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Hematological Analysis of Acute Myelogenous Leukemia Using RI-LBP and Hausdorff Dimension

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ABSTRACT: Leukemia is a type of cancer that affects the blood cells and most commonly WBCs or leukocytes. There are two types of acute leukemia: Acute lymphoblastic Leukemia and Acute Myelogenous Leukemia that is ALL and AML respectively. A series of preprocessing steps such as color correlation and contrast enhancement are included for the microscopic blood smear images having multiple nuclei are exposed, when it is considered only AML. Old age human affected with AML. The requirement for automation of leukemia detection arises since trending methods involve manual analysis of the blood smear as the first step toward diagnosis. It took lot of time and its accuracy depends on the operator's ability. We have a simple technique that automatically detects and segments AML in blood smears is presented in this paper. The simplicity is phenomenon of proposed approach that differs others; classification of complete blood smear images as opposed to sub images; and use of these algorithms to segment and detect nucleated cells. The work here is to show how we can detect acute myelogenous leukemia with its feature extraction by using hausdorff dimension and Rotate Invariant Local Binary Pattern (RI-LBP).

KEYWORDS: Hausdorff Dimension (HD), Acute Myelogenous Leukemia (AML), Feature Extraction, Rotate Invariant Local Binary Pattern, Support Vector Machine (SVM).

I. INTRODUCTION

Medical imaging has become one of the most important visualization and interpretation methods in biology and medicine over the past decade. It has witnessed a tremendous development of new, powerful instruments for detecting, storing, transmitting, analyzing, and displaying medical images. The most challenging aspect of medical imaging lies in the development of integrated systems for the use of the clinical sector. Main objective of analyzing through images is to gather information, detection of diseases, diagnosis diseases, control and therapy, monitoring and evaluation. Now a days identification of blood disorders has been done through visual inspection of microscopic images of blood cells. From the identification of blood disorders, it can lead to classification of certain diseases related to blood. One of the most feared human disease is cancer. Leukemia is a type of blood cancer, and if it is detected late, it will result in death. Leukemia occurs when many abnormal white blood cells produced by bone marrow. When abnormal white blood cells are a lot, the balance of the blood system will be disrupted. The existence of abnormal blood can be detected and examined by haematologists. Blood is the main source of information that gives an indication of changes in health and development of specific diseases.

Microscopic examination of blood cells, still remains as the standard leukemia diagnosis technique. This analysis suffers from time delays and it presents not a standardized accuracy since it depends on operator's capabilities and

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tiredness. The microscopic images are used to identify the types and maturity of blood cells but it is a time consuming and tedious job and is inadequate to identify the type of the cell. Also the equipment required is very costly and may not be exist in all hospitals and clinics. The practice of manual counting of the white blood cells suffer from the disadvantages associated with human errors. So there is always a need for a cost effective and robust automated system for leukemia screening which can greatly improve the output without being influenced by operator fatigue. Accurate segmentation of the white blood cells is very important to locate the cancer region.

The main objective of this paper is to demonstrate that the classification of peripheral blood smear images containing multiple nuclei can be fully automated. To segment the image more efficiently and to validate the segmented images, this work can be used as ancillary/ backup service to the physician in order to improve efficiency and accuracy of clinical practice. Two new features, namely cell energy and Hausdorff dimension (HD) have been used in our work. Our work provides software based cost effective and an efficient alternative tool in recognizing and analysing blood cells. Here tedious human task is transformed in to a computer based process in which system outperforms the manual system.

