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Research Article

Efficient Segmentation of Lymphoblast in Acute Lymphocytic Leukemia

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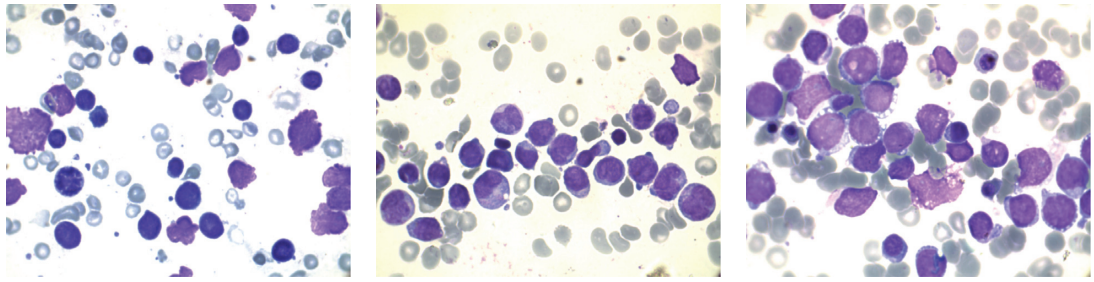
Microscopic examination of peripheral blood smears and bone marrow is the preliminary step for the diagnosis of several life-threatening diseases. Acute lymphocytic leukemia (ALL) is the most common disease in children that also needs an early diagnosis for on-time treatment as it spreads rapidly in the blood and forms immature lymphocytes. This might cause death in some weeks if left untreated. Manual methods in clinical laboratory being applied for the diagnosis of these diseases are inefficient and expensive, and the results are less accurate. A computer-aided system is the need of the day in which the most important step is segmenting the region of interest in blood or bone marrow for the detection and cure of the diseases which is the most challenging task. This study aims to propose a simple threshold-based segmentation technique by processing the S component of the HSV color space to segment the lymphoblasts in the bone marrow images of ALL patients. The technique was applied to 230 RGB bone marrow images having all the three types of ALL, i.e., L1, L2, and L3 resulted in the overall accuracy of 96.8%.

1. Introduction

Blood and its components are the key substances for the microscopic examination of most life threat diseases such as leukemia, HIV, anemia, tumor, cancer, and thalassemia [1–5]. Leukemia is the type of cancer starting in bone marrow from immature lymphocytes called the lymphoblasts and then spreads through the blood in all over the body. The on-time treatment has a good chance of recovery for the patient. Lymphoblasts are mainly present in the bone marrow or peripheral blood slides of a patient having acute lymphoblastic leukemia [6–8]. According to French American British (FAB) classification, ALL is subclassified as L1, L2, and L3 on the basis of morphological structures exhibited in Figure 1. L1 type consists of nucleus and may or may not have a basophilic cytoplasm and have a small size, L2 having irregular nucleus and having a cytoplasm. L3 is large in size and have vacuoles in the cytoplasm. To diagnose ALL, it is totally dependent on the detection and morphological examination of blast cells in bone marrow and peripheral blood images. This process is performed by the hematologists' manually in clinical laboratories, which is a slow process, and it also depends on the experience of the laboratory expert and his physical condition. Hence, to overcome the limitations of these manual processes, fast and automated system is the need for the diagnosis of these lives in danger diseases. For the designing of this automated system, the most essential part is the segmentation of the region of interest, and it is the most difficult task to be done as the whole system depends on it. The aim of this study is to segment the blasts from bone marrow images and to introduce an effective segmentation approach. This can



(a) (b) (c)

Figure 1: Three types of lymphoblast in acute lymphoblastic leukemia. (a) L1 blasts. (b) L2 blasts. (c) L3 blasts.

help the experts in the designing of the whole diagnostic system.

The further paper is organized into four main sections: Section 2 explores related work, Section 3 presents materials and methods reported in the paper, and Section 4 exhibits experimental results and discussion. Finally, Section 5 presents the conclusion.

