

Acute myelogenous leukemia detection in blood microscopic image by local binary pattern

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Abstract— Acute myelogenous leukemia (AML) is a subtype of cancer which is mainly observed in the people above the age of 65 years. Since current methods involve manual examination of the blood sample as the first step toward diagnosis. Manual examination is less accurate and very complex so we are proposing this method. In this paper, a simple technique that automatically detects and segments AML in blood smears is presented. The proposed method differs from others in (A) It does not involve any complexity; (B) We can easily detect the cancer cells. Here SVM (support vector machine) is used which will help to easily compare the results b/w the existing and proposed method. Which shows the drastic improvement and also give high accurate result.

Index Terms— CIELAB, Morphological filter, GLCM features, SVM.

I. INTRODUCTION

AML is the type of cancer which is mainly observed in elder people. This disease increases along with the age. So to identify the AML take the blood microscopic images. generally Leukemia is broadly classified as Two types Acute Lymphoblastic Leukemia (ALL) and Acute Myeloid Leukemia (AML).. Acute myelogenous leukemia (AML) is a heterogeneous clonal disorder of haemopoietic progenitor cells, which lose the ability to differentiate normally and to respond to normal regulators of proliferation. This loss leads to fatal infection or organ infiltration, typically, in the absence of treatment, within a year of diagnosis.. Only AML is considered in this paper[1].

And also cancer is also observed in two type one is with high amount and other one is with low amount. Here in this paper at the end there is a clear difference is observed in between these two types.

After taking the samples in this paper crop the image manually to find the mean , area , standard deviation of the cancer cell. By taking these shape features by using the results cancer cell is compared with no-cancer cell. Then segment the cropped image. In the existing method k-mean clustering algorithm is used. K-mean algorithm will separate the layers of the blood sample like plasma, nuclei[3]. By using the k-mean clustering algorithm there is problem occurred the problem is when we segment the image into three segments the complexity is increased. To reduce the

complexity and also improve the accuracy in finding the cancer in the proposed method morphological filtering is used so that the accuracy in finding is increased. After segmentation, Local Binary Pattern (LBP)[7] is used to extract the features. Then compare existing method outputs and proposed method outputs by using Support vector machine (SVM)[5][6].

II. PROPOSED METHOD

The overall system working is explained in block diagram(see Figure 1). Where each block has its own role in the system. The first step involves the cropping the image and then the cropped image is the pre-processed it is converted to CIELAB to avoid the unwanted contrast made by the camera while taking image. After this the by the cropped image shape features are calculated to the cancer cell and no cancer cell. k-means clustering algorithm is applied to the cropped image to extract the GLCM features. Then SVM is applied to the image before LBP and after LBP[5][6][7].

To reduce the complexity image is converted into gray scale image[2]. Shape features are extracted by cropping image manually. In shape features are , standard deviation, mean values are calculated . After this it is given to the morphological filtering block. The morphological filter will perform the segmentation process like which helps to separate the nuclei from other content of the blood sample. Finally, it is given to LBP (local binary patter) so the we can extract the GLCM features in these features contrast , correlation , homogeneity , energy are calculated. Followed by classification by SVM. SVM will create a separate platform to make decision surface for differentiating the methods. SVM is mainly of two type Linear and Non-Linear SVM. linear SVM is used to get the better analysis.

Finally images with k-means algorithm and morphological filtering are compare so that best method for detecting cancer cells. So that the accuracy of finding cancer cells is improved. The brief explanation of each block is seen in the next pages. first the input image is taken then it is preprocessed after that morphological filtering is applied to it then after LBP is applied after that SVM Is used to classify the results to show the difference between the existing and proposed one. By seeing the output images and tables we can clearly compare the results as shown in the last page of the paper.

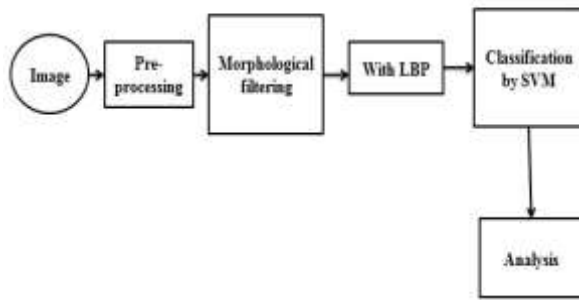


Fig 1: Block diagram

III. DESCRIPTION

A. Pre-processing

The image is cropped according to our requirement then the image is converted to CIELAB. The images generated by digital microscopes are usually in RGB color space. Usually the blood cells and image background vary greatly with respect to color and intensity. This is caused by multiple reasons such as camera settings, varying enlightenment, and aging blemish. Cell segmentation is different with respect to these variations, so a process is used to convert RGB input image into the CIELAB color space [2]. The a and b components is used to make accurate color balance corrections. The $L^*a^*b^*$ color space with dimension L represents the lightness of the color, element a^* that represents its position between red/magenta and green, and element b^* that represents its position between yellow and blue. In the proposed method image is converted into gray scale image.

