iJRASET
International Journal For Research in Applied Science and Engineering Technology



INTERNATIONAL JOURNAL FOR RESEARCH

IN APPLIED SCIENCE & ENGINEERING TECHNOLOGY

Volume: 9 **Issue:** VIII **Month of publication:** August 2021

DOI: https://doi.org/10.22214/ijraset.2021.37536

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International Journal for Research in Applied Science & Engineering Technology (IJRASET)
ISSN: 2321-9653; IC Value: 45.98; SJ Impact Factor: 7.429
Volume 9 Issue VIII Aug 2021- Available at www.ijraset.com

Detection of Blood Cancer Cells Using Microscopic Images

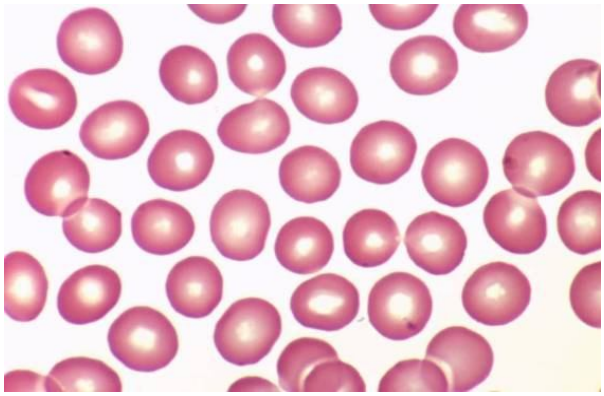
Vidyashree M S[1], Dr. Divakar H R[2], Mamatha M[3]
[1, 2]*Dept. of MCA, PES College of Engineering, Mandya*
[3]*Sri Siddaganga College of Arts, Science and Commerce, Tumakuru*

Abstract: ***Blood Cancer cells forming a tissue is called lymphoma. Thus, disease decreases the cells to fight against the infection or cancer blood cells. Blood cancer is also categorized in too many types. The two main categories of blood cancer are Acute Lymphocytic Lymphoma and Acute Myeloid Lymphoma. In this project proposes a approach that robotic detects and segments the nucleolus from white blood cells in the microscopic Blood images. Here in this project, we have used the two Machine learning algorithms that are k-means algorithm, Support vector machine algorithm. K-mean algorithm is use for segmentation and clustering. Support vector machine algorithm is used for classification.***

Keywords: k-means, Support vector machine, Lymphoma, Acute Lymphocytic Lymphoma, Machine Learning.

I. INTRODUCTION

Cancer is the growth of abnormal cell uncontrolled in the body. The cancer cells stop the functionality of normal cells working in body due to the huge growth of cells. The older malignant never dies instead of it will spread various part of the body. cancer is caused by large damage to gene. Cancer is having the same symptoms which may cause the cancer they having the illness, giddiness, lot of hair fall, headache, vomiting, one part of body pain, swelling, lump. Bleeding, vision problem, weight loss, fever. Acute Myeloid lymphoma is a one classification of cancer that spreads fastly, it mostly affected the bloodline and bone essence. In bone marrow abnormal white blood cells are caused. These blasts are immaturely growing and it does not able to fight against the affected cell or infected cell. These lymphoma cells are multiply rapidly and affected in the blood stream. One of the indications of Cancer is Occurs of a greater number of Cancer cells in blood stream. In Acute Myeloid Lymphoma “Acute” indicates fast development of disease. The myeloid cells usually develop in to the different grown-up blood cells for example RBCs, WBCs and platelets. The symptoms of Blood Cancer are frailty, delirium, prostration, or pain in joints or bones. Cancer of Blood bodily flesh is called Lymphoma.



A) Normal Blood



B) Cancer Blood

II. LITERATURE SURVEY

The process was done outhard way it requires well known person to do them test by hand. The approach replica decreases the expectation of errors in the hard way process by deep learning methods, namely convolutional neural networks. This is followed by n training the replica with the upgrade thick Convolutional neural network structure.[1].

Detection of white corpuscle cancer diseases such as Acute Myeloid lymphoma Acute Lymphocytic Lymphoma, and Myeloma is a hard task in medical field. For split-up they used the union of Gaussian Distribution, flexible thresholding and for grouping they have used k- mean method. Using Gray level co-occurrence matrix, the similarities are examining and they are used for classifying using convolutional neural network.[2].

