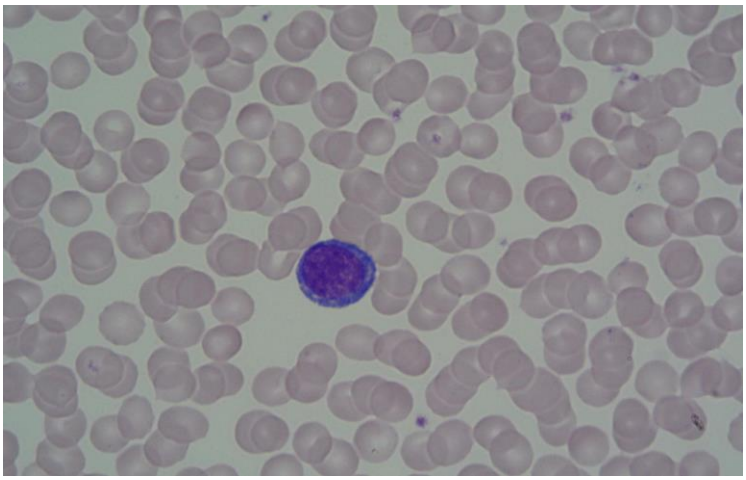
Title: **Leukemia Detection**

Analyze the microscopic blood cell images and focus on the changes in the geometry of cells and statistical parameters for separates white blood cells from other blood components by using image enhancement, image segmentation and feature extraction (Leukemia Detection)



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SCOPE

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Chapter 1
ABSTRACT

Leukocytes, produced in the bone marrow, make up around one percent of all blood cells. Uncontrolled growth of these white blood cells leads to the birth of blood cancer. Out of the three different types of cancers, the proposed study provides a robust mechanism for the classification of Acute Lymphoblastic Leukemia (ALL) and Acute Myeloid Leukemia(AML) is a type of cancer where the bone marrow forms too many lymphocytes. They crowd out and prevent the production of healthy blood cells. Conventionally, the process was carried out manually by a skilled professional in a considerable amount of time. The proposed model eradicates the probability of errors in the manual process by employing machine learning techniques . The model, trained on cells' images, first pre-processes the images and extracts the best features. This is followed by training the model and finally predicting the type of cancer present in the cells. The model was able to reproduce all the measurements correctly while it recollected the samples exactly 94 times out of 100. The overall accuracy was recorded to be 97.2%,

which is better than the conventional machine learning methods like Decision Trees, Random Forests, Naive Bayes, etc. Thus, the model can be used effectively as a tool for determining the type of cancer in the bone marrow

Keywords: Acute Lymphoblastic Leukemia, Acute Myeloid Leukemia, Classification algorithms, Machine Learning, Image processing

CHAPTER 2

OBJECTIVES

Leukemia means blood cancer which is characterized by the uncontrolled and abnormal production of white blood cells (leukocytes) by the bone marrow in the blood.It is one of the serious cancers that threaten the existence of human beings.In spite of its prevalence and serious consequences, it is mostly diagnosed through manual practices.Counting and examination of blood cells manually by microscope is tedious, time intense and entails a lot of technical expertise.It may lead to wrong analysis due to which patients are treated wrongly.Hence there arises a need to come across for automated blood cell detection and counting system that can facilitate physician for diagnosing diseases in fast and efficient way that can replace the manual process. Detection through images is a fast and cheap method as there is no special need for equipment for lab testing. Distinctive image processing processes like Image acquisition,Image preprocessing,Image segmentation,Feature extraction ,Image enhancement, Clustering, Mathematical process and Labeling has been used.After enhancement, segmentation is done to concentrate on the area of interest; in this case it is the nucleus. We apply Feature extraction after that we have connected it to the classifier to get the desired results as whether the cell is cancerous or not.Therefore automatic image handling framework can overcome related limitations in visual investigation from manual processes which provide early detection of disease and also type of cancer.

CHAPTER 3

LITERATURE REVIEW

3.1. National Status

Paper	Findings and conclusion	Methodology	Reliability
1.	-In this paper, ineffective ancient method of cancer detection has been replaced by present (effective) method of cancer detection -Along with leukemia, a brief information about detection of other diseases like brain cancer and diabetes has been included.	**- Image acquisition**- From nearest university lab **-Image Preprocessing**- Elimination of undesirable noise, contrast enhancement, histogram equalization **- Image Segmentation**-thresholding **-Feature extraction**-. **-Geometrical** - cell volume, perimeter, radius, eccentricity, symmetry and concavity **-Texture**-correlation factor,entropy, contrast and power. **-Statistical-** mean, variance, standard deviation and skew of the object matrix histogram.	Yes
2.	-Automatic handling framework can detect leukemia earlier and more precisely than the hematologist -In this paper Symptomatic radio-graphy has been used for image processing that assigns the technological parts of medicative pictures	**-Image acquisition** -Images of Blood are collected from hospitals **-Image preprocessing** -Color image is converted to gray scale Followed by filtering the image, removal of noise from the image and finally histogram equalization is done **-Segmentation**- k-mean clustering is used where the nucleus is concentrated for the detection process. **-Feature extraction** -features of nucleus are extracted using GLCM and GLDM.f **-Features of the cancerous cell:** Its type is found among acute myeloid leukemia	**no**

3.	The paper discusses that there is a need for an automatic diagnosis and classification method that can replace the manual process that is not reliable.	**-Image acquisition** -Microscopic images Blood is collected with proper magnification **-Preprocessing** -The first stage in which distortions in image are removed . A Gaussian filter is used to change the weight at a damaged distance. **-Enhanced Multi-Parameters Clustering Algorithm Segmentation**-Image components are segregated under different groups where specific focus has been given to clustered image segmentation. **-Functions used in Feature extraction:** Energy, Contrast, Correlation, Homogeneity, Mean, Skewness, Kurtosis **Classification** identification of specific morphology of WBCs so that its relative functions can be developed.	**Yes**
4.	-The paper tells about an advanced method for detection of leukemia that uses cell count and some other parameters like area and perimeter. -It has the facility of converting RGB image to gray colour image and converting grey colour image to binary image directly. installing macros for each step also facilitates the process. .	**-Image acquisition**: Input sample image is taken from the research labs. -**Preprocessing**-Input RGB image is converted into the grey colour image for identifying and differentiating the cells present . **-Segmentation**-The method of thresholding is used for segmentation . **-Feature Extraction** The parameters like area and perimeter and number of blood cells present in the given input sample image are detected.	**Yes**

5.	In this paper an automated blood cell detection and counting system has been introduced that uses image processing to overcome the past problems of the blood testing.Blood are classified on the basis of color, texture and morphology.	**-Image Acquisition**- Images taken from hospital labs for detection**.** **-Image Segmentation**-Segmentation based on thresholding has been used to segment the image in constituent objects based on some threshold criteria T. **-Image Morphology for Feature Extraction** - extracts the elements of any image such as boundary extraction, morphological filtering etc that prepares the image for further processing. **a.Median Filtering**:Nonlinear smoothing spatial filter often used for noise reduction to enhance the quality of the edges in an image. **b.Edge detection** -Sobel edge detection operator is used here which uses a 3*3 mask around each pixel value of an image to approximate the corresponding image gradient. **c.Smoothing Using Erosion:**Enhances the quality of edges in an image.	**No**
6.	- The paper says that the Existing microscopic image processing approaches are unable to analyze the ALL data with non-stationary nature so the focus of this research is to design hybrid Convolutional Neural Network (CNN) to detect the ALL from microscopic images of human blood cell into malignant -To train the ALL-DC model, a fuzzy based CNN classifier is used which helps to achieve better detection and classification accuracy.	**-Acquisition**- Images were extracted from research labs. **-Image preprocessing**-Here, Lighting based Microscopic Image Enhancement (LMIE) technique is used for image preprocessing . **-Segmentation**-K-mean with FOA is proposed as an optimization approach for minimization of irrelevant area from the segmented ROI of microscopic image. **-Feature Extraction:**Feature is extracted from the ROI of the cell portion of a microscopic image based on the HOG feature extraction algorithm. **-Classification**-CNN	**Yes**
7.	-In this paper , a machine learning model to detect and classify immature leukocytes for efficient diagnosis of AML is presented. -Images of leukocytes in AML patients and healthy controls were obtained from a publicly	**-Dataset** Labelled images of leukocytes from the peripheral blood of 100 AML patients and 100 healthy controls are collected from the dataset . **-Segmentation:** Morphological dilation followed by erosion was used to separate noise from the region of interest (ROI).	**Yes**

	available dataset in The Cancer Imaging Archive.The nucleus to cytoplasm area ratio was a discriminative feature for both detection and classification ranked using the Gini importance, which is defined as the loss of Gini impurity caused by each feature in the random forest.	**-Feature Extraction:** From each image, 16 cytomorphological features were extracted, which could be divided into four categories: nucleus size etc. **-Classification** A random forest algorithm is chosen for classification. Binary classification between immature and mature leukocytes is first performed, followed by classification of immature leukocytes into four types.	
8.	In this paper, Simple modifications to standard neural network architectures have been proposed to achieve high performance in the malignant leukocyte classification problem. -Transformations such as mirroring, rotation, blurring, shearing, and addition of salt and pepper noise were used.	**-Methodology:** images of healthy and malignant lymphocytes from C-NMC 2019 Dataset were used for training variations of the Exception and VGGNet architectures, in order to create a classifier capable of distinguishing the two cell types. .All the steps related to image preprocessing, image enhancement, lymphocyte segmentation, and stain normalization were performed using standard image processing techniques and inhouse methods.	**Yes**
10.	For the detection through images focus has been made on the changes in the geometry of cells like area, perimeter and statistical parameters like mean and standard deviation which separates white blood cells from other blood components using processing tools like MATLAB.	**-Image Preprocessing-**Contrast enhancement , histogram equalization **-Image Segmentation**- thresholding **- Feature extraction**- Mean, variance, standard deviation and skewness of histogram of image matrix of cell and gradient matrix are acquired. **-Textural**:homogeneity, correlation factor, entropy, contrast etc. **-Edge Detection by Sobel operator** **-Classification:** k-means clustering	**Yes**
11.	-The paper discusses about computer vision system that can detect and estimate the number of cancerous cells in blood Using KNN and Hough Transform Algorithm. -Overall every information about the blood and the blood samples	**-Preprocessing:** contrast enhancement **-Segmentation:** performed by thresholding **- Feature Extraction:** · Geometrical Features. · Texture Features · Color Features · Statistical Features **-Classification:**	**No**

