



Leukemia Blood Cell Image Classification Using Machine Learning: A Systematic Review

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Article information

Article history:

Received: June, 26, 2023

Accepted: July, 27, 2023

Available online: Sept., 16, 2023

Keywords:

Leukemia,
Machine Learning,
Image Classification.

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Citation: Mohammed, Z. M., & Mohammed, E. Z. (2023). Leukemia Blood Cell Image Classification Using Machine Learning - A Systematic Literature Review. *Journal of Advanced Sciences and Nanotechnology*, 2(2), 204–214.

Abstract

A rise in the quantity of young blood cells in the both blood and bone marrow is the primary cause of leukemia, a malignant condition that affects the system that produces blood. This disease appears in the elderly and represents the most common type of disease among young people. Symptoms appear in the form of bleeding, bruising, a feeling of fatigue, a high temperature, and a high rate of transmission of the disease. These symptoms occur due to a deficiency of mature and normal blood cells. The cause of this disease is unknown, as there are different causes depending on the type of leukemia. The genetic factor, weather and environmental conditions have a major and major role in the causes of the disease. Where there are factors that lead to an increase in the chances of contracting the disease, such as smoking, ionizing radiation, and some chemical elements. Also, individuals with a family history of the disease also have an increased chance of developing the disease. The disease can be detected and diagnosed with a blood test or by taking a dose of bone tissue. White blood cells are capable of divided into the following categories: neutrophils, monocytes, eosinophils, lymphocytes and basophils. During this period, the authors designed a CNN to classify and detect normal white blood cells. The following two actions are taken by the system in order to identify the type and shape of a typical white blood cell. Finding the primary traits and characteristics of typical WBCs is the first step. The classification of mature WBCs according to kind is the other duty. The device will be able to detect mature and normal WBCs using CNN by comparing their properties to those of higher level normal WBCs. With the amount of data used, the accuracy of the suggested method was up to 96.78%. The most pertinent studies showing the value of machine learning and its algorithms in detection, medical image segmentation, tagging, and classification, particularly leukemia, are presented and discussed in this paper.

DOI: <https://doi.org/10.55945/joasnt.2023.2.2.204-214>,

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1. Introduction

A definition of leukemia is the malignancy of the both bone marrow and blood [1]. The annual cause of death in the United States due to leukemia was estimated to be 24,500 deaths in 2017. generally, according to the rate of disease progression and the type of aberrant cell identified in bone marrow and peripheral blood, Acute and chronic leukemia are the two subtypes that are recognized. Blast cells are the most immature malignant cells that are specific of acute leukemia which is characterized by high proliferation