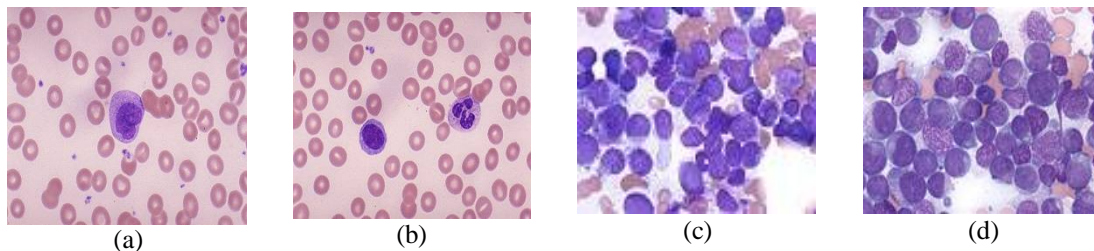


Fig.1 (a) – (b) From non-AML patients. (c) – (d) From AML patients

The main symptoms of AML are lack of normal blood cells as shown in fig.1(c) and fig.1(d) of AML patients compare with the fig.1(a) and fig.1(b) of non-AML patients which may include anemia due to lack of red cells. Lack of red cells causes persistent tiredness, dizziness, paleness, shortness of breath when physically active, frequent or repeated infections and slow healing due to a lack of normal white cells, especially neutrophils increased or unexplained bleeding or bruising due to a very low platelet count. Other symptoms may include bone pain, swollen lymph nodes, swollen gums, chest pain and abdominal discomfort due to a swollen spleen or liver. This technique relies on the operator's ability. During diagnosis, due to imitation similar signs by other disorders confusion also occurs. So this paper is about developing a cost effective and robust automated system for AML segmentation and classification. In the system, the microscopic blood images containing multiple nuclei are exposed to series of pre-processing, segmentation and feature extraction.

II. RELATED WORK

Digital image processing techniques have been used to analyse the cells that lead to more accurate, standard, and remote disease diagnosis systems. However, there are some complications in extracting the data from WBCs due to wide variation of cells in shape, size, edge, and position. Since illumination is imbalance, the image contrast between cell boundaries and the background varies depending on the condition during the capturing process. In addition, the cost of leukemia treatment can be overwhelming [1].

The effectiveness of an automatic morphological method to identify the Acute Lymphocytic Leukemia by peripheral blood microscope images is showed in this paper. In this system, they first individuate the leucocytes in the blood image from the other blood cells, then it selects the lymphocyte cells (the ones interested by acute leukemia), it evaluates morphological indexes from those cells and finally it classifies the presence of the leukemia. They used FAB Classification and Sobel Image Enhancing method. Features such as Canny Image Detection. Structured Image Dilation and Hole Filling have been extracted. This results in improvement in accuracy of detection but lacks from the process of segmentation [2]. F.Scotti [3] showed the effectiveness of an automatic morphological method to identify the Acute Lymphocytic Leukemia by peripheral blood microscope images. In this system, they firstly individuate in the blood

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image the leucocytes from the others blood cells, then it selects the lymphocyte cells (the ones interested by acute leukemia), it evaluates morphological indexes from those cells and finally it classifies the presence of the leukemia. Methods used in this paper are FAB Classification, Sobel Image Enhancing, Canny Image Detection, Structured Image Dilation and Hole Filling. Advantages of Optimal Classification, Improve accuracy. Disadvantages were discussed in this paper are Lack of image segmentation. C.Reta [4], et.al., have presented the methodology for analyzing morphology of the abnormal leukocytes images In this using data mining techniques subtypes of acute leukemia are classified. First phase includes extraction of leukocytes, cytoplasm's and nucleus from bone marrow images using color and texture information. Second phase consists of feature extraction to Segmented region in order to classify subtypes of leukemia. 92% accuracy is achieved overall. T.Markiewicz [5], et.al., built a system to detect leukemia cells of images of bone marrow. Using Support Vector Machine (SVM) classifier and blood cell images features that are related to geometry, texture, and statistical analysis, the system was built. The pressure is on selection and generation of features for getting out the best recognition.