	has been discussed in this paper ,like cell count,detection, other prevention and treatment like chemotherapy,radiotherapy etc.	. KNN(K-Nearest Neighbor Algorithm)	
12.	-The leukemia cell has been extracted and detected using the watershed technique. -The Simulation of blood cells will be done on MATLAB from the original blood sample image from Lab.	**-Image acquisition:** Blood image from slides with effective magnification is taken. **-Segmentation by Watershed algorithm:** Starting from user-defined markers, the watershed algorithm treats pixel values as a local topography (elevation). **-Abnormal blood cell detection and feature extraction:** Total number of cells in blood sample image has been calculated to find the average parameters for a single cell and Compactness and Form Factor for cells were calculated to calculate the time for code execution.	**Yes**
13.	In this paper, a technique for automatic detection and classification of AML in blood smear is presented. For the different image processing technique K-means algorithm ,spatial and spectral features , Genetic algorithm ,Local ternary pattern were used	**-Image acquisition:** Blood image from slides with effective magnification is taken. **-Image preprocessing:** Pre-processing is done by contrast stretching. **-Segmentation-** K-means clustering algorithm is used for segmentation that uses three clusters corresponding to nucleus, background and other cells. **-Feature Extraction:** Spatial and spectral features are used.The **texture features** such as energy, contrast, homogeneity, correlations and Hausdorff Dimension are used . **Color based features** like Mean, standard deviation and energy are the important color features used for classification. **-Classification:** In the proposed work, Support Vector Machine (SVM) is used for classification.	**Yes**
14.	-This paper analyzes the work done on leukemia detection and	**-Image Acquisition:**Blood sample is taken by a trained pathologist from the lab**.**	**Yes**

	diagnosis using machine learning, deep learning and different image processing techniques using the bibliometric methods.	**-Pre-processing and segmentation purpose.** Popular algorithms include watershed transform, Zack algorithm, gray scale transformation, edge detection **-Feature Extraction:** Different features are extracted for the purpose of selecting the region for classification that include statistical features, texture features, color features	
15.	Different strategies for detecting WBC have been proposed in this research. Segmenting, detecting groups of leukocytes, and extracting their characteristics are some of the approaches used. .	**-Image acquisition:** Blood image from slides with effective magnification is taken. **-Image preprocessing:** Various pre-processing techniques so that the images are appropriate for contrast and the further footstep in the processing. **-Feature Extraction**- large amounts of data is taken and turned into a reduced representation by taking advantage of the features of the existing data. **-Features used**:Fractal Dimension, Local Binary Patterns (LBP),Texture Features,Shape Features,Color Features.	**No**

3.2. International Status

Paper	Findings and Conclusion	Methodology	Reliability
1	This paper has discussed different preprocessing techniques, and leukemia classification techniques. Also it contains a brief knowledge about recent available methods used for classification with results and analysis. So, leukemia disease can be classified using many	**-Image Preprocessing** To perform noise reduction, a Wiener filter and median filter is used. **-Feature Extraction** Feature extraction can be done by separating the similar gray values together. It contains shape features,	**YES**

	latest machine learning algorithms.	edge features, number of connected components, area and perimeters of image. **-Image Segmentation** Repetitive thresholding algorithmic rule is employed for segmentation purposes particularly from noisy pictures. **-Image Classification** SVM with 95% efficiency	
2	The proposed model annihilates the likelihood of blunders in the manual procedure by utilizing a profound learning strategy in particular convolutional neural systems. It predicts the type of cancer in the given image with an accuracy evaluated to 97.2%. The proposed model performed better than the baseline methods like SVM, decision trees.	**-Image Acquisition** Dataset consists of images of patients diagnosed with Multiple Myeloma. **-Data Augmentation** The dataset is first augmented by rotating the image and extracting edges. **-Feature Extraction** We extract the features such as Color, Geometry, Texture features and statistical features. **-Image Preprocessing** **-Image Classification** An optimized Convolution Neural Network(CNN)	**No**
3	This research work has presented a complete architecture based on deep learning techniques for the classification of ALL and achieved 97.78% accuracy	**-Image Acquisition** Microscopic images of bone marrow are taken with a Euromax digital camera microscope **-Image Preprocessing** The image is first converted into HSV (Hue, Saturation, Values) color space, and then processed by the S component of the specified color model to get the region of interest (Lymphoblast). **-Image Segmentation** Simple threshold is applied that is the maximum threshold and the image is then converted back to RGB **-Image Classification** Deep learning technique using Alexnet model with CNN for the classification of ALL into its subtypes and normal condition.	**NO**

4	This paper has proposed an algorithm that combines the lobes of nuclei using their own characteristics, and then detect WBC using the location of the nucleus of leukocyte, which is timeless and accurate in experiments. It has an automatic recognition system for WBC, a method for detecting WBCs from peripheral blood images directly and classifying them without manual operation.	**-Image Acquisition** Blood image from slides with effective magnification is taken. **-Image Detection** It detects WBCs from the microscope images based on the simple relationship of colors and the morphological operations. **-Feature Extraction** Different statistical parameters **-Features Used** Convolution Neural Network(CNN),SVM,PRICoLBP	
5	The main aim of this paper is nucleus segmentation followed by feature extraction to detect Leukemia.	**-Image Acquisition** Microscopic images of blood cells are acquired with a digital microscope having an inbuilt camera inside it. **-Image Enhancement** A global contrast stretching and segmentation based on HIS color space is used to improve the image quality. **-Image Segmentation** Automatic Otsu's Thresholding along with morphological operations and watershed transform. **-Feature Extraction** Geometrical features	**YES**
6	The automatic detection and counting of lymphoblasts aims to provide additional support to medical practitioners while diagnosing acute lymphoblastic leukemia.	**-Image Acquisition** Blood samples taken from healthy and infected patients . **-Image Preprocessing** The lymphoblasts can be identified by converting the blood sample from RGB to CMYK **-Image Segmentation** Zack algorithm or triangular method is used to find the thresholding value. Then a histogram of the image is applied. **-Feature Extraction** Hough transform is a feature extraction technique used to detect lines, circles, ellipses and other features when their parametric equations are known.	**YES**

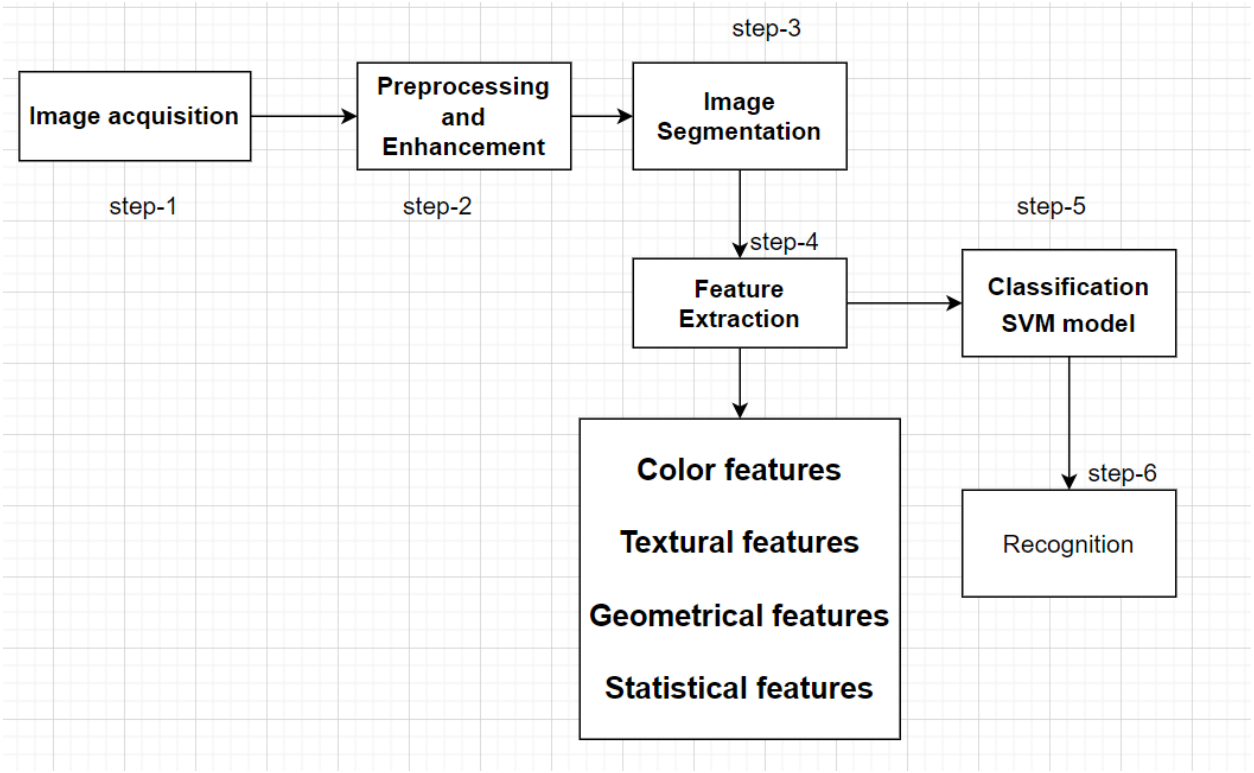
7	This system performs automated processing, including color correlation, segmentation of the nucleated cells, and effective validation and classification. A feature set exploiting the shape, color, and texture parameters of a cell is constructed to obtain all the information required to perform efficient classification.	**-Colour Correlation** An adaptive procedure is used: the RGB input image is converted into the CIELAB. **-Image Segmentation** Segmentation is performed for extracting the nuclei of the leukocytes using color-based clustering. **-Feature Extraction** Shape features: One of the shape features for classifying AML by their shape is compactness. **-Image Classification** For the classification purpose various machine learning algorithms like support vector machines are used.	
9	In this paper, the segmentation procedure is a result of an optimization problem which is tackled by using a genetic algorithm, which represents, in a 3-D space, the real spots of the microarray image with spot models.	**Classical method with CNN**	**YES**
10	This paper, we presented a low cost digital pathology system capable of detecting Malaria, providing a CBC, and WBC count from a blood smear image.Overall system is cost-effective and has a performance relatively close to a human pathologist. So, its use may enable cheaper and faster treatment of patients.	**-Image Acquisition** Obtained from four different databases: LISC, IUMC, MAMIC, KAGGLE database. **-Image Preprocessing** The binary masks of the samples obtained **-Image Segmentation** The CNN	**NO**
11	Image enhancement at the preprocessing stage becomes the most crucial process for a successful feature extraction and diagnosis of leukemia. The fully segmented nucleus can be achieved by using the same threshold value even though different samples of ALL and AML had been used. Hence, it can be used as the basis for extracting the features from the blood slide images.	**-Image Acquisition** Blood image from slides with effective magnification is taken. **-Image Enhancement** Global contrast enhancement techniques by implementing the threshold and stretching value on the selected images is applied. **-Feature Extraction** **-Image Segmentation** Due to color space being convenient to convert from RGB and also intimately	**NO**

