An Automated Blood Cancer Detection System to Detect Leukemia Using Improved Machine Learning Techniques

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Abstract: An improved machine learning technique called Automated Blood Cancer Detection System (ABCDS). The proposed system (ABCDS) automatically classifies the Leukemia into Cancerous or Non-Cancerous. In this present system we focuses on an ameliorate machine learning tactic for a classification of Leukemia blood cancer. The Proposed system contains six stages. In the first stage, the white blood sample images are collected. In the next stage the proposed system will undergo preprocessing which improves the performance by handling missing values, normalizing features. In third stage feature extraction involves the use of white blood cells to identifying the shape and color by using Convolutional Neural Network (CNN). In the fourth stage, training the model enables accurate enable of Leukemia Blood Cancer. In the fifth stage the proposed system will classify the data into clusters based on its features or characteristics using K-Means Clustering Algorithm. Following the previous stages the final stage has the proposed system resulting whether the Leukemia is cancerous or non-cancerous.

Keywords: CNN Algorithm, K-Means Algorithm, Machine Learning Technique, Leukemia Detection

I. INTRODUCTION

The widespread of legions of people are beseted with leukemia, a blood malignancy that is complicated and potentially fatal. Blood cells are created in the bone marrow, the soft substance found inside bones, where it all begins. The body overproduces aberrant white blood cells in leukemia, which prevents the normal blood cell from proliferating. The fast growth of this cancer prevents normal blood cells from being produced, which is crucial for a healthy immune response in many body organs. On the other hand, the aberrant cells spread to vital organs like the brain and liver, where they seriously harm them. An elevation or diminution in the aggregate of white blood cells (WBC) in blood plasma is indicative of a disease. White blood cells come in five different varieties: neutrophil, monocyte, lymphocyte, eosinophil, and basophil.

Any fluctuation in the leukocytes.count is cause for concern. The condition most commonly linked to a low leukocytes. (WBC) count is leukemia. Our bodies may become unhealthy and contribute to disease when WBC levels are abnormally high. Leukemia is a form of cancer and a potentially fatal illness. Because of the abnormal white blood cells' fast proliferation, it damages the bone marrow and blood. These abnormal WBCs impair the bone marrow's capacity to produce red blood cells and platelets and are unable to fend off illness. Leukemia comes in two flavors: acute and chronic. Compared to chronic leukemia, acute leukemia grows more quickly and exhibits more severe symptoms. There are two forms of leukemia: myelogenous and lymphocytic.

The immune system is aided by lymphocytes, a subtype of white blood cell. Excessive growth of tumors in the gist that develop into those lymphocytes is known as lymphhocytic leukemia. In myelogenous leukemia, the hematopoietic cells that give rise to RBCs, WBCs, and platelets proliferate abnormally. Leukemia is categorized into four categories of diseases: ALL, AML, CLL, and CML (chronic lymphocytic leukemia). Acute lymphocytic leukemia is also known as acute myelogenous leukemia.

Leukemia is the most prevalent type of blood cancer in every demographic community, with children being the most affected. -This aberrant occurrence is brought on by the overproduction and undevelopement of blood cells that can maltreat bone marrow, the immune system, and red blood cells. A hematologist diagnoses patients under a microscope. As a result of technological advancements, machine learning tactic have become powerful tools in the province of healthcare, enabling automated and precise detection of various diseases, including leukemia. Timely and accurate diagnosis is crucial for effective treatment and improved patient outcomes.

II. RELATEDWORK

In [1], the author Faysal Ahmed et al have design a descriptor using HOG feature and logistics regression algorithm to predict the microscopic images of Leukemia. This paper implemented as callable Leukemia prediction method based on a publicly available ALL_IDB dataset using the HOG feature descriptor and Logistic Regression. The proposed model initially detects the shape of the blast cell from images. Then, PCA for data dimension reduction of the feature vector etc. Finally, for the classification the HOG feature descriptor and logistic regression is being used.

The author Jakkrich Laosai et al [2] have implemented acute leukemia Classification using medical-knowledge-based morphology and CD marker. This paper implemented a method of morphological features based on medical knowledge and classify blood cells into ALL, AML, and healthy groups. The results are classified and then compared with CD markers in a final-decision-making process to confirm the sub-type classification of ALL and AML. In performance evaluation by experiments using 200 and 300 samples for training and testing, respectively.