rate, arrest of the function of normal cells while in chronic leukemia the rate of proliferation of the malignant cells is much slower with the course of the disease being longer and less aggressive in comparison with acute leukemia. The malignant process in chronic leukemia involves the mature cells of the blood. Leukemia is sub classified according to the involved lineage into myeloid and lymphoid, myeloid lineage include granulocytes, erythrocytes and thrombocytes while the lymphoid lineage is classified into B and T-lymphoid cells. The four principal types of leukemia are acute lymphoblastic leukemia, acute myeloid leukemia, chronic lymphocytic leukemia, and acute lymphoblastic leukemia. as show in Figure 1. Regarding the affected age group, acute lymphoblastic leukemia (AML) most commonly affects children between the age of (3-7) years old and it has another peak in the elder age group beyond 65 years old. AML is prevalent in the elderly and seldom affects the pediatric age group. It is a type of blood cancer represented by the accumulation of cancer cells in lymph nodes, bone marrow, and secondary lymphoid organs. One of the most common types of leukemia worldwide. All is a blood cell starting from the bone marrow cancer. It is It is characteristic an unchecked, accelerated proliferation of immature blood cells and affects both kids and adults. Leukemia is a common cause of death among blood illnesses, with cancer ranking second in the world behind cardiovascular diseases. According to the global burden of illness report from 2017, 9.6 million people worldwide cancer caused an early death, making it one of the worst global health issues [2]. The distinguishing feature of the disorder, which is the leading cause of death for chronic lymphoblastic leukemia (CLL) patients, is the imbalance in the body's immune system and the associated infections³. AML It is one of the deadliest types of blood cancers, due to immature leukocyte proliferation in the bone and peripheral marrow circulation. AML is traditionally diagnosed by Peripheral blood smear images and microscopic samples are used by expert examiners, which is a laborious and time-consuming technique [4]. Chronic myeloid leukemia (CML) is a type that requires early detection to allow for effective treatment. Rapid, error-free, and automated diagnostic methods are therefore requiring [5]. The diagnosis of leukemia is achieved by proper history taking and clinical examination of the patient as most of the patients present with fatigue, fever, lymphadenopathy, hepatosplenomegaly and bleeding problems such as epistaxis, bruises and ecchymosis, also weight loss is a major manifestation due to the catabolic process of the disease. as shown in Table 1, Microscopic examination by performing complete blood count and picture with bone marrow aspiration/biopsy is very vital as by which identifying of the abnormal cell occurs and sometimes the type of the leukemia can be determined through only microscopic examination. More advanced techniques include immunophenotyping by flowcytometry and cytogenetic and molecular analysis. By far AML is the most serious type of leukemia as the survival rate of the affected individual is only 27% [6]. ALL is known to have better prognosis in children and by the aid of chemotherapy, the survival rate approaches almost 90%. CML has excellent prognosis especially after the administration of tyrosine kinase inhibitors treatment which initiated a dramatic change in the survival rate. CLL has a chronic course with periods of relapse and remission and the treatment can range from only watch and wait to heavy chemotherapeutic agents according to the stage of the disease. The modalities of leukemia management vary according to the type whether acute or chronic, acute leukemia is treated by heavier regimens and higher doses of chemotherapy. The chemotherapeutic agents have many types according to their mechanism of action such as alkylating agents, antimetabolites, cytotoxic antibiotics, demethylating agents, signal transduction inhibitors and monoclonal antibodies. Radiotherapy has a role in the treatment of leukemia especially in localized disease and the most modern modality of treatment is bone marrow transplantation which has two types' allogenic bone marrow transplantation which is beneficial in acute leukemia and autologous bone marrow transplantation which is used in the chronic setting of the disease after failure of chemotherapy treatment.

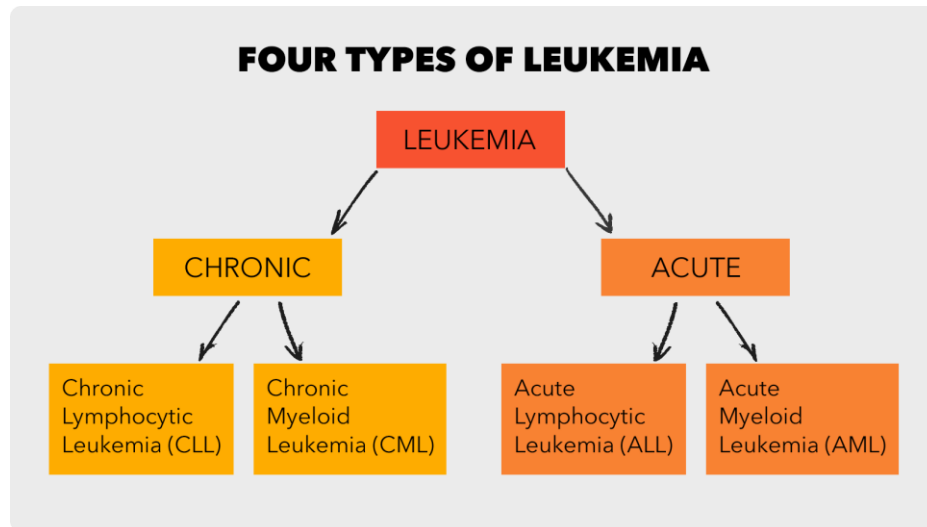


Figure 1: Types of Leukemia

Table 1: Diagnostic of Blood Cancer

Types of Blood Cancer	Diagnostic Tests
Leukemia	Complete Blood Count (CBC)
Lymphoma	Biopsy, CT Scan, X-Ray
Multiple Myeloma	CBC, Bone Marrow, X-Ray

2. BACKGROUND

The basic building blocks of a picture are called pixels, which are collections of data used to depict a two-dimensional image in digital form. A passing monochrome or grayscale image has a numerical number for each pixel's intensity. One of the methods for segmenting images most significant issues in image processing and analysis. It entails dividing the image into a few portions that adhere to a specific uniformity standard. Segmentation's main objective is to make it easier to represent and state the analysis of diverse issues[7].

