

Comparison of Segmentation Algorithms for Leukemia Classification

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Abstract: Leukemia is a deadly cancer that results from the proliferation of non-differentiated white blood cells in blood as compared to the other two types of cells, i.e., red blood cells and platelets. These cells are known as blasts cells which overcrowd other cells rendering those cells as inefficient in their functions and are themselves non-functional. This paper presents a comparative study of four different segmentation techniques on the images of peripheral blood smear and the classification of these images into diseased and healthy cells using the SVM classifier. The best result was obtained by a custom threshold method of segmentation with a classification accuracy of 96.89%.

Keywords: Acute Leukemia, Machine Learning, Support Vector Machine. Image Processing, Image Segmentation

1 Introduction

Human Blood mainly consists of three types of cells, i.e., white blood cells(WBC), red blood cells(RBC) and platelets. RBCs play an essential role in the transportation of oxygen to all body organs and the removal of carbon dioxide through the blood. White blood cells, on the other hand, are the fighter cells of our body which help our body to fight infections, whereas platelets help in blood coagulation[1]–[3][4]. All these types of cells are developed from stem cells produced in the bone marrow present in bones, via a process known as hematopoiesis. Leukemia, also known as ‘liquid cancer’ or ‘cancer of blood’ may result due to exposure to radiations, certain chemicals or due to genetic history[5]. As per American Cancer Society statistics, 60,530 new leukemia cases are estimated in 2020 and estimated deaths are projected to be 23,100. Leukemia is the seventh leading cause of cancer death in USA as per the National Cancer Institute. It is preliminarily diagnosed by the complete blood count (CBC) clinical blood test and is caused by the uncontrolled accumulation of partially developed leukocytes or white blood cells, also known as blast cells. Based on the progression of disease, Leukemia may be categorized as acute leukemia, characterized by fast progression and speedy deterioration of patient and chronic leukemia, characterized by slow progression of disease. All components of blood originate either from myeloid progenitor cells or lymphoid progenitor cells. Hence Leukemia may be further categorized on the basis of origin of lymphoblasts and the speed of progression into various categories as shown in figure-1. Though the disease is diagnosed by a preliminary assessment of blood components, the final diagnosis is dependent on biopsy of bone marrow, cytogenetics, immunophenotyping, or PET scan tests. Analyzing blood smear or bone marrow biopsy under the microscope is very time consuming, and the results chiefly depend on the expertise of the hematopathologists.[6],[7], which calls the need to automate the process of diagnosis[8][9]. Various researchers from the field of medicine, computer science, and hematopathologists are working together to develop a sound model of leukemia diagnosis[10].

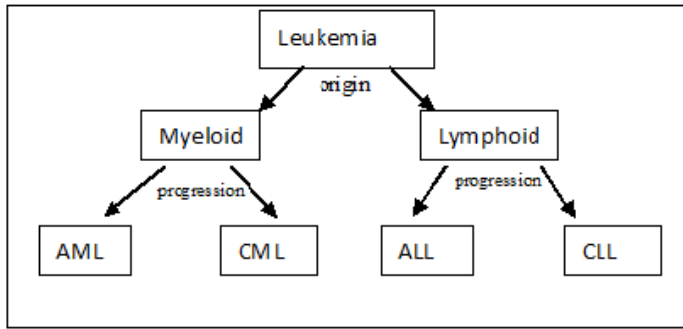


Figure 1: Classification of Leukemia

Image processing techniques and machine learning have proved to be a boon for this task. Researchers have tried and tested various methods of classification to the features extracted from the images using image processing techniques[11][12]. The images of blood smears are first captured, preprocessed for various types of enhancements, and segmented to find the region of interest(ROI)[13]–[15][16]. The features extraction and selection are then carried out, which are then fed into machine learning-based classifiers for classification into healthy or diseased. The classification can also be applied to identify different types of leukemia, i.e., acute or chronic, AML or ALL, or further categories of AML or ALL, etc.[17], [18][19]–[21]. Various machine learning techniques have been used for classification in the literature e.g., SVM[8], [22]–[29], KNN[30], [31], decision tree[6], [14], [21], [32]–[35] and random forests[32], [36]–[40] to name a few.

