Effective Preprocessed

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Effective preprocessed thin blood smear images to improve malaria parasite detection using deep learning

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Effective preprocessed thin blood smear images to improve malaria parasite detection using deep learning

W Swastika*, G M Kristianti and R B Widodo

Informatics Engineering Study Program, Universitas Ma Chung, Malang, Indonesia

*windra.swastika@machung.ac.id

Abstract. Malaria can be difficult to detect from thin blood smears. Image recognition methods such as convolutional neural network can be used to detect malaria, but the training process takes a long time. Previous research created a new architecture and compares it to several other architectures such as VGG-16 and ResNet. The effect of preprocessing is analyzed in this research. VGG-16, ResNet, and the custom architecture created by the previous research are being used in this study. The preprocessing methods being analyzed in this research include gray-world normalization and comprehensive normalization. The highest accuracy improvement per epoch (0.5256% using ResNet-50 and 0.0352% using custom architecture) is achieved through gray-world normalization, that also improves final accuracy (90.1% using ResNet-50 and 93.1% using custom architecture) when compared to other methods with the same epochs for ResNet and custom architecture.

1. Introduction

Malaria is a life-threatening disease that affected 90 countries and killed 435 thousand people in 2017 [1,2]. In Indonesia, only 266 out of 514 districts were declared free of malaria [3]. About 10.7 million people still lives in areas with high risk of malaria, as of 2018 [4].

Early detection of malaria is detrimental to the patient's survival. However, access to malaria detection may not be accessible to everyone in remote regions where malaria is prevalent. Methods such as polymerase chain reaction (PCR) and rapid diagnostic test (RDT) are two of the effective, but less accessible methods to detect malaria, and are costly [5].

Thin blood smear, on the other hand, depends on simple tools such as microscope and staining. However, reading the microscope slides require experts that can distinguish between malaria-infected red blood cells and healthy red blood cells. This method also suffers from accuracy degradation that might occur when the experts have to perform large scale diagnosis with limited manpower [6]. This calls for a method to help identifying whether a thin blood smear contains malaria parasite or not. This problem causes studies such as Rajaraman et al [7] to use convolutional neural network to identify malaria on thin blood smear images taken from the microscope slides, in order to augment the identification process.

Rajaraman et al. [7] shows success with malaria identification using CNN, using pretrained AlexNet, VGG-16, ResNet-50, Xception, and DenseNet-121. It also proposes a new architecture (which will be called "Rajaraman model" in this paper). However, the study suffers from problem with the training time. It is hypothesized that adding preprocessing may enhance training time and accuracy. The purpose of this study is to determine the effect of image preprocessing on training time and detection accuracy.

It is expected that preprocessed images as the input of CNN yield faster training time and better accuracy.

2. Methods

Malaria is a blood disease caused by the Plasmodium parasite carried by female Anopheles mosquito bites. It can also be transmitted directly through blood transfusions, syringes and pregnant women to their babies. In humans, there are 4 species of Plasmodium, namely falciparum, vivax, malariae and ovale. Characteristics of malaria are fever, anemia, thromocytopenia, and splenomegaly. The severity of malaria depends on the type of plasmodium and the immunity of patients.

Malaria diagnosis consists of diagnosis based on clinical presumptive diagnosis as well as diagnosis based on laboratory examination. Clinical presumptive diagnosis is a diagnosis of malaria based on clinical examination of the patient, generally consisting of examination of symptoms of fever (periodic), heat, level awareness, dizziness, etc. The experience of medical personnel who make a diagnosis determines whether or not the diagnosis is correct. The clinical diagnosis cannot be used as the main reference in the treatment of malaria because the error rate is quite high. Laboratory examination to diagnose malaria are microscopic thick and thin blood smear examinations. Thick blood smears help in detecting the presence of parasites, whereas thin blood smears help to identify type of parasitic species that cause infection. Laboratory examination is the most commonly and reliable to diagnose disease. However, according to the protocol established by WHO, the diagnosis of malaria involves intensive examination of blood smears with a magnification of 100X and the calculation of the number of red blood cells containing parasites is usually done manually.

2.1. Deep learning

Manually diagnosing classification of infected and uninfected cells on a blood smear image is a process that requires special expertise. In the recent years, deep learning models, especially convolution neural network (CNN), have proven to be very effective to solve image and pattern recognition problems [8-11], including identification of plasmodium in thin blood smears images [7].

