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Paper:

# Computer-Based Blood Type Identification Using Image Processing and Machine Learning Algorithm

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**Blood type identification is a method used for determining the specific blood type of a person. It is a requirement before blood transfusions or blood donations is undertaken especially during emergency situations. Presently, the tests are performed manually by medical technologists in the laboratories. Sometimes, manual blood typing is prone to human error, resulting to incorrect blood grouping and wrong typing in the report, leading to fatal transfusion reactions. The study was focused on the development of a device that is capable of identifying the blood type of an individual using an image processing and machine learning algorithms. The study covered the identification of eight blood types, specifically rhesus positive and negative, A, B, O, and AB, by developing a capturing box integrated with a web camera system that could effectively capture blood sample images. In this study, the methodologies utilized were image processing through segmentation, feature extraction by color and texture properties, and different machine learning algorithms. After training, the results showed that coarse tree DT has the best performance accuracy score of 97.77% using 70 : 30 holdout validation. The testing results showed that the system is 100% accurate as validated by a registered medical technologist.**

**Keywords:** blood type identification, image processing, feature extraction, machine learning algorithms, coarse tree DT

## 1. Introduction

Blood typing is necessary to ensure the safety of the patient. Receiving blood that is incompatible with the blood type can lead to a potential life-threatening transfusion reaction. Blood grouping tells us what type of blood a person has [1]. In cases reported in 2018 by the Food and Drug Administration, in the US, there were transfusion-related deaths due to labeling errors. Similarly, in another study [2], a total of 2,229 errors out of 32,672 requisitions for blood transfusion, typing and cross-matching over a period of a year. Common errors include sample labelling errors, inappropriate request for blood components, and mismatched information on requisition forms versus samples. Given these situations, errors regarding blood type identification, especially during blood donation must be prevented to avert potential fatalities.

Moreover, in the study presented by Rathod and Pathan [3], the typical blood type testing is conducted in the laboratories by medical technologists and the result may be slow and inaccurate since it depends on the operator's capabilities, tiredness, and availability. To avert inaccuracy, and in order to successfully perform blood typing without such common human errors, this study purported a system that would automatically identify the different human blood types. This system could then have the database of any donor's personal information and have blood types identified through image processing and machine learning. Other features of the system including the automatic printing of blood bag labels indicating the blood type and the date of extraction and collection were added.

Thus, this study imperatively highlights the importance of blood typing as a precursor to any medical procedure. In the Philippines and elsewhere, blood typing is administered by the Red Cross Organization before any blood donation is conducted. It is a method to determine the blood type of a patient or donor [4]. There are many types of blood group, but the major two types of blood groups are ABO blood system and rhesus blood system. A blood group is a classification of blood based on the presence or absence of inherited antigenic substances on the surface of red blood cells (RBCs) [5].

In the existing system, a licensed medical technologist is the authorized person to do the blood typing. The willing donor must have accomplished the personal information sheet that serves as registration. After that, the medical technologist will extract the blood sample from the donor and perform the blood typing procedure. During bloodletting activities outside medical facilities, there are cases wherein the medical technologists are not present. When collected, the blood samples from such activities are re-tested in the laboratories, thus causing delay. Since only expert medical technologists can tell the blood type by seeing at the agglutination process, we need a more ef-

ficient way to identify such blood types. Previous studies used image processing alone to identify the blood types as in the cases of [3, 5, 6]. In these studies, a machine learning algorithm was used but the images were obtained from the laboratories. Correlation analysis and feature selection were not implemented to identify the most significant features of a blood sample. Thus, an automated system was proposed to easily identify the different human blood types to address the problems.

The proposed system was composed of a capturing box for image acquisition, where MATLAB was used to perform the image processing, feature extraction, and machine learning. This proposed system was also capable of storing the personal information of a donor for future reference. Other features of the system included its capability to print the summary of results and print the blood bag labels. The device was developed with the intention to deploy in bloodletting activities of Red Cross Philippines and similar groups to help them retrieve and document data from donors and to utilize a fast, accurate, and reliable system of blood type identification. Current existing fully automated blood typing and cross-matching machines are bulky and expensive, and can only be installed in medical facilities, which this system purports to address.