		related to human perception, therefore, the HSI color space is adopted. Thus, out of these three color spaces, only the S component is used for transforming the RGB image. **-Image Classification**	
12	This paper is specifically designed for the evaluation and comparison of the performances of algorithms for segmentation and image classification. The actual state of the art related to the automatic systems for the detection of ALL is examined, and a metric to evaluate the performances of these algorithms is proposed.	**-Image Segmentation** The cells are separated from the background by using algorithms based on different characteristics of the cells (e.g. shape, color, inner intensity). **-Image Classification** Identification of white cells - The cells are classified in white cells and red cells. The classifier can search for the presence of the nucleus by using color information. Identification of lymphocytes Identification of candidate lymphoblasts.	**YES**
13	This research used microscopic images from the ALL_IDB dataset to classify the blast and non-blast cells for Leukemia prediction. The proposed model initially detects the shape of the blast cell from images.	**-Image Acquisition** Blood image from slides with effective magnification is taken. **-Image Preprocessing** It applies the Canny edge detection algorithm with a gaussian filter to reduce noise. **-Feature Extraction** The histogram of Oriented Gradients (HOG) feature is calculated from the output images. **-Image Classification** The proposed model is trained using the logistic regression classifier.	**YES**
14	The implementation of this system would save lives and reduce financial and emotional costs imposed on patients. CAD-SFA would allow for reproducible diagnosis by diminishing the inter-observer variability. CAD-SFA can also be used for educational purposes where the trainee can validate their findings. Finally this paper proposed an image	**-Image Enhancement** Conversion from RGB image to HSV color image, Histogram equalization for contrast stretching operations. **-Image Segmentation** Watershed segmentation operation is used to separate connected cell components. Minimum bounding box for each cell is calculated using	**YES**

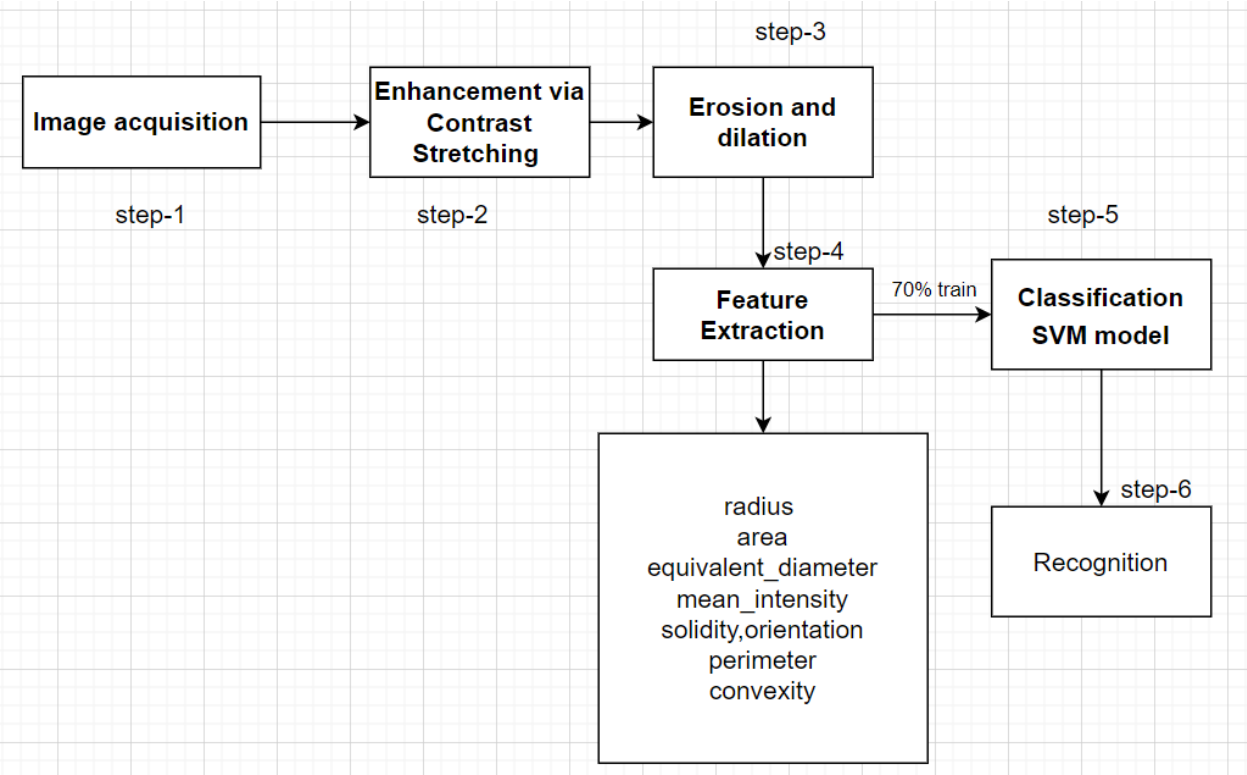
	processing based ALL diagnosis which is outstanding in greater accuracy and sensitivity.	'regionprops()' function and then 'imcrop()' function is used along with the bounding box to separate nucleus and cytoplasm. **-Feature Extraction** Morphological and functional changes are reflected by the nucleus and cytoplasm of lymphoblast so morphological features,textural features and color features are used. **-Image Classification** Some of the classifiers used are KNN, SVM and Tree.	
15	This paper puts forward a method to automatically detect whether the given microscopic blood smear image is infected by AML or not. The accuracy of the system running both, SVM with full feature set and SVM with reduced feature set is 95%.	**-Image Preprocessing** The RGB input image is converted into the CIELAB color space or more appropriately the CIEL*a*b* color space. This consists of 3 components namely L*, a* and b*. L* is the luminosity layer which depicts the lightness of the color. A* and B* are known as chromaticity layers. **-Image Segmentation** A center-based clustering algorithm has been used. **-Feature Extraction** It contains two features: Texture Features Shape Features **-Image Classification** The Support Vector Machine (SVM) algorithm was chosen as it is a promising nonlinear, nonparametric classification technique.	**NO**

CHAPTER 4
Design

4.1 Proposed architecture



4.2 Proposed Image processing



CHAPTER 5

INVENTION DETAILS

5.1. Objective of the invention:

The microscopic images for disease detection used to be inspected visually by hematologists and the process was very time consuming and tiring. An automatic

image processing system is needed to overcome related constraints in visual inspection. The proposed system will be on microscopic images to detect Leukemia. The early and fast identification of Leukemia greatly aids in providing the appropriate treatment which is the major objective of the invention.This model provides results with greater accuracy hence increasing the reliability in comparison to pre-existing model for Leukemia detection.We developed method consist of four main stages as follows: enhancement, segmentation, feature extraction, and image classification.There are previous research related to leukemia disease detection and computing. However, our model aims to have higher precision and increased efficiency with respect to many methods developed by other researchers. The preprocessing of the image is carried out by contrast stretching followed by histogram equalization. After this step the image segmentation is carried out by thresholding and segmentation is also done under morphological operation since in medical image segmentation, morphology plays an important role. Both dilation and erosion are performed under morphological operations. In the third step feature extraction is performed considering various features such as Color, Geometry, Texture features and statistical features. The accurate feature extraction and leukemia classification are proportionately dependent on the correct segmentation of the maximized and cropped lymphocytes.Lastly, classification is done using SVM. In this way we have carried out this project for the faster, efficient and reliable method for the detection of leukemia.

5.2. Detailed Description with the functional block

5.3 Steps with their mathematical intuition

- **Image Enhancement**

Histogram equalization is a very common method that utilizes the image histogram to adjust the contrast of image. This method is suitable for enhancing dark background/foreground and low contrast blood smear images.Contrast stretching evenly distributes a histogram's pixel values across the full range of available pixel values. This technique is ideal for enhancing the contrast of an image with pixel values concentrated in one area of the intensity spectrum, such as the original low-contrast image above. It may increase the contrast of background noise, while decreasing the usable signal.

(a) The Blood cells image I(x,y) is initially converted to gray scale image g(x,y) by using equation (1) to define the nuclei of the WBCs as dark regions.

