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AUTOMATED CELL NUCLEUS SEGMENTATION AND ACUTE MYELOGENOUS LEUKEMIA DETECTION IN BLOOD MICROSCOPIC IMAGES

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Abstract: Acute myelogenous leukemia (AML) is a subtype of acute leukemia, which is common among adults. The average age of a person with AML is 65 years. The need of automation for leukemia detection gets up since current methods involve manual examination of the blood smear as the first step toward determination. This is time consuming and its accuracy depends on operator's ability. In this work a simple technique that automatically detects and segments AML in blood smear is used. The propose methods different from the others in: 1) The simplicity of developed approach; 2) Classification of complete blood smear images as opposed to sub images; 3) Use of this algorithms to segment and detect nucleated cells. Linear binary pattern (LBP) is used for texture classification and support vector machine (SVM) is employed for classification.

Keywords: Acute myologenous leukemia, Feature Extraction, Segmentation, classification algorithm

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INTRODUCTION

White blood cells (WBC) or leukocytes play a major role in the determination of different diseases; as a result, to get information about them is valuable for hematologists. Determination of leukemia is based on the fact that white cell count is increased with not fully developed blast cells (lymphoid or myeloid), and neutrophils and platelets are decreased [1]. Therefore, hematologists routinely query blood smear under microscope for proper identification and classification of blast cells [9]. The presence of the excess number of blast cells in peripheral blood is a significant symptom of leukemia. Leukemia is broadly classified as: 1) acute leukemia (which progresses quickly); and 2) chronic leukemia (which progresses slowly).

PROPOSED METHOD

A. System overview

Acute myelogenous leukemia (AML) is a heterogeneous clonal disarrangement of haemopoietic progenitor cells ("blasts"), which lose the ability to differentiate normally and to respond to normal regulators of proliferation. AML is a fast-expanding cancer of the blood and bone marrow. It is causing death if left untreated, due to its fast spread into the bloodstream and other vital organs [2]. Furthermore, AML is the most common myeloid leukemia, with a frequency of 38 cases per 100 000 increasing to 179 cases per 100 000 adults aged 65 years and older [49]. AML also build up 15-20% of childhood leukemia, roughly 60% of cases appear in people aged younger than 20 years. That is about 500 children and adolescents in the U.S. each year are affected by AML. Survival in childhood acute lymphoblastic leukemia is approaching 90%, but treatment in infants (i.e., children younger than 12 months) and adult's needs improvement. Early diagnosis of the disease is fundamental for the recovery of patients, particularly in the case of children [2]. AML is often difficult to diagnose since the precise cause of AML is still unknown. In addition, the symptoms of the disease are very similar to flu or other common diseases, such as fever, weakness, tiredness, or aches in bones or joints [2]. If the described symptoms are present, blood tests, such as a full blood count, renal function and electrolytes, and liver enzyme and blood count, have to be done [2]. Since there is no staging for AML, there are different types of treatment can differ from chemotherapy, radiation therapy, bone marrow transplant, and biological therapy. Fig. 1 shows six different images, three depicting healthy cells from non-AML patients and three from AML patients [7].

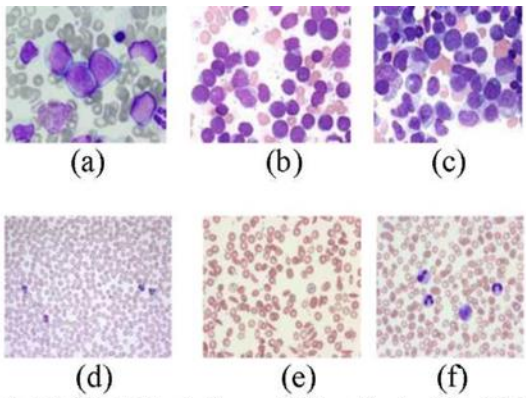


Fig 1: Images from ASH. (a)–(c) Myeloblasts from AML patients. (d)– (f) Healthy cells from non-AML patients.

