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Detection of Cancer Cells in Human Blood Samples Using Microscopic Images

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ABSTRACT

Blood testing is now widely regarded as one of the most important clinical examinations. A blood cell's characteristics (volume, shape, and color) might reveal vital information about a patient's health. On the other hand, inspection process takes time and requires a high level of expertise knowledge. As a result, automated medical diagnosis technologies are needed to help clinicians identify illnesses promptly and reliably. The main objective of normal blood segmentation is just to isolate defective/abnormal units from a complex background and segments them into architectural elements utilizing image processing techniques such as contrast enhancement, thresholding, and morphological procedures, among others. The suggested method here reduces noise and enhances visual segmentation. All previous methods used different segmentation strategies, which resulted in less efficiency than the suggested method. This work can be implemented using MATLAB environment.

Keywords - Blood cell, abnormal cell, Image processing, Image segmentation, Image enhancement, Thresholding techniques.

I. INTRODUCTION

A gram stain is just a little amount of blood thinly spread on a microscope slide, which is then colored and then are examined. Blood smears have usually been checked manually with a microscope by experienced laboratorians. Blood smear analysis has recently been made easier with the use of automatic computerized digital devices.A gram stain is indeed a photograph of something like the blood cells in the body only at moment such sample is drawn. A blood gram stain can be used to assess the following cells:

• WBCs (leukocytes) — aid in the attack against infections and play a role in immunological responses.
• Platelets (thrombocytes) — small cell fragments required for effective blood clotting
• RBCs (erythrocytes) are red blood cells that deliver oxygen to the tissues.

The bone marrow produces and matures these cellular components, which are then discharged further into blood circulatory system as needed. In the bloodstream, the quantity and types of cells change, but the body regulates them within specified parameters.

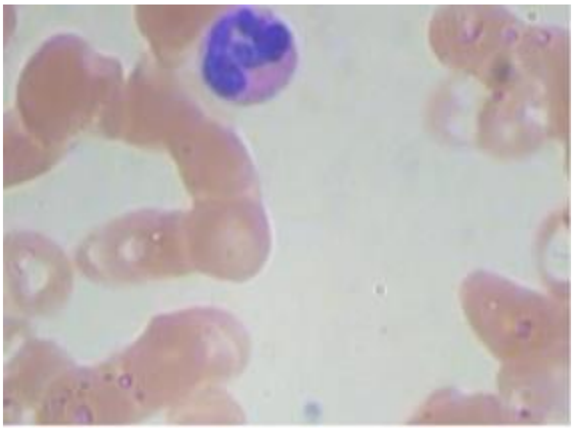

Figure 1: Picture of blood on slide

Millions of RBCs, thousands of WBCs, and some hundred thousand of platelets make up a bit of blood on a blood smear slide.

A wide variation of disorders and conditions which can influence the amount and visibility of blood cells. The outcomes of a gram stain examination would be used to back up the results of other examinations. Erythrocytes that are thinner and coarser than normal, for instance, can help to confirm other anemic symptoms. Likewise, the existence of premature Leucocytes could help in cancer detection, infection or other disorders by supplementing data from other tests.

In the field of digital computer vision, the process of splitting an image is known as segmentation, partition of image information into numerous pieces (pixels, picture elements). Segmentation seeks to make an image more intelligible and easier to examine by decreasing and/or changing its description. Image segmentation refers to the process for locating objects and boundaries that present in images (lines, arcs, edges and so on). Image segmentation, to look at it another way, is the method of giving a label to every other pixel in a picture because that pixels with a certain label have similar features.

Convolutional Neural Networks are sophisticated algorithms that are improved to Artificial Neural Networks in the Deep Learning approach. The disease in an input image is classified using these Convolutional Neural Networks. With the use of Convolutional Layers, training choices, and comparison with trained datasets, this will extract relevant features from the input image. Convolutional Neural Networks (CNNs) are the current hot technology in the field of object recognition and classification from images.