The paper is further described in various following sections. Section 2 gives an overview of the proposed model. Section 3 provides the segmentation techniques used; section 3 gives a brief of the classification method used, and section 4 describes the results and its analysis. Finally, the concluding remarks are given in section 5.

The proposed Model

The paper presents the study of four different segmentations on classification, as shown in figure 2.

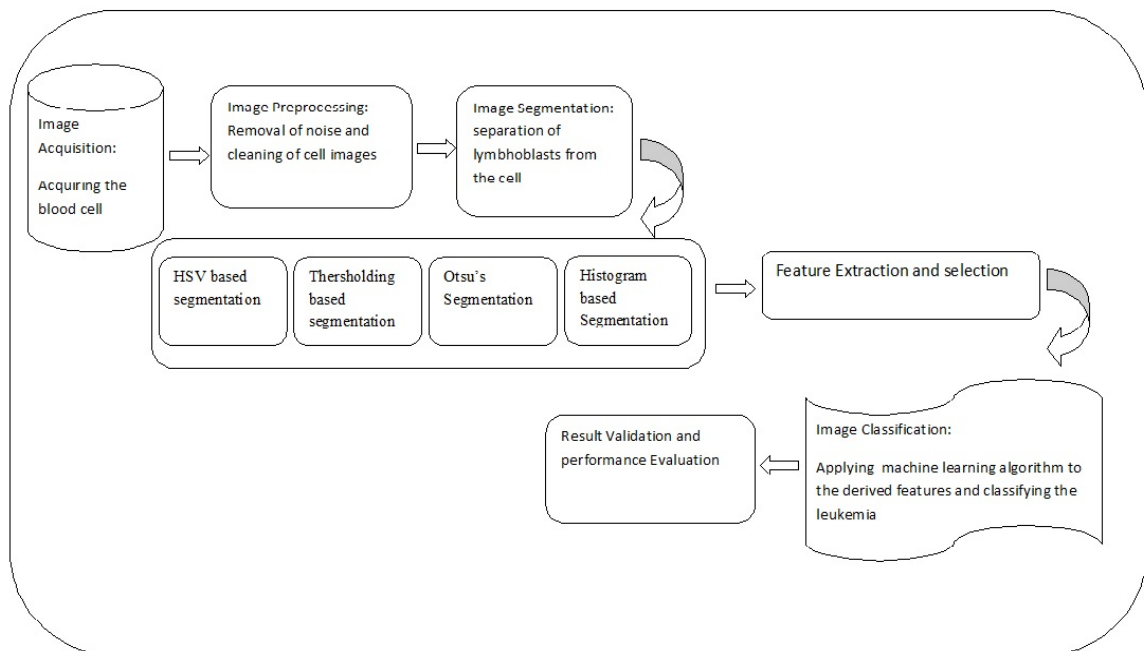


Figure 2: Research Framework

As described in the literature, image processing techniques include image acquisition, image enhancement, image segmentation, feature extraction, and classification.

Step 1: Acquiring Dataset

The study of leukemia has been affected by the lack of availability of public datasets [14], [28][41][13], [15]. The only dataset which is in the public domain and is available on request is ALL-IDB from Fabio Scotti, R.D. Labatti, and Vincenzo Piuri, which has been extensively used by the researchers in this domain. [[42]–[44]. The dataset consists of two datasets ALL-IDB1 and ALL-IDB2. ALL-IDB1 consists of 108 blood smear images collected during September 2005. It comprises of 49 ALL affected images from leukemic patients while 59 images from healthy people. On the other hand, ALL-IDB2 consists of the segmented area from both normal and diseased cell images from the ALL-IDB1 dataset and consists of 260 images of segmented leukocytes or lymphoblasts having fifty percent each [47][48].

