

An Analysis of Classification Techniques for Leukemia Detection

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Abstract

Leukemia is a popular Blood cancer form that begins in the bone marrow. It can be treated early enough to stop the disease from progressing. The approach of detecting leukemia using blood microscopic images is described in this research. The classification of blood cells is critical for assessing and diagnosing illnesses. Diseases involving blood can only be classified in medical diagnosis systems once blood cells have been classified. In this paper the efficiency of image processing is utilized with effective classification techniques to identify leukemia. Previous classification techniques used for Leukemia detection are discussed in detail in the paper. Different tests which measure the cell counts of blood, its features and possible extraction of disease are well explained to provide detailed information about the scenario.

Keywords: Leukemia, Feature Extraction, Classification.

I. Introduction

In the past, the combined deep learning approaches blended with image processing techniques were utilized to predict many different forms of tumors. It is incredibly difficult to detect cancer at an early stage. When it comes to cancer analysis, the results are inconclusive [52]. Blood Cancer like Leukemia starts in the bone marrow and ultimately spreads throughout the body. It can produce an increase in the production of white blood cells, which causes the blood stream to swell. Chronic Myelogenous Leukemia (CML) is diagnosed

with a full blood count, bone marrow biopsy, and cytogenetic test.

1.1 Complete Blood Count (CBC):

Complete Blood Count (CBC) is a type of blood test that measures the various components in the stream of blood. These include the number of red blood cells, the hemoglobin count, and the Hematocrit.

1.2 White Blood Cells (WBC) Count:

White Blood Cells are not actually infections. They are the components of the blood that break down foreign matter in the blood. In some cases, they can cause illness or even death.

1.3 The count of Red Blood Cell (RBC) :

The total number of RBCs is the amount of blood that is missing from the blood. Depending on the findings of a blood test, it can be reduced or increased.

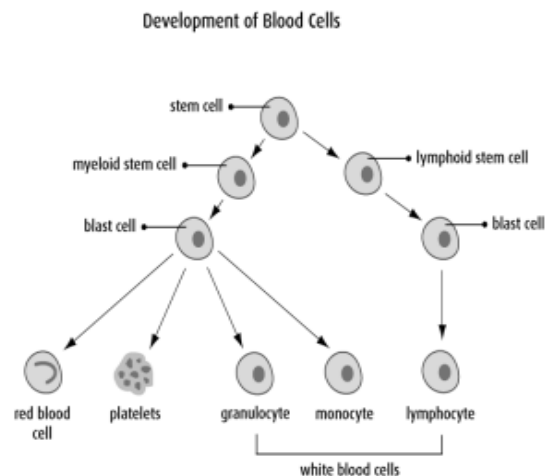


Fig 1: Formation of leukemia Blood Cells

1.4 Hemoglobin:

Hemoglobin is the type of protein found in RBC that circulates oxygen to various parts of the body. Patients with leukemia frequently don't have it.

1.5 Platelet Count:

There is a gross count of platelets discovered in blood platelets that are used to help clot blood when the skin is scraped or opened to the outside.

1.6 Hematocrit:

This metric assesses how much space the various components of red blood cells take up. It displays the proportion of total red blood cells in the mass range.

The objective of this work is to categorize the immediate characteristics of leukemia depending on its type and various classification techniques. The study's major goal is to classify cancer cell types based on their characteristics.

2. Related Work

R. B. Hegde et al. [4] proposed an image processing strategy for detecting leukocytes in peripheral blood smears that improved accuracy. Computer Aided Acute Lymphoblastic Leukemia (CAALL) detection method based on image analysis was discussed by A. M., Sahlol, A. T., Elhoseny, M., and Hassanien, A. E., et al [18]. D. Minnie and S. Srinivasan proposed to use modified K-Means Algorithms and formulation of Association Rules to cluster the Preprocessed Automated Blood Cell (ABC) Counter Data [22]. P. Aiswariya, S. Manimekalai, et al. [51] describe a leukaemia segmentation methodology for successfully evaluating blood cells. The proposed GLEHE entails a two-stage approach that includes entropy estimation and histogram equalization. Classification System based on texture on Transrectal Ultrasound Image for Prostatic Cancer Identification was proposed by Xiaofu Huang, Ming Chen, Peizhong Liu, Yongzhao Du, et al., and accuracy was achieved (89.5 %) [2].