B. Morphological filtering

An image is partitioned into several regions depending on the features to be extracted. Employing morphological filtering ensures that perceptibility and visibility of these regions improve. The following actions were performed in order to obtain the desired outcome. Once these actions are performed, the following texture and shape-based features are then extracted from these whole images[1].

In morphological filtering close operation is a dilation processes followed by an erosion of image, the erosion option will erode the grey scale image. After erosion original image is multiplied with erode image.. using the same structuring element for both operations To connect the separated points of the membrane in a better way it gives a good outline of the perimeter of the nuclei.

C. Local Binary Pattern

The concept of Local Binary Patterns (LBP) was introduced for texture classification . The LBP combines the structural and statistical image analysis approaches into a single high efficiency transformation which is invariant with respect to monotonic gray scale transformations and scaling. In the LBP method each pixel is replaced by a binary pattern which is derived from the pixel's neighborhood. Each gray scale pixel P of an image is used as a center of a circle with radius r. The number of samples M determines the amount of points that are taken uniformly from the contour of the circle. These points are interpolated from adjacent pixels if needed. The sample points are compared against the pixel P one by one

with a simple comparison operation which result a binary zero if the center point is larger than the current sample point and one otherwise. When doing this operation for example clockwise from a certain starting point the result will be a binary pattern with length M(see Figure 2) [7].

256	254	251
280	260	263
260	240	230

Fig 2: Simple LBP

Here the center bold value is taken as P compared with all its neighbors there are M=8 neighbors.

Some of the advantages by using the LBP are:

- They are very fast to compute.
- They require less parameters to compute.
- They are not variant with respect to the monotonic grey level transformations.
- The process is very easy to understand.

D. Feature extraction

Feature extraction is done after converting the image to required format and cropped . In the feature extraction there are two types of features: shape features and gray level co-occurrence matrix features[4].

1) Shape features:

In the shape features we are going to find the values of mean, standard deviation, area of the nuclei(see Table 1 and Table 2).

Table 1. Shape features extraction by k-means algorithm





Features	Value of normal cell	Value of cancer cell
Image		
Mean	0.3708	0.2652
Standard deviation	0.4831	0.4416
Area	2271	497.12

Table 2. Shape features extraction by morphological filtering

Features	Value of normal cell	Value of cancer cell
Image		
Mean	0.7866	0.5062
Standard deviation	0.4097	0.5000
Area	1802	1303

2) GLCM features:

GLCM features the special features which are also known as texture features. Second-order statistics describes Gray-level pixel distribution second-order statistics such as the probability of two pixels having particular gray levels at particular spatial relationships[8]. Some of these features are the following (see Table 3).

Energy:

It shows the uniformity in the image.

Contrast:

The contrast feature show the local variation in the image



Homogeneity:

This parameter measures the disorder of an image

Correlation:

It is measure of regional-pattern linear dependence in the image.

Table 3. GLCM features

Features	k-means	Morphological
Image		
Contrast	2.4593	3.6654
Correlation	0.8843	0.7875
Energy	0.5187	0.5791
Homogeneity	0.9561	0.9345

E. Classification by SVM

Support vector machine which helps to Support vector machine (SVM) is used for constructing 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[5][6].

An SVM is primarily a two-class classifier. It can be either linear or nonlinear. In linear SVM all the input values or multiple inputs are taken and worked on it at a single time. As in case of non-linear SVM only one single input is taken and solved at a time this is the difference between the linear and non linear SVM's.

Here linear SVM two-class classifiers used because it is not computationally expensive, and it has good performance. By using SVM specificity, accuracy are defined. The main components required for finding these parameters are

TP – true positives

TN – true negatives

FP – false positives

FN – false negatives

- Sensitivity = $T1/(T1+F0)*100$
- Accuracy = $(TP+TN)/(TP+TN+FN+FP)*100$
- Specificity = $TN/(TN+FP)$
- Precision = $TP/(TP+FP)$

IV. EXPERIMENTAL RESULTS

In this project two images are considered one is with low cancer cells and other is with high cancer cell. And compare the results with k-means algorithm and morphological filtering method.

Now, take the image with less number of cancer cells (see Figure 2)then apply both k-mean and morphological filtering then extract the SVM outputs (see Table 4). Plot the graph according to table(see graph 1).