3. Aim and Objectives

This review aims to identify studies and research related to the diagnosis, Detection and classification of blood cancers and related items using special techniques for machine learning, so that the dose of blood taken as well as the surrounding blood is analyzed.

4. Literature Review

The majority of the photos in the dataset were taken with an optical microscope and a digital camera. in a lab. The images are in the JPG format. Using various image processing methods and approaches will be absolutely necessary to process and enhance photos and their quality [6]. Because leukemia, the majority of past studies have concentrated on dividing white blood cells rather than red blood cells and platelets is a form of disease that affects white blood cells. Several techniques, such as clustering, growth region, segmentation, color, and thresholding, are employed while dividing a cell. The author typically draws out characteristics like contrast, color, shape, and energy. Most researchers at the classification steps used traditional machine learning (ML) methods such as support vector machine (SVM) and convolution neural network for classification [1], and the paragraphs below explain the most important studies conducted in this field, and explain the most important techniques that gave accuracy results.

[1] (Detection of leukemia based on morphological contour division using

Fuzzy C mean) by Viswanathan et al in 2015

The proposed system using the Fuzzy c-means method ensures accurate stratification of leukemia by blood subtypes. The suggested method therefore offers wider applicability to the scale for the identification, categorization, and treatment of both healthy and diseased blood cells. Less time spent counting and fewer inaccuracies. A microscopic blood sample was used to evaluate the suggested algorithm on a collection of samples with acute lymphoblastic leukemia. Fine contrast enhancement is utilized in the analysis and processing of the blood sample and image to highlight infected white blood cells. Processed by subtraction and addition operations using the morphological process to scan other small parts. Nuclear fractionation is done by detecting a curve that provides correct and accurate detection of leukocytes it is then from a microscopic blood sample. Where a performance score of 98% was obtained [8].

[2] (Reducing features for improved identification of AML cells in microscopic specimens using principal components analysis) by MoradiAmin et al in 2015

In this research, fuzzy means c were used to classify cancerous and non-cancerous cells using characteristics based on PCA extracted from a nucleus sample. Also, the outcomes demonstrated that the suggested approach can be adopted as an auxiliary diagnostic tool for oncologists. In addition, the clinical impact of this research is the ability for pathologists to test a blood sample for cancer cells. A 98% confidence level was obtained in the results. The algorithm can also distinguish non-cancerous elements from the cell subtype with enhanced sensitivity, as the classifiers were evaluated by statistic parameters including sensitivity, specificity, accuracy, and false negative rate [9].

[3] (Adjunctive diagnosis of acute myeloid leukemia using an HMRF-based segmentation method) by Su et al in 2017

This approach was applied to six cells Groups consisting of 61 bone marrow aspirate samples using the clustering method and cell image formation by automatic Markov field, and its performance was compared to other methods and algorithms in whole sample analysis, nucleus segmentation, and computational efficiency.

Optimized segmentation results are shown in both samples, helping to provide the basis for extraction and characterization of lower cell characteristics. A 96% confidence level was obtained in the results. Segmentation of sample images using these proposed methods can help the analyzer to distinguish the six groups of cells and also to determine the number of claudicating [10].

[4] (Use of transformational learning in CNNs and SVMs for the blood being tested for leukemia slides) by Romuere R. Veras et al in 2018

In this study, a novel approach of identifying and categorizing leukemia in blood samples is described. It is possible to test the feature extraction capability of pre-trained CNNs based on the findings acquired with 99% accuracy by the used approach. By feature choice: While developing the suggested methodology, we used two approaches: using the outputs of each of the three structures independently, and using vector collection sequences [11].

[5] (Classification of acute leukemias utilizing a system for decision-making that is based on digital microscopic pictures) by Ahmed S Hassan et al in 2018

The proposed approach was used to conduct image segmentation and classification on a public database of blood samples. A pre-treatment phase and a post-treatment process make up the suggested methodology. To track the frequency of some randomly repeated cells, image segmentation was used. For blast detection in AML pictures, the proposed technique using K means was contrasted with LBG and KPE. With a confidence level of 99.5% [12], the results demonstrated that the K-means outperformed the Algorithms KPE and LBG.

