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# Detecting Anemia Based on Palm Images using Convolutional Neural Network

Ahmad Saiful Rizal[1], Alfian Futuhul Hadi[2], Sudarko[3], Supangat[4]

[1]Department of Mathematics, Faculty of Mathematics and Natural Sciences, Jember University, Indonesia
Email: ahmadsaifulrizal13@gmail.com
[2]Department of Mathematics, Faculty of Mathematics and Natural Sciences, Jember University, Indonesia
Email: afhadi@unej.ac.id
[3]Department of Chemistry, Faculty of Mathematics and Natural Sciences, Jember University, Indonesia
Email: darko@unej.ac.id
[4]Department of Pharmacology, Faculty of Medicine, Jember University, Indonesia
Email: drsupangat@unej.ac.id

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***Keywords*— Classification, Clustering, Convolutional Neural Network, Hemoglobin, Image Processing.**

***Abstract*— *Hemoglobin is a protein in the blood that conveys oxygen from the lungs to the body's tissues. Hemoglobin levels under the normal limit cause anemia. Hemoglobin estimation is generally utilizing a needle to take the patient's blood as a sample and afterward testing it at the chemicals laboratory. This technique has a shortcoming, specifically, it is less proficient because it requires a few hours. Likewise, it needs to hurt the patient's skin with a hypodermic needle. In this study, we will discuss the Convolutional Neural Network (CNN) in classifying hemoglobin levels based on palm images. Hemoglobin levels are partitioned into two classes, to be anemia and non-anemia. The image size utilized is 500×375 pixels with the number of Red, Green, and Blue (RGB) channels. The data utilized in this study were images of the patient's palm. The first important phase in this research was data retrieval, which went on with preprocessing data, then the data is clustered into two clusters using a random state, then at that point, each cluster will be classified using the CNN algorithm.*

*The best results are obtained by the value of accuracy reached 96.43% with a precision score of 93.75% achieved, recall of 100%, and specificity of 92.31% for cluster 1 in random state 1, and the similar random state for cluster 2 is obtained the value of accuracy reached 96.43% with a precision score of 93.33%, recall of 100%, and specificity of 92.86% were achieved this way.*

## I. INTRODUCTION

Machine Learning (ML) is a modeling technique that can recognize patterns in data automatically without human assistance. ML enables the analysis of massive quantities of data [1]. Algorithms in machine learning can predict based on the given dataset. Machine learning in the medical sector can be utilized for breast cancer classification [2], pneumonia detection based on chest X-Ray images [3], classify Covid-19 contamination [4], early diagnosis of Coronavirus impacted patients [5], myocardial infarction detection [6], recognizing cardiovascular disease from mammograms [7], brain tumor detection [8], and dermatologist level classification of skin cancer [9]. There is additionally related research, for example, Ozturk et al. [10] have detected covid-19 automatically using raw chest X-ray images for binary classification (Covid-19 cases vs Normal) and multiclass classification (Covid-19, Normal and Pneumonia). Rajpurkar et al. [11] presented radiologist-level pneumonia detection on chest X-rays, containing more than 100000 frontal view X-ray images with fourteen diseases. Talo et al. [12] designed a convolutional neural network for brain disorder classification. Comelli et al. [13] employed deep learning for lung segmentation on high-resolution computerized tomography images.

The model of machine learning can make a prediction based on current observations. The results of the prediction will be compared to the actual data that has been tested to measure the exactness of the model. Machine learning can make a model for image recognition. One of the algorithms is Convolutional Neural Network (CNN). CNN is one of the deep neural networks that apply a model based on an Artificial Neural Network (ANN) with multi-layers consisting of two or more hidden layers. ANN has the principle of imitating the brain process in the visual cortex with its main components being neuron cells and synapses. The model of the deep neural network can be trained utilizing existing data and ANN structures [14].

