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Accurate Machine Learning Algorithms Based on Detection of Leukemia Disease: A Review

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Abstract

Blood cell disorders are often detected in advanced stages as the number of cancer cells is much higher than the number of normal blood cells. As one of the important aspects of diagnosing leukemia and determining its progress is identifying malignant cells. This paper illustrates the discovery of leukemia and its four main types through machine learning algorithms, as it was found that Computer-Aided Diagnosis (CAD) has progressed rapidly over the past few years. To identify leukemia, multiple machines learning algorithms have been created for early detection. Leukemia is a condition synonymous with white blood cells (WBC) that affect the bone marrow and/or blood. The early, healthy, and reliable diagnosis of leukemia has a major role in treating patients and saving their lives. To define leukemia in relation to its subtypes, several methods have been developed. However, these approaches include improvements in efficiency, learning process, and performance. This research paper is explained to enhance and provide rapid and stable detection of leukemia. To facilitate real-time collaboration between patients and healthcare providers for leukemia research, early diagnosis, and treatment. Thus it can save patients and doctors time and money. While the use of machine learning algorithms has shown accurate results, it depends on the shape and size of the sample and the type of algorithm used to classify the subtypes of leukemia (leukemia).

Keywords — Leukemia, Blood Cancer, Machine Learning.

1. INTRODUCTION

Leukemia is a form of blood tissue cancer. The delicate inside of the body, called bone marrow, is leukemia. Leukemia. Hematopoietic stem cells compose of the bone marrow. It evolves over time into multiple blood components such as white blood cells (WBCs), platelets, and red blood cells (RBCs), which each have distinct functions. [1][2]. Cells (RBC) are responsible for the transfer of oxygen from the lungs to the tissues of the body. Though (WBC), also known as leukocytes, is responsible for combating disease and inflammation, platelets help with clotting and control bleeding [3]. The first type of leukemia consists of two categories: chronic leukemia and acute leukemia [4]. Acute leukemia is actually referred to as acute myeloid leukemia (AML) and acute lymphocytic leukemia (ALL) and is categorized as chronic myeloid leukemia (CML) and chronic lymphocytic leukemia (CLL) [5].

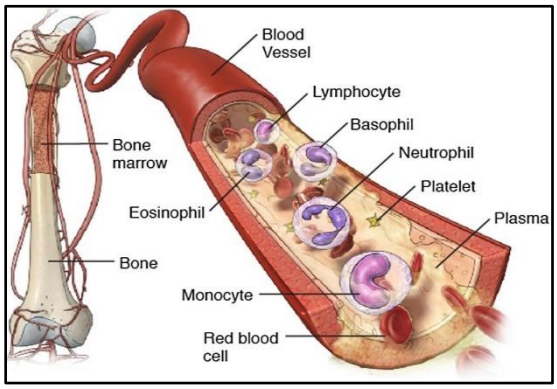

Figure 1: Leukemia in Human Blood and marrow [6]

In American culture, leukemia is a severe issue, affecting all children and adults and even babies below the age of 12 months. The most prevalent form of cancer is pediatric leukemia, although the study on adults by the Health Organization indicates that leukemia has been one of the 15 most common cancer types [7]. An important feature that makes cancer killer is the rapid development of irregular cells that develop past their

natural boundaries, then invade neighboring cells and spread to other organs is an essential trait that causes cancer killers. The term used for this process is metastasis. The World Health Organization's website reveals that cancer is the second leading cause of death globally, causing nearly 9.6 million deaths in 2018 [8]. According to report from the National Cancer Institute (NCI), there are expected to be 62,130 new cases of cancer treatment in the United States and 245,000 fatal or extremely serious cases [9][10][11][12]. And its ranks ninth among diseases (tumors) in children in India [13].