(b) Contrast stretching is applied to improve image contrast done by stretching the range of intensity values. The lower and upper limits are defined as a =0 and b=255, histogram (h) of the original image is evaluated using equation (2) by no of pixels(N) is used to initialize the limit of lower(c) and upper(d) in histogram. Then image **g(x,y)** contrast is stretched to **L(x,y)** using equation (3).

$$h=\frac{g(x,y)}{N} \quad \rightarrow (2)$$

$$L = (g(x,y) - c) * \left(\frac{b-a}{d-a}\right) + a \quad \rightarrow (3)$$

(c) Histogram equalization(H) of equation (4) is used for adjusting the image intensities which enhances the contrast of the nuclei where l is the level of intensity.

$$H=\text{floor}(g-l) * \sum_{l=0}^{g(x,y)} h(l) \rightarrow (4)$$

Here we will get a histogram image that needs to undergo the segmentation process for extraction of our region of interest.

- **Image Segmentation:**

  The segmentation phase, which is concerned with extracting individual object components carrying pivotal information.Image segmentation can also be performed under morphological operations since in medical image segmentation, morphology plays an important role.

  Morphological operations apply a structuring element to an input image, creating an output image of the same size. In a morphological operation, the value of each pixel in the output image is based on a comparison of the corresponding pixel in the input image with its neighbors.The most basic morphological operations are dilation and erosion. Dilation adds pixels to the boundaries of objects in an image, while erosion removes pixels on object boundaries. The number of pixels added or removed from the objects in an image depends on the size and shape of the structuring element used to process the image. In the morphological dilation and erosion operations, the state of any given pixel in the output image is determined by applying a rule to the corresponding pixel and its neighbors in the input image.

  In all detection, morphological operation is used for the segmentation of leukaemia cells. It efficiently enhances the cells by filling small holes and gaps, smoothening their boundaries, and removing the salt or pepper noise from the nucleus

  For image segmentation two morphological operations are used namely opening and closing • are defined below.

  The opening of an image E by the structuring element is an erosion followed by dilation.

$$E \circ S = (E \ominus S) \oplus S.$$

Closing of an image E by structuring element S can be defined as dilation followed by erosion.

$$E \bullet S = (E \oplus S) \ominus S.$$

After performing the morphological operation we will be able to get our region of interest and hence it undergoes feature extraction.

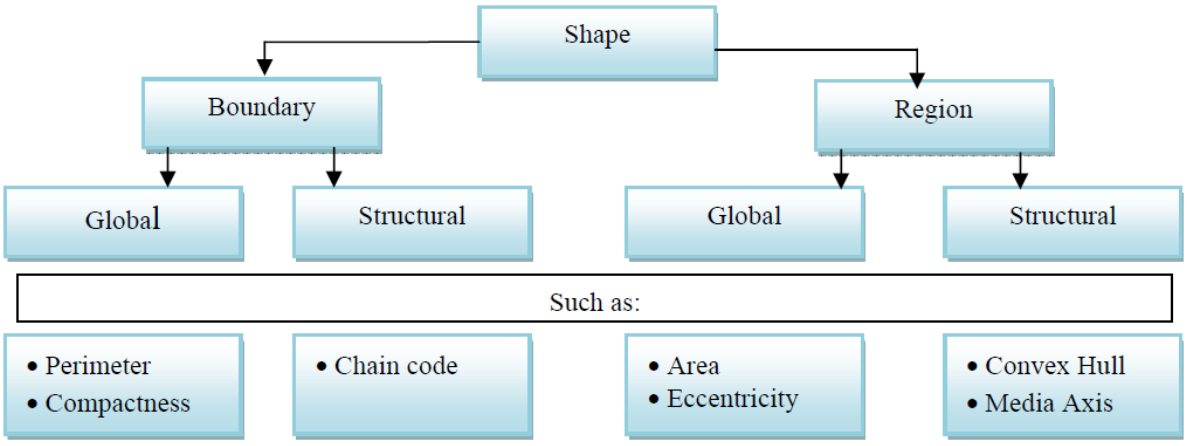
- **Feature Extraction:**

  In feature extraction we extract relative information from the images. We extract the features such as Color, Geometry, Texture features and statistical features. The goal of feature extraction is to obtain a set of image descriptors. By finding the relationship between these descriptors, the patterns determining the images can be discovered. The accurate feature extraction and leukemia classification are proportionately dependent on the correct segmentation of the maximized and cropped lymphocytes.

  Feature extraction is a part of the dimensionality reduction process, in which an initial set of the raw data is divided and reduced to more manageable groups. So when you want to process it will be easier. The most important characteristic of these large data sets is that they have a large number of variables. These variables require a lot of computing resources to process them. So Feature extraction helps to get the best feature from those big data sets by selecting and combining variables into features, thus, effectively reducing the amount of data. These features are easy to process, but still able to describe the actual data set with accuracy and originality.For leukaemia detection, feature extraction plays a vital role because blast cells may have a lot of information including different characteristics of their nucleus and cytoplasm.

We extract the features such as Color, Geometry, Texture features and

statistical features.



- Geometric Features – It includes perimeter, radius, area, rectangularity, compactness, convexity, concavity, symmetry, elongation, eccentricity, solidity etc.

1) Roundness: $\frac{4\ X\ \Pi\ X\ area}{convex\ perimeterr^2}$

2) Solidity: $\frac{Area}{Convex\ area}$

3) Elongation: $1\text{-}\frac{major\ axis}{minor\ axis}$

4) Eccentricity: $\frac{\sqrt{major\ axis\ ^2 - minor\ axis^2}}{major\ axis}$

5) Compactness: $\frac{4 * \Pi X\ area}{perimeterr^2}$

6) Rectangularity: $\frac{area}{major\ axis * minor\ axis}$

7) Convexity: $\frac{Perimeter\ convex}{Perimeter}$

- **Image classification**

A Support Vector Machine (SVM) is a binary linear classification whose decision boundary is explicitly constructed to minimize generalization error. It is a very powerful and versatile Machine Learning model, capable of performing linear or nonlinear classification, regression and even outlier detection.

Classification is done using SVM.The SVM classifier is formally defined for the separation of the hyperplane.

Our classifier i.e function is :

$$b = \frac{\sum_{(s \in S)} (y_s - \sum_{m \in s} \lambda_m y_m x_m \cdot x_s)}{N_s}$$

$$h_{w,b}(x) = g(w^T x + b)$$

g(z) = 1 if z ≥ 0, -1 otherwise

where , hw,b is our desired return of a function

Model:

Input → features(radius, area,convexity,rectangularity..etc.)

Output → (Acute Myeloid Leukemia or Acute Lymphocytic Leukemia)

- **Image recognition**

After the classification model we can predict if the image is suffering from which type of leukemia like Acute lymphocytic leukemia (ALL), Acute myelogenous leukemia (AML). The final recognition of ALL from peripheral blood smear images is accomplished by optimized support vector

machine (SVM). The SVM model predicts the disease and if it is suffering then it will try to make a circle in the image and hence it is recognized.

5.4. Summary of Invention

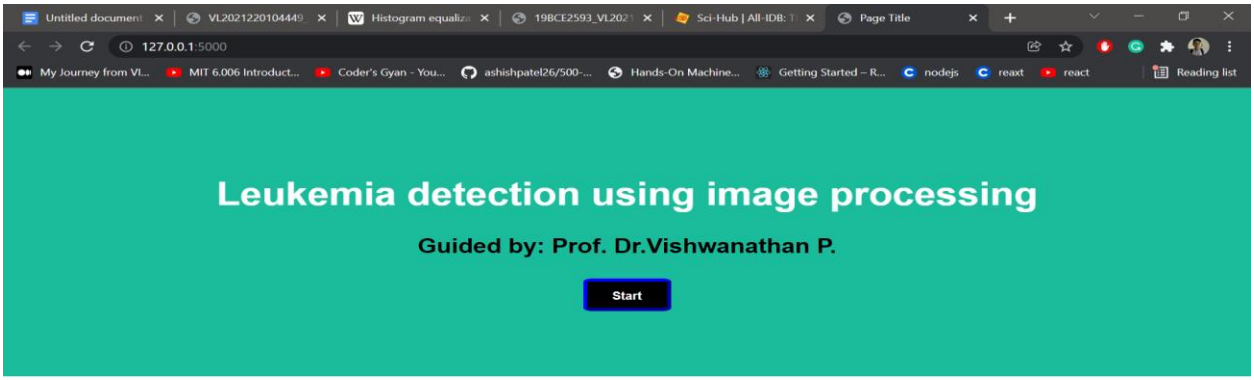
The proposed model is comparatively effective and reliable. It is observed it returns the accuracy of (>=90%) with lesser computational cost.

Less demand for processors in our model because there is no neural network for classification computation. Hence it is regarded as the best fit for small scale projects and effective.

