

Enhanced Machine learning algorithms Lightweight Ensemble Classification of Normal versus Leukemic Cells

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DOI: 10.47750/pnr.2022.13.S09.056

Abstract

Leukemia is type of cancer in blood which impacts the lymphatic framework and the bone marrow and also impacts white blood cells. Leukemia, in contrast to other types of cancer, does not produce solid tumors; instead, it produces a huge number of aberrant white blood cells that crowd out the healthy blood cells. Machine learning algorithms that are widely utilized in the treatment of leukemia, whether it is to classify the various forms of leukemia or to determine whether a patient has the disease. It is a malignant kind of cancer that results in a number of medical issues. Expert hematologists and pathologists manually examine blood samples under the microscope to make a diagnosis. Techniques like image processing and pattern recognition can be utilized to help these experts. In order to attain excellent performance in the categorization of malignant leukocytes challenge, this paper suggests straightforward modifications to conventional neural network topologies. Consequently, there is considerable interest in the trustworthy and precise recognition of nonmalignant and malignant cells. Leukemia can be automatically detected using computer-aided diagnostic (CAD) models, which can help doctors and be useful for leukemia early identification. In this single-center study, we attempted to develop a deep learning model for classification of leukemic B-lymphoblasts. Data augmentation methods were utilized to manage the little dataset size and an exchange learning technique was utilized to accelerate learning and upgrade the presentation of the recommended network in order to create a trustworthy and accurate deep learner. The outcomes demonstrate that our suggested approach surpassed separate networks with a test accuracy of 95.59% in the Leukemic B-lymphoblast examination, and was caable to merge characteristics extracted from the top deep learning models.

Keywords: leukemia, machine learning, deep learning, ensemble classification.

INTRODUCTION

Children and adolescents can develop leukemia, a bone marrow blood cell cancer. Depending on how quickly it advances, leukemia can be classified as acute or chronic. Based on the afflicted blood cell type, acute leukemia could in upcoming studies split in the acute lymphoblastic leukemia (ALL) and [1] acute myeloid leukemia (AML) . ALL is the most prevalent kind of leukemia in children. In ALL, lymphocytes, a kind of the white blood cell (WBC), within bone marrow multiply uncontrollably and doesn't gets matured into the normally formed cells as they should. [2] Cancerous cells can spread to other organs and harm the entire body by infiltrating the blood cells. When suspective cells grow quickly, the bone marrow can fail, which can be fatal if discovered too late in the disease's progression or if treatment is put off. Age is a significant clinical factor that should be considered in the diagnosis of ALL. The risk then gradually decreases until the mid-20s, and it starts to rise once more after that, around age 50.

Leukemia

A condition associated with white blood cells is leukemia (WBC). Blood has several different components, including platelets, WBC, and red blood cells (RBC). Blood clots and bleeding are controlled by platelets. Erythrocytes, a kind of RBC, are in

charge of carrying oxygen from the lungs into the tissues of body. WBC, sometimes referred to as leukocytes, are in charge of battling illnesses and infections. Large quantities of immature WBC are produced in leukemia. It is a specific sort of cancer that damages the immune system of an individual's body while impacting the bone marrow and blood. Acute and chronic leukemia are the two primary classifications of leukemia according to progression. In contrast to chronic leukemia, which allows WBC to operate properly and grows more slowly, acute leukemia causes infected WBC to increase fast and exhibit abnormal behavior. This, however, can be serious because it might be difficult to tell it apart from the regular WBC.

Acute Lymphocytic Leukemia

The majority of cases of ALL, a WBC malignancy brought on by the excessive and ongoing proliferation of immature WBC in the bone marrow, are in youngsters. It is exceedingly challenging to diagnose ALL since its symptoms, such as fatigue, weakness, and joint and bone pain, are remarkably similar to those of the viral and also in other usual fever. L1, L2, and L3 are the three forms of ALL.