Hemoglobin is an important component in red blood cells. The main capability of hemoglobin is responsible for carrying oxygen and carbon dioxide in the body [15]. The lack of hemoglobin level can cause anemia, while hemoglobin conditions above the normal limit can cause polycythemia. Anemia is a decrease in the concentration of red blood cells that are circulating or the concentration of hemoglobin which hinders the most common way of transporting oxygen [16]. One of the clinical symptoms that are many times found in anemia patients is pale skin and conjunctiva. Therefore, paramedics frequently check the fingertips and conjunctiva to determine the condition of anemia patients [17]. The normal level for hemoglobin in the blood is as given: women 12-16 g/ 100 ml blood, men 14-18 g/ 100 ml blood, and newborns 14-20 g/ 100 ml blood [18].

Hemoglobin measurements are generally carried out using a hypodermic needle to take the patient's blood as samples and keep on testing at the chemicals laboratory. Their hemoglobin levels will be recognized after a few hours. Symptoms of anemia and non-anemia should be visible based on hemoglobin levels. This method is less efficient because it requires a long process and causes pain to patients. It is also considered less kindly for certain individuals since it should hurt the patient's skin with a hypodermic needle, especially in infants, elderly patients, and other vulnerable groups.

In this study, we will detect anemia and non-anemia based on palm images using a Convolutional Neural Network (CNN) to give development to patients without utilizing a hypodermic needle. This algorithm is used with the expectation of having high accuracy. By using the accuracy of the model, the detection of anemia and non-anemia should be possible only with a palm image.

## II. METHOD

### 2.1 Image Processing

An image might be characterized as a two-dimensional function that contains a set of pixels. Every pixel is represented by two integers to indicate its area in the image field, while to show the brightness of the pixels, it frequently utilizes a value of 8 bits, and that implies there are $2^8$ or 256 degrees of gray with the interval [0, 255], where 0 is considered black, 255 represents white and all intermediate values between 0 and 255 are shades of gray varying from black to white or gray level. A digital image is an image that can be processed directly using a personal computer. Digital image size $M \times N$ is represented with matrix size $M$ rows and $N$ columns :

$$f(x,y) = \begin{bmatrix} f\,(0{,}0) & f\,(0{,}1) & \cdots & f\,(0, N-1) \\ f\,(1{,}0) & f\,(1{,}1) & \cdots & f\,(1, N-1) \\ \vdots & \vdots & \ddots & \vdots \\ f\,(M-1{,}0) & f\,(M-1{,}1) & \cdots & f\,(M-1, N-1) \end{bmatrix}$$

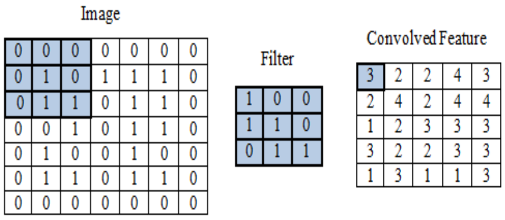
Indexes of $x$ and $y$ are utilized to denote the rows and columns. The $x$-index moves down and the $y$-index moves right. The origin is $f\,(0{,}0)$ which is located in the top-left corner and finishes in $f\,(M - 1, N - 1)$. It intends to show the area of pixels [19].

### 2.2 Convolutional Neural Network (CNN)

CNN is an improvement of the Multi-Layer Perceptron (MLP) and the most recent technique for processing two-dimensional data. CNN is a deep learning algorithm because of its network depth and is widely applied to image data. CNN consists of an input layer, output layer, and hidden layer. Hidden layers generally contain convolutional layers, pooling layers, and fully connected layers [20].

#### 2.2.1 Convolutional Layer

The convolutional layer is the core of CNN, most of the computation is finished in this layer. The convolutional layer in the CNN architecture generally uses more than one filter. The filter as a feature detector, convolved with an image input, thereby producing the convolved feature by using a stride until all receptive fields are covered [21]. The convolution process can be illustrated in Fig 1.