## 2. Methodology

### 2.1. Project Design

The project design is applicative since it aimed to find a solution for an immediate need, through a practical solution with the purpose of improving an existing system. This study is intended to create a device capable of identifying human blood types in a more efficient and effective way, with the hope of reducing human error, particularly in offsite activities.

#### 2.1.1. Hardware Design

The hardware design includes the correct selection of the camera for the capturing box. Specifications, availability, and cost were considered in the selection. The physical design must satisfy the aesthetic and functional requirements of the system, thus, proper component placement and connection should be considered. The image capturing box is the hardware component which contains the web camera for the image acquisition.

#### 2.1.2. Software Design

The software design started with the establishment of a MATLAB-based program and graphical user interface. Different programs for image processing, feature extraction, and different machine learning algorithms were run and simulated, and served as guide to develop the best algorithm for the project. For the study, texture analysis using the gray-level co-occurrence matrix (GLCM) was used for examining texture that considers the spatial relationship of pixels in the retrieved images as the statistical method. The GLCM functions characterize the texture of an image.

For image processing, with reference to different literatures and studies presented, acquisition, segmentation, RGB to grayscale, and thresholding are the image processing algorithms to be done. After processing, features were then extracted. Region and image properties of the blood sample were considered such as the area, mean, and standard deviation of the objects. Texture analysis using GLCM was used. Contrast, correlation, energy, entropy, and homogeneity were the features extracted using GLCM. Coding, flowcharting, debugging, and simulation were done to create an error-free program and graphical user interface.

Classification [7] is used to find out in which group each data instance is related within a given data set. It is also used for classifying data into different classes according to some constrains [8]. Different machine learning algorithms [9, 10] are used and compared for classification such as support vector machine (SVM), decision tree (DT), linear discriminant analysis (LDA), logistic regression (LR), *k*-nearest neighbor (KNN) classifier, and Ensemble.

### 2.2. Project Development

#### 2.2.1. Hardware Development

The hardware development includes the assembly of the image capturing box. The essential part in the image acquisition is the selection of the appropriate camera based on the required specifications. A high-definition web camera with at least 8 megapixel is enough for good quality blood sample image. A plain white background was considered with lighting components such as LEDs for clearer image. The thermal printer, which will print the gathered data including the patient's personal information, blood image, and blood type, is part of the hardware system too. The laptop, which contains the developed programs for image processing, feature extraction, machine learning, and GUI, is also included in the hardware system. The laptop contains the MATLAB 2018b software with at least 3 USB 2.0 sockets for the USB devices. It will display the created graphical user interface.

**Figure 1** shows the actual photo of the casing. The casing is made up of 1 cm thick plywood covered with white vinyl sticker. The dimensions are 11 in $\times$ 15.5 in $\times$ 5.5 in (L$\times$W$\times$H) for the front side and 11 in $\times$ 15.5 in $\times$ 7.5 in (L$\times$W$\times$H) for the back part. The durability of the material was also considered so that the laptop can be placed on the box.

#### 2.2.2. Software Development

Software development includes the coding and programming in order to develop the system. Image processing, feature extraction, and establishment of trained model were designed and programmed using MATLAB 2018b.

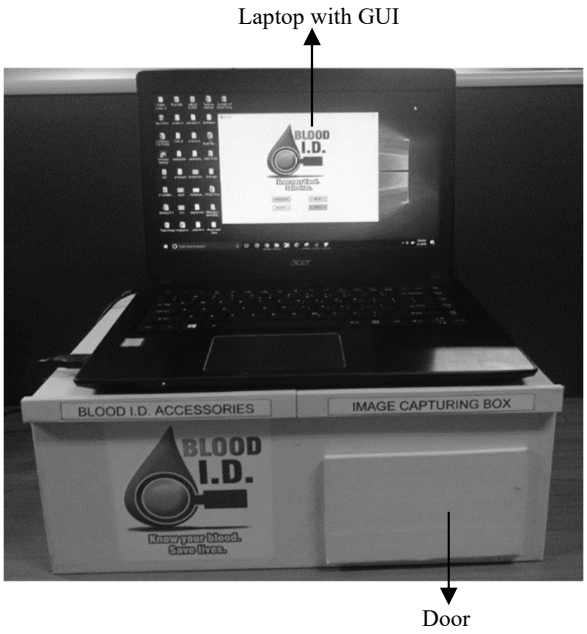


**Fig. 1.** Actual photo of the prototype's casing.

Image acquisition

After developing the image capturing box, the web camera was interfaced with the MATLAB to test the image data acquisition. Image acquisition is the first step and one of the most critical steps in image processing. Correct image must be captured so that the next procedures will function according to the expected output.