Leukemia Acute Myeloid

AML, the most prevalent form of acute leukemia, develops at the time bone marrow begins to produce blasts and the unmaturing WBC. Additionally, aberrant RBC and platelets could be produced. Early-stage AML's typical symptoms can resemble those of the flu or other common illnesses. The signs and symptoms may differ depending on kinds of the blood cells affected. Feverish, pain in bone, tiredness, breath shortness, pale complexion, continue infections, susceptibility to bruising, and abnormal bleeding, such as frequent nosebleeds and gum bleeding, are all symptoms of AML. Eight distinct subtypes of AML set it apart from other kinds of leukemia.

For the categorization of cancer using gene expression data, numerous supervised and the unsupervised machine learning techniques also deep learning techniques have been developed. Also in multi-class classification of cancer challenge, several research found that machine learning techniques performed more predictably. The techniques utilized for feature (gene) selection, however, vary amongst these investigations. In the feature selection among microarray and the RNASeq data, specifically utilized differential expression analysis and the least-redundancy and the maximum-relevancy technique used RNASeq data to apply a algorithm of group genetic for feature selection in 5 distinct malignancies.

The uninformative genes were eliminated by using support vector machines (SVM) and a recursive feature technique of elimination. These studies mainly focused on using machine learning techniques to solve a multi-class classification problem. According to reports, several methods created through various authors for cancer classification of multi-class perform more predictably than those currently in use given a brand-new ensemble classifier for the categorization of over 31 distinct cancer tumors obtained from the TCGA repository, named the predictor of cancer utilizing an ensemble model (CPEM). They also evaluated other input properties, including mutation spectra, profiles, rates, and signatures. Then, they looked into several machine learning and the feature selection models in order to identify the top model, it got used 10 folds of cross-validation and achieved an accuracy of 84%. Additionally, they took use of the six most prevalent malignancies out of the 31 kinds, and model's accuracy of classification was 94%. Certain statistical techniques produced outcomes that surpassed those of machine learning algorithms.

Researchers, medical professionals, and haematologists have long had difficulty making an early diagnosis of leukemia. Leukemia symptoms include swelling of the lymph nodes, pallor, fever, and weight loss, however they can also be present in other illnesses. Early leukemia diagnosis is challenging because the symptoms are usually minor. The most popular method for diagnosing leukemia is microscopic examination of PBS; however, only bone marrow samples should be collected and examined.

Several research have used machine learning (ML) and the computer-aided diagnostic techniques for image analysis in laboratory over the past 20 years in an effort to get beyond the drawbacks of a late leukemia diagnosis and identify their short groups. For the purpose of diagnosing, distinguishing, and number of the cells in various forms of leukemia, blood smear pictures have been studied in these investigations.

ML is known subfield of the artificial intelligence which uses mathematics based relationships and algorithms, also was swiftly applied to the field of clinical research. Without explicit experience, ML makes it possible to programme computers, and they learn from their experience. These techniques have produced incredible results when processing medical data, and they have had outstanding performance when diagnosing diseases. According to research, by extracting and subsequently assessing the

properties of these images, ML approaches impressively help complex clinical dynamic cycles in clinical picture handling. More sophisticated data processing techniques were desperately needed as medical diagnosis tools proliferated and a vast amount of top-quality info was generated. Traditional approaches were unable to evaluate or discover patterns in such a massive number of data.

Objectives of Study

For the photos of all leukemia, the suggested aggregated model, which is depend over deep learning based architectures, performs best in perspectives of the accuracy, recall., and precision As far as we are aware, the very first investigation into the application of the aggregated modelling relied on the fine-tuned deep learning algorithms for classification of ALL leukemia images got processed to the ISBI 2020 challenge the dataset.

We painstakingly analyzed the effect of calibrating the different models with different settings of analyzers and picture standardization to give a more discriminative portrayal to improve expectation execution. With these modifications, our suggested model outperformed other cutting-edge deep learning-based architectures and machine learning models independently in ALL classification accuracy.

