Feature Extraction and Detection of White Blood Cells from Microscopic Images Using Neural Network

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Abstract

In today's society, doctors and physicians face numerous obstacles when it comes to diagnose patient's illnesses. Many traditional and automated tools are developed in the medical field for the exact identification of the disease. Accurate leukemia prognosis is critical for providing better treatment, which differs depending on several factors. The medical field will benefit greatly from the provision of an automation technology for leukemia assessment. Many barriers exist in the identification and categorization of leukemia, such as noise in textual data, low sample size and so on. This paper discusses the feature extraction method and segmentation of leukemic cells. Aspects of color and texture features are extracted. After being analyzed, these traits are fed into a Back Propagation Neural Network (BPNN) and classified as malignant or normal using the Levenberg-Marquardt (LM) algorithm. The RGB input images are converted into YCbCr. After the noise removal, Gaussian filters are applied. A segmentation procedure is used to create a binary image from which 14 texture features and 72 color features are obtained and fed through a LM algorithm-trained BPNN. The proposed method was applied to 260 images, 130 of which were malignant and 130 of which were normal blood cells, with an accuracy of 96.92%.

Key Words: Leukemia, Levenberg-Marquardt (LM) Algorithm, Gaussian Filters.

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Introduction

Human cells divide and replicate to replace the old ones. Cells eventually grow older or become damaged and new cells take their place. Sometimes abnormal or damaged cells grow and multiply which form tumors (can be cancerous or non-cancerous), which are lumps of tissue. Malignant tumors are cancerous tumors that have spread to other areas of the body. Non-cancerous or benign, tumors do not spread to other regions of the body and can be surgically removed [1]. Cancer is one of the diseases that most people are too scared of. Cancers come in many forms, one of which being Leukemia. The term Leukemia is derived from the Greek word Leukemia, which means "white blood". Blood is indeed a sophisticated structure made up of over 4000 cellular organelles. In the modern medicine, blood samples may be used to diagnose most of the physiological problems [3]. The production of blood is shown in Fig. 1.

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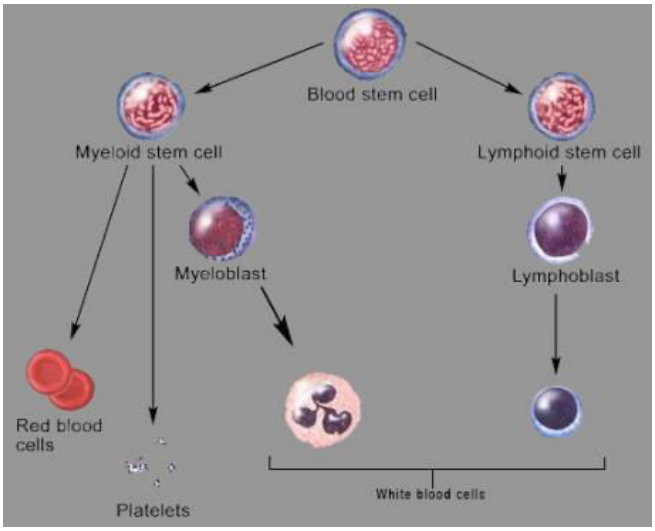

Fig. 1. Production of Blood

The role of RBC or erythrocytes is to transport oxygen to the bodly tissues and return CO_2 to human lungs. WBC or leukocytes protects the body from diseases. White blood cells come in a variety of shapes and sizes. Platelets, also known as thrombocytes, aid in blood clotting and bleeding management. Plasma is a dissolved ion-rich fluid found in blood that is essential for cell activity.

Leukemia is referred to be a variation of cancerous growth that starts in the marrow of bone and causes an abundance of malicious WBC. Blasts or leukemia cells are WBC that has not fully matured. A shortage of regular blood cells causes these symptoms. Blood analysis and bone marrow biopsy are typically used in diagnosis. The symptoms of leukemia includes pain or tenderness in joints, shortness of breath, lymph nodes welling, muscular weakness, loss of appetite, skin bleeding, night sweats, enlargement of spleen or liver, fever and weight loss. Leukemia can be either Acute or Chronic [4]. Acute Lymphocytic Leukemia (ALL) arises if the bone marrow cell's genetic structure, or DNA, alters (mutates). Chronic Lymphocytic Leukemia (CLL) occurs when healthy cells perish; malignant lymphocytes keep existing and expanding. These abnormal cells accumulate in the blood and healthy organs, creating complications. Healthy cells may be pushed out of the bone marrow, interfering with the creation of blood cells. This disease almost never affects children. Acute Myelogenous Leukemia (AML) occurs when blood cell formation gets uncontrollable. The bone marrow creates immature cells that grow into myeloblasts, which are leukemic WBC. These malicious cells might accumulate and crowd out healthy cells. AML is found more commonly in men. Chronic Myelogenous Leukemia (CML) is associated with the abnormalities in DNA. This disease occurs mainly in adults. The cell structure of different types of leukemia is illustrated in Fig. 2.

