

Software Proposal Document for project Automated Detection of White Blood Cells Cancer Diseases

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Abstract

The main idea of this project is Automated blood cancer detection is the key to improve accuracy of blood tests. Automated blood cancer systems should provide quick results with high accuracy, decreasing false positive and false negative cases. So, we propose a system for detection of white blood cancer diseases. We aim to detect several types of white blood cancer diseases like Leukemia and Myeloma, moving forward to improving the accuracy of results along with receiving results faster. We also aim to decrease the cases in which the case is diagnosed to be false positive or false negative. Our system will be desktop based in which blood sample images are acquired and the system process them to classify whether its positive or negative case. Also, showing which subtype of the disease it corresponds to and if its in early or late stage.

1 Introduction

1.1 Background

The blood is an essential fluid in the human body that carries out the critical functions of transporting oxygen and nutrients to the human body cells and eliminate carbon dioxide, ammonia, and other waste products via the Red Blood Cells (RBC'S). In addition, the White Blood Cells(WBC'S) play a vital role in our immune system and the platelets help in preventing clots in the blood. Therefore, a disorder in any of those main components will surely affect the balance of the human body. For instance, the disorder of the White Blood Cells in the normal blood will affect the immune system badly and the body will be exposed to certain types of cancer such as leukemia, myeloma, lymphoma and myelodysplastic syndrome. First of all, Lymphoma is a blood cancer that occurs in the bodys lymphatic system. Your white blood cells change and grow out of control. Hodgkins lymphoma and non-Hodgkins lymphoma are

the two major types of lymphoma. Moving to Leukemia, it is blood cancer in which malignant white blood cells multiply inside human body's bone marrow. Leukemia may be either acute or chronic. Chronic leukemia advances more slowly than acute. Myelodysplastic syndrome (MDS) is a condition affecting the white blood cells in your bone marrow. The body produces too many immature cells, called blasts. The blasts multiply and crowd out the mature and healthy cells. Myelodysplastic syndrome may progress either slowly or quite fast. It sometimes leads to leukemia. Finally, Myeloma is a type of cancer that develops from cells in the bone marrow called plasma cells. And while the process of manually inspecting the microscopic images for diagnosing is time consuming as the experts do it themselves. Moreover, Hematologists experts find it is difficult to classify the leukemia cells, their manual classification of blood cells is not only time consuming but also inaccurate [10]. In addition, experts are not available in all small villages so, an automated system for diagnosing microscopic images is in urgent need to save time and effort for both the experts and the patients. so we propose to develop an automatic system for detecting most commonly white blood cells disorder diseases such as (leukemia , myeloma , lymphoma and MDS) to help increasing the accuracy of the diagnosis and save time with an affordable cost for the patients .

1.2 Motivation

This project takes into consideration how hematologist experts find it difficult to classify the white blood cells diseases, their manual classification of blood cells diseases is not only time consuming but also inaccurate. So laboratories need to have a system which make the process of diagnosis easier and enhance the accuracy of results. According to some similar systems which are already implemented, it was found that each system was able to detect only one type of blood cancer, also some of white blood cancer diseases were not taken into consideration and no one tried to implement a system that can detect them.

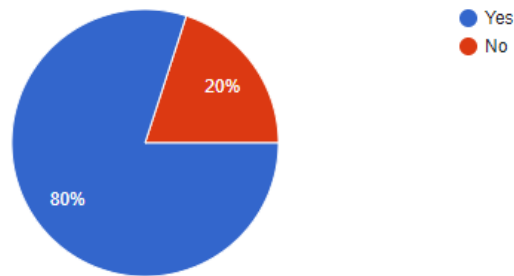
According to the survey we have made,

Who has responded?

Email
rawdammohammed91@gmail.com
nyny_65@hotmail.com
sobhsalem92@yahoo.com
nora92oka@gmail.com
shereen_mohamed9@yahoo.com
tharwatalex@yahoo.com
raghda.saleem91@gmail.com
z_saleem@hotmail.com
drhanan9590@gmail.com
magedmater@hotmail.com

11. In your opinion, is misdiagnosed cases a good reason to develop automated blood cancer diagnosis ?

10 responses



12. Which cancer diagnosis method would you prefer (Automated or Manual) ?

10 responses

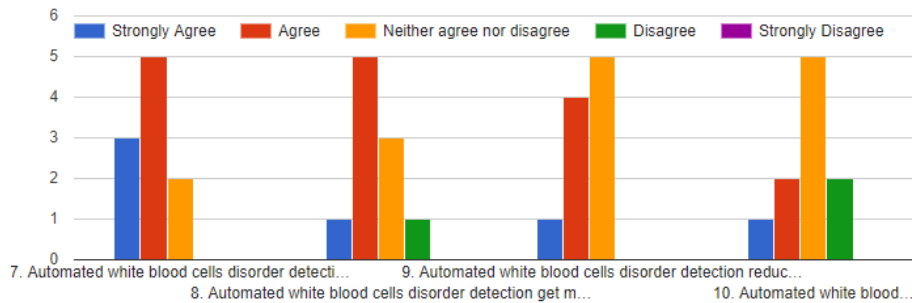
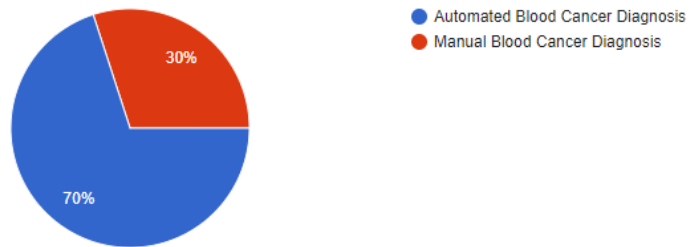
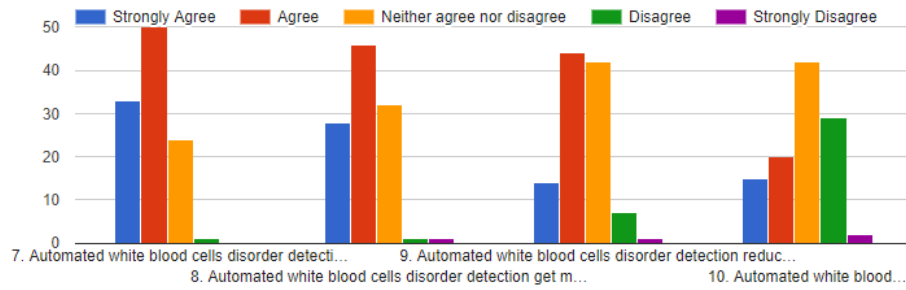
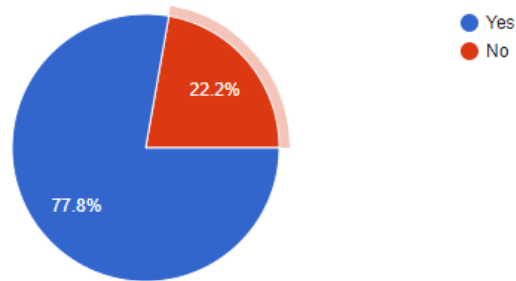