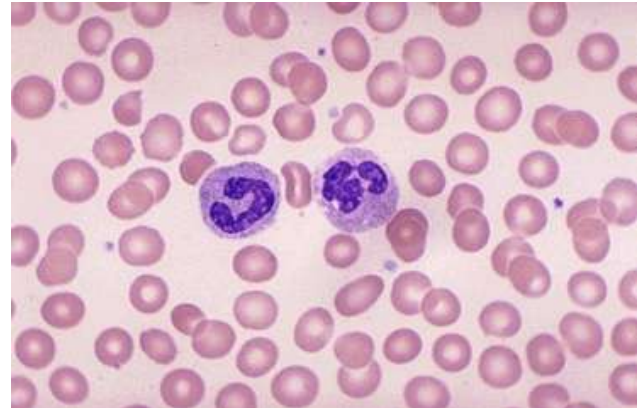
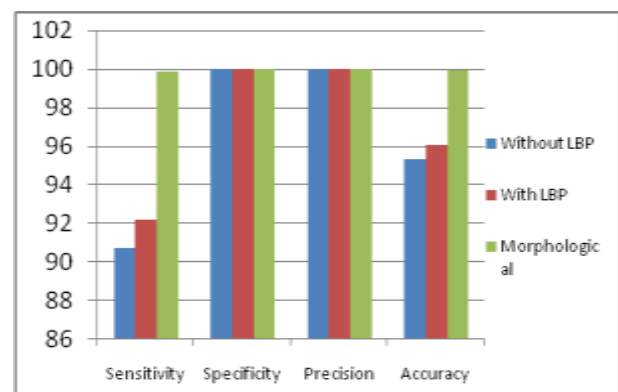


Fig 2: Image with less number of cancer cells

Table 4. results for cameraman image

Parameters	Without LBP	With LBP	Morphological
Sensitivity	90.7013	92.1860	99.8886
Specificity	100	100	100
Precision	100	100	100
Accuracy	95.3506	96.0936	99.9443



Graph 1: graph for Low cancer cell image

The Table 4 and Graph 1 shows the values of the SVM output and comparison between k-means and morphological filtering.

Now we go for the image which has high amount of cancer cells (see figure 3). And also compare the values of SVM with respect to the different types of algorithms like k-means with LBP and with out LBP along with morphological filter(see Table 5 and Graph 2).

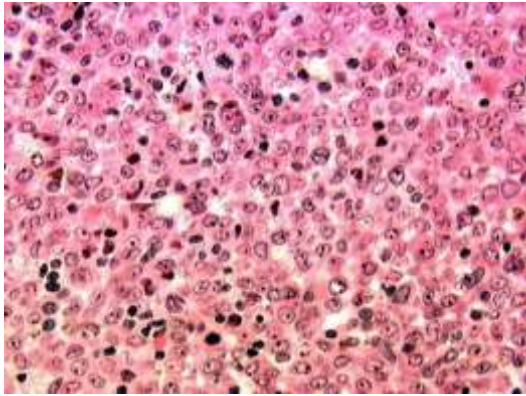
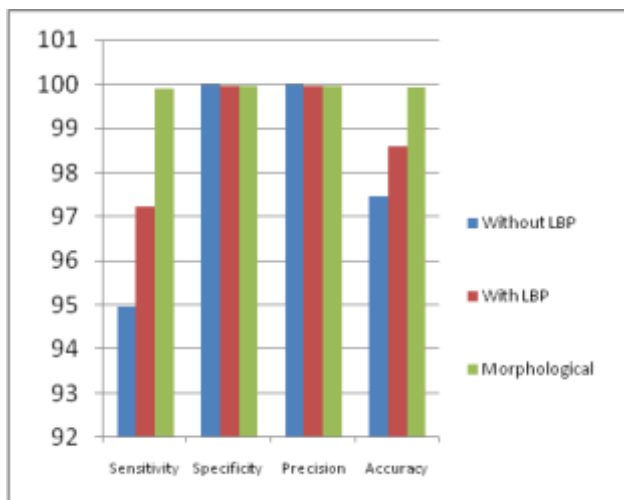


Fig 3: Image with high number of cancer cells

Table 5. results for cameraman image

Parameters	Without LBP	With LBP	Morphological
Sensitivity	94.9532	97.2374	99.8906
Specificity	99.973	99.9624	99.9639
Precision	99.9716	99.9613	99.9638
Accuracy	97.4637	98.6002	99.9273



Graph 2: graph for High number of cancer cell image

After results I conclude that the morphological filter is much better than the k-means clustering algorithm.

V. CONCLUSION

In this paper morphological filtering is used which increases the sensitivity and accuracy. By using k-means algorithm we can not exactly extract the nuclei at one time so to avoid this morphological filtering is used. SVM outputs are compared for existing and proposed method.

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