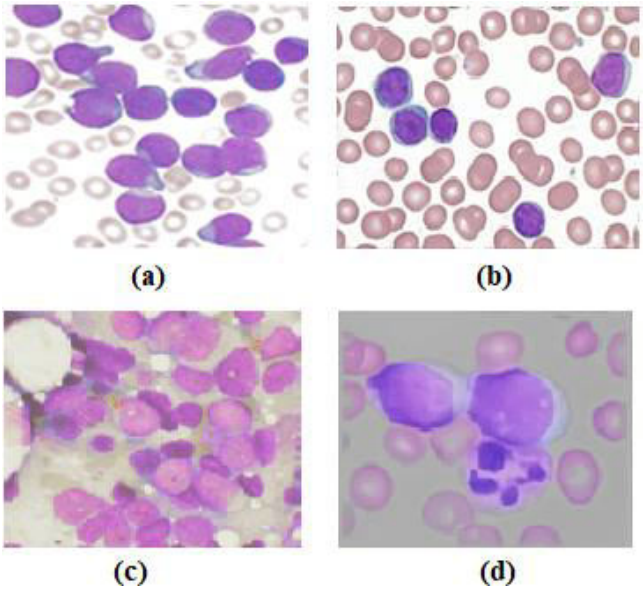

Fig. 2. Cell structure of Leukemia (a) ALL, (b) CLL, (c) AML, (d) CML

A unique computer-assisted diagnosis approach that is based on GLCM and contour characteristics has been proposed by Rawat *et al.* [5]. To determine the existence of lymphoblast cells, the extracted feature is categorized using a binary classifier called Support Vector Machine (SVM). Mohapatra *et al*. [6] has proposed color based clustering, fractal geometry, contour signature and texture based techniques for nucleus feature extraction using SVM. Shahin *et al.* [7] proposed a Convolutional Neural Network (CNN) based on transfer learning along with fine-tuned activation features. The "WBCsNet" is a unique end-to-end CNN architecture developed exclusively for Leukemia detection. Putzu *et al*. [8] suggested isolating the whole leukocyte before separating the nucleus and cytoplasm. The characteristics of shape, color, and texture are extracted. SVM was utilized along with Gaussian Radial Basis Kernel model.

Madhukar *et al.* [9] presented a classification method for whole blood smears with numerous nuclei. For the SVM classifier to operate, shape, texture, features were obtained. For separating WBCs from other blood components, Mohapatra *et al.* [10] presented a fuzzy oriented two step color separation. Shape characteristics based on Hausdorff Dimension and contour signature features were applied in an SVM classifier. On

peripheral smear of blood, Madhloom *et al.* [11] demonstrated the use of cell categorization to distinguish between different cancerous cells. K-means clustering was introduced by Patel *et al.* [12] for identifying WBCs. On the needed section of the images, certain filtering techniques were included. The Zack algorithm, as well as several feature extraction approaches, was employed. WBC was classified using SVM. Nasir *et al.* [13] trained the Multilayer Perceptron using LM and Bayesian Regulation algorithms, which is included to categorize inputs. Muntasa *et al.* [14] implemented a model for detecting of ALL based on color image object properties. Tomari *et al.* [15] employed an Artificial Neural Network (ANN) to recognize and identify RBC in blood smear images and classify them as normal or abnormal.

Materials and Methods

To create a system for WBC categorization that is both efficient and reliable, a novel algorithm for image processing is proposed. It is comprised of 4 major processes such as pre-processing, segmentation, feature extraction and classification. Each process is well optimized to generate precise outputs at each level. Preprocessing is performed to remove noise and other artifacts. Otsu thresholding based segmentation approach is adopted to elevate the performance of proposed system. GLCM is utilized for the extracting texture related features and it can minimize the data necessary for categorizing WBC images. Finally BPNN is used as the classifier which is trained using LM algorithm. Overall steps involve in Leukemia classification is illustrated in Fig. 3.

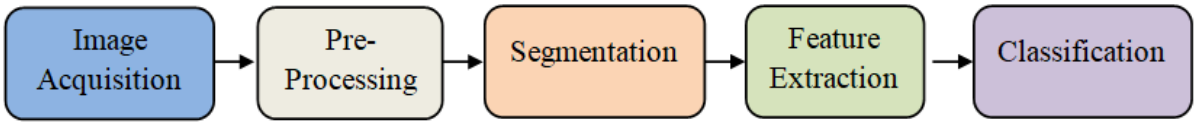

Fig. 3. Block Diagram of Proposed Leukemia Classification System

Data Acquisition

The acquisition of a digital image in RGB color space is the first step. Blood sample images have been generated for the segmentation operation by transforming input images from RGB to YCbCr space due to the red as well as blue pigmentation in the blood samples. When images are shifted to YCbCr format, the returned Cb and Cr coefficients are used for cell segmentation. The conversion of an image from RGB to YCbCr color space is shown in Fig. 4.

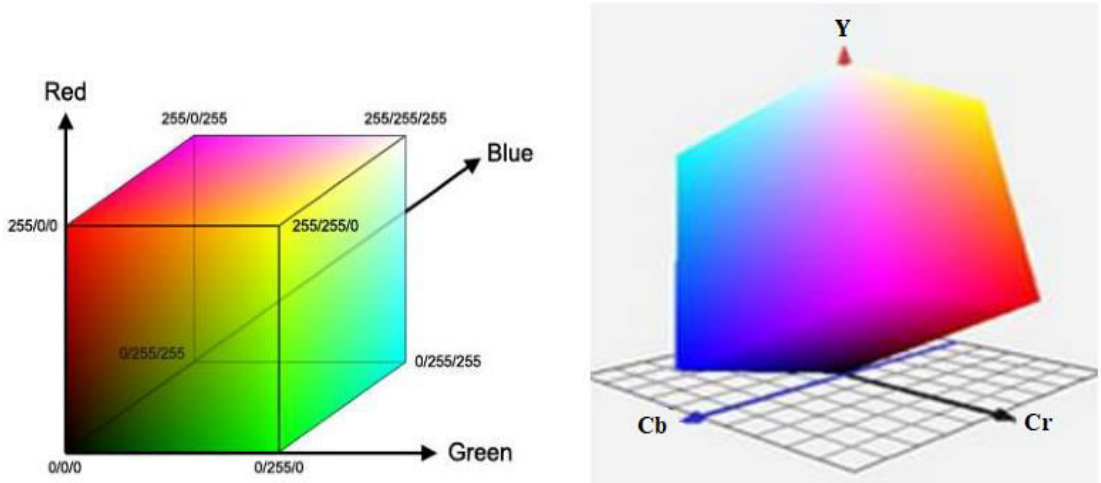

Fig. 4. RGB to YCbCr Conversion

Image Enhancement

Image enhancement is a technique for improving image quality varying contrast and brightness, reducing noise and sharpening fine details. After converting to YCbCr, we apply Gaussian filter to the Cb and Cr channel. The Gaussian filter is used for the smoothening of an image. Eqn. 1 provides the Gaussian filter transfer function $G(x, y)$ used for

smoothening the image having pixel co-ordinates (*x*,*y*) and variance (σ^2).