II. RELATED WORKS

Ritika in [1], Picture enhancement is among the most exciting yet visually pleasing parts of image recognition. In order to improve any image's quality, it comprises techniques such as increasing contrast and removing noise. This research compares the mathematical morphological approach to a variety of other state-of-the-art techniques for dealing with low contrast problems in photographs. One of the most prevalent approaches for increasing contrast in digital photos is histogram equalization (HE). The following method is easy and an efficient way for enhancing globally contrast in photos, but this has certain downsides. CLAHE (Contrast Limited Adaptive Histogram Equalization) improves image locally contrast without amplification of noise. In article [2], Picture capture, image segmentation, image analysis, image preprocessing, and image post-processing are the five essential components of image processing. Segmentation of the image is the most crucial phase in processing of image. In this paper, we look at a few of the generic segmentation techniques which has been used in categorization in biomedicine image processing, particularly in the processing of blood cells. Essentially, image segmentation separates the entire image into distinct disjoint parts. The truth that the segmented image must keep as much valuable information as possible while discarding irrelevant data makes the entire procedure crucial.

In [3] the author presented pictures taken from peripheral blood smear slides, we describe an unsupervised blood cell segmentation technique. The method is fast, fully automated, it's been proven to deal with a variety of RBC morphologies. It recognizes the markings within for each object; determines a precise one-pixel vast border to every element; separates things that merely contact; and has been found to function with only a diverse variety of erythrocytes morphologies. Two sets of photos were used to test the entire method.
Cooccurrence probabilities are the statistical way for identifying the spatial arrangement of gray-tones that can be used to determine the texture of a gray-scale image. We use grey level cooccurrence matrices (GLCM) to construct five textural attributes: entropy, local homogeneity, energy, and, inertia, and test the features present in leukocyte detection. Because few factors must be calculated in order to produce GLCM, we use datamining methods to estimate appropriate scales. The best discriminative qualities for defining cellular patterns are also defined using feature selection approaches. To distinguish between the 5 types of typical leukocytes and chronic lymphocytic, texture criteria are required, highlighting the importance of genetic features. Such nuclear chromatin and cytoplasmic granularity, which are considered by hematologists in [4].

Image processing procedures are used to change the attributes of an image or to edit it. Especially those methods are used here to segment the cancer cell in human blood samples. To overcome these issues, this study proposes a vision-based technique that uses a deep architecture of convolution neural networks (CNNs) to classify the blood sample. The paper suggests extracting features automatically using CNNs, which are capable of learning picture features automatically for the better training of the system.

The Methodology session describes the implementation process and techniques used in this work, the Results and Discussions session shows experimental results or a brief explanation of our model execution, and the Conclusion session summarizes our work, which is followed by the References session.

III. METHODOLOGY

In the proposed work, it consists of two phases. They are the segmentation phase in which the cancer cells get segmented and the classification phase in which the blood sample is then classified either as normal or abnormal solely rely on the distinct features extracted by the convolution neural network.
The below is the flow of our proposed work:

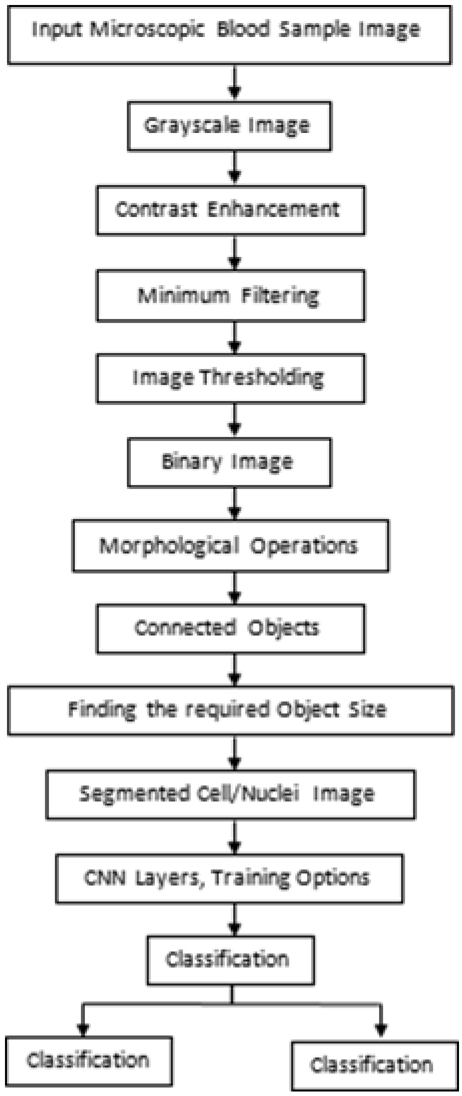

Figure 2: Flow diagram of our method

A grayscale image just contains the light intensity information since each pixel intensity is indeed a small body representing only a luminance. Grayscale photos, also referred to as grey monochrome or black-and-white photos, are constructed entirely of grayscale shades. The contrast is black when it's weakest and white when it's strongest. In the field of computer imaging, Gray - scale images differ through one bi-tonal mixed race (BW) images, that have simply black and white as colors (also called bi-level or binary images). Grayscale images show a variety of grey tones.

Image thresholding is a simple and quick way to separate foreground and background elements in a photo. By converting grayscale photos into binary images, this type of image segmentation technology isolates objects. With photographs with a lot of contrast, image thresholding works nicely.

Morphological operations are well suited to the processing of binary images because they rely completely on a promotion of pixel intensity values instead of their quantitative data. Gray - scale pictures could also be subjected to architectural treatments wherein the illumination transfer functions are uncertain and the precise pixel intensity values are immaterial or insignificant. Morphological approaches employ a small structure or sequence called a standard technique to investigate an image. The standard technique is compared to pixels in the near surroundings in all feasible positions in the image.

The photograph can indeed be separated or partitioned into various segments. It is not really a fine decision to examine the actual picture in one go because there may be areas of the picture that are void of data. We can use the key portions for image preprocessing by separating the picture into distinct segments. That's just how photo segmentation functions in a summary. A picture contains a large number of distinct pixels. Image segmentation is a technique for separating pixels with comparable characteristics into groups.

Convolution 2D-layer:

The convolutional 2D layer is by far the most essential element of a CNN and it is where the majority of the computation actually occurs. It requires data input, a kernel filter, as well as a feature map, among many other things. A feature detector, often referred as a kernel or a filter, analyzes the picture's receptive fields for something like the existence of the feature. Convolution is indeed the label for this technique. The feature detector is indeed a two-dimensional (2-D) weighed array that signifies a portion of the picture. The kernel size, that can vary enormously, is typically a 3x3 matrix, that determines the dimensions of the receptive field too though. After trying to apply the filter to a section of the image, the dot product of the input image and the filter is calculated. The dot product would then be written to the output vector. By altering the filter by something like a stride, the kernel would then be wiped throughout the entire image, and the process repeats until the kernel has drifted throughout the image plane. A region of interest, activation function map, or convolved feature is the end product of a series of dot products from source and the filters.

Parameter sharing ensures that the feature detector's weights remain constant as it traverses across the picture. Backpropagation and stochastic gradient are used to change some characteristics during training, such as weighting factor. However, three hyperparameters that determine the higher size must always be presented yet when the neural network can indeed be trained. Here are few examples:

1. The intensity of the result is associated with the quantity of filters employed. For instance, three distinct maps would come from three various filters, yielding a depth of 3.

2. The kernel's stride is perhaps the number of pixels it traverses with in input matrix. Despite the reality that two or more stride values are uncommon, a longer stride means less output.

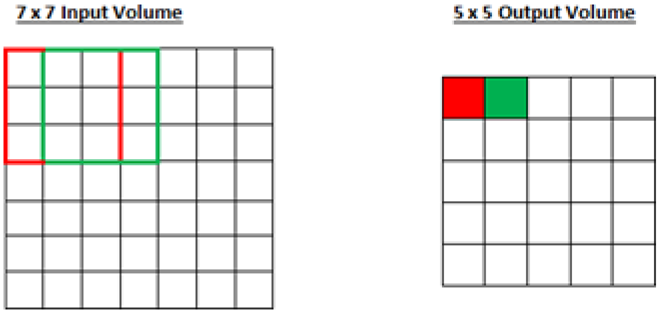

Figure 3: Stride

3. Whenever the filters don't accommodate the image as input, zero-padding is regularly utilized. All elements are set to zero outside of the input matrix, resulting in a greater or equal result.

Rectified Linear Unit Layer (ReLU):

To train deep neural networks employing stochastic gradient with backpropagation of defects, an activation function which resembles and functions just like a linear function is however truly a nonlinear function is essential. In order to prevent overloading, the goal needs to be more responsive to the activated aggregate input. A rectified linear activation unit (or ReLU for short) has been used to construct this activation function. Neural networks having hidden convolution layers that use the rectifier function are commonly known to as rectified networks.