Local binary decoration for automatic identification of Acute Lymphoblastic Leukemia (ALL) was proposed by Singhal, V., and Singh, P., et al [31]. M. Durairaj, R. Deepika, and others [29] suggested a survey on the use of datamining to predict acute myeloid leukemia malignancy. Automated detection of acute lymphocytic leukemia utilizing blast cell morphological traits was explored by S. Mohapatra, S. Hariprasath, T.

Mohammad, and others [34]. An extensive study on Feature Extraction for Leukemia Detection in Blood Microscopic Imageries was proposed by P. Aiswariya, S. Manimekalai, and others [50]. These include extraction methods for leukemia categorization procedures that are relevant to the analysis of benefits and drawbacks.

3. Classification

The selection of the appropriate technique for classification is a challenging task. This procedure should be done carefully to improve the accuracy of the results.

3.1 Classification using Machine Learning Classifiers

A segmentation technique is used to identify leukemia. In this procedure, Otsu's thresholding and morphological operators were utilized to segment the image of the blood cell. Despite the fact that this technique incorporated leukemia categorization strategies, classification was done using ML classifiers, Deep learning classifiers and Ensemble classifiers. In order to shorten training time, it was important to improve the accuracy of multiple independent training data sets for the categorization of leukemia. A classification scheme for recognizing leukemic cells was devised by F. Soni et al. [48]. ALL-L1, L2, and L3 leukemia cells were separated into three groups using this method. In terms of detecting and classifying leukemia cells, this method was more reliable. This technique, however, does not include the GLCM characteristics or Haralick for categorization.

Faisal Asadi et al. [3] explored Acute leukemia categorization using LVQ with blood cell imagery extraction utilizing blood smear pictures. This approach was used to detect acute lymphoblastic leukemia by morphologically distinguishing lymphocytic cells. Although this method was quite accurate in discriminating between blast and ordinary lymphocytic cells, it was unable to maintain the accurateness range when categorizing photos in a large dataset. S. Shafique et al. [5] used image processing to develop an approach for diagnosing. The Acute Lymphoblastic Leukemia (ALL) was processed with microscopic blood images for detection. This process was used to segregate the lymphocytes that had been clustered using the Watershed Segmentation (WS) algorithm, and the lymphocytic cells were classified as normal or blast cells using the SVM classifier. Overall, this method demonstrated a good level

of accuracy. This method, however, was unable to distinguish the image's numerous visual features.

Asadi et al. [17] developed a system in which the blood cells abstraction images and back propagation neural network technique for categorizing acute leukemia. The properties of blood cells were extracted using a back propagation neural network technique. Digital image processing techniques were used to identify the leukemia. When it comes to classifying acute leukemia, however, this approach had a lower accuracy rate. The possible Forecast of cranial dealing in pediatric for ALL patients using machine learning is presented by Amirash Kashef learning et al. [10]. To classify acute leukemia cells, this method determined the features of white blood cells. Because it was more reliable, efficient, and time-consuming, this method produced more accurate classification results. This method, on the other hand, was more prone to errors.

Sarnmad Shafiq et al. [11] discussed computer based acute lymphoblastic leukemia detection and diagnosis for ALL classification. The feature matrix was created in this way by using 2D-DWT to separate the cytoplasm and nucleus regions. The Bhattacharyya distance and PCA were used to select uncorrelated and important characteristics. A back propagation neural network was used to classify the lymphocyte cells. Although this method was more accurate, the combination of features took a long time to categorize. Singhal, V. et al. [21] devised a method for detecting lymphocytes from blood sample images automatically. For classification, the geometric features and the Local Binary Pattern (LBP) features were taken out from the images of the collected blood samples. The SVM classifier for lymphocyte cell categorization was trained using the gathered features. This system delivered higher accuracy during the classification process. The texture variants, on the other hand, were not provided in this way.

