Sinkron : Jurnal dan Penelitian Teknik Informatika
Volume 6, Number 3, July 2022
DOI : https://doi.org/10.33395/sinkron.v7i3.11488

e-ISSN : 2541-2019
p-ISSN : 2541-044X

Detection Malaria Base Microscope Digital Image with Convolutional Neural Network

Muhammad Muttaqin[1)*], Media Cahyo Untoro[2], Muhammad Arif Algifari[3)], Amir Faisal[4)]
[1,2,3)]Teknik Informatika, Institut Teknologi Sumatera, Indonesia,
[4)]Teknik Biomedik, Institut Teknologi Sumatera, Indonesia
[1)]cahyo.untoro@if.itera.ac.id, [2)] muhammad.14117138@student.itera.ac.id

Submitted : Jun 27, 2022 | **Accepted** : July 22, 2022 | **Published** : July 23, 2022

Abstract: Malaria is a tropical disease that infects human red blood cells caused by infection with the plasmodium parasite. Plasmodium parasites spread to humans through female Anopheles mosquitoes and can reproduce in human blood cells. Malaria is a health problem that is at risk of causing other health problems such as anemia and even death. The current gold standard for malaria diagnosis is laboratory diagnosis by microscopic examination to find the malaria parasite through the blood cells of the patient. However, the diagnosis of malaria through microscopic observation of blood cells has the potential to take a long time, because the plasmodium parasite has a very small size. The malaria detection system using the Convolutional Neural Network (CNN) method is designed to detect malaria in human blood cells. CNN is a machine learning method designed to classify objects in an image. The system was built in three stages of development, namely the development of a CNN model for malaria detection, software development and hardware development. The hardware components used in the system include Raspberry pi, Raspberry Pi camera module, and LCD. The results of the malaria detection test using the CNN model gave an accuracy of 98.76% which was tested on blood cell images from a microscope.

Keywords: CNN, Image, Malaria, Microscope, Parasite

INTRODUCTION

Malaria is a tropical disease that infects red blood cells, malaria is caused by infection with the plasmodium parasite that can multiply in human red blood cells (Febrianti & Christi, 2017). Malaria is transmitted to humans through the bite of a female Anopheles mosquito, malaria symptoms begin to occur about 10 to 15 days after being bitten by an infected mosquito (Pratiwi et al., 2021). Malaria is a health problem that is at risk of causing other health problems such as anemia and can even cause death, especially among infants, toddlers, and pregnant women (Puasa et al., 2018).

Based on data from the malaria website published by Indonesia Ministry of Health, malaria has long been one of the highest causes of death in the world, including in Indonesia. It was recorded that in 2021 there were 94,610 malaria cases that occurred in Indonesia, in the current malaria management effort and elimination certification target in 2030. Malaria handling efforts are carried out starting from strengthening in the fields of diagnostics, therapy, and control of malaria vectors. The level of malaria endemicity in Indonesia has decreased in many districts and cities in Indonesia and has even reached 58% of the malaria elimination target. In Lampung Province which now consists of 15 urban districts have 4 malaria endemic areas, namely 3 low endemic areas (Pesisir Barat Regency, South Lampung Regency, Bandar Lampung City) and 1 medium endemic area (Pesawaran Regency) (Kemenkes RI, 2021).

In the management of malaria infection, malaria must be treated properly and as quickly as possible. Correct diagnosis is the main key to successful control of malaria infection and can reduce mortality from malaria. The most common treatment for malaria and the gold standard for malaria diagnosis today is laboratory diagnosis with microscopic examination to find malaria parasites through blood cells from patients. However, the diagnosis of malaria through microscopic observation of blood cells has the potential to take a long time This is because the Plasmodium parasite has a very small size and to avoid errors that occur (Yohannes et al., 2020).

Microscopic examination for the detection of malaria has several advantages, namely it is quite cheap and can identify malaria well. However, this microscopic examination requires several stages and is greatly influenced by the ability of the health personnel concerned (Untoro & Buliali, 2018). The microscopic

*name of corresponding author

examination stage for the detection of malaria requires at least 100 fields of view to be checked, so the inspection activity takes a long time and is less efficient (Susanti et al., 2017). In addition, this microscopic examination requires skilled and experienced human resources and has a specificity rate of 99% and a sensitivity rate of 57% (Setiawan et al., 2021).

