Non-Invasive Anemia Detection Tool with Application of Mini Spectrometry Base Machine Learning

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Abstract:

Anemia is a condition in which the level of hemoglobin (Hb) in the body is reduced. Prolonged anemia can cause heart problems, pregnancy disorders, and even death. According to the 2018 basic health research data, anemia sufferers in Indonesia have increased to 48.9%. to reduce the level of anemia, early detection is needed, but the existing tools are usually invasive, namely using blood samples, which certainly reduces public interest. This study aims to make an efficient non-invasive anemia detection tool as an option in anemia detection. This tool was developed using the working principle of mini spectrometry, which recognizes light sources in mini spectrometry using Near-infrared because the Hb wavelength is within the near-infrared wavelength range. The Hb wavelength is 1700-1725 nm and the near-infrared wavelength is 1000-2500 nm. The Photo-NIR detector is used as a sensor because it can capture signals according to the near-infrared wavelength. The method used in signal processing is the Principal Component Analysis (PCA) method for feature extraction and two feature variations are produced. Furthermore, grouping was carried out using the Fuzzy C Means (FCM) method so as to produce anemic and non-anemic data based on the degree of membership. The results of this study obtained an accuracy of 88%. In conclusion, the non-invasive detection tool succeeded in separating anemic and non-anemic samples. Therefore, a non-invasive detection tool is needed as an option for the detection of anemia.

1 INTRODUCTION

According to the 2018 basic health research data, anemia sufferers in Indonesia increased to 48.9% from the previous37.1%, with the age group 15-24 years and 25-34 years (Sholikhah et al., 2021). Based on data from the 2019 Semarang City Health Office, the prevalence of anemia in Semarang in the group of young women has increased to 43.75% and in the group of pregnant women to 15.4%. meanwhile, data from Kendal District Health Office in 2018, 715 itu 721 pregnant women experienced anemia, so in 2019, the maternal mortality rate reached 103.28 out of 100,00 live births caused by bleeding.

Anemia is a health disorder caused by a lack of red blood cells in the blood. Red blood cells are also known as hemoglobin (Hb) (Agustina et al., 2022). The normal standard for hemoglobin levels in the blood is 12 g/dL, if the hemoglobin level in the blood is below the normal standard, it can be said that the person has entered symptoms of anemia. Currently, anemia detection is still using invasive methods. The use of invasive methods in detecting ane-

mia has several drawbacks, namely it is less efficient and causes discomfort to its users because it requires taking blood samples to detect anemia by inserting a needle into the patient's arm, then conducting a laboratory examination and finding out the results takes a long time (Bernecker et al., 2019; Dervieux et al., 2020). Therefore, one of the efforts that must be made in overcoming this problem is to make a detector or tool to detect anemia that does not need to use needles (non-invasive), as the newest innovation that can be an option in anemia detection.

Based on previous research related to non-invasive detection of anemia, namely through the conjunctiva of the eye based on digital image processing. In this study, the feature extraction method was carried out using the SVM classification. The results obtained have an accuracy of 72,916%. However, this study still has drawbacks, namely the accuracy of the detection results is affected by the intensity of light. If the light intensity obtained is less, then the resulting accuracy results are less precise (Hasan and Ismaeel, 2020). In addition, research related to anemia detection has also been carried out before detecting Hb. In

this study, Hb detection was carried out based on the light intensity received by the sensor. However, in this study there were still some data that could not be read (Morscher et al., 2014).

This non-invasive technology was developed using the working principle of mini spectrometry, which recognizes light dispersion using pastern recognition algorithms on the finger of anemic patients (Mumtazmi et al., 2022). The light source in mini spectrometry uses near-infrared because the Hb wavelength is within the near-infrared wavelength range. The Hb wavelength is 1700-1725 nm and the near-infrared wavelength is 870-2500 nm (Nasruddin et al., 2021; Nidianti et al., 2019). The photo-NIR detector is used as a sensor because it can capture signals according to the near-infrared wavelength. The catch of the photo-NIR detector is in the form of analog signal data that is converted to digital (ADC). The ADC signal data is then processed using the principal component analysis (PCA) feature extraction method, then using the fuzzy c-means (FCM) classification method is used to find points in clusters based on their degree of membership to separate anemic and non-anemic data. Data resulting from the detection of anemia or non-anemia can be viewed quickly in realtime, without requiring a long time, namely by using the Blynk IoT application which can be accessed using a smartphone/PC.