Image

| | | | | | | |
|---|---|---|---|---|---|---|
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 1 | 0 | 1 | 1 | 1 | 0 |
| 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| 0 | 0 | 1 | 0 | 1 | 1 | 0 |
| 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| 0 | 1 | 1 | 0 | 1 | 1 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Filter

| | | |
|---|---|---|
| 1 | 0 | 0 |
| 1 | 1 | 0 |
| 0 | 1 | 1 |

Convolved Feature

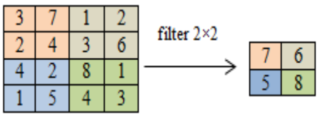
| | | | | |
|---|---|---|---|---|
| 3 | 2 | 2 | 4 | 3 |
| 2 | 4 | 2 | 4 | 4 |
| 1 | 2 | 3 | 3 | 3 |
| 3 | 2 | 2 | 3 | 3 |
| 1 | 3 | 1 | 1 | 3 |

*Fig 1: Convolution process*

The convolution operation is the sum of products of the elements that are located at the same position of two matrices.

### 2.2.2 Pooling Layer

The pooling layer can keep up the size of data during the convolution process, by doing downsampling. In this layer, we can represent data to be smaller, easier to manage, and simple to control overfitting. The pooling system that is normally utilized is max pooling, which chooses the maximum value in a specific area [22]. The pooling system is shown in Fig 2.



| | | | |
|---|---|---|---|
| 3 | 7 | 1 | 2 |
| 2 | 4 | 3 | 6 |
| 4 | 2 | 8 | 1 |
| 1 | 5 | 4 | 3 |

| | |
|---|---|
| 7 | 6 |
| 5 | 8 |

*Fig 2: Max pooling operation*

### 2.2.3 Activation Function

The activation function is a function to initiate neurons and its process should be possible after the convolutional or pooling process [23]. There are three activation functions:

*Sigmoid* function, the output of this function is dependably in the range 0 and 1. The disadvantage of the sigmoid is that the gradient tends to be small or zero when the dataset is too small or large. This causes the network to refuse to learn further or learning is drastically slow. This function is used for classification problems.

*Tanh* function, the output has a range between -1 and 1. This function tends to learn slowly but is slightly faster or quite stronger for *Tanh* than *sigmoid*. This is used for machine learning classification.

*ReLu* function, the output value of this function will be 0 if the input value is negative, if the input value is positive then the resulting output is the activation value itself. The advantage of this function, it is more computationally efficient and converges faster because it's linear than *sigmoid* and *Tanh*, meaning it overcomes the weakness of *sigmoid* and *Tanh*.

### 2.2.4 Fully Connected Layer

In this layer, every neuron has a full connection to all activations in the previous layer. Each neuron in the convolution layer should be changed into one-dimensional data with the goal that the data can be classified linearly. The fully connected layer can be implemented at the end of the network.

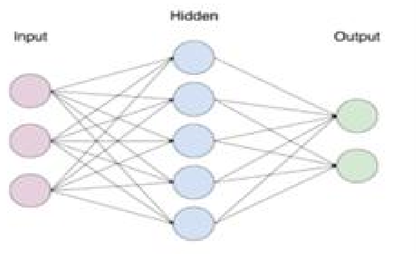


*Fig 3: Fully connected layer*

Overall, this is a Convolutional Neural Network model for image classification, consisting of convolutional layers, pooling layers, fully connected layers, and output layers [24]