[6] (Using DCN to detect AML and classify its subtypes) by Sarmad Tehsin et al in 2018

The percentages of blast cells (abnormal white blood cells) in bone marrow or peripheral blood determine how severe acute lymphoblastic leukemia is. It is challenging for lab staff to precisely identify the traits of blast cells since hand microscopic analysis of bone marrow is less reliable, time-consuming, and prone to mistakes. Researchers have used a variety of computational techniques to determine the makeup of blast cells, but these techniques suffer from significant drawbacks that prevent them from accurately segmenting leukocytes, such as a lack of object-to-background contrast, sensitivity to grayscale, sensitivity to image noise, and large computational sizes. Therefore, the creation of a novel and enhanced method for leukocyte cell segmentation is essential. 97% segmentation accuracy under various lighting situations. [13].

[7] (Convolutional neural network usage to classify leukemia in images of peripheral blood cells) by Thanh Park et al in 2018

This paper presents two data augmentation methods to expand the set of data to prevent over fitting and draw attention to the specifics of the training image manager. Where traditional methamphetamine is easy to implement and does not take long, other methamphetamine techniques for expanding the dataset show promising solutions for reducing neural network error rates. Also, we proposed a Leukemia Net Convolution construct to detect active AML images of normal cell ages at high resolution. A confidence rate equal to 96.72% was obtained [1].

[8] (Use of local pixel information for acute lymphoblastic leukemia segmentation) by Wafaa Mustafa et al in 2019

In this systematic study, an automated leukocyte fractionation process is piloted based on machine learning approaches and image processing techniques. Leukocyte fractionation was conducted using statistics characteristics determined by genetic algorithm (GA). The data consisted of 108 microscopic blood samples and were segmented. As follows: 59 normal blood cells and 49 abnormal cells. Information about cells and other organisms obtained in six iterations, in each iteration. The level of confidence in the results obtained was 97% [13].

[9] (Image analysis for automatic identification of many acute kinds leukemias in perivascular blood) by Angel Acevedo et al in 2019

In order to distinguish between several blast cell types different mononuclear cells present in the blood, the LDA experiment obtained extremely high diagnostic accuracy. By using linear discriminant analysis to pick 700 characteristics, high classification accuracy was attained. In comparison to actual detection and diagnosis, the six categories of cell types overall classification accuracy was 85.8%, whereas The average sample's total categorization accuracy was 94%. [14].

[10] (Using a convolutional neural network to identify leukemia subtypes from microscopic images) by Ahmed, Nizar Yigit et al in 2019

In this systematic approach, we show a current study that uses a CNN architecture to detect and diagnose leukemia using microscopic images and blood samples, through which the other four classes of leukemia can be identified. We found that the SGD optimizer performs more efficiently and is significantly superior to the ADAM optimizer with regard to loss measures as well as accuracy [15].

[11] (Detection of AML by texture feature for microscopic blood smear classification) by Sonali Majhi et al in 2019

The proposed methodology illustrates a good study for the classification of healthy leukocytes from virulent cells in the images of microscopic samples. The suggested technique uses both the

thresholding triangle method and the Y component of the CMYK picture to process pre-inserted images. Then a discrete orthogonal S transform (DOST) is used to extract the texture properties. Then the reduced properties of the Adaboost algorithm are provided with the random forest are utilized as the basic classifier along with an RF classifier (ADBRF). The outcomes revealed that the suggested strategy provides a high level of accuracy of (99.66%) [16].

[12] (Depth learning and conventional image manipulation techniques are contrasted. identifying uncolored blood cells in photos of perivascular blood smears) by Brij Mohan Kumar et al Singh in 2019

Six categories of the detection and classification for uncolored blood cells uncolored blood cells—basophils, monocytes, eosinophils, neutrophils, lymphocytes, and aberrant cells—were demonstrated in this study. For the categorization and diagnosis of uncolored blood cells, we compare DL techniques using conventional image processing techniques. We also assessed the neural network classifier's performance using the extracted and manually created features, and we obtained a 99.8% accuracy rate. Also, we applied the entire training curriculum. The neural network's full training yielded accuracy of around 99% [17].

[13] (Making a diagnosis of AML by identifying, locating, and classifying contaminated leukocytes using the random forest technique) by Satvik Huo et al in 2020

This study demonstrates the formation of an automated forest model and method for diagnosing, classifying, and detecting infected leukocytes using the RF method to eliminate the methodological limitations of manual detection of AML. The study showed the system's ability to diagnose abnormal particles with a 93% accuracy and an 0.98 AUC-ROC. The proposed method also achieved an accuracy of 65% for each class of leukemia [18].