Step 2: Image Enhancements

Images are enhanced to remove the noise and get better results. Various types of enhancements are done to ALL-IDB 1 images like RGB to gray conversion, histogram stretching, separating HSV components, etc.

Step 3: Image segmentation

The enhanced images are then segmented using:

- a) **Histogram stretching based segmentation**
- b) **Manual Thresholding**
- c) **HSV based Segmentation**
- d) **Otsu's Segmentation**

a). Histogram based segmentation

Preprocessing :

- i) Image converted to greyscale (E1)
- ii) Image enhancement is performed using contrast stretching (E2)
- iii) Histogram equalization is performed on contrast stretched image (E3)

Segmentation:

- i) Added image (S1) = E2 + E3
- ii) Subtracted Image (S2) = E2 – E3
- iii) Background Removed Image = S1 + S2

The result of histogram-based segmentation is given below in figure 3, and figure 4. The result of manual thresholding, which was set at 80, is depicted in figure 5. The result of automatic Otsu's segmentation is illustrated in figure 6, while figure 7 shows the results of HSV based segmentation.

b) Manual Thresholding

Pixel intensity values were observed with Matlab inbuilt tool, and then several threshold values were tried and tested out of which pixels in the image with intensity greater than 80 were assigned a pixel value equal to 1.

c) HSV based segmentation

Image is converted from RGB (Red, Green, Blue) to HSV color model wherein H stands for Hue (color) component, S for Saturation, i.e., shade or amount of gray, and V stands for brightness value. S component of HSV is extracted from the image as it gives the structural information of the leucocyte nucleus [45], [46].

