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A SURVEY ON DETECTION OF LEUKEMIA USING IMAGE PROCESSING TECHNIQUES

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ABSTRACT

Leukemia is a class of illnesses that often affects the blood and is sometimes referred to as blood cancer. Leukemia is a malignancy of white blood cells. If not caught in time, it could be dangerous. Hematologists examine microscopic pictures to find cancer. The procedure of detection becomes extremely difficult and time-consuming. If discovered earlier, leukemia can be treated. However, the conventional approach causes the late identification of cancerous cells. Therefore, a machine-learning strategy might be utilised to lower the number of deaths brought on by late detection. In this article, 16 research papers are discussed. This review study's goal is to examine the literature on leukemia identification. and classification utilising deep learning, machine learning, and other image processing methods.

Keywords: Leukemia Blood Cancer, Machine Learning Algorithms, White Blood Cells, Survey.

I. INTRODUCTION

Leukocytes, which make up around 1% of all blood cells, are created in the bone marrow. The uncontrolled expansion of these white blood cells leads to bone marrow cancer. Platelets, red blood cells, and white blood cells are the three main types of blood cells that are created in the bone marrow and discharged into the circulatory system as blood cells. The three main types of blood cancers caused by abnormal blood cells preventing the development of healthy ones are leukemia, myeloma, and lymphoma [1].

As one of the main causes of mortality in people, leukemia is a kind of blood cancer that affects white blood cells. A kind of blood cancer that affects white blood cells is called leukemia. Currently, diagnosis is carried out by visual inspection, which requires experienced personnel, requires time to complete, and is tiring. In Ethiopian hospitals, a significant problem is the lack of an autonomous, quick, and efficient leukemia diagnosis method [3].

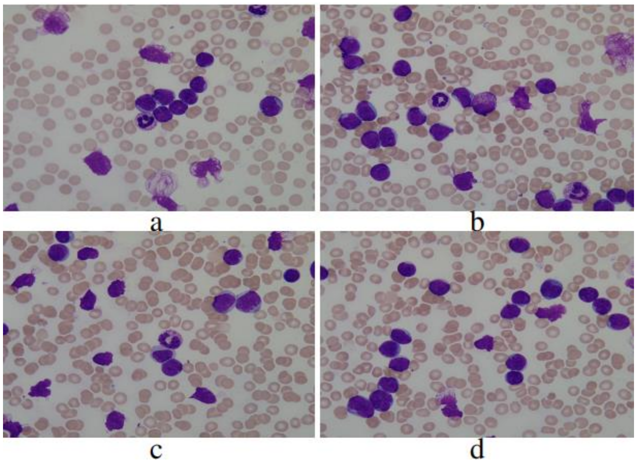

Fig 1. pictures of blood samples from the ALL-IDB-1

The four primary kinds of leukemia are:1.Acute lymphocytic leukemia (ALL) 2.Acute myelogenous leukemia (AML) 3.Chronic lymphocytic leukemia (CLL) 4.Chronic myelogenous leukemia (CML).

The most frequent kind of leukemia in children, adolescents, and teenagers up to age 39 is acute lymphocytic leukemia (ALL). ALL may have an effect on adults no matter their age. Senior citizens are particularly vulnerable to it. people above 65. Youths may be affected by AML. Chronic lymphocytic leukemia (CLL) is the most common kind of chronic leukemia in adults. CLL signs may not appear for months. Chronic myelogenous leukemia (CML) can affect anyone of any years of age, even though elder people are more likely to have it (individuals who are 65 or older are most at risk). Youngsters typically ever go through it. Symptoms of CML may not appear for long periods of time.

The detection of various leukemia stages using microscopic pictures is an area of deep learning and convolutional neural networks. Image processing goes through six phases to identify the disease stage. Image acquisition is followed by image pre-processing, image segmentation, extraction of features, cell detection, and ultimately cell classification. Some recent works classified as belonging to the WBCs and RBCs division rely on a shading space, including the HSI shading space and RGB. The alternative method makes use of standard AI techniques, image processing methods, and data processing methods including K-Means clustering, Watershed segmentation, Support Vector Machines, and fuzzy logic, Clustering using C-Means, etc.

In this work, many categorization and detection methods for leukemia by various researchers are further explored.