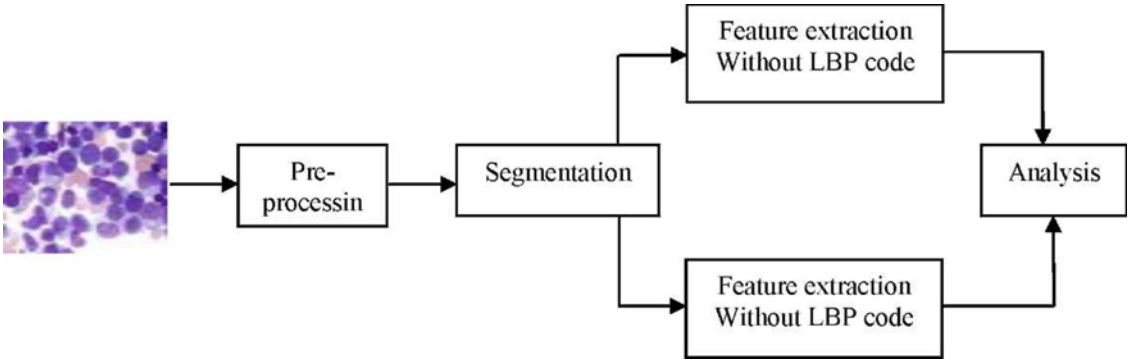


Fig 2. AML classifier system overview

Input image apply to preprocessing in preprocessing RGB image is converted into CIELAB. For segmentation k-mean clustering algorithm is used. Every pixel is assigned to one of these classes using the properties of the cluster center. Each pixel of an object is classified into *k* clusters based on the corresponding a and b values in the Lab color space. Therefore, each pixel in the Lab color 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. The feature set is classified into,

1. Texture feature
2. Shape feature
3. Color feature
4. Hausdroff dimension

B. feature extraction

Feature extraction in image processing is a approach of reexamine a large set of redundant data into a set of features of reduced dimension. Converting the input data into the set of features is called feature extraction. Feature selection grandly weighted the classifier performance; therefore, a correct choice of features is a very critical step. In order to build an effective feature set, several published articles were studied, and their feature selection methodology was observed. It was famed that certain features were widely used as they gave a good classification. We implemented these features on whole images in our system. Those features were considered to raise the classifier performance. Feature set is chosen to categorize the image database.

HD: Fractals have been used in medicine and science in the past for various quantitative measurements [1]. The fractal dimension D is a statistical quantity that gives an suggestions of how completely a fractal appears to fill space. There are many precise definitions of fractal dimension. The most important theoretical fractal dimensions are the Renyi dimension, the HD, and the packing dimension. Practically, the box-counting dimension is broadly used, partially due to their ease of implementation. In a box counting algorithm, the number of boxes masking the point set is a power-law function of the box size. The procedure for HD measurement using the box counting Method is carried out below as an algorithm:

1) Binary image in acquired from the gray-level image of the blood sample;

2) Edge detection technique is used to trace out the nucleus boundaries;

3) Edges are superimposed by a grid of squares;

4) The HD may then be defined as follows

tog ***(R(SJ)***

Where *R* is the number of squares in the superimposed grid, and *R(s)* is the number of filled squares or boxes (box count). Higher HD implies higher degree of roughness. Thus, HD turned out to be a critical feature in our system particularly since we considered whole images of the blood sample. In the whole images, the number of nuclei under the field of view was much higher for a cancerous case as placed to the noncancerous case. This resulted in steep distinguish in box count between the two cases and thereby demonstrated to be an effective feature.

LBP: The idea of local binary pattern (LBP) was inserted for texture classification. This way has many advantages. For example, the LBP texture features have the following characteristics: 1) They are strong against illumination changes; 2) they are rapid to compute; 3) they do not require many parameters to be set; 4) they are local features; 5) they are uniform with respect to monotonic grayscale transformations and scaling; and 6) they have executed very well in many computer vision image retrieval applications. The LBP method has proved to be greater than many existing methods, including the linear discriminant analysis and the principal component analysis. In order to trade with textures at different scales, the LBP operator was later figurative to use neighborhoods of different sizes. 1. Shape features. One of the shape features that has proven to be a good measure for classifying AML by their shape is compactness [1]-[4]. The shape of the nucleus, according to hematologists, is an essential feature for separation of myeloblasts. Region and boundary based shape features are getting for shape analysis of the nucleus.

- *Area:* The area was determined by counting the total no. of nonzero pixels within the image region.

- *Perimeter:* It was measured by calculating distance between sequential boundary pixels.

- *Compactness:* Compactness or roundness is the measure of nucleus as defined as

perimeter" Area

Solidicity: The ratio of actual area and convex hull area is known as solidicity and is essential feature for blast cell categorization. The measure is defined as

Solidicity =

Convex area

- *Eccentricity:* This parameter is used to measure how much a shape of a nucleus irregular from being circular.