Textural parameters such as entropy, contrast, mean value and angular second momentum have been used. Geometrical parameters are compactness, perimeter, concavity points and symmetry radius, area and filled area. For statistical analysis parameters are mean value and for nucleus standard deviation and for gradient matrix cytoplasm, mean and standard deviation are considered. Kurtosis and Skewness for image and gradient matrix. M.C., Colunga [6], et.al., use EM-Algorithm to identify types of leukocyte. First, using principal component analysis, the image pattern is changes into a lower dimensional space. They obtain the Gaussian functions parameters to model each class probability distribution function of cells, EM-algorithm is used. Classification of the images are done by using Bayes' theorem and finally by choosing the class with the highest probability.

Many attempts have been made in the past to construct systems that aid in acute leukemia segmentation and classification. There are four main categories in segmentation techniques: thresholding techniques and boundary-based and region-based segmentation and hybrid techniques that combine boundary and region criteria. When it comes to peripheral blood or bone marrow smears, region-based or edge-based schemes are the most popular. A proper combination of both boundary and region information may present better results than those obtained by either method on its own. From a survey conducted by Ilea and Whelan on color image segmentation algorithms, it was concluded that color images present more reliable image segmentations than graylevel images. Many segmentation algorithms were presented in literature are Otsu segmentation and automated histogram thresholding were employed to segment WBCs from the blood smear image. The work in employed contour signature is to identify the irregularities in the nucleus boundary. The work employed in selective filtering is to segment leukocytes from the other blood components.

III. THE AUTOMATED SYSTEM FOR ACUTE MYELOGENOUS LEUKAEMIA DETECTION

A cost effective and robust automated system for leukemia screening is developed in this work. The method has evaluated using a set of images (with abnormal samples and normal samples). In the proposed system, the microscopic blood images containing multiple nuclei are exposed to series of preprocessing steps, which include color correlation, and contrast enhancement. Pre-processing of the image has done in order to reduce the background non-uniformities and perform color correlation. In order to exploit all the available a-priori information and thereby achieving a robust identification of the nuclei of the white cells, segmentation on whole images by combining different methods is performed and extraction of different sets of features has performed for a database of images. Finally, classifier performs classification of Cancer and Non-cancer blood cells and validation has done on the output based on the results obtained. Fig 2 illustrates the step-by-step processing of the proposed system. A detailed depiction of the sequence of steps that are to be followed for efficient classification of acute leukemia gives the overview of the system.

A. Image acquisition

Blood cell image will be obtained from nearby hospital with effective illumination and also from the image bank of the American Society of Hematology (ASH). They provide high-quality images captured using different microscopes in different resolutions. Pixel, used as the resolution for our classification is 184×138 . The blood cell images obtained are stored in the computer system for the further processes.

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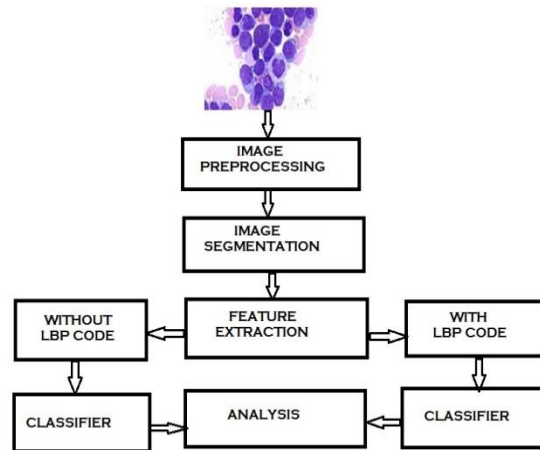


Fig 2 AML classifier system overview

B. Preprocessing

During image acquisition and excessive staining, the images will be disturbed by noise. The noise may be due to illumination or shadows that make region of interest (ROI) appear as blurred image region. Background will be excluded since our ROI will be white blood cells. During this preprocess, image enhancement will be done as the contrast enhancement technique is capable to improve the medical image. In RGB chrominance and luminance component are mixed that is why RGB is not choose for color analysis and color based segmentation algorithm. This can be overcoming by CIE Lab CIE (Commission International d'Eclairage) specifies three: CIE*XYZ, CIE*Lab, and CIE*Luv. In CIE*Lab or CIE Lab, the three component represent luma component that is illumination information and ab represent the chroma information. $L^*=0$ provide the black color and $L^*=100$ provides white color. The a^* , the values $a^*<0$ that indicate green while the values $a^*>0$ indicate magenta. The b^* , the values $b^*<0$ that indicate blue and values $b^*>0$ indicate yellow.