Based on the above problems, research to create an image-based malaria detection system by implementing an algorithm model with the best accuracy from the research that has been done. There are several methods that have been used in previous research such as Support Vector Machines (SVM), Backpropagation, K-Nearest Neighbors, Decision Tree, Random Forest, and Convolutional Neural Network (CNN). (Banyal & Dayat, 2016) aimed to detect malaria plasmodium through blood cell images, results of this study used the SVM method with an accuracy of 75%. Research conducted (Hamid et al., 2016) aimed to create a tool to identify the presence of plasmodium parasite cells in blood cell images, results used Backpropagation method with an accuracy rate of 86.8%.

Research conducted by Michael Olaolu Arowolo, et al aims to evaluate the classification performance of the KNN algorithm and decision tree, to obtain higher classification accuracy as a recommendation for malaria prediction. The results of this study obtained an accuracy of 86.7% for the KNN method and an accuracy of 83.3% for the decision tree method (Arowolo et al., 2020). Aims to create a malaria detection system from microscopic images of blood cells. using the CNN method, results this study have an accuracy rate of 95.83% (Pratiwi et al., 2021). Research conducted by Sushil Kumar Mishra aims to identify malaria in blood images using the Random Forest method. The results of this study have an accuracy rate of 91% (Mishra, 2021). CNN-LSTM can classify heart health better on ECG Myocardial Infarction (MI) data 98.1% and arrhythmias 98.66%. (Abdullah & Al-Ani, 2020). (Aldahoul et al., 2021) classification of cartoon images with normal and pornographic classes with the CNN algorithm obtained an accuracy of 87.87%, F-measure 87.87%, and AUC 94.40%. Before classifying the dataset, a model will be made first with training data which results in 79.92% accuracy and 80.85% F-Measure.

CNN is the development of Multilayer Perceptron (MLP) for image data processing and is commonly used in classifying an image. MLP is the development of Artificial Neural Network (ANN) which is made to cover the shortcomings of ANN with Single-layer Perceptron (Pangestu & Bunyamin, 2018). This malaria detection system will be implemented on a microscope and integrated using a raspberry pi, so that the results of malaria detection can be displayed directly through the monitor. One of the expected contributions of this research is that the results obtained can be used to detect malaria quickly and accurately and to speed up the process of detecting malaria infection in red blood cells. So that it can improve health services in Indonesia, especially in dealing with malaria

LITERATURE REVIEW

Malaria is a disease caused by the Plasmodium parasite through the bite of the female Anopheles mosquito. Symptoms of malaria begin about 10-15 days after being bitten by an infected mosquito. Malaria can cause other health problems such as anemia and is at risk of causing death, especially among infants, children under five, and pregnant women. Based on data from the malaria website published by the Indonesian Ministry of Health, malaria is one of the highest causes of death in the world, including in Indonesia. In 2021, there were 94,610 cases of malaria in Indonesia. Malaria must be appropriately handled as quickly as possible so that there will be no further transmission of malaria and avoid unwanted things. The process of diagnosing malaria through red blood cells has the potential to take a long time because the plasmodium parasite has a minimal size.

In 2016 there was a study conducted with the title "Implementation of Principal Component Analysis Methods and Support Vector Machines in Detecting Plasmodium Malaria in Blood Sample Images". In this study, the dataset was taken from PROF Hospital using the Principal Component Analysis and Support Vector Machines methods. DR. H. ALOE SABOE Gorontalo City. This study obtained the results of malaria detection with an accuracy rate of 75% (Banyal & Dayat, 2016).

2016 there was a study title "Application of Color Features for Plasmodium Falciparum Identification in Blood smear Preparations Using MK-Means and Backpropagation Networks". In this study, using the Modified K-Means (MK-Means) and Backpropagation methods, the dataset was obtained from the Public Health Image Library (PHIL) website. This study received malaria detection results with an accuracy rate of 86.66% (Hamid et al., 2016).

2020 there was a study conducted title "PCA Model For RNA-Seq Malaria Vector Data Classification Using KNN And Decision Tree Algorithm". In this study evaluating the performance of the KNN and Decision Tree classification algorithms for malaria detection, the dataset used was malaria data from West Kenya obtained from the National Institute of Health. This study received the results of malaria detection with a precision value of 86.1%, recall of 94.9%, and an accuracy rate of 86.7% for the KNN method. Meanwhile, the Decision Tree

Classification method has a precision value of 85.4%, a recall of 89.7%, and an accuracy rate of 83.3% (Arowolo et al., 2020).