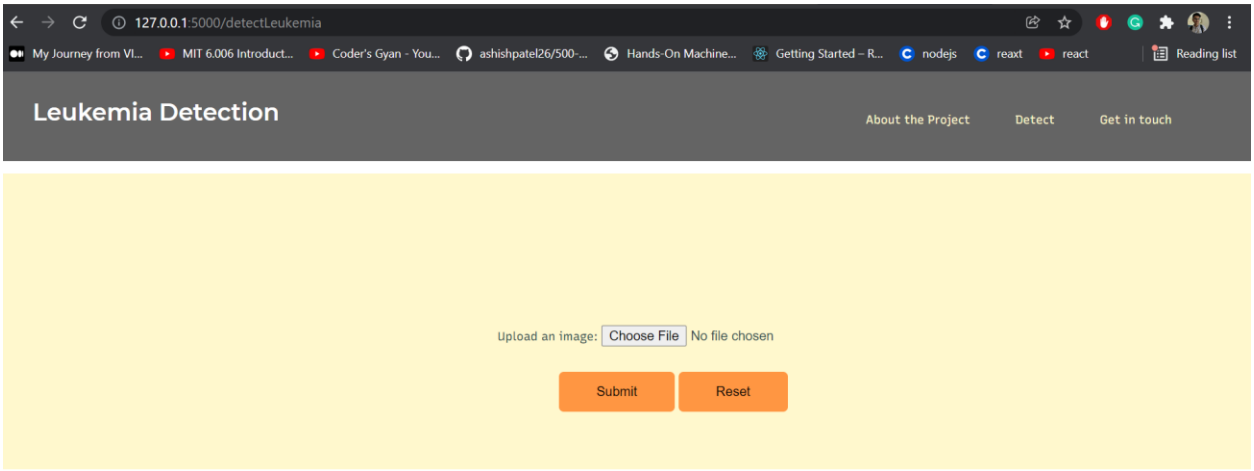
CHAPTER 6

Implementation - Snapshot of Prototype

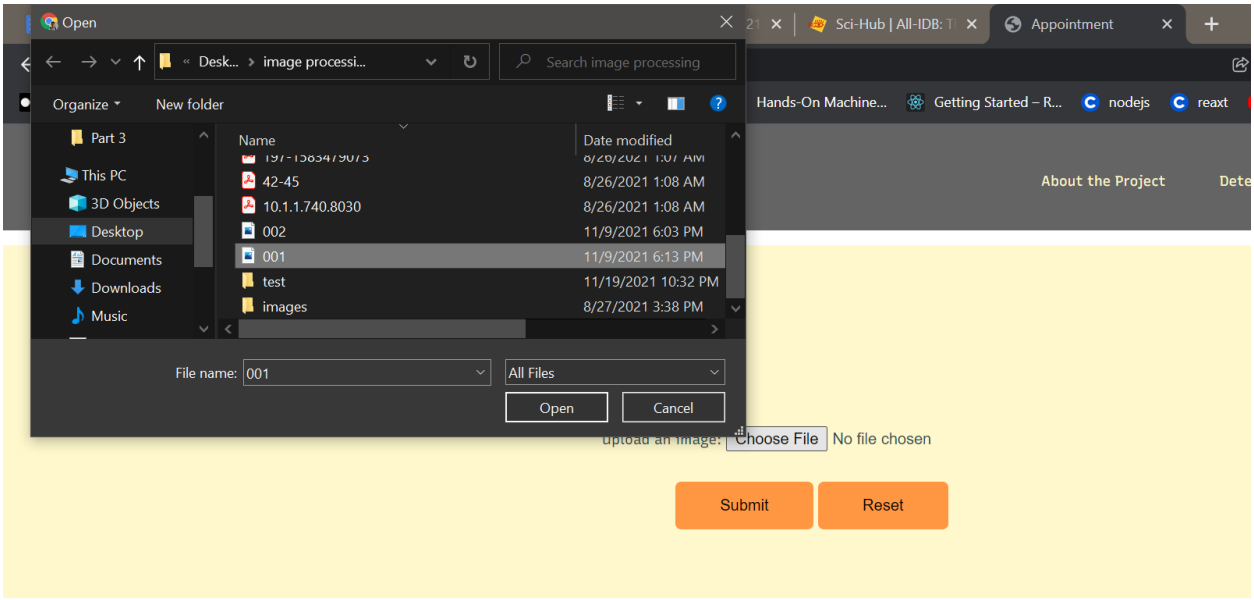
Step-1: application is hosted in local server using FLASK(a library of Python Programming Language)



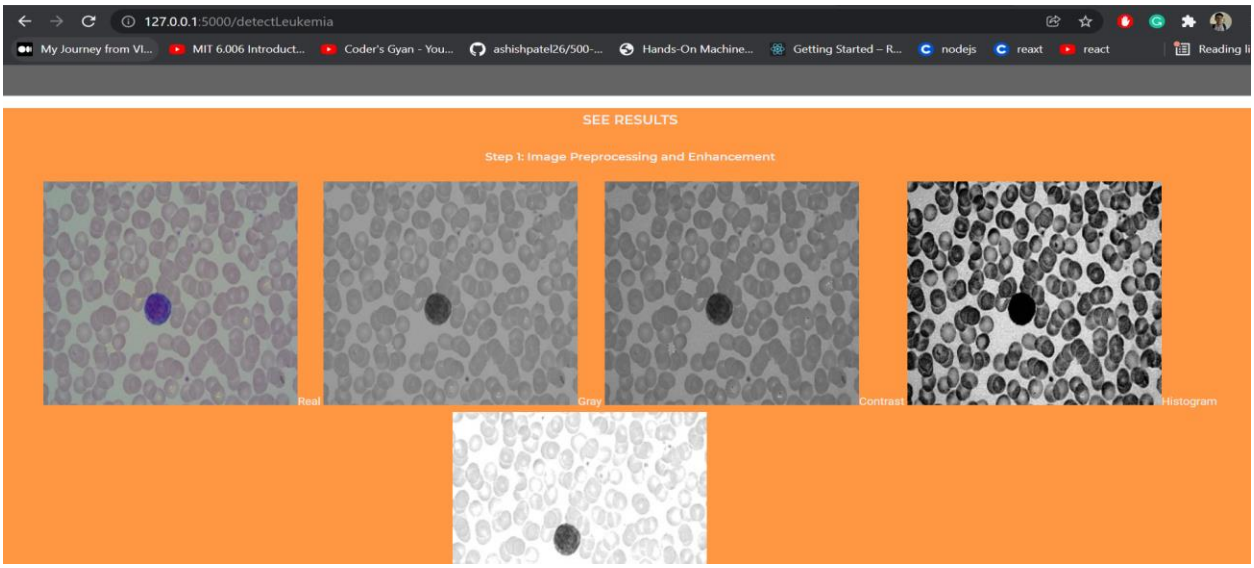
Step-2: go to localhost/detectLeukemia

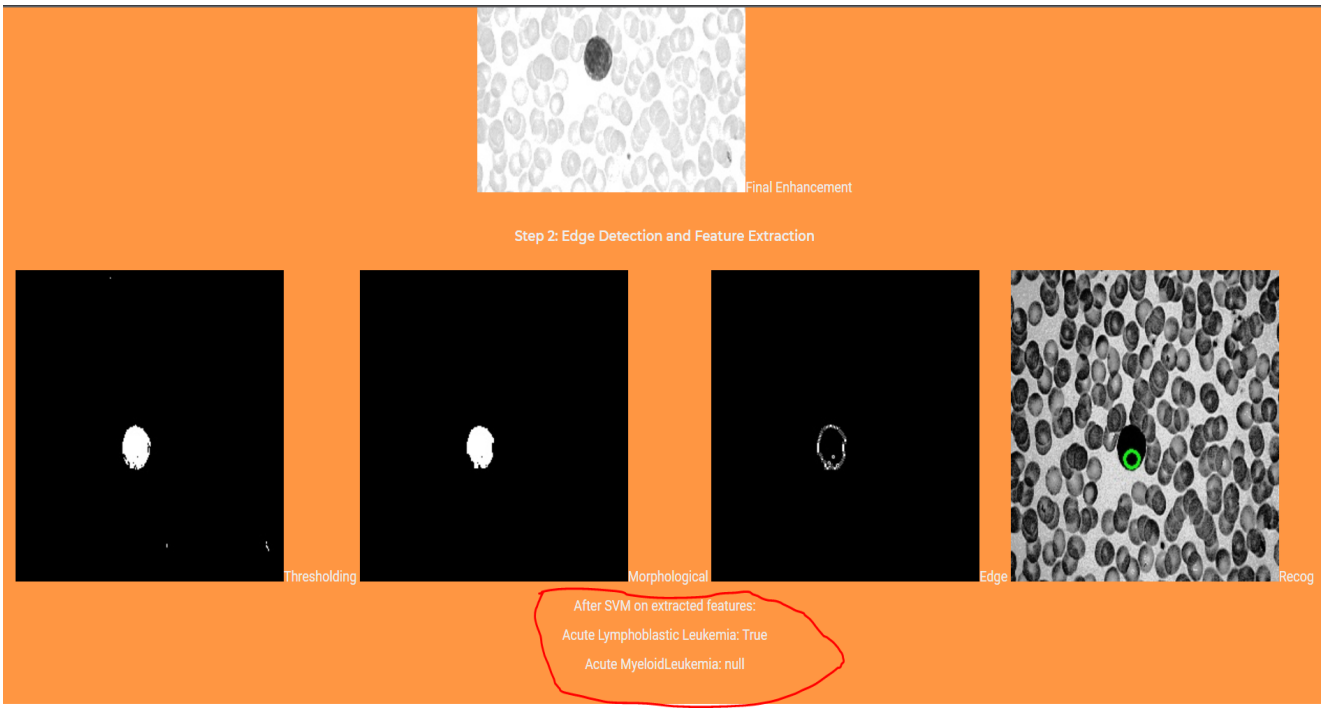


Step-3: Load a Image



Step-4: Output





6.1. Pseudo Code for overall implementation

Preprocessing

```
ab_global=[]
for image in images:
        file_name=dirname.file
        input_image=read from the directory
        inputImLAB = rgb2lab(input_image);
        % Extract a* and b* channels and reshape
        ab = double(inputImLAB(:,:,2:3));
        ab = reshape(ab,nrows*ncols,2);
        ab_global = [ab_global;ab];
```

end

Enhancement

enhanced=contrast_stretching(preprocessed_image)

Segmentation

Erosion=erosion(enhanced)

Dilation=dilation()

segmented_image = imbinarize(min_data_3d_ind)

Feature extraction

Compute radius, area, diameter, convexity…

```
centers = reshape([stats.Centroid], 2, CC.NumObjects);
majors = [stats.MajorAxisLength];
minors = [stats.MinorAxisLength];
diameters= [stats.EquivDiameter];
radii = [diameters./2];
```