Survey of Literature

The IoMT research community has carried out a number of studies regarding computer-aided diagnosis (CAD) of leukemia. Researches shows various machine learning and deep learning strategies for leukemia detection. With 94.4% accuracy, Random Forest is used in to classify and identify cancer of WBC and certain of its various other types. In with an accuracy of 92.9%, the suggested model identified ALL using KNN and Naive Bayes Classifier. On 60 sample photos, the classifier is put to the test. For the classification of leukemia cells, a novel Principal Component Analysis (PCA) based on the ABC-BPNN method is proposed in and achieved an average accuracy of 98.73% while taking less computation time. The ALL is recognised in. First, BSA-based clustering is used to segment images of leukemia..

The ALL-IDB collection of is set to predict ALL in K-medoids are show with 97.50% accuracy in the DOST, PCA, and LDA are suggested in accuracy rate of 99.67%. Jinvestigates a strategy based on generative adversarial optimization (GAO), which has an accuracy rate of 93.87%. presents a 97.08% accurate Genetic Algorithm (GA) and Artificial Neural Network (ANN). Chronological Sine Cosine Algorithm (SCA) was test and demonstrated accuracy of 98.60%. uses the ALL-IDB1 dataset and the ASH image repository to categories lymphoblast cells. Convnet is examined, and 81.74% accuracy was attained. The data which is heterogeneous datasets ALL-IDB1 and ALL-IDB2 are used in. Utilizing a pre-trained model of CNN with the SVM, it obtained 98% accuracy, leukemia (whether pathological or non-pathological) is diagnosed with high precision. In, CNN is used to diagnose leukemia (normal vs. abnormal) using the ALL-IDB1 dataset, with an accuracy rate of 96.50%.

The ALL detection in uses the ALL-IDB1 and ALL-IDB2 datasets. SVM, the algorithm in use, achieved 89.82% accuracy. The ALL-IDB2 dataset is utilised in to identify ALL, and a customised KNN with 96.26% accuracy is the approach under investigation. In, using the ALL-IDB1 dataset, ALL is categorised using SVM with a 95.00% accuracy rate based on cell energy features. Using the ASH image bank dataset, the authors of first identify FAB ALL subtypes with 97.2% accuracy using GA and the multilayer perceptron kernel (MLP) function. Second, FAB AML subtypes are identified with 98.6% accuracy utilizing heredity based mechanism and a Gaussian radial basis kernel function. Finally, a GA with a Gaussian Radial Basis kernel is used to identify healthy, ALL, and AML with an accuracy of 99.40%.

The literature demonstrates that practically all earlier approaches classified leukemia according to healthy, AML, or ALL kinds. These methods, however, did not deal with the issue of correctly classifying leukemia in terms of all of its subtypes, including ALL, AML, CLL, and CML. In order to classify leukemia in terms of all of its forms, deep CNN-based techniques are described in this paper.

Setup of Experiment

The setup of experimental for carrying out the study is described in this section. After describing dataset retrieval and data augmentation, the deep learning models that were utilised to categorise the various kinds of leukemia are next elaborated.