1.1. ***Acute Myeloid Leukemia*** **(AML)*:*** Acute leukemia, which happens when the bone marrow starts to develop immature WBC and blisters, is the most common form. This also allows irregular platelets and red blood cells to develop. Symptoms can be similar to those associated with influenza or other common diseases. In addition, the terrain and markings can vary according to the cell types affected. Acute myelogenous leukemia is usually symptomatic with fever, fatigue and exhaustion, bone pain, skin phaleness, shortness of breath, sudden swelling, recurring diseases and bleeding, such as hemorrhage gums and common nose bleeds (AML). (AML) has eight other subtypes which vary from other leukemia types [14].

1.2. ***Acute Lymphocytic Leukemia*** **(ALL):** (ALL) is the most often seen carcer (WBC) in children caused by overproduction in the bone marrow of premature WBC and a chronic overproduction. The symptoms of both flu and other common illnesses, such as bone and joint fatigue, stiffness and discomfort, make it difficult to diagnose. Three variants (ALL) labeled L1, L2, and L3 are available [3].

1.3. ***Chronic Myeloid Leukemia*** **(CML):** The Chronic myeloid leukemia is rare at a young age [15]. It is a slow-growing type of leukemia, and it can progress to fast-growing acute leukemia and difficult treatment. It can be seen in three phases, i.e., accelerated, chronic, and eruption phases. As it is in the chronic phase, leukemia grows slowly and is in the strongest case. The second stage, however, goes through a stage in which the blood cells are immature, usually known as the extended stage. Finally, it passes through the third stage, which is the explosion stage, known as the transformation stage of the explosion or the acute stage [14].

1.4. ***Chronic Lymphoblastic Leukemia*** **(CLL):** It is known as a blood disease that slowly gets worse. It is not very common in children but is most commonly observed in adults, its symptoms include night sweats, fever, weight loss, and periodic infections [14].

The types of leukemia and a pictorial representation of the blood structure are shown in figure 2 [14]