Figure 1: Experts respondings from the survey



11. In your opinion, is misdiagnosed cases a good reason to develop automated blood cancer diagnosis ?

108 responses



12. Which cancer diagnosis method would you prefer (Automated or Manual) ?

108 responses

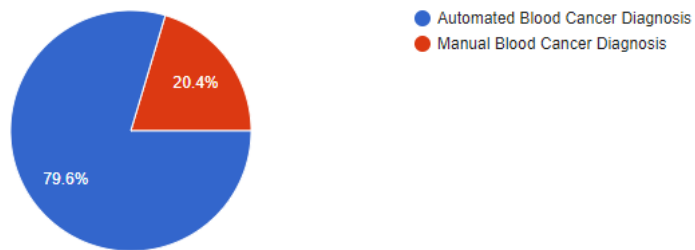


Figure 2: Community respondings to this survey

Academic Motivation

1. Automated detection of MDS and Myeloma which werent previously implemented.
2. [5][6] Training to new datasets.
3. [2][3] WBC diseases detection algorithms.
4. [1] Accelerate segmentation processing time.

1.3 Problem Definitions

We have different challenges that this project will solve. Most of existing systems can detect one type of white blood Cells (WBC) disorders so they couldnt cover all types. Our system will detect Leukemia, Myeloma, Lymphoma and MDS generally taking into consideration that MDS and Myeloma hadnt been detected in existing systems. We will enhance the accuracy of the detection of white blood cells disorders in blood microscopic images and consider high performance and high processing speed. We will focus on building an overall system for white blood cells disorders classification.

2 Project Description



Figure 3: Project Description photo

2.1 Objective

As the process of manually inspecting the microscopic images is costly,time consuming and not that accurate somtimes relative to human errors as mentioned.”Even hematologist finds it difficult to classify the leukemia cells, there

manual classification of blood cells is not only time consuming but also inaccurate” in [10]. So, there is an urgent need for an automated cancer detection system which saves time for experts and provides more accurate results and costs less than manual inspection when the experts inspecting the microscopic images themselves. therefore, our proposed automated system is considered to detect white blood cells diseases such as (leukemia ,lymphoma, myeloma and MDS (Myelodysplastic syndrome) and detect the stage of the cancer too ,striking to reduce the possibilities of false negative and false positive diagnosis.

2.2 Scope

- 1- The system will detect white blood cells diseases such as(leukemia , lymphoma,myeloma and MDS).
- 2- The doctors can view the stage of cancer.
- 3- The system will reduce the possibilities of false positive and false negative diagnosis to take place.

2.3 Project Overview

1. Fuzzy-C-Means which is a clustering method which allows single data to belong to more than one cluster and it is a pattern recognition method.
2. Adaptive-K-Means which manipulates the local minimum and maximum values based on the RGB color space during the initialization step.
3. Expectation Maximization.
4. Support Vector Machine (SVM) and k-means clustering algorithms.
5. discriminative dictionary learning algorithm to learn a small dictionary including few atoms from huge amounts of original information.

Pre-Processing: Test image passes by some processes before segmentation like converting it to different color spaces (Grayscale, YCBCR) and cropping the image to get a certain cell. Segmentation: The cropped cell is segmented using two techniques like K-means and YCBCR segmentation. Feature Extraction: Features from the segmented image are extracted using multiple ways like texture, gradient and geometrical extraction. Classification: After extracting the features from the image, all of them are sent to the classifier in order to get the results.

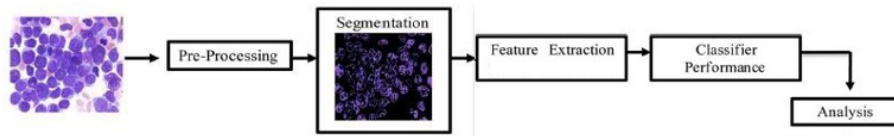


Figure 4: SystemOverview

3 Similar System Information

I. [10] Analysis of Microscopic Blood images for Detecting Leukemia using Nuclear Segmentation

A system proposed by R. Saravanakumar, G. Kiruthiga, K. Lubna, P. Nivedha and K. Pavithra for detection of Leukemia using nuclear segmentation. This system managed to count the number of RBCs and WBCs in blood sample image using image processing techniques like Threshold and Circular Hough Transform. The main purpose of this system was to detect leukemia in blood at an early stage so it can be cured easily. The system was based on five main steps which are Image acquisition; Image preprocessing, Image segmentation, Feature extraction and Detection of cancer cells. Image acquisition is the first step to go through the system then preprocessing of the image requires noise removal to make it suitable for further stages of processing using some image enhancement techniques like contrast enhancement including linear contrast and histogram equalization, Image segmentation means partitioning the image into a set of pixels to locate the WBCs structure which are abnormal and finally for feature extraction is done to decide whether the cell is blast or normal. Following are the features which are considered while detection of leukemia: Statistical, Textural and Geometrical.