Image processing

The image processing algorithm was developed to enhance blood sample image before extraction [5]. The image passed through a series of image processing techniques such as segmentation or division of image into three parts, RGB to gray conversion, thresholding or binary image conversion, segmentation, and feature extraction.

Segmentation and RGB to grayscale

As suggested by [11], image processing should involve segmentation which divides the image into three parts. For the study, the region of interest was defined to have a size of $65 \times 65$ pixels. Image segmentation is the most important step and a key technology in image processing which directly affect the next processing [12]. Using the segmentation process helps the system in identifying the region of interest for segment A, segment B, and segment D where agglutination and non-agglutination occur. After segmentation, the segmented images will be converted to grayscale [13].

Thresholding

Thresholding or binarization convert a pixel image into a binary image according to [14]. First, the image is converted into grayscale then a threshold is applied.

Feature extraction

In the study of [15], the transformation of the input data into a set of features is called feature extraction. For the study, the region and image properties of the object and texture analysis were used to extract features such as area, mean, standard deviation, entropy, contrast, energy, correlation, homogeneity, variance, smoothness, kurtosis, and skewness. The standard deviation is the parameter to distinguish occurrence of agglutination [16].

### 2.3. Correlation and Feature Selection Using MINITAB

To examine the correlation of each feature with other features, correlation analysis using MINITAB 17 was conducted. Correlation assesses the strength of relationship between two variables through correlation coefficient $R$ and the Pearson product moment correlation. The correlation coefficient $R$ measures the strong linear relationship between the two variables. Pearson's coefficient of correlation $R$ and $p$-value were used to assess if the two features of blood samples have weak or strong relationship. For Pearson's coefficient of correlation $R$, if the value is less than $\pm 0.5$, one feature can be eliminated. For the $p$-value, at 95% confidence interval, if the $p$-values are greater than 0.05, one feature can be also eliminated. Using these two parameters, the identified features will be decreased or trimmed down, thus the most significant features will be generated.

### 2.4. Machine Learning Algorithm

Developing the training model is the next step after identifying the most significant features. These features will have comprised the data set to be imported to the classification learner application of MATLAB. It is composed of one response and eight predictors. Per segment, the workspace variable is composed of $400 \times 9$ table including the label, and used 5-fold cross validation, 10-fold cross validation, 80 : 20 holdout validation, and 70 : 30 holdout validation. Cross validation was used to protect the data against overfitting by partitioning the data set into folds and estimating the accuracy on each fold. $k$-fold validation partitions the data into $k$ (5 and 10 were used in this study) randomly chosen subsets (or folds) of roughly equal size. One subset is used to validate the model trained using the remaining subsets. This process is repeated $k$ times such that each subset is used exactly once for validation. On the other hand, holdout validation partitions the data into exactly two subsets (or folds) of specified ratio for training and validation. **Fig. 2** shows the pipeline of the machine learning, training, and testing stage of the system. The training was done using the classification learner of MATLAB. The extracted features per segment were compared with the saved trained model. Different machine algorithms were used and compared based on the accuracy and training time. Prediction was based on the presence of agglutination (1) and non-agglutination (0). As shown in **Fig. 2**, the data set

