Developing an Automated Decision-Supporting System to Diagnose Malaria Parasite from Thin Blood Smear Images Using Deep Neural Networks

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□ ABSTRACT □

Malaria is a life-threatening disease caused by a parasite called Plasmodium, which is transmitted to humans through the bite of infected female Anopheles mosquitoes. The accurate detection of malaria parasite from thin blood smear images is imperative to improve diagnosis.

Purpose: This study aims to investigate the use of a deep neural networks for developing automated clinical decision-making system to improve malaria detection and evaluate its performance.

Materials and Methods: A deep neural network was proposed and trained on a dataset of microscopic images of thin blood smears to detect the presence of the malaria parasite. The collection of data comprises 27,558 pictures of red blood cells, where the number of infected and uninfected cells is equal. To test the model's effectiveness, a subset of 2000 images was taken, and the accuracy, precision, sensitivity, and f1-score were used as performance indicators.

Results: The results showed that the proposed deep neural network achieved an accuracy of 0.96, indicating its effectiveness in detecting the disease. The precision score of 0.98 indicates that the model has a low rate of false positives, while the sensitivity score of 0.947 indicates that it can detect most cases of malaria. The f1-score of 0.96 shows a good balance between precision and sensitivity.

Conclusion: The study demonstrates the potential of using a deep neural network for accurate and efficient malaria detection. The high accuracy, precision, and sensitivity scores suggest that the model is effective in detecting the disease and can minimize the risk of misdiagnosis. Therefore, the proposed deep neural network approach can serve as a promising tool for malaria diagnosis and control.

Keywords: Deep Learning, Deep Neural Networks, Malaria, Thin Blood Smear Images.

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تطوير نظام دعم قرارآلي لتشخيص طفيلي الملاريا من صور لطاخة الدم الرقيقة باستخدام الشبكات العصبية العميقة

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□ ملخّص □

الملاريا هي مرض يهدد الحياة يسببه طفيلي البلاسموديوم والذي ينتقل إلى الإنسان من خلال لدغة أنثى بعوضة الأنوفوليس الحاملة للمرض. يعد الكشف الدقيق عن الطفيلي المسبب للملاريا في صور لطاخة الدم أمراً بالغ الأهمية لتحسين عملية التشخيص.

الهدف: يهدف هذا البحث إلى استكشاف استخدام الشبكات العصبونية العميقة لتطوير نظام آلي لدعم القرار لتحسين كشف الملاريا وتقييم أدائه.

المواد والطرائق: تم تدريب شبكة عصبونية عميقة على مجموعة بيانات من الصور المجهرية للطاخة الدم الرقيقة للكشف عن وجود طفيلي الملاريا. تتضمن مجموعة البيانات 27,558 صورة للخلايا كريات الدم الحمراء، حيث يتساوى عدد الخلايا المصابة وغير المصابة. لاختبار فعالية النموذج، تم اختيار عينة فرعية من 2000 صورة، كما تم استخدام كل من: الدقة والإحكام والحساسية إضافة إلى معامل f1 كبارمترات تقييم لأداء عمل النموذج.

النتائج: أظهرت النتائج أن الشبكة العصبونية العميقة المقترحة حققت قيمة دقة 0.96 ، مما يشير إلى فعاليتها في الكشف عن المرض. وبلغت قيمة الإحكام 0.98 مما يدل على أن النموذج لديه معدل منخفض للإيجابيات الكاذبة، في حين تدل قيمة 0.95 للحساسية إلى أنه يمكن للنموذج اكتشاف معظم حالات الملاريا. كما يوضح معامل f1 بقيمة 0.96 أنه يوجد توازن جيد بين الدقة والحساسية.

الاستنتاجات: توضح الدراسة إمكانية استخدام الشبكة العصبية العميقة للكشف الدقيق والفعال عن مرض الملاريا. تشير القيم المرتفعة للدقة والضبط والحساسية إلى أن النموذج فعال في الكشف عن المرض ويمكن أن يقلل من خطر التشخيص الخاطئ، مما يسمح باستخدام النموذج المقترح للشبكة العصبية العميقة كأداة مثمرة لتشخيص ومكافحة الملاريا.

الكلمات المفتاحية: التعلم العميق، الشبكات العصبونية العميقة، الملاريا، صور لطاخة الدم الرقيقة.

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Introduction:

Malaria is one of deadliest disease, it is caused by two types of species: Plasmodium falciparum and Plasmodium vivax. According to the World Health Organization (WHO), there were an estimated 247 million malaria cases and 619,000 malaria deaths worldwide in 2021 [1,2].