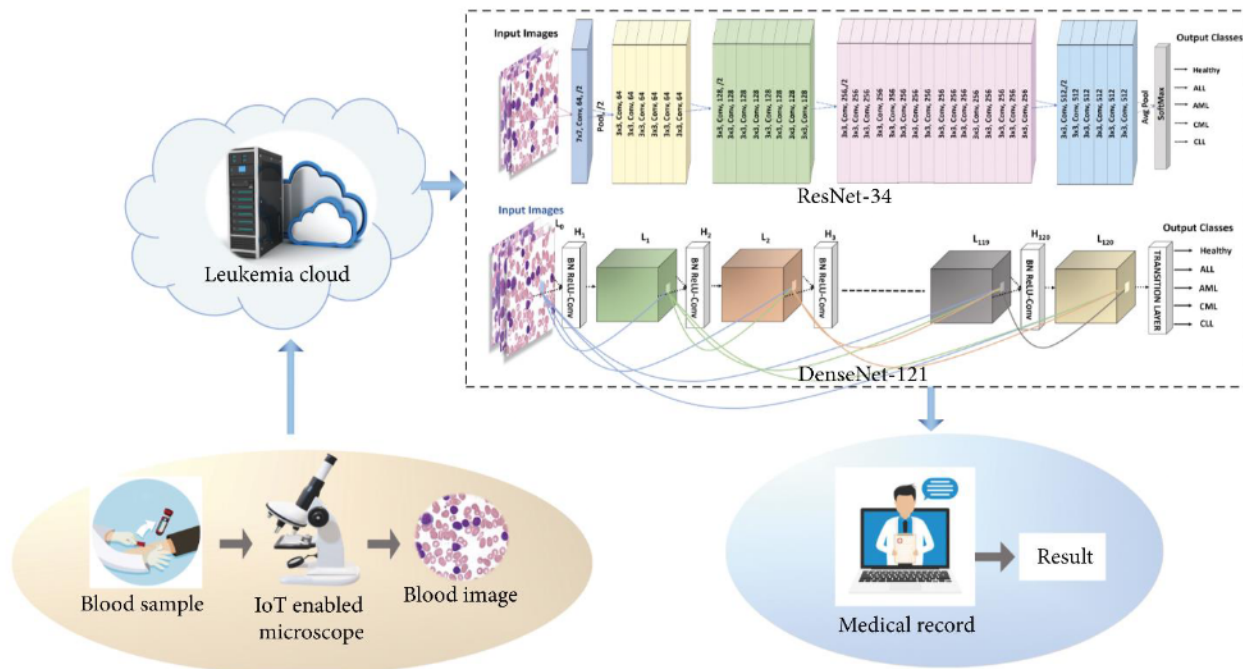


Figure 1: Setup of experiment

Dataset Description

The ASH bank of image and ALL-IDB are the two sources from which the dataset is compiled. The ASH bank of image is freely available online and offers a comprehensive collection of photographs on a range of haematological subjects. All available annotated cell photos of blood leukemia, including any one of the four subtypes, were chosen for this article.

The ALL-IDB dataset offers blood cell micrographs with annotations that were created for segmentation, assessment, and classification. Only healthy and ALL forms of leukemia samples are included in the ALL-IDB. The ALL-IDB dataset lacks the remaining leukemia subtypes specified. Because knowledgeable oncologists assigned the ALL categorization to each image in the dataset, the ALL-IDB is regarded as being more trustworthy. Figure displays a few examples of photos from datasets.

Models of Deep Learning

The dataset is enhanced before being sent to CNNs, the deep learning models. In this study, CNNs are used in place of standard machine learning methods, which require time and effort to learn and come with hand-crafted features. CNNs have the capacity to automatically learn from unprocessed data. Convolutional and pooling layers come first in a typical CNN, which ends with a fully connected layer. Convolutional, pooling, and dense layers can be added to a CNN to produce new models. New light CNN models like VggNet and AlexNet have been developed by layering CNN architectures. The next level CNN models, including ResNet and DenseNet, these are intricate and capable of learning better, as explained in the result section. In order to identify and classify leukemia according to its types, ResNet-34 and DenseNet-121 type of modelling is utilised in the work that is being presented. The following subsections provide a description of each model's specifics.