II. [12] White Blood Cell Segmentation Techniques in Microscopic Images for Leukemia Detection

A system proposed by Biji G1 , Dr.S.Hariharan2 for detection of Leukemia by segmentation of white blood cells images. This system managed to use two clustering techniques to compare the performance of the image segmentation. The 2 techniques are Fuzzy-C-Means (FCM) and adaptive K-Means (AKM). The first technique is Fuzzy-C-Means which is a clustering method which allows single data belong to more than one clusters and it is a pattern recognition method. The second technique is adaptive K-Means which manipulates the local minimum and maximum values based on the RGB color space during the initialization step. The enhanced initialization method returns a two-element array with minimum and maximum RGB values from the whole pixel area. The

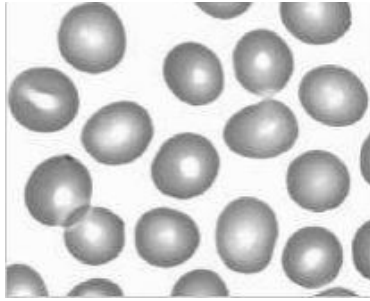


Figure 5: Normal blood.

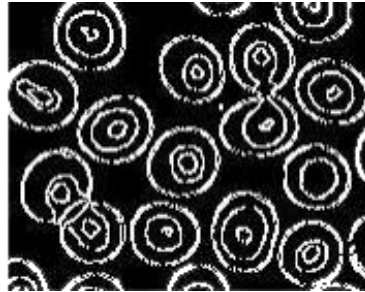


Figure 6: Normal blood After Feature Extraction.

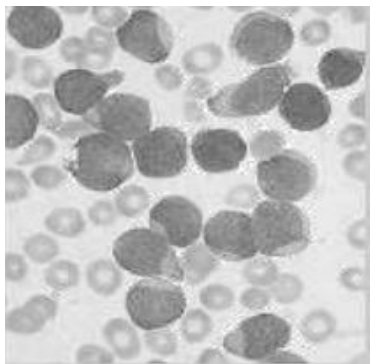


Figure 7: Affected Blood cells.

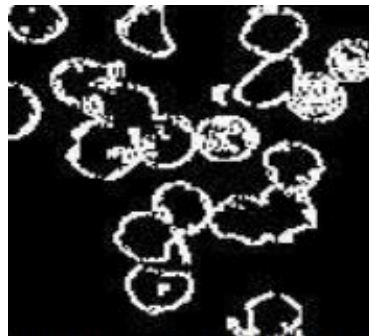


Figure 8: Affected Blood cells after feature extraction.

operator computes the maximum and minimum pixel values for each band of a rendered image within the region of interest. The adaptive method is an iteration-based clustering that produces an optimal value of initial k-centroids by minimizing the objective function.

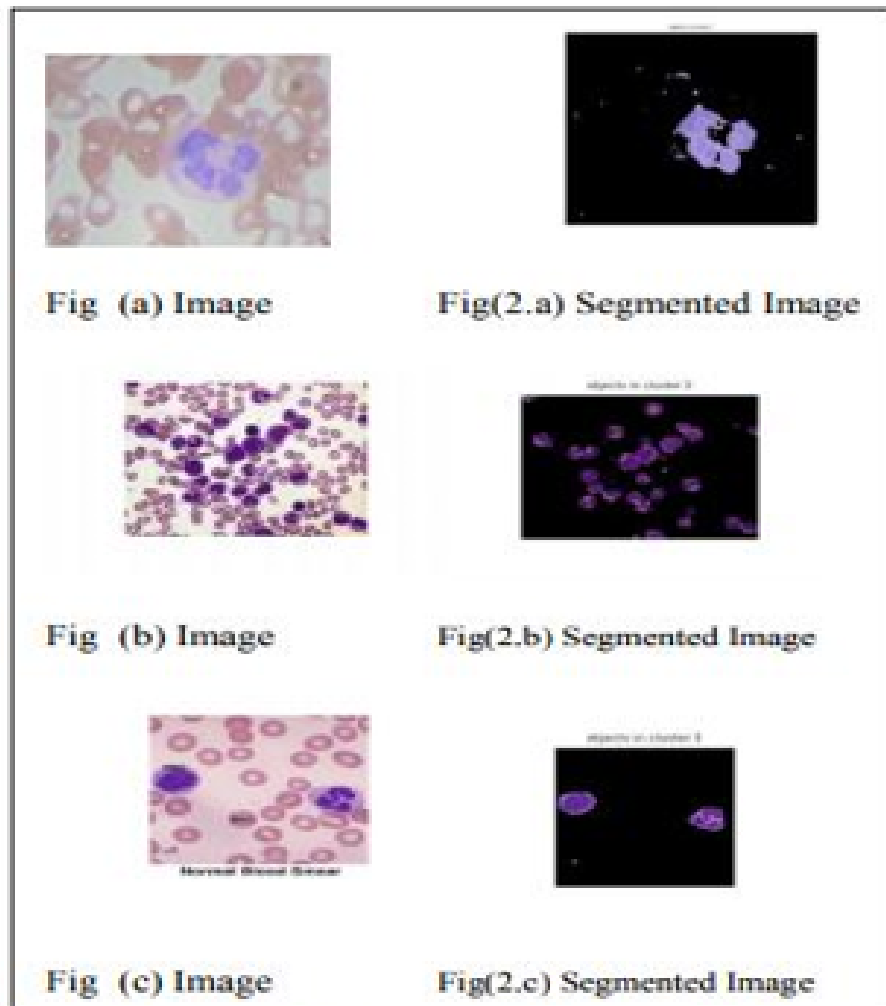


Figure 9: Image and segmented image using k-means

III. [6] Detection of Centroblasts in H and E Stained Images of Follicular Lymphoma

A system proposed by Emmanouil Michail, Evgenios N. Kornaropoulos, Kosmas Dimitropoulos, Nikos Grammalidis, Triantafyllia Koletsa, Ioannis Kostopoulos for automatic detection of malignant cells in microscopic images acquired from

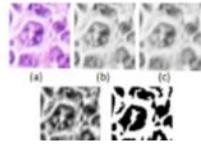


Figure 10: Normal blood.

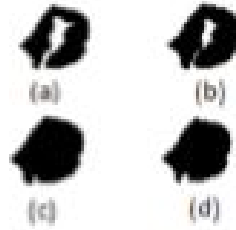


Figure 11: Normal blood After Feature Extraction.

