

# ANALYSIS OF AUTOMATED DETECTION OF WBC CANCER DISEASES IN BIOMEDICAL PROCESSING

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**Abstract** – Medical industry is one of the most prominent industry where deep learning can play a huge role especially when it comes to medical imaging. Automated diagnosis of WBC cancer diseases such as Leukemia and Myeloma having similar symptoms. Therefore, from the doctor’s side, they might be confused to diagnose those two diseases. In this paper, a new approach named-Random forest classifier is applied for final decision. The system learning methodology is reduce the misdiagnosis cases. The proposed system will produce the parameters such as Mean, Accuracy, Texture features will be evaluated and the experimental result shows that the increase in the three parameter values will reduce the noise of an image.

**KeyWords:** white blood cell, random forest, diseases

## INTRODUCTION:

Leukemia is a type of cancer that affects the bone marrow causing increased production of white blood cells which influx the blood stream[1]. White blood cells help the body to fight infections and other diseases. Red blood cells carry oxygen from the lungs to the body's tissues and take carbon dioxide from the tissues back to the lungs[2]. The images generated by digital microscopes are usually in RGB color space, which is difficult to segment[3]. The blood cells and image background varies greatly with respect to color and intensity[4]. The approach of leukocyte classification consists of two parts: (1) The segmentation of leukocyte, cytoplasm, and nucleus; (2) The classification of the segmented leukocytes using a set of features[5]. For the segmentation procedure the input image contains at least one leukocyte. Image pre-processing, feature extraction and classification plays major role in detection of white blood cell cancers[6]. The removal of noise is another main factor that yields accuracy to final result. The main goal is to de-noise the input image. Pre-processing also includes color relevance wheel RGB images are converted to Grey color space images[7]. When there is huge data, it is inefficient and consumes more time, and multiple comparisons of persons at a time are not possible and finding the stages is difficult. So here we are going to

develop an innovative approach for finding the optimal sequence alignment to reduce the time, space complexity and increase the efficiency of sequence alignment in the large data set and find the stages of CML. Here we are using innovative DSDPM algorithm, it is dynamic and recursive optimal distance calculation method to reduce the execution of time and making it cost effective for finding the mutation and optimal sequence alignment.

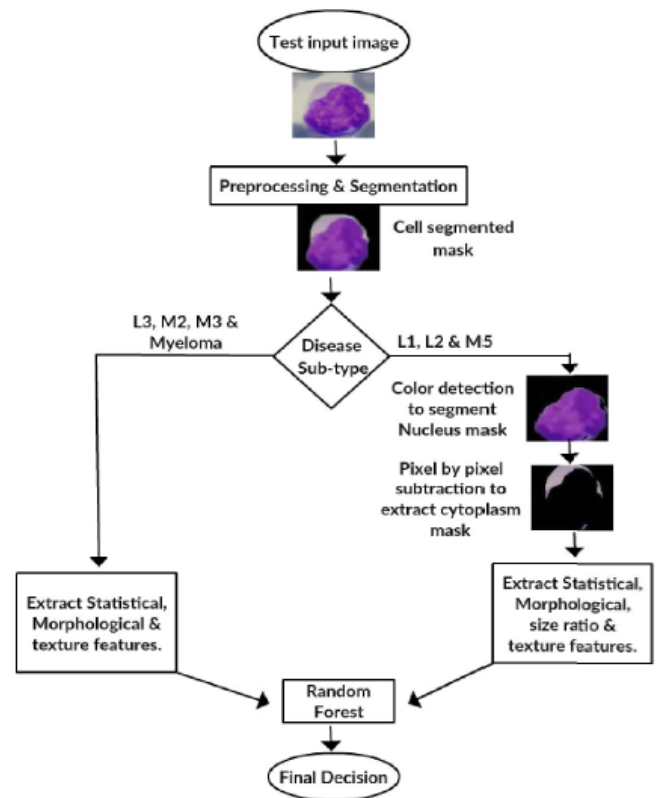


Fig:1 Process flow chart

## 2. METHODOLOGIES

Dr.T. Karthikeyan (2017) This paper proposes the White blood cells may be produced in excessive amounts and are unable to work properly which weakens the immune system. Careful microscopic examination of blood smear