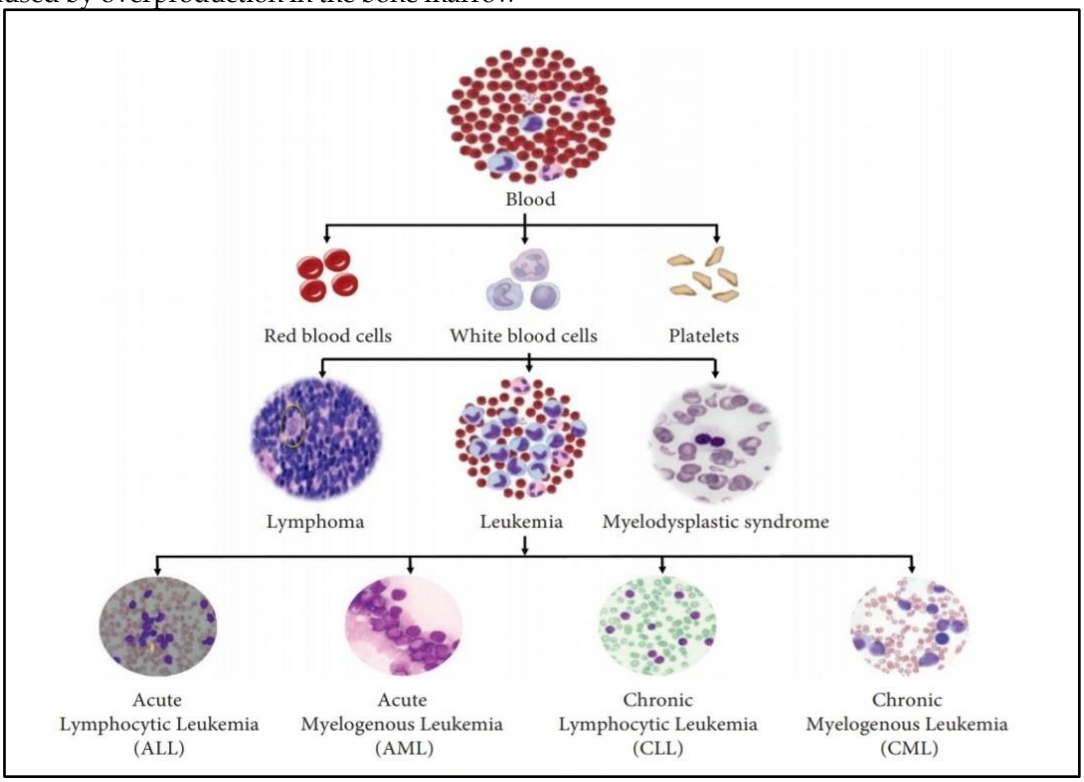

Figure 2: Types of leukemia [14]

2. CLASSIFICATION ALGORITHMS USED IN THE TREATMENT OF LEUKEMIA TYPES

Classification is the theoretical decision-making of identifying parts of an image or even an entire image. Image categorization is an important and widely used branch of artificial intelligence (AI) within a set of predefined categories using only samples from a category. The image classification is divided into two types; an uncontrolled image classification exists [16][17]. Although current work is focused on mild algorithms of classification, not unexpected algorithms of classification. The main classification in the machine vision classification is also regulated [18].

2.1. ***Support Vector Machines algorithm*** **(SVM):** (SVM) is a powerful data classification tool based on the HLP classifier. This classification is achieved through a discrete surface (linear or non-linear) in the input space of the data set. It's basically a classifier that improves the margin between classes. Features based on the shape and texture of the image core sample are extracted and recorded. The number and structure of the nucleus lobes is one of the salient features used to define the (WBC) class. Among all the features, the most relevant features are identified and used for training (SVM) such as the number of lobed nuclei characterizing the nuclei of each species, the ratio of periphery to nuclei and entropy, and the ratio of nuclei to cell [19].

2.2. ***K-Nearest Neighbor algorithm*** **(KNN):** K-Nearest Neighbor algorithm works without a training phase so it is considered a lazy learner and it performs classification or regression as soon as it saves its training data set. K-NN is also used to classify blasts in leukemia cells and to classify cells into two parts namely acute myeloid leukemia (AML) and acute lymphocytic leukemia (ALL) and it works with 80% accuracy [20]. KNN is a simple algorithm that classifies new states based on a measure of similarity (e.g., distance functions) and stores all available states. This algorithm was already used in the early 1970's as a non-parametric method for pattern recognition and statistical estimation [18]. Also, K-NN was used to search for a set of k-organisms among the training datasets whose results were closer to the test data and the class naming base prevailing over neighboring regions [21].

2.3. ***Neural Networks algorithm*** **(NN):** A Neural Network is used to detect all cells in slices of blood samples. It's a network built from several interconnected neurons. Neurons are characterized as simple processing units that, based on current inputs, alter or trigger their internal state and generate outputs that are dependent on input and current activation. By making many of these neurons run in parallel and connecting some neurons via weighted connections to others, NNs are created, creating a weighted and guided network of various layers [22]. It determines the design and training of the NN, which usually depends on the application and the data form. Since the layers of the architecture are an input layer that determines the size of the image and corresponds to the height of the NN, the width and number of the image channels defined [23]. Pre-tested (NN) were examined to extract classifiers and features of the clusters used to classify normal cells and blast cells [3].