[14] (Use the improved YOLOv2 and its portfolio of features to learn about the different types of leukocytes) by Arshad Anjum Seifedine et al in 2020

Two tests were undertaken as part of this review to assess how well the suggested algorithm for localization using YOLOv2 performed. A confidence level of 97.2% was attained in the findings of the second test, in which BoF was extracted for cell categorization and experiments were conducted on standard LISC and ALL-IDB data sets of leukocytes [19].

[15] (An enhanced feature swarm optimization for the efficient classification of leukemia by white blood cells) by Ahmed T Kollmannsberger et al in 2020

A hybrid categorization approach for leukemia images of uncolored blood cells was put forth in this study. The procedure uses a deep neural convolutional network as its foundation (VGGNet) to extract traits from white blood cell samples, followed by filtering the obtained traits using the Statistically Improved Salp Swarm Algorithm (SESSA), which only extracts relevant traits and eliminates unimportant traits. With a confidence level of roughly 83%, the performance of the hybrid method adopted was excellent in terms of both lowering complexity and accuracy. In order to generate 10 combinations for each of the 10 possible qualities, SESSA was carried out in 10 independent runs. Six categorized algorithms (Linear KNN, SVM, Naive Bays, Decision Trees, Multi-Layer Perceptron) were used to analyze these groups[20].

[16] (Diagnosis of leukemia in blood cells using deep learning conversion) by Mohamed Naman et al in 2020

This methodology proposed two classification models that distinguish between a microscopic sample of healthy blood from cancer and an infected sample. A pre-trained CNN known as Alex Net was used in the first model, to extract the characteristic features. Experiments showed that the SVM classifier excelled with a confidence level of 93.57%. The second model uses Alex Net to extract and classify features. According to tests, this model performed better than the original model Across a range of performance metrics. Instead of just classifying images as cancer- or leukemia-free, researchers can expand future studies to differentiate between various kinds of leukemia [21].

[17] (Analysis of blood leukemia image with point detection and deep learning) by Di Ruberto et al in 2020

This review proposes a novel and effective leukocyte counting and classification system that provides automated procedures for the determination of ALL using the convolution neural network (CNN) method to overcome the problems of manual examination, fatigue, or subjective opinion. Step 1 the authors evaluated the performance of the method used on the first 33 images of an acute leukemia dataset, which is a general screening data for cancer, and the results obtained showed that it accurately detected 99.7% of the uncolored blood cells present in the first 33 images of leukemia. The system also accurately identified 94.1% of the lymphocytes, at the stage of classification [22].

[18] (Using CNN for automatic detection and diagnosis of leukemia from bone marrow microscopic samples) by Aayush Mittal et al in 2020

In this review, the method used eliminates the possibility of error in manual examination using DL techniques in some convolutional neural systems. The method is implemented on images and focuses on the best salient features of them and then follows them up by preparing the model with the structure of the variable convolutional nervous system. Finally, the chosen sample's cancer type is predicted by the model that was employed. A 97.2% accuracy rate was attained [23].

[19] (Using machine learning to classify treatment outcomes for people with ALL using clinical data) by Amirarash Khatibi et al in 2020

This article describes the classification of treatment outcomes for patients under 18 years of age with medical and clinical information using ML. All pediatric patients under the age of 18 are analyzed. In this review, data are collected manually from patient reports for 241 patients. The data used included are medical information, patient demographics, side effects, and complications related to treatment. In this review, two methods are suggested for data analysis. While the second technique does not include individuals whose reason of death is uncertain, the first strategy takes into account all pediatric patients where the most well-liked classification methods were put to use and contrasted to find the model that performs better. According to the results, the XGBoost algorithm performed better than other classifiers in the first proposed technique, with an accuracy of 88.5%. SVM, contrasted with, second-generation model technique is the better, with a 94.90% accurate outcome. The results also indicated that the patient's fever rising again and again is the main symptom. predictor of every treatment result [24].

[20] (ML for accurate Leukemia diagnosis and classification from images of samples taken) by Dese Yemane et al in 2021

In this study, the proposed system was able to diagnose and detect the four most common various leukemias, including acute and ongoing myelogenous leukemia, by means of a powerful image segmentation process, then an SVM algorithm classification stage. The results obtained were specificity, sensitivity, and accuracy of 100%, 97.86%, and 97.69%, respectively, for the data used for the test. The method used also showed an accuracy of 94.75% for the white blood cell count which includes monocytes and lymphocytes [25].