or bone marrow aspirate is the only way to effective diagnosis of leukemia. The need for automation of leukemia detection arises since the above specific tests are time consuming and costly. A low cost and efficient solution for quantitative examination of stained blood microscopic images for leukemia detection. Fuzzy c means is compared with k means for image segmentation, in which Fuzzy c means gives higher accuracy than k means, Gabor Texture Extraction method is used to extract color features from images and finally extracted features are used for classification. Fuzzy c means gives 90% accuracy whereas k means gives 83% accuracy. Support Vector Machine is used for classification. The work has been developed using MATLAB 7 environment.

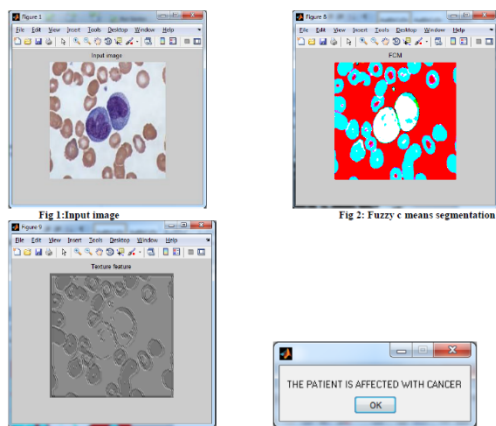


Fig:2 Leukemia Classification

Fuzzy c means gives 90% accuracy whereas k means gives 83% accuracy. Based on this segmentation result, the patient will be affected by cancer.

Romel Bhattacharjee (2015) This paper describes a large number of diseases can be diagnosed. One type of the most common blood diseases is Acute Lymphoblastic Leukemia (ALL). Rapid and uncontrolled growth of immature leukemic cell is used to characterize ALL. The morphological analysis of the bone marrow and blood smear is the primary step of diagnosis. Valuable information is provided by the features extracted from the blood cells for the confirmation of the diagnosis. For each class, two intensity and label dictionaries are designed for representation using image patches of training samples. New image is represented by all dictionaries and the one with minimum error determine the type of class. We considered M2, M3 and M5 subtypes for evaluation of the method.

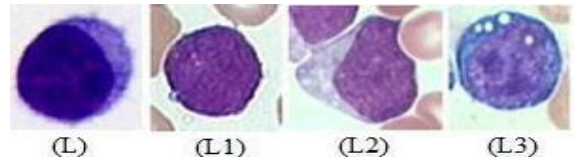


Fig:3 Morphological variability of blast cells (L) healthy lymphocytic cell, (L1), (L2), (L3) are lymphoblasts.

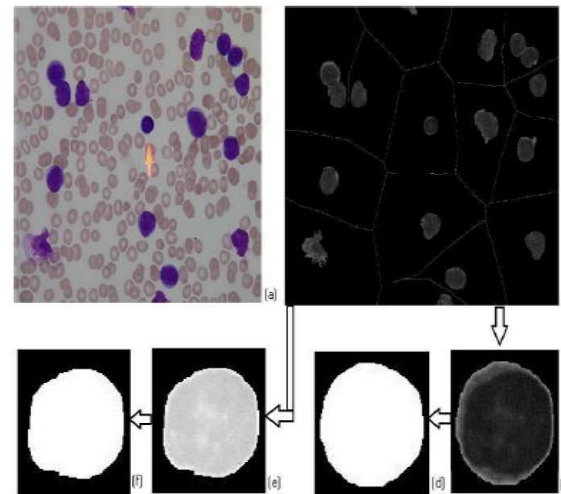


Fig:4 Segmentation of the lymphocytic image. (a) lymphocyte cell image in RGB; (b) segmented image; (c) isolated lymphocyte cell; (d) isolated lymphocyte cell in binary; (e) isolated cell nucleus; (f) isolated cell nucleus in binary.

