

AUTOMATIC SYSTEM FOR BLOOD TYPE CLASSIFICATION USING IMAGE PROCESSING TECHNIQUES

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Abstract: There is still not yet available a low-cost commercial equipment to determine blood types in an emergency situation. This paper presents the development of a low cost system, based on image processing techniques, that allows the automatic determination of human blood types in emergency situations. The experimental method is based on the plate test where the serums specifics of blood types determination are mixed with the sample blood of the donor. The mixtures blood/serums are captured through a CCD camera and analyzed using the software IMAQ Vision from National Instruments. The developed image processing methodology and the obtained results are detailed. The first prototype for automatic human blood determination is presented.

1 INTRODUCTION

The determination of blood type can be performed using various experimental tests (Datasheet of Diamed, 2008) (Datasheet of Diamed-ID, 2008). The plate test, used in this work, allows the determination of blood type in a short time. It consists of mixing the specific reagents of blood type determination, with the patient blood. The result depends on the occurrence or absence of agglutination (Datasheet of Diamed, 2008). The agglutination of erythrocytes is observed macroscopically, in a short time, allowing using image processing techniques to detect the occurrence or absence of agglutination and therefore the determination of the corresponding blood type. In Figure 1, it is presented an image that shows the difference between the occurrence and absence of agglutination.

Currently, for the determination of blood types it is required human intervention, not only in performing the analytical procedures, as well as in reading and interpreting the results, being then the process more susceptible to errors (Alexander, 2007). With the aim to fulfil that gap and to automate the determination of blood types, some devices were developed (Alexander, 2007) (Anthony, 2005) (Lambert, 2005). However, they

have high costs and present some limitations compared to the method proposed in this work.

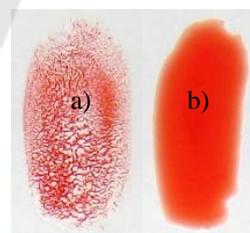


Figure 1: (a) Occurrence of agglutination. (b) Absence of agglutination.

Preliminary studies performed by the research team allowed the development of a software tool based on image processing techniques, able to detect the occurrence of agglutination. However, the methodology was not fully automatic, requiring the users to select the image area to quantify (Ferraz, Carvalho and Brandão, 2008) (Ferraz, Carvalho and Brandão, 2010). In this sense, this paper presents a new system to automatically determine the blood type. The methodology presented in this work is innovative and at low-cost, being an added value to commercial solutions.

2 IMAGE ACQUISITION PROCESS

As the reaction of agglutination is macroscopically visible, the sample images were captured in real size, using a CCD camera (Sony Cyber-shot DSC-S750) with 7.2 megapixel resolution.

To analyze the acquired images, an image processing application was developed using the IMAQ Vision software from National Instruments (IMAQ, 2004). Figure 2 shows the schematic of the designed system.

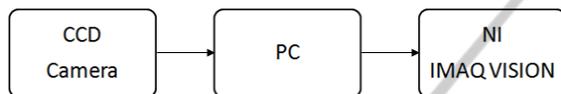


Figure 2: Designed system schematic.

3 DEVELOPED SOFTWARE

The software application developed is presented in this section, where it is detailed each image processing technique employed. For each step (3.1 to 3.10), it is shown the effect that the applied technique has in the former image, using IMAQ Vision software.

3.1 Image Buffer: Add Copy (1)

Stores a copy of the original image with the four samples (mixed blood/serum) in Buffer # 1 of the image buffer for later use, Figure 3. Final results will be overlaid on this image (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

As the original image will suffer a series of changes, later there is a need for the original image, this function allows saving the original image.

3.2 Color Plane Extraction: RGB Green Plane

Allows extracting the green plane from an RGB image, Figure 4 (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

The original image is a RGB image that must be processed to allow the determination of the occurrence of agglutination.



Figure 3: Original image.

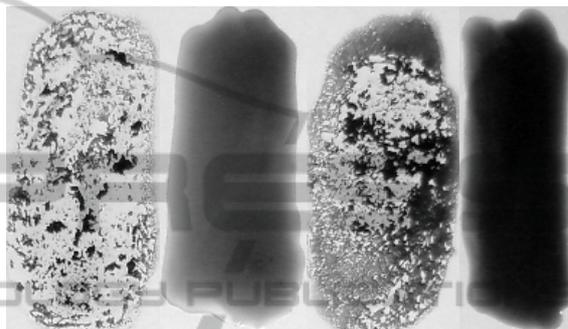


Figure 4: Image resultant from applying the Color Plane Extraction: RGB Green Plane function.

