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ANALYSIS OF ACUTE LYMPHOBLASTIC LEUKEMIA CLASSIFICATION WITH MACHINE AND DEEP LEARNING TECHNIQUES

B. REVATHI[1], M. KALIAPPAN[2], E. MARIAPPAN[3], S.K. KEZIAL ELIZABETH[4]
[1]Assistant Professor, Ramco Institute of Technology, Department of Artificial Intelligence and Data Science, India.
[2]Professor, Ramco Institute of Technology, Department of Artificial Intelligence and Data Science, India.
[3]Associate Professor, Ramco Institute of Technology, Department of Artificial Intelligence and Data Science, India.
[4]Assistant Professor, Mangayarkarasi College of Engineering, Department of Computer Science and Engineering, India.
E-mail: [1]revas85@gmail.com, [2]kalsrajan@yahoo.co.in, [3]mapcse.e81@gmail.com, [4]kezialcse@gmail.com

ABSTRACT

Leukemia is a term for a cancerous condition that affects the organs that produce blood. The inordinate batch of crude white blood cells (WBS) in the bone marrow is the cause of leukemia, a fatal disease. There is a greater possibility of recovery if leukemia is discovered early. In the treatment of leukemia, Deep Learning and Machine Learning algorithms are commonly employed, especially in detecting whether leukemia is progressing in patients. Conventional machine learning and deep learning approaches are practical guides in computer vision that improve the speed and accuracy of identifying and categorizing images (medical), including minuscule blood cells. This survey offers a thorough examination of the recognition and assortment of WBCs and acute leukemia in microscopic blood cells. In this survey, various directions of classification of Acute Lymphoblastic Leukemia (ALL), including the following steps in the methods: Data enhancement, preprocessing, segmentation, extracting features, selecting features(reduction), and classification, with an emphasis on the classification stage. The models using these classifiers have higher performance metrics when compared to the other model. Our suggestion is to offer for identifying and categorizing acute leukemia.

Keywords: *Leukemia, Classification, Medical Imaging, Cancer, Performance Metrics*

1. INTRODUCTION

The condition known as cancer is incredibly diverse. White blood cells and other cell types can develop cancer, which is known as leukemia. Leukemia diagnosis is difficult in several fields, including hematology. The area under artificial intelligence that deals with machine learning (ML) [19]. One kind of blood cancer that causes leukemia is one that causes the body to produce more white blood cells (WBCs). These aberrant blood cells have strike on the bone marrow and blood, which weakens the immune system. They may also reduce the ability of bone marrow to make blood cells, such as platelets.

These WBCs that are Cancerous cells have the ability to enter the bloodstream. and injure various bodily systems, including the brain, liver, kidney, spleen, and so on. This damage can then result in the development of additional deadly cancer types. Unusual WBCs are individuals who have not reached their full potential and function inadequately inside the immune system. Blood cancer, also known as leukemia, is brought on by the lymphatic system and spinal cord producing aberrant white blood cells out of control [2].

2. TYPES OF ACUTE LYMPHOBLASTIC LEUKEMIA

Consequently, four subgroups of leukemia. Different methods have been devised to distinguish leukemia according to its subgroups. They are L1, L2 and L3. L1 type cells often have a modest size, a comparable shape, a little cytoplasm. They have a well-organized, discoid core. Collate to L1 type cells [1], L2 type cells are larger and exhibit from variety. They have irregular nuclei with differences in their cytoplasm. L3 type cells have an oval or round nucleus and have the same size and shape. They have a good number of vacuoles-containing cytoplasm. Frequently, they are bigger than L1. Deep Learning algorithms can summarize from images to understand how to carry out necessary tasks. The main goal of this study is to improve several deep learning, Machine learning techniques. Both experience and explanation-based learning are possible in deep learning [22].

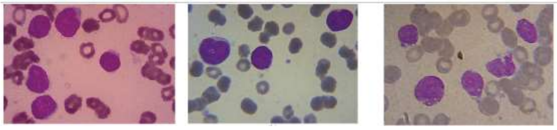

Figure 1: ALL Subtypes

The above figure 1 represents the Multi-cell blood microscopic images of the ALL subtype show the following morphology: (a) L1 (b) L2 and (c) L3. Curious white blood cells functions poorly as a component by abnormal white blood cells developing uncontrollably in the spinal cord and lymphatic system referred to as blood cancer.