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They are done an overview of image analysis based on the region of images. Thisis a summary of several studies in the subject of blood cancer, with a focus on detecting and classifying distinct kinds of lymphoma. This research looks at how distinct aspects of digital images of white blood cells can be utilised to segment and detect the type of lymphoma. Finally, a comparison of alternative segmentation and classification strategies is made, as well as their relationships.[3].

Lymphomameaning blood cancer, characterised by the bone marrow's unregulated and abnormal synthesis of white blood cells (leukocytes) in the blood. Diseases can be found and diagnosed early by examining microscopic blood cell images. Recently, Antigen has been employing an image processing approach to evaluate detect and identify lymphoma types in patients. Image detection is a quick and low-cost technology.[4].

The method extracts features of microscopic blood images by extract the changes on various features like the cell textures, shade, and where its located, geometry and numerical analysis input.[5].

AML is represented as the classification of the myelotomies is prevent the growth of antigens which is fight against the illness. Here, travelling exhaustive and also mean is under contrast to automaticsystem. The important to design the automated system to grow theorder toidentify the cancer in early stages.[6].

Risk of MDS it's a very challenging diseases of the diseases group to treat and cure. Few therapies are available to treat and cure the diseases approved by FDA. Those therapies are available for treatment often while take some months. For example, some diseases are taken 6-7 months to cure. Some diseases like cancer takes 10-12 months. cancer is in early stages it takes to cure 6-7 months. Cancer is in advanced / final stage it will take more time to cure and some cases the person will died [7].

Cancer occurs the when the lot of informal white blood cells produces by the. bone marrow. Antigen use of microscopic study of human blood, which methods is used to detect the cancer cells. which includes, breaking, classifying and grouping that identify tocase toache from lymphoma [8].

It requires more time to detect the cancer in the manually. So, we are proposed that the extraction of features of cancers that can be extracted by the MATLAB and classifies with some of the classification with their Algorithm as CNN, FNN, SVM, and KNN it will get the more accuracy than the other algorithm [9].

In this paper we have to discusses the related method to automatic counting the blast cells on the Acute lymphoma based on the blood sample of the cancer. Here they are used to MATLAB 7.0 software to use the known about the counting of the blasts cell in the image this way is very accurate to known about the count of the blast cells in the Blood samples [10].

Here they have developed accurate automatic system for the blood cell segmentation from the colour Blood smear images. They have to segment the cells for the Blood cell to the better Segmentation results.[11].

In this paper they have presented contour aware segmentation approach to classify the normal cell sickle cell, burr cell, helmet cells, and classifies the all the types of cells in the blood smear [12].

III. METHODOLOGY

In this project we have to detect the affected cancer cells based on the microscopic blood images in ordered to classified the images. First this image to pre-process andpartition thecanter and examine the similarities from the image. The Microscopic image give has to the put in system contains the Thrombocyte,erythrocyte and haemocyte. Firstly, the input images will be undergoing to the pre-processing. In these pre-processing to detect the thresholding. In thresholding the foreground and background layer will be separated and the next it will go to grayscale and the next we do the Binarization. In binarization to convert the grayscale image to black-white image. After pre-processing then it will go for Segmentation. In these segmentations. in these segmentations these only segment the cells presented area for the purpose of testing. After the segmentation to detect the Region of interest. Next it will identify the features from the image and then compared with the dataset and to identify the affected cells and non-affected cells and the radius, diameter value of the normal and affected cells and also identified the cancer cells and normal cells in the image.

A. Dataset

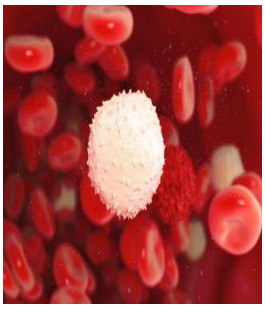
The Blood sample Dataset that contains more images including augmented images from Kaggle.com Repository.