3.3 Filters: Convolution Highlight Details

The convolution filter highlights the regions in the image where there are sharp changes in pixel values. These regions correspond to the boundaries of the samples and other noisy pixels that may be present in the image. The convolution kernel highlights the edges of an image and in this case, the function uses a 3 x 3 kernel (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

The next function is a threshold function that is used to separate certain structures of the image. In this case, it is used to separate the samples blood/serum of the background, once this function segments the image in two regions, designated region "particle" and "region background" (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

3.4 Threshold

This function applies a threshold to the image resulting of previous function based on the Minimum and Maximum threshold values introduced. All pixels that are not contained between the Minimum and Maximum values are set to 0 and all pixels that fall inside the range are replaced by 1

(IMAQ, 2004) (Klinger, 2003) (Relf, 2003). In this function the Minimum value is 128 and the Maximum value is 255.

The Minimum and Maximum threshold values were determined by trial and error, when developing the algorithm, and were kept constant afterwards. The result of applying this function is presented in Figure 5.

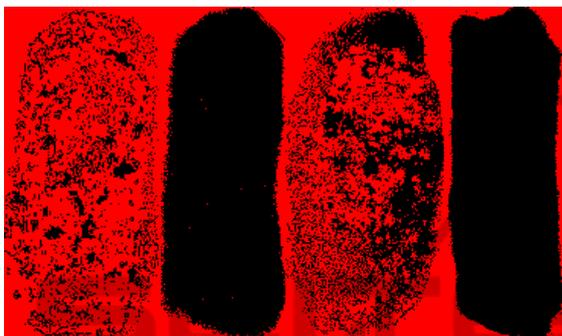


Figure 5: Image resultant from applying the Manual Threshold.

This function is then combined with the Local Threshold: Niblack function, allowing isolating the particles corresponding to the mixed blood and serum.

3.5 Local Threshold: Niblack

Calculates a threshold value for each pixel based on the statistics of the surrounding pixels. This algorithm compensates the high lighting variations. This function uses a kernel; in this case the kernel size is 115 width and 132 height (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

Using the previous feature to define the borders in the image to isolate particles, results in the image shown in Figure 6.

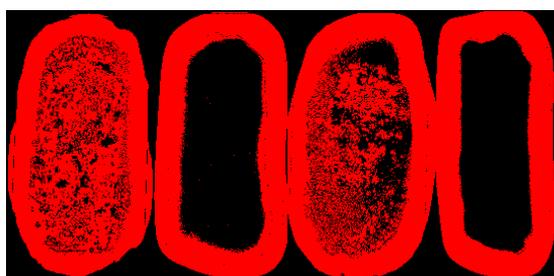


Figure 6: Image obtained by applying the Local Threshold: Niblack function to Figure 5.

3.6 Adv. Morphology: Fill Holes

Fills all the holes that are present in the particles. Holes are filled with a pixel value of 1. The resulting binary image contains entire particles, without holes, corresponding to the samples blood/serum (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

3.7 Adv. Morphology: Remove Small Objects

This function removes the small particles and the possible noise in the binary image resulting from the previous function. It eliminates particles that are not relevant to the analysis. The particles that are removed by an iteration of erosion are assumed to be noisy particles (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

This function is used to eliminate the small particles that can interfere in the analysis of the image. Small drops of blood or serum in the background of the image are not relevant to the analysis, and should be therefore removed.

3.8 Adv. Morphology: Remove Border Objects

It eliminates particles that are at the border of the image. It removes particles that are not needed for the analysis of the image, preventing interference from unwanted particles (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

This step is necessary to eliminate particles that are joined together due to high kernel placed in the Local Threshold: Niblack function, but in fact should be separated.

3.9 Particle Analysis

This step is particles corresponding to each mixture blood/serum. These necessary to analyze the properties of the particles in the image, considered as four particles can be analyzed using various properties, being the determination of the center of mass the most important in this work (IMAQ, 2004) (Klinger, 2003) (Relf, 2003). This function is essential because it defines a coordinate system and the region to analyze.

The result of the previous function is a table that contains the properties selected and their values. The values of Center of Mass X and the Center of Mass Y will be used in the following function.

3.10 Threshold

As described in 3.4. The result of this function is presented in Figure 7.