$$G(x,y)=\frac{1}{2\pi\sigma^2}e^{-\frac{x^2+y^2}{2\sigma^2}} \quad (1)$$

Image Segmentation

In a typical digital image, segmentation aids in the identification of various boundaries and objects [16]. After the segmentation procedure, the visual description may be simply evaluated and made more meaningful. Identical pixel intensities are allocated the very same tag during the segmentation procedure for easy analysis [17]. On the blood smear image, the Otsu thresholding technique is used to create a binary image with distinct areas.

The occurrence of pixels in image can indeed be expressed in the form of two classes. One class is the background class denoted by C_{bg} and the other class is the foreground class denoted by C_{fg}. The goal of Otsu's algorithm is to locate the best value of threshold by minimizing the variance within the class or by maximizing the variance between classes. Consider that the input gray scale image consist of pixel intensities in the range [1,2,3, ... L]. Total count of pixels having intensity value *i* is indicated by n_i. The overall count of pixels in the image is indicated as, $N=n_1+n_2+n_3....+n_L$. Main objective of this algorithm is to choose an optimal threshold value T_{opt} such that the sum of variance σ_{bg}^2 (for background class C_{bg}) and σ_{fg}^2 (for foreground class C_{fg}) is a minimum value. Let the pixel intensities in class C_{bg} are in the range [1,2,3,.... k] and the pixel intensities in class C_{fg} are in the range [k+1,...L]. The weight (*w*), mean (μ) and variance (σ^2), for C_{bg} and C_{fg} are calculated as:

For C_{bg} (background class),

$$w_{bg}=\sum_{i=1}^{k}\frac{n_i}{N} \quad (2)$$

$$\mu_{bg}=\frac{\sum_{i=1}^{k} i*n_i}{\sum_{i=1}^{k} n_i} \quad (3)$$

$$\sigma_{bg}^2=\frac{\sum_{i=1}^{k}(i-\mu_b)^2*n_i}{\sum_{i=1}^{k} n_i} \quad (4)$$

For C_{fg} (foreground class),

$$w_{fg}=\sum_{i=k+1}^{L}\frac{n_i}{N} \quad (5)$$

$$\mu_{fg}=\frac{\sum_{i=k+1}^{L} i*n_i}{\sum_{i=k+1}^{L} n_i} \quad (6)$$

$$\sigma_{fg}^2=\frac{\sum_{i=k+1}^{L}(i-\mu_b)^2*n_i}{\sum_{i=k+1}^{L} n_i} \quad (7)$$

The sum of the weighted variances (σ_w^2) given by,

$$\sigma_w^2=w_{bg}\sigma_{bg}^2+w_{fg}\sigma_{fg}^2 \quad (8)$$

By minimizing the weighted intra-class variance can be minimized to estimate the optimum threshold value [18]. Another approach to estimate the threshold value is to maximize the inter-class variance (σ_{IC}^2) denoted by:

$$\sigma_{IC}^2=\sigma^2-[w_{bg}w_{fg}(\mu_{bg}-\mu_{fg})^2] \quad (9)$$

Algorithm 1. Otsu's Thresholding Algorithm

Step 1. Provide gray scale image as input.
Step 2. Obtain the histogram of input.
Step 3. Choose an initial threshold value T and compute variance for C_{bg} and C_{fg}.
Step 4. Compute intra-class variance.
Step 5. Repeat step 3 and 4 for all combinations of threshold value T.
Step 6. The optimum threshold T_{opt} is obtained for which the interclass variance σ_{IC}^2 is maximum.

Feature Extraction

Color moments and color histogram are the two types of color features. 14 Haralik's features are deduced by utilizing GLCM and are employed in training the BPNN using LM algorithm.

a. Color Moments

Color moments are measurements that can be used to distinguish objects depending primarily on their color characteristics. These seconds give a gauge for color similarity among objects once they've been computed. We employ the three centre moments of a color distribution in a picture. The mean (μ), standard deviation (σ), and skewness (*k*) are the three variables. Three or more values can be used to define a color. For both these

channels in an image, moments are computed. As a result, an image is defined by 9 moments, one for each of the three color channels. The 3 moments are indeed being represented using the following equation.

$$\mu = \sum_{j=1}^{N} \frac{1}{N} K_{ij} \quad (10)$$

$$\sigma = \sqrt{\left(\frac{1}{N} \sum_{j=1}^{N} \left(K_{ij} - E_i \right)^2 \right)} \quad (11)$$

$$k = \sqrt[3]{\left(\frac{1}{N} \sum_{j=1}^{N} \left(K_{ij} - E_i \right)^3 \right)} \quad (12)$$

Where, N is the number of pixels in the image and K_{ij} the value of the j^{th} pixel of the image at the i^{th} color channel. E_i is the mean value, or first color moment, for the i^{th} color channel of the image.

b. Color Histogram

Color histogram is calculated for R, G and B channels of the given image. The distribution of colors in the image is indicated by the color histogram. In the histogram there are eight bins. As a result 72 color histogram features are extracted. The value of bin is chosen as 8 and it provides standard results. The percentage of the number of distinct sorts of colors in a color histogram is the only thing that matters, regardless of where the colors are in space. A color histogram's parameters are extracted using statistics. They depict the statistical distribution of colors and the image's basic tone.

c. Texture Features

These features pertain to cell details such as holes and granules. A collection of 14 Haralick's features are computed by using GLCM through 4 directions of adjacency. The GLCM approach for extracting textural information from blood smear images is a popular statistical tool. The spatial dependence of distinct grey levels in a blood smear image is calculated using GLCM [19]. Therefore, a total of 113 features are extracted. Fig. 5 shows how to create a GLCM from a grayscale image.