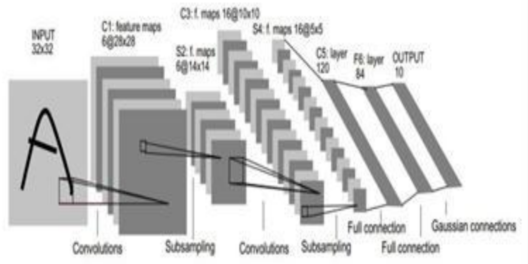


*Fig 4: CNN Architecture*

### 2.3 Performance Evaluation

The confusion matrix is a two-dimensional matrix that describes the performance of the model on the test data. Each column of it represents the predicted class and each row represents the actual class. In the confusion matrix, there is a true negative (TN) indicating a correct prediction for a negative class, false negative (FN) implying that the actual data is positive but predicted to be negative. True positive (TP) shows the correct prediction for the positive class, while false positive (FP) is the actual negative data but is predicted to be positive. From the results of the confusion matrix, it may be utilized to calculate the value of accuracy, recall, specificity, and precision [25].

### 2.3.1 Accuracy

Accuracy is a comparison between correct value prediction and general data. It describes how precisely the model can predict accurately.

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN} \qquad (1)$$

### 2.3.2 Recall

Recall or sensitivity (True Positive Rate) is the correlation of a true positive prediction with the general positive actual data.

$$Recall = \frac{TP}{TP + FN} \qquad (2)$$

### 2.3.3 Specificity

Specificity (True Negative Rate) is the proportion of true negative prediction with the general negative actual data.

$$Specificity = \frac{TN}{TN + FP} \qquad (3)$$

### 2.3.4 Precision

Precision is the ratio of positive correct predictions with the general positive predicted data.

$$Precision = \frac{TP}{TP + FP} \qquad (4)$$

## 2.4 Data

The data used in this study were images of patients' palms obtained directly from Soebandi General Hospital, Jember Regency, Indonesia. Data retrieval was taken using an android camera with the right health protocol. The research population was patients in the hospital. Every image and label embedded is to be utilized as a dataset. The image data obtained 193 images. The patients have tested their hemoglobin levels in the clinical laboratory. In the image data, 57 patients with anemia (25 men and 32 women) because hemoglobin level is under the normal limit, and 136 patients with non-anemia (73 men and 63 women). The examples of image data are shown in Fig 5.

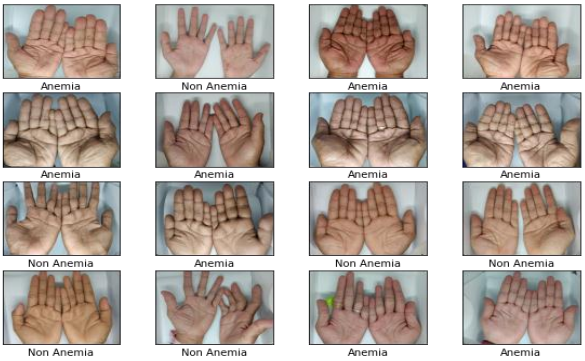


*Fig 5: Image Data*

This research was finished with systematic steps, the architecture can be shown in Fig 6.