Load into the dataset

```
stats(i).Contrast = out.Contrast;
stats(i).Correlation = out.Correlation;
  stats(i).Energy = out.Energy;
stats(i).Homogeneity = out.Homogeneity;
```

```
stats(i).ent = ent_result;
stats(i).std_dev  =std_dev ;
stats(i).skew  = skew ;
stats(i).kurtosis  =kurtosis ;
stats(i).meanval = meanval;
```

SVM

Break dataset into training and testing

model = svm(train_data,test_data)

prediction=model(dependencies)

Implementation in python programming:

Contrast Stretching

```
def contrastStretching(img,r1,r2,a,b,c):
    s1 = a*r1
    s2 = b*(r2-r1)+s1
    imgC = np.zeros((256,256), dtype=np.int32)
    for i in range(0,256):
```

```
    for j in range(0,256):
        r = img[i,j]
        if r<r1:
            imgC[i,j] = a*r
        elif r>r1 and r<r2:
            imgC[i,j] = b*(r-r1) +s1
        else:
            imgC[i,j] = c*(r-r2) + s2

  imgC = imgC.astype(np.uint8)
  return imgC
```

Histogram:

```
def histeq(img):
    a = np.zeros((256,),dtype=np.float16)
    b = np.zeros((256,),dtype=np.float16)
    imghist = img
```

```
height,width=img.shape


#finding histogram
for i in range(width):
    for j in range(height):
        g = imghist[j,i]
        a[g] = a[g]+1


#performing histogram equalization
tmp = 1.0/(height*width)
b = np.zeros((256,),dtype=np.float16)


for i in range(256):
    for j in range(i+1):
        b[i] += a[j] * tmp
    b[i] = round(b[i] * 255)


# b now contains the equalized histogram
b=b.astype(np.uint8)
```

```
    #Re-map values from equalized histogram into the image
    for i in range(width):
        for j in range(height):
            g = imghist[j,i]
            imghist[j,i]= b[g]

    imghist = imghist.astype(np.uint8)
    return imghist
```

Erosion and Dilation:

```
def dilation(img,mask):
  img = img.astype(np.float16)
  dilimg = np.zeros((256,256), dtype=np.float16)
  for i in range(1,255):
    for j in range(1,255):
      imgtemp = img[i-1:i+2, j-1:j+2]
      res = np.multiply(imgtemp,mask)
      dilimg[i,j] = np.amax(res)
```

```
    dilimg = dilimg.astype(np.uint8)

    return dilimg
```

```
def erosion(img,mask):

    img = img.astype(np.float16)

    eroimg = np.zeros((256,256), dtype=np.float16)

    for i in range(1,255):

        for j in range(1,255):

            imgtemp = img[i-1:i+2, j-1:j+2]

            res=[]

            for k in range(0,3):

                for m in range(0,3):

                    if mask[k][m] ==1:

                        a = imgtemp[k,m]

                        res.append(a)

            eroimg[i,j] = np.amin(res)

    eroimg = eroimg.astype(np.uint8)

    return eroimg
```

Feature extraction:

```
def featureExtraction(img):

    cells=img[:,:,0]



    pixels_to_um = 0.454

    ret1, thresh = cv2.threshold(cells, 0, 255,
cv2.THRESH_BINARY+cv2.THRESH_OTSU)



    kernel = np.ones((3,3),np.uint8)

    opening = cv2.morphologyEx(thresh,cv2.MORPH_OPEN,kernel, iterations = 2)



    from skimage.segmentation import clear_border

    opening = clear_border(opening) #Remove edge touching grains

    plt.imshow(opening, cmap='gray') #This is our image to be segmented further using
watershed

    sure_bg = cv2.dilate(opening,kernel,iterations=10)

    plt.imshow(sure_bg, cmap='gray') #Dark region is our sure backgroundm
```

```
    dist_transform = cv2.distanceTransform(opening,cv2.DIST_L2,5)

    plt.imshow(dist_transform, cmap='gray') #Dist transformed img.

    print(dist_transform.max()) #gives about 21.9

    ret2, sure_fg = cv2.threshold(dist_transform,0.5*dist_transform.max(),255,0)

    plt.imshow(sure_fg, cmap='gray')

    sure_fg = np.uint8(sure_fg)  #Convert to uint8 from float

    unknown = cv2.subtract(sure_bg,sure_fg)

    plt.imshow(unknown, cmap='gray')

    ret3, markers = cv2.connectedComponents(sure_fg)

    plt.imshow(markers)

    markers = markers+10



# Now, mark the region of unknown with zero

    markers[unknown==255] = 0

    plt.imshow(markers, cmap='jet')   #Look at the 3 distinct regions.



#Now we are ready for watershed filling.

    markers = cv2.watershed(img,markers)
```

```
#Let us color boundaries in yellow.
#Remember that watershed assigns boundaries a value of -1
    img[markers == -1] = [0,255,255]

#label2rgb - Return an RG~B image where color-coded labels are painted over the
image.
    img2 = color.label2rgb(markers, bg_label=0)
    imr1 = cv2. resize(img, (960, 540))
    imr2 = cv2. resize(img2, (960, 540))
    plt.imshow(img2)
    # cv2.imshow('Overlay on original image', imr1)
    # cv2.imshow('Colored Grains', imr2)
    cv2.waitKey(0)

##############################################################################
##############
#Now, time to extract properties of detected cells
#Directly capturing props to pandas dataframe
```

```
  props = measure.regionprops_table(markers, cells,
                    properties=['label',
                                'area', 'equivalent_diameter',
                                'mean_intensity', 'solidity', 'orientation',
                                'perimeter'])
```

Load into dataset:

```
 import pandas as pd
  df = pd.DataFrame(props)
  print(df.head())


#To delete small regions...
  df = df[df['area'] > 50]
  print(df.head())


#####################################################################
#Convert to micron scale
  df['area_sq_microns'] = df['area'] * (pixels_to_um**2)
```

```
df['equivalent_diameter_microns'] = df['equivalent_diameter'] * (pixels_to_um)

print(df.head())



df.to_csv('safal.csv')
```

Classification/Recognition:

SVM:

```
import pandas as pd

import numpy as np

import matplotlib.pyplot as plt

import seaborn as sns

from wrapper import leukemia

%matplotlib inline

cancer=read_csv()

df_cancer = pd.DataFrame(np.c_[cancer['data'], cancer['target']], columns =
np.append(cancer['feature_names'], ['target']))



df_cancer.head()
```

```
X = df_cancer.drop(['target'], axis = 1) # We drop our "target" feature and use all the remaining features in our dataframe to train the model.

X.head()



from sklearn.model_selection import train_test_split

y = df_cancer['target']

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random_state = 20)

from sklearn.svm import SVC

svc_model = SVC()

svc_model.fit(X_train, y_train)

y_predict = svc_model.predict(X_test)

from sklearn.metrics import classification_report, confusion_matrix

dataread=pd.read_csv('safal.csv')

cm = np.array(confusion_matrix(y_test, y_predict, labels=[1,0]))

confusion = pd.DataFrame(cm, index=['is_cancer', 'is_healthy'],

                         columns=['ALL','MLL'])



print(string1)
```

Edge Detection:

```
def edgeDetection(img):
    imgS = img.astype(np.float16)
    sobx=[[-1, -2, -1],
          [0, 0, 0],
          [1, 2, 1]]
    sobx = np.array(sobx, np.float16)
    soby =[[-1, 0, 1],
          [-2, 0, 2],
          [-1, 0, 1]]
    soby = np.array(soby,np.float16)
    for i in range(1,254):
        for j in range(1,254):
            imgtemp = img[i-1:i+2, j-1:j+2]
            x = np.sum(np.multiply(sobx,imgtemp))
            y = np.sum(np.multiply(soby,imgtemp))
```

```
            pixvalue = np.sqrt(x**2 + y**2)

            imgS[i,j] = pixvalue

    imgS = imgS.astype(np.uint8)

    return imgS
```

Detect Circle:

```
def detectCircles(img,openedimg):

    imgcircle = cv2.cvtColor(img, cv2.COLOR_GRAY2BGR)

    detected_circles = cv2.HoughCircles(openedimg,

                cv2.HOUGH_GRADIENT, 10, minDist= 10, param2= 30, minRadius = 1,
maxRadius = 13)

    ctr=0

    if detected_circles is not None:



        # Convert the circle parameters a, b and r to integers.

        detected_circles = np.uint16(np.around(detected_circles))



        for pt in detected_circles[0, :]:
```

```
        a, b, r = pt[0], pt[1], pt[2] #a,b are the coordinates of the center and r is the
radius



        # Draw the circumference of the circle.

        imgcirclefinal = cv2.circle(imgcircle, (a, b), r, (0, 255, 0), 2)



        # Draw a small circle (of radius 1) to show the center.

        #cv2.circle(img1, (a, b), 1, (255, 0, 0), 3)

        ctr+=1

    return imgcirclefinal,ctr
```

We have deployed into the server using a framework of Python- **Flask:**

Code of Deployment:

```
import os

from flask import Flask, redirect, url_for, send_from_directory,request, render_template

from detectLeukemia import *
```

```
import cv2

import matplotlib.pyplot as plt

from queue import Queue

import random

from threading import Thread

import time



UPLOAD_FOLDER = 'C://Users/ASUS/Desktop/Leukemia-
Detection/static/images/user'



ALLOWED_EXTENSIONS = set(['png', 'jpg', 'jpeg', 'bmp'])



app = Flask(__name__)

app.config['UPLOAD_FOLDER'] = UPLOAD_FOLDER

app.config['SEND_FILE_MAX_AGE_DEFAULT'] = 0



def allowed_file(filename):

    for i in range(len(filename)):

        if filename[i]=='.':
```

```
            ext = filename[i+1:]
            break
    if ext in ALLOWED_EXTENSIONS:
        return True


@app.route('/',methods=["GET", "POST"])
def index():
    return render_template('homepage.html')


@app.route('/detectLeukemia',methods=["GET", "POST"])
def detectLeukemia():
    if request.method== 'POST':
        if 'file' not in request.files:
            return render_template('detectLeukemia.html')
        file = request.files['file']
        if file and allowed_file(file.filename):
            filename= file.filename
            file.save(os.path.join(app.config['UPLOAD_FOLDER'], filename))
```

```
print('filename is', filename)

a = cv2.imread('static/images/user/{}'.format(filename))

featureExtraction(a)

a = cv2.resize(a,(256,256))

img1 = cv2.cvtColor(a,cv2.COLOR_BGR2RGB)

imgcopy = img1.copy()

img = cv2.cvtColor(img1, cv2.COLOR_RGB2GRAY)

cv2.imwrite(UPLOAD_FOLDER+'/file1.jpg',a)

cv2.imwrite(UPLOAD_FOLDER+'/file2.jpg',img)


img2 = contrastStretching(img, 20, 150, 0.1, 1, 2)

cv2.imwrite(UPLOAD_FOLDER+'/file3.jpg',img2)


imghist = histeq(img)

cv2.imwrite(UPLOAD_FOLDER+'/file4.jpg',imghist)


imgfinal = enhancement(img2,imghist)

cv2.imwrite(UPLOAD_FOLDER+'/file5.jpg',imgfinal)
```