Both adults and children are susceptible to leukemia. Leukemia often presents with symptoms that are similar to other diseases, making diagnosis challenging. Early examination and detection are therefore necessary in order to provide leukemia patients with the proper care and lower their chance of dying [5]. An overview of the various deep learning neural networks used to treat acute lymphoblastic leukemia is given in this section. Normally the images can be getting from the dataset, after that it will be segmented. The Segmentation can be done by segmentation module. Each leukocyte cell's nucleus and cytoplasm are divided by this module [23]. Blood smear shows the different types of leukocytes, including infected white cells, known as lymphoblast cells [24-26]. There are no zero pixels in the nucleus region in the binary equivalent image of the nucleus, which extracts all the features [29].

3. LITERATURE SURVEY

Subhan, et, al. [3] proposed to develop a computer system that can count the number of malignant cells in a blood sample(specimen) and identify them. segmenting the image of a blood slide and then extracting features to find leukemia cells. The Hough transform and KNN algorithm were used to segment the bone marrow aspirate. Individual cells were chosen, and features were generated based on texture, statistical analysis, and geometric analysis of the cells, as well as an examination of the characteristics of abnormal cells, including their radius, area, perimeter, shape, and color. We are able to identify the aberrant cells using the reference measurement. For improved detection and extraction accuracy, nucleus shape characteristics such area, perimeter, circularity, code implementation time, etc., are taken into account. Using the proposed feature, leukemia detection was categorized with an overall accuracy of 93% using the KNN classifier and Hough Transform.

Adnan Saeed, et.al. [4] proposed the cutting-edge deep learning architectures Multi-Attention EfficientNetV2S and EfficientNetB3, A fine-tuning technique based on transfer learning is used to distinguish between normal and blast cells, the images of blood smears that were scanned microscopically. Both systems are pretrained on an image network that spans a large area. We merely added extra layers to each model and changed the final block of each. The model is simplified not only by this Multi-Attention Mechanism, but it also effectively identifies its network. The accuracy has increased and the total loss has been reduced by applying the suggested strategy. Accuracy of 99.73% is EfficientNetV2S and 99.25% is EfficientNetB3 accordingly.

Pradeep Kumar Das, et.al.[6] presented that a weight factor based novel probability has a major role to play in effectively combining the advantages of both MobilenetV2 and ResNet18 through hybridization. The ALLIDB1 and ALLIDB2 public benchmark datasets are used to verify its performance. The experimental findings show that, for the ALLIDB1 is 99.39% and ALLIDB2 97.18% accuracy of the datasets (70% of the training is given and 30% of the testing is given). Like, it attains the highest accuracy of 96.92 percent and 96.0 percent (50% training and 50% testing), respectively. Furthermore, it outperforms the more modern transfer learning-based approaches in the majority of scenarios when it comes to some of the performance metrics like sensitivity, specificity, accuracy, precision, F1 score, and receiver operating characteristic (ROC) in both datasets.

Anil Kumar K.K, et.al.[7] proposed using Deep Convolutional Neural Networks (DNN's), ALL will be classified using the WHO categorization scheme without the need for computationally intensive image segmentation and feature extraction. Images from the American Society of Haematology's (ASH) online image bank were employed in the categorization. A custommade deep learning network was developed by using a pretrained CNN AlexNet and LeukNet to isolate B-cell and T-cell images created by the introduced work, the study achieves a classification accuracy of 94.12%. Additionally, the study contrasted the classification results using three distinct training techniques. The classification of ALL utilizing DNNs instead of image segmentation and feature extraction methods.

Lorenzo Putzu,et.al. [8] proposed comprehensive and entirely automated technique for classifying and identifying WBCs using microscopic images. This method is required to thoroughly analyze every cell component. Using a novel method for background pixel removal, many properties, including form, color, and texture, are retrieved from each cell component. Several classification models were trained using this feature set to see which one would work best for leukemia detection. By utilizing image processing techniques, the suggested method allows for the automatic analysis of blood cells and serves as a medical tool that circumvents the many disadvantages of manual observation. Given its high performance and ability to provide suspicion of early diagnostics, which may then be verified by a haematologist using specialized procedures, this procedure could also be utilized for counting.