Subrajeet Mohapatra, S. et al. [45] developed a lymphocytic cell categorization method based on a blood image. The anomalies in the border nucleus were mainly identified with the effective utilization of hausdorff dimension and contour signature characteristics. The qualities of the image, such as pigment, form, and texture, were retrieved to its most. The initial segmentation of WBC from other blood components was performed using Kmeans clustering. The roughness at the periphery of the lymphocytic cell nucleus was quantified using the hausdorff dimension for classification. A. M., Sahlol et al. [18] developed a computer-aided acute lymphoblastic

leukemia detection system based on image processing from blood smear pictures. Contour signature and hausdorff dimension were used to measure border anomalies on the nucleus. Color, shape, and texture were all taken into account while categorizing the items. The SVM classifier was used to categorize the image. The method's main problem was that it couldn't tell the difference between lymphoblast cell subtypes. Bhattacharjee, R. et al. [39] devised an ALL classification and segmentation approach based on a blood smear picture. The data was segmented based on the Watershed Transform (WT), and classification models were used to diagnose ALL in this technique. This approach altered the visual contrast both manually and automatically. This method, however, took a lengthy time to compute.

Min Zhou et al. [7] developed a method for detecting leukemia. Utilizing the process, the texture characteristics and form features with contour signature were extracted from the image. Using Otsu's method, the image was segmented automatically. This method identified leukemia faster and evaluated both malignant and benign cells. This approach, which was self-determining of the stains in the smear image of the blood, was used to segment the overlapping cells. This method, however, took a lengthy time to compute.

Computer Aided Diagnostic (CAD) system was formulated by Rawat, J. et al. [40]. It was formulated on the form of Gray level co-occurrence matrices (GLCM). The cancer identification is challenging process as the overall procedure needs to be carefully scrutinized in a unplanned area, where Computer Assisted Diagnosis can be of great utilisation. Segmenting the cancer cell precisely is an important operation in a computer-assisted diagnostic method aimed at earlier diagnosis of cervical cancer [53]. The existence of leukemic cells was detected by classifying the obtained features with an auto Support Vector Machine (SVM) type of binary classifier. The position of nucleus shape in the identification of ALL was demonstrated using this method. This method, on the other hand, has a high computational complexity.

3.2 Classification using Ensemble Classifiers

In MM Amin's work, the lymphocyte image was divided into cytoplasm and individual nucleus areas using K means clustering. The texture and form of the lymphocyte samples were used to determine whether they were cancerous or healthy. On the other hand, the classifier was slower to compute and failed to contain ALL of the sub categorization kinds [36]. Moshavash,

Z. et al.[6] developed the approach of segmentation for identifying Acute Leukemia from the microscopic images of the blood. Color pattern, form, LBP-based texture, and features based on hematologist criteria of visualization were extracted for leukocyte recognition from a photo. While more accurate, our approach lacked robustness when it comes to recognizing leukocytes in images with touching cells and excessive staining.

Using a machine learning technique, Keyvan karami et al. [8] suggested survival predictive variables in patients with acute myeloid leukemia. A method for classifying leukemia that is automated. This method examined the textural, morphological, and color features of blood microscopic pictures for the detection and classification of leukemia. This approach took longer to classify leukemia, although being more accurate in terms of malignancy classification and white blood cell detection.

3.3 Deep Learning System of Classification

Marzahl, C. et al. [15] used the deep learning system which was based on attention and also on advanced augmentation techniques. It was utilized to classify leukemic b-lymphoblast cells from the blood smear microscopic pictures. WBC categorization and localization were replicated using a deep network. The WBC majority portions in the snap were identified with the help of the average pooling layers. This method correctly identified ALL in a blood smear image, but it did not reliably identify all lymphocytes in a whole slide image.

Rehman, A. et al. [47] developed a deep learning and image processing system to classify ALL. The discussed model was trained by the efficient utilization of the max-pooling and the extensive convolution layers. To classify the image, the SoftMax, completely connected layer, and classification layer were employed. This method resulted in a quick processing time and great accuracy. The overlapping cells, on the other hand, were not segmented using this procedure.