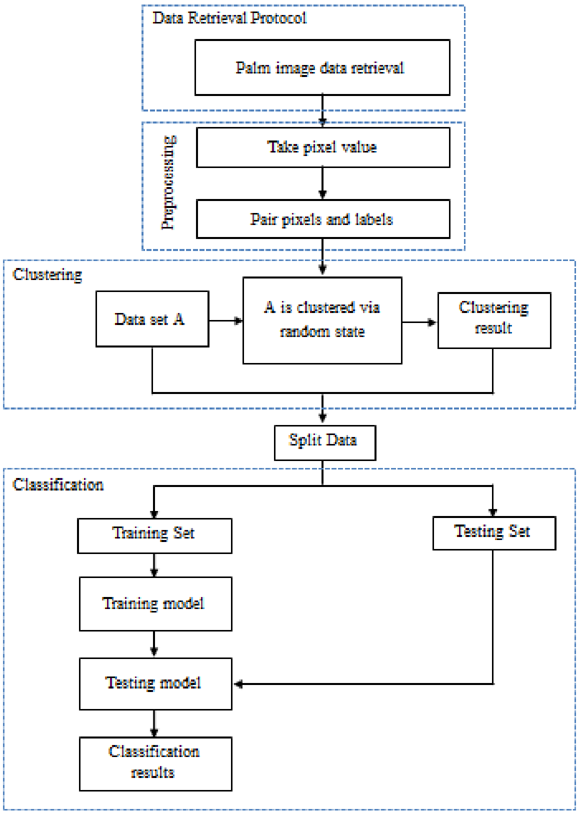


*Fig 6: Research Framework*

First, data retrieval was done by applying the right health protocol. Data that has been got will be preprocessed. The image will be taken its pixel values so the machine can analyze the pattern of pixel values. Next stage, these pixels will be matched with its label. This step needs a balancing strategy to adjust samples for classification cases.

After that, data was clustered into two clusters via a random state. Cluster results were separated into a training set (80%) and a testing set (20%). Data is fit to be applied to a current model. This study uses the CNN model. The model is trained using the accessible training set. This training process goes through several repetitions. In one repetition, the model will learn the pattern of all training data so it can do a decent prediction. This model is hoped to have high accuracy and low loss. In this process, the model will check the accuracy value of validation data. Then, the process has not been completed. Sometimes necessary to change parameters to get the accuracy of a decent model.

Testing model is a truly important part of machine learning since it aims to test the model that has been made, so classification results are obtained. Likewise, its result is evaluated by the standard goodness of fit predictive models with machine learning by analyzing accuracy, precision, recall, and specificity.

There is also a hyperparameter, that can be adjusted and plans to control the model improvement. Different hyperparameter values can affect model training. The next phase is the hyperparameters used in the training process. Epochs, the number of times to iterate over the dataset. Batch size is the quantity of sample data that should be visible to the model each time. Learning rate, the amount to update the model parameters at each batch. A small value of learning rate will make the training process run slowly.

In this study, we use Python programming on the web application also known as Google Colab. Its official site is www.colab.research.google.com. The Google Colab has various libraries including NumPy, Pandas, TensorFlow, Matplotlib, etc. It additionally gives storage media connected to google drive. In this research, we use the processor Graphics Processing Unit (GPU) because it has more cores so it's able to do parallel computing and is suitable for image processing [26].

## III. RESULTS

In the classification results, there are 2 classes namely anemia and non-anemia. The testing model uses 28 images on each cluster for the different random states. Here are the results of the testing model that has been done:

*Table 1: Classification results for Cluster 1*

| RS | loss | Accuracy | Precision | Recall | Specificity |
|---|---|---|---|---|---|
| 0 | 2.26 | 78.57 | 84.62 | 73.33 | 84.62 |
| 1 | 0.26 | 96.43 | 93.75 | 100 | 92.31 |
| 2 | 0.18 | 92.86 | 92.86 | 92.86 | 92.86 |
| 3 | 0.03 | 96.43 | 91.67 | 100 | 94.12 |
| 4 | 1.39 | 71.43 | 60.00 | 81.82 | 64.71 |
| 5 | 0.54 | 89.29 | 93.33 | 87.50 | 91.67 |
| 6 | 0.65 | 89.29 | 83.33 | 90.91 | 88.24 |
| 7 | 0.17 | 96.43 | 90.00 | 100 | 94.74 |
| 8 | 0.39 | 82.14 | 80.95 | 94.44 | 60.00 |
| 9 | 0.99 | 89.29 | 93.33 | 87.50 | 91.67 |

