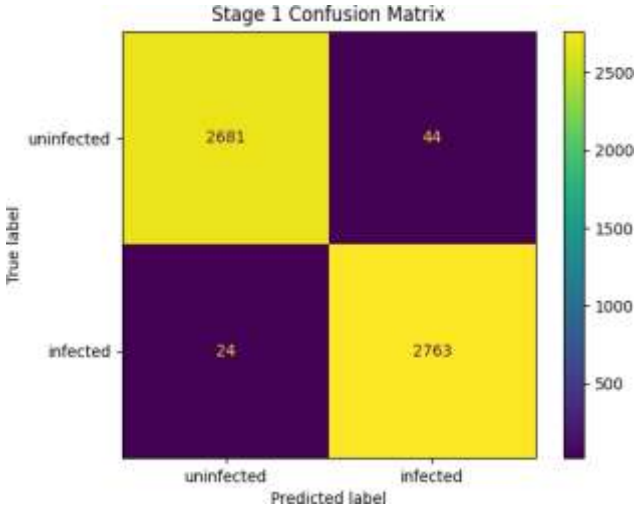

Fig. 2: Confusion Matrix for Stage 1

The model classified 2681 uninfected and 2763 infected samples as uninfected and infected, respectively. A total of 44 uninfected samples were misclassified as infected and 24 infected samples as uninfected. These findings suggest that both the false positive and the false negative rates are low and almost equal.

It's worth noting that the dataset is balanced, with a similar number of infected and uninfected samples. Therefore, the model is not biased towards any class. This also reflects the fact that the classifier has a consistent performance across both classes.

The quantitative performance metrics are as follows:

- **Accuracy:** 98.9%
- **Precision (Infected):** 0.987
- **Recall (Infected):** 0.992
- **F1-Score:** 0.989

The high recall value is important for medical diagnosis, as it increases the likelihood of detecting most infected cases, thereby minimising false negatives. In summary, the Stage 1 model shows outstanding performance, stability and readiness for deployment.

B. *Stage 2: Life-Cycle Classification Performance*

The second stage of the framework is a multi-class classification model identifying parasite life-cycle stages (ring, trophozoite, schizont or gametocyte).

The model has learned well for all the classes, with better performance for the majority classes. The ring stage exhibits the highest accuracy, suggesting the model identifies its distinctive characteristics. The trophozoite stage also exhibits consistent performance, with occasional confusion with the ring stage.

The schizont and gametocyte stages show relatively lower performance, which can be attributed to the scarcity of samples and the similarities between these classes. But the model can still learn these classes to some extent, suggesting that it learns some features even with limited data.

In summary, the Stage 2 model attains an average accuracy of around 75-80%, which is deemed acceptable for multiclass microscopic image classification problems.

Crucially, the model does not suffer from class bias. The model's predictions are spread over all classes instead of heavily favoring one class. The misclassifications can be

attributed to inherent similarities between parasite stages, such as visual overlap between ring and trophozoite stages. This is expected due to the nature of the problem.

C. *Grad-CAM Visualization and Interpretability*

To improve Interpretability, Grad-CAM was incorporated into the architecture of the system, allowing for visualization of the areas of the image that are most important for influencing the model's predictions. The Grad-CAM generated heat maps performed consistently in that they highlight the area of biologically relevant regions within the red blood cells and especially highlight the area in the red blood cell that contain the parasitic structures.

This provides additional evidence that the model is "learning" the relevant structure and useful features rather than simply reacting to "background noise"; therefore, this finding strengthens the overall conclusions regarding how Life-Cycle classification is performed by the model since Grad-CAM also demonstrated that the model can identify differences between parasite stages in terms of localized morphological features.

The ability to incorporate explainability improves the transparency of the system and will increase the trust between the system and future users who may want to use the system for the purposes of clinical adoption.

D. *Confidence-Based Prediction Analysis*

A confidence-based thresholding mechanism was developed to increase the reliability of the model's predictions. Each prediction is assigned a probability score, which serves as a measure of the model's confidence; thus, the predictions with high confidence are considered reliable and therefore can be used directly, while those with low confidence are flagged to indicate that the prediction is uncertain. Uncertain predictions can then be provided to an appropriate medical professional for further evaluation.