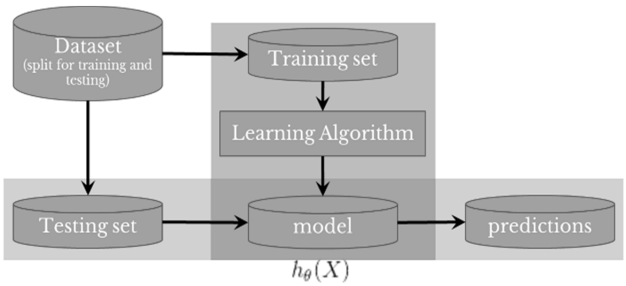


**Fig. 2.** Machine learning pipelines.

was divided into training and testing sets. The training data set is used to develop the learning algorithm to establish the model. Once the target accuracy of the training model is achieved, the model was tested using the testing data set. Different machine learning algorithms were compared and used such as SVM (linear, quadratic, cubic, fine Gaussian, medium Gaussian, and coarse Gaussian), DT (fine tree, medium tree, and coarse tree), discriminant analysis (linear discriminant and quadratic discriminant), LR, nearest neighbor classifier (fine, medium, coarse, cosine, cubic, and weighted), and ensembles (boosted trees, bagged trees, subspace discriminant, subspace KNN, and RUS boosted trees).

### 2.5. Testing the Blood Type Identification

In testing the system, certain steps and factors in blood sample preparation must be considered. Use of proper materials like the antisera must be carefully observed in order to achieve the desired results. The following shows the steps done in blood sample extraction as well as the expected appearance of the extracted blood.

Blood preparation starts by cleaning the area of the finger to be pricked for blood extraction. In order to determine the blood type, a medtech will mix the donor's blood with antibodies A and B using a toothpick. Also, by using a monoclonal antibody D, the medtech will be able to determine if the blood type is negative or positive.

After securing the capturing box and blood sample, testing the functionality and accuracy follows. Functionality is used to verify that a system performs and functions correctly according to design specifications. Accuracy as explained by [17] was defined as the number of correct assessments over the number of all assessments. The accuracy of the system was evaluated by letting the medical technologist identify the extracted blood sample first before testing it with the system. If the assessment of medical technologist and the result of the system is same or matched, then the system is said to be accurate. Eq. (1) shows the formula used in determining the accuracy of the system. In testing the whole system, at least 30 individuals will be needed as volunteers.

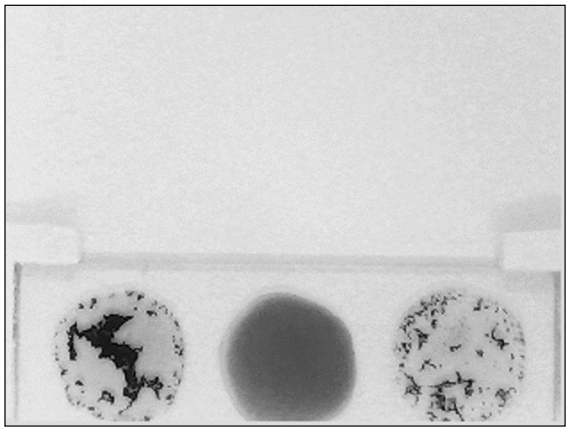

**Fig. 3.** Captured image of blood sample inside capturing box.

$$Accuracy\ [\%] = \left(\frac{A}{B}\right) \times 100\%, \quad \ldots\ldots \quad (1)$$

where $A$ represents the total number of correct assessments and $B$ represents the number of all assessments.

## 3. Results and Discussions

The purported system is a software-based system developed especially for Red Cross Philippines Organization and similar organizations that need to easily identify the blood type of a donor during bloodletting activities, for the purpose of documentation and accuracy in the event of a blood transfusion.

The system is composed of the image capturing box, a laptop with GUI, and a printer. The inner part of the box is divided into two compartments. The left compartment is intended for the accessories or the needed supplies and materials to extract the blood and to prepare the blood sample. This includes the glass slides, lancing device, antisera, alcohol, cotton, and tape. Alcohol and cotton are used to clean the area of the finger to be pricked. A lancing device is used to prick the portion of the finger to extract the blood. The blood will then be placed on the glass slide and will be mixed with the antisera. On the other hand, the right compartment is the capturing part of the box. It is composed of a webcam and a white platform for the glass slide. It has LED strips on the front and back walls of the inner box for controlled illumination of the sample since the webcam is enclosed inside the box. The right part of the box has an opening on the front side enough for the hands to place the glass slide. Concurrently, the image of the blood sample in a glass slide with antisera will be placed inside the capturing box.