2021, there was a study title "Plasmodium Parasite Detection in Microscopic Image of Blood Smear with Deep Learning Method". In this study, the dataset was obtained from the National Library of Medicine (NLM) website using the CNN method. This study received the results of malaria detection with the highest precision and recall value of 0.98 and an accuracy rate of 95.83% (Pratiwi et al., 2021). 2021 there was a study conducted by Sushil Kumar Mishra under the title "Human Malaria Detection and Stage Classification using Random Forest Classifier". In this study, the dataset was obtained from the National Library of Medicine (NLM) website using the Random Forest method. This study received malaria detection results with a precision value of 0.90, a recall of 0.90, and an accuracy rate of 91% (Mishra, 2021).

As for this study, malaria detection was carried out using the convolutional neural network method of blood cell images. The use of the CNN method in this study is based on previous research conducted (Pratiwi et al., 2021) which produces the highest accuracy compared to other algorithms. CNN is one of the machine learning methods developed by Multi-Layer Perceptron (MLP)(Pangestu & Bunyamin, 2018), designed to process and be used in classifying an image. The difference between the research conducted by the author and previous studies is that the malaria infection detection model application will be applied directly to the light microscope and integrated into an application connected via a raspberry pi (Raspberry_Pi_Trading_Ltd., 2019).

The ReLU activation function is used to make the result of the previous layer non-linear. This layer uses the ReLU activation function, namely (x) = max (0, x). The development of this process essentially creates a limit on the number zero. If the value of x or the input from the node in the kernel is less than 0, then the value of x = 0, while for the value of x that is greater than 0, the value of x is the number x itself.

METHOD

System that can help the malaria detection process quickly and accurately to make it easier to detect malaria infection in red blood cells. This system is expected to improve health services in Indonesia, especially in dealing with malaria. The stages of the research carried out by the author are described in the flow chart (Figure 1).

Figure 1 Diagram Method

Identify Solutions

Plasmodium malaria detection system on blood sample images from a microscope using the Support Vector Machines method gets 75% accuracy and backpropagation with 86.66% accuracy (Banyal & Dayat, 2016). K-Nearest Neighbors and Decision Tree have a precision of 0.86, a recall of 0.94 and an accuracy rate of 86.7% for the KNN method (Arowolo et al., 2020). Decision Tree Classification obtains malaria detection results with a precision value of 0.85, 0.89 recall and 83.3% accuracy (Arowolo et al., 2020). Random Forest for malaria detection with precision value 0.90, recall 0.90 and accuracy 91%. malaria detection system on microscopic blood images using the CNN method architecture with a precision and recall value of 0.98 and an accuracy of 95.83% (Pratiwi et al., 2021). Creating a system that can detect malaria infection based on microscopic images of red blood cells using the CNN method. This system will be implemented on a microscope and integrated using a raspberry pi, so that the results of malaria detection can be displayed directly through the monitor.

Data Collection

In this study using a dataset obtained from the website of the Lister Hill National Center for Biomedical Communications, U.S. National Library of Medicine (NLM) which was used in the development and training phase of the CNN model for malaria detection. The dataset named malaria datasets used has 27,556 image data, which is divided into two classes, namely the parasitized class (infected) with 13,778 data and the uninfected class with 13,778 data. Example image for infected blood and uninfected images (Figure 2). From the dataset, it will be divided into two groups of data, namely 26,000 image data will be used in the model training process and the remaining 1556 image data will be used for testing. With details of data grouping as follows.