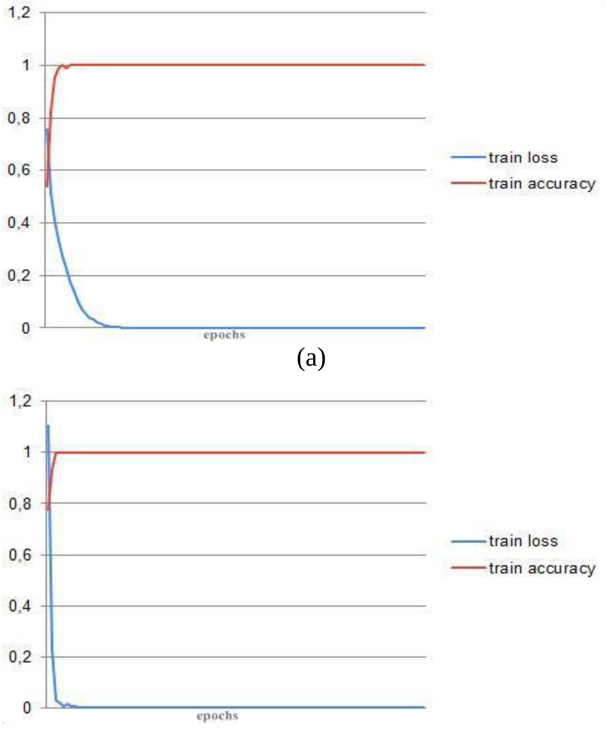
RS: Random state

Based on the test results above, this indicates that the model can classify anemia well. The value of accuracy reaches 96.43%, it is called excellent classification. Meanwhile, the testing model for Cluster 2 is shown in Table 2.

*Table 2: Classification results for Cluster 2*

| RS | loss | Accuracy | Precision | Recall | Specificity |
|---|---|---|---|---|---|
| 0 | 1.27 | 89.29 | 91.67 | 84.62 | 93.33 |
| 1 | 0.11 | 96.43 | 93.33 | 100 | 92.86 |
| 2 | 1.01 | 85.71 | 84.62 | 84.62 | 86.67 |
| 3 | 1.31 | 89.29 | 92.86 | 86.67 | 92.31 |
| 4 | 0.61 | 92.86 | 88.24 | 100 | 84.62 |
| 5 | 0.17 | 92.86 | 85.71 | 100 | 87.50 |
| 6 | 0.87 | 92.86 | 92.86 | 92.86 | 92.86 |
| 7 | 1.22 | 82.14 | 87.50 | 82.35 | 81.82 |
| 8 | 0.82 | 82.14 | 88.89 | 84.21 | 77.78 |
| 9 | 0.72 | 89.29 | 100 | 76.92 | 100 |

In model optimization, a loss and an optimizer are needed to train the model. The best model of training data is Cluster 1 in random state 1. Meanwhile, for Cluster 2 in random state 1 as well, as shown in Fig 7.



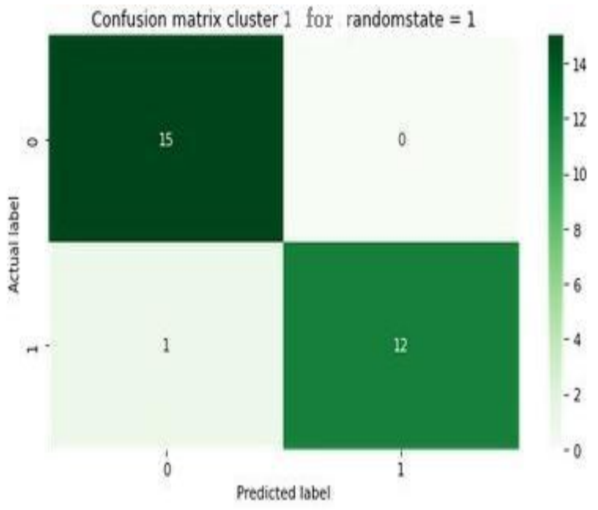
(a)

(b)