C. Image Segmentation

Segmentation of white blood cell (WBC) and determine ROI that is nucleus for WBC only. This is because in leukemia cell images, the cytoplasm is scanty. So, focus will be on nucleus of WBC only. Determination the types of WBC should be done from the nucleus. Only lymphocytes and myelocytes should be considered and need to determine them whether they are blast cells or not. Others like neutrophils, basophils and eosinophils should be excluded. Once the blast cells are determined, then proceed to the next step. Sub images containing nucleus only will be considered. This is to reduce errors since there are similar color scales in WBCs with other blood particles.

Segmentation in this system is performed for extracting the nuclei of the leukocytes using color-based clustering. Cluster analysis is the formal study of methods and algorithms for grouping, or clustering, objects according to measured or perceived intrinsic characteristics or similarity. Cluster analysis does not use category labels that tag objects with prior identifiers, i.e., class labels. k-means, which is one of the most popular unsupervised learning algorithm and is also a simple clustering algorithm, was first published in 1955. k-means is still widely used. This speaks to the difficulty in designing a general-purpose clustering algorithm and the ill-posed problem of clustering. In this paper, we chose clusters corresponding to nucleus (high saturation), background (high luminance and low saturation), and other cells (e.g. erythrocytes and leukocyte cytoplasm). Here, every pixel is assigned to one of these classes using the properties of the cluster center.

Segmentation is typically associated with pattern recognition problems. It is considered the first phase of a pattern recognition process (shown next) and is sometimes also referred to as object isolation. Cluster analysis is done to segment the nucleus. The k-means algorithm requires three user-specified parameters: the number of clusters k , cluster initialization, and distance metric. A k-means clustering procedure is used to assign every pixel to one of the clusters. 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

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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 (e. g., erythrocytes and leukocyte cytoplasm). Each pixel of the entire image will be labelled to a particular color depending on the minimum distance from each indicator. 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.

D. Feature Extraction

Feature extraction in image processing is a technique of redefining a large set of redundant data into a set of features of reduced dimension. Transforming the input data into the set of features is called feature extraction. The most important problem in generation of features of blood cells that characterize them in a way enabling the recognition of different blast types with the highest accuracy. The features to be used are for nucleus of lymphocytes and myelocytes.

- *Geometrical Features* – which includes area, radius, perimeter, symmetry, concavity, compactness, solidity, eccentricity, elongation, form factor will be obtained.
- *Texture Features* – which includes homogeneity, energy, correlation, entropy contrast, angular second momentum will be obtained.
- *Color Features* – the RGB color spaces will be transformed into HSV or L^*a^*b color spaces. Their mean color values will be obtained.
- *Statistical Features* – the mean value, variance, skewness, kurtosis of the histograms of the image matrix and the gradient matrix for RGB or HSV or L^*a^*b color space.

GLCM features:

Texture is defined as a function of the spatial variation in pixel intensities. The GLCM and associated 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 depicted in 2-D gray-level co-occurrence matrices, which can be computed for various distances and orientations. In order to use information contained in the GLCM, Haralick defined some statistical measures to extract. Some of these features are, 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 variations present in an image. Entropy: This parameter measures the disorder 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.

HD (hausdorff dimension) - Fractals have been used in medicine and science in the past for various quantitative measurements. The fractal dimension D is a statistical quantity that gives an indication of how completely a fractal appears to fill space.