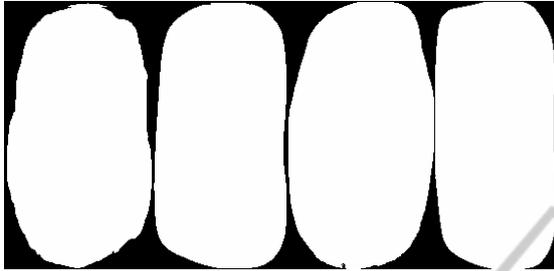


Figure 7: Image obtained by applying the Manual Threshold function.

3.11 Image Buffer: Retrieve Buffer # 1

It retrieves the copy of the original color image, so that it can be used by the next function. The original image has the four samples blood/serum, Figure 8 (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).



Figure 8: Image obtained by applying the Image Buffer: Retrieve Buffer function in the image of Figure 7.

3.12 Color Operators: Not Or

This step performs a logical OR operation between the original image input image and the original image stored in the buffer. This is a bit-wise operation (IMAQ, 2004) (Klinger, 2003) (Relf, 2003). The result of this function is presented in the image of Figure 9.

3.13 Color Plane Extraction: HSL Luminance Plane

This function is used to extract the luminance plane from the color image obtained with the previous function (IMAQ, 2004) (Klinger, 2003) (Relf, 2003), Figure 10.

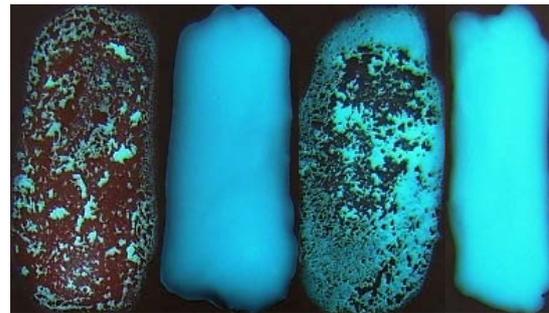


Figure 9: Image obtained by applying the Color Operators: Not Or function in the image of Figure 8.



Figure 10: Image obtained by applying the: HSL Luminance Plane function in the image of Figure 9.

3.14 Set Coordinate System

This function defines a coordinate system based on the stage of particle analysis. The particle analysis function gives the coordinates necessary to calculate the center of mass, used in this function. Chosen the mode horizontal and vertical motion because it allows adjusting the region of interest positions along the horizontal and vertical axes (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

The definition of the region of interest is an important task in this method. Based on the coordinate system, it is selected the region to be analyzed, depending of the center of mass of the particle calculated through the particle analysis function.

This function will be repeated for each of the particles in analysis. In this case, it will be repeated four times, one for each blood/serum sample.

3.15 Quantify

It measures the intensity of the pixels in the region of interest selected, Figure 11. This step uses the Reposition Region of Interest that when enabled, it dynamically repositions the region of interest based on the coordinate system previously defined. Also, it

uses the Reference Coordinate System that indicates the coordinate system to link the region of interest (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

The result of the application of this function consists of a table that contains the area (percentage of the analyzed surface in relation to the complete image), the mean value (mean value of the pixels), the standard deviation (standard deviation of the pixels) and the minimum and maximum values of the pixels (IMAQ, 2004) (Klinger, 2003) (Relf, 2003).

This function allows identifying the occurrence of agglutination in a sample blood/serum based on the standard deviation value of the pixels.

As in the previous function, this step is repeated for each of the particles in analysis.

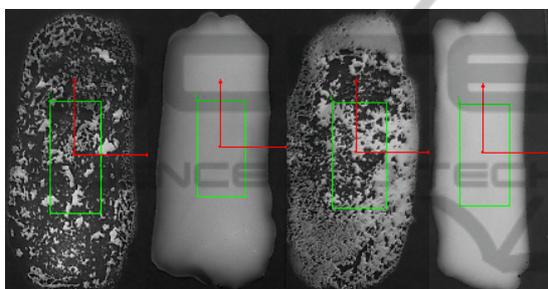


Figure 11: Result of applying the Quantify function.

4 SYSTEM PROTOTYPE

A prototype system that automatically determines the human blood type, based on the plate test procedure, was designed (Figure 12).



Figure 12: Prototype developed.