2 MATERIAL AND METHODS

2.1 Hardware Design

In designing non-invasive anemia detection hardware, the tools needed are ESP32 to function as a microcontroller, and near-infrared as a light source with a wavelength of 1000-2500 nm Near-infrared is used as a light source because the wavelength of Hb 1700-1725 nm is included in the near-infrared wavelength range (Nasruddin et al., 2021). Furthermore, a photo-NIR detector is used as a sensor because the photo-NIR detector is a sensor that can capture the wavelengths generated by near-infrared itself, a USB cable as a connection device with a voltage source, a polycarbonate chip that functions in decomposing light from near-infrared. DC to DC stepdown is used as a liaison near-infrared, sensors and also servo motors to ESP32, and servo motors that function to rotate polycarbonate plates.

The first step in making this detection tool is to connect the servo motor, near-infrared and photo-NIR detector to the ESP32 using a DC to DC stepdown cable. After that, the polycarbonate chip is placed on the device parallel to the near-infrared above the servo

motor, so that the light produced by near-infrared can be decomposed using the polycarbonate chip. The last process is to connect the voltage source to the ESP32 using a USB cable to operate properly.

The workings of this anemia detection tool use the working principle of mini spectrometry, namely recognizing light dispersion using pattern recognition algorithms on the fingers of people with anemia (Mumtazmi et al., 2022). Detection is carried out by decomposing light from near-infrared through polycarbonate chips to obtain a light color with the same wavelength as the Hb wavelength, namely 1700-1725 nm (Nasruddin et al., 2021). Light with the same wavelength as the Hb wavelength is directed to the patient's index finger which is in the finger slot. Some of the light is absorbed by the finger and some of the light is passed on. The transmitted light will be captured by the photo-NIR detector and used in the detection of anemia. The following is a hardware manufacturing block diagram shown in Figure 1.

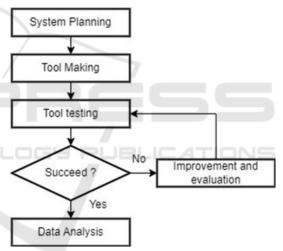


Figure 1: Hardware Manufacturing Block Diagram.

2.2 Machine Learning

The steps taken during the data processing began with taking the ADC data obtained from the measurement process directly using a non-invasive anemia detection tool, in the form of the resulting wavelength data. Then the data is read by the system and characterized by calculating the maximum value, standard deviation, and average (mean) of each data to produce a feature vector value. Furthermore, the feature extraction process was carried out using the PCA method to reduce the number of variables (which were initially very large) to fewer to facilitate analysis at a later stage. The next step after feature extraction using the PCA method is the clustering process. The clustering

process was carried out using the FCM method, which aims to determine the results of grouping anemic and non-anemic data. After the data has been successfully grouped, a testing process is carried out to determine the accuracy of the system so that the results obtained are accurate.

A block diagram of the data processing process is shown in Figure 2.

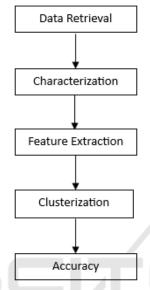


Figure 2: Data Processing Process.

1. Data Sampling

Data sampling was carried out at the Muhammadiyah Kendal Hospital with as many as 20 anemic samples and 20 non-anemic samples. In one patient five times data collection was carried out, whereas in 1 retrieval 50 data will be taken so that the total data taken in one patient is 250 data. The sample data forms a matrix with a size of 250 rows x 40 columns which will be used as input for the time characterization domain.