Training Data

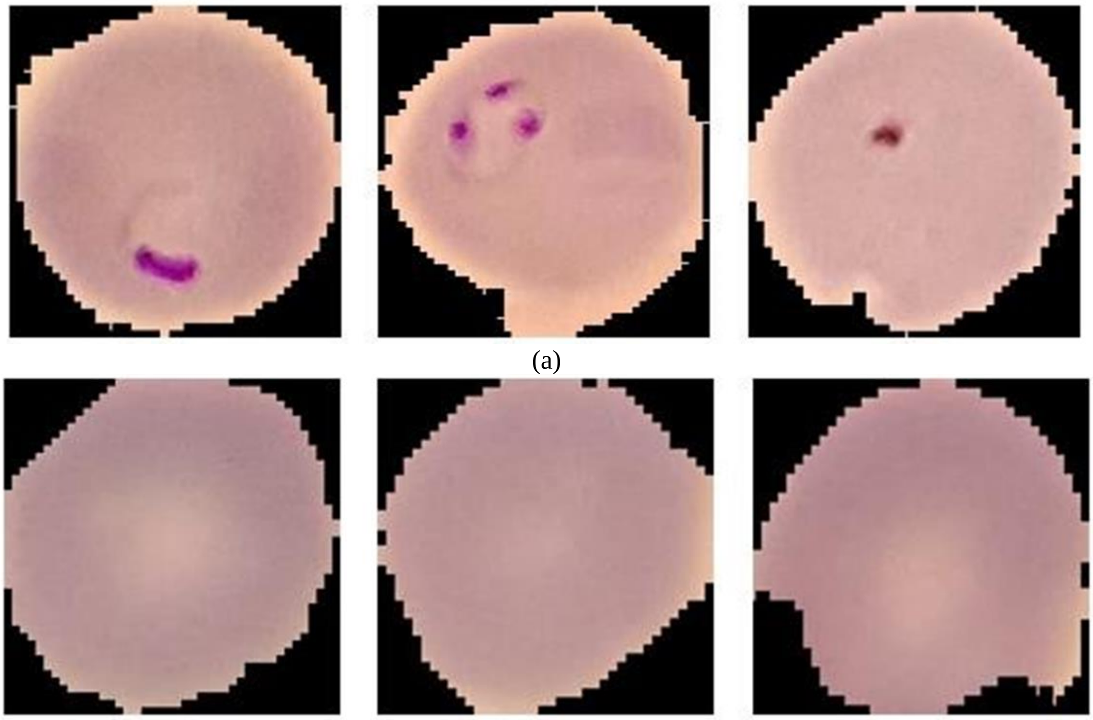
*name of corresponding author

The training dataset will be used to train the model, in the training process this model will be divided into 2 more dataset namely training data and validation data. The total training data group is 26,000 images from a total of 27,556 images in the dataset, while the distribution of training data and validation data is as follows.

1. 75% of the training data are 19,500 images, with details of 9,750 images parasitized (infected) and 9,750 uninfected images (not infected with malaria).
2. 25% of the validation data are 6,500 images, with details of 3,250 images parasitized (infected) and 3,250 uninfected images (not infected with malaria).

Test Data

The test data group will be used to test the model that has been trained, the data used as test data should not be involved or used in the training process. The test data used are 1,556 images from a total of 27,556 images in the dataset. This study will also use the image data of malaria preparations obtained from the public health center to test the model based on the original image from the microscope, image retrieval from this public health center will be carried out at the implementation stage.



(a)

(b)

Figure 2 Infected Blood Image (a), Uninfected Blood Image (b)

Design CNN

The CNN architecture that will be used in this study has several stages, namely input image, convolution layer, ReLU, pooling layer using max polling and fully connected layer Table 1.

Table 1 Model CNN

No	Layer	Output	No	Layer	Output
1	Input image	64, 64, 3	9	ReLU Activation 3	16, 16, 64
2	Convolutional 1	64, 64, 16	10	Max Pooling 3	8, 8, 64
3	ReLU Activation 1	64, 64, 16	11	Dropout	8, 8, 64
4	Max Pooling 1	32, 32, 16	12	Flatten	4096
5	Convolutional 2	32, 32, 32	13	Dense	200
6	ReLU Activation 2	32, 32, 32	14	Dropout	200
7	Max Pooling 2	16, 16, 32	15	Dense	2
8	Convolutional 3	16, 16, 64			

The input image used is the image for CNN training obtained from the National Library of Medicine website. The convolution layer will use a layer with a size of 64x64 pixels with a filter size of 3x3 pixels, after going through the convolution process each layer is processed using the ReLu activation function. Next is max pooling with a size of 2x2 pixels with a stride or a shift of 2. Then at the end a flattening process will be carried out which converts the image features into a one-dimensional vector, the goal is that it can be used as input from the fully connected layer and can be classified. In the fully connected layer, after passing through the flatten stage, the shape of the image feature has become a one-dimensional vector. In table 3.1 above, the output of the flatten layer is 4096 pixels which is obtained from the number of pixels from the previous layer which has been converted into a one-dimensional vector. Next, the dropout layer is the stage of temporarily removing some pixels to speed up the process. After that, the dense function is to add a fully connected layer to classify according to the class in the output. In table 3.1 above the dense layer has an output of 2 because in this study the classification results are divided into 2, namely infected or not infected.