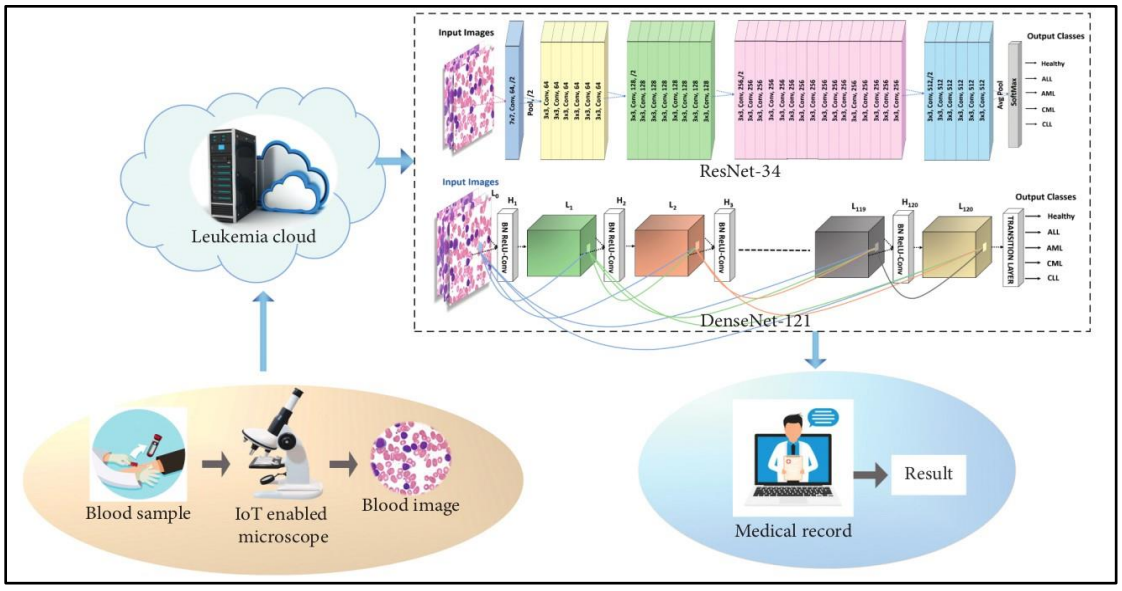

Figure 3: A proposed framework for diagnosis of leukemia [14]

2.4. ***Naïve Bayes algorithm:*** The main goal of the Naïve Bayes algorithm is to detect the presence of blast cells by using features extracted from the pieces. They carry blast cell information and this information is analyzed using the proposed classifier to detect the presence of blast cells. The suggested GFNB is to combine the Naïve Bayes classifier with a gene index. The classification procedure is the work of the classifier to gather the Naïve Bayes index results. It is easy to understand and successful. As it converges rapidly and can deal with inequality measures [24].

2.5. ***Deep Learning:*** Deep learning is one of the branches of machine learning that is inspired by the work of the nervous system and the human brain [25]. Therefore, many works have demonstrated that the human expert can be compared to deep learning methods due to the accuracy of prediction. It also demonstrated a method based on deep learning to identify cancer metastases and that the combination of a human pathologist's diagnosis with deep learning methods can improve the accuracy of pathological diagnoses. Moreover, advances in deep learning have enabled algorithms to outpace the performance of medical experts in general [26][27].

2.6. ***K-Means clustering algorithm*:** k-means the clustering algorithm using the Attractive Clustering method creates the midpoint based on the potential value of the data points to find white blood cell nuclei. The blood cell segmentation process coupled with image optimization and computation for WBCS segmentation and two-stage segmentation of lymphocytes identified the white blood cell nucleus from the background by clusters of k-means applied to the color space of the LAB. For images with low contrast cells, the k-means algorithm does not work well. To overcome this problem k-means clustering and a global threshold in the HSV color space and the morphological process of cell division were used [6]. When color images are converted to grayscale images, the WBC regions become the darkest area in the images. Next we apply Zack's algorithm equation and white blood cell assembly graph [28][29].