2. Characterization

Characterization is the stage used to find the characteristics of each signal. The results of the characterization process are in the form of a feature or ordinary matrix called a feature vector. Time domain characterization is done in a way that calculates the maximum value, standard deviation, and average (mean) of each finite data. The feature vector returns a value of 200 rows x 3 columns, where data one-100 = anemia and data 101-200 = non-anemia.

3. Feature Extraction Using Principal Component Analysis (PCA) Method Principal Component Analysis (PCA) is an algorithm that is used to reduce or reduce data information but does not eliminate the information contained in the data. The reason for using the PCA method in the first data processing is because the PCA method is a simple and easy method to implement but produces great accuracy in the data reduction process [10]. The function of PCA itself is to reduce the number of variables (which were initially very large) to become fewer to facilitate analysis at a later stage. In the initial stages, the data measured by the photo-NIR detector is characterized by an n x m matrix, where n indicates the amount of data and m indicates the characteristics of the data. Next, the calculation of the average difference value for each data is carried out, using equation (1).

$$C = \sum_{i=1}^{n} (x_i - \bar{x})$$
 (1)

After calculating the average difference value for each data, then calculating the variance and covariance matrices of the sample data using equation (2).

$$\begin{bmatrix} \sigma_{1}1 & \sigma_{1}2 & \dots & \sigma_{1}n \\ \sigma_{2}1 & \sigma_{2}2 & \dots & \sigma_{2}n \\ \dots & \dots & \dots & \dots \\ \sigma_{n}1 & \sigma_{n}2 & \dots & \sigma_{n}n \end{bmatrix}$$

$$\sigma_{i}j = \frac{\sum_{i}^{j}(i-\bar{i})(j-\bar{y})}{n-1}$$
(2)

Next, the search for eigenvectors and eigenvalues from the previously obtained covariance matrix is carried out. The process of finding eigenvectors and also eigenvalues using MATLAB, where if the matrix A is square, and the eigenvalues are $x_nx1 \neq 0$, then it is known that AX is a scalar multiple of X. eigenvalues are scalars which when multiplied by the column vector X is the same as matrix A multiplied by the same column vector, or can be defined by equation (3).

$$AX = \lambda X \tag{3}$$

The results of the eigenvectors that have been obtained are then sorted from the largest to the smallest value. After sorting, the eigenvector table is then multiplied by the initial matrix so that the PCA results are PC1, PC2, and PC3. In processing this data, the PCA results taken were PC1 and PC2 had an eigenvalue of more than 1. The data processing algorithm using PCA can be seen in Figure 3.

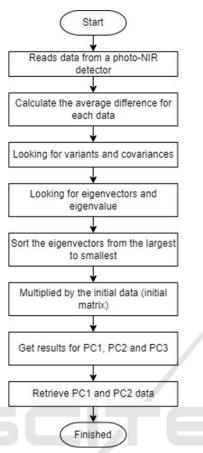


Figure 3: Data processing algorithm using PCA.

4. Clustering Using the Fuzzy C Means (FCM) Method

The FCM algorithm is used for data clustering after the data has been reduced using the PCA method. The FCM algorithm process begins by reading the data to be lustered in the form of an i x j matrix, where i is the number of rows of data and j is the number of columns of data. Next is to determine the reference constant values to be used such as the number of clusters (k), then the rank (w), the maximum iteration (maxiter), the smallest error (e), and the initial iteration (iter). The value of this reference constant will determine the number of iterations and the accuracy of the clustering results. After determining the value of the reference constant, the initial matrix U is formed by randomly generating $u_i k$ numbers. In generating uik values, the rule is that the number of numbers in one row must equal one. After that, the cluster center value is calculates as described in the V_k jmatrix. V_k jis known by using equation (4).

$$V_{kj} = \frac{\sum_{i=1}^{n} ((U_{ik})^{w} (X_{ij}))}{\sum_{i=1}^{n} (U_{ik})^{w}}$$
(4)

Then the objective function (P(iter)) is calculated using equation (5).