Convolutional Layer

The process at this layer, will process the input image with a pixel size of 64. Convolution layers use several parameters such as filters and strides in the process. The convolution process in this study uses a kernel size of 3x3 and uses a filter with a size of 3x3. In the convolution process, the dot product calculation operation is carried out between the kernels of the 3x3 size image with a 3x3 filter, and the number of stride shifts is 1. The convolution calculation process is carried out sequentially and a displacement or shift of 1 is carried out until all parts of the image pixels have been processed. The calculation simulation at this layer can be seen in Figure 3.4 with an example of a 6x6 input image.

Polling Layer

In this layer the kernel size used is 2x2. Pooling layer aims to reduce the dimensions of the results of the convolutional process or commonly called down sampling. In this study, we will use the max pooling technique in the pooling layer process, which is where the largest value will be used. The simulation process of the max pooling layer can be seen in Figure 3.6 using a size of 2x2 with a stride or a shift of 1

Fully Connected Layer

This layer will be processed at the last layer after all hidden layers are processed, which then results into an output, namely one class label. In a fully connected layer, there is a flatten process, which is the unification of each pixel into a one-dimensional vector, a dropout layer, which is the process of temporarily removing some hidden layers to speed up the process, and a dense process, which is to add layers to fully connected using the sigmoid activation function to classify and then become a output is one of the class labels.

Create Model CNN

The stages of making a convolutional neural network model for the detection of malaria. The process at this stage of implementation includes model making which has been planned in sub-chapter 3.5 to the programming stage. The CNN model will be created in the python programming language, while the training data and validation data for model training and model validation will use the dataset described in data collection. After the model has passed the training and validation stages, the model will be saved in H5 format. Furthermore, the H5 model will be tested to test the accuracy of the model obtained using the confusion matrix which will be explained in the testing.

Evolution

The testing phase of this model is to determine whether the model that has been made is able to detect malaria and has good accuracy. The tests were carried out using the malaria dataset from the NLM website which has been described in data collection. To find out whether the model is working well, that is by using a confusion matrix. The confusion matrix will compare the actual value and the predicted value which will result in 4 categories, namely true positive, true negative, false positive and false negative. With the confusion matrix can calculate the accuracy of the image that has been identified correctly using the equation below, in this study an accuracy of 80% is expected as a measure of the success of the model that has been made. The formula for calculating accuracy, precision, recall and F1 Score is quoted from research conducted by Sushil Kumar in 2021, which can be seen in equations 3.1 - 3.4 below [12].

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{FP} + \text{TN} + \text{FN}} \tag{3.1}$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{3.2}$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{3.3}$$

$$\text{F1} - \text{Measure} = \frac{2\text{xRecall} * \text{Precision}}{\text{Recall} + \text{Precision}} \tag{3.4}$$

RESULT

Taking pictures of malaria samples from a microscope

The sample preparation stage has been carried out, images are taken using a raspberry pi camera which will capture images directly from a light microscope. Before taking pictures of malaria preparations, make sure the observations from the microscope are clear. The results of taking pictures of malaria preparations can be seen in Figure 3 below, the results of taking pictures of malaria preparations from a light microscope can only be caught by a raspberry pi camera.

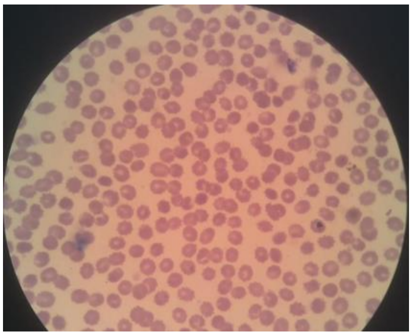


Figure 3 Filming of Malaria Preparations

Grouping of datasets

The first stage is grouping malaria datasets, in this study using datasets obtained from the Lister Hill National Center for Biomedical Communications website, U.S. National Library of Medicine, and annotated by Mahidol-Oxford Tropical Medicine Research Unit in Bangkok, Thailand. The dataset is called malaria datasets which has 27,556 image data, consisting of 13,778 parasitized data (infected) and 13,778 uninfected data. The dataset grouping is done by dividing the image into several data groups, namely training data, validation data and test data. Details of the distribution of images from the dataset can be seen in sub-chapter 3.4 of data collection. The grouping of images is divided into one folder, each of which has a parasitized and uninfected sub folder, the structure of the malaria dataset grouping folder. Tested the model using data validation. To measure the accuracy of the CNN model using a confusion matrix, which will produce 4 categories, namely true positive, true negative, false positive and false negative. From the confusion matrix of the classification of the validation data, the prediction results obtained are:

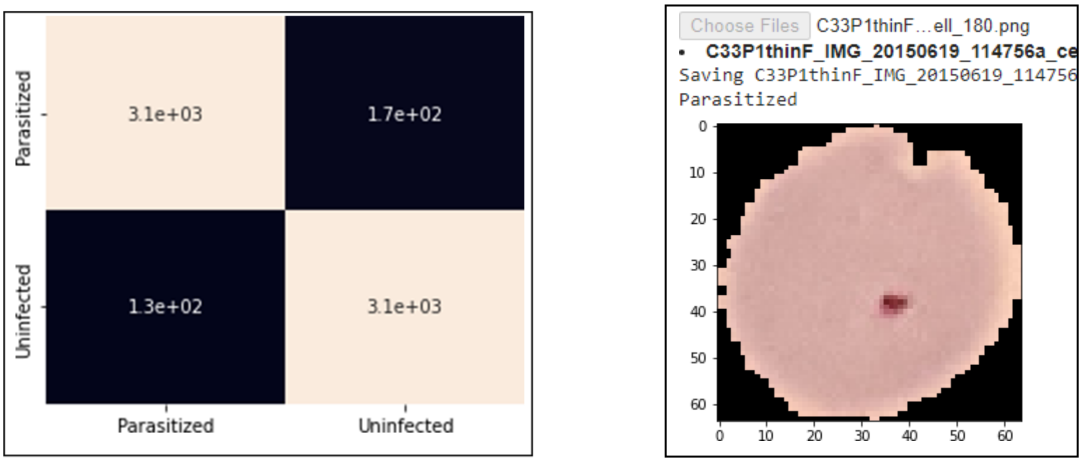
1. Correct prediction with 3107 parasitic detected images (true positive).
2. Correct prediction with 3099 detected uninfected (true negative) images.
3. The prediction was wrong with the prediction results being detected by parasites, it turned out that the image was not infected/uninfected (false positive) as many as 167.
4. The prediction was wrong with the prediction result of not being infected/uninfected, it turned out that the image was infected with parasites (false negative) as many as 130.

$$Accuracy = \frac{3107 + 3099}{3107 + 167 + 130 + 3099}\ x\ 100 = 95.43\%$$

The model that has been created is saved in a file with the extension h5, to perform testing with input data directly from the user, a function will be created to access the CNN model created using google collaborative. To access the model, you need the hardware library.models.load_model, the program code to access the h5 model. the image will be resized to a size of 64x64 pixels, to classify the image into the model that has been created, the image will be represented in the form of an array using the img_to_array() command. After the array form can

*name of corresponding author

be predicted using the CNN model by running the CNN.predict() command, which will output the classification results in the form of parasitized or uninfected classes. Program to upload images and make predictions



```
C33P1thinF...ell_180.png
• C33P1thinF_IMG_20150619_114756a_ce
Saving C33P1thinF_IMG_20150619_114756
Parasitized
```

Figure 4 Result Classification Citra Malaria

To measure the accuracy and performance of the CNN model of malaria detection classification using a confusion matrix, the confusion matrix can measure the performance of the classification model of two or more classes. The confusion matrix will compare the actual value and the predicted value which will result in 4 categories, namely true positive, true negative, false positive and false negative. Testing the accuracy of this model uses test data or data testing that has been described in sub-chapter 3.4 above with detailed data, namely 779 infected data and 778 non-malaria infected data. From the confusion matrix of the classification of the test data, the prediction results obtained are:

1. Correct prediction with 758 parasitic detected images (true positive) out of a total of 779 parasitic images.
2. Correct prediction with 766 uninfected images detected from a total of 778 uninfected images.
3. Incorrect prediction with the prediction results being detected by parasites, it turns out that the image is not infected/uninfected (false positive) as many as 21.
4. Incorrect prediction with the prediction result of not being infected/uninfected, it turns out that the image is infected with parasites (false negative) as many as 12.

