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# An Approach to Detect Acute Myelogenous Leukemia in Blood Microscopic Images

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***Abstract:*** *Acute Myelogenous leukemia (AML) is a specific kind of cancer where the blood cells, bone marrow get affected. This is usually common among adults with an average age of 65 years. The current method for the detection of Acute Myelogenous leukemia is inefficient, since it needs the manual examination of blood smear. Its accuracy depends on the operator's ability and it is time consuming. This paper presents a simple approach that automatically detects AML cells in the blood smear. The proposed approach mainly comprises of preprocessing where the noise contents are removed and the conversion of RGB images into CIELAB color space. This step is followed by segmentation which extracts the important information from an input image. Classification and validation are performed based on feature extraction.*

***Keywords:*** *Acute Myelogenous Leukemia (AML), Classification, Segmentation, Feature extraction*.

## I. Introduction

Acute Myelogenous Leukemia is a cancer of the myeloid line of blood cells, characterized by the rapid growth of abnormal white blood cells that accumulate in the bone marrow and interfere with the production of normal blood cells [1].AML is the most common acute leukemia affecting adults. Although AML is a relatively rare disease, accounting for roughly 1.2% of cancer deaths in the United States, its incidence is expected to increase as the population ages.

The symptoms of AML are caused by replacement of normal bone marrow with leukemic cells, which causes a drop in red blood cells, platelets, and normal white blood cells. These symptoms include fatigue, shortness of breath, easy bruising and bleeding, and increased risk of infection. Several risk factors and chromosomal abnormalities have been identified, but the specific cause is not clear. As an acute leukemia, AML progresses rapidly and is typically fatal within weeks or months if left untreated [2].

AML has several subtypes: treatment and prognosis vary among subtypes. AML is cured in 35-40% of people less than 60 years old. Older people who are not able to withstand intensive chemotherapy have an average survival of 5-10 months. AML is treated initially with chemotherapy aimed at inducing a remission; patients may go on to receive additional chemotherapy. Recent research into the genetics of AML has resulted in the availability of tests that can predict which drug or drugs may work best for a particular patient, as well as how long that patient is likely to survive. Most signs and symptoms of AML are caused by the replacement of normal blood cells with the leukemic cells. A lack of normal white

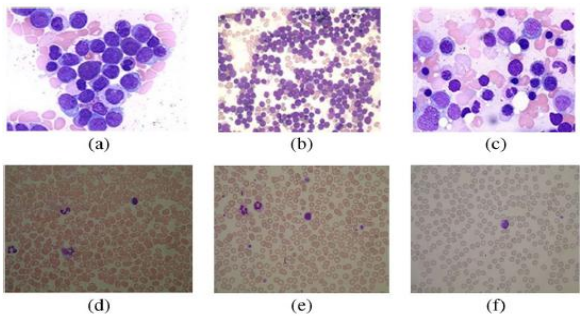


Fig. 1. (a)-(c) AML cells. (d)-(f) Healthy cells from non AML patients.

blood cell production makes the patient susceptible to infections, while the leukemic cells themselves are derived from white blood cell precursors; they have no infection-fighting capacity. A drop in red blood cell count can cause fatigue, plateness, and shortness of breath. A lack of platelets can lead to easy bruising or bleeding with minor trauma. Fig. 1 shows images from AML and non AML patients.

Confusion in diagnostic can occurs due to the similarities in the signs by other disorders [13]. Digital imaging techniques have been used in the past, which helps to analyze the cells accurately. But there are several complications in extracting data from the WBCs. The proposed system helps to automatically detect the AML cells in the blood smear.

## II. Related Works

Many attempts have been made for classifying AML cells from the blood smear [1-10]. Madhloom [11] performed some arithmetic operations and threshold operations for finding the white nuclei. The challenge he faced in developing the system is the selection of the thresholding method. But the technique used in this system is not providing efficient result for the segmentation of AML cells. Kovalev [12] developed a system to classify five types of leucocytes from the blood image. But the classification is done only for the subimages.The work in [13] explains an unsupervised segmentation algorithm for the separation of white blood cells. Nallaperumal and Krishnaveni [14] presented a watershed segmentation algorithm for the separation of the nucleus from the surrounding cytoplasm.

A common drawback found in all the system is that they classify only subimages. But in the proposed system classification is done for the entire image. And here the classification is done with a linear support vector machine. The result is then compared with the existing models.

## III. Process Overview

The overall system is depicted in Fig. 2. The overview of the system shows the sequence of steps that are to be followed for the efficient classification of acute myelogenous leukemia. The first step is the preprocessing step which will remove the unwanted noise contents present in the input image. It also includes the conversion of RGB images into the L*a*b color space image. This step is followed by the segmentation technique, which uses k-means clustering. After that feature extraction based on which classification and validations are done.

## IV. Preprocessing

*Image Acquisition:* American Society of Hematology *(ASH)* is providing a web based image library that contains growing collection of AML images. We are accessing the images of ASH as it provides high quality images with different resolutions. The resolution used for our classification was 200 X 200 pixels.