Nilam Nur Amir S jarif etal [3] developed acute lymphoblastic leukemia segmentation using local pixel data. This study presented a segmentation process for A-leukocyte cells based on a machine learning approach and an image processing technique. The routine was found to cause blast cell segmentation. It was found that the segmentation results obtained while checking the accuracy of white blood cell segmentation were close to the results of standard methods. In addition, blast cells were correctly identified in collected microscopic images of blood cells taken under different lighting conditions with different cameras.

In [4], author Preetham Kumar et al reported the utilization of data mining and imagery segmentation algorithms for the determination of acute lymphoblastic leukemia.. The aim of the proposed work is to map different computer system techniques used for blood sample image segmentation. The segmentation method is fully unmanned without the need to frame the image separately. Cytoplasmic extraction plays a key role in inducing segmentation between the nuclear region, and the cytoplasmic region is a pathologically important feature in cancer detection. The proposed algorithm takes into account images stained with different stains and cells with different abnormalities to effectively detect malignancy.

The author Pradeep Kumar Das et al [5] have implemented Detection and Classification of Acute Lymphocytic Leukemia. The research work aims to develop an computerized methodology for authentication and categorization for ALL. Extraction of lymphocytes is accomplished by k-means clustering technique. This paper presents an efficient scheme to detect healthy and unhealthy (ALL)- lymphocytes. The scheme employs GLCM and GLRLM to extract texture features. Moreover, it also emphasizes to extract shape and color features. Finally, SVM with RBF kernel is employed to classify WBCs into healthy and ALL affected cell.

Astha Ratley et al [6] have designed Leukemia Disease Detection and Classification Using Machine Learning Approaches. This paper focuses on analyzing different image processing and machine learning tactic used for classification of leukemia detection. This paper concludes that leukemia disease can be classified using many latest machine learning algorithms. Also the paper

contains a brief knowledge about recent available method used for classification with results and analysis.

In [7], the author Arjun Singh Parihar et al have presented a overarching complete scrunity of the various machine learning based approaches employed for automated blood leukemia detection highlighting the salient features of each approach. It can be concluded that AI based techniques can prove to be a strong supporting tool to medical practitioners aiming to detect blood leukemia. It can be concluded that image enhancement and feature extraction are as important as the effectiveness of the automated classifier, hence appropriate data processing should be applied to attain high accuracy of classification.

Author Arash Roshanpour et al [8] applied machine learningtothe detection and classification of leukemia using blood images. This review study provides a comprehensive and systematic overview of the state of all published ML-based leukemia detection and classification models that process PBS images. Thissystemimprovesaccuracy, shortens diagno sis time and provides faster, cheaper and safer diagnosticservices.DL, among other new advanced M L algorithms, may be useful for applications in computer-aided detection systems, whole-slide imaging (WSI), and even in software in hematology laboratories, creating an opportunity for research. Pathologist and oncologists to better detect leukemia.

Anjali Chavan et al [9] have designed Leukemia Blood Cancer Detection. This paper implements a method for detecting leukemia that is both quick and accurate. The designed methodology intends to detect leukocyte cancer early and reduce cases of false positives. This apparatus has High reliability, accuracy, efficiency, reduced processing time, reduced error, and robustness. In this paper, a fully automatic system that would accurately identify Leukemia cancer was designed. Firstly, for model creation blood microscopic images from train and testing dataset are collected and then utilized 3 pre- trained deep-learning models for checking accuracy.

In [10] the convolutional neural network and IOT update were used by M Sai Lasya et al. to encounter and segregate leukemia. This doc ument covers using lOT to save results with a specific username and password. Information extracted from microscopic images of blood samples can be useful to humans because it predicts, resolves, and immediately treats blood disorders in an individual patient. The system is very efficient, reliable, less processing time, less errors, high accuracy, lower cost and must be robust to existing subject strains, testing protocols, time, etc.

The author Sonali Mishra et al [11] have implemented Texture feature based classification on infinitesimal blood smear for acute lymphoblastic leukemia detection. This paper implements the method initially pre-processes the input images using Y component of the CMYK image and a triangle method of thresholding. Subsequently, it utilizes discrete ortho normal Stransform (DOST) to extract the texture features, and its dimensionality is reduced using linear discriminant analysis. The work can be extended towards the sub-classification of acute lymphoblastic leukemia into cancerous or non-cancerous cells.