Procedure for HD: HD is considered an essential feature considered in our proposed system. The procedure for HD measurement using the box counting method is elaborated below as an algorithm:

- Binary image is obtained from the gray-level image of the blood sample;
- Edge detection technique is employed to trace out the nucleus boundaries;
- Edges are superimposed by a grid of squares

The HD may then be defined as, $HD = \log(R)/\log(R(s))$; where R is the number of squares in the superimposed grid, and $R(s)$ is the number of occupied squares or boxes (box count). Higher HD signifies higher degree of roughness.

RI- LBP (Rotate Invariant Local Binary Pattern)

Local binary patterns (LBP) is a type of feature used for classification in computer vision. It has been found to be a powerful feature for texture classification; it has been determined that when LBP is combined with the Histogram of oriented gradients (HOG) descriptor. LBP only considers the signs of the differences to compute the final descriptor.

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The information related to the magnitude of the differences is completely ignored. The magnitude provides a complimentary information that has been utilized to increase the discriminative power of the operator. Especially in the neighbourhood with strong edges the magnitude of the differences can provide an important information. The dominant direction is defined as the index in the circular neighbourhood for which the difference is maximum. As an image undergoes a rotation the dominant direction in a neighbourhood also undergoes the rotation by the same angle. To make the LBP invariant to rotation we circularly shift the weights according to the dominant direction. The dominant direction (D) in a neighbourhood is the index of neighbour whose difference to the central pixel is maximum. For each pixel in a cell, compare the pixel to each of its 8 neighbours (on its left-top, left-middle, left-bottom, right-top, etc.). Follow the pixels along a circle, i.e. clockwise or counter-clockwise. where the center pixel's value is greater than the neighbour's value, write "1". Otherwise, write "0". This gives an 8-digit binary number (which is usually converted to decimal for convenience).

E. Image Classification

There is a plenty of statistical techniques, which aim at solving binary classification tasks. In this paper, we use a support vector machine (SVM) 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. SVMs is a promising nonlinear nonparametric classification technique, which already showed good results in the medical diagnostics, optical character recognition, electric load forecasting, and other field.

Evaluation

Classification using the SVM, a statistical method called cross-validation is used for evaluating and comparing learning algorithms. Cross-validation is a technique for judging how the results of a statistical analysis will generalize to an independent data set. It is mainly used in settings where the goal is prediction and where one wants to estimate how precisely a predictive model will perform in practice. Three kinds of validation techniques have been used: K-fold, holdout, and leave-one-out. Hold-out: The data are split into two no overlapped parts: one or testing and the other for training. The test data are held out and not looked at during training. K-fold: In K-fold cross-validation, the data are first partitioned into K equally (or nearly equally) sized sets or folds. Leave-one-out: Leave-one-out cross-validation is a special case of K-fold cross-validation where K represents the number of instances in the data.

IV. PROPOSED SYSTEM

Acute myelogenous leukemia (AML) is a subtype of acute leukemia, which is prevalent among adults. The average age of a person with AML is 65 years. The need for automation of leukemia detection arises since current methods involve manual examination of the blood smear as the first step toward diagnosis. This is time-consuming, and its accuracy depends on the operator's ability. In this paper, a simple technique that automatically detects and segments AML in blood smears is presented. The proposed method differs from others in:

- The simplicity of the developed approach;
- Classification of complete blood smear images as opposed to sub images;
- Use of these algorithms to segment and detect nucleated cells.

The detection design is intended to be featured using LBP and simulated through Matlab. The extraction and performance of detection of the proposed design should assure the percentage of extraction with hausdorff with LBP and without LBP results in greater difference.

A. Computer Simulation

The selection of a classification technique for classification is a challenging problem because an appropriate choice given the available data can significantly help improving the accuracy in credit scoring practice. The proposed technique has been applied on peripheral blood smear images obtained from two places, as aforementioned. To evaluate the proposed method, the following four measures of accuracy used in this paper. A microscopic blood image of size 184×138 is considered for evaluation. The superiority of the scheme is demonstrated with the help of an experiment. Feature extraction with LBP operator and with RI-LBP presented very interesting results. The system

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constructed without having to employ the LBP operator gave a higher efficiency. All the three validation methods incorporated into our system. However, the performance of HD, in particular, after using RILBP increased the classifier performance by 4%. By employing LBP, the edges of the nuclei of the myleoblasts were extracted in a very pronounced manner.