Both the rectification layer and the non-linearity function will be combined in the Rectified Linear Unit Layer. These combinations will operate in between convolutional neural network layers as a rectified linear unit layer. In a nutshell, the ReLU layer is a rectified Linear unit.

$Y(l) = \max(0, Y(l{-}1))$ … (1)

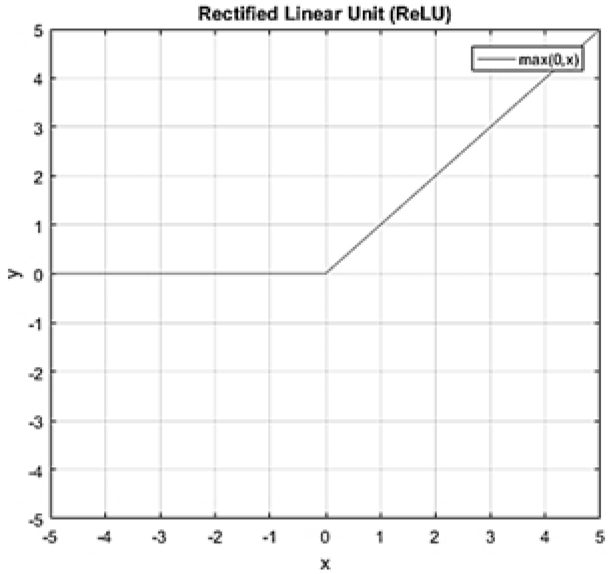

Figure 4: ReLU curve Maximum Pooling Layer:

Down-sampling, also referred as max pooling, is a form of dimensionality reduction which limits the number of input elements to the bare minimum. The pooling technique, like the convolutional 2d layer, runs a filter throughout the entire input image, but this filter has no weights. Rather, the kernel uses an summation function to populate the result array with the values of the receptive field.

Since feature detection is much more crucial to the accurate location of such feature, particularly in picture identification projects, the pooling layer's main purpose should be to provide feature lessening. Max pooling produces greater results as compared to average pooling. As a result, we will conduct our investigation using the maximum pooling layer.

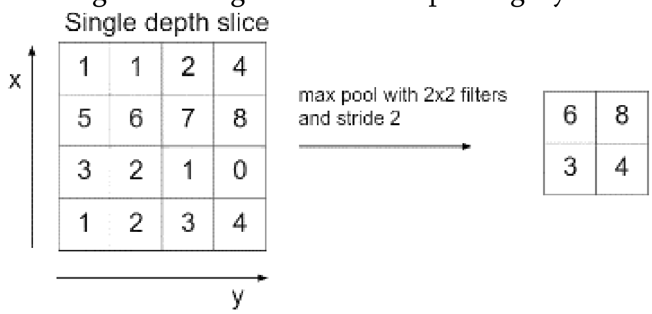

Fig 5: Maximum Pooling

Softmax-Layer:

A multidimensional generalization of the logistic function is the softmax functionality. It really is generally implemented as the final activation functionality of a network in multiple regression analysis to standardize the network's result to a probability distribution function over possible output class. The soft-max function normalizes the vector x of J real numbers into a probability distribution with J probabilities proportional to input number exponentials. In this example, some vector components may be below zero or greater than one, and that they might not stack up to the value one; nonetheless, but upon performing softmax, every other component will be in the range (0,1), and also the components will total to 1, letting them to also be interpreted as chances. Furthermore, the higher the input component, the higher the probability.

FC Layer:

The full-connected layer gets its name from the fact that it is completely connected. In partly linked layers, as previously mentioned, the pixel values of such test pictures are not specifically correlated to the output hidden layers. Every output node node creates a connection to such a node as in preceding layer mostly in fully-connected structure. Utilizing the information and filters gathered by the earlier layers, the present layer performs the multi class classification tasks. Although convolution layers categories inputs using ReLU activation functions, FC layers utilize a softmax activation function that serve a probability in between 0 and 1.