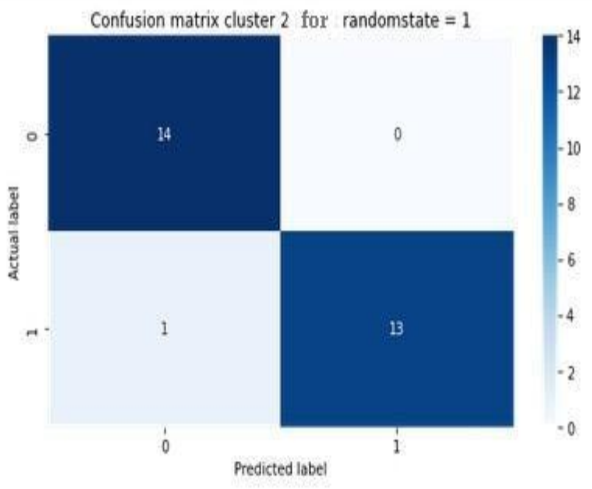
*Fig 7: The best model training of all random states*

*(a) Cluster 1; (b) Cluster 2*

A confusion matrix is also needed to evaluate the performance of the model. It is utilized to show how the model when making predictions, not only provides information about the errors made by the model but also the types of errors made. The best result confusion matrix is shown in Fig 8.



(a)



(b)

*Fig 8: The best result testing of all random states (a) Cluster 1; (b) Cluster 2*

Detailed classification results for the random state in ranges 0 and 9 are shown in Table 3 and Table 4 :

*Table 3: Classification results for the random state in ranges 0 and 9 for Cluster 1*

| Random State | TP | FN | FP | TN |
|---|---|---|---|---|
| 0 | 11 | 4 | 2 | 11 |
| 1 | 15 | 0 | 1 | 12 |
| 2 | 13 | 1 | 1 | 13 |
| 3 | 11 | 0 | 1 | 16 |
| 4 | 9 | 2 | 6 | 11 |
| 5 | 14 | 2 | 1 | 11 |
| 6 | 10 | 1 | 2 | 15 |
| 7 | 9 | 0 | 1 | 18 |
| 8 | 17 | 1 | 4 | 6 |
| 9 | 14 | 2 | 1 | 11 |

TP: True Positive; FP: False Positive

FN: False Negative; TN: True Negative

*Table 4: Classification results for the random state in ranges 0 and 9 for Cluster 2*

| Random State | TP | FN | FP | TN |
|---|---|---|---|---|
| 0 | 11 | 2 | 1 | 14 |
| 1 | 14 | 0 | 1 | 13 |
| 2 | 11 | 2 | 2 | 13 |
| 3 | 13 | 2 | 1 | 12 |
| 4 | 15 | 0 | 2 | 11 |
| 5 | 12 | 0 | 2 | 14 |
| 6 | 13 | 1 | 1 | 13 |
| 7 | 14 | 3 | 2 | 9 |
| 8 | 16 | 3 | 2 | 7 |
| 9 | 10 | 3 | 0 | 15 |

## IV. DISCUSSION

The loss function will measure the level of dissimilarity of predicted data to the target data. To calculate the loss value, we make a prediction using the given input data sample and compare it with the actual label value. The lower the loss value, the more accurate the prediction model. The loss function used in this study is BinaryCrossEntropy. The loss value of the testing data for each random state is shown in Table 1 and Table 2.

Optimization is the process of adjusting model parameters to reduce model errors in every step of the training process. Optimization aims to do a fitting process between training data and target data, also avoiding overfitting. It occurs because the model is too focused on training data and the performance of the model will be bad when tested with other data.

In Fig 7, the loss function of the model represented that Cluster 2 converged faster than Cluster 1. For Cluster 2, loss value reached 0,0065 in 5 epochs. While Cluster 1 for the same loss value needs 17 epochs.

Based on the results of testing accuracy in Table 1, the model produces the highest accuracy 96.43%, meaning that it can recognize the images very well. The lowest accuracy is 71.43% however still includes fair classification. While for Table 2, the highest accuracy was 96.43% achieved. The lowest accuracy is 82.14%.