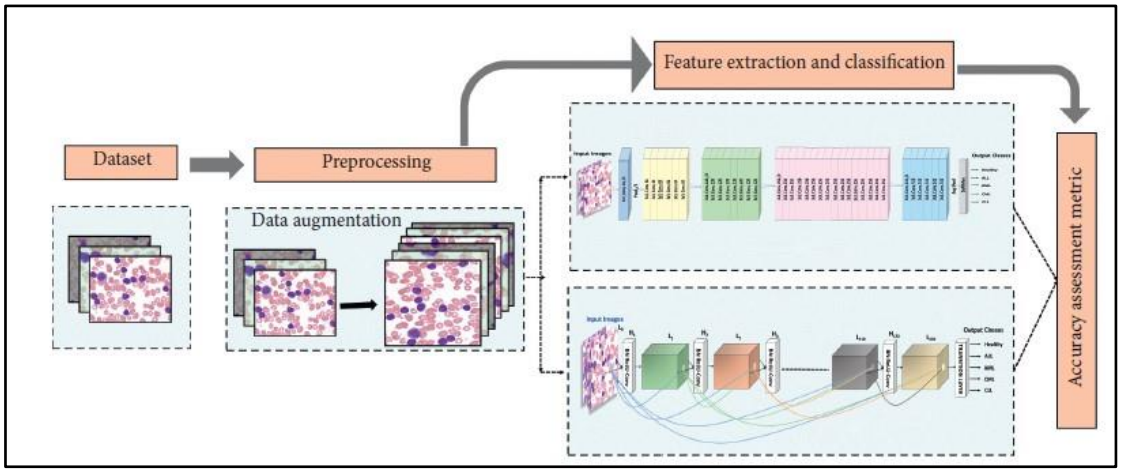

Figure 4: Proposed Methodology for leukemia [14]

2.7. ***Random Forest (RF):*** The features extracted by the random forest classifier are used to classify a lymphocyte as either a normal cell or a burst cell. The random forest classifier is a passionate learner at the time of training that works by generating various decision trees and outputting the class i.e., class mode[30]. It works well on large and stable databases, especially in high dimensional spaces. The random forest algorithm was used to generate a random sample with subgroups. This formation produced an observed accuracy of 95% [31].

3. RELATED WORKS

Over the years, numerous approaches for identifying leukemia have been suggested and several of these experiments have provided solutions for classifying the two most common forms of leukemia: Acute myeloid and acute lymphoblastic leukemia (AML) (ALL) [32]. Many studies present technology in algorithms for machine learning.

I. J. Maria *et al.* [20] used the Support Vector Machines algorithm (SVM), It is a binary algorithm used to separate the blood samples between myeloid and lymphoid cell stem cells and separate it from acute myeloid and acute leukemia. Splits the input space of the dataset, maximizing the class margin. The training

algorithm defines the help vectors for the classifier. A sample form and texture-based characteristics for each nucleus are collected and reported. Of all the features, the most important features are chosen and are used to train the SVM.

T. Engineering [19] used methods could classify leukocytes in this work and categorize them into 2 main groups, Lymphoid stem cells and Myeloid stem. A robust classifier framework separates and classifies the blood in this job. The findings of the experiment revealed that 100 sample photographs could be divided between Lymphoid stem cells and Myeloid stem cells by the effectiveness of detecting leukemia. Using K-Means clustering, the procedure was tested. The visual signs of structure and form are inspired by features derived from the segmented cytoplasm and nucleus. The description of Foil of Bretagne (Lymphoid) and Almeida Lloyd is the subject of our work (Myeloid).

P. M. Gumble [18] used the KNN algorithm because it is a simple algorithm that classifies new states based on a measure of similarity (for example, distance functions) and stores all available states. This algorithm was already used in the early 1970s as a non-parametric method for pattern recognition and statistical estimation. A total of 72 samples were taken out of 66 found to be correctly identified. The accuracy of the system is 91.66%.

S. Kumar *et al.* [1] presented an algorithm for acute leukemia detection systems. Using a K-mean clustering algorithm, the implemented procedure implements simple improvements, anatomy, filters and segmentation techniques. A 92.8% accuracy algorithm is suggested and is tested on a range of 60 by Nearest Neighbor (k-NN) and Naïve Bayes Classifier.