2. Related Studies

There is no simple technique for the segmentation process as most of the researchers addressed this problem and reported their techniques in state of the art [5, 9]. Sadeghian et al. [10] proposed a segmentation method for ALL blast in peripheral blood images for which canny edge detection algorithm was used with gradient vector flow GVF for the detection of the nucleus and then zack threshold was applied for cytoplasm. However, this method is applied to a single WBC image. Osowski et al. [11] recognized myoblasts in bone marrow by segmenting it and applied watershed transformation algorithm, but due to the crowded marrow, it resulted in oversegmentation. Madhloom et al. [12] proposed a method in which they used contrast stretching and arithmetic for the localization and segmenting white blood cells with 95% accuracy; however, the method was used for the nucleus component, and that's why this is not identifying the leukemia cells as it required nucleus as well as the cytoplasm. In this study, we have proposed a method based on thresholding with the HSV color model, which could accurately segment the lymphoblasts for the detection of ALL in microscopic bone marrow images.

Tabrizi et al. [13] proposed snake contour for the segmentation of leukocytes; LVO, PCA algorithms, and SVM classifier is used for the identification. Mohamed and Far [14] segmentation was intensity based on Gram–Schmidt orthogonalization. Abbas and Mohamad [8] proposed a convolution mask along with Otsu method for the segmentation of nuclei of the lymphocytes for the detection of leukemia having the same limitation as faced by Madloom et al. [12] to detect leukemia nucleus, cytoplasm is needed. Mohapatra et al. [15] separated the interested region using *K*-means clustering and then used shadowed C-means (CSM) on the CIELAB color model for the segmentation of nuclei and cytoplasm of the leukocytes and then used an ensemble of classifiers for the classification. Adollah et al. [16] reviewed different methods for the segmentation of leukocytes in which different authors addressed the problem with different techniques, i.e., Otsu threshold and circular histogram were used for the segmentation of WBCs, entropy with higher order is used as a feature, gray level threshold, filters with color matching, different morphological operators, shape information of binarizing and generating maximum intensity, watershed with seeds, and combining filters with scale-space were used for the segmentation purpose.

Comaniciu and Meer [17] recommend an image-guided decision support (IGDS) for the classification of different lymphomas and uses mean shift algorithm for the accurate segmentation; however, the system is not checked for acute leukemia. Abbas and Dzulkifli Mohamad [8] applied 2∗2/6 convolution mask for repressing high values of RGB, and then Otsu method is applied to obtain nuclei, small areas were removed, and nuclei have been dilated for the required results of segmenting nuclei and detecting leukemia resulting in accuracy of 96.5%.

Bhattacharjee and Saini [18] used a watershed algorithm for the segmentation of blast cells to detect ALL, and the segmentation process was followed with morphological operators, binary search tree, and Gaussian mixture model to classify the blasts. Pan et al. [19] employed extreme learning machine to segment the leukocytes on the basis of gradient threshold and entropy for the segmentation of multicolor objects on the HIS color model with Otsu's thresholding to properly segment leukocytes. Abbas et al. [6] applied a convolution filter of 3×3 on the red channel of the RGB image and then converted that image into the binary mask and on the analysis of the histogram, and after that, both the binary images were added which results in nuclei of leukocytes. Amin et al. [20] used *K*-means clustering to segment the lymphoblasts cells from the blood images. Geometric and statistical features were employed to classify that lymphoblast into subtypes of ALL using support vector machine (SVM).

Dhanachandra et al. [21] enhanced the contrast of the images for which the author used partial contrast stretching, then used subtractive clustering method followed by *K*-means clustering and calculating potential for each pixel, then finds the center cluster using Euclidean distance, and then reshapes the image. For noise removal, they use a median filter. Rawat et al. [22] proposed histogram equalization followed by global threshold and morphological

opening to segment the nucleus of the blast cell and finally subtracted an image from the preprocessed image to obtain cytoplasm. To classify the images, geometrical, statistical, and chromatic features were extracted and fed to classifiers PCA-KNN, PCA-PNN, PCA-SVM, and PCA-ANFIS in hierarchical; this took a long time to classify the images. Nighat Bibi et al. [23] used dense convolution neural network and residual CNN with cloud framework for the detection and classification of all types of leukemia.