This methodology of having a confidence-based thresholding mechanism increases the safety of the system, by minimising the number of instances in which incorrect automated decisions will be made, and it also supports a Human-In-The-Loop diagnostic workflow.

E. *Qualitative Results and Analysis*

Qualitative analysis of Model Predictions and Interpretability Outputs was done to analyze the results of the system's ability to identify infected cells and correctly identify parasite regions. In addition, the model is capable of making use of subtle visual cues to differentiate between parasite life-cycle stages. Although there is some ambiguity in identifying closely related life-cycle stages, the biological features associated with the predicted life-cycle stages remain within the expected values.

F. *Summary of Findings*

The results from the experiments demonstrate that the proposed two-stage system is both effective and reliable for the automated diagnosis of malaria.

In Stage 1, the model produces very accurate results with both balance and unbiased predictions, which make it a robust tool for detecting infections. Stage 2 produces strong multi-class classification, no significant class bias and produces meaningful learning for all stages of the parasite's life cycle. The incorporation of Grad-CAM enhances interpretability in addition to the use of a confidence-based mechanism enhances the reliability and safety of the system. Additionally, the combination of accuracy, transparency, and practicality results in the system being suitable for use in medicine in real-world applications.

The qualitative results of the proposed system are illustrated in Fig. **3**, demonstrating the effectiveness of infection detection, Grad-CAM-based interpretability.

CONCLUSION AND FUTURE WORK

This research presents a two-stage deep-learning framework that takes advantage of data provided by Microscopic Blood Smears (MBSs) to help detect and classify malaria. The first stage consists of a deep-learning algorithm demonstrating a two-class (malaria-infected vs. non-infected) classification by accurately and consistently separating two classes using a low error rate.

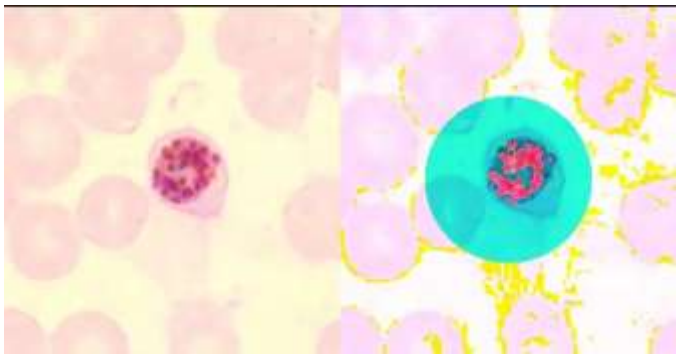

Fig. 3: Infected Input Image with Grad-CAM Highlighted Output Image

The second stage of the framework consists of using deep learning to classify infected blood samples into four different parasite life-cycle stages (i.e., trophozoite, schizont, gametocyte, or unstageable). While the limited sample sizes (with fewer than 25 available samples) posed challenges for this stage, the second-stage model demonstrated sufficient generalization and validity (with respect to the classifier evaluation metrics) to indicate that the model was able to extract pertinent features from the MBSs. In addition, to facilitate better interpretability of the classifier's predictions, a Gradient-weighted Class Activation Mapping (Grad-CAM) approach was applied to provide visualizations of the portions of the image that contributed most significantly to the classification outcome. With this approach, the potential for transparency to clinicians is greatly increased and trust in automated systems is established.

Furthermore, a confidence-based thresholding mechanism was supplied to support a human-in-the-loop approach to enable the safe deployment of the framework.

The automated malaria detection and classification framework achieved an appropriate balance between accuracy, interpretability, and reliability, indicating that it could represent an effective tool for the automated diagnosis of malaria, particularly in resource-limited environments.

In the future, work will focus on improving the performance of multi-class classification through increasing the size of the data sets and balancing the number of classes within each data set. Future work will also look into more sophisticated architectures, integrating the classification system with real-time diagnostic systems and demonstrating its clinical utility through practice.

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