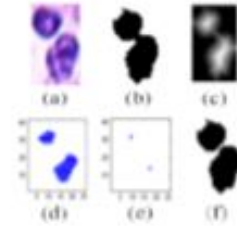


Figure 12: Normal blood After Feature Extraction.

tissue biopsies of follicular lymphoma. This system consists of five main steps which are image preprocessing, image segmentation, touching-cell splitting, selection of candidate CBs and classification. Starting with Pre-processing as the algorithm uses as input HPF images of FL stained with Hematoxylin and Eosin (H and E), Noise removal is needed. So image is converted to grayscale and filtered using a Gaussian filter with a 3x3 kernel. Additionally, histogram equalization is applied to differentiate between nuclear membrane and background. Moving to image segmentation, some initial enhancements need to be done to eliminate unnecessary components then Otsu thresholding is done to segment nuclei. But due to the transparency of large cells, their interior appears hollow after Otsu thresholding. Furthermore, in some cases, the perimeter of the cells remains open after segmentation (open cells) and a simple hole-filling operation is not able to sufficiently fill the inner area of the cell so post-processing procedure consisting of three steps is applied to each object in the image a) the cell is extracted from the image, b) image dilation, c) hole-filling, d) image erosion. Touching-cell splitting is done based on Gaussian mixture modeling. Expectation Maximization (EM) algorithm is used to estimate a) the order of the mixture by using the minimum description length (MDL) criterion and b) the parameters of the Gaussian mixture. Selection of candidate CBs at this step candidate CB cells are being selected, based on their size, shape and intensity histogram. Classification is the final stage instead of extracting a set of textural or morphological features, for classifying between CBs and non-CBs; the whole image of the cell with its surroundings was used as a feature vector. In that way, all the features able to distinguish between CBs and non-CBs are incorporated. Furthermore, redundant features are removed through dimensionality reduction.

IV. [11] Application of Support Vector Machine and k-means Clustering Algorithms for Robust Chronic Lymphocytic Leukemia Color Cell Segmentation

A system proposed by Emad A.Mohammed, Behrouz H.Far, Mostafa M.A. Mohamed and Christopher Naugler for segmentation of lymphocyte color cell using Support Vector Machine (SVM) and k-means clustering algorithms. These algo-

rithms overcome the occlusion problem when lymphocytes are tightly bound to the surrounding Red Blood Cells. Following are the four main steps used. Nucleus Segmentation in which the goal is to classify every pixel as nucleus pixel or background pixel, Cell Segmentation, Cytoplasm Segmentation and Accuracy Measurement in which there are two metrics used to estimate the segmentation accuracy. The first metric is direct pixel count of the ground truth mask (manually segmented mask) and the segmented mask resulting from the segmentation algorithm. The output results it was found that the algorithm could process all the 440 images even if the lymphocyte cells were tightly tied to RBCs. The problems of over and under-segmentation were reduced significantly.

V. [8] Detection of Leukemia in Microscopic Images Using Image Processing

A system proposed by Chaitali Raje, Jyoti Rangole which mainly focus on the nucleus segmentation followed by feature extraction to detect Leukemia. This automated system detect Leukemia when lot of abnormal white blood cells produced by the bone marrow. Initial segmentation is done using Statistical parameters such as mean, standard deviation which segregates white blood cells from other blood components i.e. erythrocytes and platelets. Geometrical features such as area, perimeter of the white blood cell nucleus investigated for diagnostic prediction of Leukemia. The proposed method is successfully applied to a large number of images, showing promising results for varying image quality. Different image processing algorithms such as Image Enhancement, Thresholding, Mathematical morphology and Labelling are implemented using LabVIEW and MATLAB.

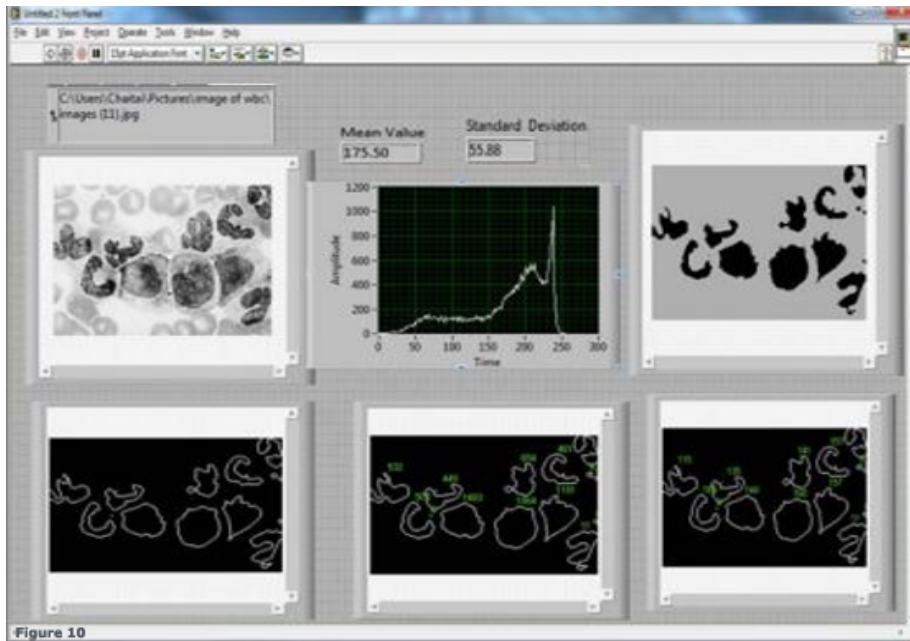


Figure 13: Screenshot of the system

VI. [9] DETECTION OF LEUKEMIA USING MATLAB

A system proposed by Shailesh J. Mishra, Mrs.A.P.Deshmukh which mainly focus on Leukemia Detection at earlier stage. This automated system knows the presence of leukemic cells, a study of morphological bone marrow and peripheral blood slide analysis is done. In order to classify the abnormal cells in their particular types and subtype of leukemia, a haematologist will observe some cells under a light microscopy looking for the abnormalities presented in the nucleus or cytoplasm of the cells. The clinical behaviour of the disease can be predicted using this classification and accordingly treatment should be given to the patient. And uses Read Cell Image, Gradient, Dilate the Image, Fill holes, Clear Border, Final Segmented Cells.