T. T. P. Thanh *et al.* [4] recommend a system based on the Neural Network (NN) to differentiate between regular and abnormal images of blood cells. The system proposed achieves an accuracy of up to 96.6 percent. In a largely augmented dataset, the authors carried out the proposed method to validate the accuracy and reliability of the proposed NN architecture. Since only one form of leukemia disease, acute lymphoblastic leukemia (ALL), was added to the dataset, the researchers used a new data set to test the architecture, including four forms of leukemia. In future work, researchers would like to use some algorithm tuning in terms of weight initialization, activation functionality to boost the efficiency of the NN architecture.

R. D. Souza *et al.* [31] presented the features extracted by the random forest classifier are used to classify the lymphocytes as either normal cell or blastocyst. Random Forest Classifier is a passionate learner in training time who works by generating different decision trees and class output i.e., class mode. It works well on large and stable databases, especially in high-dimensional spaces. A random forest algorithm was used to generate a random sample with subsets. This configuration produced a remarkable accuracy of 95%.

D. Umamaheswari *et al.* [33] Introduced in conjunction with simulating differential measures (SDMs) in the nucleus and cytoplasm segmentation of both lymphocytes and lymphocytes, using a clustering algorithm, a decision support system to describe

U. N. Wisesty *et al.* [21] presented two principal objectives. The first is to remove cells containing functions. The second goal is to distinguish two types of lymphocyte cells, namely regular and abnormal lymphocytes. The researcher used a combination of shape feature and histogram feature in conducting this analysis, and the classification algorithm is k- nearest Neighbor with k variance was 1, 3, 5, 7, 9, 11, 13, and 15. The best precision, sensitivity, and specificity levels were 90 percent, 90 percent, and 90 percent, and were obtained with k=7 from combined area-perimeter-mean-standard deviation characteristics.

B. K. Das *et al.* [24] used the Naïve Bayes algorithm and the main goal of this algorithm used of the features extracted from the pieces was to detect the presence of blast cells. It holds information about the blast cells and this information is analyzed to detect the presence of blast cells using the proposed classifier. The recommendation is to merge the Naïve Bayes classifier with the gene index. The classification procedure is the work of the classifier to gather Naïve Bayes indicator results. It is easy to understand and effective. Because it converges quickly and is able to deal with measures of inequality.

A. Rehman *et al.* [23] suggested a tool for classifying everything in stained bone marrow images into its subtypes and reactive bone marrow (normal). The comprehensive segmentation and deep learning techniques with the neural network are used to shape the model on images of the bone marrow to obtain correct rating outcomes. This led the series of experimental observations and comparison with the effects of the Naïve Bayesian, KNN and SVM classifiers. Experimental results indicate that the suggested technique reached 97.78 percent accuracy. The findings have demonstrated that the method proposed could be used as a way of recognizing and assisting pathologists in the production of acute lymphoblastic leucemia and sub-types.

Everything was implemented. In the scheme, classifiers were used, such as Multi-Level Perceptron (MLP), SVM and Dempster Shafer. Of these, Dempster Schafer showed a 96.72 percent accuracy score.

R. Bhukya *et al.* [34] detecting ALL, Otsu used the threshold for banalization and morphological operations to segment the nucleus of leukocyte cells. Then, using the shape features, SVM is used to discriminate fit and injurious cells with the accuracy of 92.7 percent. unsupervised algorithms. K-NN and SVM are good for small datasets, Naïve Bayes, K-mean, and Neural Networks work with large and small datasets and deep learning works well when the dataset is large.

Minakshi Arya [35] emphasized on an automated framework based on image processing algorithms to

identify blood cells for acute lymphocytic leukemia detection (ALL). There were 20 PCA models for experimentation, and seven models had an accuracy of 99.9%, including Medium KNN, Coarse KNN, Cosine KNN, Cubic KNN and Weighted KNN, Ensemble Boosted Bake Trees. These models were tested on the basis of predictive tempo, training time, insecurity and ROC. The weighted KNN classifier was the best of all models when using PCA.