Currently, the most widely used diagnostic technique for malaria is microscopy, microscopists often examine blood samples using both thick and thin smears to diagnose this condition. The accuracy of this procedure, however, is reliant on the caliber of the samples and the skill of the analyst. When attempting to diagnose malaria on a wide scale, this might be a difficult undertaking. In recent years, computer-aided diagnosis (CADx) technologies using microscopic pictures of blood samples and machine learning algorithms have been created. These techniques examine the morphological, textural, and positional differences of the regions of interest using hand-engineered features [3,4].

Machine learning algorithms have been used to detect the presence of malaria parasites in medical images, such as convolutional neural networks (CNNs) and random forests. CNNs are particularly effective for image classification tasks and have been used to classify images of blood cells as infected or not infected with the malaria parasite. Random forests, which are a type of ensemble learning method, have also been used for this task and have been shown to have good performance. Other algorithms also been used [5].

At present, researchers have started to use deep learning and machine learning algorithms to detect malaria parasite. Rajaraman et al. used CNNs to diagnose malaria parasite from microscopic images by providing end-to-end feature extraction and classification algorithm. This evaluated the performance of pre-trained CNNs models as feature extractors for classifying infected and uninfected cells. The results showed that pre-trained CNNs are a promising tool for improved disease screening [6]. Shah et al. presented a custom CNNs model to differentiate between healthy and infected blood samples. The CNNs model is composed of multiple convolutional and fully connected layers and has a good accuracy according to the resources available. After the model is trained, it is tested using several blood sample images, and the CNNs classifier has shown high accuracy even under limited computational resources with 95% [7]. Qadir et al. compare the performance of different transfer learning models on identifying infected malaria cells by feeding them a large dataset of uninfected and infected cell images. The results indicated that DenseNet models performed the best, with DenseNet-201 achieving the highest accuracy and f1-score of 0.9339 and 0.9321, respectively [8].

The current methods for diagnosing malaria can be time-consuming and require skilled technicians, which can lead to human error and potentially inaccurate results. Therefore, developing new algorithms for detecting malaria parasites is crucial for improving the speed, accuracy, and cost-effectiveness of malaria diagnosis, particularly in areas with limited resources. Automated algorithms can help to identify malaria parasites quickly and accurately, reducing the time required for diagnosis and enabling more effective treatment. Moreover, new algorithms can facilitate the development of portable and low-cost diagnostic tools, which are particularly important in remote and low-resource settings.

The remaining content of this paper is organized in the following manner. In Section 2, you will find a detailed account of the materials and methods used in this study, encompassing information regarding the dataset, image preprocessing, model Architecture, and model evaluation. The results are reported in section 3, followed by a discussion of the findings in section 4. Finally, the paper concludes with a summary of the results in the conclusion.

Research Materials and Methods:

-1 Dataset

Researchers at the "Lister Hill National Center for Biomedical Communications (LHNCBC)", have developed a method to lessen the workload for microscopists in areas with limited resources and increase diagnostic precision. They gathered **thin** blood smear slides stained with Giemsa from 150 patients' falciparum-infected and 50 healthy patients. The collection of data includes 27,558 images of cells, with an equal number of cells that are infected and not infected with Plasmodium. Positive examples show the presence of Plasmodium, while negative examples do not contain Plasmodium but may have other types of objects such as staining artifacts or impurities [9]. The positive examples (infected) and the negative ones (uninfected) are shown in Figure 1. For this study, the first 2000 images were used, with 1030 being infected and the rest being healthy.

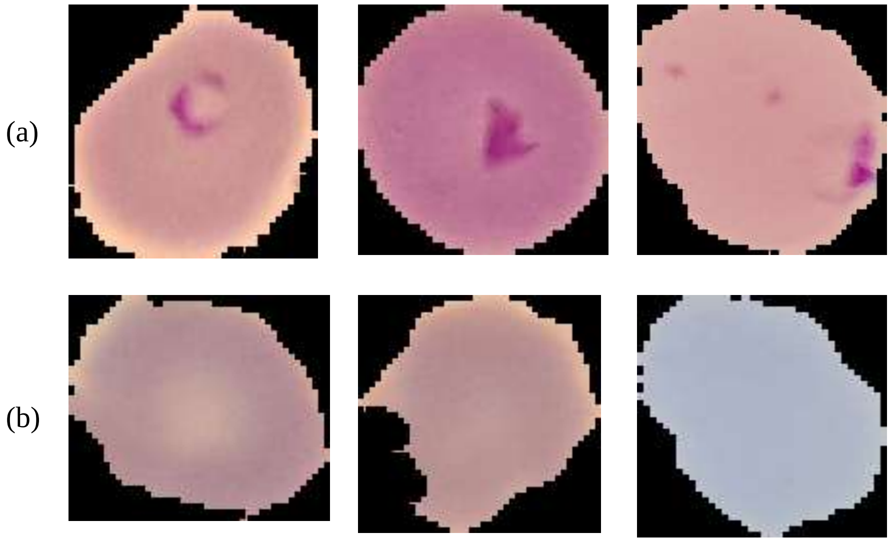

Figure 1. Examples from both the malaria-infected (a) and non-infected (b) groups are selected from the malaria dataset.