Image acquisition

**Figure 3** shows the captured image of a blood sample. Here, the glass slide is placed in a designated slot inside the box, where the sample glass slide must be completely captured. Given that the blood samples are evenly distributed in the glass slide, the presence of agglutination

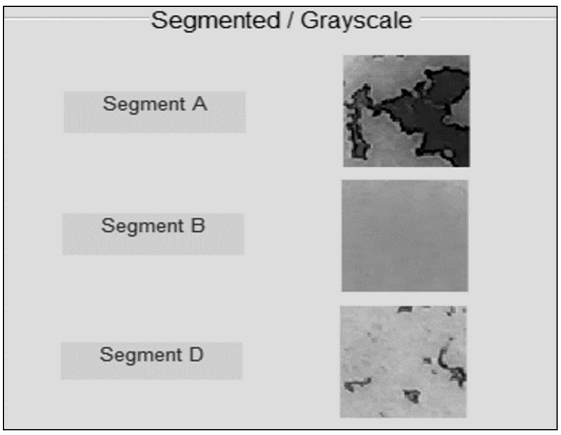


**Fig. 4.** Output image after segmentation and RGB to grayscale.

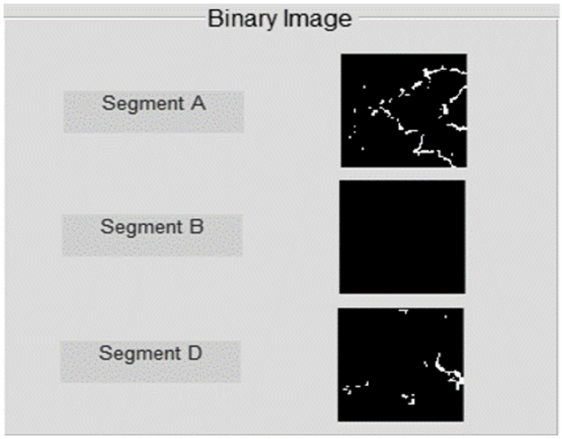


**Fig. 5.** Output image after thresholding.

and non-agglutination is very noticeable. The web camera used in this study is a 16-megapixel A1Tech camera with manual focus.

Segmentation and RGB to grayscale

**Figure 4** shows the segmented and grayscale images. These processes were used to capture the correct location where the agglutination occurs. Here, the image is divided into segment A, segment B, and segment D. The RGB image is automatically converted to grayscale. The agglutination of the blood sample is presented in black pixels, as shown in **Fig. 4**, segment A and segment D have agglutination.

Thresholding

After thresholding, as shown in **Fig. 5**, the binary image is composed of black and white pixels. The white pixels represent the agglutination part of the segment while the background or black pixels represent non-agglutination in the segment. As shown in **Fig. 5**, in segment A and segment D, the agglutination occurred as represented by white pixels and black pixels. On the other hand, in segment B, since there is no agglutination, the converted image is composed of black pixels only.

Feature extraction

All the parameters are different in each segment, and it depends if the agglutination occurred or not. For example, since agglutination occurred in segment A and segment D, the areas are larger (728) than segment B with smaller area (16) since there is no agglutination. Similarly, the entropy values for segment A (4.02) and segment D (3.89) are higher, because agglutination occurred. The system will then use these values to learn and identify the blood type based on such combinations of results.

Correlation and feature selection using MINITAB

To determine the correlation of each feature with other features, correlation analysis using MINITAB 17 was conducted. For segment A, $R$-values are less than $\pm 0.5$ for variance and mean (0.310), variance and standard deviation ($-0.392$), smoothness and area ($-0.048$), smoothness and mean (0.052), smoothness and standard deviation ($-0.065$), and smoothness and entropy ($-0.048$), which means that the area, mean, and standard deviation are not correlated with variance and smoothness. Therefore, the variance and smoothness will be eliminated. The $p$-value supports this claim since with respect to variance and smoothness all $p$-values are greater than 0.5. Thus, for segment A, variance and smoothness will be eliminated. Kurtosis and smoothness (0.049) and skewness and smoothness (0.050) have $R$-values, which are less than 0.5. This means that these features are not correlated. The $p$-value supports this claim since with respect to kurtosis–smoothness and skewness–smoothness, the $p$-values (0.332 and 0.315, respectively) are greater than 0.05. Thus, for segment A, kurtosis and skewness will also be eliminated. This case is similar to segment B and segment D.