3.4 Other type of Classifier

Joshi, M.D., et al. [28] developed an ALL identification process was mainly focused on medical imaging. This method used an image quality development and arithmetic development, as well as the Otsu threshold the targeted blood cell segmentation method, to segment blood cells.

The KNN classifier was used to separate the blast cells from the normal cells. Although the detection accuracy was great, it lacked resilience when it came to contacting cells and excessive staining in the images. Using a dual-threshold method, Li, Y. et al.[9] developed a method to efficiently segment the white blood cell. The HSV and RGB color spaces were combined in the dual-threshold approach. Preprocessing, threshold segmentation, and postprocessing were the three aspects of this approach. The image was preprocessed to produce the H-component image and also the contrast stretched gray scale resultant image. The dual threshold approach was used to segment the data, and the golden section search was used to find the best thresholds. Using median filtering and mathematical morphological techniques, the incomplete WBCs were eliminated in the post-processing stage. This approach had a high level of segmentation accuracy.

Feedforward is the neural network and also one of the first and most prominent algorithms for learning. They are often referred to as deep networks or multi-layer preceptor networks. Each layer in the network processes an aspect of the data, and it selects entities that appear in the background. The feedforward layer is composed of the neurons that receive the inputs. It is typically equal to the number of neurons in the dataset. There are many hidden layers within the output and input layers. These layers contain a large number of neurons and are used to transform the inputs before they are processed. Neuron weights are often used to describe the strength or amplitude of an independent connection between two neurons. They can also be used to compare weights on inputs. Random Variable and the edges are probabilistically dependent on it.

4. Methodology

4.1 Learning Vector Quantization (LVQ):

LVQ is a pattern recognition classification algorithm that uses a competitive layer, where each output unit denotes a distinct class or category. The output unit is changed during data training (by supervised training, altering the weight value), to calculate the Bayes classifier theory's decision surface. It is expected that a set of training patterns is available as well as an initial distribution of reference vectors (each one unique). The LVQ is neural network architecture and it is similar to the self-organizing mapping (SOM) architecture in that it lacks a topological structure and each output unit is aware

of the class it represents. This learning vector quantization neural network architecture is illustrated in Figure 2.

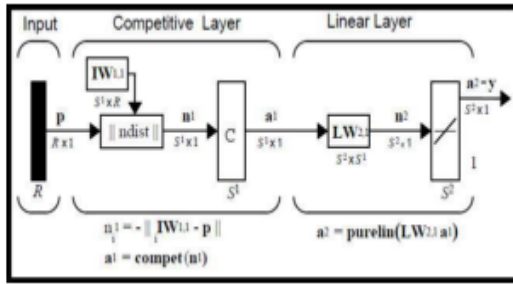


Fig 2: Learning Vector Quantization Neural Network Architecture

4.2 Support Vector Machine (SVM):

For the classification step, we utilized the SVM classifier, which is a well known Supervised learning technique. It's especially useful for binary classification, which is why we used it when we had to distinguish between two classes. The two classes were namely normal and blast. We provided the SVM with our extracted feature vector, and it separated the cells into normal and blast categories based on their characteristics. To achieve maximum accuracy in high-dimensional domains, SVM is combined with a linear kernel. When the set of characteristics is huge, other kernels might not be able to cope up to map the results quickly enough. The linear kernel is more exact and faster, and it's used to generate somewhat distinct decision bounds. On the supplied feature vector, it can be shown that SVM performs effectively for detecting ALL. The SVM classifier is shown in Figure 3.

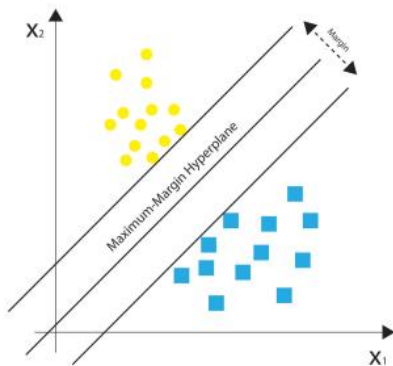


Fig 3: SVM Classifier

4.3 Ensemble Method:

Whenever there are a plenty of feature differences amongst the models, ensembles work to produce better outcomes. As a result, several ensemble approaches aim to create variations in the different models which were blended. More random algorithms (like random decision trees) can yield a stronger ensemble than extremely purposeful algorithms, which may seem counterintuitive (like entropy-reducing decision trees). However, it has been proven that utilizing a range of strong learning algorithms is more beneficial than using strategies that aim to dumb down models in order to foster diversity.