$$P_{iter} = \sum_{i=1}^{n} \sum_{k=1}^{c} \left(\left[\sum_{j=1}^{m} (X_{ij} - V_{kj})^{2} \right] (U_{ik})^{w} \right)$$
 (5)

After P(iter) is determined, whether or not the iteration continues is determined by two conditions. The first requirement is that the iteration must be more than or equal to the maximum iteration value, otherwise the iteration will continue. If so, it will proceed with checking for the second condition, namely the difference in the value of the objective function of the i-th iteration with the (i-1) iteration must be less than or equal to the smallest error. If not, then the iteration will continue. To continue the iteration, it is necessary to update the u_ik value. The u_ik value is updated using equation (6).

$$U_{ik} = \frac{\left[\sum_{j=1}^{m} (X_{ij} - V_{kj})^{2}\right]^{\frac{-1}{w-1}}}{\sum_{k=1}^{c} \left[\sum_{j=1}^{m} (X_{ik} - V_{kj})^{2}\right]^{\frac{-1}{w-1}}}$$
(6)

If these two conditions are met properly, the iteration is complete and the $V_k j$ matrix resulting from the iteration will be used as the cluster center. So that the data will be clustered based on its distance to the canter of the $V_k j$ cluster. The data clustering process using the FCM method is shown in Figure 4.

5. Testing

Testing on data processing begins with setting the cluster center point each data, namely for the first cluster center point is anemia and the second cluster center point is non-anemic. The testing process is then carried out by finding the distance between the first cluster and the second cluster in each data using equation (7).

$$Cluster Distance = \sqrt{(x_{measures} - C1_x)^2 + (y_{measures} - C1_y)^2}$$
 (7)

After calculating the cluster distance, the next step is to find the value minimum distance between cluster 1 (C1) and cluster 2 (C2). For anemia data if the value minimum = cluster distance 1 then the data can be said to be correct, while for non-anemia data is said to be correct if the minimum value = cluster distance 2. After knowing the correct amount of data, accurate calculations are carried out from the results of data processing that has been done using the formula equation (8).

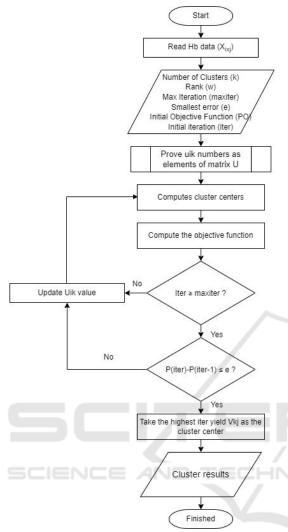


Figure 4: Data clustering process using the FCM method.

$$Accuracy = \frac{Correctamount}{Totalnumber} \times 100$$
 (8)

2.3 Blynk IoT

Blynk is an IoT platform that is used to remotely control hardware, display sensor data, store data, and visualize it using iOS and Android applications (Septiana et al., 2018). Several types of microcontrollers are compatible with Blynk IoT such as NodeMCU ESP8266, Arduino, Rasberry Pi, and ESP32 via the Internet (Utari et al., 2019). Blynk IoT consists of several main components, this is shown in Figure 5.

- 1. Blynk App: used to control hardware and display data on widgets.
- 2. Blynk Server: this is a storage service that is responsible for all the relationships between appli-

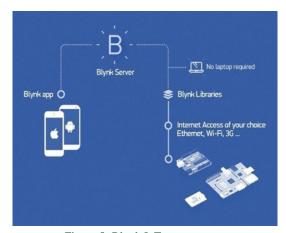


Figure 5: Blynk IoT components.

cations and hardware.

3. Blynk Libraries: This includes various widgets such as control buttons, display formats, notifications and time management that allow hardware to send data obtained from sensors to be displayed on applications effectively.

3 RESULT

3.1 Hardware Design

After the process of designing the system, making the toll, testing and also repairing the tool that was developed, the following is a display of the implementation of the tool that has been made. The display of tool implementation is shown in Figure 6.