Images and their histograms

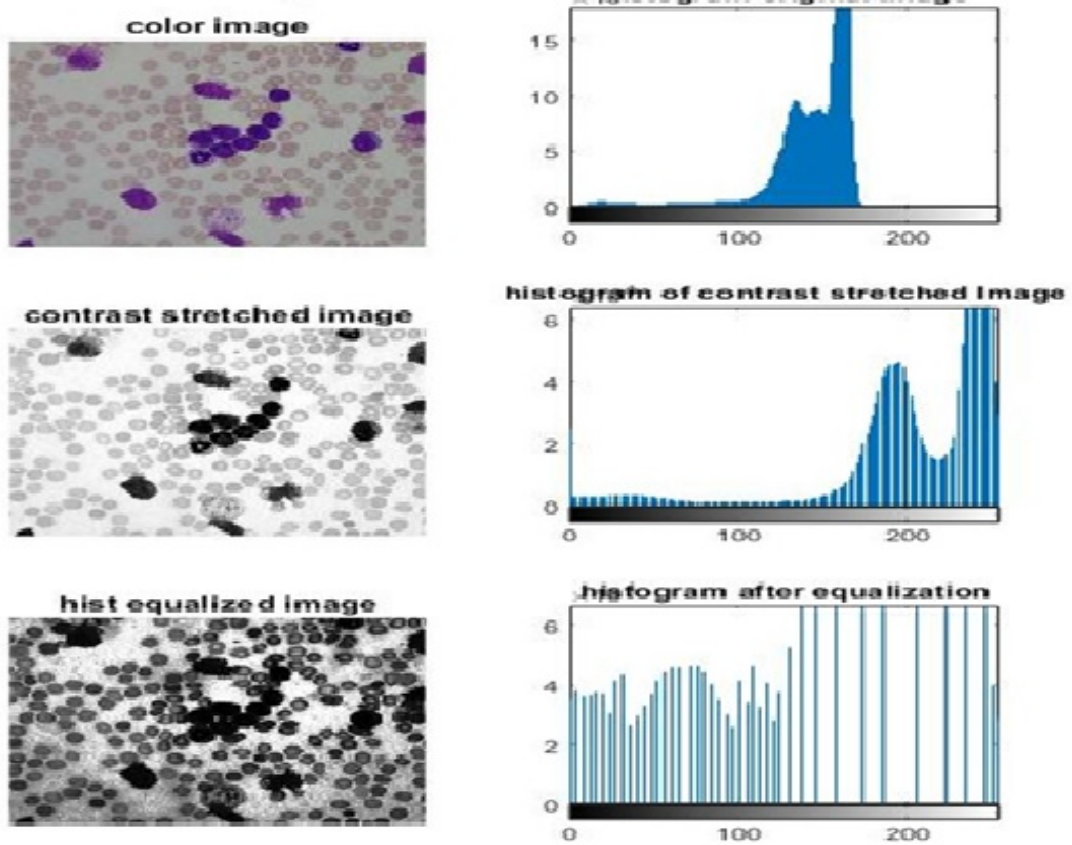


Figure 3: Histogram of images

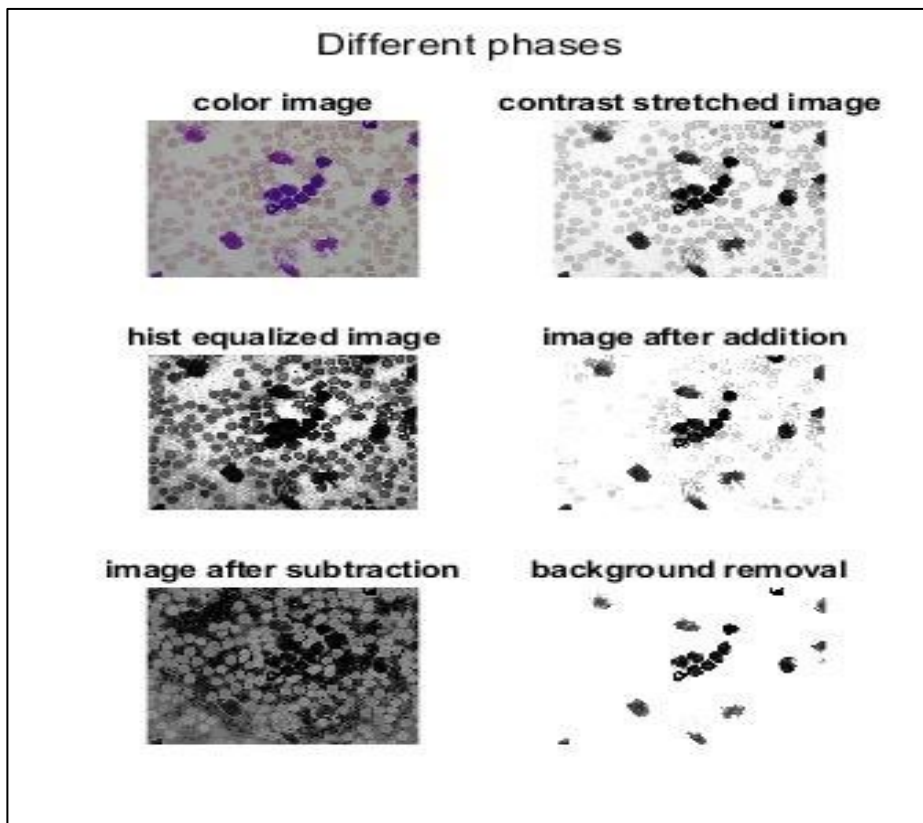


Figure 4: Histogram based Segmentation

d) Otsu's Segmentation

The Otsu's thresholding method proceeds by iterating through all the possible threshold values, and measures the spread of the pixel levels along each side of the threshold to find whether the pixels fall in foreground or background. A threshold value having the minimum value for the sum of the foreground and the background spreads is thus found.