After correlation, the selected features for segment A, segment B, and segment D are area, mean, standard deviation, entropy, contrast, energy, correlation, and homogeneity, thus forming the data set. The study included eight blood groups such as A+, B+, AB+, O+, A−, B−, AB−, and O−. Each group in the data set contains 50 samples, for a total of 400 samples or observations. These will be used in training to develop the trained model using different machine learning algorithms.

Machine learning algorithm

Different types of machine learning algorithm were used and compared to develop the trained model such as SVM, DT, LDA, LR, KNN, and Ensemble.

Based on the results of training showed in **Fig. 6**, course tree DT has the best performance having an accuracy of 97.77% using 70 : 30 holdout validation, thus, the system for deploy will use this algorithm.

To check the performance per class, the confusion matrix plot and receiver operating characteristic (ROC) curve were used. This plot shows how the currently selected classifier performed in each class. In **Fig. 7**, confusion matrix shows the true positive rate or percentage. It also shows the false negative rate or percentage is smaller,


**Fig. 6.** Training accuracy and time.

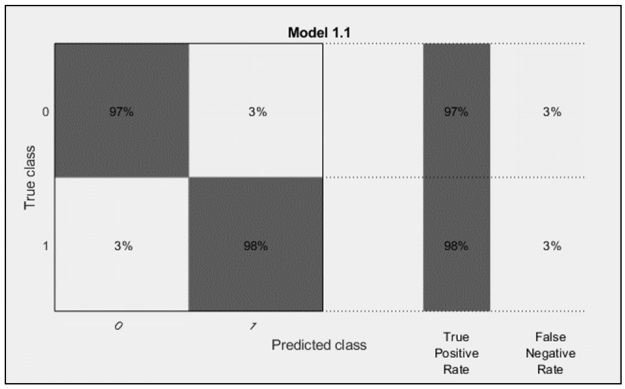


**Fig. 7.** Confusion matrix using 70 : 30 holdout validation.

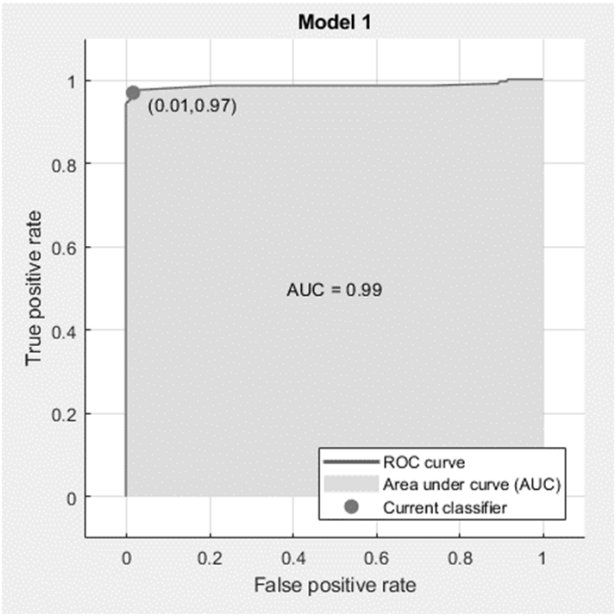


**Fig. 8.** ROC curve using 70 : 30 holdout validation.

which is 3%. This means that only 3% of the data set were confused if there is occurrence of agglutination or non-agglutination. The true positive rate for agglutination (1) is 98%, while the true positive rate for non-agglutination (0) is 97%, thus the accuracy is 97.5%.

The ROC curve was also observed, as shown in **Fig. 8**. ROC curve [18], or ROC is a graphical plot that plots true positive rate (same as sensitivity) against the false positive rate (same as the complementary of specificity), at various threshold settings [19]. Major concern is the area under the ROC curve (AUC). Recently, the correctness of ROC curves has been questioned because in some cases AUC can be quite noisy as a classification measure. Nevertheless, it gives a good enough result in this study. The more the area, the better it is. Based on the ROC curve, it can be seen that the false positive rate of the ROC is 1%, while the true positive rate is 97%.