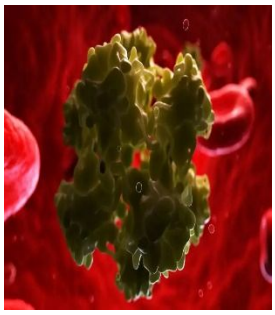
B. Dataset Samples

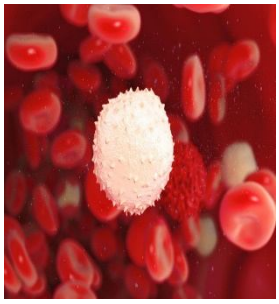
In this images A, B, C, D images that are the samples of the Cancer.

E, F these images are non-cancer images.

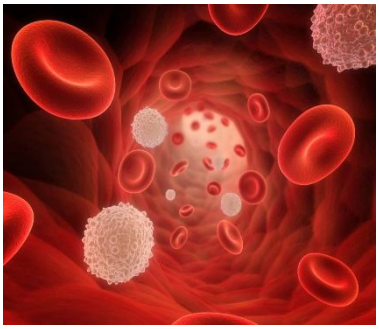
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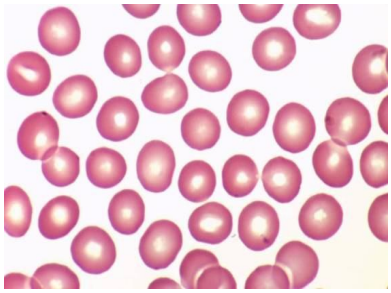

A


B


C

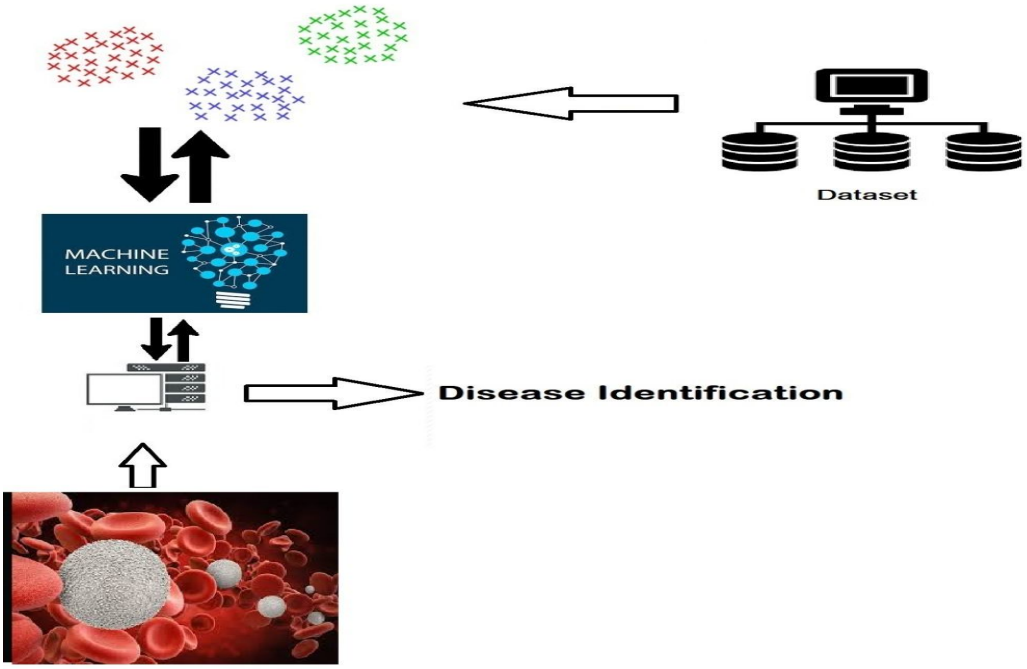

D


E


F

In this Dataset samples we have to extract features that are circumference, radius, diameter.

C. System Architecture



In this Architecture, it indicates the upload of the blood cancer image to application. The application process it and the extracts the features and generates clusters of features to compare with the trained dataset to provide prediction. that are process some steps to extract the feature and detect the output of the images. The images data is taken from the Kaggle and it will be adding into our working folder. data will be collected from various sources.

