

# Leukemia Detection Using Image Processing

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## ABSTRACT

Digital image processing for medical images has advanced so much in a very short period of time, but we still have to figure out very narrow issues which can be very important sometimes. One such problem is to successfully differentiate between a normal bone marrow slides images with an abnormal one. This needs to be done with high accuracy because these classification results will be going for classification of different types of Leukemia. In order to work through the process, a number of features will be extracted from each image. A set of images will be used to get the features and another set will be used to test out the features extracted from the training dataset. This classification technique is done at a high accuracy rate to identify a malicious Leukemia image.

**Keywords:** Leukemia, image processing

## INTRODUCTION

From multiple types of cancers, Leukemia is one type of blood cancer. As per <sup>1</sup>, about 4.5% cases of cancer in Malaysia are for Leukemia. This type of cancer starts in bone marrow. The main cause of Leukemia is extra formation of malignant white blood cells (WBCs) which are also immature in nature <sup>2</sup>. Unfortunately, children are more likely to have Leukemia as compared to adults. There are four types of this cancer:

- AML - Acute Myelogenous Leukemia
- ALL - Acute Lymphocytic Leukemia
- CML - Chronic Myelogenous Leukemia
- CLL - Chronic Lymphocytic Leukemia

Types of WBCs which can be affected by Leukemia are neutrophils, basophils, along with eosinophils, monocytes and lymphocytes. The progression speed of acute Leukemia (AML and ALL) is more than chronic

Leukemia (CML and CLL). If caught at early stages of the disease, Leukemia is very much curable and treatable. A hematologist recommends a complete blood count (CBC) test to check for the disease. A detailed study of morphological marrow of bone smear analysis needs to be conducted if there are found any form of abnormal counts of the cell from the test. This is finalized to ensure the presence and detection of leukemic cells in the blood <sup>3</sup>. There are instances where the counts of platelets and RBCs becomes very low in leukemia. Based on the current scenario in medical industry, the presence of leukemia is observed by taking a look at the nucleus and the cytoplasm via a microscope <sup>4</sup>. The only problem is that this task of looking under the microscope is a very tedious task to accomplish, and that goes even for an expert too. Because of this process's extensive nature of diagnose, the final results might lead to misdiagnosis.

Classification of leukemia is a long and complicated process with multiple steps. The first step is to separate the images of bone marrow into normal and abnormal category. Again, this classification is also a multistep process. These processes are as follows:

- Image enhancement
- Image segmentation
- Features extraction
- Classification

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In medical imagery, the first step which is image enhancement plays a very important and crucial role. Reason being this step improves and enhances the quality of the image and it becomes easy and efficient for human viewing. But medical images comes with their own issues and weaknesses. This issue is missing contrast from the image which is due to the bad lighting at the time of image acquisition. Hence, image enhancement steps are taken so that this problem can be overcome with. The steps which leads into image analysis and image interpretation is none other than image segmentation, in this step the medical image is separated into regions <sup>5</sup>. The tasks which follows this one, such as feature extraction and image classification relies heavily on the quality and efficiency of image segmentation <sup>6</sup>. In Leukemia, WBCs holds very important information about the diagnosis of leukemia. Hence, during the segmentation process the RBCs and background will be segmented and we are left with the WBC only which will go further into the analysis. The next step is to extract the features out of the image having only WBCs. These are the features holding vital information about the classification and diagnosis. A hematologist observes the WBCs from the image on various parameters <sup>7</sup>:

- Size
- Shape
- Nucleus chromatin structure and its characteristics
- Nucleoli's size and color
- Cytoplasm's color
- Characteristics of granules and their presence/absence

These are some of the features which are extracted in order to classify efficiently. Color based features are extracted in this paper, which are as follows:

- Standard deviation
- Mean
- Variance

These features are extracted for red, blue and green channel separately. These features are then used to classify the faulty and non-faulty leukemic cells. We can categorize the whole implementation is broadly divided

into two parts:

This would be our base dataset, which we will use to create a baseline for comparison with other images.

We then need to process the other half of raw data i.e. we process the remaining images to as to make a decision for test images. This decision will be in regards to whether the test images belong to cancerous or non-cancerous category.

The whole project will be divided into 2 parts. Part 1 involves extracting features from a set of sample images, part 2 is about comparing the extracted features with images to mark them as cancerous or not. We have employed 35 distinct sample images to create a baseline data as well as comparison with the test images. This data size can obviously be increased or decreased as per the user's requirements. But as per the author's guidelines, the bigger the training dataset images, the better. More number of input images will yield better baseline and hence better results to compare with. Once the extraction process is complete, we define the optimal range for each feature. This range for every feature will be used in the next step in order to classify the images into cancerous and non-cancerous category. Part 2 takes a test image as input and extracted feature range from part 1 as well is taken as input. Features are extracted for the test image. These new features will be compared with the feature database and baseline. This is how the new image is classified into cancerous and non-cancerous categories.

## METHODOLOGY

In the given paper, the author has used the following methodology for the implementation of a generic system to classify leukemic cells in the blood samples. The process is automated so that manual interventions like looking under a microscope could be dealt with and an efficient result could be obtained. Because a misdiagnosis in this case could be a heavy mistake from the medical perspective.