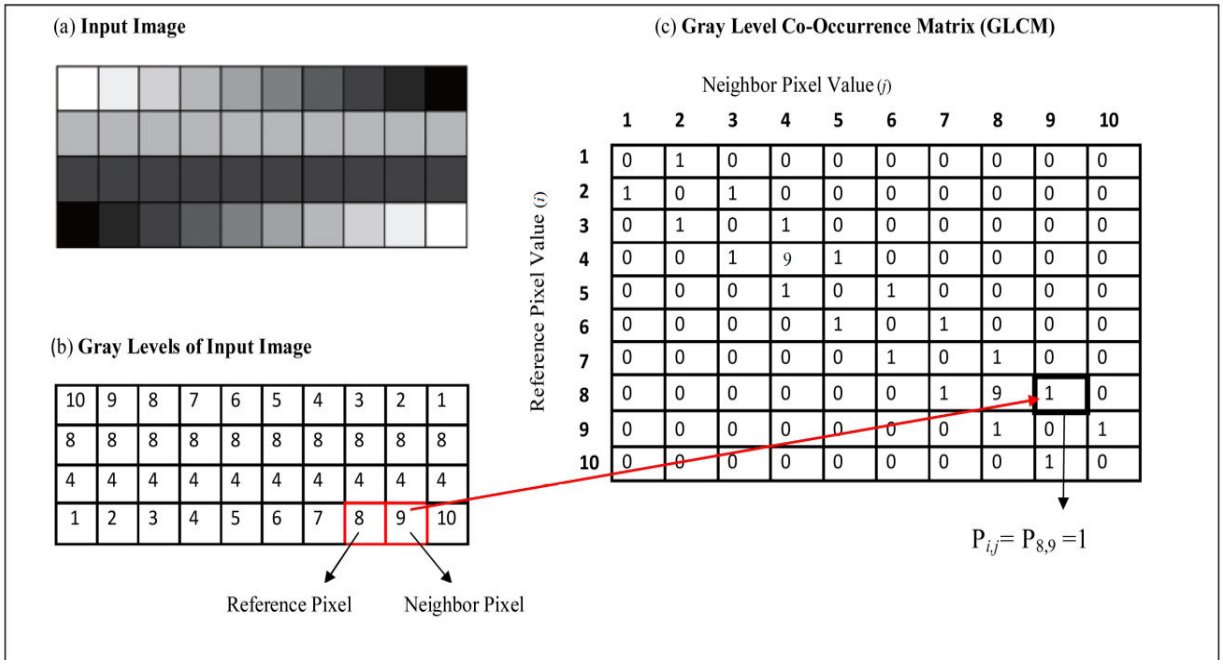

Fig. 5. GLCM construction from grayscale image

The count of column members and row members in GLCM matches the gray level count in the segmented image perfectly. The GLCM can be formed in four different orientations in space (0°, 45°, 90° and 135°). The mean of the previous matrices is used to create a new matrix. Let's call the GLCM as $P_{i,j}$ having matrix dimension NxN. The frequency through which pixels with grey levels I are connected in the space with pixels having grey value of j is denoted by the GLCM elements (i,j). Fig.6 depicts the distribution of GLCM in space [20].

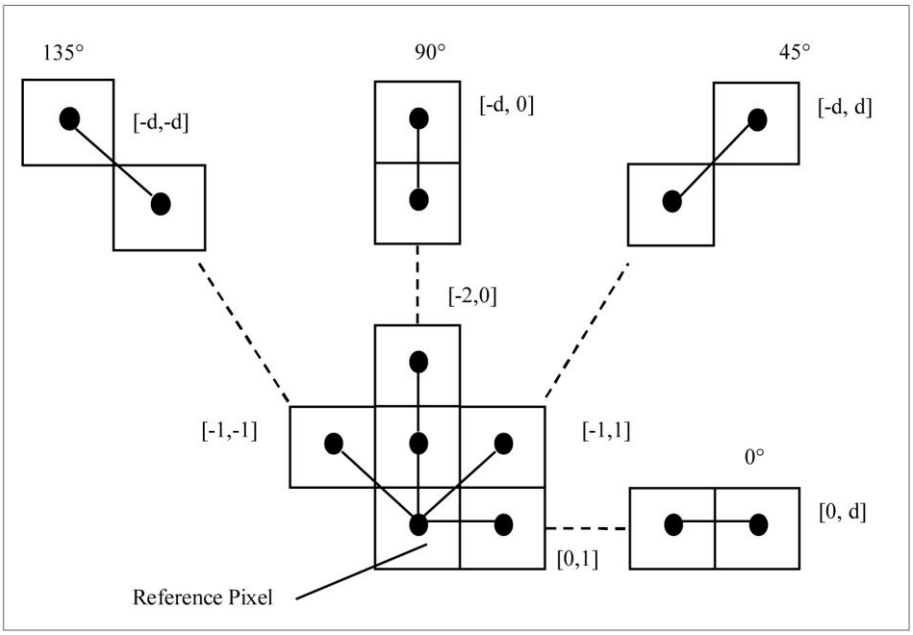

Fig. 6. Directions and Spatial Orientations of Co-occurrence Matrix

Classification

In order for the nets to provide the required mapping of input to output, ANN must be trained towards the task of classification. The dataset is randomly split into three sections: train (70%), validation (15%), and test (15%). The LM algorithm is utilized to modify the connection weights, also known as synaptic weights. Training of ANN using Back Propagation Algorithm (BPA) resembles training with an instructor. This means, it is mandatory to make a set, which contain reference input values and reference output values. This set is called training set and the corresponding values are called templates. If teacher identifies that student has a problem, then the teacher has to compel the student to learn the material. Neural network represents a student and the check mechanism verifies the input and output of network. If the network does not make a correct response, it is necessary to change the values of the weights so long, that the network will make a correct response. The general model of the Back Propagation Neural Network (BPNN) is depicted in Fig. 7. A link is used to interconnect nodes of two adjacent layers of ANN. A link is the representation of weights that denotes the amount of correlation between adjacent nodes.