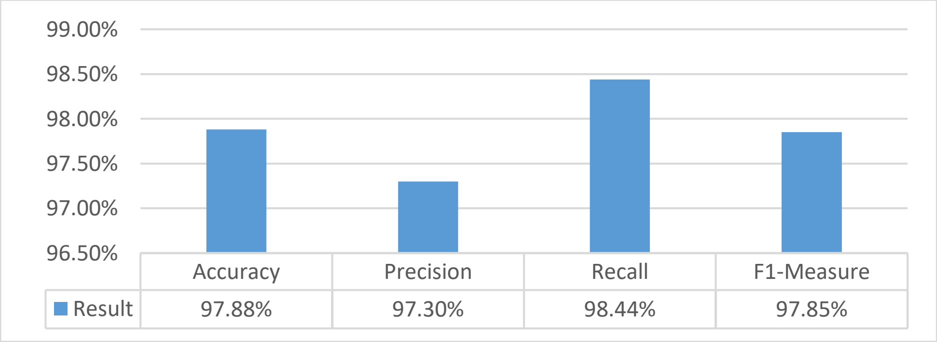


Figure 5 Calculation of accuracy, precision, recall and f1-score of malaria detection model

In this test, the blood cell image will be tested using a CNN model that has been created through the google Collaboratory, from the image of the malaria preparation, manually cropping to get an image of one blood cell. After the image cropping process, 243 images of blood cells were obtained which can be classified with the following details.

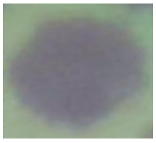
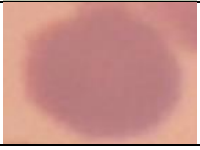
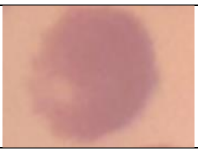
1. 240 images are uninfected blood cells, which are named sequentially 1.png – 240.png.
2. 3 pictures are blood cells infected with malaria, which are named 241.png, 242.png and 243.png.

The blood cells that have been cropped above are classified to detect the presence of malaria parasites in the image. This malaria classification test is carried out on all images and the results of the classification will be displayed with the label "parasitized" for images that contain parasites and "uninfected" for images that do not detect parasites.

From the tests carried out using the CNN model that has been made, the classification results are:

1. Correct prediction with 3 parasitic detected images from a total of 3 images.
2. Correct prediction with 237 images detected not infected with parasites out of a total of 240 images.
3. The prediction was wrong with the prediction results being detected by parasites, it turned out that the image was not infected as much as 3.

Based on the results of these tests, it can be calculated that the malaria classification accuracy level is 98.76% using equation 3.1, so that the test is successful and has passed the expected accuracy parameter limit of 80%.

No	Image	**Result CNN**	**Conclusion**	**No**	Image	**Result CNN**	**Conclusion**
1		Uninfected	Prediction Right	8		parasitized	Wrong Prediction
2		Uninfected	Prediction Right	9		Uninfected	Correct Prediction
3		Uninfected	Prediction Right	10		parasitized	Wrong Prediction
4		Uninfected	Prediction Right	11		Uninfected	Correct Prediction
5		Uninfected	Prediction Right	12		Uninfected	Correct Prediction
6		Uninfected	Correct Prediction	13		Uninfected	Correct Prediction
7		Parasitized	Wrong Prediction				

DISCUSSIONS

The malaria detection system that was created was successfully tested for malaria detection using blood cell images captured from a microscope with an accuracy of 98.76%, with less than 3 seconds for each blood cell image processed with CNN and IoT. Research can be developed again by adding the auto cropping feature of blood cells. Development of detection of specific types of malaria suffered.

REFERENCES

Abdullah, L. A., & Al-Ani, M. S. (2020). CNN-LSTM based model for ECG arrhythmias and myocardial infarction classification. Advances in Science, Technology and Engineering Systems, 5(5), 601–606. https://doi.org/10.25046/AJ050573

Aldahoul, N., Karim, H. A., Abdullah, M. H. L., Wazir, A. S. B., Fauzi, M. F. A., Tan, M. J. T., Mansor, S., & Lyn, H. S. (2021). An Evaluation of Traditional and CNN-Based Feature Descriptors for Cartoon Pornography Detection. IEEE Access, 9, 39910–39925. https://doi.org/10.1109/ACCESS.2021.3064392

