Automatic *Plasmodium vivax* Infected Red Blood Cell Detection and Classification in Blood Smear Images

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***Abstract*—Malaria is one of the major public health issues throughout the world. As a serious parasitic infection, it is a leading cause of morbidity and mortality in tropical and sub-tropical countries. Moreover, malaria cannot be treated until it is diagnosed, if a delayed diagnosis or treatment occurs, which will lead to anemia and blocking the capillaries that carry blood to the brain. Thus, fast diagnosis and acute treatment of this illness are very helpful to reduce the mortality. Currently, the most common method to diagnose malaria is microscopic examination. This kind of method is conventional but time consuming, and for this kind of examination, highly trained microscopists are required. Meanwhile, to address the limitations of manual microscope examination, a cost-saving, accurate and fast computer diagnosis system is required. This research proposed a two-staged malaria diagnosis system based on a YOLO algorithm for cell detection and based on a convolutional neural network (CNN) algorithm for cell classification. The results show that it achieves detection accuracy of 89.19%. While in the cell classification stage, the classification accuracy reaches 93% on the test images.**

Keywords*—*Malaria*, *Plasmodium vivax*, *Deep Learning*, *YOLO*, *Faster-R CNN*, *CNN

I. Introduction

One of the major public health issues throughout the world is malaria, a disease transmitted by the female anopheles mosquito. As a serious parasitic infection, it is a leading cause of morbidity and mortality in tropical and sub-tropical countries. According to the World Health Organization, though due to effective prevention in recent years, malaria deaths have reduced steadily over the period 2000–2019, it still caused approximately 400 thousand deaths arising from 229 million malaria cases in 2019 [1]. There are five different species of Plasmodium parasite that can affect humans which are *P. falciparum*, *P. vivax*, *P. ovale*, *P. Malariae*, and *P. knowlesi*, all of which have four different stages of their life cycle: ring, trophozoite, schizont, and gametocyte [2]. Among them, *P. falciparum* is the deadliest type, while *P. vivax* has a wider distribution than *P. falciparum* due to its ability to develop in anopheles mosquitoes at lower temperatures [3]. Though malaria is a disease that can be completely prevented and treated [4], for the reason that different species of Plasmodium parasites have a variety of morphologies in theirs different life stages, to classify a certain type and stage of malaria parasite in laboratory diagnosis, an experienced technician is required.

Currently, the most common method to diagnose malaria is microscopic examination. There are two kinds of Giemsa stained blood films (thin films and thick films) that are recommended in malaria microscopy [5]. This kind of method is conventional but time consuming, and for this kind of examination, highly-trained microscopists are required. It is

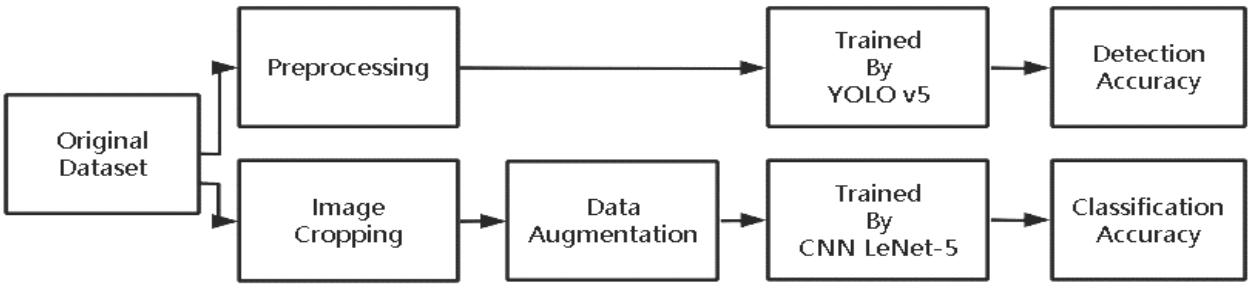

Fig 1. Overview of the proposed methods.

common that a well-trained technician can diagnose malaria accurately and effectively in well-funded medical facilities in large cities where malaria seldom appears. On the other hand, in some developing countries, particularly in some remote villages where malaria is most prevalent, the diagnosis is often inaccurate and inefficient. The potential problems of this diagnosis arise from (a) The high cost of training microscopists (b) Inaccurate diagnosis results due to duplication work, limited experience or mental and physical exhaustion [6]. Moreover, malaria cannot be treated until it is diagnosed, if a delayed diagnosis or treatment occurs, which will lead to anaemia and blocking the capillaries that carry blood to the brain. As a result, the infected and destroyed red blood cells will kill malaria-infected patients [7]. Thus, fast diagnosis and acute treatment of this illness are very helpful to reduce the mortality.