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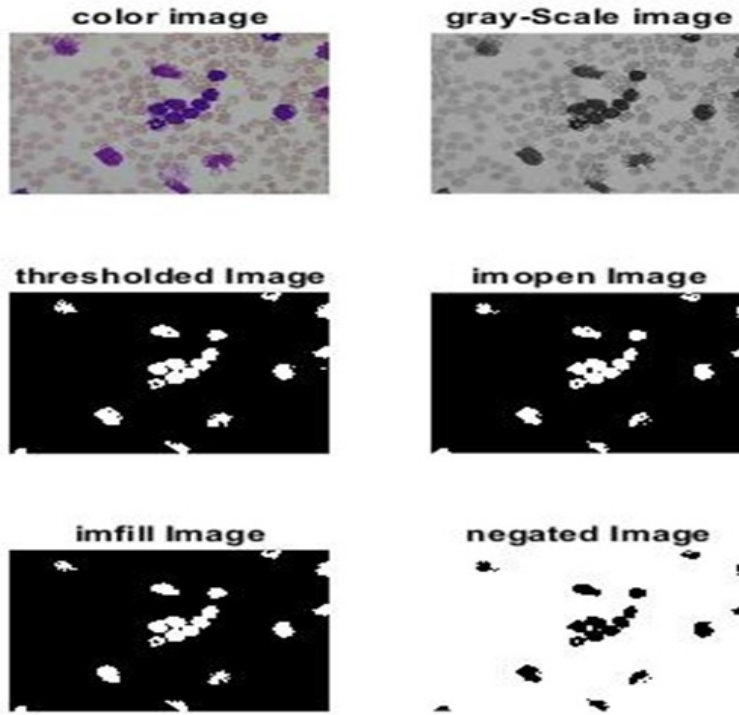


Figure 5: myThresh Segmentation

Step: 4 Feature Extraction:

After successful segmentation, the connected components are found, and for each connected component, the following morphological features are extracted from each blood cell image. The following features are then averaged to find the mean features which are then fed into the SVM classifier.

| | | | | |
|--------------|-------------|------------|-------------|----------------|
| Area | perimeters | majorAxis | minorAxis | eccentricities |
| orientations | convexAreas | FilledArea | Eq_Diameter | solidity |
| extent | Roundness | | | |