3. Materials and Methods

The main purpose of the segmentation process is to collect the lymphoblasts from the slides containing all the blood components. It will help in the detection and classification of acute leukemias [7]. The original images obtained from digital camera microscope are in the RGB color model. However, for speedy and accurate segmentation, it is converted to the HSV color model to process the S component.

3.1. Image Database. Images for this study were taken in the department of hematology lab at Saidu Medical College, Swat, KPK, Pakistan, using Euromax digital camera microscope. The slides were stained with Giemsa under the supervision of Dr. Amreek Lal, and the images were taken with 100x lens and oil immersion. The total images of $L1$ type 102, $L2$ type 120, $L3$ type 30 were kept in different folders classified according to (FAB) with the help of concerned hematologist.

3.2. Proposed Methodology. A simple method for the segmentation of lymphoblasts is proposed. The images were first converted to the HSV color model, and then the S component is processed further to achieve good segmentation results. There are the subtypes of acute lymphoblastic leukemia according to the French American British classification, i.e., $L1$, $L2$, and $L3$ having different morphologies [20]. So, we tested different threshold values for each class according to the morphological structures of the lymphoblast. In the S component image, we found the maximum threshold value to find out the value (T_{rh} value) in which the blast could only segment, while the rest of the objects should be removed.

$$\mathrm{TT} = \mathrm{Max}\left(\mathrm{Max}\left(S\left(i,\ j\right)\right)\right) - \mathrm{T}_{rh}. \quad (1)$$

Different values of T_{rh} were checked with equation (1) for all classes and then take that value on which the lymphoblasts were segmented accurately. After this, a MATLAB command Imfill holes were applied to all the images to restore the lost information and then find out a seeded value of RGB color of the blast in the original input image to convert back the image into its original RGB color. The proposed research framework is exhibited in Figure 2.

3.3. Pseudocode. The proposed algorithm processed the image and segmented lymphoblast according to the following pseudocode:

(i) Read the image img(i, j) from the directory in RGB color space

(ii) Convert RGB image img(i, j)to HSV color space img_seg(i, j) for further processing

(iii) Get the S component of the HSV color model, $S(i, j)$ as they have more information about blasts and segmentation occur easily

(iv) Find out the maximum threshold in $S(i, j)$ and then subtract that value on which other small objects remove and only the lymphoblasts remain

(v) If $S(i, j)$ is greater or equal to the threshold value, find out in the previous step and then give the value 1, otherwise 0

(vi) For the lost information function, Imfill holes are used to fill the gaps and information

(vii) Wherever the value is 1, convert to its original color in RGB img(i, j)

4. Experimental Results

Different T_{rh} values were checked for the accurate segmentation in different experiments. Firstly, the value for L1 blasts was kept 0.40 but could not produce efficient results and then changed to 0.45 in which it is segmented accurately over 102 images. It has an irregular shape nucleus and in rare cases have a cytoplasm. For L2 blast, due to the morphology of having cytoplasm, we checked the value 0.47 and 0.48, but the results were not satisfactory. On $\mathrm{T_{rh}}$ value 0.50, it produced good segmentation results. This was applied to 120 images having L2 morphology. L3 blasts are large in size and having vacuoles in the cytoplasm part of the cells for that the value was set higher than that of L2 0.52 to segment the blasts with vacuoles to turn out satisfactory results. After hole filling is applied to fill the gaps which occurred during the whole process, results are exhibited in Figures 3–5 for ALL subtypes L1, L2, and L3, respectively.

The segmentation results are shown in Figures 3–5 for lymphoblasts of types L1, L2, and L3, respectively, giving efficient results as compared to other methods. Performance accuracy of the technique used in our study is shown in Figure 6.

4.1. Performance Analysis. The proposed technique was also compared in terms of segmentation accuracy for the evaluation with three different existing methods which is shown in Figure 7. It is used for the segmentation of five types of white blood cells, and those methods were proposed by Madloom et al. [12]; Tabrizi et al. [13]; and Mohamed and far [14] presented in Figure 7. The only limitation in this study is that sometimes it results in oversegmentation and sometimes the very important information is missing especially in the case of L3 subtype of the ALL which affects the overall accuracy. Further segmentation results of all the three types of lymphoblasts are shown in Figure 8. Finally Table 1 presents accuracy for each subtype. The algorithms were also checked with ground-truth data, and the result is shown in Table 2.