2- Image preprocessing:

As the dataset contains images of varying resolutions, they were resized to a uniform 50 x 50 resolution to ensure consistency before being fed. To standardize the gray-level values of the images, a rescale parameter was applied to adjust the values to a range between zero and one.

-3 Model Architecture

A Deep Convolutional Neural Network (CNN) design is utilized to differentiate between malaria-infected and healthy images for classification purposes. The model consists of three convolutional layers and one dense layer followed by the output layer. The first two layers are identical, each with a 32-node convolutional layer, followed by a max pooling layer. The third layer is a 64-node convolutional layer followed by another max pooling layer. After the convolutional layers, the model includes a flattening layer that reshapes the output of the convolutional layers into a 1D vector. Following the flattening layer, there is a dense layer with 64 nodes, which acts as a hidden layer. To prevent overfitting, the model includes a dropout layer after the dense layer, which drops 50% of the connections between the hidden layer and the next layer. Finally, the model ends with an output layer with a single node, which is used for malaria binary classification task. Table 1. shows a summary of the deep CNN sequence model. The binary crossentropy loss function is implemented, and the Adam optimizer with a learning rate of 0.001 is chosen for its computational efficiency, simplicity, and memory advantages.

Table 1. A summary of the deep CNN sequence model.

Layer (type)	Output shape	Number of parameters
conv2d (Conv2D)	(None, 48, 48, 32)	896
max_pooling2d (MaxPooling2D)	(None, 24, 24, 32)	0
conv2d_1 (Conv2D)	(None, 22, 22, 32)	9248
max_pooling2d_1 (MaxPooling2D)	(None, 11, 11, 32)	0
conv2d_2 (Conv2D)	(None, 9, 9, 64)	18496
max_pooling2d_2 (MaxPooling2D)	(None, 4, 4, 64)	0
flatten (Flatten)	(None, 1024)	0
dense (Dense)	(None, 64)	65600
dropout (Dropout)	(None, 64)	0
dense_1 (Dense)	(None, 1)	65
Total params: 94,305 Trainable params: 94,305 Non-trainable params: 0		

-4 Model Evaluation

The dataset was split into two parts in a random manner, where 80% of the data was assigned to the training set and the remaining 20% to the test set. Various performance metrics were taken into account to assess the predictive ability of the CNN classification model. These metrics included sensitivity, precision, f1-score, and accuracy. Equations (1)-(4) define each of these metrics.

$$Sensitivity = \frac{TP}{TP + FN} \times 100\% \quad (1)$$

$$Precision = \frac{TP}{TP + FP} \times 100\% \quad (2)$$

$$f1 - score = \frac{2TP}{2TP + FN + FP} \times 100\% \quad (3)$$

$$Accuracy = \frac{TP + TN}{TP + FN + TN + FP} \times 100\% \quad (4)$$

The term "true positive" (TP) refers to the number of individuals with malaria who are accurately identified as having the disease. Conversely, "false negative" (FN) refers to individuals who have malaria but are incorrectly identified as not having it. The sum of TP and FN represents the total number of malaria patients. "True negative" (TN) describes the number of individuals who do not have malaria and are accurately identified as such, while "false positive" (FP) refers to individuals who do not have malaria but are incorrectly identified as having the disease. The sum of TN and FP represents the total number of non-malaria patients. Accuracy measures the percentage of correct predictions, while the f1-score reflects a balance between precision and sensitivity.

Results and Discussion:

1- Results:

The CNN model was trained on a malaria dataset, consisting of 2000 images that were nearly balanced (1030 infected and the rest being healthy), for a period of 25 epochs. A batch size of 64 was used during the training process.

The classification results suggest that the model has achieved high accuracy, with an accuracy score of 0.96, indicating that the model can correctly classify 96% of the patients as malaria or non-malaria. Precision score of 0.98 suggests that out of all the patients predicted as having malaria, 98% of them are correctly classified, indicating that there is a low false positive rate. The sensitivity score of 0.95 indicates that the model can correctly identify 95% of the malaria cases. Therefore, there is a low false negative rate, meaning the model can identify most of the actual malaria cases. The f1-score of 0.96 indicates that the model has a balanced performance between precision and sensitivity. Overall, the results suggest that the model has a high accuracy and performs well in identifying patients with malaria, with high precision and sensitivity scores. Figure 2 shows the curves for the accuracy and loss for both the training and validation sets.