Fahimeh Alaei, et.al.[10] have proposed to assess the effectiveness of 26 distinct texture features from the four primary categories of texture features based on their effectiveness such as statistical, transform, model and etc., approaches- on the task of retrieving document images. The evaluation of document image retrieval systems' distinctive features involves using three document image datasets, MTDB, ITESOFT, and CLEF_IP, with different content and page layouts. The same evaluation metrics precision, recall, and F-score of the retrieval results are calculated, and a comparative analysis of the outcomes is also given. The texture-based feature approaches' feature dimensions and temporal complexity are further contrasted. Ultimately, a few conclusions are reached and recommendations for further lines of inquiry are given. some of the methods allows the analysis of blood cells, and it represents using medical tool. This tool is used to avoid the numerous (count, performance) drawbacks.

Jakkrich Laosai,et.al. [11]. The suggested technique determines the class of each White Blood Cell (WBC) using color images of stained peripheral blood smears as input. Segmentation, feature extraction, and classification are steps in the process. The classification of Almeida Lloyd (Myeloid) and Foil of Bretagne (Lymphoid) is the main focus of our investigation. in order for medical professionals to assess, find irregularities, and confirm the diagnosis. Based on our image processing approaches, we were able to identify leukemia and classify 100 sample photos into two groups: myeloid stem cells and lymphoid stem cells. K-Means clustering has taken place. From the divided cytoplasm and nucleus are used to drive the features that are extracted for Shape and texture signals. The investigation of various classification systems has been extensive using various feature set combinations. The outcomes displayed here are derived from experiments carried out using normal cells. 92% was the maximum performance achieved with SVM.

Liyan Pan,et.al. [12] when it comes to juvenile acute lymphoblastic leukemia (ALL), the prognosis of relapse is crucial for efficacious therapy and subsequent planning. The main objective of Building an ALL-relapse prediction model using machine learning techniques. Randomly splitting the datasets was achieved using Monte Carlo cross-validation that was layered with 10-fold cross-validation. ALL children, and the shortest list of highly penetration factors was found using a forward feature selection technique. Besides the separation of test sets of 150 cases, they added an additional independent data set of 84 patients to assess the prediction model impartially for use with new patients. The 14-feature Random Forest model succeeded in 0.798 accuracy.

Fatma M. Talaat, et.al.[13] proposed a novel classification model that separates non-cancerous form leukemia-affected images in blood microscopic images. The three primary steps that comprise the general recommended method in this paper are as follows: (i) Preprocessing the image; (ii) Extracting features; and (iii) Classification. For classification, an optimized CNN (OCNN) is employed. CNN's hyperparameters are optimized by fuzzy optimization. Fuzzy logic is a very beneficial tool for CNN tuning. Based on the results, it can be observed that the best outcomes were obtained by enhancing the CNN's performance through the use of an OCNN classifier and hyperparameter modification. Using the C-NMC Leukemia dataset, the OCNN shows 99.99% accuracy.

S. Alagu, et.al.[14] proposed a key characteristic for ALL detection. The required input photographs can be found in an internet database. To give every image a consistent size, resizing is done. U-Net segments the nuclei of blast cells and healthy cells. The output from the several CNN models, including AlexNet, GoogleNet, and SqueezeNet, about 1000 deep features are recovered. Concatenating all the features is done via deep feature fusion. Some of the feature selection techniques, including selection process involves mutual information (MI), minimal recursive maximal relevance (mRmR), and recursive feature elimination (RFE). All of the prime features are intersected to yield the distinguishing characteristics. ANOVA is used to statistically analyze dissimilar feature sets. A comparison is made between the suggested system's performance with fused features and feature sets without fusion. With p =.00001, 50% of the crossed deep features exhibit greater significance. These characteristics will be useful for making wise clinical judgments to accurately pinpoint the blast cells at an early stage.

Maila Claro, et.al.[18] proposed a CNN model called Alert Net-RWD is used to automatically diagnose acute myeloid and acute lymphoid leukemia. The obtained outcomes show promise, as Alert Net-RWD uses less parameters than other systems described in the literature. Furthermore, the suggested approach is more appealing to employ in mobile applications due to its decreased file size. Convolutional neural networks (CNNs) that can distinguish between blood film with ALL, AML, and healthy blood slides (HBS). These studies yielded an accuracy of 97.18% and a precision of 97.23% using 16 datasets including 2,415 photos. Comparing the findings from the suggested model against those produced by cutting-edge techniques was carried out, some of which also relied on CNNs.