Extracted features classified using SVM.Support Vector Machines (SVMs) are a popular machine learning method for classification, regression, and other learning task. SVM first uses a nonlinear mapping function for transforming the input data from the observation space to a higher dimensional feature space, and then creates a maximum margin hyper plane to separate the two given classes. Nonlinear mapping functions transform the nonlinear separation problem in the input plane into a linear separation problem in feature space facilitating easier classification in the higher dimensional feature space.An SVM is primarily a two-class classifier. We choose a linear SVM two-class classifier; because it is not computationally expensive [1]. Three kinds of validation techniques have been used: K-fold, holdout, and leave-one-out

V. EXPERIMENTAL RESULTS

In order to ensure the effectiveness of the presented system, we employed features measures based on which decisions made.The features measuresdefined in relation to the possible outcomes of the classifier system. When attempting to classify a specimen, there are four possibilities: true positive when cancer cells are correctly identified,false positives, when non-cancer cells identified as cancerous,true negatives, when non-cancer cells correctly identified, and false negatives, when cancer cells identified as noncancerous.

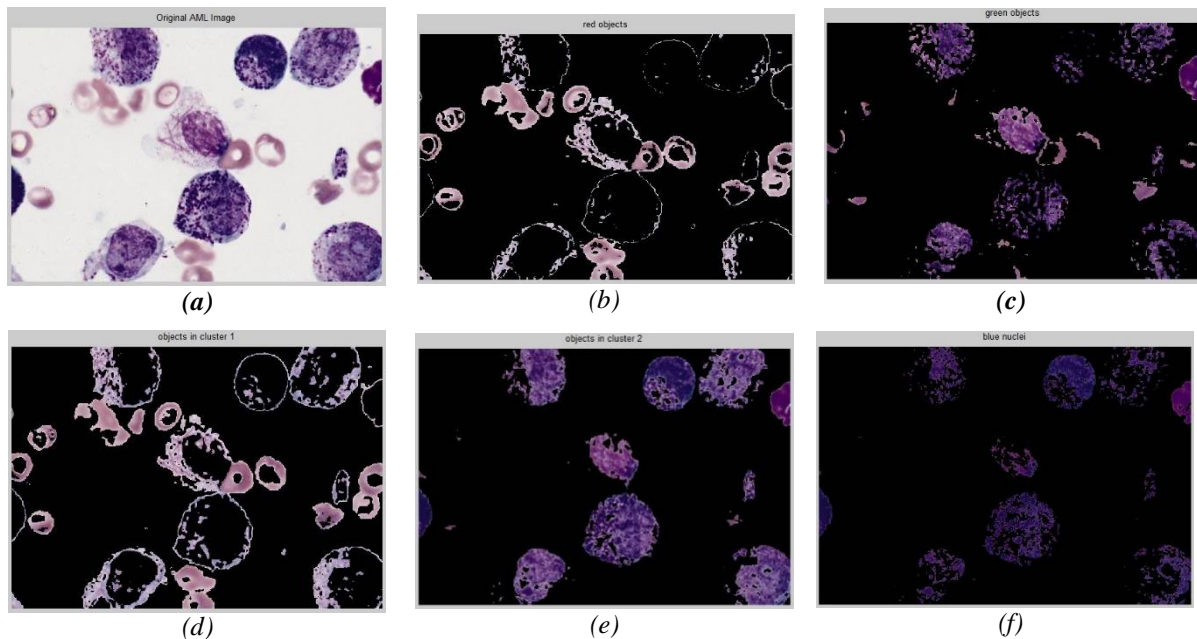


Fig 3 Detection with LBP (a)Original Image, (b) Red Image, (c) Green Image, (d) Objects in Cluster 1, (e) Objects in Cluster 2, (f) Blue Nuclei Extraction