DenseNet-121 Model

On the CIFAR-10 and ImageNet datasets, dense convolutional networks, or the DenseNet, produced the top classification outcomes. Dense connectivity are employed in the DenseNet architecture, like ResNet architecture. In DenseNet-121, there are 121 layers. Each layer in the DenseNet design is connected to every layer below it. As a result, each layer of the network receives significant features that were learned by any earlier layers, which improves the effectiveness of network training [55]. In comparison to ResNet, the DenseNet architecture trains the network with fewer parameters. Small datasets cause the model

to be overfit, however the thick connection fixes this issue. A dense block, a key component of DenseNet, is used to improve flow of information in between layers. It is made up of 33 conv, BN, and ReLU. The specific formula is given in for the dense block.

$$L_l = H_l([L_0 L_1 \dots L_{l-1}])$$

The implementation of the models is made easier by the use of open source fastai and the deep learning package in Python for both pre-trained models.

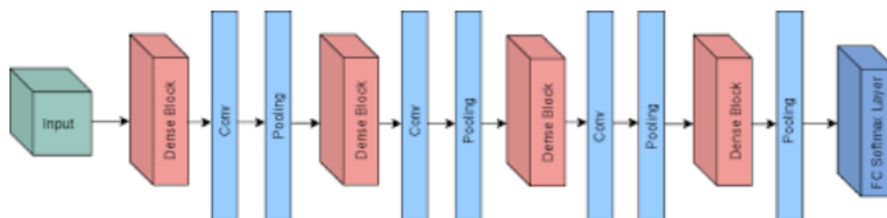


Figure 2: Structure of DenseNet-121

ResNet-34 Model

The 34-layered pre-trained model is called ResNet-34. Deep neural networks' effectiveness is affected by the framework and the dataset. Better performance is produced by the deep network of the CNNs and a huge dataset. The network is drilled deeper, performance starts to suffer. The diminishing gradient is the root cause of this issue. By bypassing some levels, the ResNet is able to fix this issue when gradients advance from the initial layers to the final ones. The ResNet model's layers can be calculated mathematically using

$$y = f(x) + i d(x) = f(x) + x$$

The gradient can simply flow by omitting the connections between layers, which speeds up layer training. A total of 34 layers make up ResNet-34, including one convolutional and the pooling layer also four additional layers that use identical pattern. Every layer is convolved with three-way convolution using a feature map with the corresponding sizes of 64, 128, 256, and 512.