- Input all the images (cancerous only) into the system
- Extract the following parameters from these images, one by one
  - o Mean value of red channel pixels
  - o Mean value of blue channel pixels

- o Mean value of green channel pixels
- o Standard deviation of red channel pixels
- o Standard deviation of blue channel pixels
- o Standard deviation of green channel pixels
- o Variance of red channel pixels
- o Variance of blue channel pixels
- o Variance of green channel pixels

- In this code, we are using a total of 35 images (we can increase this number by including more images)

- Hence, we will get a total of 35 sets of parameters for all the cancerous images

- After getting all the values, we will decide a range for maximas and minimas for all the parameters used.

- After this, we will have a range for each parameter.

- To test an image, again calculate all the above parameters for that test image

- Now, if any of the parameter of test image comes under the range of our dataset, the image comes closer to be a cancerous image

- But, if even 1 of the parameter is out of range, then test image is declared not cancerous.

- To test, a set of random images is also given.

### RESULTS AND DISCUSSION

Following are the images which passes the test and are termed as healthy cells based on the classification criteria.

Based on the above experiment, it is evident to say that the implementation based on feature extraction specifically on the color features of these images works really well and efficiently.

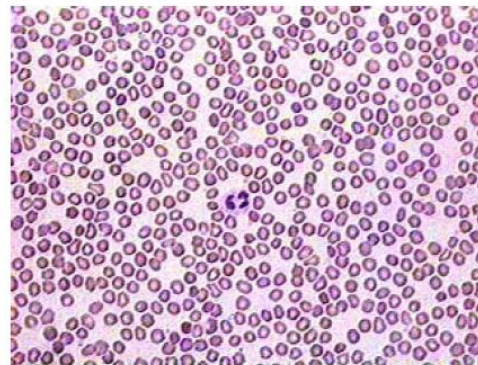


Figure 1. First case image after calculate Mean value

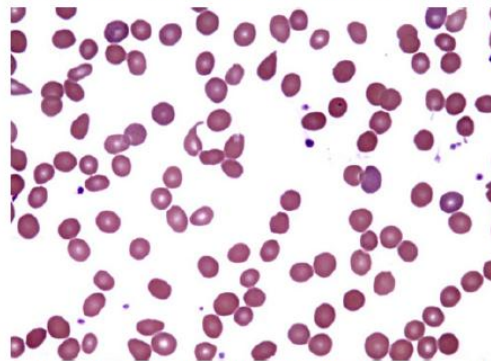


Figure 2. First case image after calculate Standard deviation value

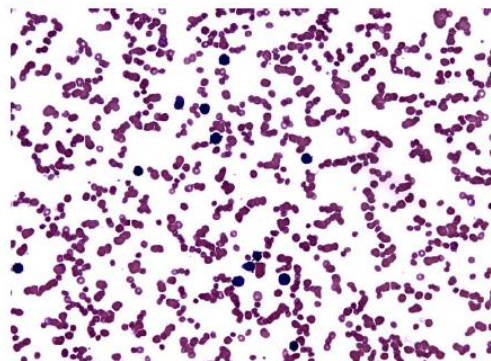


Figure 3. First case image after calculate Variance value

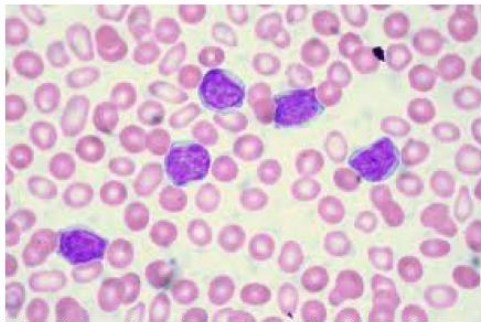


Figure 4. Second case image after calculate Mean value

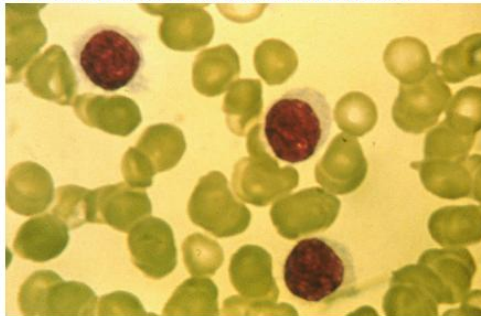


Figure 5. Second case image after calculate Standard deviation value

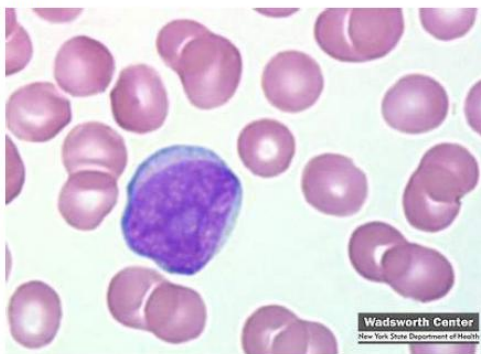


Figure 6. Second case image after calculate Variance value

### CONCLUSION

This paper study involves classification of leukemic affected cells from the general lot of healthy cells. This is done using the microscopic blood sample images. The proposed system uses the microscopic images and extract the features in terms of standard deviation, mean and variance of red, green and blue channel of the microscopic blood sample images. The algorithm used in the above discussion is able to identify the infected cells in RBCs when used for an infected individual.

The system showed efficiency, reliability, was able to perform calculations in a considerable less amount of time and with much less error, high accuracy, cheaper computation cost and a robustness in finding the exact solution. This way, it'll become easier to identify the diseased patient.

**Financial Disclosure:** There is no financial disclosure.

**Conflict of Interest:** None to declare.

### Ethical Clearance

All experimental protocols were approved under the College of education for pure science, University of Babylon, Iraq and all experiments were carried out in accordance with approved guidelines.

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