After pre-processing the acquired image, the images have to undergo segmentation, feature extraction and classification. In this work, two clusters are formed, namely clusters of nucleus and other cells. Among them, the desired cluster is to be selected by the system. In the figure above (Fig.3), the nuclei are in the first cluster. But this will not happen always. Sometimes, the second cluster will contain the nuclei. To avoid the confusion and selection of clusters, a new colour-based algorithm is implemented.

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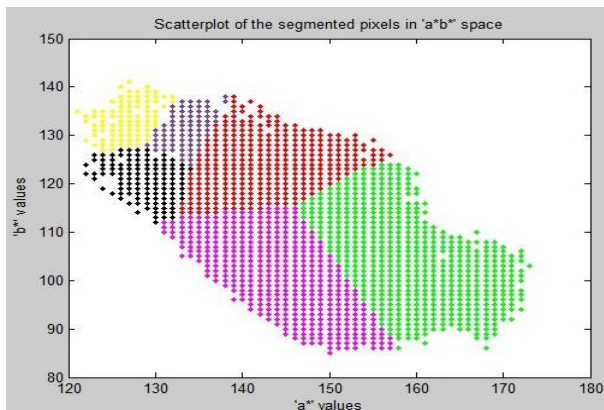


Fig. 4 Scatterplot of the segmented pixels

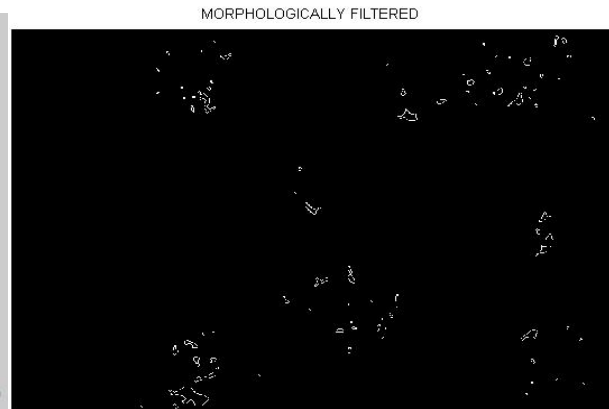


Fig. 5 Morphological Filtering

Above Figure 4 gives the scatterplot of the segmented pixel of the original images for the Hausdorff Dimension of cancerous cell and figure5 shows the segmented cell images for cancerous cell using Morphological filtering. After segmentation, a set of features of the nuclei are extracted. Based on the Hausdorff Dimension with LBP feature, the result of HD of cancerous cell is given in figure7 below for morphologically filtering method which is equal to 1.0017. The HD is found out on the basis of box counting. The number of white blood cells in the images of cancerous case is more than that of the normal case. This will result in a comparable difference in HD.