The implementing of the proposed method achieved 97.53% average accuracy for different sub-types of AML.

Monica Madhukar (2014) Acute myelogenous leukemia (AML) is a subtype of acute leukemia, which is prevalent among adults. In this paper, a simple technique that automatically detects and segments AML in blood smears is presented. Computer simulation involved the following tests: comparing the impact of Hausdorff dimension on the system before and after the influence of local binary pattern, comparing the performance of the proposed algorithms on subimages and whole images, and comparing the results of some of the existing systems with the proposed system. Eighty microscopic blood images were tested, and the proposed framework managed to obtain 98% accuracy for the localization of the lymphoblast cells and to separate it from the subimages and complete images.

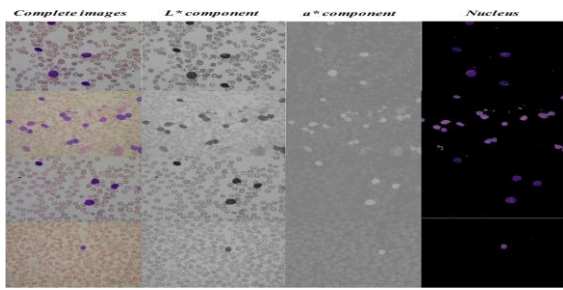


Fig:5 RGB to CIELAB conversion and segmentation

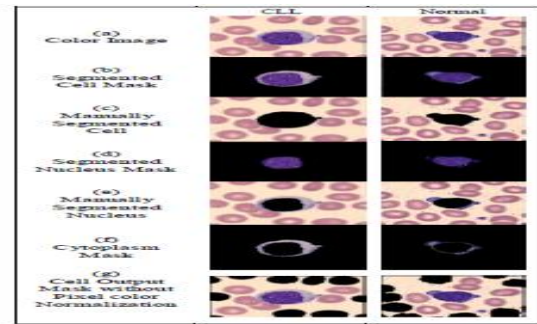


Fig: 7 The segmentation method output.

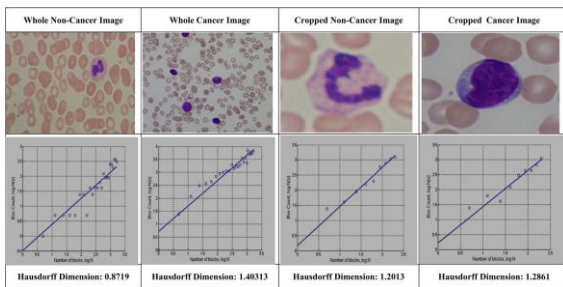


Fig: 6 Results of HD

This is observed that the LBP operator enhanced the overall performance by a very high margin

Emad.A.Mohammed (2013) Chronic lymphocytic leukemia (CLL) is the most common type of blood cancer in Canadian adults. CLL cell morphology maybe similar to normal lymphocytes. There are a low number of related works on image analysis in CLL. This is focused on lymphocyte color cell segmentation using Support Vector Machine (SVM) and k-means clustering algorithms. The algorithm overcomes the occlusion problem when lymphocytes are tightly bound to the surrounding Red Blood Cells. Over and under-segmentation problems are significantly reduced. In this paper we used 440 lymphocyte images (normal and CLL), in which 140 images are used for segmentation accuracy measurement and 12 images for SVM training. The algorithm obtained 98.43% maximum accuracy for nucleus segmentation, and 98.69% for cell segmentation. The cytoplasm region can be extracted by 99.85% maximum accuracy with simple mask subtraction.

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Ruggero Donida Labati (2011) Automated systems based on artificial vision methods can speed up this operation and increase the accuracy and homogeneity in telemedicine applications. In this paper, we propose a new public dataset of blood samples, specifically designed for the evaluation and the comparison of algorithms for segmentation and classification. For each image in the dataset, the classification of the cells is given. Similarly a specific set of figures of merits to fairly compare the performances of different algorithms. This initiative aims to offer a new test tool to the image processing and pattern matching communities, direct to stimulating new studies in this important field of research.