Dr B Leela Kamari et al [12] have designed Detection of Leukemia & its Staging Using Image Processing; Artificial Intelligence. This paper designed an automated detection & staging of leukemia using combination of image processing & artificial intelligence technique. Also, detection of white blood in blood stain image, accurately, is crucial for prediction of leukemia with accuracy. In this paper, they presented a low cost detection of leukemia & its staging using image processing and artificial intelligence.

The Machine Learning hinge System for Automatic Detection of Leukemia Cancer Cell was reported by Supriya Mandal et al. in [13]. They have found that the classification algorithms used by Gradient Boosting Decision Tree outperform Support Vector Machines. Additionally, they have deduced a few

key mannerism that have a big influence on the detection of cancer cells, such as the existence of neighboring nuclei and the measurement of irregularity in a nucleus' shape. Based on our research, the GDBT-based classifier performs better than the SVM model. Furthermore, our feature analysis shows that area difference and the presence of neighboring cell nuclei have a major influence on the detection of cancer cells.

An inquisitiveness-based convolutional neural network has been used by the author Muhammad Zakir Ullah et al. [14] to classify acute lymphoblastic leukemia cases. This paper provides a non-invasive method based on convolutional neural networks (CNNs) that performs the diagnosis task using medical images. The implemented solution, which consists of a CNN-based model, extracts higher-quality deep aspect from the effiy dataset using the discernible geometry group from Oxford (VGG16) and an intentness module called Efficient Channel Attention (ECA). This improves feature representation and classification outcomes. The study's conclusions manifested that the deep learning-based model that was built works better than the most advanced methods. Enhancing the deep swotting architectures with the attention module could result in a notable improvement in performance.

Uzma Ghulam Mohammad and colleagues [15] have developed a vision-based technique that is effective in predicting acute lymphoblastic leukemia. Using four machine learning algorithms—K-Nearest Neighbor, Support Vector Machine, Random Forest, and Naïve Bayes(NB)—this study builds an ensemble automated prediction approach. This study suggested a method for predicting acute leukemia (ALL) using ensemble voting classifiers with predefined CNN architectures (VGG16, ResNet50, or ResNet101) and machine learning algorithms (RF, SVM, KNN, NB).

An Efficient Blood-Cell Segmentation for the Detection of Hematological Disorders was described by Leela Kamari et al. in [16]. When the residue

offset parameter is used properly, segmentation becomes more accurate with the right EF. This approach is contrasted with the most recent techniques.

In terms of precision, F1 score, Jaccard score, and dice similarity, it performs better than the current EF approaches. There could be more medical and cybernetics uses for it. Algebraic EFMs typically have biased fitting parameters and unintentionally weighted fitting errors, which results in imprecise boundaries and challenges with hematological disorder diagnosis.

The author pradeep kumar das et al [17] have implemented A Systematic Review on Recent Advancements in Deep and Machine Learning Based Detection and stratification of Acute Lymphoblastic Leukemia. In this purpose, segmentation schemes are predominantly categorized into signal and image processing-based techniques, conventional machine learning-based techniques, and deep learning-based techniques. From this review unsupervised schemes are preferred for segmentation tasks, where as supervised schemes are preferred for classification tasks.

Advika Parthv et al [18] have designed A horizontal scrutiny using Machine Learning and Data Mining Approach for Leukemia. These projects have done rigorous analysis and study of many research articles based on Leukemia diseases interesting majorly in the classification algorithm. The prime objective of this review article is to analyze and compare techniques on Leukemia disease. In this review, the authors have reviewed several research articles on existing work for Leukemia disease.

In [19], the author Umid Kumar Dey et al reports Genetic Expression Using Machine Learning Analysis To Detect type Of Leukemia Using Machine Learning. The purpose of this study is to take into account the gene expression data of several people and predict what type of leukemia they have by using three machine learning algorithms, XG

Boost, Random Forest Classification and Artificial Neural Networks. The use of PCA to decrease the dimensionality of the data set not only made the computation faster but also gave better results since when the dimensionality wasn't reduced at all, the results were far poorer, which is why they weren't included here.