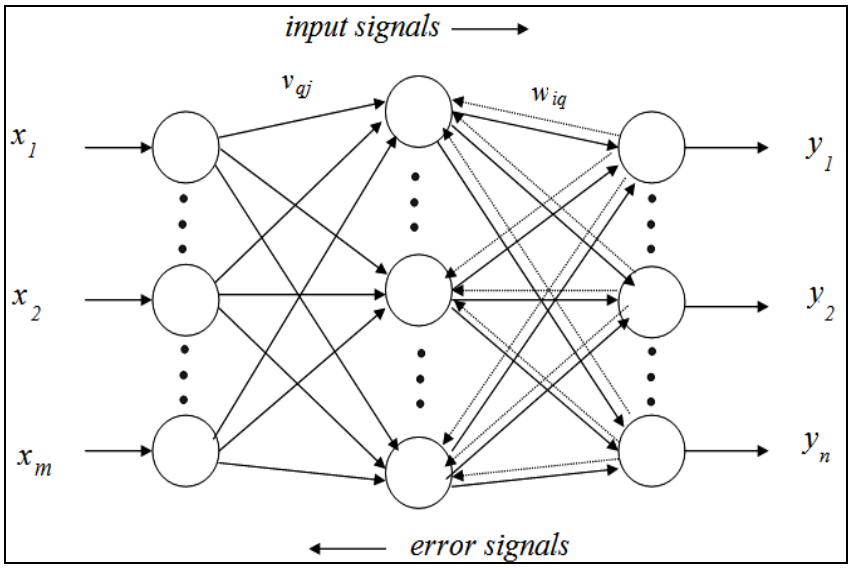

Fig. 7. General Structure of BPNN

In order to classify blood smear images into normal and abnormal, we used a BPA with Levenberg-Marquardt (LM) optimization method to categorize inputs target categories according to the extracted feature vectors. The LM scheme is a higher order adaptive method used to reduce MSE of BPNN. This scheme is implemented on ANN for the classification of medical conditions. In this work BPNN- LM scheme is used to discover the presence of leukemia and experiments are further performed to compute the sensitivity, specificity and accuracy of the LM optimized methodology. LM algorithm for identifying leukemia in blood smear slides is given below.

Consider blood smear classification for leukemia detection as a nonlinear model,

$$x_i = p(y_i, \alpha) + e_i, i = 1,2,3,....m \qquad (13)$$

Where α is a vector having **n** parameters and m>n. Assume, **g** is nonlinear in $\alpha_T = [\alpha_1, \alpha_2, \ldots\ldots \alpha_n]$. Least squares rule is utilized to estimate the indefinite parameters in non-linear regression function. In proportion to this scheme, the estimates of α_1, α_2, …… α_n are obtained by minimizing, $\sum g_i^2(\alpha)$.

The sum of squares of errors during the classification of leukemia can be derived as:

$$g_i(\alpha) = x_i - p(y_i, \alpha) \qquad (14)$$

Algorithm 2. LM Algorithm

Step 1. Calculate the Jacobian matrix having (*i,j*) elements.
Step 2. Calculate the gradient of error $\nabla^2 g(\alpha)$.
Step 3. Approximate Hessian Function using the Jacobian Matrix $\nabla^2 g_i(\alpha) \approx -J(\alpha_k)^T F(\alpha_k) + \tau \mathrm{I}$ Step 4. $[J(\alpha)^T J(\alpha) + \tau l]p = -J(\alpha)^T F(\alpha)$ is solved to find the direction *p*.
Step 5. Update weights of the network, ***w*** using the direction *p*. In order to improve function value, let α = α+ p and τ = τ/2.
Step 6. Using updated weights, the sum of square of errors are recomputed.
Step 7. If squared sum of errors is not reduced, discard newly updated weights, then increase the τ value using α and go to step 4.
Step.8. Else decreases the value of τ using α and stop.

Experimental Results

All microscopic blood images in the datasets are taken from ALL-IDB database. The images are taken from ALL-IDB2 which has 130 cancerous images and 130 normal images. All images are of .jpg format of size 257x257. Fig. 8(a) displays the input test images having ALL disease which is taken in RGB color space. Fig. 8(b) shows the preprocessing of RGB color space image YCbCr where Y, Cb, Cr components are extracted.