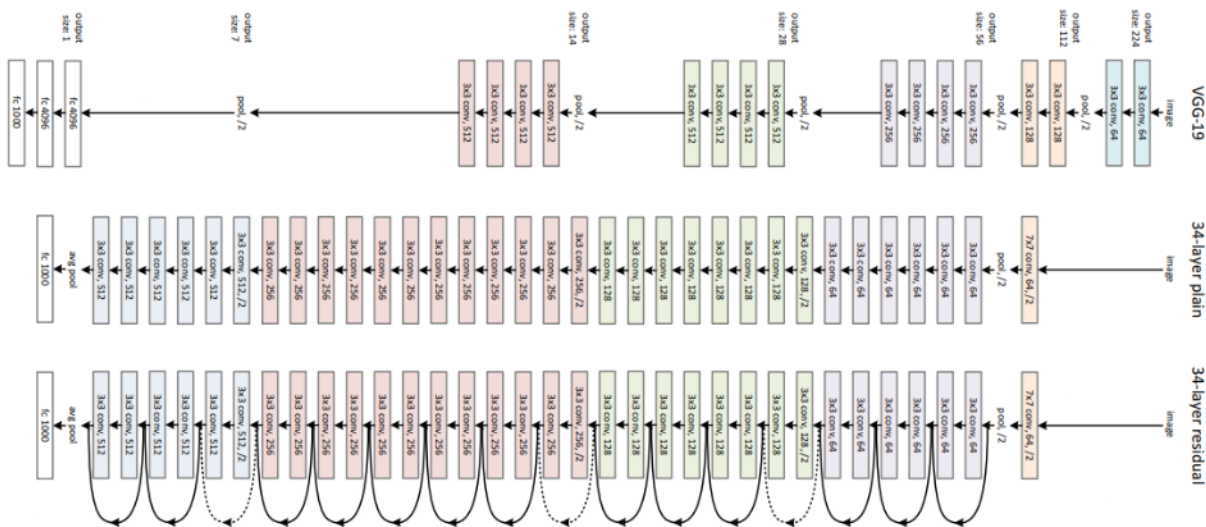


Figure 3: Architecture of Resnet-34

Results

Recall, Precision, F1 score, and the accuracy are utilized as performance indicators to assess the proposed models. The Table provides a description of mathematical equation of every parameters. Here, the terms true positive rate are (TP) and the false positive rate is shown as (FP) refer to positive classes that have been determined to be positive, false positive rate represented as (FP) and true negative rate (TN) to negative classes that have been determined to be negative, and false negative rate (FN) to positive classes determined to be negative . Recall, on the other hand, measures how well a leukemia subtype class is predicted. For the known leukemia and non-leukemia subtype gatherings, precision is the expectation. F1 score is the consonant mean of review and accuracy, where accuracy is the proportion of accurately anticipated positive leukemia subtype classes to projected positive leukemia subtype classes.

Type of Measure The Derivations

$$\text{Accuracy ACC} = \frac{(TP + TN)}{(P + N)}$$

$$\text{Precision PPV} = \frac{TP}{(TP + FP)}$$

$$\text{Recall TPR} = \frac{TP}{(TP + FN)}$$

$$\text{F1 score and F1} = \frac{2TP}{(2TP + FP + FN)}$$

Various parameters, including the precision and recall along with F1 score, and accuracy, are utilized to demonstrate the effectiveness of the procedures used.

Classification of leukemia subtypes utilizing ResNet-34 and DenseNet-121, continuously, is represented by the confusion matrix. Figures and 5 clearly show how well the presented models predicate.