The author D. Umamaheswari et al [20] have implemented Segmentation and Classification of Acute Lymphoblastic Leukemia Cells Tooled with Digital Image Processing and ML Techniques. In this project the algorithm is proposed by investigating the existing segmentation algorithms in the field of leukemia research for the sake of supporting hematopathologists to recognize Acute Lymphocytic Leukemia (ALL) by analyzing the blood cell images. The algorithm proficiently segments the largest nucleus blob in the obtained blood cell image for the cause of supplementing hematologists in detecting leukemia.

III. METHODOLOGY

The proposed system takes an input image set depicting white blood cells including both normal and leukemia-affected samples. The images are given as input to data pre-processing. This involves resizing an image, Conversion of RGB to Grayscale image and Reducing Noise. Next Identify relevant features from the blood samples which may be utilized to distinguish between normal and leukemia cases. A common feature includes shape, color and other characteristics visible in microscopic images. Train the model using the training dataset. This involves adjusting the model parameters to learn the patterns and features that distinguish between normal and leukemia samples. A separate model's performance Evaluation model is used to validate the dataset and to ensure it generalizes well to new, unseen data.

A. Data Collection
An Image of the form jpg will be taken as input. An input image set would refer to a collection of images depicting white blood cells. These images are used as input to the data preprocessing phase.

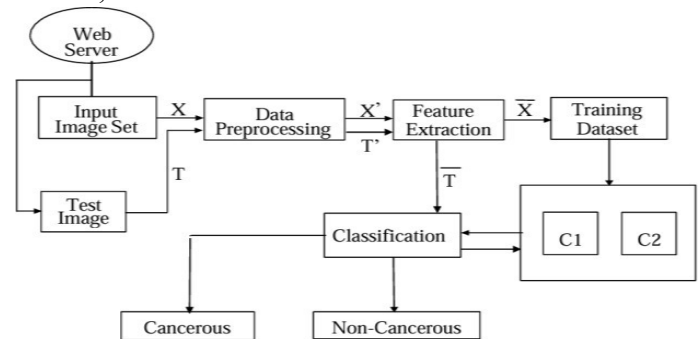The data would be preprocessed to remove noise, artifacts, and other inconsistencies.

Fig.1 System Architecture

B. Data Preprocessing
The procedures and methods used on raw data prior to feeding it into machine learning algorithms for testing and training are referred to as data preparation. Pre-processing aims to improve the image data by reducing unwanted distortions and enhancing certain image attributes that are important for tasks involving additional processing and analysis. The preprocessing stages that need to be followed are:

1) Resizing an Image
X is the input image and X should be resized to a new size X resized, there sizing process typically involves interpolation to determine pixel values in there sized image. X should be resized to a new width while maintaining the aspect ratio preservation. The aspect ratio is typically defined as the ratio of the width to the height of an image. The original width is denoted as W0 and the original height as H0. The aspect ratio (AR) is given by:

$$AR = W0 / H0 \qquad (1)$$

To preserve the aspect ratio when resizing, new width is denoted as Wn and to find the corresponding height Hn the mathematical formula is given by:

$$AR = W0 / H0 = Wn / Hn \qquad (2)$$

The above equation can be rearranged as:

$$Hn \text{ or } Xresized = Wn / AR \qquad (3)$$

2) Conversion into gray scale image
Xresized is the input given to convert into gray scale. The Technique used here is Luminosity method. In this method, the grayscale intensity is calculated using weighted sum of its Red, Green and Blue values. To

convert Xresized matrix into grayscale the mathematical equation is given by:

$Xg = 0.2989\ R(Xresized) + 0.5870\ G(Xresized) + 0.1140\ B(Xresized)$ (4)

3) Reducing noise

The tactic used in reducing noise is Gaussian Blur. Gaussian blur is a sought-after image processing technique used for smoothing and noise reduction.