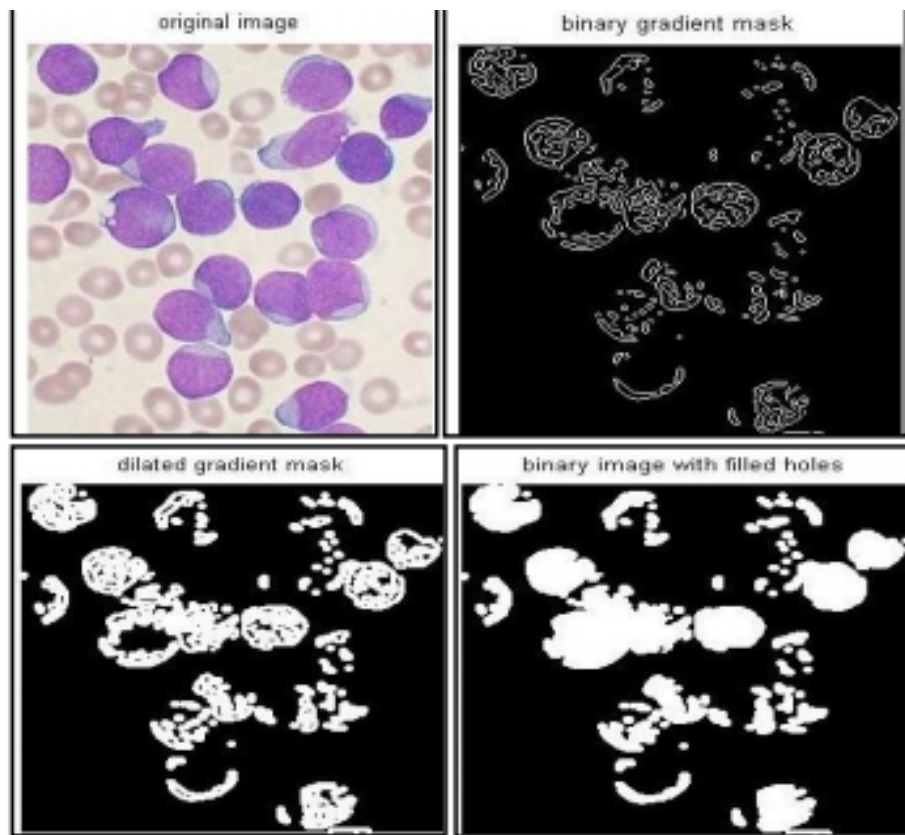


Figure 11

Figure 14: System Steps

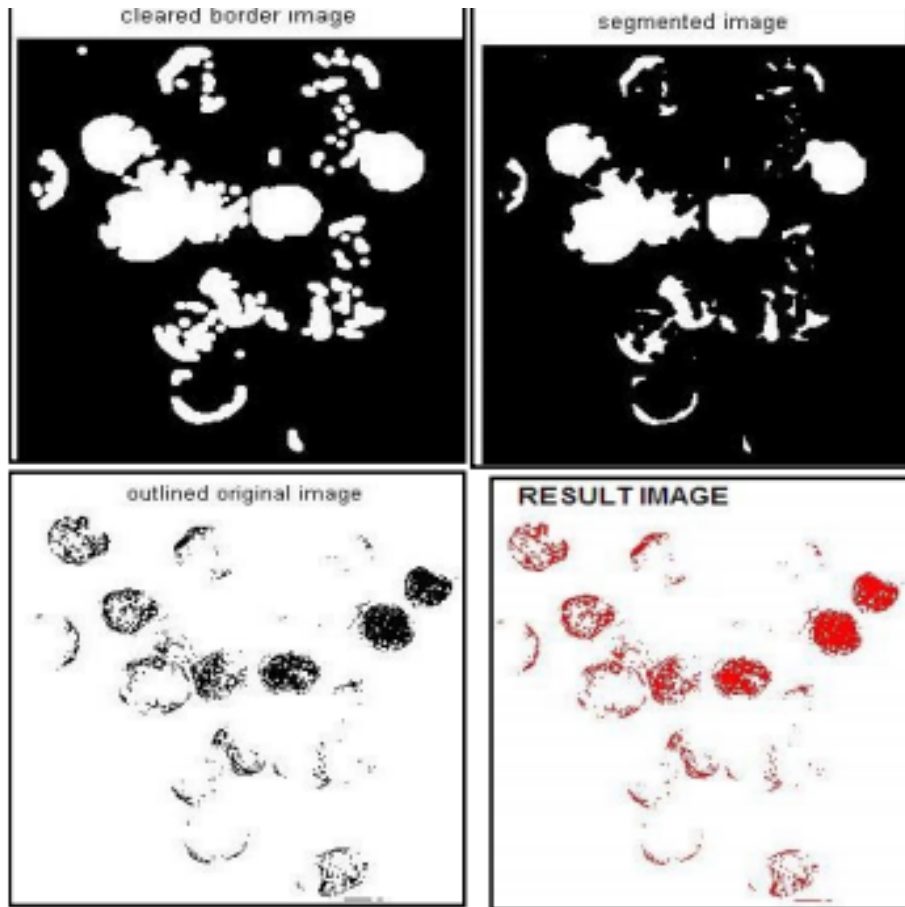


Figure 12

Figure 15: System Output

VII. [1] *Exploiting GPUs to Accelerate White Blood Cells Segmentation in Microscopic Blood Images*

A system proposed by Qanita Bani Baker and Khaled Balhaf to accelerate white blood cells segmentation in microscopic blood images as its an essential step in the automatic cell analysis and classification that generally includes WBC segmentation. This system managed to accelerate the use of k-means clustering method in WBC segmentation by using CUDA programming to take the advantages of parallel processing of the large number of cores in GPU. The main 3 steps are pre-processing step where they convert colors space and extract color from images. In the second step, they apply cell segmentation in CPU using K-mean clustering approach. Finally, they implement the two previous steps in parallel computing using CUDA programming. Moreover, they proposed a

hybrid (CPU and GPU) platform where some steps are required to execute in GPU side and other steps in CPU side to accelerate the process of segmentation. And they conducted that the hybrid approaches (GPU and CPU) are 3X faster than sequential and does not affect the segmentation accuracy implementation as illustrated in the table below. In my opinion this system strikes a very powerful side which focuses on accelerating the Processing time of the segmentation of white blood cells which is a primary stage in any automated system that detect WBC.