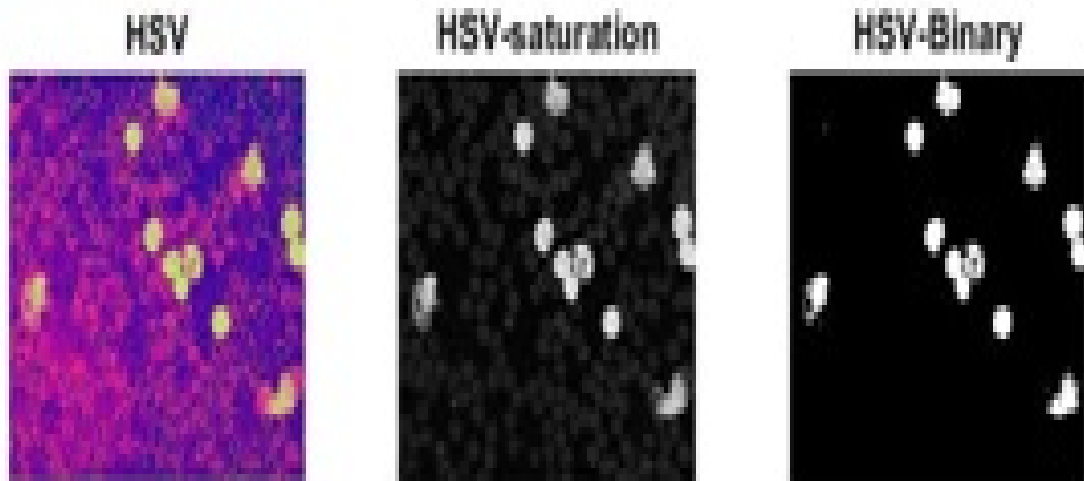


Figure 6: HSV based segmentation

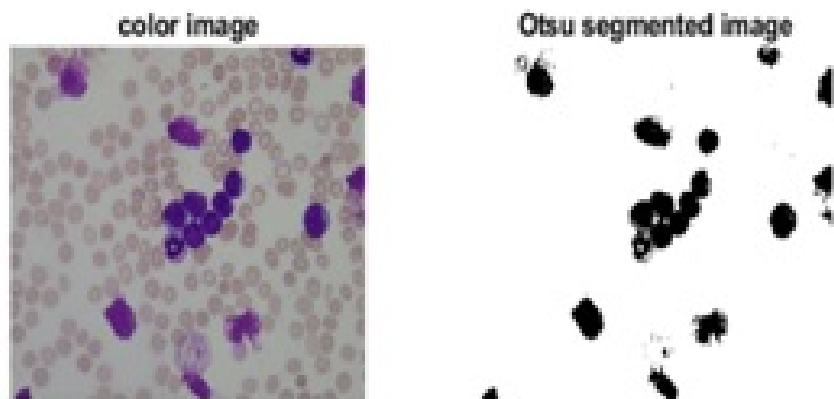
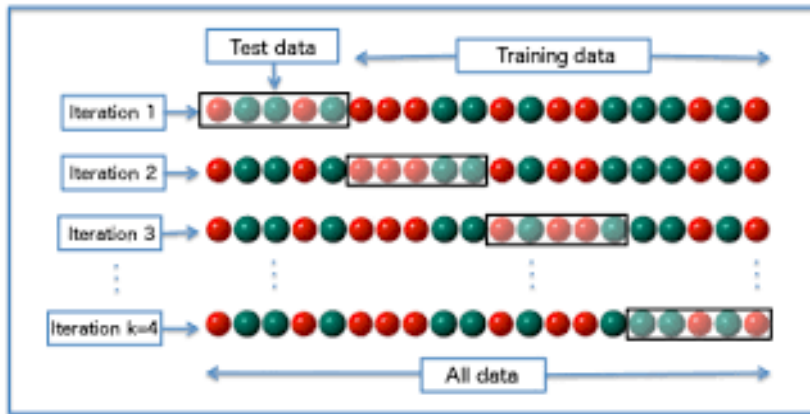


Figure 7: Otsu's Segmentation

3. Classification

The mean features thus obtained are further fed into the SVM classifier. We implemented the classification using a two-class SVM classifier with a radial basis kernel. SVM has been extensively used by researchers to classify the blood smear images. The input images are divided into training image data and testing image data in various ratios, i.e. (70:30), (80:20), and (75:25), etc. The SVM model is trained using the training data. K-fold cross-validation is used with $k=10$ to avoid over-fitting and over-training.

In this method, the training data is divided into K equal-sized folds or sets. In each of the K -iteration, one set or fold is used for validation, and rest $K-1$ folds are used for training, as shown in figure 8.



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Figure 8: Cross-Validation

Image courtesy- [https://en.wikipedia.org/wiki/Cross-validation_\(statistics\)](https://en.wikipedia.org/wiki/Cross-validation_(statistics))

4. Results and Discussion:

The SVM classification results for various segmentation algorithms are summarized in table 1 given below:

Table 1: SVM Classification Results

| S.No | Segmentation | Accuracy |
|------|---------------|----------|
| 1 | HSV | 88.9% |
| 2 | MyThreshold | 96.89% |
| 3 | Otsu | 86.8% |
| 4 | Hist_Contrast | 86.95% |

The results demonstrate that the same SVM gives different results when applied to the images segmented by various techniques. Thus it directly supports the effectiveness of segmentation methods and its correctness. The better the segmentation, the better will be the classification. The experiment was conducted with a small set of segmentation methods. The same experiment may be performed with a broader set of segmentation techniques. The given research demonstrates that the feature extraction and selection also depend on the correctness of segmentation. It was found that the threshold of 80, which was manually selected to divide the intensity values, gives the best result among other segmentation i.e. 96.89%

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