Zhencun Jiang, et.al.[20] suggest using the Vision Transformer (ViT-CNN) ensemble model to categorize photos of cancerous and healthy cells to help diagnose acute lymphoblastic leukemia. The vision transformer model, which differs from the CNN model in terms of feature extraction, the transformer structure is the foundation of this image classification model. Classification results in the ViT-CNN ensemble model can extract the characteristics of cell images in two alternative approaches The ViT-CNN ensemble model's classification accuracy on the test set is 99.03%, and an experimental comparison demonstrates that this model performs better than the others. The suggested approach can effectively be employed for the diagnosis of acute lymphoblastic leukemia is aided by computers and can distinguish between cancerous and normal cells with accuracy.

4. CLASSIFICATION

To classify leukemia morphologically, it is necessary to identify leukemia cells and determine the stage of cell differentiation. Basically there are three types of ALL Classification [30]. They are,

L1: The structure of lymphoblastic leukemia is homogenous with blasts being homogenous and having a regular nucleus that may be small.

L2: The characteristics include irregular and large nuclei surrounded by heterogeneous chromatin structure.

L3: It was a rare subtype. Large last cells with prominent nuclei and abundant cytoplasm can be used to identify it. The nucleus will have a stippled homogenous chromatin structure and vacuoles will surround it.

In this survey, various features and performance metrics are used. Here, some of the existing algorithms were analyzed. Based on the techniques the results produced.

5. METHODOLOGY

In this Proposed methodology, Figure 2 displays the system's architecture. The process of obtaining relevant information from medical images, frequently with the aid of computational techniques, is also called as medical image analysis. Among the tasks involved in medical image analysis are the exploration and visualization of 2D and 3D volumes. Pre-processing, segmentation, extraction of features, and classification of images. The various stages of Proposed Methodology are as follows,

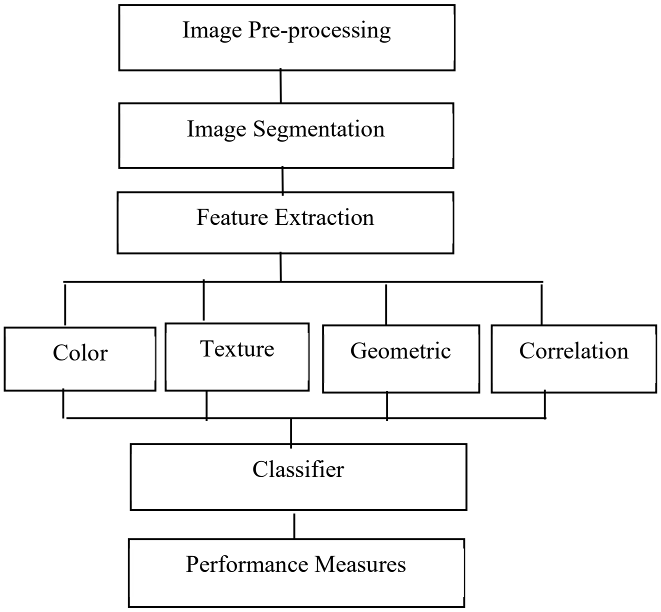

Figure 2: Image Processing Steps

5.1 Image Preprocessing:

The region of interest (ROI) may appear blurry due to illumination or shadows, which could be the cause of the noise. Background will not be included White blood cells represent our ROI [3]. The quality of medical images can be enhanced by using the contrast enhancement method during this preprocess. Several methods are employed for edge detection, morphological operations, and pre-processing grayscale transformation (linear, histogram, logarithmic, and so on).

5.2 Image Segmentation:

A subfield of digital image processing called image segmentation finds various uses in the fields of machine vision, augmented reality, and image analysis. The segmentation of organs, illnesses, or anomalies in medical images has become more difficult as the area of medical image analysis expands. The different artifacts included in medical imaging make it extremely difficult to separate the images [17]. Deep neural models have been demonstrated to be useful in a variety of image segmentation tasks recently. The noteworthy expansion can be attributed to the accomplishments and superior efficacy of deep learning methodologies. It looks at the many commonly used medical image datasets, the numerous criteria for assessing the segmentation tasks, and the various CNN-based networks results.