Architecture of CNN generally consists of input images, several layers of convolution with pooling, followed by a fully connected layer, and the output layer. In previous studies, the CNN architecture used by Rajaraman et al. are AlexNet, VGG-16, ResNet-50, Xception, DenseNet-121, and a custom architecture.

The CNN training process in previous study requires a long time. It dues to the slow increase in accuracy that can be caused of several factors, for example large image sizes, overly complex CNN architectures, inadequate optimizers, or also because of the amount of data used for training is very large.

In this study, we propose additional preprocessing to images that will be used as training data. It is expected that with proper image preprocessing the training time will decrease and the accuracy will increase.

2.2. Image preprocessing

We test the effects of preprocessing on three CNN architectures, namely VGG-16 [12], ResNet-50 [13], and custom model (Rajaraman model [7]). Preprocessing method used in this study is color normalization. Color normalization emphasizes colors on objects that often appear faded due to lighting constraints or image capture devices. Examples of color normalization methods include: gray world normalization, comprehensive normalization, and histogram specification (matching). In this study, we focus on gray-world normalization and comprehensive normalization. The formula for gray-world normalization [14] and comprehensive normalization [15] are shown in the (1) and (2).

$$R_{new} = \frac{R_{old}}{R_{avg}}, G_{new} = \frac{G_{old}}{G_{avg}}, B_{new} = \frac{B_{old}}{B_{avg}} \quad (1)$$

$$R_{new} = \frac{R_{old}}{R_{old}+G_{old}+B_{old}} \quad G_{new} = \frac{G_{old}}{R_{old}+G_{old}+B_{old}} \quad B_{new} = \frac{B_{old}}{R_{old}+G_{old}+B_{old}} \quad (2)$$

Where R_{new}, G_{new}, and B_{new} are new pixel intensity for red, green and blue pixel, respectively. R_{old}, G_{old} and B_{old} are original pixel intensity for red, green and blue pixel, respectively. R_{avg}, G_{avg} and B_{avg} are the average pixel intensity for red, green and blue pixel, respectively.

2.3. Dataset

Data for analysis of thin blood smear images came from researchers at the Lister Hill National Center for Biomedical Communications (LHNCBC), which is part of the National Library of Medicine (NLM). Data collection was carried out for images of healthy blood smears and those infected with malaria. To acquire red blood cell images on a microscope, a mobile application was developed.

Thin blood smear images that had been stained with Giemsa from 150 patients infected with malaria and 50 healthy patients, were collected and photographed at Chittagong Medical College Hospital, Bangladesh.

The obtained images were then given information manually by an expert slide reader at the Mahidol-Oxford Tropical Medicine Research Unit in Bangkok, Thailand. The initial image and annotation note are archived in NLM (IRB # 12972). The dataset contains a total of 27,558 cell images with the same number of blood cells infected with parasites and healthy blood cells.

Figure 1 shows some examples of healthy and infected cell images taken from the dataset.

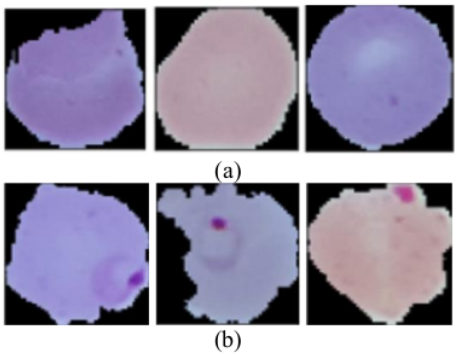


Figure 1. Example of cell images from dataset. (a) uninfected cell images; (b) infected cell images.

2.4. Evaluation

Confusion matrix is used to evaluate the performance of CNN architecture and optimizer. Some of the metrics that are the focus of the evaluation are True Positive, False Positive, False Negative, True Negative, Accuracy, Sensitivity and Specificity (Table 1).

Table 1. Metrics used to measure CNN performance.