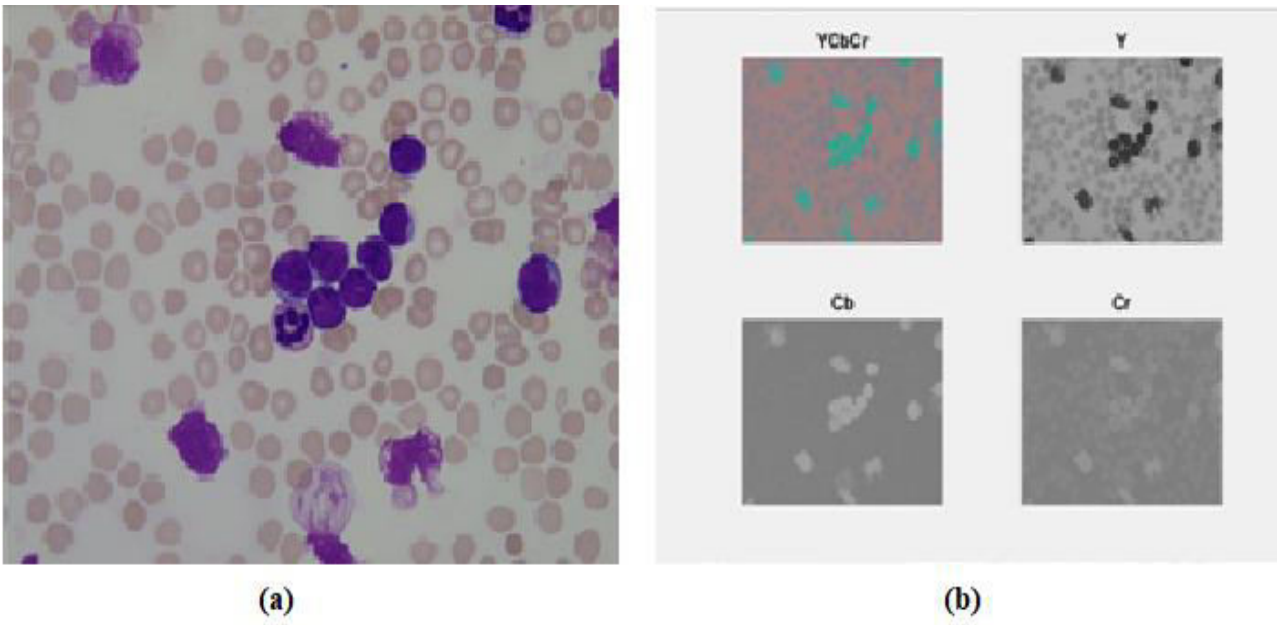

Fig. 8. (a) Input image having ALL, (b) YCbCr components extraction

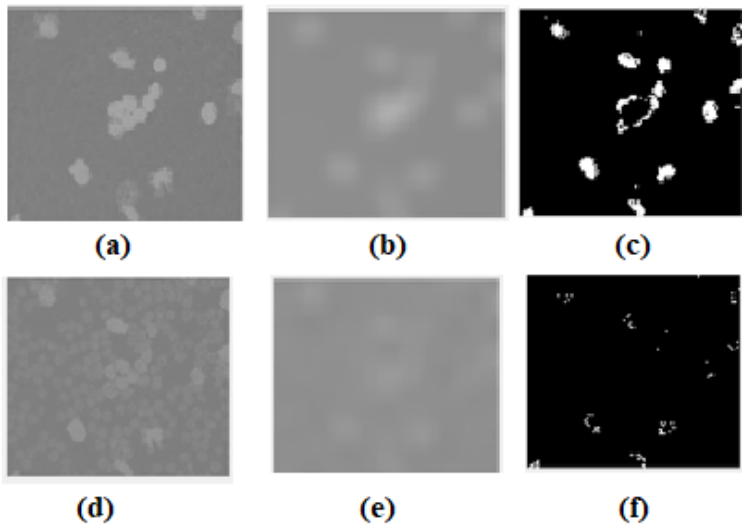

Fig. 9. (a) Gaussian Filtering on Cb, (b) Adaptive thresholding on Cb, (c) Mask on Cb, (d) Gaussian Filtering on Cr, (e) Adaptive thresholding on Cr, (f) Mask on Cr

Fig. 9 depicts a Guassian filter for noise removal is applied to Cb and Cr channel. It is followed by Adaptive image threshold using local first-order statistics to the Gaussian Filtered Cb or Cr channel. Combining Gaussian filter and Adaptive thresholding of Cb or Cr a binarization is applied and a mask is created for Cb as Mask Cb and for Cr as Mask Cr is obtained. As illustrated in Fig.10 common regions are taken from Mask Cb and Mask Cr morphological operations are performed and a binary mask is created. Here, needed regions appear as white and unwanted regions appear as black and then a segmented mask is formed.

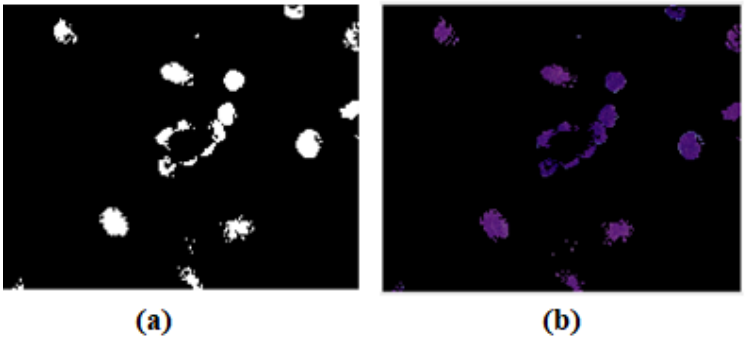

Fig. 10. (a) Binary mask, (b) Segmented Mask

From segmented mask we extract color features of 2 types (a) color moments (b) color histogram of RGB, HSV, YCbCr and using GLCM texture features [22] are extracted as shown in Fig.(11).

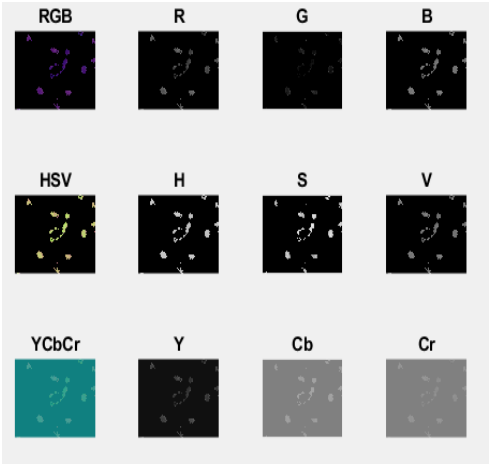

Fig. 11. Color Moments

Combining color moments (27 features), color histogram (72 features), color texture features (14 features) (total 113 features) are passed through a neural network. Fig. 12 depicts the neural network model and the result of cancer detection [23].