It involves convolving the image with a Gaussian filter, which assigns weights to surrounding pixels based on a Gaussian distribution. This results in a softened appearance, reducing high-frequency noise and enhancing overall image quality. The mathematical equation of Gaussian Blur is given by:

$$G(x, y) = \frac{1}{2\pi\sigma^2} e^{\frac{-x^2+y^2}{2\sigma^2}}$$ (5)

A. Feature Extraction

Feature extraction in image processing is a technique of redefining a large set of redundant data into a set of features reduced dimension. This transformation of the input data into the set of features is called feature extraction. Feature extraction refers to the process of identifying and extracting important characteristics or features from raw data. It helps to focus on the most relevant information and discard relevant or redundant data.

Shape feature extraction technique is one of the key methods in feature extraction field. Shape features refer to quantitative measurements or descriptors that characterize the geometric shape of objects in an image or dataset. These features provide valuable information about the structure and form of objects. Extracting shape information using CNN Algorithm involves leveraging the activation maps of convolutional layers to capture hierarchical features.

B. Training

The goal is to train a stereotype that can make meticulous predictions on new, unseen data by learning patterns and relationships from the pedagogy set. The pedagogy phase consists of the following steps:

1) Design a CNN stereotype is suitable for image classification. It typically includes convolutional veneer for feature lineage and pooling veneer for spatial down sampling.

2) Choose an appropriate loss function and optimizer. Compile the model.

3) Feed the training data into the CNN and adjust the model's weights through back propagation. Monitor training metrics such as accuracy and loss.

4) Evaluate the model on the validation dataset to ensure it generalizes well and doesn't over fit.

5) Fine-tune hyper parameters, including learning rate and batch size, to optimize the model's performance.

6) Assess the model's accuracy on the testing dataset to evaluate its overall performance.

7) Analyze metrics such as precision, recall, and F1 score to understand the model's strengths and weaknesses.

8) Based on evaluation results, fine-tune the model or adjust its architecture for better performance. Iterate if necessary.

9) Once satisfied with the model's performance, deploy it for real-world use in a blood cancer detection system.

C. Clustering

Clustering is a technique in machine learning and data analysis where data points are grouped together based on similarities, aiming to find patterns or structures within the data. Clustering is a fundamental unsupervised learning technique that involves grouping similar data points together based on certain characteristics or features.

The K-means clustering algorithm is a popular unsupervised machine learning technique used for partitioning a dataset into K clusters. K-means aims to group data points into K clusters, where each point belongs to the cluster with the nearest mean. The objective is to minimize the intra-cluster variance. Partition the data into K clusters, where each cluster is represented by its centroid, such that the sum of squared distances between data points and their respective cluster centroids is minimized.

D. Classification

CNN Algorithm is a Supervised Learning Algorithm used in various applications, especially in image recognition task like detecting blood cancer such as

Leukemia. It consists of various layers: an input layer, convolutional layer, pooling layer, fully connected layer, and a classification layer, as displayed in Fig. 2.

1) Input Layer

In this layer of a CNN model, inputs (images) are given. Here, the size of the inputs is also defined.

2) Convolutional layer

As its name signifies, a convolution operation is performed in this layer. It is done by performing a dot multiplication between kernel pixels with the respective image pixels on which the kernel pixel is currently lying and then adding all these results to evaluate a convolution output at particular pixel. Then, the kernel slides over the whole image based on the predefined stride. The objective of this layer is to extract the different features from its previous layer.
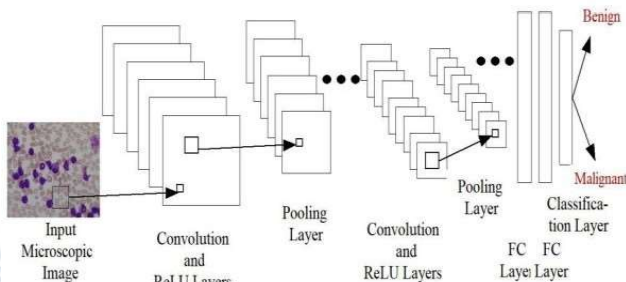
Fig.2 CNN Architecture

3) ReLu Layer

ReLu stands for Rectified Linear Unit. This layer is employed to enhance non-linearity in the CNN model. Here, ReLu activation functions are employed to add nonlinearity instead of traditional tanh or sigmoidal activation functions. ReLU does not saturate near1, unlike these two functions. More importantly, it makes the network faster with maintaining similar accuracy by improving the learning speed. It is a popular activation function since it is easy to use and is successful at eliminating the drawbacks of other formerly well-liked activation functions.