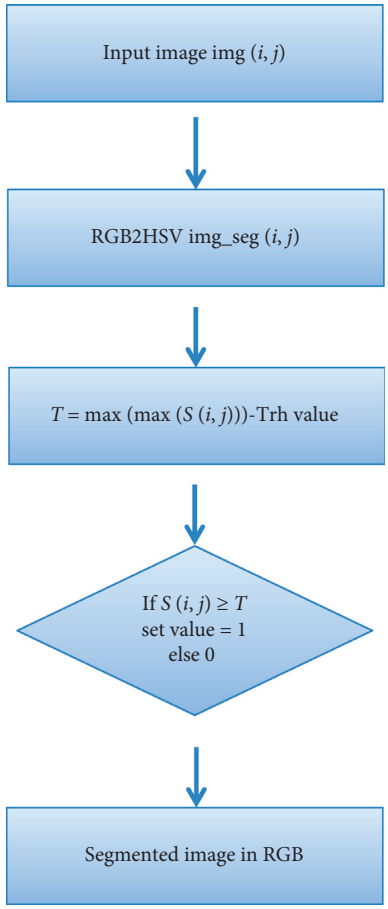
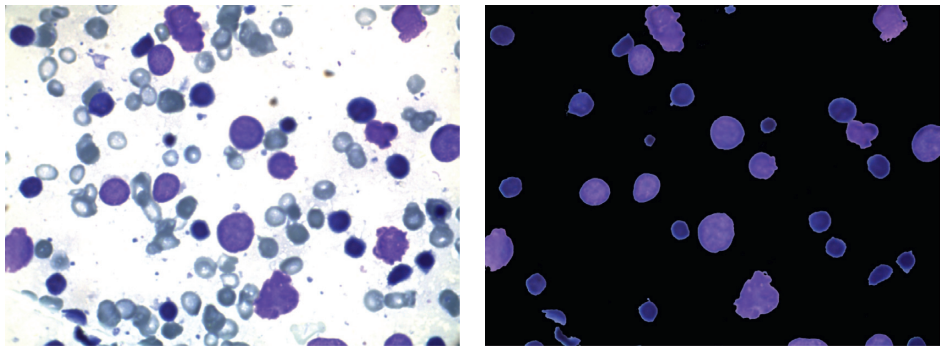
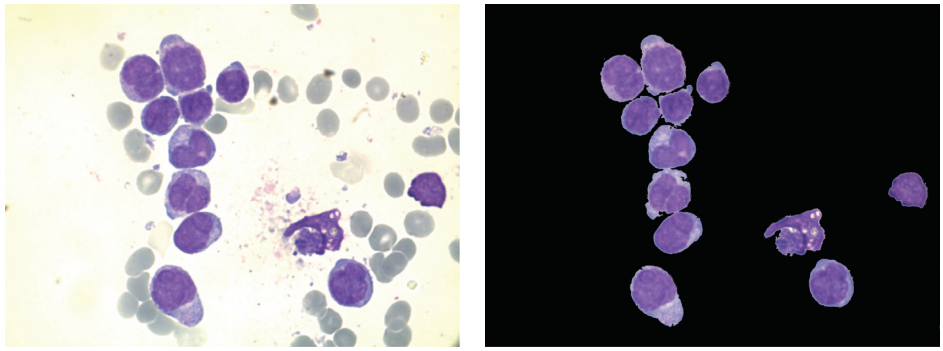


Figure 2: Proposed research framework.