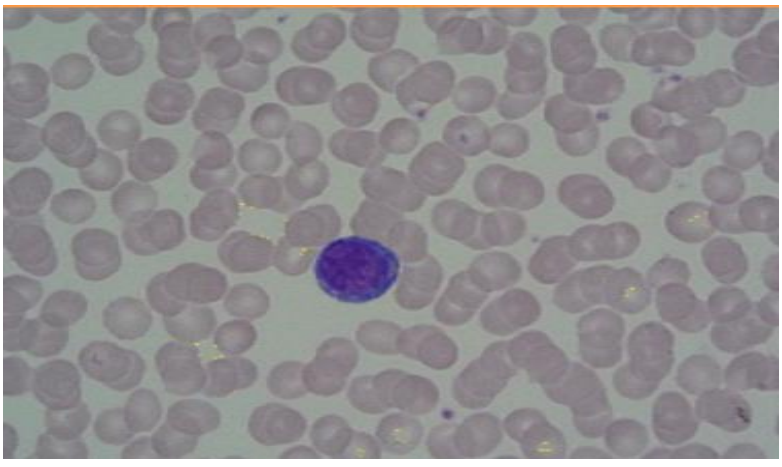
```
        imgthresh = thresholding(imgfinal, 150)
        cv2.imwrite(UPLOAD_FOLDER+'/file6.jpg',imgthresh)
        mask = [[1,1,1],
                [1,0,1],
                [1,1,1]]
        erodedimg = erosion(imgthresh,mask)
        openedimg = dilation(erodedimg,mask)
        cv2.imwrite(UPLOAD_FOLDER+'/file7.jpg',openedimg)
        imgEdges = edgeDetection(openedimg)
        cv2.imwrite(UPLOAD_FOLDER+'/file8.jpg',imgEdges)
        imgcircle,ctr = detectCircles(img,openedimg)
        cv2.imwrite(UPLOAD_FOLDER+'/file9.jpg',imgcircle)
        #time.sleep(30)
        return render_template('result.html', cells=ctr)
            #redirect(url_for('detectLeukemia', )


return render_template('detectLeukemia.html')
```

```
if __name__ == "__main__":

    app.debug =True

    app.run()
```

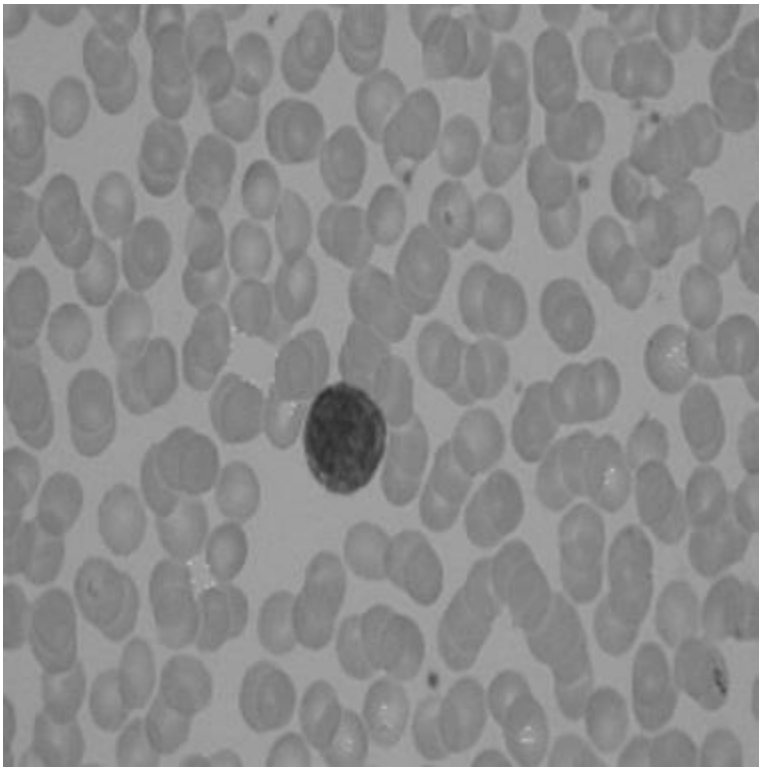
CHAPTER 7
RESULTS

Experimental result:

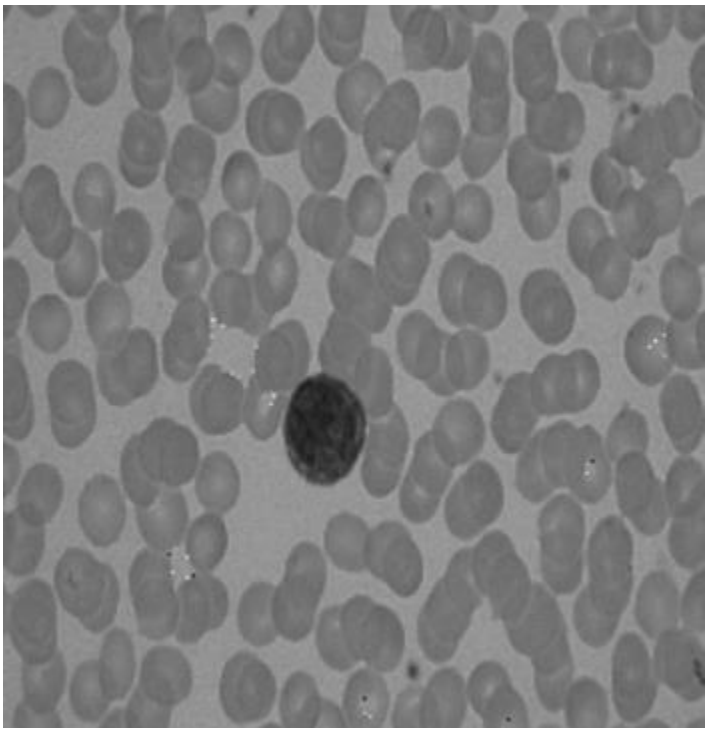
a. Original Image



b. Gray Scale Image

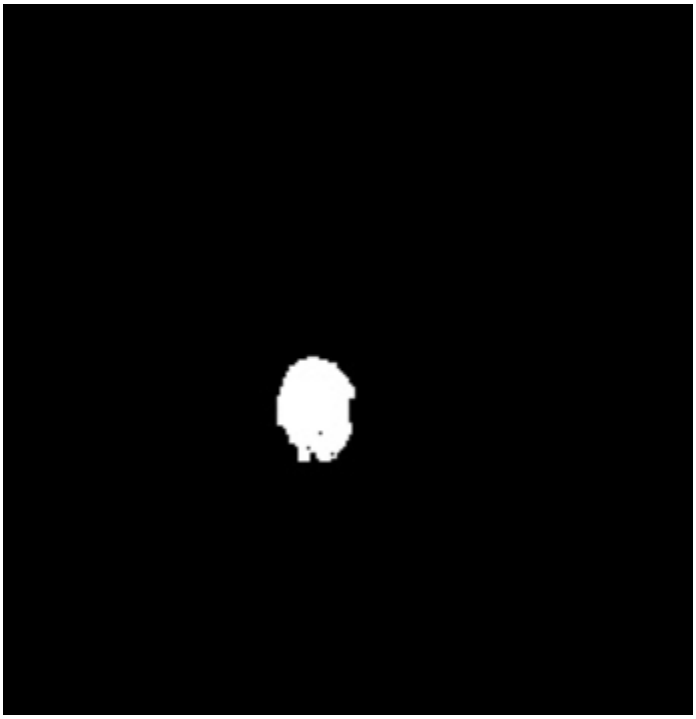


c. Enhanced Image

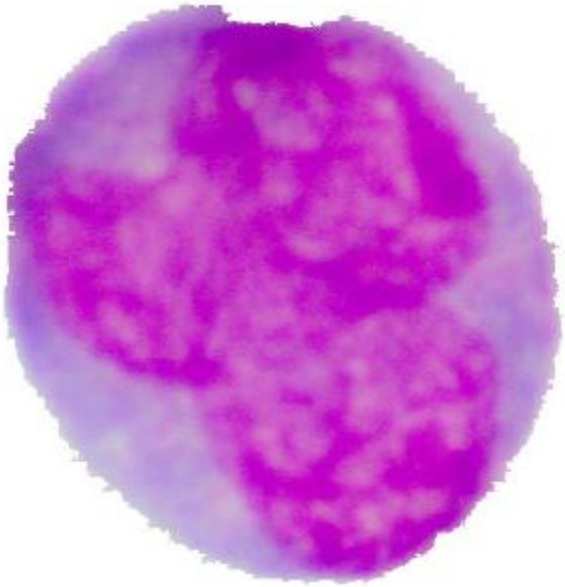


d. Morphological Operation

We find the region of interest



e. Feature extraction



Extracts the necessary features

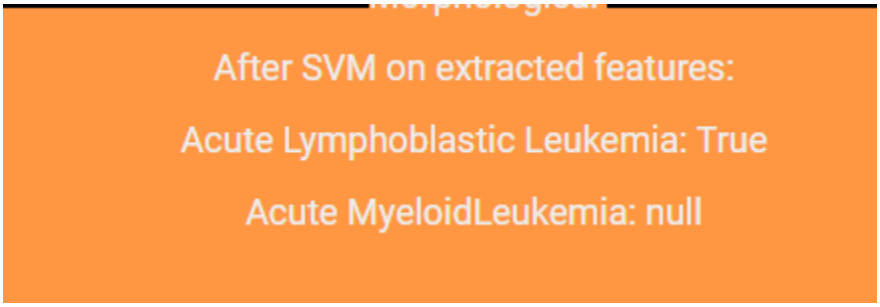
predict.ipynb U | safal.csv U | wrapper.py U | detectLeukemia.py 6, M | app.py 2, M | result.html 1, M