Stochastic gradient descent is used to train the network. The cross-entropy that penalises at each place is defined as:

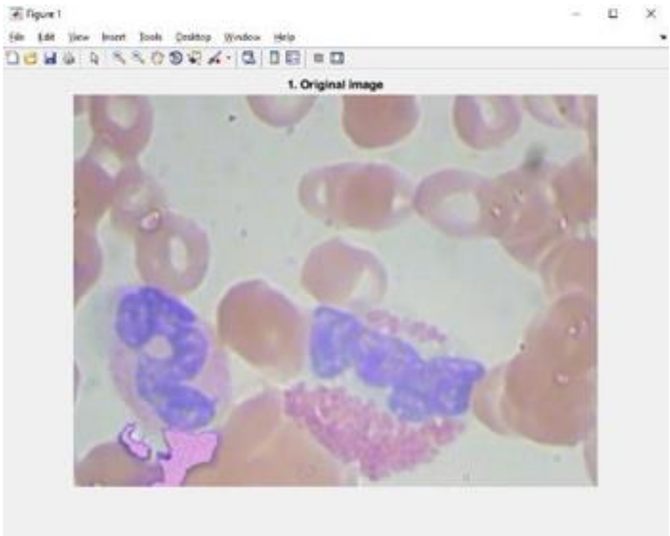

Figure 6 : Input Image

The above picture of blood on slide is considered as the input image that undergoes the process of image segmentation.

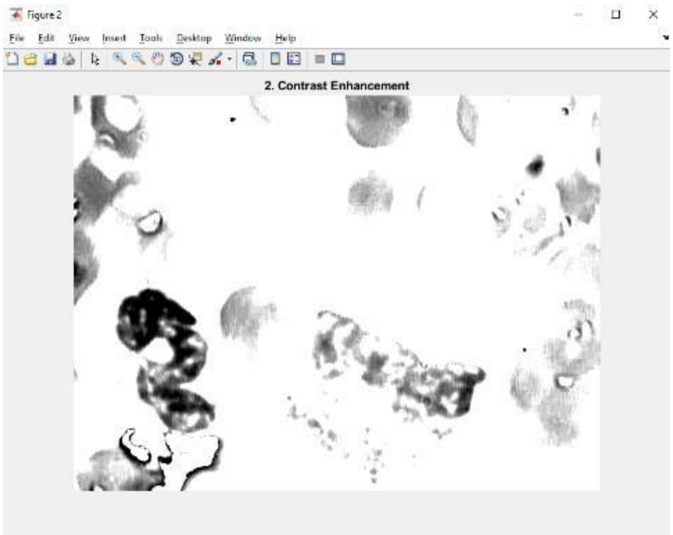

Figure 7 : Contrast Enhanced Image

For the first few steps, the given image undergoes the preprocessing of the image like contrast enhancement, minimum filtering to filter the given image.

$$En = \Sigma xg\ \Omega\ \omega(x) \log(pl(x)(x)) \quad \cdots (2)$$

The separation border is calculated using morphological processes. The weight map is then calculated as follows:

$$\omega(\mathrm{i}) = \omega(\mathrm{i}) + \omega \ \exp(-((d1(\mathrm{i})+d2(\mathrm{i}))2) \ldots (3)$$

$c\,0 \qquad 2\sigma 2$

The weight map is ωc(i) and the distance to the border/boundary is d 1 and d 2.

IV. RESULTS WITH DISCUSSIONS

The below shown figures are the experimental results of the proposed work:

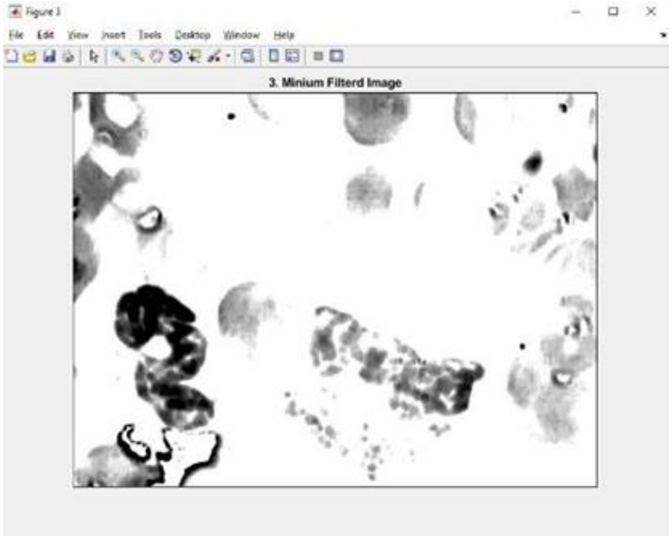

Figure 8: Minimum Filtered Image

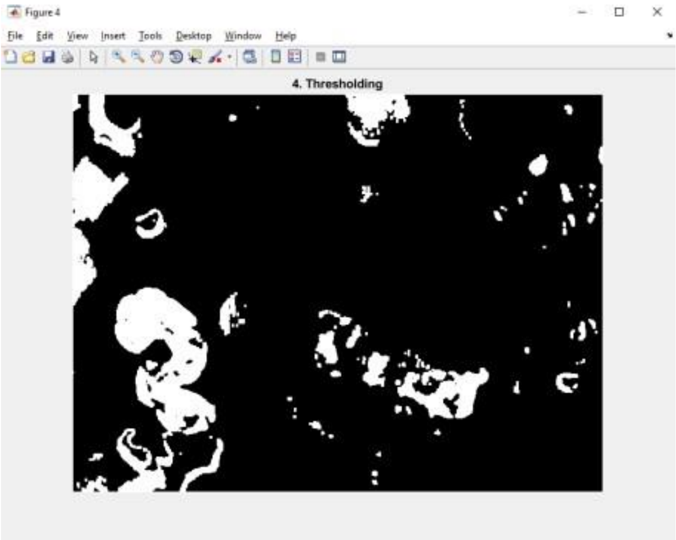

Figure 9: Thresholding

Thresholding is the process of image segmentation that helps in segmenting the interesting regions and removes all the unwanted information in the picture.

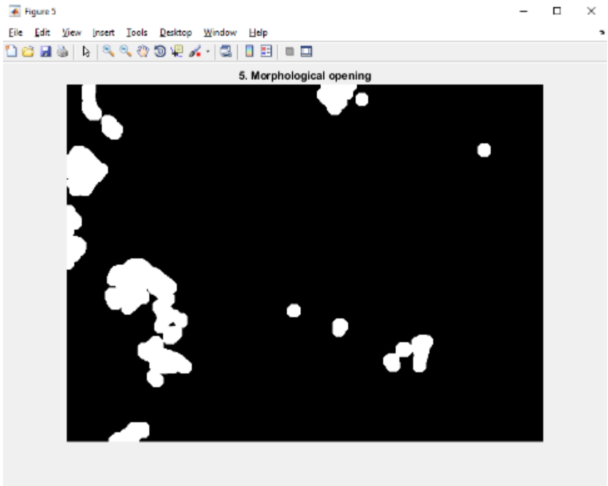

Figure 10 : Morphological Operations

In the above picture the morphological operated image can be seen with the minimal and required information from the picture.

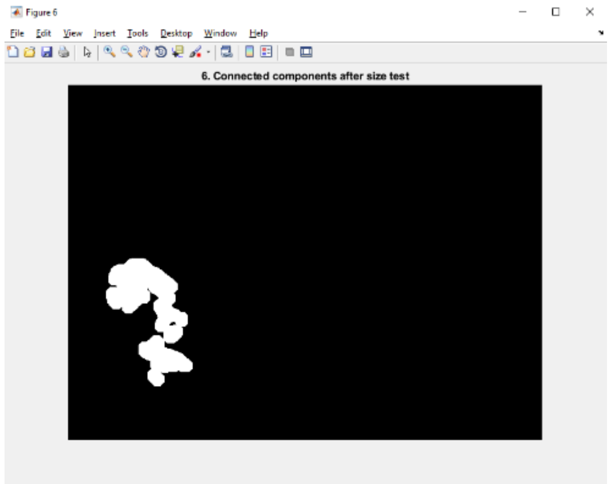

Figure 11 : Connected Components

The above picture filters out the connected components and removes all the components that are not connected. This also comes under morphological operations.