Metrics	Formula	Evaluation focus
True Positive (TP)	TP_i	Correctly identify i^{th}class (uninfected image)
False Positive (FP)	$\sum_{j=1}^{i-1} E_{c_j c_i} + \sum_{j=i+1}^{n} E_{c_j c_i}$	Incorrectly identify j^{th} class (infected image) as i^{th} class (uninfected)
False Negative (FN)	$\sum_{j=1}^{i-1} E_{c_i c_j} + \sum_{j=i+1}^{n} E_{c_i c_j}$	Incorrectly identify i^{th} class (uninfected image) as j^{th} class (infected)
True Negative (TN)	$N\text{-}(TP_i + FP_i + FN_i)$	Correctly identify infected class
Accuracy (acc)	$\frac{\sum_{i=1}^{n} TP_i}{N}$	Correctly identified i^{th}class ratio
Sensitivity (sn)	$\frac{TP_i}{TP_i + FN_i}$	True positive rate of i^{th}class
Specificity (sp)	$\frac{TN_i}{TN_i + FP_i}$	True negative rate of i^{th} class

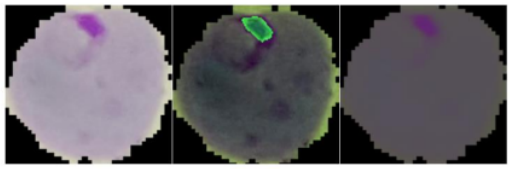
The training system is run using a computer with 8GB of RAM running on Ubuntu Bionic 18.04 LTS version and a Core 2 Duo E7500 CPU. VGA used is the NVIDIA GTX 650 Ti. Tensorflow which uses CUDA is installed using Docker.

3. Results and discussion

In this study, color normalization preprocessing was examined. There will be three conditions that are tried as preprocessing on CNN. The three conditions are as follows:

- Without preprocessing
- Color Normalization: Gray-world Normalization
- Color Normalization: Comprehensive Normalization

Fig. 2 shows an example of red blood cell before and after preprocessing using gray-world normalization and comprehensive normalization.



(a) (b) (c)

Figure 2. Red blood cell example. (a) Without preprocessing (original image); (b) preprocessed using gray-world normalization; and (c) preprocessed using comprehensive normalization.

For ResNet-50 architecture, three training sessions are conducted in accordance with the preprocessing conditions mentioned in the previous section. Each training was carried out with 60 epochs, according to the number of epochs conducted in previous studies [7]. Summary of confusion matrix results obtained from the training are shown in Table 2.

Table 2. Results of accuracy, sensitivity and specificity using ResNet-50.

Image condition	Accuracy	Sensitivity	Specificity
Without preprocessing	0.830	0.713	**0.998**
Gray-world preprocessing	**0.901**	0.854	0.969
Comprehensive preprocessing	0.790	**0.894**	0.645

As shown in Table 2, for ResNet-50 architecture, the best accuracy is achieved by using the Gray-World Normalization preprocessing. The accuracy achieved also has 7.1% difference with the results of training that does not use preprocessing. However, the sensitivity of training using Gray-World Normalization is smaller than the specificity of the training.

Because this research is expected to help the rapid diagnosis process from patients, it requires high sensitivity. With the ResNet-50 architecture, it can be seen that the highest sensitivity is achieved by comprehensive preprocessing.

For VGG-16 architecture, three training sessions are conducted in accordance with the preprocessing conditions mentioned in the previous section. Each training was carried out with 60 epochs and the summary of confusion matrix results obtained from the training are shown in table 3.

Table 3. Results of accuracy, sensitivity and specificity using VGG-16.

Image condition	Accuracy	Sensitivity	Specificity
Without preprocessing	**0.980**	**0.977**	0.986
Gray-world preprocessing	0.972	0.974	0.970
Comprehensive preprocessing	0.979	0.974	**0.987**

In Table 3, it can be seen that training using VGG16 has an accuracy value above 97%. Training with the best accuracy and sensitivity is achieved by without preprocessing. For custom architecture, three training sessions are conducted in accordance with the preprocessing conditions mentioned in the previous section. Each training was carried out with 300 epochs and the summary of confusion matrix results obtained from the training are shown in table 4.

Table 4. Results of accuracy, sensitivity and specificity using custom model.

Image condition	Accuracy	Sensitivity	Specificity
Without preprocessing	0.862	0.709	**0.994**
Gray-world preprocessing	**0.931**	**0.922**	0.945
Comprehensive preprocessing	0.865	0.805	0.950

As shown in Table 4, it can be concluded that custom architecture training has the best accuracy when using Gray-World Normalization preprocessing. As in the ResNet-50 architecture, the difference between without preprocessing and Gray-World Normalization preprocessing is about 10%. In custom architecture, the highest sensitivity is also achieved by using Gray-World Normalization preprocessing.

4. Conclusion

This study has shown the usage of image preprocessing can be beneficial for model training in some of CNN architectures. However, it should be noted that the benefit does not apply to all architectures, as shown in VGG-16. Gray-World normalization seems to be the best performing preprocessor for 2 architectures, namely ResNet-50 and Custom Model.

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