Image Size	CPU (sec)	GPU (sec)	CPU & GPU (sec)	GPU Improvement	Hybrid Improvement
200*100	2.4	2.4	1.5	1	1.6
250*150	3.6	3.2	2.3	1.125	1.565
300*200	4.9	3.6	2.7	1.361	1.814
350*250	5.6	3.9	2.9	1.435	1.931
400*300	6.6	4.3	3.5	1.534	1.885
450*350	7.3	4.5	3.8	1.622	1.921
500*400	9	5.3	4.5	1.698	2
Original	13.7	6	4.55	2.283	3.01

Function Name	CPU time	GPU time
Color Space Function	0.95 sec	1.65 sec
Extract Color Function	0.35 sec	1.1 sec
K-means cluster	12.4 sec	3.25 sec

Figure 13

Figure 16: Comparison between different sizes of images and performance

VIII. [2] DETECTING DIFFERENT SUB-TYPES OF ACUTE MYELOGENOUS LEUKEMIA USING DICTIONARY LEARNING AND SPARSE REPRESENTATION

Omid Sarrafzadeh, Hossein Rabbani, Alireza Mehri Dehnavi and Ardeshir Talebi proposed an automated leukemia detection system to detect different sub-types of Acute Myelogenous Leukemia using dictionary learning and sparse representation. They used different approach in this regard, 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. They considered M2, M3 and M5 sub-types for evaluation of the method. They used discriminative dictionary

learning algorithm to learn a small dictionary including few atoms from huge amounts of original information. The parameters used for building the dictionaries are size of atom, number of atoms, number of patches and number of iterations. Their algorithm is tested on the self-provided dataset contains 27 microscopic images of three sub-types of AML; 9 AML-M2, 10 AML-M3 and 8 AML-M5. Their results showed that by increasing atom size of DL, the performance would be better and the best average accuracy (97.53 percent) achieved for atom size of 49.

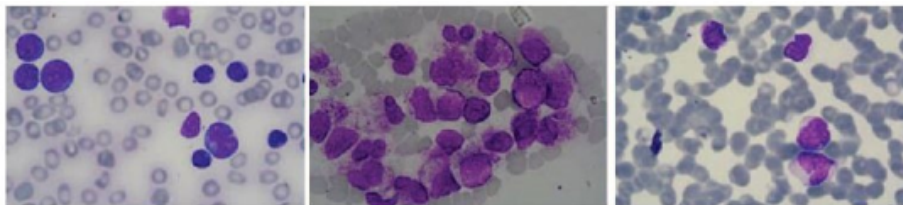


Figure 17: Sample images of AML (a) M2 (b) M3 (c) M5

IX. [7] Automated Screening System for Acute Myelogenous Leukemia Detection in Blood Microscopic Images

Sos Agaian, Monica Madhukar and Anthony T. Chronopoulos proposed a simple technique that automatically detects and segments AML in blood smears. The proposed method differs from others in the simplicity of the developed approach, classification of complete blood smear images as opposed to sub-images and use of these algorithms to segment and detect nucleated cells. The constructed system is applied to complete blood smear images containing multiple nuclei. Two new features, such as cell energy and Hausdorff dimension (HD) have been used. They used k-Means clustering algorithm in nuclei segmentation. Segmentation in this system is performed for extracting the nuclei of the leukocytes using color-based clustering. They applied some enhancement filters to improve the visibility of some regions so, they used Sobel operator, Canny edge detection, dilation and hole filling. In feature extraction, they used fractals dimensions such as HD and box counting dimension. They used a support vector machine (SVM) for constructing a decision surface in the feature space that bisects the two categories, cancerous and noncancerous, and maximizes the margin of separation between two classes of points. The developed algorithm presents accuracy of (98 percent) and thereby providing an effective and reliable source of classification of AML.

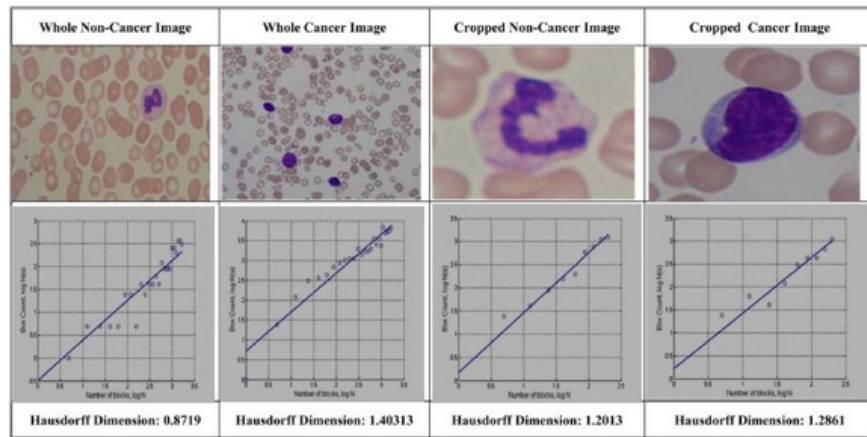
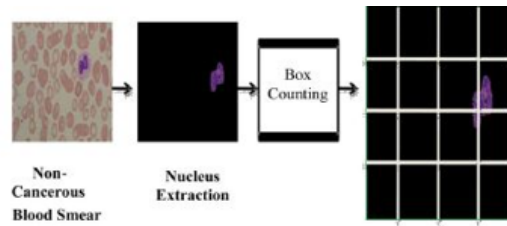