[21] (automatic detection of leukemia using deep networks of neurons that have already been trained) by Anilkumar et al in 2021

The suggested approach uses a computer-aided detection and using a CNN for diagnosis with prior training as the identification and detection of leukemia samples. The microscopic samples utilized in the suggested model were obtained from a publicly accessible data set. Without using any techniques for feature extraction or image separation, the samples in the proposed study were classified. The method used pre-trained string networks like Residual networks like ResNet-101 and ResNet, Directed Acyclic Graph (DAG) networks like GoogLeNet, VGG-16, AlexNet, and VGG-19 -50 to perform classification and comparison. The categorization accuracy for the outcomes was 100% [26].

[22] (Diagnosis of acute lymphoblastic leukemia from convolutional neural network array micrographs) by Mondal et al in 2021

The purpose of employing CNN to automatically diagnose ALL is described in this review. The method was evaluated and trained using data from dataset C-NMC-2019 ALL. In the initial test set, the suggested weighted group model generated a weighted F1 score of 89.7%, an AUC of 0.948, and an accuracy of 88.3%. [27].

[23] (Improved convolutional neural utilization Grids for image classification of leukocytes) by Sarah S et al in 2022

This study gave a general overview of how contemporary neural network models performed when used to diagnose and categorize leukocyte samples. Using the RS and GR approach, the CNN structure was used to identify and categorize photos of four different types of leukocytes. In the test set and training set, the suggested technique had accuracy levels of roughly 97% and 99%, respectively [28].

[24] (Classification and segmentation of leukemia) with contributions by Muhammad Mallah et al in 2022

To identify and diagnose leukemia, this methodology looked at the classification, pre-treatment, selection, extraction, and segmentation of white blood cells and cells. The most challenging part is that deep learning techniques require enormous quantities of data sets and information that have been prepared for training. We used deep models including Boltzmann machines, CNN, and restricted auto encoders to achieve high random classification accuracy, and we reached the best accuracy of 97.78% [29].

[25] (The use of a learning algorithm to design an independent scheme to make a diagnosis and detection of leukemia based on the hybrid CNN model) by Fredric Samson et al in 2022

In this review, it is proposed to process the images generated by data overload models to remove noise and data overload. We used the hybrid cnn with Interactive Self-School Algorithm (HCNN-IAS), whose function is to perform feature extraction, classification and merging operations. The HCNN-IAS algorithm classified highly efficiently the different of leukemia, including ALL, AML, CLL, and CML (CLL), (CLL) The experimental results showed higher and better diagnostic and classification accuracy in terms of accurately diagnosing leukemia and recovery rates about 99% [30].

[26] (Analysis of the experimental setting for the diagnosis and detection of supervised and classified ALL) by Elrefaie et al in 2022

This study describes two methods of classifying leukemia: normal leukemia and blast cell leukemia. Modern techniques were used to pre-treat samples to obtain, improve and transform data. Also, the bundling technique was used to precisely divide the cores. By using experimental decomposition (EMD) based on the Hilbert-Hung transform, the majority of the prominent features were retrieved (HHT). The Bayesian regularization (BR) technique was used to create the neural network (NN) classifier. NNs were contrasted with classifiers (SVM), KNN, Random Forest, and Nave Bayes. According to the trial findings, the NN algorithm performed better than average, with a classification precision of 98.7%. The specificity and sensitivity are, respectively, 98.1% and 99.3%. [31].

[27] (Diagnosis of acute lymphoblastic leukemia using VKCS with an attention mechanism) by Masoudi et al in 2022

In this study, a more accurate diagnostic method for acute lymphoblastic leukemia was presented, and the approach proposed the variable nucleus channel spatial attention, based on a three-stage model transformational learning (VKCS). A knowledgeable deep network captures high-level properties from images of blood sample in the first step. The suggested model is improved in the second stage by two processes that simultaneously take into account spatial and channel information: variable nucleus spatial attention and variable nucleus channel attention. The classification unit is relevant to the last step. For the ALL-IDB2VKCS data set and ALL-IDB1 data set, respectively, accuracy was roughly 99.6% and 100% [32].