Table 1. Comparison of classification algorithms

Ref.	**Year**	**Classification algorithms**		
		Methods	***Dataset***	***Accuracy***
[20]	2020	SVM	ALL - AML	92%
[24]	2020	Naïve Bayes	ALL	94.94%
[35]	2019	PCA - KNN	ALL	99.9%
[23]	2018	Naïve Bayes – KNN - SVM	ALL	97.78%
[1]	2018	KNN - Naïve Bayes	ALL	92.8%
[31]	2018	Random Forest	ALL	95%
[4]	2018	Neural Networks	ALL	96.6%
[21]	2017	K-Nearest Nighbour	ALL	90%
[18]	2017	KNN	ALL	91.66%
[34]	2017	SVM	ALL	92.7%

Table 2. Merits and Demerits of classification algorithms

Algorithms	**Supervised / Unsupervised**	**Merits**	**De-Merits**
SVM	Supervised	* High accuracy. * Works for unstructured and semi-structured knowledge well. * Linearly separable feature space is not necessary. * Matches well with high-dimensional data.	* Binary classification only. * It consumes a lot of memory. * Long training time. * Not suitable for large data sets.
KNN	Unsupervised	* Easy to implement. * No training period required. * New data can be added smoothly.	* Cannot handle high dimensions. * Cannot handle large data sets. * Needs a scaling feature. * Account cost is high.
Neural Networks	Both	* Works efficiently for both small and large data sets. * Capable of discovering complicated non-linear interactions between variables. * It only needs less statistical training * Error tolerable.	* Prone to over-processing. * Large arithmetic overload. * Causes problems in the unjustified behavior of the network. * Works with numerical data. * The network duration is unknown.

Naïve Bayes	Supervised	* Convergence is fast and simple classifier. * Only needs less training data. * Works efficiently for both small and large data sets. * Highly scalable.	* All traits are assumed to be linearly independent but in reality it is not. * Dependencies cannot be modified. * Chance of losing accuracy. * Assume that digital features are a habit.
Deep Learning	Both	* Reduces the need for feature engineering and is automated deduction. * It can be applied to many different data types and applications.	* His requirements are expensive. * Training is very expensive due to complex data models. * It is not easy to understand what is being learned.
Random Forest	Supervised	* Show all components of the image except for the cell nucleus. * Highlight entire image objects with cell nucleus. * Reducing noise and preserving edges * Convert grayscale image to binary image. * Lymphocyte division with good accuracy.	* Since it builds multiple trees to combine their outputs, it requires a lot of computing power as well as energy. * It also requires a lot of preparation time as it combines multiple decision trees to decide the class. * It also suffers from interpretability because of the collection of decision trees and fails to evaluate the importance of each variable.

4. DISCUSSION

In general, it is not possible to say, on the basis of the accuracy values provided in Table 1, which algorithm is better for the accurate detection of leukemia forms, since the comparison is not based on the same dataset. It can be shown, however, that the K-NN algorithm operates with the PCA algorithm more specifically according to those requirements. Additionally, In Table 2, we find the benefits and drawbacks of the various algorithms discussed. Although Neural Networks, and K-NN are unsupervised algorithms, Naïve Bayes and SVM are supervised algorithms. The first and only binary classifier is SVM, although more than two classes can be categorized into all other algorithms. For small datasets, SVM and k-NN are appropriate, while Neural networks and Naïve Bayes function for large and small datasets, and when the dataset is massive, deep learning works well. Naïve Bayes classifies linear data, k-NN, neural networks, and deep learning work for nonlinear data, and SVM works well with both linear and nonlinear data.

5. CONCLUSION

Machine learning algorithms are becoming increasingly popular and this paper is an attempt to compare the classification of six machine acquisition algorithms used: Help Vector Machine, K-Nearest Neighbor, K-mean, Neural Networks, Naïve Bayes, Deep Learning, and Random Forest. The literature on these leukemia classification and prediction algorithms was taken for review. Further work in this research will lead to determining the effectiveness of treatment provided to leukemia patients, through effective use of appropriate machine learning algorithms and classification of all types of leukemia, which can be executed in parallel for better response time and accuracy.

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