I J C T A, 9(5), 2016, pp. 2147-2151

Detection of Leukemia in Blood Microscope Images

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ABSTRACT

Leukemia is a cancer of the blood and bone marrow, the spongy tissue inside the bones where blood cells are made. Acute myeloid leukemia (AML) is one of the most common types of leukemia among adults. The signs and symptoms of leukemia are non-specific in nature and also they are similar to the symptoms of other common disorders. Manual microscopic examination of stained blood smear or bone marrow aspirate is the only way to effective diagnosis of leukemia. But this method is time consuming and less accurate. In this paper, a technique for automatic detection and classification of AML in blood smear is presented. K-means algorithm is used for segmentation. Both spatial and spectral features are used for classification. Genetic algorithm is used for optimizing the spectral features. Local ternary pattern is used for texture description. Blood microscope images were tested and the performance of the classifier was analyzed.

Keywords: Acute myelogenous leukemia (AML), Feature extraction, Genetic algorithm, Classification.

1. INTRODUCTION

Leukemia is a type of cancer. All cancers begin in cells which make up blood and other tissues. Bone marrow is the soft material in the center of most bones. In people with leukemia, the bone marrow produces abnormal white blood cells [1]. These abnormal cells may crowd out normal white blood cells, red blood cells and platelets. Acute myeloid leukemia (AML) is one of the most common types of leukemia among adults.

The initial symptoms of AML are not specific and are similar to other disease such as generalized weakness, anemia, fever, joint pain, etc. Currently, the microscopic investigation of blood cells is performed manually by hematologists through visual identification under the microscopic. However the manual recognition method is time consuming . Moreover diagnostic confusion also occurs due to imitation of similar signs by other disorders. Digital image processing methods have been applied for automatic classification and detection of acute myeloid leukemia [9], [3]-[6], [13]. Earlier gray level images were used for segmentation. It is proved that [3] color images present more reliable image segmentation than gray level images.

The work in [10], [11] employs k-means clustering algorithm for segmentation. It is an unsupervised color based segmentation method. The work in [1] uses local binary pattern for texture classification. Xian-Hua et al. [2] proposed the use of robust local ternary pattern for texture classification as the local binary pattern is sensitive to noise. The work in [1], [4], [10], [11] uses spatial features for classification. Many of the systems presented in literature uses SVM classifier. It has been proved by the work of Jing Zhou et al. [12] that the use of genetic algorithm for parameter optimization improves the classification capability of SVM classifier. The common drawback in these systems is that many of them classify only sub images.

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The work in [1] has proposed a system to classify whole images. But local binary pattern is used for texture classification which is sensitive to noise.

The goal of the proposed work is to design a fully automated classifier for detecting and classifying acute myeloid leukemia. This paper is structured as follows. Section II focuses on the proposed methodology. Section III gives the results obtained. Section IV presents conclusion and future work.

2. METHODOLOGY

The step-by-step processes involved in the proposed system are depicted in Fig. 1. The first step is image preprocessing. This step is followed by K-means clustering method to separate the blue nucleus from the blood smear. Features are extracted after segmentation in order to be used for classification. Spectral features are optimized using genetic algorithm before using them in classification process. Finally, classification is done using SVM classifier.