The accuracy curve demonstrates that the model's accuracy improved gradually during the training process, reaching a plateau of around 0.96 for both the training and validation sets. This indicates that the model was able to effectively classify the majority of the images in the dataset. The loss curve shows that the model's loss decreased steadily during training, indicating that the model was successful in minimizing its error.

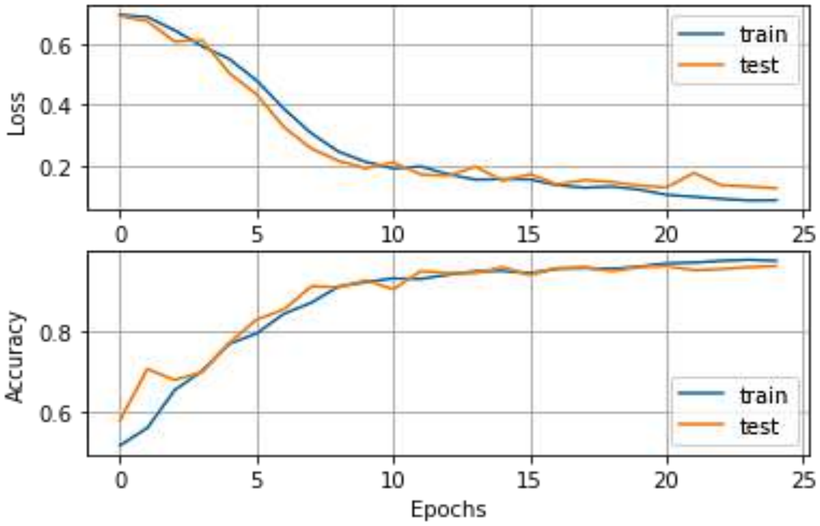

Figure 2. Accuracy and Loss curves of the proposed CNN model.

2- Discussion

In this paper, I explored the use of deep neural networks for the detection of malaria. Results showed that a deep learning approach can achieve high accuracy in detecting malaria from thin blood smear images of blood samples. This is particularly promising, given the challenge of accurately diagnosing malaria in areas with limited access to healthcare professionals and diagnostic tools. However, this analysis also revealed some potential limitations of applied approach, the accuracy of the model may be affected by variations in the staining of blood samples, which can affect the contrast and visibility of the parasites.

Huq et al. developed a "robust deep neural network model for identification of malaria parasites in cell images". The researchers suggested using CNN models to classify cell images due to its ability to recognize intricate features and assign appropriate labels. They employed a type of CNN called VGG16 to identify the images. To ensure correct classification even with adversarial images, they trained the model with adversarial images labeled correctly. Prior to adversarial training, the model achieved an accuracy of 95.96%, which decreased slightly to 95.79% after adversarial training. The model was able to correctly classify 93.38% of adversarial images [10].

Vijayalakshmi et al. proposed a novel deep neural network model that can identify falciparum malaria parasite in infected patients using transfer learning. This method combines the existing Visual Geometry Group (VGG) network with Support Vector Machine (SVM) through the "Train top layers and freeze out rest of the layers" strategy. The VGG19-SVM model achieved a classification accuracy of 93.1% in identifying infected falciparum malaria [11].

Devi et al. conducted a system to categorize erythrocytes infected with malaria using a set of histogram features. The technique involved several stages such as pre-processing, segmentation, feature extraction using histogram data from different color channels, feature selection, and classification of malaria-infected erythrocytes using various machine learning algorithms including Artificial Neural Networks (ANN), Support Vector Machine (SVM), k-Nearest Neighbor (k-NN), and Naive Bayes. According to the experimental results, ANN provides the highest classification rate among all the classifiers with an overall accuracy of 96.32% and an f1-score of 85.32% [12].

This study proposed a customized CNN architecture to detect malaria cells, which demonstrated better accuracy than existing models. It reveals that deep learning approaches have the potential to significantly improve the accuracy and efficiency of malaria diagnosis. To address the limitations I identified, future research could focus on developing methods to generate high-quality annotated images of parasites and exploring alternative imaging techniques that may be less affected by staining variations. Overall, the study's findings demonstrate the promise of deep learning in the fight against malaria.

Conclusions and Recommendations:

For decades, malaria has been a significant problem worldwide. It is common knowledge that medical models should be compact for easy deployment, as large models can present a challenge. Therefore, this approach considered this issue and produced a compact model without sacrificing accuracy. This study reinforces the notion that AI can have boundless applications in healthcare industries, making medical work more cost-effective. Automated models such as presented in this study can efficiently and economically detect various diseases, making a significant contribution to the medical field.

Conflicts of Interest

No conflict of interest to declare.

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