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The image is converted into grayscale by converting RGB values in the image. Change of a shad image into grayscale image to comprehensive to taken the noted points in the images. Automatic thresholding is extracting the what we required area only other noise data will be reduced. Segmentation partitions of an image is containing same pixels and same values. We have used unit testing to verify the segmentation of the blood cancer images to extract ROI of the cells. Return on investment is a performance degree used to assess the performance of a funding or compare the performance of a number of exclusive investments. ROI attempts to at once measure the amount of go back on a particular funding, relative to the investments price. we have used integration testing to verify the ROI of test images and trained dataset. The data features obtained from ROI is compared with the trained dataset features. The key to a comparison of machine learning algorithms is ensure that each algorithm is compared in the same way on the same data. The prediction of the blood cancer and its stage will be provided.

D. Algorithm

1) *SVM [Support Vector Machine]:* "Bolster Vector Machine" (SVM) is an administered device selecting up facts on set of regulations which may be utilized for each or relapse asking for situations in any case, its miles mainly applied in type troubles. in the svm set of policies. We plot each file thing as a perspective in n-dimensional images (in which n is form of abilities you have got) with the rate of each potential being the price of a selected setup. At that point we perform class with the guide of finding the hyper-plane that separates the two making ready nicely usual. Bolster Vectors are essentially the co-ordinates of individual prediction. The SVM classifier is a wilderness which freat in grouping. Recognize that cluster for take a look at realities. here we have three bunch statistics and all are isolating the suggestions pleasantly presently. how may we see the quality viableclass? Here increasing the separations amongst closest statistics sections and bunch information will help us to decide the perfect kind. This separation is known as margin. The aspect for organization is radical in contrast with every irregularity dataset. Consequently, we call the correct class. Another lightening purpose for choosing the group with better edge is energy in the event that we pick out a category having low fact. At that factor there can be useless opportunity of a void over brilliance. From the elegance were geared up to determine what frames is recognized till a way and may from this foresee the abnormality which were fit for bypass and produce real outcome.

E. Working Steps

1) In first step, we use image Acquisition
2) In second stage it will generate image pre-processing on tested data.
3) Then apply segmentation, feature extraction , and classification method
4) Identify the counting area (the area where cells do not interfere with each other and are properly separated).
5) Perform colour normalization on the image.
6) Separate white blood cells from the image by performing image segmentation.
7) Specify the region of interest.
8) Extract the region of interest.
9) Feature vector analysis is performed which includes extraction and selection of features of the cell images including the size of the cell, the circularity of cells, count of cells, the area of cytoplasm and nucleus, nucleus/cytoplasm ratio etc.
10) Initial classification of lymphoid or myeloid series is done by the shape of the nucleus.
11) The extracted features are then compared with those stored in the database and classification is done into AML or ALL categories.
12) The extracted features are compared and verified with the SVM methodology to identify the layer-based comparison.

F. SVM Mathematical Model

Length of a vector

The distance between vectors x and y is known as their norm, and it is written as ||x||. The Euclidean norm equations are used to calculate a number's norm vector x = (x1,x2,...,xnx1,x2,...,xn) is:

||x||=x21+x22+...+x2n−−−−−−−−−−−−−−√||x||=x12+x22+...+xn2

Direction of a vector

supervision of a vector x = (x1,x2x1,x2) is denoted by the letter w, and is described as follows:

w=(x1||x||,x2||x||)w=(x1||x||,x2||x||)

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look at figure 1,
cos(θ)=x1‖x‖cos(θ)=x1‖x‖ and cos(α)=x2‖x‖cos(α)=x2‖x‖. Then, the supervision vector w can also be write as:
w=(cos(θ),cos(α))w=(cos(θ),cos(α))

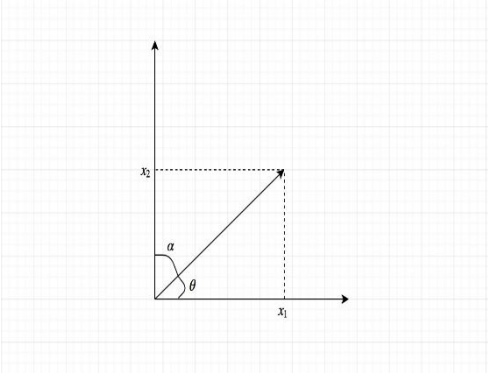


Figure 1

G. Dot product

The result of the dot product of two vectors is nonzero. It helps us comprehend how the two vectors are connected.
Figure 2 depicts two vectors, x and y, as well as the angle θθbetween both of them The mathematical equations for the dot product are as follows: x·y=||x|| ||y|| cos(θ)x·y=||x|| ||y|| cos(θ)