5.3 Feature Extraction:

A variety of techniques, including as statistical analysis, mathematical transformations, and the use of trained models, can be used to extract features [16]. There are various features involved in the medical image processing. They are,

1. Total amount of pixels with in the center
2. Primary axis of the ellipse encircling the nucleus length, measured in pixels.
3. Color Extraction
4. Texture Extraction
5. Geometric Extraction
6. Correlation Feature

5.4 Color Features:

A color distribution is how an image's chromatic composition is viewed. Color histograms are the most widely used and simplest way to represent color content or information [9]. It records the total color distribution of an image and displays the probability innate to the intensities of the three color channels. The color attributes used in this study are derived from the RGB and HSV color spaces. The color image was divided into three separate color channels, each of which included values for hue, saturation, and value in the HSV color space and red, green, and blue in the RGB color space. Next, each color band in the image's histogram is assessed. As a result, a total of 36 color features are recovered for each nucleus sub image

5.5 Texture Features:

Patterns or structures in a image that are not captured by more conventional features like color or shape can be recognized using these features. Texture features can be extracted from an image using a variety of techniques, including statistical techniques.

5.6 Geometric Features:

Features of an item made up of a collection of geometric components, such as surfaces area, curves, points, and lines, are referred to as geometric features. These features, which can be found using feature detection techniques, can include corner features, edge features, blobs, ridges, prominent points, image textures, and more.

5.7 Correlation Features:

CAD model parameters are extracted using a correlation-based method. It is demonstrated that the problem is high dimensional when CAD parameters are used as input. A curtain airbag's volume simulation is utilized as a case study. 'Sleeping Parameters' are introduced using area, medial axis, etc.

6. PERFORMANCE METRICS

To guarantee the efficacy of the system that was presented, we implemented specific measurements that informed the decisions that were made. In this section, specific measures that are employed to assess the classifiers are discussed [21,28].

6.1 Accuracy:

Accuracy is one metric for evaluating classification models.

$$\text{Accuracy}=(TP+TN)/(TP+TN+FP+FN) \quad (1)$$

6.2 Precision:

Number of positive class predictions that truly belong to the positive class is measured by precision. It is computed by dividing the total number of false positives and true positives by the number of true positives.

$$\text{Precision}=TP/(TP+FP) \quad (2)$$

6.3 Recall:

It is computed by dividing the total number of false negatives and true positives by the number of true positives.

$$\text{Recall}=TP/(TP+FN) \quad (3)$$

6.4 F1-Score:

A single score is provided that balances recall and precision in a single figure. The mean of precision and recall is used to evaluate it.

$$\text{F1 Score}=2(P*R)/(P+R) \quad (4)$$

Table 1: Performance Analysis.

Methods used	Accuracy (%)
Support vector Machine (SVM)	92
Random Forest Model	79.8
CNN (AlexNet)	97.23
ViT-CNN	99.03

KNN	93
EfficientNetV2S	99.73
EfficientNetB3	99.25
Optimized CNN(OCNN)	99.99

The Performance of various techniques for Leukemia Classification processing given in table 1. Optimized CNN(OCNN) achieves high accuracy of 99.99%. Random Forest secures lowest accuracy 79.8% and so on. The performance of model graphically shown in Figure 3.

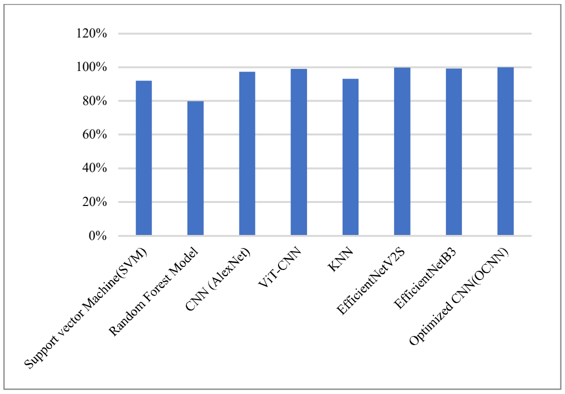

Figure 3: Experimental Results

7. CONCLUSION

The literature that has used or implemented machine & Deep learning models for leukemia classification is reviewed in this study. Several publicly accessible data sources for those research are also included in the paper. Finding datasets for machine learning is quite challenging, particularly for data related to healthcare. The majority of the research made use of their own data that was gathered in a lab or clinical environment. We can't find a study that includes datasets that are accessible to the general public, to the best of our knowledge. It is clear from the analysis of the literature that the studies that are now in existence only concentrate on a small amount of data for classification.

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