[28] (Knowledge instillation of peripheral blood leukocytes using a deep learning classification network)

by Wenfei et al in 2022

In this methodology, a deep educational training framework is provided, which introduces a pressure model method to distill knowledge in the diagnosis and classification of leukocytes, by creating accurate results with small models. Using a leukocyte dataset with 25,830 original samples, pre-training large-format CNN structure models was the first stage. Then, KD extracts the large model's hidden information, and the little model is subsequently trained. The best tiny model, which had a test accuracy of 98.31% on the mixed dataset, is then selected as the final prediction model [33].

[29] (Evaluation and comparison of DL methods in the automated classification of leukocyte images and samples) by Amin Salih et al in 2022

This paper presents the study and understanding of the role of convolutional neural network and ML techniques in achieving excellent performance in classifying samples and images of depends on the properties of the shape of granular information in leukocytes and leukocytes. Hematologists, who are experts in the division of plasma cells, classify them into two groups: non-granulocytes (lymphocytes and monocytes), and granulocytes (eosinophils, basophils, neutrophils). We employed two alternative approaches, the first of which utilized live photos from CNN. The SVM algorithm was utilized in the second method. The accuracy of the support vector device is approximately 90.6%, but the accuracy of the convolutional neural network is 98.4%, according to the comparison of the results [34].

[30] (Using ML and DL techniques to automatically classification of chronic leukemia in a heterogeneous data set) by Arjun Jha et al in 2022

This study presents a new data set of 500 samples, which contain images of normal AML ALL. The data contains about 1,700 blood cancer cells. The process of increasing the volume of data is done by adding new samples to the data set. This group is used for automated binary classification. The proposed approach performs classification functions of two and three categories using the latest algorithms that are built on ML and DL. In the case of completely connected layers set with the final CNN layers for its VGG16 algorithm, the proposed binary classification approach obtained an accuracy of up to 97%, 98 percent for DenseNet 121 when combined with a SVM [35].

[31] (Using DL for the diagnosis and automatic detection of ALL in B cells and T cells) by Anilkumar et al in 2022

Leukemia is typically diagnosed and detected by examining peripheral blood samples and bone marrow. swabs by the use of microscope. Where it can be used methods based on image processing, which are fast, cheap and simple methods, to diagnose and determine the types of leukemia cells with analyzing and processing pictures of laboratory samples. The suggested methodology to categorize acute lymphoblastic leukemia using DL algorithms. The study used the DL network to classify All. The accuracy of the results was approximately 94.12%. The study also compared the performance and efficiency of classification using three different training algorithms [26].

5. DISCUSSION

Microscopic assessments of samples' images are the most prevalent and are considered one of the basic methods for detecting leukemia in its initial stages, as the traditional examination of these images can be the cause of many errors in diagnosing the two types and class of the disease and may also lead to inaccurate results. In addition, the agnostic accuracy suffers due to the laborious and time-consuming nature of these samples' evaluation. In order to give high diagnosis accuracy, automated approaches were therefore urgently required. Without affecting the expertise of technicians or being affected by work pressures. Therefore, there is an urgent need to use artificial intelligence techniques in detecting, diagnosing and categorizing different types and types of leukemia depending on the images of a television program. And the detection of leukemia, as the results of accuracy reached 100% in some of the researches that we mentioned.

6. CONCLUSION

The identification of leukemia using images of tiny blood samples is the subject of this study. By The system uses statistical analysis, texture, geometry, and color changes analysis as classifier input. A classifier will be created utilizing features in the micrographs. The program must perform well, be dependable, process data faster, make fewer mistakes, generate high-quality findings at a lower cost, and be tolerant of changes in user techniques, sample collection procedures, etc. The SVM algorithm can handle this condition (slack variables) by using the trade parameter (cost) and punishment parameter. Support Vector Machines can calculate the maximum level of hyper-margin that can exist between training examples by utilizing the kernel function to convert the data (implicitly) to a higher dimension space.

7. Future WORKS

Numerous suggestions and recommendations for future work were sparked throughout the construction of the suggested system, which may boost the system's effectiveness. These suggestions and recommendations include the following: Build more efficient learning models that can be trained on national and international datasets. The model may be trained with different batch sizes to prevent the over fitting problem. It is accomplished by providing more leukemia-related images. Improve the model's performance as a result. To obtain more reliable results, increase the training model's epoch count until it reaches stability and stops learning. Huge databases to produce forecasts with more accuracy. We need to make further improvements to the data in our created dataset.

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