Arowolo, M. O., Adebiyi, M., Adebiyi, A., & Okesola, O. (2020). PCA Model for RNA-Seq Malaria Vector Data Classification Using KNN and Decision Tree Algorithm. 2020 International Conference in Mathematics, Computer Engineering and Computer Science, ICMCECS 2020, March. https://doi.org/10.1109/ICMCECS47690.2020.240881

Banyal, N. A., & Dayat, A. R. (2016). Malaria Dalam Sel Darah Merah Manusia Dengan Menggunakan Metode Multi Class Support Vector Machine (SVM). Jurnal Ilmiah ILKOM, 8(Agustus), 111–118. https://media.neliti.com/media/publications/258814-klasifikasi-citra-plasmodium-penyebab-pe-d8c974da.pdf

Febrianti, E. L., & Christi, T. (2017). Peneraan Forward Chaining Untuk Mendianogsa Penyakit Malaria Dan Pencegahanya Berbasis Web. Jurteksi, 4(1), 93–100. https://doi.org/10.33330/jurteksi.v4i1.32

Hamid, M., Mudjirahardjo, P., & Yudaningtyas, E. (2016). Penerapan Fitur Warna Untuk Identifikasi Plasmodium Falciparum pada Sediaan Apus. MATICS : Jurnal Ilmu Komputer Dan Teknologi Informasi, 8(2), 73–77.

Kemenkes RI. (2021). Malaria: Penyebab Kematian Tertinggi di Dunia. Online, 1–3. https://www.malaria.id/profil

Mishra, S. K. (2021). Human Malaria Detection and Stage Classification using Random Forest Classifier. 6(6), 214–218.

Pangestu, M. A., & Bunyamin, H. (2018). Analisis Performa dan Pengembangan Sistem Deteksi Ras Anjing pada Gambar dengan Menggunakan Pre-Trained CNN Model. Jurnal Teknik Informatika Dan Sistem Informasi, 4, 337–344.

Pratiwi, N. K. C., Ibrahim, N., Fu'Adah, Y. N., & Rizal, S. (2021). Deteksi Parasit Plasmodium pada Citra Mikroskopis Hapusan Darah dengan Metode Deep Learning. ELKOMIKA: Jurnal Teknik Energi Elektrik, Teknik Telekomunikasi, & Teknik Elektronika, 9(2), 306. https://doi.org/10.26760/elkomika.v9i2.306

Puasa, R., H, A. A., & Kader, A. (2018). Identifikasi Plasmodium Malaria Didesa Beringin Jaya Kecamatan Oba Tengah Kota Tidore Kepulauan. Jurnal Riset Kesehatan, 7(1), 21. https://doi.org/10.31983/jrk.v7i1.3056

Raspberry_Pi_Trading_Ltd. (2019). Karta katalogowa - Raspberry Pi 4 Computer Model B. June. www.raspberrypi.org

Setiawan, A. W., Rahman, Y. A., Faisal, A., Siburian, M., Resfita, N., Gifari, M. W., & Setiawan, R. (2021). Deteksi Malaria Berbasis Segmentasi Warna Citra dan Pembelajaran Mesin. Jurnal Teknologi Informasi Dan Ilmu Komputer, 8(4), 769. https://doi.org/10.25126/jtiik.2021844377

Susanti, I., Handayani, S., Ekowatiningsih, R., Prasetyorini, B., Yusnita, E. A., Ardianto, D. A., & Widjaya, S. K. (2017). Pengembangan Mikroskop dengan Mikrokontroler dan Cahaya Monokromatis untuk Mendeteksi Parasit Malaria. Jurnal Teknologi Laboratorium, 6(2), 75–82. https://doi.org/https://doi.org/10.29238/teknolabjournal.v6i2.59

Untoro, M. C., & Buliali, J. L. (2018). Penanganan imbalance class data laboratorium kesehatan dengan Majority Weighted Minority Oversampling Technique. Register: Jurnal Ilmiah Teknologi Sistem Informasi, 4(1), 23. https://doi.org/10.26594/register.v4i1.1184

Yohannes, Y., Devella, S., & Arianto, K. (2020). Deteksi Penyakit Malaria Menggunakan Convolutional Neural Network Berbasis Saliency. *JUITA: Jurnal Informatika*, *8*(1), 37. https://doi.org/10.30595/juita.v8i1.6671