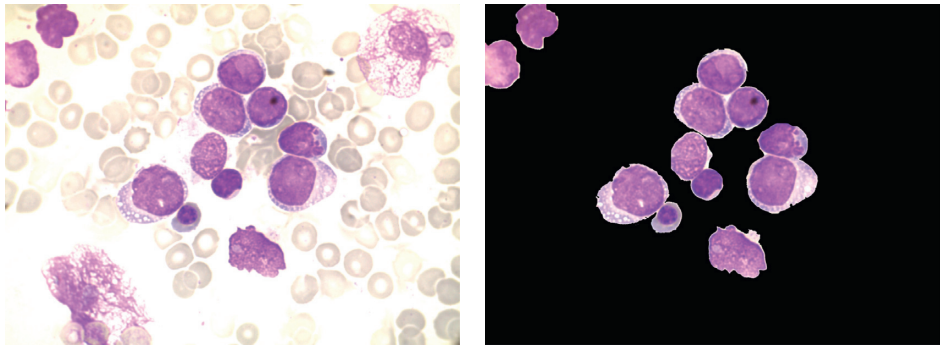
(a) (b)

Figure 3: ALL subtype L1. (a) Original image. (b) Segmented lymphoblast.



(a) (b)

Figure 4: ALL subtype L2. (a) Original image. (b) Segmented lymphoblast.



(a) (b)

Figure 5: ALL subtype L3. (a) Original image. (b) L3 segmented lymphoblast.

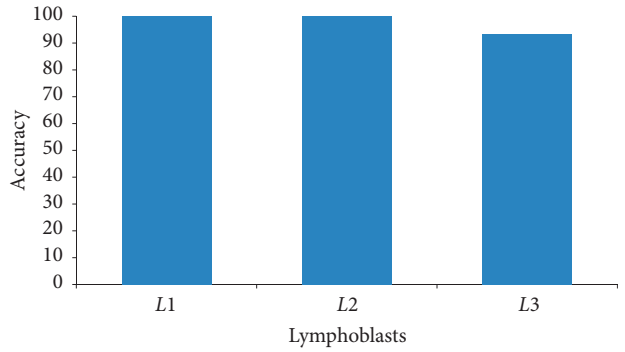


Figure 6: Performance accuracy of the proposed system.

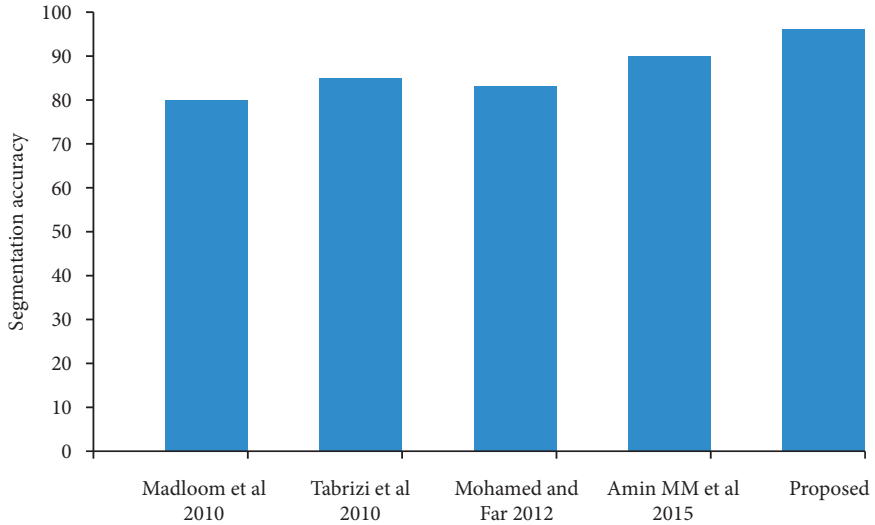
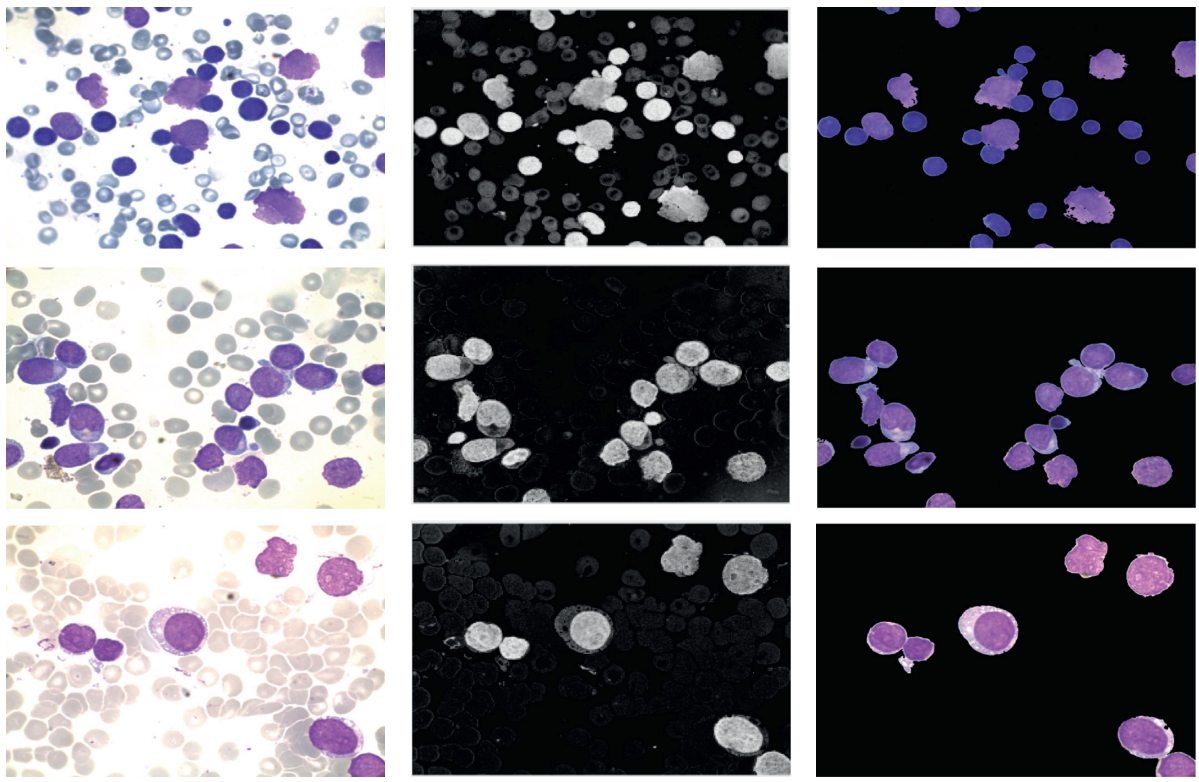