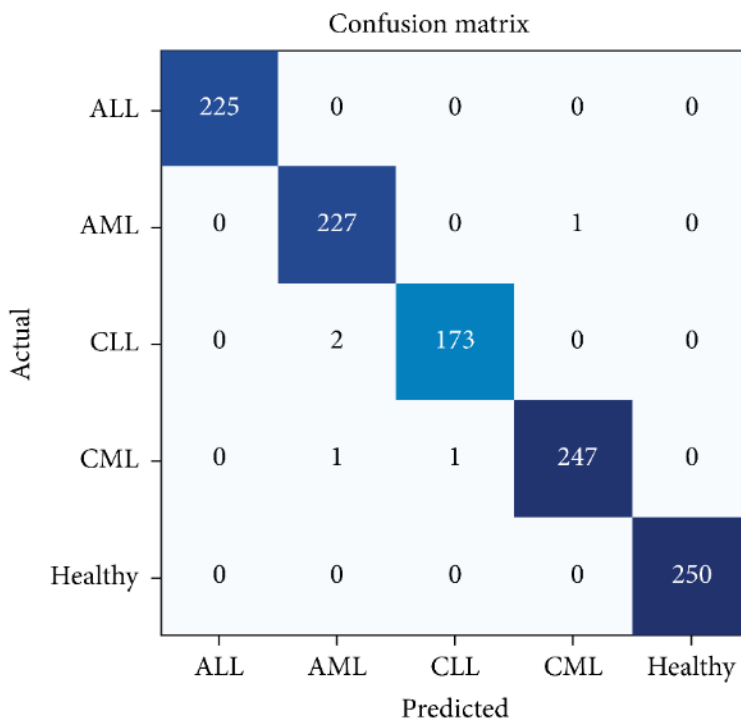


Figure 4: Resnet-34 Confusion Matrix

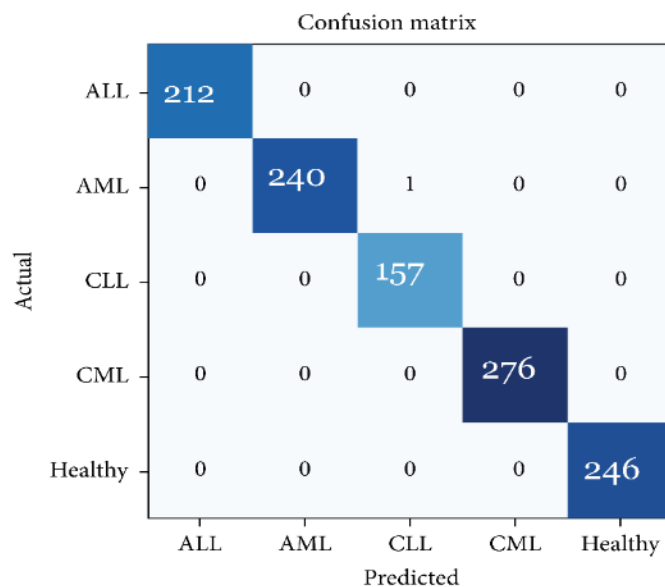


Figure 5: Matrix of DeneNet-12

For ALL and healthy cases, ResNet-34 and the DenseNet-121's prediction of accuracy is 100%, and their precision and recall also F1 score are also 100%, or 1.0. ResNet-34's AML prediction accuracy is 99.66%; its precision at 1.0%; its recall is the 0.99%; and its F1 score is also 0.98%. ResNet-34 has a 99.74% precision and recall also F1 score for the CLL. Precision, recall, and F1 score are all 0.99%, though. ResNet-34 predicts CML with an accuracy of 99.73%, precision of 0.99%, recall of 1.0%, and F1 score of 0.98%; DenseNet-121 predicts AML with an accuracy of 99.92%. Precision, recall, and F1 score are all 1.0%, though. DenseNet-121's prediction accuracy for CLL is 99.92%; its precision is 1.0%; its recall is 0.98%; and its F1 score is 1.0%. The DenseNet-121 F1 score, recall, precision, and accuracy for CML predictions are all 100%.

Discussion

When it comes to smear preparation, a number of variables (such as lighting conditions, staining times, blood film thickness, and film flaws) might result in unfavourable visual artefacts or various colour distributions in the lab photographs. These problems make it more difficult to detect and monitor blood stains precisely. Preprocessing is required since it is difficult for ML to process these smear images. Data pretreatment (such as preparation, normalisation, and segmentation) might increase the accuracy of leukemia detection when employing ML algorithms. A collection of preprocessing strategies should be used to prepare datasets for accurate leukemia identification with the least amount of error using ML methods.

The fundamental step in processing blood smears using ML techniques is choosing effective features. The key issue was choosing these qualities to identify leukemia in circumstances in that the various researcher has hold over the selections and the analysis of the blood cell properties. As characteristics of blast cells, some research have employed colour and shape, where the others has used texture and various metrics of texture. The manual selection of the most crucial elements is always seen as a difficult task because it always involves some degree of mistake. None of these manually chosen features has ever been referenced in medical texts as the only way to diagnose leukemia. As a result, selecting a few key features from a big pool of features is entirely an algorithmic process, and the algorithm's approach will determine how effective the process is. The research showed that approaches that extracted fewer cell characteristics had a lesser degree of precision for diagnosing leukemia.

Conclusion & Future Scope

The diagnosis of many blood-related disorders depends heavily on the image analysis of blood smears. Early detection of leukemia and the first smear results can result in an accurate diagnosis and prompt treatment. In order to diagnose early-onset

leukemia and identify subtypes with the least amount of error and the quickest turnaround possible, blood smear image analysis using machine learning techniques could be used. The utilization of novel ML calculations, especially DL, in CAD frameworks, entire slide imaging (WSI), and even applications and programming at hematology labs to help pathologists and oncologists in better identifying leukemia can be an expected future course for research.

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