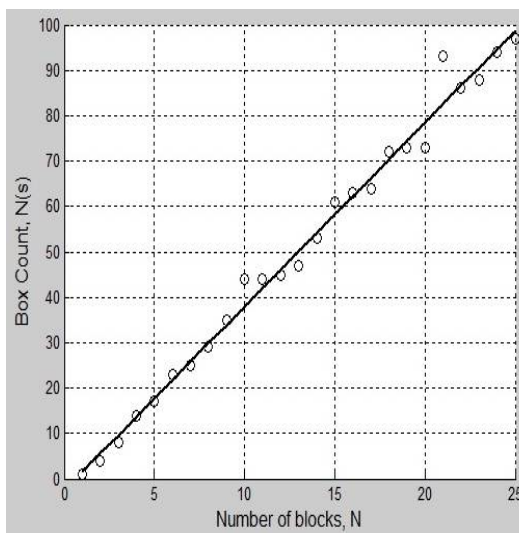


Fig.6 Hausdorff dimension with LBP

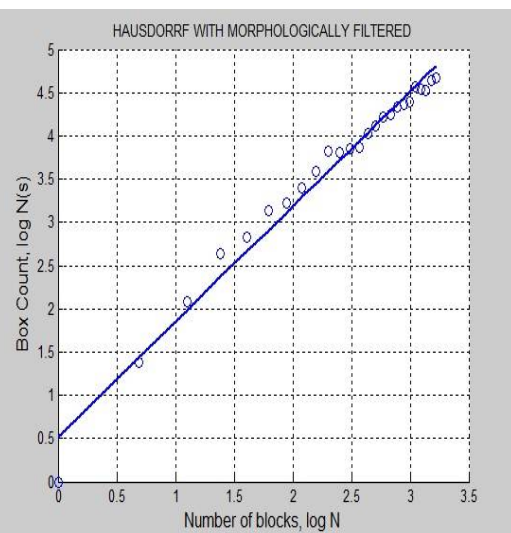


Fig. 7 Hausdorff Dimension = 1.0017

Based on the Hausdorff Dimension with RI-LBP feature, the result of HD of cancerous cell is given in figure9 below for morphologically filtering method which is equal to 1.8415. The HD is found out on the basis of box counting. The number of white blood cells in the images of cancerous case is more than that of the normal case. This will result in a comparable difference in HD

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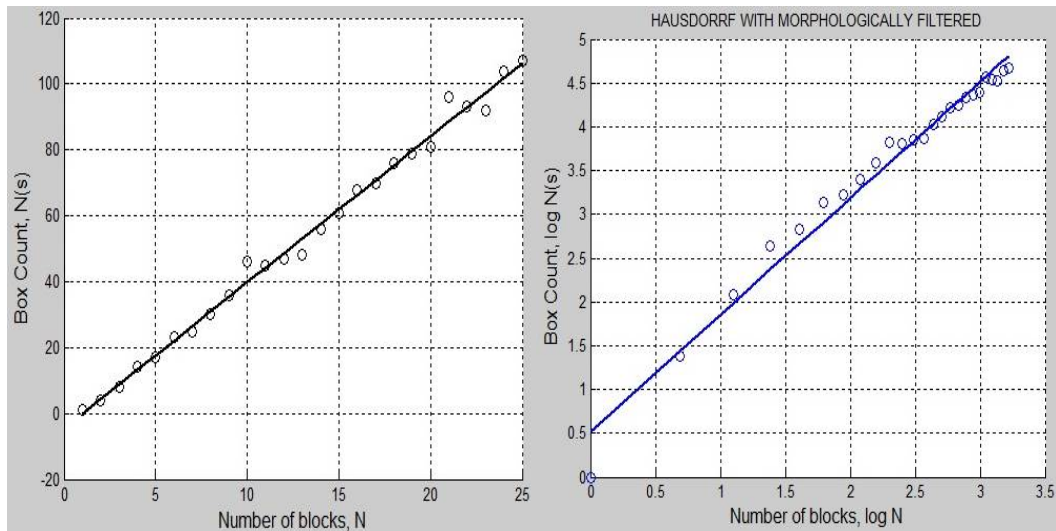


Fig 8 Hausdorff dimension with RI-LBP

Fig. 9 Hausdorff Dimension = 1.8415

VI. CONCLUSION

This work has reported the design, development, and evaluation of an automated screening system for AML in blood microscopic images. It uses 80 high-quality 184×138 size images. The presented system performs automated processing, including color correlation, segmentation of the nucleated cells, and effective validation and classification. A feature set exploiting the shape, color, and texture parameters of a cell is constructed to obtain all the information required to perform efficient classification. The impact of the RI LBP operator on the HD proved to be a promising feature for this analysis. The future expansion is to focus on collection of more samples to yield better performance. And the same is to be utilized for detection of various leukemia which is under research still now.

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