Figure 7: Performance evaluation of the proposed method with different techniques in state of art.



(a) (b) (c)

Figure 8: Experimental results. (a) Original images. (b) *S* component of HSV color space. (c) Segmented images.

Table 1: Accuracy for each subtype.

ALL subtype	*L*1	*L*2	*L*3
Total images	102	120	30
Accurate segmented	102/102	120/120	28/30
Accuracy	100%	100%	93.3%

Table 2: Proposed method evaluation with ground-truth data.

Lymphoblast type	Recall	Precision	F-measure
L1	0.9622	0.9811	0.9703211
L2	0.9501	0.9712	0.96010211
L3	0.9211	0.9322	0.9313221

5. Conclusion

This paper has presented an effective approach to segment lymphoblast in a robust and accurate manner for the detection of leukemia by using simple threshold-based method with the HSV color model and attained an overall accuracy of 96.8%. The proposed segmentation technique is easy to implement and then applied to 230 RGB images of bone marrow slides images of ALL patients. The segmentation accuracy for the subtypes L1 and L2 was 100%; for the third subtype L3, the accuracy was 93.3% because of the vacuoles present in the cytoplasm area. Furthermore, the method is compared for performance evaluation with three other existing methods in terms of accuracy. We can also use the proposed method in general for the segmentation of blast cells in other types of leukemia. This is witnessed from our experimental results that the proposed method in this paper is more helpful in the segmentation of lymphoblasts specially for ALL. For future work, segmentation accuracy for L3 subtype of ALL could be improved and limitations will be covered.

Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Additional Points

Summary. Acute lymphocytic leukemia (ALL) is a crucial disease, and manual methods are inefficient and expensive. Automated system is proposed to identify ROI in blood/marrow for the detection and cure of the disease by processing *S* component of HSV of lymphoblast.

Conflicts of Interest

The authors declare no conflicts of interest.

Acknowledgments

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