The blood and the four serums drops are manually placed in the plates inserted in the mobile drawer, actuated by a DC motor. In the first blade, it

is placed reagent anti-A, in the second reagent anti-B, in the third anti-AB reagent and finally in the fourth, reagent anti-D, in accordance to the testing procedure previously described.

The system is switched on and the drawer moves to the mixing area, where the mixture blood/serum is promoted in each blade. It must be referred that there is no contamination between the four samples. Next, the drawer moves to the image capture zone. A step motor moves a *Glossy 5* Mega pixels webcam along the samples for capturing the four images. The images are saved for future analysis. The system is controlled by Arduino microcontroller (<http://www.arduino.cc/>).

5 RESULTS

The proposed methodology was tested with several standard blood types samples. In this section, are presented the results obtained when applying the image processing methodology to four blood/serum samples of a donor blood type, Figure 13.

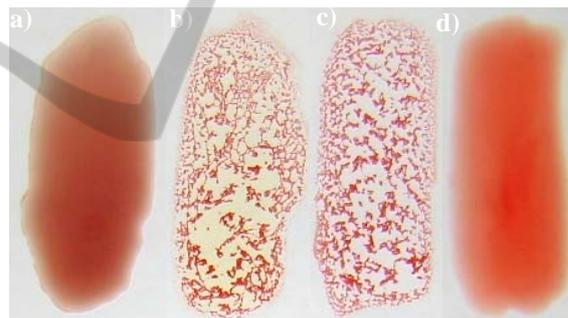


Figure 13: Blood/serum samples. (a) Serum Anti-A. (b) Serum Anti-B. (c) Serum Anti-AB. (d) Serum Anti-D.

Figure 14 shows the final images obtained with the application of image processing techniques to the original sample images of Figure 13. The corresponding quantification is presented in Table 1.

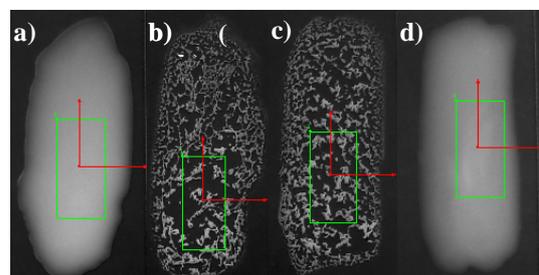


Figure 14: Image resulting from application of the image processing techniques developed, to images of Figure 13.

Table 1: Results of quantification of images of Figure 14.

Fig.	Area	Mean Value	Standard Variation	Min Value	Max Value
(a)	0,9	162,1	7,7	137,0	181,0
(b)	0,8	56,9	45,1	5,0	201,0
(c)	0,9	62,2	42,7	9,0	199,0
(d)	0,8	146,0	8,8	109,0	173,0

Analyzing Figure 14, it is observed that the agglutination occurred in images (b) and (c), but not in images (a) and (d). By correlating this information with the information from Table 1, it is observed that the standard deviation, in the images (b) and (c) is well above 16, while in the images (a) and (d), the standard deviation is less than 16. The value 16 for the standard deviation is a limit established for determining the occurrence of agglutination in a sample. This value was established from trial and error. Thus, it is observed that when agglutination occurs, the standard deviation is much higher than the one obtained when agglutination does not occur, allowing thus identifying the occurrence of agglutination and consequently identifying the blood type of a patient. In this example, given that the agglutination has occurred in the presence of serum anti-B (Figure 14-b) and in the presence of serum anti-AB (Figure 14-d), the blood type presented is B negative. Note that the agglutination occurs in the presence of serum anti-AB, because the patient had B antigens in their red blood cells that agglutinated in the presence of anti-B antibodies existing in serum. However, the serum anti-AB, also had anti-A antibodies, that have not reacted because the patient did not have A antigens, justifying the slightly less value of agglutination (42.7), compared to that obtained with serum anti-B (45.1).

4 CONCLUSIONS AND FUTURE WORK

With the proposed system, based on image processing techniques, it is possible to automatically determine the blood type of a patient, by detecting the occurrence of blood agglutination. This approach allows the determination of blood type of a patient, safely, and it can be used in emergency situations as the results are obtained within a short time (2 minutes). The PC hardware requisites of the prototype are minimal and IMAQ software package allows the correct and fast determination of blood types.

In future, we intend to optimize the prototype, reducing human intervention in the procedures. Another objective is to ensure that the developed device is portable, allowing its use near the patient, avoiding travel to the lab that only cause more time consuming.

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