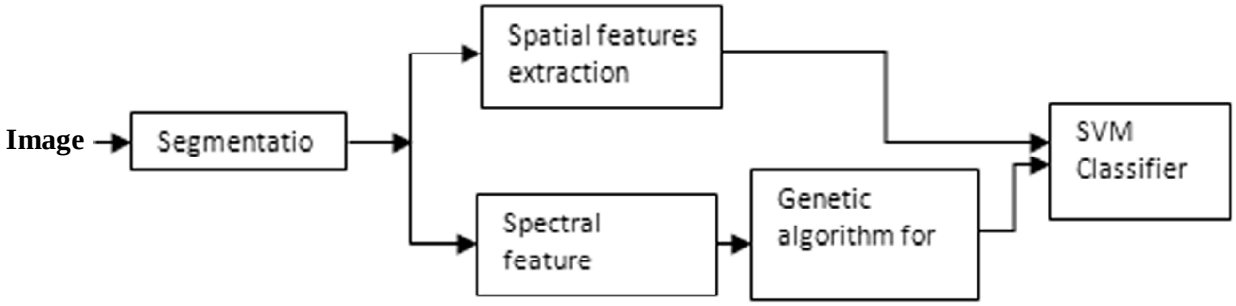


Figure 1: Block diagram of the proposed system

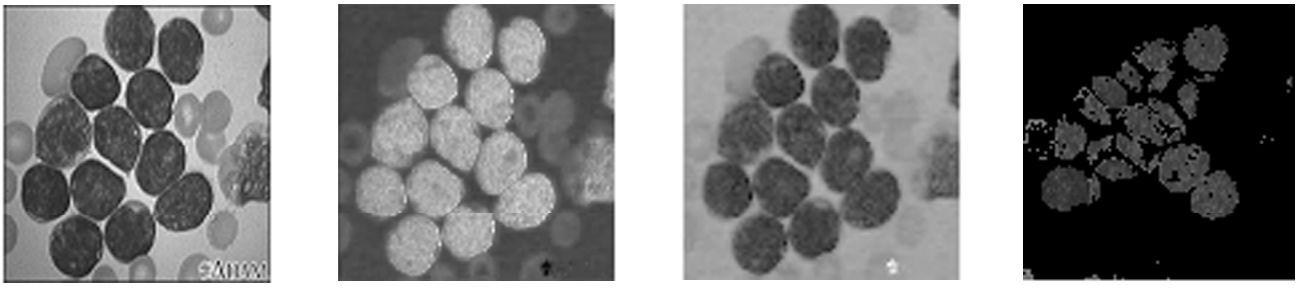
2.1. Preprocessing

The images are obtained from the online image bank of American Society of Hematology (ASH) [7]. In order to make the cell segmentation effective, the RGB input image is converted into the CIEL*a*b color space [1]. Fig.2 gives the illustration of RGB to CIELAB color conversion process and segmentation.

2.2. Segmentation

K-means clustering algorithm is used for segmentation [5]. The proposed system uses three clusters corresponding to nucleus, background and other cells. Every pixel is assigned to one of the clusters based on the properties of cluster center.

The *k*-means algorithm requires three user-specified parameters: the number of clusters *k*, cluster initialization, and distance metric. *k*-means clustering is a partitioning method. The algorithm partitions data into *k* mutually exclusive clusters, and returns the index of the cluster to which it has assigned each



(a) **(b)** **(c)** **(d)**

Figure 2: (a) input image (b) a*component (c) b* component (d) nucleus

observation. Each cluster in the partition is defined by its member objects and by its centroid, or centre. The centroid for each cluster is the point to which the sum of distances from all objects in that cluster is minimized. Each pixel of an object is classified into *k* clusters based on the corresponding *a and *b values in the L*a*b color space. Therefore, each pixel in the L*a*b colour space is classified into any of the *k* clusters by calculating the Euclidean distance between the pixel and each color indicator. These clusters correspond to nucleus (high saturation), background (high luminance and low saturation), and other cells (e. g., erythrocytes and leukocyte cytoplasm). We consider only the cluster that contains the blue nucleus, which is required for the feature extraction..While performing *k*-means segmentation of complete images, it was observed that, in some of the segmented images, only the edges of the nuclei were obtained as opposed to the whole images of the nuclei. This shortcoming was overcome by employing morphological filtering.

2.3. Feature Extraction

Feature extraction is the process of defining a set of features, or image characteristics, which will most efficiently or meaningfully represent the information that is important for analysis and classification. Feature selection greatly influences the performance of the classifier and therefore a correct choice of features is very crucial. In this paper, both spatial and spectral features are used for classification. According to hematologists, the shape of the nucleus is an essential feature for discrimination of cancerous and normal myeloid cells. The lymphocytes are more circular than the myeloblasts. The shape features are extracted from the binary equivalent of the image where the nucleus region is represented by nonzero pixels.

Local ternary pattern is a method used for texture classification. LBP can achieve effective description ability with appearance invariance and adaptability of patch matching based methods. However, LBP only thresholds the differential values between neighbourhood pixels and the focused one to 0 or 1, which is very sensitive to noise existing in the processed image. In this system LTP is used, which considers the differential values between neighbourhood pixels and the focused one as negative or positive stimulus if the absolute differential value is large; otherwise no stimulus (set as 0). Unlike LBP, it does not threshold the pixels into 0 and 1, rather it uses a threshold constant to threshold pixels into three values. Neighbouring pixels are combined after thresholding into a ternary pattern. Defining the local neighbourhood as a set of sampling points evenly spaced on a circle centred at the pixel to be labelled allows any radius and number of sampling points. When a sampling point does not fall in the centre of a pixel, bilinear interpolation is employed. Each gray scale pixel is compared with these sampling points one by one. A threshold value is assumed. Based on the above condition, each pixel is replaced by a ternary pattern. Further the ternary patterns are split into two binary patterns namely LTP lower pattern and LTP upper pattern.