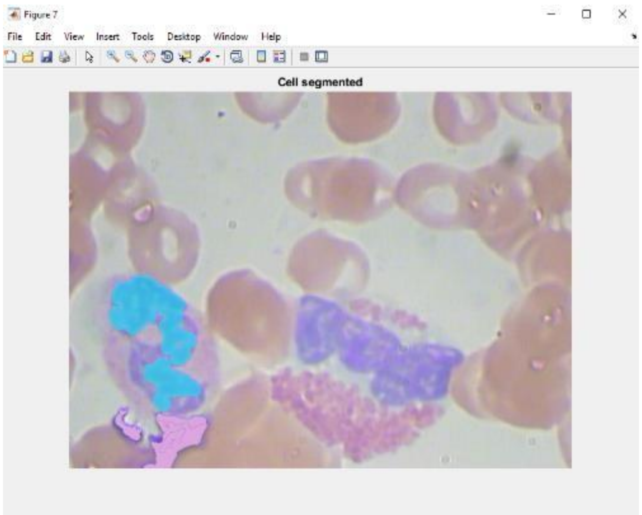

Figure 12 : Segmented Cell

In the above figure, the blood slide image and the segmented cancer cell in it can be seen clearly after the segmentation process.

Now we take the mask images to train the layers in CNN for the classification of whether it is normal or abnormal.

The below is the masked image that's used in training the system,

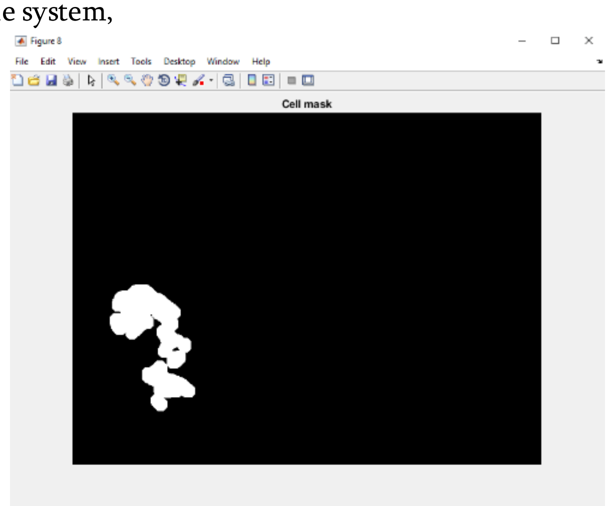

Figure 13: Cell Mask

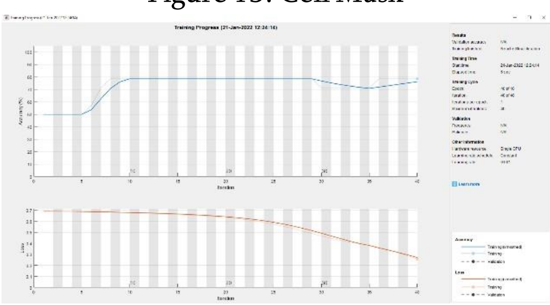

Figure 14: Training Progress

The above figure is the training progress of the system for the classification and to display the outcome from the system.

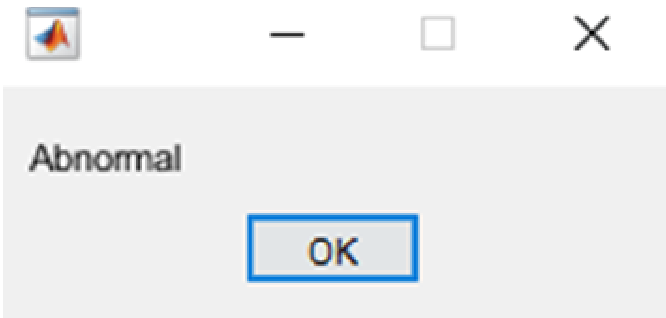

Figure 15: Output

The above figure is the output that displays after the testing for the given input blood slide image.

V. CONCLUSION

We tested an image based on the segmenting the cancer cells and identification in a blood drop sample in this study. Techniques such as segmentation, augmentation, and thresholding perform better than pre-existing models. The sensitivity of binary image and color-based segmentation is higher than that of any other approach. And the classification using CNN layers for training and testing of the same is done successfully.

There is a scope of, after detecting the abnormal cell, we can specify the type of abnormality (Leukemia, Lymphoma, Myeloma etc.) using the deep learning techniques.

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