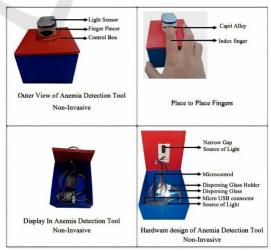


Figure 6: Display of tool implementation.

3.2 Machine Learning

1. Data sampling

Table 1: Anemia sample data.

No.	Number of Patient with Hb Levels								
1.	4	2	3	2	2	2			1
2.	7	6	5	5	5	5			2
3.	16	10	5	6	6	6			5
4.	18	10	11	13	13	13			7
5.	21	10	12	14	14	14			7
250.	42	46	46	43	43	43			45

Table 2: Non-Anemia sample data.

No.	Number of Patient with Hb Levels								
1.	5	6	5	6	5	5			5
2.	5	13	12	7	9	6			12
3.	6	14	15	9	13	8			15
4.	10	16	18	12	17	15			17
5.	10	17	19	15	21	16			20
250.	55	52	46	55	56	47			53

Based on Table 1 and Table 2, analogous data were found on the results of anemia measurements in anemic patients and also in non-anemic patients who had been carried out.

2. Characterization

Table 3: Vector feature values.

Data	Maximum	Standard Deviation	Mean
-1	19,06	27,24	48,20
2	21,33	19,46	48,80
3	19,20	26,22	48,80
4	18,78	27,36	48,00
5	16,02	20,66	42,60
100	21,46	24,98	61,20
101	16,47	22,30	45,60
102	20,76	16,04	52,20
103	14,89	24,14	47,20
104	17,05	23,86	44,80
105	17,46	22,80	43,80
200	17,46	22,80	43,80

Table 3 shows the result of the characterization process, namely the value of the feature vector. Each data will be searched for the maximum value, standard deviation and average value. Data 1-100 are data taken from anemic patients, while data 101-200 are data taken from non-anemic patients.

3. Feature Extraction Using Principal Component Analysis (PCA) Method

Feature extraction will be carried out using feature vector data measuring 200 rows x 3 columns

as shown in Table 3. Where the data will be extracted using PCA features using Matlab to find the eigen values which have been sorted from the largest number as in Table 4 and the eigen vector values which are sorted according to the order of the eigen values as shown in Table 5.

Table 4: Eigen values.

Eigen Values		
	112,5291	
	16,9215	
	1,1329	

Table 5: Eigen vector.

Eigen Vector						
0,8833 -0,3162 -0,3462						
0,3112	-0,1570	0,9373				
0,3507						

The matrix values of the eigen vectors are then multiplied by the transpose of the initial matrix which measures 200 rows x 3 columns to produce the Principal Component (PC) as shown in Table 6, with 1-100 anemic data and 101-200 nonanemic data.

Table 6: Principal Component.

		•	
Data	PC1	Ekstraksi	PC3
00		PCA PC2	
1	2,9189920	3,7818193	0,8478797
2	1,4286449	-4,0443551	2,4594854
3	3,1339610	2,6162275	0,7277167
4	2,6967718	4,0015579	0,6579699
5	-5,2803313	-0,1259826	-0,3266830
			•
			•
100	14,3562939	-2,8171040	-1,4957786
101	-1,9160600	0,3886640	-0,8788068
102	3,0524977	-8,2283799	0,6027757
103	-0,3493570	1,8525220	-2,8399143
104	-1,8936031	2,0093340	0,0091286
105	-3,0207303	1,2692095	0,6978164
	•	•	•
		•	
200	-3,0207303	1,2692095	0,6978164

4. Clustering Using the Fuzzy C Means (FCM) Method

The result of the FCM classification is in the form of a cluster center point, where there are 2 cluster

center points, namely cluster 1 center point (non-Anemia) and cluster 2 center point (Anemia). Where is the center point of cluster 1 (c1x,c1y) and the center point of cluster 2 (c2x,c2y) as shown in Table 7.

Table 7: FCM classification results.