Meanwhile, to address the limitations of manual microscope examination, a cost-saving, accurate and fast computer diagnosis system is required. For instance, an image processing method based on machine learning has the potential to provide fast and consistent estimates of examination results. In an early study of automatic malaria examination, morphological methods were considered for the recognition of red blood cells and malaria parasites [8]. On the other hand, compared with direct observation of blood smears by the technician, image processing is more advanced. After the advent of deep learning algorithms, there have been many advancements in the field of computer vision, especially in the abnormalities detection in medical images field. Algorithms such as such as YOLO series (V1 [9], V2 [10], V3 [11] , V4 [12] , V5) , SSD [13], and some others, also known as one-stage object detection algorithms, which take the object detection process as one complete regression problem rather than proposing region of interests separately [14].

In our research, we proposed a two-staged method to detect and classify infected red blood cells. The input groups with maximum accuracy were selected respectively to get the best solution to this blood smears data set. The experimental results show that the method proposed in this research can reach 88.19% accuracy in the cell detection stage, and the accuracy in the cell classification stage can reach 93%.

II. Related Research

Here are some other approaches that applied to *P. vivax* detection in blood smears.

Thin blood smear images were cropped into a certain size, and then applied a fuzzy divergence-based segmentation method on *P. vivax* infected parts [15]. Based on the pre-segmented objects, four textural features (average intensity, skewness, uniformity and entropy) and a feature called fractal calculation were extracted and Support Vector Machine (SVM) and Bayesian classifiers were applied for *P. vivax* identification [15]. Their classification algorithm on cells from 100 uninfected patients and 100 infected patients achieved an accuracy of 95% for SVM classifier and 98% for Bayesian classifier respectively [16].

An artificial neural network (ANN) was applied on segmented cells to classify the parasite species in thin blood smears images [17]. The researchers reported that their ANN classifier achieved an accuracy of 96.2% in recognizing *P.vivax* from other plasmodium species on 205 infected cell images.

A parasite segmentation through connected components analysis was performed, and Convolutional Neural Network (CNN) was applied for parasite species classification in thin blood smears [18]. Evaluation on 363 images showed that the classifier achieved an accuracy of 87.9% for parasite species classification.

A method comprises two steps was proposed in [19]. The first stage partitioned the cell regions using Mask R-CNN segmentation. The second stage defined the whole cell area by classifying the segments from the initial stage. Then a smaller VGG-like Net was employed to classify the segmentation results. The result showed it reached 98.1% accuracy for classification.

III. Methodology

The proposed method consists of two parts, i.e., cell detection and cell classification. The overview of the method is shown in Fig. 1. The cell detection performance and cell classification performance are evaluated separately.

The first stage is cell detection. The preprocessing method of this part consists of histogram equalization, contrast stretching, median blur, and two other methods that combined histogram equalization with contrast stretching together

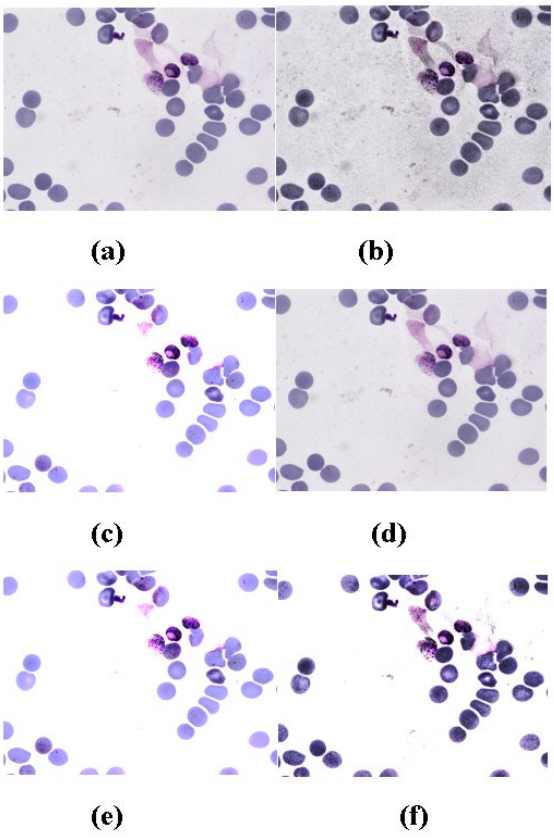

Fig 2. Sample output images of preprocessing (a) Original image, (b) Histogram equalization, (c) Contrast stretching, (d) Median Blur, (e) Contrast then Hist, (f) Hist then Contrast