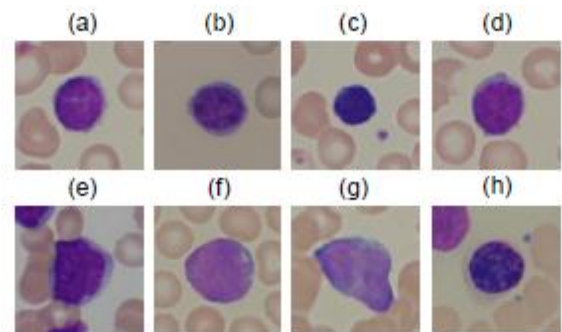


Fig: 8 Example images contained in the ALL-IDB2: healthy cells of non-ALL patients (a-d), lymphoblasts from ALL patients (e-h).

Subrajeet Mohapatra(2011) Acute lymphoblastic leukemia (ALL) are a group of hematological neoplasia of childhood. ALL makes around 80% of childhood leukemia. The non specific nature of the signs and symptoms of ALL often leads to wrong diagnosis. Diagnostic confusion is also posed due to imitation of similar signs by other disorders.. Techniques such as

fluorescence in situ hybridization (FISH), immunophenotyping, cytogenetic analysis and cytochemistry are also employed for specific leukemia detection. The need for automation of leukemia detection arises since the above specific tests are time consuming and costly. A low cost and efficient solution is to use image analysis for quantitative examination of stained blood microscopic images for leukemia detection. A fuzzy based two stage color segmentation strategy is employed for segregating leukocytes or white blood cells (WBC) from other blood components. Discriminative features i.e. nucleus shape, texture are used for final detection of leukemia. In the two novel shape features i.e., Hausdorff Dimension and contour signature is implemented for classifying lymphocytic cell nucleus. Support Vector Machine (SVM) is employed for classification.

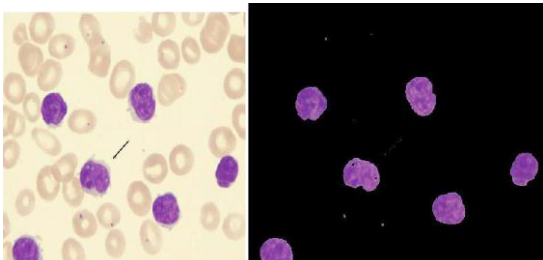


Fig: 9(a) Input and Segmented Output

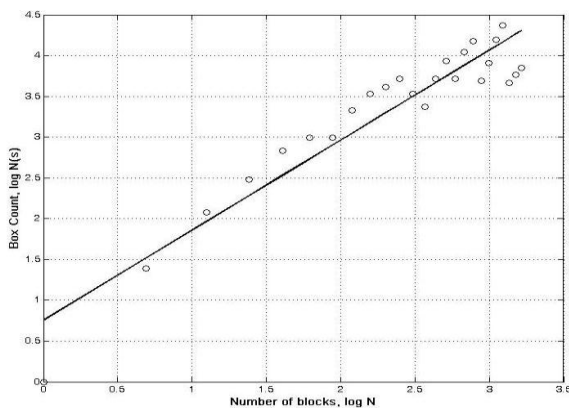


Fig: 9(b) Box Counting Algorithm Results

In this scheme the available images were used for training SVM classifier and an accuracy of 93% was observed.

## RESULT AND DISCUSSION

In this paper, the shape, mean, accuracy, color and texture features gives the better detection accuracy to identify the subtypes of leukemia and myleoma.

## 4. CONCLUSION

In this survey paper, various wbc cancer diseases and its subtypes are identified. By comparing the other classifiers, random forest classifier will produce better accuracy (94.3%). It is the best classifier for identification process.

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