4) Pooling layer

Pooling or sub-sampling is done to reduce the dimensionality of the image, which decreases the image's feature dimension to minimize the computational costand make the learning faster. It is

also used to suppress over-fitting issues. In CNN, Max Pooling and Average Pooling are two popular methods of pooling.

5) Fully Connected Layer

An aggregate of fully connected layer(s) is added after the convolutional and downsample layers in the CNN model. As the name implies, every neuron in this layer connects to every neuron of the previous layer. This layer integrates every data that the earlier layers had learned to uncover the larger patterns. The final fully connected layer integrates information (features) for image classification. Thus, the output size of the final fully-connected layer is selected the same as the aggregate of classes that we intended to rank the input data.

6) Classification layer

It is the last layer in the CNN model, which exploit the probabilities estimated by the Soft Max activation function for every input to predict the class effectively.

IV. RESULTS & ANALYSIS

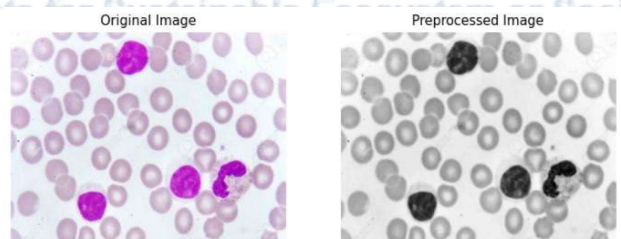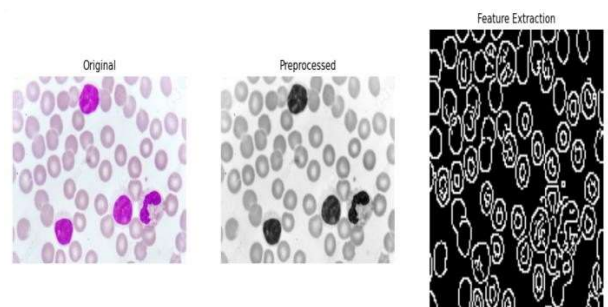**Fig. 3 An Original Image and a Preprocessed Image**

Fig.4An Original Image, Preprocessed Image and a Feature Extracted Image

Once the features are extracted, the further action is usually to snap the data into separate sets for training and testing the machine learning model. This is done to assess how well the model generalizes to new, Unseen data. The data splitting is performed such that 80% of the images are allocated to the grounding set, and the remaining 20% are allocated to the testing set. By splitting the data into learning model and testing sets, machine learning practitioners can train the model on one set of data.

After the data splitting process, where the images have been classified into training and testing sets, clustering using the k-means algorithm is performed on the training data. k-means clustering can be applied to the extracted features from the images to group similar images together based on their feature representations.
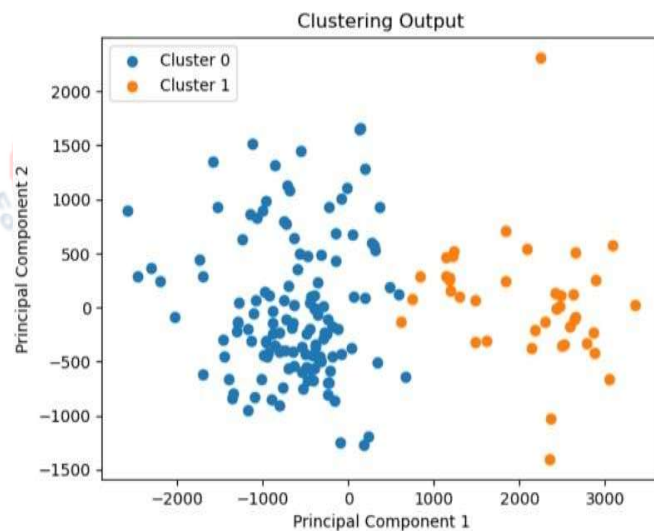