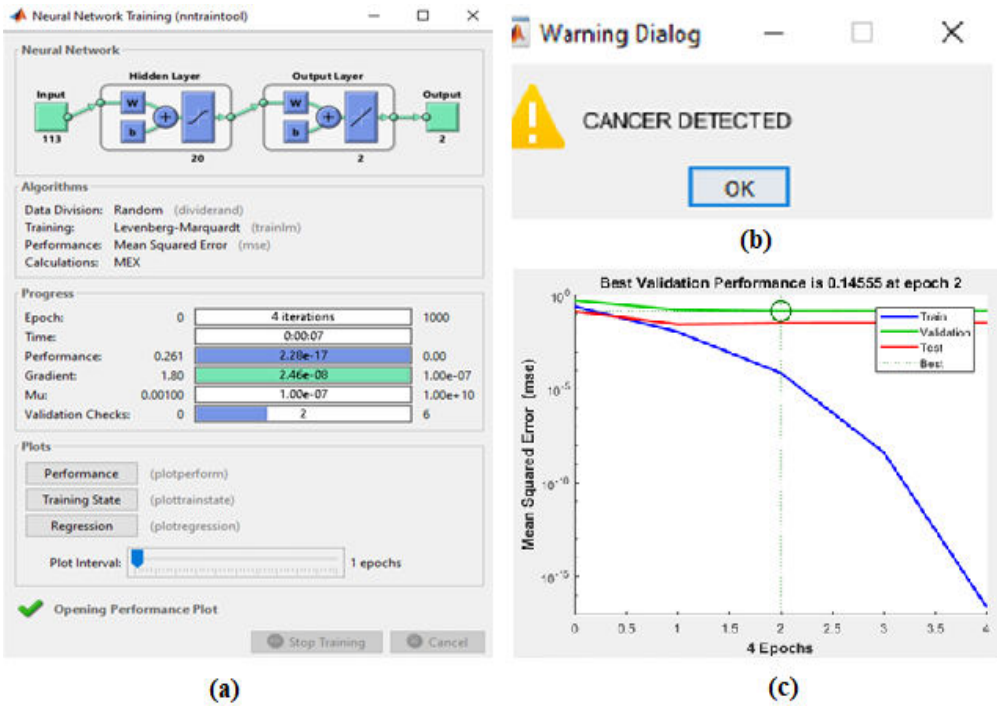

Fig. 12. Classifier (a) Neural Network, (b) Result, (c) Performance

The training states of LM algorithm [24] for given dataset is shown in Fig. 13. This figure illustrates the variation in gradient, Mu and validation check during each epoch. These values changes during each epoch and an optimum value is attained so as to minimize the MSE value. After obtaining the optimum value for MSE, four iterations are performed to validate the training algorithm. For this dataset, the gradient value is 0.024612 and Mu value is 1x e^{-7} at 4^{th} epoch. The next step in validating the neural network is to build a regression plot, which exhibits the relationship between the outputs of the neural network and the target outputs. The regression rate [25] obtained for DC200 is 0.95179 and it is the best among all other input data sets.

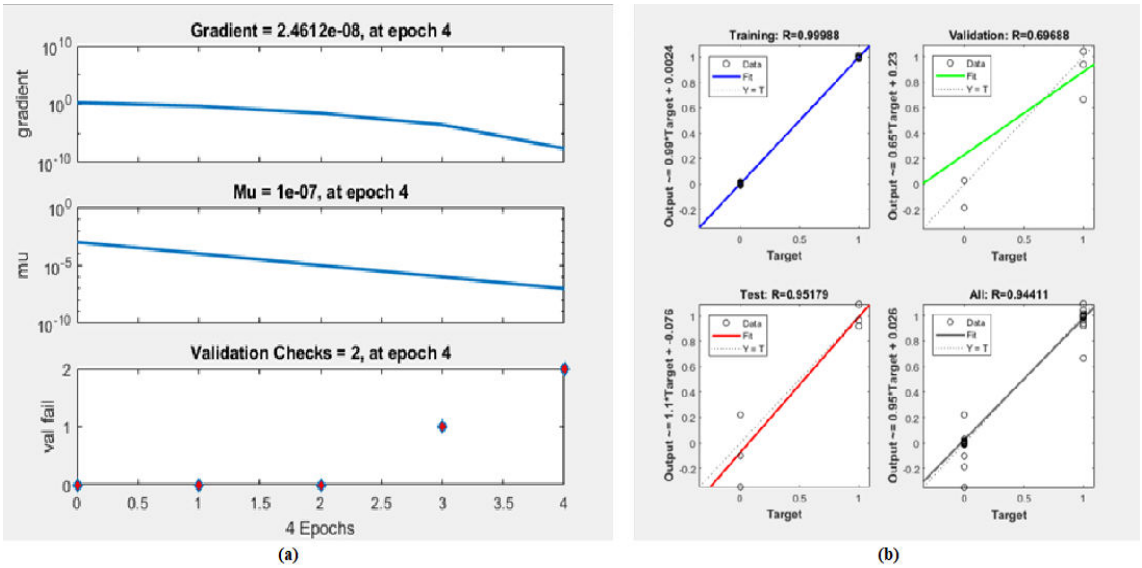

Fig. 13. (a) Training State, (b) Regression

While considering various machine learning aproaches, proposed algorithm provides better accuracy in terms of leukemia detection. The proposed optimized LM based machine lerning algorithm provides an accuracy of 96.9231%. KNN provides an accuracy of 79.6154%, which is the second best performer. Accuracy of the proposed classifier is 17.3077% higher than KNN based leukemia classifier. Performanceanalysis of the proposed work with various machine learning approachesis illustrated in Fig. 14.