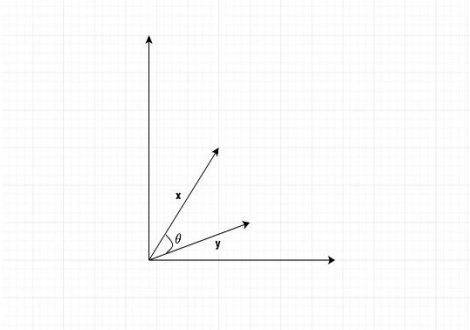


Figure 2

looking at figure 3, we can see θ=β−αθ=β−α. Then we can get:
cos(θ)=cos(β−α)=cosβcosα+sinβsinα=x1||x||y1||y||+x2||x||y2||y||=x1y1+x2y2||x||
||y||cos(θ)=cos(β−α)=cosβcosα+sinβsinα=x1||x||y1||y||+x2||x||y2||y||=x1y1+x2y2||x|| ||y||

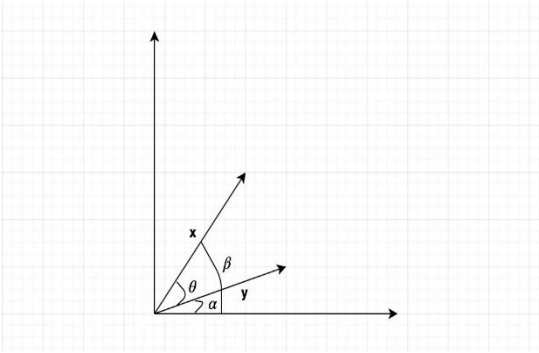


Figure 3

When we plug this into the mathematical dot product equation, we obtain the following:x·y=||x|| ||y|| x1y1+x2y2||x||
||y||=x1y1+x2y2x·y=||x|| ||y|| x1y1+x2y2||x|| ||y||=x1y1+x2y2
For two n-dimensional vectors, the dot product can be calculated as follows:x·y=∑i=1nxiyix·y=∑i=1nxiyi

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ISSN: 2321-9653; IC Value: 45.98; SJ Impact Factor: 7.429
Volume 9 Issue VIII Aug 2021- Available at www.ijraset.com

H. Linear Separability

One of the most significant concepts in SVM is linear separability. Although data strength may not be linearly separable in practise, we will begin with the linearly separable situations (because they are the easiest to grasp and deal with) and work our way to the non-linearly separable ones.

Figure 4 shows how a line separates two-dimensional data. We stated that the data are linearly separable in this scenario.

Figure 5 shows an example of non-linearly separatingdata, which implies that we cannotfindinga line that divides two-dimensional data in the same way, theWe told three-dimensional data that if we can locate a plane to separate them, they will separate linearly.

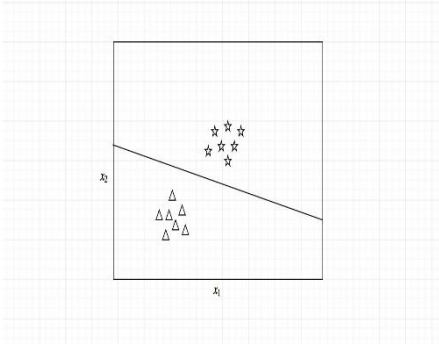


Figure 4

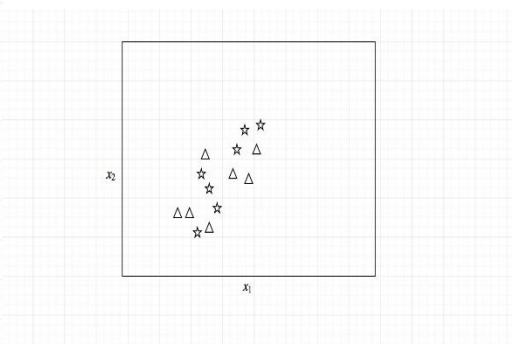


Figure 5

I. Hyperplane

Let's look First, consider the two-dimensional situation. Two-dimensional linearly separable data can be separated by a single line The function the end of the line y=ax+by=ax+b. We give x a new namex1x1 and y with x2x2 and this is what we get:

ax1−x2+b=0ax1−x2+b=0

define x = (x1, x2) (x1, x2) and w = (a, −1) (a, −1), we get:

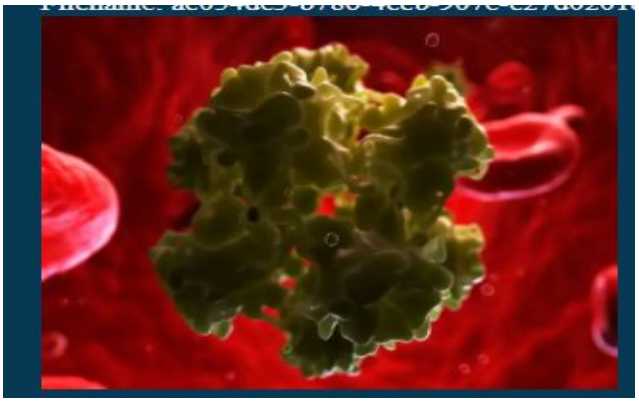
w·x+b=0w·x+b=0

Classifier

The hyperplane is a tool that can be used to able generate predicted. The hypothesis function h is defined as follows:

h(xi)= {+1−1if w·x+b≥0if w·x+b

IV. RESULTS AND DISCUSSIONS

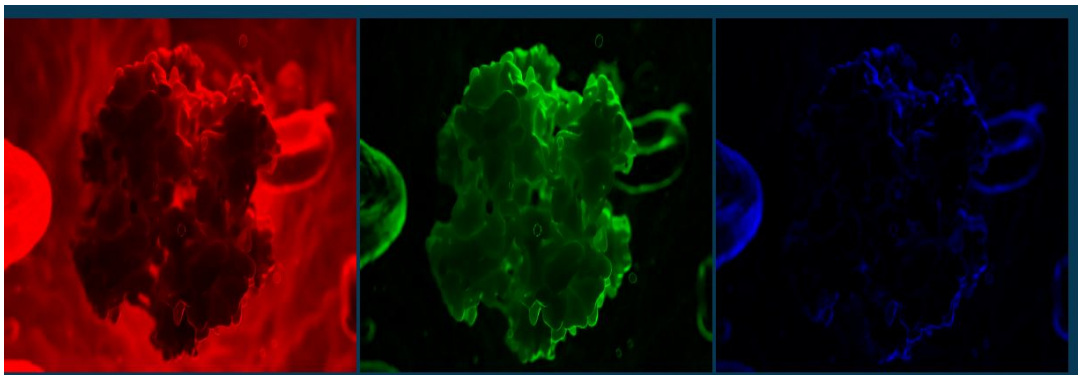


a) Uploaded image

The uploaded image will be under goes to the pre-processing stage. Here the image will be pre-processing then it will be converted into green and blue image. Here we have extracted the affected area of the cells in the blood sample. After that affected area off the blood sample will be detected and that part of image only taken and then it will go to the feature extraction.

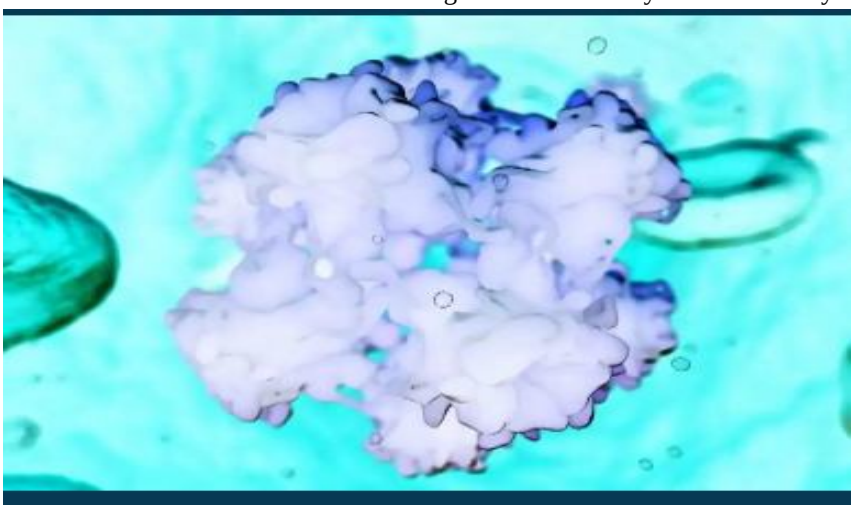
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b) Filtered images