Fig.5 Clustering Output

This visualization likely results from a clustering algorithm that grouped data points based on their similarity across these two principal components. These components are likely attained from a dimensionality reduction technique, such as Principal Component Analysis (PCA).
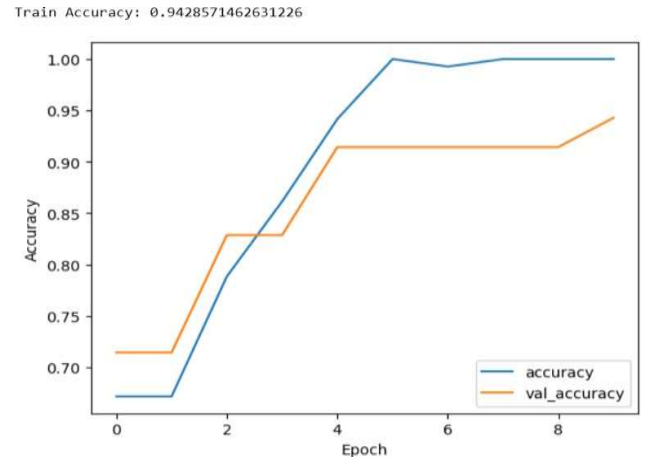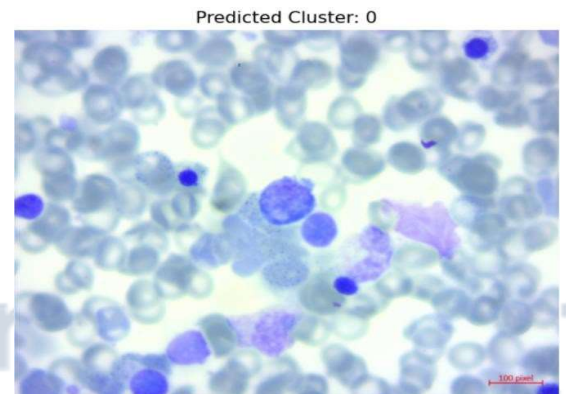

Fig.6Accuracy Graph

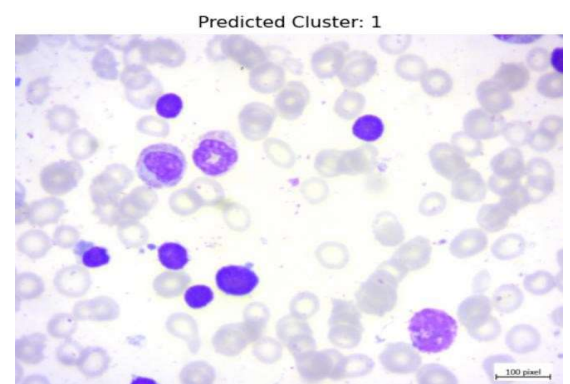**Fig.7 Shows the classified image as Non-Cancerous**

Fig.8 Shows the classified image as Cancerous

V. CONCLUSION

This automated blood cancer detection system represents a significant advancement in leveraging

machine learning techniques, particularly in the context of detecting Leukemia. Traditional diagnostic methods can be time-consuming and rely heavily on manual interpretation, which may lead to delays or inaccuracies. The system addresses these challenges by harnessing the power of machine learning, specifically through Convolutional Neural Networks (CNNs), a type of deep learning algorithm known for its effectiveness in analyzing complex patterns in images. In this case, the system utilizes CNNs to extract features, such as the shape of cells, from white blood samples.

By employing CNNs, the system can automatically learn and identify subtle patterns and abnormalities indicative of leukemia within these samples. This automated feature extraction process significantly reduces the reliance on manual labor and subjective interpretation, potentially leading to more consistent and reliable results. Furthermore, the system enhances its diagnostic capabilities through the integration of the K-Means clustering algorithm. This algorithm helps to organize and group the extracted features into clusters based on similarity, allowing for a more refined analysis and interpretation of the data.

After the extraction of the features, the system employs the K-Means clustering algorithm to group similar features together. This clustering process aids in identifying patterns and structures within the data, which is essential for distinguishing between cancerous and non-cancerous cells. The system achieves an impressive 94% accuracy in this clustering step, highlighting its efficacy in identifying potential leukemia indicators. Following the clustering process, the system utilizes CNN algorithms to classify the clustered features into either cancerous or non-cancerous cells. Overall, this integrated approach combining feature extraction via CNNs, clustering using K-Means, and classification through CNN algorithms demonstrates the system's robustness and potential in automating

the detection of leukemia from white blood samples.

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