Eccentrici ty = —-—

- *Elongation:* Abnormal swelling of the nucleus is also a feature which weighted toward leukemia. Hence nucleus is measured in terms of a ratio called elongation.

Elongation -

"ruin

- *Form factor:* This is an dimensionless parameter which changes with surface irregularities and is defined as

4 * si * Ares

***Form factor* = j-**

perimeter*

2. GLCM feature: Texture is defined as a function of the spatial fluctuations in pixel intensities. The GLCM and attended texture feature calculations are image analysis techniques Gray-level pixel distribution can be described by second-order statistics such as the probability of two pixels having particular gray levels at particular spatial relationships. This information can be described in 2-D gray-level co-occurrence matrices, which can be calculated for various distances and orientations. In order to use information contained in the GLCM, Haralick defined some statistical measures to educe textual characteristics. Some of these features are the following.

- *Energy:* Also known as uniformity (or angular second Moment), it is a measure of homogeneity of image.

- *Contrast:* The contrast feature is a difference moment of the regional co occurrence matrix and is a measure of the contrast or the amount of local variation present in an image.

- *Entropy:* This parameter measures the disarrangement of an image. When the image is not texturally uniform entropy is very large.

- *Correlation:* The correlation feature is a measure of regional-pattern linear dependence in the image.

C. Classification

Classification is the job of assigning to the unknown test vector a label from one of the known classes. ago the patterns are very close in the feature space, SVM is a strong tool for classification based on hyper plane classifier. This classification is achieved by a separating surface (linear or non-linear) in the input space of the data set. They are basically two class classifiers that optimize the margin between the classes. The classifier training algorithm is a process to find the support vectors.

D. Flow graph

SVM is employed for classification. There are two phases training phase and testing phase which is shown below

2. Testing Stage

1. Training Stage

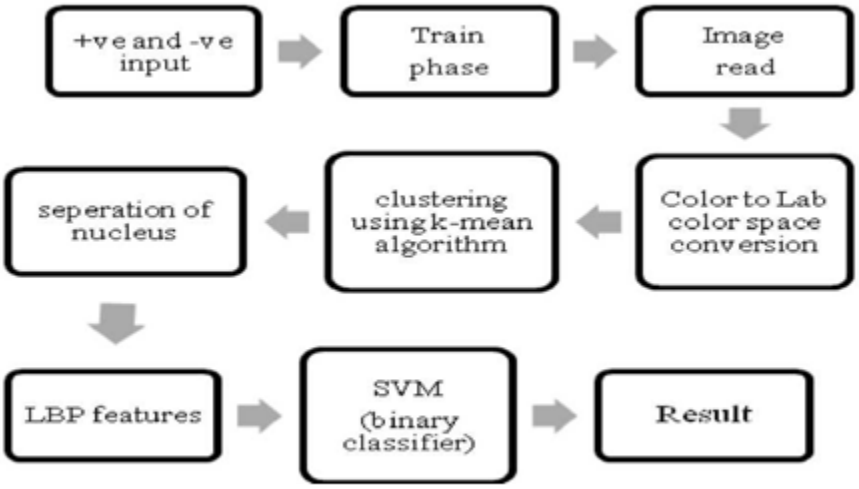


Fig 3: Flow diagram for training of blood cancer detection using SVM

2. Testing Stage

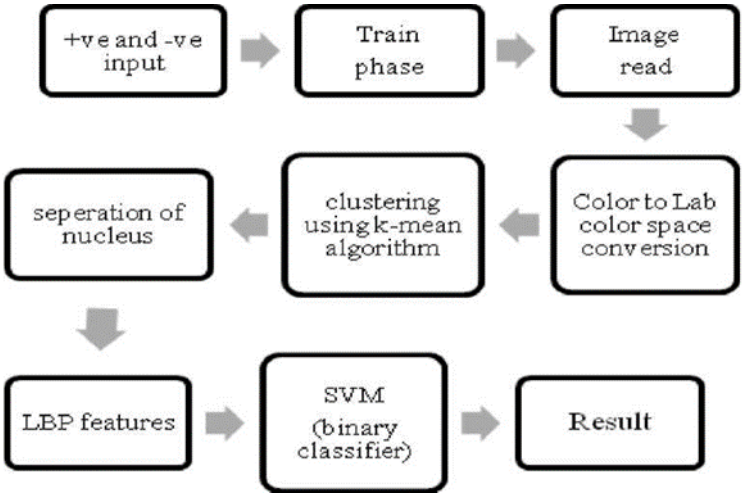


Fig 4: Flow diagram of testing phase of defected image for the representation SVM

Step1. Training phase and testing phase takes image as a input, it may be AML or NONAML.