In feature extraction the uploaded image and training dataset images that are extracted the features of the shape,radius, diameter, geometry, colour that are extracted by the training dataset images and uploaded image. Feature extraction process is done by more accurately and efficiently. And here the feature extraction of all images that are done by more accurately and efficiently.



c) Cancer cell image

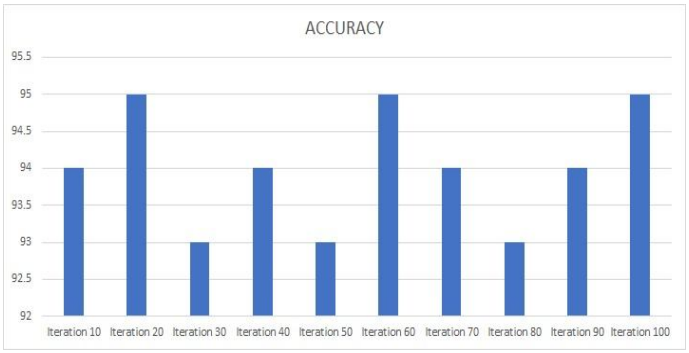
If the feature of extraction of the blood sample images will done after that the images will be compared with uploaded image and dataset image. After that comparison the features are matched with each other the expected output will be predicted about the cancer cells. In case the images will not compare with each other the process will be continue with another images of dataset and the process will continue to process of comparison until the comparison process done. And the comparison process will accurately be done with efficient manner.

And also find the values of the infected cells such that radius, diameter, circumference of the cells.

In this project we have to expect the stage of the cancer detections and their cells value. The user will upload the image to the application that uploaded image will firstly that image will be pre-processing and then pre-processing image will be converted in to the Gray scale image. In the Gray scale image they take only a affected area in the image other area of the image will be not taken. After that the image will be extracted the features in the image and then it will be compared with the data set and predict the output. And also, here we have used to Xfan image segmentor to segment the image. And also, we have to use the KNN and k means Algorithm. Here we finding theclosest values and collateto thedataset. all the nearest values are merge and form a cluster. k means algorithm are used to the finding the meane value off the data and it will be compared with the training data. output of the Algorithms is the input to the SVM Algorithm

it will give some iterations and that accuracy that is given in the below.

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Accuracy Iterations

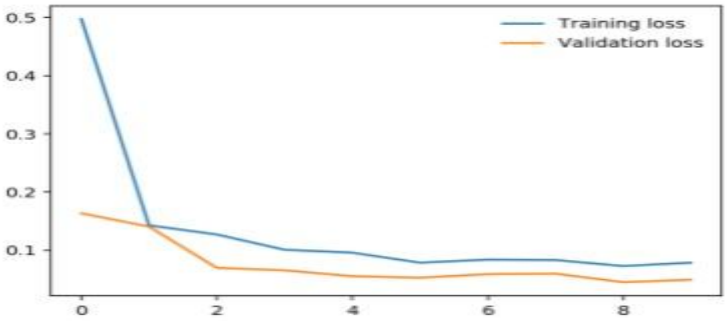
The details of test indicate the result of instruction dataset size is shown in table

TrainSize	Precision	Recall	F1
100	0.94	0.92	0.85
200	0.93	0.90	0.88
300	0.92	0.92	0.84
400	0.92	0.91	0.83
500	0.92	0.91	0.81
600	0.92	0.90	0.82
700	0.91	0.92	0.83

a) Table: Precision, recall, F1 score

We present our examine result and to testament of out instruct replica. In this paper we have shown the cell values of the cancer cells and to predict that image is belongs to cancer or not. If it is Belongs cancer to show the stage of that cancer.