safal.csv

```
,label,area,equivalent_diameter,mean_intensity,solidity,orientation,perimeter,area_sq_microns,eq
0,10,9954543,3560.1289017908607,141.56295110684638,0.9931402831402831,1.5702999110115896,16707.6
1,11,35895,213.78244422372165,153.0203928123694,0.7835967516590988,1.2685061282573644,1114.00523
2,12,3703,68.66444519658124,150.53713205509047,0.7567954220314735,-1.376925377628658,370.0548698
3,13,4133,72.54170551062629,151.5429470118558,0.8119842829076621,-0.42504771663644375,348.918830
4,14,2622,57.77918384933796,152.71662852784135,0.741306191687871,0.045663593957817855,365.268073
5,15,11312,120.01202327285446,152.8497171145686,0.8235893702220605,0.328615162136571,594.5828278
6,16,4700,77.35777827895049,152.27893617021277,0.7587988375847594,0.8271443353725824,458.3807716
7,17,1558,44.538828124428505,152.55263157894737,0.7728174603174603,0.7657817809151569,224.728968
8,18,1667,46.07049295453128,152.80263947210557,0.8289408254599702,0.302197183933418,210.20205614
```

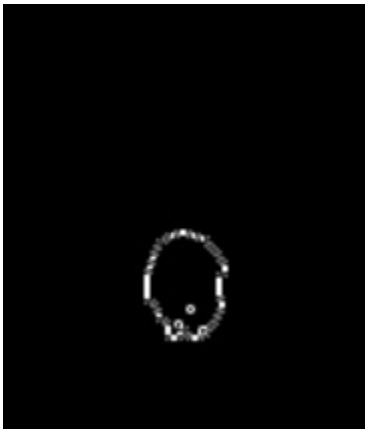
f. Classification

Classifies the disease



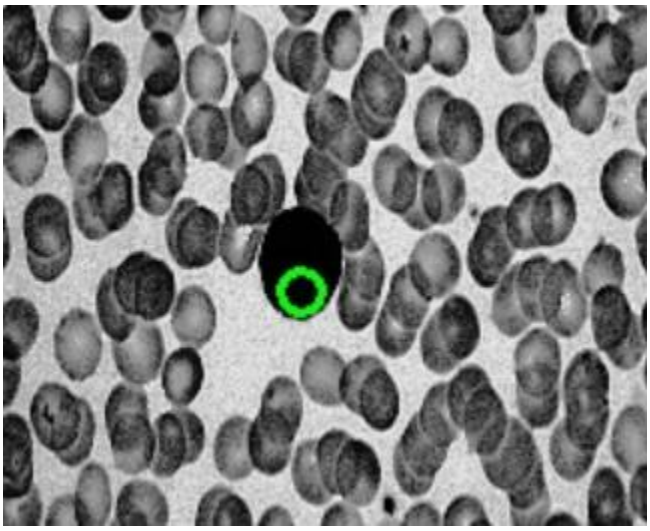
g. Edge Detection

Detects the edge



h. Recognition

Points the affected area

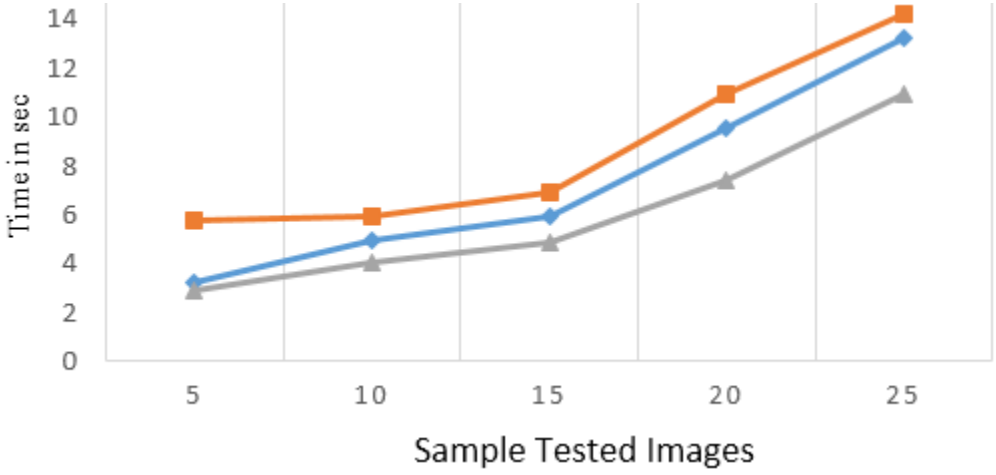


Analysis of result and accuracy:

Time complexity:

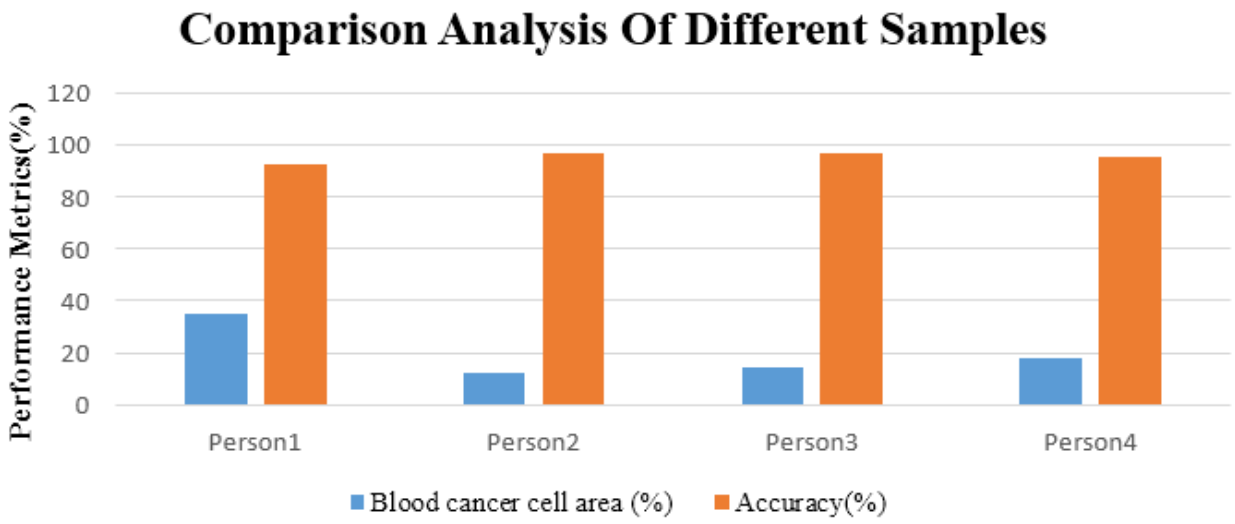
Time complexity=N*(N-1)/proces. Time

N= number of images



In the above graph the orange color denotes the accuracy of the SVM model, hence computationally fast.

Individual and accuracy:



By performing this project the overall accuracy is around 92% and hence computationally fast for distinguishing the ALL and AML.

Therefore this project is regarded as the successful project.

CHAPTER – 8
CONCLUSION AND FUTURE WORK

To overcome the limitations of the manual diagnosis methodology for leukemia, an image processing along with SVM model for automatic detection and classification of immature leukocytes was presented. The model was capable of detecting immature leukocytes with 92% accuracy which is on par with the current state of art . Furthermore, the model achieved precision of above 65% for each of the four immature leukocyte classes during multiclass classification, despite imbalance in numbers across classes, which is an improvement over previous research.The proposed color features of the nucleus in the B channel of LAB color space were calculated to be important for classification. This may stand as a tool for doctors to reduce the time and cost required for

the diagnosis of leukemia. The proposed model can expedite the detection of leukemia by identifying immature leukocytes, especially in developing countries where diagnosis takes numerous weeks, and potentially save lives because early diagnosis is vital for treatment success in leukemia patients. In addition, the precise classification of immature leukocytes can aid in treatment and prognosis decisions, which differ based on the type of cancerous cell. The second application of this study is in future research, where the features calculated to be most important and the proposed features can be used to elevate the classification performance. An important future direction is to gather a comprehensive dataset and develop a machine learning classifier that can classify all the types of immature leukocytes and work with imbalanced data. Future studies can expand on this work by calculating and ranking the importance of additional morphological features for the classification of leukocytes. Improving the discrimination between similar cell types, such as myeloblasts and promyelocytes, is also an avenue for future work. The difficulty of differentiating myeloblasts and promyelocytes can potentially be overcome by identifying features that are especially discriminative for the two cell types and training a specialized model to discriminate between the two cell types. Research on leukemia detection has obtained very promising results, and further work is required to develop systems that can be completely integrated into the clinical diagnosis method. Contributions of this study are an accurate model for detecting and classifying immature leukocytes, as well as calculation of the most important morphological features, which provide a basis for future research on computer-aided diagnosis of leukemia.

CHAPTER – 9
REFERENCES

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