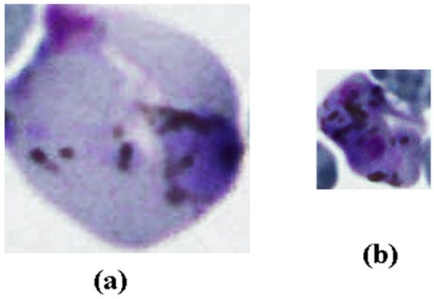

Fig 3. Sample output images of image cropping in cell classification stage (a) Direct cropping, (b) Zero padding, (c) Cell cropping with background

(Contrast then Hist and Hist then Contrast). Sample outputs of this preprocessing step are shown in Fig. 2.

The other stage is cell classification. There are three different methods of image cropping process in this stage to prepare the input images for the classifiers, i.e., direct cropping of a single cell, zero padding method, and cell cropping with background. Sample cell images cropped by the three methods are shown in Fig. 3.

A. *Preprocessing*

In the cell detection stage, to get a better detection accuracy, preprocessing the original data is necessary and effective. Through the naked eye observation, the cells parts in the images are darker than background. When we apply histogram equalization or contrast stretching [20], they create obvious effects by adjusting the brightness of different parts of the images. The background becomes brighter while the cell parts become darker. This preprocessing makes it easier to distinguish cells and backgrounds apart.

B. *Non-Maximum Suppression*

To reduce a large number of duplicated bounding boxes detected by the YOLO algorithm, here is a simply way to solve it. We set the value of intersection over union (IOU) to be greater than 0.8 and use it again to filter the detected cells, thereby increasing the accuracy of cell detection.

C. *Data Augmentation*

The data set for the *P. vivax* (malaria) infected human blood smears used in this research are from Malaria Bounding Boxes available at https://www.kaggle.com/kmader/malaria-bounding-boxes

There are 6 classes of cell images, i.e., Red Blood Cell, Trophozoite, Ring, Schizont, Gametocyte, and Leukocyte. The "Difficult" label is not really the ground truth, but it is rather the expert's opinion that expresses the difficult to label

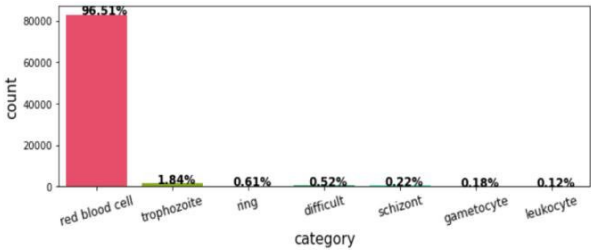

Fig 4. Distribution of different types of cells in the data set: Red Blood Cell, Trophozoite, Ring, Difficult, Schizont, Gametocyte, and Leukocyte.

those images. Hence, there are no ground truth for them and then are discarded here.

The original data set had a heavy imbalance towards uninfected red blood cells (RBCs) compared to other classes of cells, which accounts for 96.51% of the whole data set as shown in Fig. 4. This problem may become a challenge of this study, i.e., when machine learning algorithms try to identify these rare cases in rather big data sets. Due to the disparity of classes in the variables, the algorithm tends to categorize into the class with more instances, the majority class, while at the same time giving the false sense of a highly accurate model which will lead to poor classification performance.

Thus, instead of changing the number of cells in red blood cell groups, we increase the numbers of other classes of cells to the same level as that of red blood cell. This can be done via image augmentation, i.e., top-down translation, left-right translation, horizontal reflection, vertical reflection, and rotation. After image augmentation, there are 83,034 Red Blood Cell, 80,762 Trophozoite, 82,095 Ring, 79,401 Schizont, 80,257 Gametocyte, and 79,150 Leukocyte images. The size of each cell image is 250×250 pixels. The images were randomly divided into training and test sets with the ratio of 4:1.