Figure 18: Comparison between different hausdorff dimensions

3.1 Similar System Description

In the past years, blood testing mainly relied on manual diagnosis by hematologist experts. This manual process was not only time consuming but also inaccurate. A system proposed by R. Saravanakumar, G. Kiruthiga, K. Lubna, P. Nivedha and K. Pavithra for detection of Leukemia using nuclear segmentation. This system managed to count the number of RBCs and WBCs in blood sample image using image processing techniques like Threshold and Circular Hough Transform. The main purpose of this system was to detect leukemia in blood at an early stage so it can be cured easily. Another system was proposed by Biji G1, Dr.S.Hariharan2 for detection of Leukemia by segmentation of white blood cells images. This system managed to use two clustering techniques to compare the performance of the image segmentation. The 2 techniques are Fuzzy-C-Means (FCM) and adaptive K-Means (AKM). Another system with different techniques was proposed by Emmanouil Michail, Evgenios N. Kornaropoulos, Kosmas Dimitropoulos, Nikos Grammalidis, Triantafyllia Koletsa, Ioannis Kostopoulos for automatic detection of malignant cells in microscopic images acquired from tissue biopsies of follicular lymphoma. This system consists of ve

main steps which are image preprocessing, image segmentation, touching-cell splitting, selection of candidate CBs and classification. Finally, a system proposed by Emad A.Mohammed, Behrouz H.Far, Mostafa M.A. Mohamed and Christopher Naugler for segmentation of lymphocyte color cell using Support Vector Machine (SVM) and k-means clustering algorithms. These algorithms overcome the occlusion problem when lymphocytes are tightly bound to the surrounding Red Blood Cells. So, we notice that each system managed to use different techniques to solve the problem. Each one has reached an acceptable accuracy but the highest one was the one using SVM and K-means.

3.2 Comparison with Proposed Project

Paper	Function	Pre-Processing	Segmentation	Feature Extraction	Classification	DB	Accuracy	Results	Future Work
D. P. A. S. J. LAKSHMIBHATTI, Acute Myelogenous Leukemia Detection in Blood Microscopic Images using Different Wavelet Family Techniques, International Journal of scientific engineering and technology Research, 2016	Acute Myelogenous Leukemia Detection in Blood Microscopic Images using Different Wavelet Family Techniques	Median filter to remove noise.	Discrete Wavelet Transform(DWT): 1. Haar Wavelet 2. Daubechies Wavelet	1. Local Binary Patterns (LBP)	1. Neural Network (ANN)	--	1. LBP 97.48% 2. Without LBP 76.04% 3. K-means and DWT 50.099%	Experimental results shows that wavelet transform provide many possibilities of detection of image segment features owing to its multi-resolution properties and the possibility to choose different wavelet functions (Haar wavelets and Daubechies wavelet) appropriate for a given problem as well.	They will focus on collection of more samples to yield better performance and building an overall system for cancer classification
White Blood Cell Segmentation Techniques in Microscopic Images for Leukemia Detection Feb, 2016	This paper aims to segment the blood cell images of patients suffering from acute leukemia.	--	1. Standard C-Means. 2. Fuzzy C-Means 3. Adaptive K-Means	1. Feature recognition.	--	Images with resolutions of 1320 X 950	--	Experimental results shows better performance to perform image recognition and classification for acute leukemia blood cells image using the proposed adaptive system as compare to standard K-Means and Fuzzy C-Means	This research will continue to perform image recognition and classification for acute leukemia blood cells image
DETECTING DIFFERENT SUB-TYPES OF ACUTE MYELOID LEUKEMIA USING DICTIONARY LEARNING AND SPARSE REPRESENTATION, Image Processing (ICIP), 2015 IEEE International Conference on, 2015.	DETECTING DIFFERENT SUB-TYPES OF ACUTE MYELOID LEUKEMIA USING DICTIONARY LEARNING AND SPARSE REPRESENTATION	--	K-Means	--	1. Dictionary learning (DL) 2. Sparse Representation (SR)	27 microscopic images of three sub-types of AML, 9 AML-M2, 10 AML-M3 and 8 AML-M5	97.53%	Their results showed that by increasing atom size of DL, the performance would be better and the best average accuracy 97.53% achieved for atom size of 49	They aim to test the algorithm on more data and use will attempt to differentiate more subtypes. They will consider the cases of occurrence of two subtypes in a single image.
DETECTION OF LEUKEMIA USING MATLAB Feb, 2015	Detect Leukemia in microscopic images	1. Sobel filter 2. Image Dilate using the vertical structuring element followed by the horizontal structuring element. 3. Infit function	1. Incclear border function.	--	--	--	--	Only detection of leukemia in human blood cells.	--
Sot Agaian Senior Member and I. Anthony T. Chronopoulos Senior Member, Automated Screening System for Acute Myelogenous Leukemia Detection in Blood Microscopic Images, IEEE Systems Journal, 2014.	Automated Screening System for Acute Myelogenous Leukemia Detection in Blood Microscopic Images	CELLAB Color Features and Color Correlation.	1. K-Means Clustering Algorithm.	1. Hausdorff Dimension measurement using the box counting method. 2. Local binary pattern (LBP).	support vector machine(SVM)	AML comprised 80 images—40 from AML patients and 40 from non-AML patients from the American Society of Hematology (ASH) online image bank.	98%	The impact of the LBP operator on the HD proved to be a promising feature for this analysis. Furthermore, a color feature called cell energy was introduced, and results show that this feature presents a good demarcation between cancer and non-cancer cells.	They will focus on collection of more samples to yield better performance and building an overall system for cancer classification.
Morphological and textural analysis of centrioblasts in low-thickness immunohistochemical tissue biopsies of follicular lymphoma, Engineering in Medicine and Biology Society (EMBC), 2014 36th Annual International Conference of the IEEE, 2014.	Morphological and Textural Analysis of Centrioblasts in Low Thickness Biopsy Tissue Biopsies of Follicular Lymphoma	--	1. Morphological analysis of nucleus using Orthogonal Distance Regression (ODR) 2. Textural analysis of nucleus using Gray-level Run Length (GLRL)	1. Expectation Maximization (EM) using the minimum description length (MDL) 2. Gaussian mixture model	1. Naive Bayes classifier. 2. Quadratic classifier. 3. K-nearest neighbor (KNN) 4. Support Vector Machine (SVM)	300 cell images, 120 CB cells and 180 non-CB (CENTH/NOTH database)	97.44%	Different types of classifiers were tested over an annotated dataset of cropped images of CBs and non-CBs derived from HFF images. Average accuracy results of 97.44% show the great potential of the proposed method.	1. The encapsulation of the proposed classification approach on a complete framework for automatic grading of FL images and 2. The use of the proposed method in a variety of images with different concentrations of Hematoxylin and Eosin.
Emmanuel Michal, Karamouzou, Kosmas Dimitropoulos, Iliana Giannoulis ,Tsiantnylla Kolata, Ioanna Fotopoulou, Detection of centrioblasts in H and E stained images of follicular lymphoma, Signal Processing and Communications Applications Conference (ISAP), 2014 22nd, 2014.	DETECTION OF CENTRIOBLASTS IN H&E STAINED IMAGES OF FOLLICULAR LYMPHOMA	Input images are first converted to grayscale and filtered using a Gaussian filter with a 3x3 kernel then applying histogram equalization.	Otsu thresholding	1. Cell Spitting using Gaussian mixture modeling and Expectation Maximization. 2. Selection of candidate CENTRIOBLASTS using Orthogonal Distance Regression (ODR)	1. Singular Value Decomposition (SVD) 2. Linear Discriminant Analysis (LDA)	400 microscopic HFF images derived from tissue biopsies of grade II FL, stained with H&E.	82.58%	The methodology addresses the special characteristics of the images used and specifically, the transparency of the nuclei due to the small thickness of tissue sections, however, the algorithm also produces a large number of false positives.	They will detect differences between the different focus of large cells.
Detection of Leukemia in Microscopic Images Using Image Processing April 3, 2014	The proposed system will be on microscopic images to detect Leukemia.	Using LabView Histogram equalization Using Matlab 1. Convert the color image into grayscale 2. Linear contrast enhancement and Histogram equalization.	Using LabView 1. Multi-threshold (statistical parameters such as mean and standard deviation) 2. Morphological erosion 3. Sobel edge detector. Using Matlab 1. Otsu's Thresholding 2. Removal of small particles and Sobel edge detection.	Calculates the geometrical features such as area and perimeter of segmented cells.	--	Applied on 138 microscopic blood slide images.	--	LabView is more accurate than Matlab	--
Application of Support Vector Machine and k-means Clustering Algorithms for Robust Chronic Lymphocytic Leukemia Color Cell Segmentation, International Conference on e-Health Networking, Applications and Services IEEE, 2011.	Application of Support Vector Machine and k-means Clustering Algorithms for Robust Chronic Lymphocytic Leukemia Color Cell Segmentation	--	1. Thresholding the original image using Otsu's method to select the nucleus pixels only. 2. k-means clustering algorithm	--	1. Support Vector Machine (SVM)	440 lymphocyte images (normal and CLL). The images resolution is 363x360 pixels. training phase which includes 22 images out of 440 images for normal and CLL cells	1. 98.43% maximum accuracy for nucleus segmentation. 2. 98.69% for cell segmentation. 3. The cytoplasm region can be extracted by 99.85% maximum accuracy with simple mask subtraction	--	--