Graphical user interface

The accomplished graphical user interface for blood type identification is shown in **Fig. 9**. It is composed of image preview where the preview of the blood sample inside the box is being displayed. The captured image of the sample will be displayed and saved. As shown, there is no occurrence of agglutination in segment A, while there is occurrence of agglutination in segment B and segment D. The agglutination is represented by 1, while non aggluti-

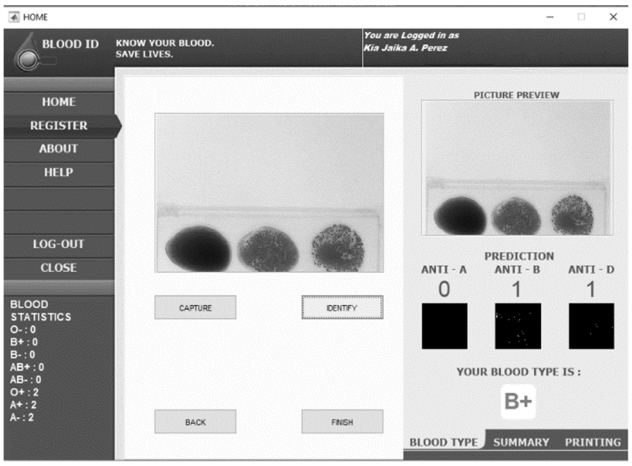


**Fig. 9.** Blood type identification GUI with blood sample and blood type.

nation is represented by 0. The prediction results showed that segment A is 0, segment B is 1, and segment D is 1. The predicted blood type is B positive (B+).

Accuracy of testing

For the evaluation of the whole system, 30 trials were performed to different individuals, as shown in **Table 1**. In this study, the results from the manual testing were assessed by a registered medical technologist. In testing the blood type, a "matched" remark means the blood type identified by the medical technologist is the same as the blood type identified by the system. An "unmatched" remark means that there is difference in the blood type identified manually by the medical technologist and the developed system. From the results, the developed system is 100% accurate.

**Table 1.** Accuracy testing for the blood type identification.

| No. | Med tech | System | Remark |
|---|---|---|---|
| 1 | A+ | A+ | Matched |
| 2 | O+ | O+ | Matched |
| 3 | O+ | O+ | Matched |
| 4 | O+ | O+ | Matched |
| 5 | A− | A− | Matched |
| 6 | O+ | O+ | Matched |
| 7 | O+ | O+ | Matched |
| 8 | O+ | O+ | Matched |
| 9 | AB+ | AB+ | Matched |
| 10 | A+ | A+ | Matched |
| 11 | O+ | O+ | Matched |
| 12 | AB+ | AB+ | Matched |
| 13 | A+ | A+ | Matched |
| 14 | O+ | O+ | Matched |
| 15 | A+ | A+ | Matched |
| 16 | O+ | O+ | Matched |
| 17 | O+ | O+ | Matched |
| 18 | A+ | A+ | Matched |
| 19 | B+ | B+ | Matched |
| 20 | A+ | A+ | Matched |
| 21 | B+ | B+ | Matched |
| 22 | A+ | A+ | Matched |
| 23 | A+ | A+ | Matched |
| 24 | AB+ | AB+ | Matched |
| 25 | A+ | A+ | Matched |
| 26 | O+ | O+ | Matched |
| 27 | B+ | B+ | Matched |
| 28 | O+ | O+ | Matched |
| 29 | O+ | O+ | Matched |
| 30 | B+ | B+ | Matched |

## 4. Conclusions

The system was successfully developed in identifying human blood type using image processing through quadratic SVM with 100% accuracy. The image capturing box was successfully established and integrated using a 16-megapixel webcam and LED strips to ensure equal lighting inside the box. Hence, the quality of the captured blood sample images is clearer and better. A MATLAB-based program was successfully developed for image acquisition, image processing, and feature extraction. Moreover, it was established that the image processing techniques such as segmentation, RGB to grayscale, and thresholding are efficient algorithms for enhancing good quality image before feature extraction. The SVM learning machine algorithm was successfully created for blood type identification. The coarse tree DT was accurately and efficiently used with a classification accuracy of 97.77% and with a training time of 0.55 s. Correlation and feature selection were effectively implemented using MINITAB 17. Pearson's moment of correlation ($R$) and $p$-value were used effectively to reduce the number of features. MATLAB-based GUIs were successfully designed and established in displaying the results such as personal information of donor, output of blood type identification, and were capable in printing the blood bag label.

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