IV. Experimental Results

The performance of cell detection and cell classification are evaluated separately. Table I illustrates the accuracy of different preprocessed inputs trained by YOLO v5. The classification results on the test set using three different cell cropping methods are shown in Table II, Table III, and Table IV. Some other performance evaluation criteria are listed as follows:

$$Accuracy = (TP + TN)/(TP + TN + FP + FN) \quad (1)$$

$$Precision = TP/(TP + FP) \quad (2)$$

$$Recall = TP/(TP + FN) \quad (3)$$

$$F1 - Score = 2TP/(2TP + FP + FN) \quad (4)$$

TABLE I. ACCURACY OF CELL DETECTION USING DIFFERENT PREPROCESSING METHODS

No.	Accuracy of different preprocessing methods	
	Methods	*Accuracy %*
1	Original	86.02
2	Histogram Equalization	88.19
3	Contrast Stretching	86.56
4	Median Blur	85.80
5	Contrast then Hist	87.60
6	Hist then Contrast	86.28

TABLE II. RESULTS ON IMAGES USING DIRECT CROPPING

	Classification performance (Direct cropping)		
	Precision	*Recall*	*F1-Score*
Red Blood Cell	0.99	0.98	0.99
Leukocyte	1.00	0.99	0.99
Ring	0.91	0.92	0.91
Trophozoite	0.84	0.80	0.82
Schizont	0.93	0.94	0.93
Gametocyte	0.92	0.97	0.94
Accuracy	0.93		

TABLE III. RESULTS ON IMAGES USING ZERO PADDING

	Classification performance (Zero padding)		
	Precision	*Recall*	*F1-Score*
Red Blood Cell	0.98	1.00	0.99
Leukocyte	1.00	0.99	0.99
Ring	0.91	0.89	0.90
Trophozoite	0.82	0.76	0.79
Schizont	0.89	0.93	0.91
Gametocyte	0.91	0.95	0.93
Accuracy	0.92		

TABLE IV. RESULTS ON IMAGES USING CROPPING WITH BACKGROUND

	Classification performance (Cropping with background)		
	Precision	*Recall*	*F1-Score*
Red Blood Cell	0.96	0.99	0.97
Leukocyte	1.00	1.00	1.00
Ring	0.93	0.89	0.91
Trophozoite	0.81	0.80	0.81
Schizont	0.91	0.90	0.90
Gametocyte	0.91	0.94	0.92
Accuracy	0.92		

V. DISCUSSION

Accounting to the experimental results, the classification accuracy of proposed method has reached 93%. However, there still are a lot of parameters in many steps in the experiments that need to be optimized. In addition, besides Yolo v5 and CNN algorithms used in this research, some other new more algorithms can be used as well, for example, YOLO v7. Except for the YOLO series, the other complicated algorithms can also be used to improve the experimental results.

It can be seen from the results in tables II to IV that the classification performances of some cells are still not good, especially schizont. Even data enhancement has been made, its classification performance is still the worst among them. Furthermore, for the future research, the collection and expansion of data set cannot be only to expand schizont data, but also to collect the data of *Plasmodium falciparum*, *Plasmodium malariae*, *and Plasmodium ovale*, the species of malaria parasites that humans can also be infected. Then in this way, the algorithm may not only detect whether a cell is infected or not, but can also distinguish the Plasmodium species.

During the training process of CNNs, there was a difficulty arising from the lack of GPU memory. It is unfortunate that the data set is too large to be trained (about 500,000 images). It is almost impossible to train the data set directly. We can only train the CNNs after size reduction via image downsampling. We believe that if the image size was not reduced, the training performance should be better.

VI. CONCLUSION

In this paper, a two-staged cell detection and classification method is proposed, which based on YOLO and CNN algorithms. Through the experimental results, it can be observed that in the cell detection stage, the input data set with best detect performance is the histogram equalization group, and its detection accuracy can reach 89.19%. While in the cell classification stage, the input group with the best classification accuracy reached 93%. This accuracy can be obtained based on a simple CNN algorithm. In the future, many parameters can still be optimized in this experiment to achieve better performance. Also, more complicated algorithms may have potential to achieve higher accuracy using the same data manipulation as in this research.

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