4 Project Management and Deliverables

4.1 Tasks and Time Plan

Our Project will be managed by Waterfall and Agile models as we have separate and distinct phases of specification and development. We also need to make it easier to change the process to reflect sudden changes in order to achieve maintainability and scalability.

Task Name	From Date	To Date
Information Gathering	09/05/17	09/15/17
Survey and Proposal	09/16/17	09/25/17
Proposal Presentation	09/26/17	09/26/17
Data set Collection	09/27/17	09/30/17
Designing System and Implementing Prototype	10/01/17	10/10/17
Designing Database	10/11/17	10/25/17
Writing SRS Document	10/26/17	11/30/17
Preparation for PROF. JIRO TANAKA	12/01/17	12/01/17
PROF. JIRO TANAKA Presentation	12/02/17	12/09/17
SRS Evaluation	12/10/17	12/10/17
SDD Document	12/11/17	01/18/18
SDD Evaluation	01/19/18	01/19/18
Implementing System	01/20/18	03/27/18
Implementation Evaluation	03/28/18	03/28/18
6 Pages Paper	03/29/18	04/03/18
Validation And Testing	04/04/18	04/30/18
Preparing for the final Presentation	05/01/18	06/13/18
Final Presentation	06/15/18	06/15/18

Figure 16

Figure 19: Time Plan Table

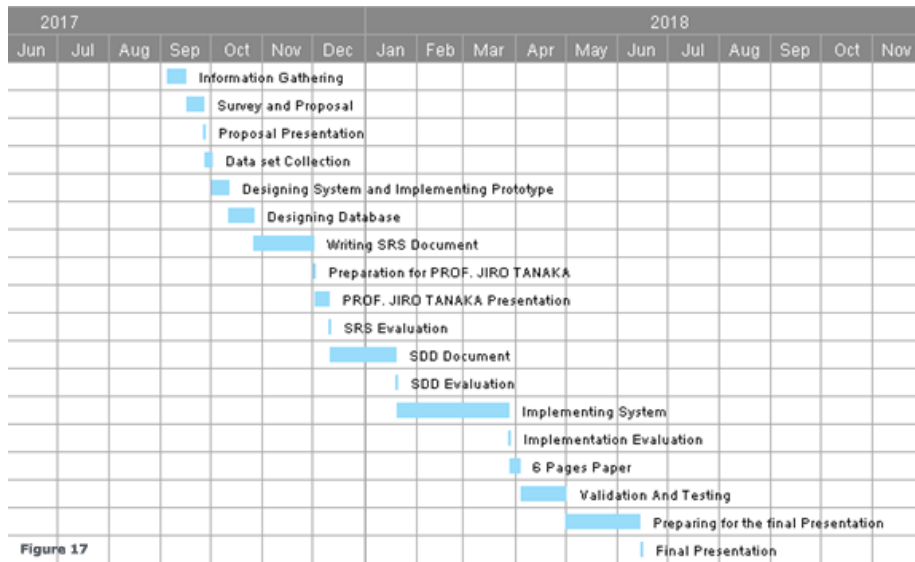


Figure 20: Gantt chart for time plan

4.2 Budget and Resource Costs

No Budget is required

4.3 Supportive Documents

The Experts that responded to this survey in Figure(1)

5 References

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