*CIELAB Color Correlation*: The digital microscope will generate RGB images which is difficult to segment. According to color and intensity the blood cells and image background varies greatly. The reasons for this can be camera settings, aging stain and varying illumination. So for making the segmentation robust, we are converting the RGB image into CIELAB color space [15], [16] or more correctly L*a*b color space, where L specifies

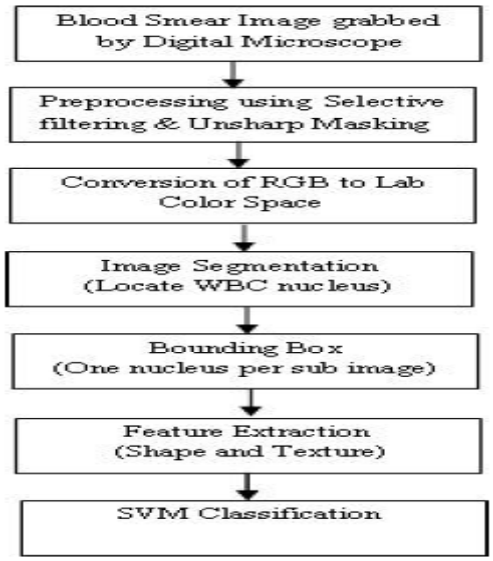


Fig. 2. Overall System

lightness of the color, dimension a* represents its position between green and red/magenta and dimension b* represents its position between yellow and blue.

## V. Segmentation

The goal of segmentation is extracting important information from an input image. For grey level images many algorithms for segmentation have been developed [17], [18]. In this system, the segmentation is performed using *k*-means clustering algorithm. Cluster analysis is the study of grouping objects with similar characteristics. In this system, the cluster corresponds to the nucleus, background and other cells. Then using the property of cluster center each pixel is assigned to one of these classes. After the segmentation is performed for preserving the nuclei of whole image, we have to perform some morphological operations.

## VI. Feature Extraction

Feature extraction is a technique of redefining a large set of redundant data into a smaller set of features. Classifier performance is influenced by the feature selection; therefore the selection of features is a crucial step. The where implemented for the blue nuclei. Fig. 3 represents the feature set used for classification.

*HD:* The fractal dimension D is a statistical quantity that shows how completely the space is filled by the fractals. Due to the ease of implementation the box counting dimension is used widely.

*LBP:* Local binary pattern are used for the classification of texture features [19], [20]. The LBP features are used because of the following reasons 1) they are robust towards the illuminationchange;2) they are computationally fast; 3) setting many parameters is not required; 4) the features are local.

*Shape features:* According to haematologists, shape of the nucleus is an important feature for classification. For analyzing the shape of the nucleus, region and boundary-based shape features are extracted.

*GLCM Features:* The GLCM feature calculation is an image analysis technique [21]. Different texture features like energy, contrast, entropy, correlation are extracted using this method.

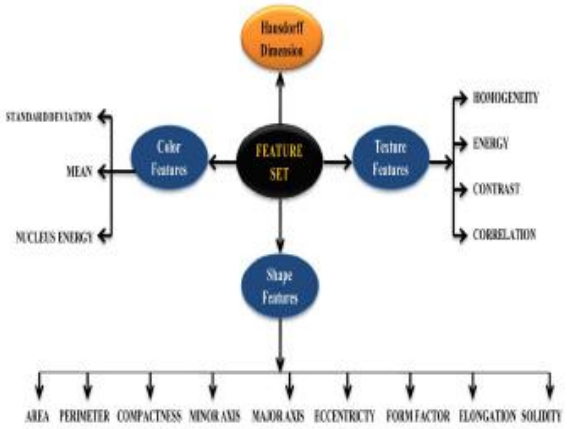


Fig. 3 Feature set for the classification

*Color features:* Since color is an important feature that human perceive while visualizing, it is considered for extraction from nucleus regions. Hence the mean color value in RGB color space is obtained for each nucleus image.

## VII. Classification

The method used for classification is a challenging problem since it will determine the accuracy of the system. Many statistical approaches are available for the binary classification tasks. The proposed methodology uses a linear support vector machine (SVM) for classifying cancerous and non-cancerous cells. After we have used the SVM for classification, a cross-validation is used for comparing and analyzing the learning algorithm.

## VIII. Conclusion And Future Work

This paper mainly focuses on the automated classification of AML cells in the blood microscopic images. It uses 108 high quality images of resolution 200 X 200 pixels. The presented system performs automated processing, including CIELAB color correlation, segmentation using *k*-means clustering, feature extraction based on which classification and validation are performed. The introduction of LBP features on HD shows a promising feature for analysis.

Further research will focus on improving the segmentation scheme, which can segment overlapped cells also. We can also use multiple classifiers to improve the accuracy of the classification. Doing so will increase the cost but the accuracy will also be improved. Extracting more features for classification will cause the system to overflow. So as a future work we can focus on how this system can be implemented accurately by removing the LBP features and thus by reducing the feature set.

## IX. Acknowledgment

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