As shown in Fig 8, anemia is symbolized by 0, and non-anemia is represented by 1. The best result is Cluster 1 in random state 1, and so does Cluster 2. In Cluster 1, the model detected 15 patients with anemia as having anemia, and 12 out of 13 patients with non-anemia as having non-anemia. However, the model can't detect one patient, the model classifies it as anemia even though the patient is non-anemia. While Cluster 2, the model can classify well but there is 1 patient as False Positive, which means is detected as anemia even though the actual is non-anemia. 14 patients True positive, the model predicts patients with anemia as having anemia. True negative consists of 13 patients with non-anemia and the model predict correctly as having non-anemia.

From Table 3, the model of Cluster 1 in random state-0 has classified 11 out of 15 patients with anemia as having anemia, 11 out of 13 non-anemia patients as non-anemia; it misclassified 4 anemia patients as having non-anemia, and 2 non-anemia patients as having anemia. In random state-1, the model misidentified one patient with non-anemia as having anemia. In random state-2, there is 1 patient as a false positive and 1 patient as a false negative. In random state-3, CNN detected 11 patients as anemia, 16 patients with non-anemia are detected correctly as non-anemia, and it misclassified 1 patient with non-anemia as having anemia. In random state-4, the model can’t predict 8 patients correctly. In random state-5, CNN has classified 14 out of 16 patients with anemia as having anemia, and 11 out of 12 non-anemia patients as non-anemia. In random state-6, one patient was a false negative, and two patients are false positive. In random state-7, the model detected one patient as anemia even though the actual is non-anemia. In random state-8, CNN has classified 17 out of 18 patients with anemia as having anemia, and 6 out of 10 non-anemia patients as non-anemia. In random state-9, the model predict 2 patients as non-anemia but the actual is anemia, also it misidentified 1 patient non-anemia as having anemia.

From Table 4, the model in random state-0 misclassified 3 patients. In random state-1, only one patient is detected as a false positive. In random state-2, CNN has predicted 11 out of 13 patients with anemia as having anemia, and 13 out of 15 non-anemia patients as non-anemia. In random state-3, there are 2 patients as false negative and 1 patient as false positive. In random state-4, the model detected 11 out of 13 non-anemia patients as non-anemia, and it detected 15 patients as anemia correctly. In random state-5, the model misclassified 2 patients with non-anemia as having anemia. In random state-6, CNN can’t predict one patient with anemia and one patient with non-anemia. In random state-7, there are 3 patients as false negative and 2 patients as false positive. In random state-8, the model detected 16 out of 19 patients with anemia as having anemia, and 7 out of 9 non-anemia patients as non-anemia. In random state-9, CNN misidentified 3 patients with anemia as having non-anemia.

There is some information about Cluster 1 and Cluster 2 in Fig 8. Cluster 1 in random state 1, the average age of patients is 47.54 years. The minimum and maximum ages of them are 14 years and 70 years. The average hematocrit level of them is 32,69. While for cluster 2 in random state 1, the minimum and maximum ages of patients are 18 years and 79 years, with the average age of them being 41,23 years. Their average hematocrit level is 33,55.

Different random state values will cause the members of each cluster to be different as well. If the image resolution is too large and there are many random states, it will cause an error in the training process. Google Colab only provides 12GB of free RAM. The error is basically because out of memory on Google Colab. The session crashed after using all available RAM

## V. CONCLUSION

The utilization of CNN is reliable enough to detect anemia, and also possibly be applied in the medical sector. This is proven by the results of accuracy of 96.43% with a loss value is 0.03 for Cluster 1, and a loss value of 0.11 for Cluster 2. Model testing gets maximum results, meaning that the model can detect categories in all experiments that were done. The results of low accuracy are due to the palm image features that are tested having many similarities with other palm image features so the model misclassified the palms.

The best result for Cluster 1 is random state 1, and so does Cluster 2. The average hematocrit level for Cluster 1 in random state 1 is 32.69 with the average age of patients being 47,54 years. While for cluster 2 random state 1, the average hematocrit level is 33.55 with the average age of patients being 41,23 years.

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