Precision: is the correlation of the divine correctlydefinite monitoring to the total correlation definitemonitoring.
Precision= TP/TP+FP.
Recall: is the correlationof the correct divinedefinitemonitoringto everyone monitoring ingenuinegroup.
Recall = TP/TP+FN.
F1 Score: is the highest possible score encumbered meanRecall and precision.
F1 Score 2*(Recall*Precision)/ (Recall + Precision).



b) Training and Validation epoch loss

V. CONCLUSION

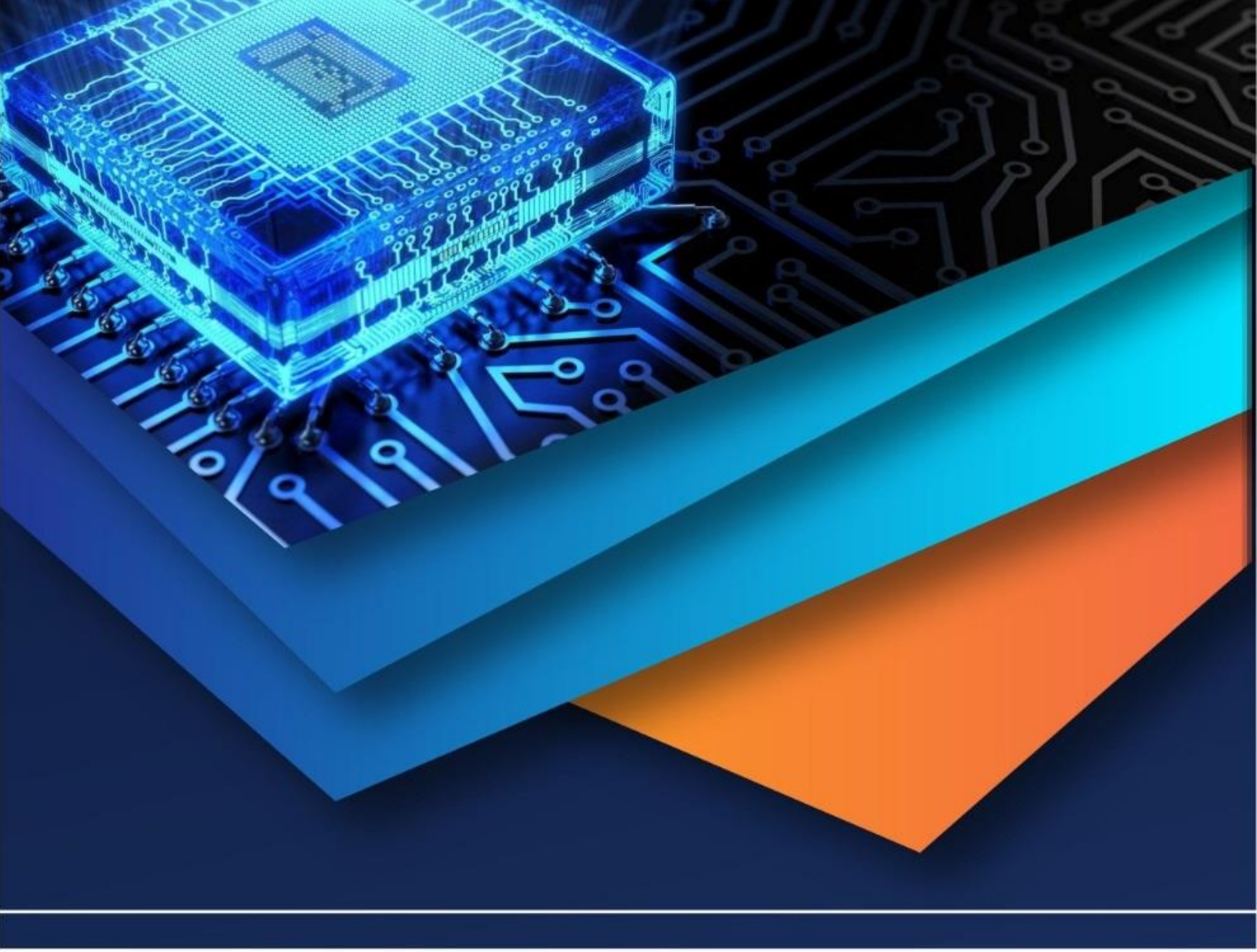
In this project we have diagnosed the cancer by uploading the Blood Sample image. Here we have uploaded the blood sample image by comparisons by the feature of the image and compared with the tested dataset and training dataset of the Blood sample image and also detecting the shape, colour, radius of the affected cells in the blood sample image. Hence the Accuracy gives in this project is 97.8%.

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