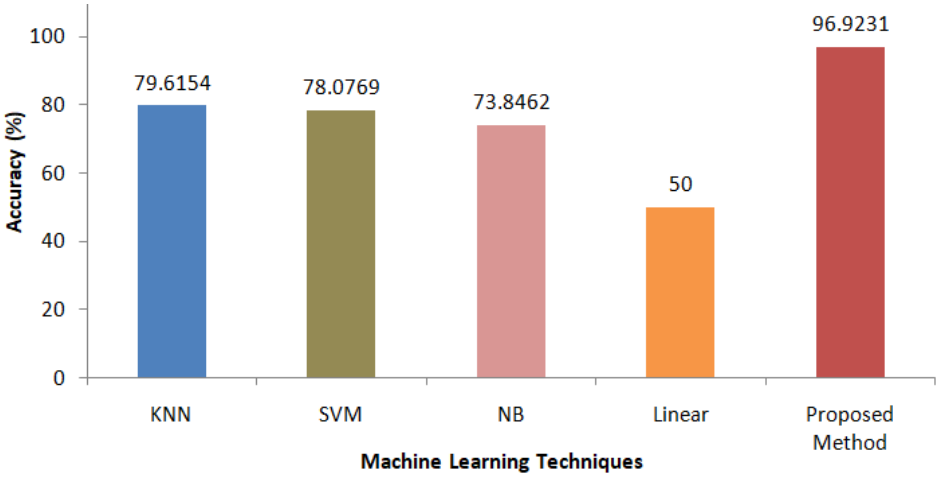

Fig. 14. Comparison of machine learning algorithms

A kernel operator collects information as inputs and converts it into a format required for computation. The deployment of "kernel" term refers to the collection of mathematical functions utilised in SVM provides a window through which data may be manipulated. As a consequence, the kernel modifies the train data, allowing a non-linear surface for decision which can be transformed into a linear equation in a wider space. Gaussian function provides an accuracy of 79.6154% which is 17.3083% lesser than that of the proposed method. The comparison of SVM kernel functions with proposed method is depicted in Fig. 15.

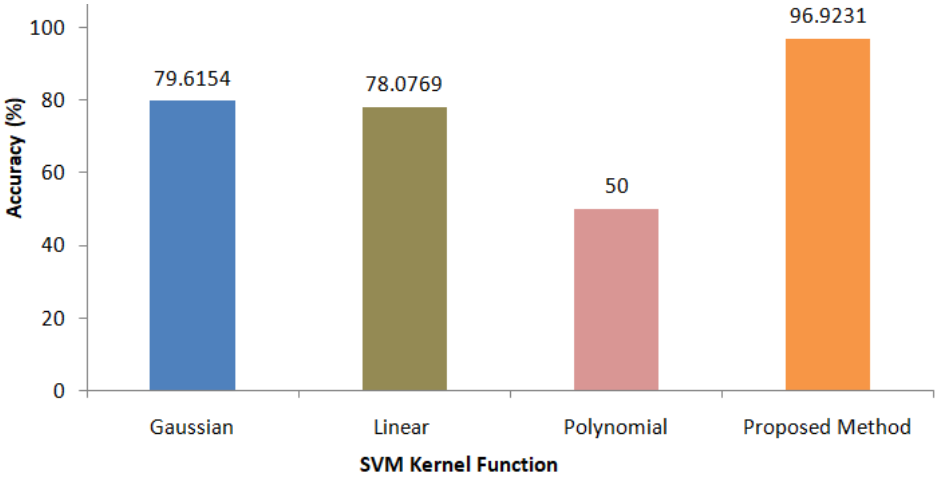

Fig. 15. Proposed method versus various SVM Kernel Functions

A kernel smoother is a statistical approach that uses the weighted average of nearby observational data to predict a factual function. The kernel determines the weight, with closer points receiving larger weights. The smoothness of the approximated function can be controlled by a single factor. By comparing various kernel smoother types, proposed classifer provides 20.7693% better accuracy. These values indicates the dominace in performance of proposed system.

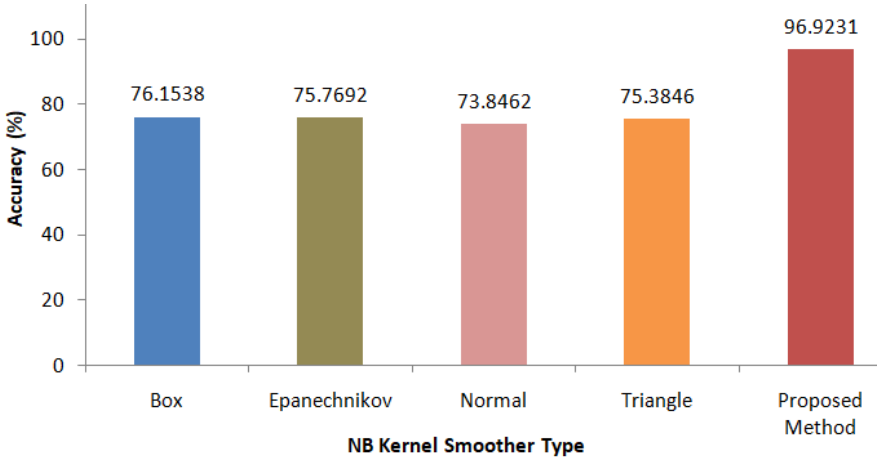

Fig. 16. Proposed method versus NB Kernal Smoother Type

Conclusion

The goal of this study is to design, build, and test an automated system that can accurately identify cancer in WBC. The system employs Gaussian filter for preprocessing, Otsu thresholding for segmentation, GLCM for feature extraction and DCNN for classification. Images are converted to YCbCr color space, and a Gaussian smoothing of Cb and Cr is generated. The classifier is then trained using color as well as texture features. In contradiction with other algorithms, this one can adapt from incorrectly categorized testing and improve the scheme's accuracy in future. The optimum classifier for distinguishing among distinct kinds and providing the greatest accuracy is based on CNN. Detection and classification accuracy for the system was 96.9231%. Our future goal is to identify several varieties of WBC for the development of a comprehensive system exclusively for WBC pathologies.

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