The texture features [1] such as energy, contrast, homogeneity, correlations and Hausdorff Dimension (HD) [8] are extracted. In addition to the features mentioned above, color based features are also used. Mean, standard deviation and energy are the important color features used for classification.

Spectral features are more reliable and stable than spatial morphology therefore the research on spectral imaging technology and its applications in biomedical engineering is one of the noticeable directions in the field of optical diagnosis at present. In this paper, Haar wavelet transform is applied and then approximation and detail coefficients are obtained. In spectral data, much of the information is repeated from image to image. This redundancy complicates analysis and classification unnecessarily. To overcome this issue, genetic algorithm is used for optimizing the spectral features.

2.4. Classification

The selection of classification technique is very crucial as an appropriate choice help improving the accuracy. In the proposed work, Support Vector Machine (SVM) is used for classification. It constructs a decision

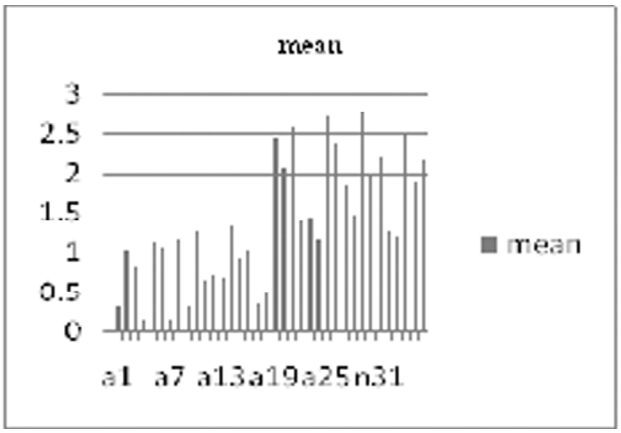
surface in the feature space that bisects the two categories, i.e., cancerous and noncancerous, and maximizes the margin of separation between two classes of points. In this paper, linear SVM classifier is used as it is computationally inexpensive and it achieves good performance.

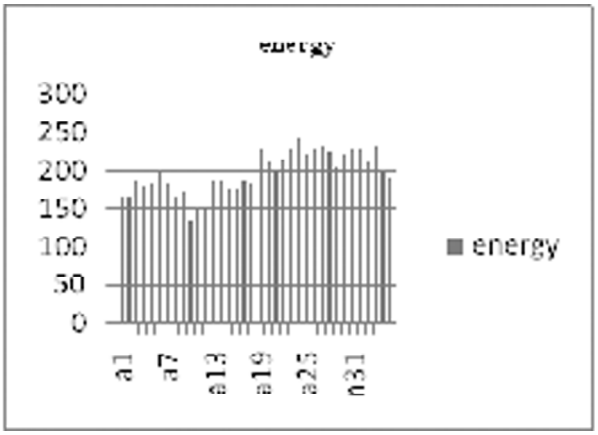
3. EXPERIMENTAL RESULTS

Images obtained from ASH have been applied to the developed system and the performance of the classifier is evaluated. Fig. 3. shows the images of segmented image after the application of LTP. Features that are extracted with the application of local binary pattern and local ternary pattern are compared. Fig. 4 shows the mean and energy plot for the image database. It has been observed that the performance of the classifier was 83.3% with LBP code and it was increased to 91.6% with the use of LTP pattern.

(a) **(a)**

Figure. 3. (a) LTP upper image (b) LTP lower image





(a) **(a)**

Figure 4: (a) Mean plot (b) Energy plot

4. CONCLUSION

This paper has given an method for automatic detection and classification of AML in blood microscopic images. The proposed system classifies whole blood images rather than sub images. A feature set containing the shape, texture, color information of the image is used. Additionally Hausdorff dimension and spectral features were extracted. Genetic algorithm was used for optimizing spectral features. Features were extracted with the application of both LBP and LTP code and the results were compared. The impact of LTP operator improved the performance of the classifier considerably. Further research will focus on the use of spectral features as essential features for classification.

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