Step2. It will read the image.

Step3. RGB image is then converted into Lab color space.

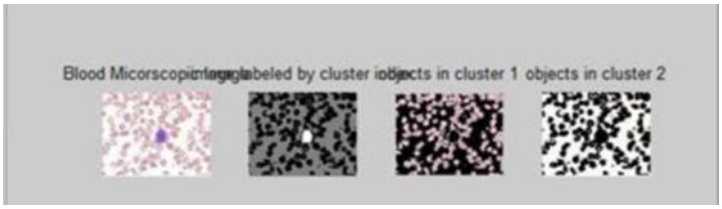
Step4. Separation of nucleus is take place in both the phases by using k-mean clustering algorithm.

Step5. Then will apply LBP features on them for finding out the texture parameter.

Step6. Output of LBP feature is given to input of SVM which stored all the steps information and generate result.

Step7. Result

III. EXPERIMENTAL RESULTS



Segmented nuclei objects in cluster 3 blue nuclei ^^^^HB

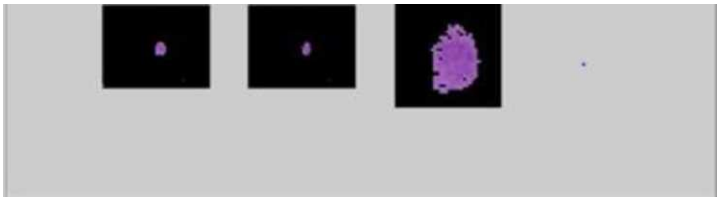


Fig 5: Segmentation of AML cell

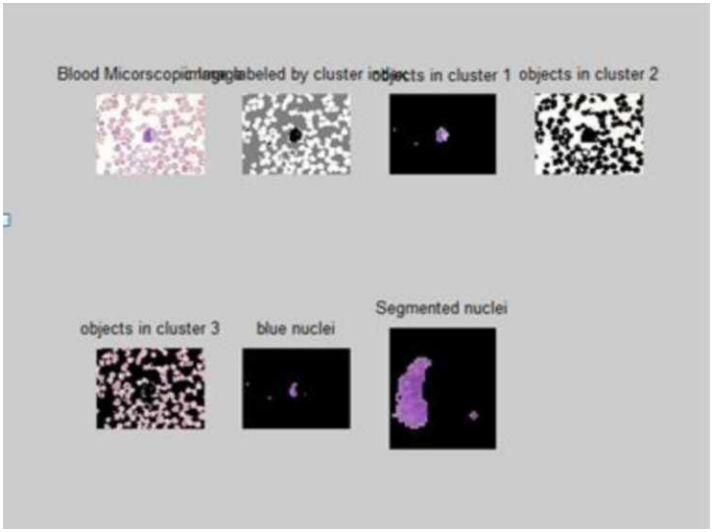


Fig 6: Segmentation of NONAML cell

TABLE I Results of shape parameter

Shape parameter	AML	NONAML
Area	203	104
Perimeter	85.4975	81.8406
Roundness	0.3490	0.1951
Eccentricity	0.625	0.9216
Convex area	253	161
Solidicity	0.8024	0.6440

TABLE II Results of texture parameter

Texture parameter	AML	NONAML
contrast	0.8328 0.8052	1.1189 1.2625
Correlation	0.8362 0.8409	0.5759 0.5248
Energy	0.1205 0.1200	0.0895 0.0874
Homogeneity	0.7886 0.8052	0.7183 07118

IV. CONCLUSION

This work has reported the design, development, and estimation of an automated cell nucleus segmentation system for AML in blood microscopic images. It uses 80 high-quality 184 x 138 size images got from the American Society of Hematology. The developed system performs

automated processing, including color correlation, segmentation of the nucleated cells, and effective validation and classification. A feature set getting the shape, color, and texture parameters of a cell is build to obtain all the information required to perform effective classification.

V. ACKNOWLEDGEMENTS

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