Cluster Center Point							
# X Y							
1 -0,5593 1,95906							
2	2 1,25848 -6,5747						

Based on the cluster center point that has been obtained. It is known that the cluster 1 center point is the non- anemia data center point and the cluster 2 center point is the anemia data center point. Therefore, the PC value of non-anemia data must be close to the cluster 1 center point and the PC value of anemia data must be close to the cluster 2 center point. If not, the data is declared wrong.

5. Testing

Table 8 shows the correct amount of data for each anemic and non-anemia data based on the results of calculating the minimum distance values in cluster 1 and cluster 2 for each data. Of the 100 anemia data, there are 10 incorrect data and 90 correct data. In non-anemic data, there are 14 incorrect data and 86 correct data.

So the total correct data from all data, both anemia data and non-anemia data, is 176 out of 200 data, and the accuracy obtained from this tool is 88%. The results in table 8 are the result of the previous process, where anemia data must be close to the cluster 2 center point and non-anemia data must be close to the cluster 1 center point. If not, the data is said to be wrong. The amount of data processed is 200, of which 100 are anemia data and 100 are non-anemic data.

Table 8: Accuracy of data processing anemia detection tool.

Patient		Accuracy		
	Amount of	Correct	Incorrect	
	Data	Data	Data	
Anemia	100 data	90 data	10 data	3*88%
Non-Anemia	100 data	86 data	14 data	
Total	200 data	176 data	24 data	

3.3 Blynk IoT

The program code is written using Arduino IDE 1.8.19 environment, this code starts to prepare the necessary library for the ESP32 module <ESP32Servo.h> and Blynk application <BlynkSimpleEsp32.h>. The anemia detection result signal is read through the ESP32 pin IO26.

The patient's index finger should be placed so that it touches the tip of the available finger slot. The ESP32 microcontroller processes data by converting analog data to digital information using Analog to digital conversion. The ESP32 module connects to the internet hotspot using the same hotspot name (SSID) and (PASSWORD) and then sends data to the Blynk application platform. The Blynk IoT application receives data through a virtual channel (V5) to be displayed so that it can be seen by users on their smartphones as shown in Figure 7.



Figure 7: Anemia detection results on the Blynk Applica-

4 DISCUSSION

The tool designed is a noninvasive anemia detection tool using the working principle of mini spectrometry as an option in the anemia detection process. This is because the currently circulating anemia detection devices still use invasive methods. This tool works by reading the wavelength of the transmitted light. The less light that is transmitted and captured by the photo-NIR detector after passing through the patient's finger, it is written that the patient is classified as anemic, conversely if more light is transmitted and captured by the photo-NIR detector, the patient is included in a non-anemia patient. Because the finger of an anemic patient will absorb more emitted light so that the light that is transmitted is less. Inversely proportional to the finger of a non-anemic patient (Ningsih et al., 2019).

Many systems have been proposed for an anemia detection system, but until now the anemia detection process still uses blood samples. Even though the blood sampling is small, if it is necessary to do it repeatedly, it still causes discomfort for the patient (Septiana et al., 2018). In addition, the anemia detection system is carried out by recognizing images of patient blood samples (Utari et al., 2019). Because the tool used still uses blood samples, we made a non-invasive anemia detection tool without the need for blood samples in the detection process.

To improve this research, in the future the authors can develop this tool as a Hb monitoring tool that is equipped with an alarm so that medical personnel can provide faster treatment if a patient is detected with a drastic decrease in Hb. This tool will be a new development and produce a sophisticated tool in dealing with cases of anemia.

5 CONCLUSIONS

This study aims to implement an anemia detection system using the working principle of mini spectrometry with the PCA data processing method and data clustering using the FCM method. This tool was created to be the tool of choice in the process of non-invasive detection of anemia.

The results obtained from the manufacture of this anemia detection system are that this tool can distinguish anemic patients from non-anemic patients with an accuracy of 88%. This tool is very useful in the process of detecting anemia, which was previously done with invasive methods now in this tool detection of anemia is done with non- invasive methods to reduce the prevalence of anemia. To improve research, this tool can be further developed as an Hb monitoring tool.

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