4.4 K Nearest Neighbor (KNN):

KNN is a classification technique that uses the distance between an object and its neighbors to determine its categorization. Its goal is to assign a classification to the new item based on its attributes. Furthermore, in KNN, the K samples of training data represent a number of nearest neighbors that are included in the voting process contribution. The value of K is determined by the situation in which it is used. The time and storage expenses increase as the number K grows larger. However, if it is little, due to the lack of information, the nearby meter will be exceedingly small. It's critical to identify the best value of K, which necessitates a trial-and-error procedure.

The existence of irrelevant features has a significant impact on the accurateness of the KNN algorithm. It is also influenced by the feature's weight, which is not the same as its categorization importance. This algorithm saves the training data's features and class vectors during the training phase. The features are derived for the testing data throughout the testing phase. When fresh data is entered, it is difficult to classify it. The distance between the new one and all of the learning data vectors is calculated, and the number of K closest to it is chosen. Most classifications of these points are expected to include the new points.

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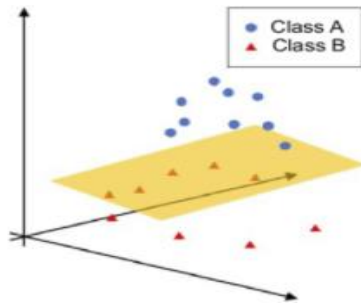


Fig 4: KNN Classifier

5. Analysis and Discussion

The Leukemia Classification and categorization is a research for long duration worldwide. Several researches have been done and many are still ongoing. Here we discuss several researches based on their accuracy and work statistics. This section also includes the evaluation and discussion of Leukemia categorization methods based on the performance metrics, accuracy range, and publication year.

5.1 Leukaemia Classification and Investigation

The numerous leukemia classification systems depending on the year of publication are described in this section. A total of 44 papers are considered in this study for the investigation of leukemia classification methods. According to the findings, the majority of research papers on the classification of Leukemia were published in 2018. The examination of Leukemia classification techniques depending on the year of publication is depicted in Figure 5.

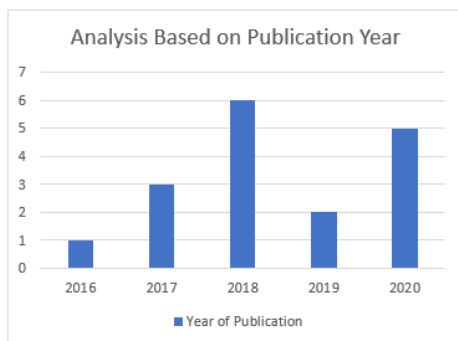


Fig 5: Analysis based on publication Year

5.2 Accuracy Based Analysis

The accuracy range study of leukemia classifying systems is described in this section. The analysis of the leukemia classification is shown in Table 1. Approaches based on the range of accuracy According to the findings, the accuracy range for most of the leukemia classification techniques is between 91% and 94%.

Accurateness %	Techniques	Research Papers
70%-80%	Learning Vector Quantization (LVQ)	[3]
82%-87%	CNN, GBT	[7], [8]
88%-90%	KNN	[19]
91%-93.7%	SVM	[11]
94.2%-95%	ENSEMBLE METHOD	[12]

Table 1: Analysis of leukemia classification based on accuracy range

6. Conclusion

Different algorithms are used to detect leukemia at an earlier stage. This paper shows how these algorithms can be used to improve the accuracy of the results. Support Vector Machine is mostly used for classification and Otsu's thresholding algorithm is mostly used for segmentation. Some of the discussed methods give good accuracy for detecting leukemia. While comparing these techniques ensemble method gives more accuracy in future work. It is also easy to implement for practical implementations and real-time usage.

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