II. LITERATURE SURVEY

Kumar et al., [1] The researcher created a system utilizing convolutional neural networks that can detect leukemia in bone marrow photographs. The system for categorization was developed using TensorFlow, a whole open-source library. 1000 iterations and 424 images were used to create a binary classification model. The Adam Optimizer's loss function optimisation produces a minimal loss at the end of each cycle. The trained model was then applied to identify the cancer kind in the pictures. Training of the model is carried out on a K80 GPU.

Mamatha balipa et al.,[2] In this paper, the authors describe a revolutionary cryptographic-based technology that interacts with patients, their relatives, and health care professionals to collect health-related data and provide useful information about diagnosis, prescribing, medication, and treatment. We propose an online social medicine recommendation system. The system looks at a user's queries on the MedHelp website and assigns a ranking to his website using an adaptive artificial neural network (AANN) and his Sentiwordnet score. The AANN weights are optimized by the Grasshopper Optimization Algorithm (GOA) and the top websites are encrypted using the Triple Data Encryption Standard (TDES) algorithm for secure data recovery.

Pradeep Kumar Das et al.,[3] In this paper the author attempts to provide an automated technique for detecting and classifying acute lymphocytic leukemia. (ALL). The colour-based k-means clustering method is used for lymphocyte extraction. Next, from the segmented picture, form, texture, and colour attributes are retrieved. The techniques for extracting the characteristics of the nucleus are grey-level co-occurrence matrix (GLCM) and grey-level run-length matrix (GLRLM). Principal component analysis (PCA) is further used for dimensional reduction. The classification of WBCs is completed using an SVM (support vector machine) using an RBF kernel.

Ranjitha P et al., [4] In order to identify leukemia and blood cancer, the author of this study used the K-means approach. Based on criteria for segmentation such as the area of fascination, cell number, border region, and cell height, they were able to locate the cancer-affected cell using the k-mean. For this method, the number of iterations is set at 40 for three vector clusters. The proportion of cancer may be calculated by multiplying the number of defective cells by the total number of cells * 100 while considering all factors into the data set. Blood cancer is categorised as being in the early stages if there are less than 25 cancer cells present, and as being in the advanced stages if there are more.

Mamatha balipa et al.,[5] In this paper, the authors discuss the difficulty in identifying and classifying medicinal Alstonia or Pale trees due to a wide variety of trees and other factors that make them difficult to distinguish from images. To address this issue, the authors propose to use pre-trained Inception V3 models and convolutional neural network (CNN) methods to detect and classify trees. Because these models offer higher accuracy than traditional methods. The goal is to identify and collect relevant information about various tree species to support specific applications.

Mamatha balipa et al.,[6] In this paper, the authors present an exploratory preliminary study that focuses on twin voice similarities and provides accurate predictions. This study aims to fill the lack of a comprehensive overview of advances in speaker identification for accurately identifying human voices. A Siamese neural network, also known as a twin neural network, is used in this work to aid in speaker identification. This model combines frame-level score representations mapped to registered functional domains and scores for final similarity measures obtained by joint optimization of functional learning, attentional mechanisms, and metric learning using end-to- Use a joint vector of utterance-level registrations. The -End procedure generates a loss function. Speech accuracy is computed by speaker representations from previous studies on speaker identification using discriminative neural networks and speech level assessment.

Mamatha balipa et al.,[7] In this paper, the authors use convolutional neural networks (CNN) and support vector machines (SVM) to detect betel nut leaf and stem diseases. In this study, we use his dataset of 181 images of healthy and infected areca nut to perform preprocessing, feature extraction, training, and classification. The proposed methodology aims to detect and treat betel nut diseases such as MAHALI, stem bleeding and yellow leaf spot. Experimental results show that the accuracy of disease detection varies depending on the input image quality and disease stage.

Sarmad Shafique et al., [8] In this paper author developed a computer-aided ALL detection and diagnosis in this research. In this study, efforts have been made to use image processing techniques to identify leukemia from microscopic blood pictures. The photos were subjected to preprocessing to eliminate any noise, and segmentation was then carried out to identify lymphocytes in the image. After obtaining shape and colour data from the clustered lymphocytes, Watershed is used to separate them, and SVM is then used to categorise the normal and blast cells.

Preetham Kumar et al., [9] This study proposes a method for automatically determining if a picture of a microscopic blood smear contains AML or not. To extract the nucleus, the photos are first pre-processed and then segmented. In the feature extraction process, the segmented picture is used to extract the form and texture features. Using an SVM classifier, the pictures are finally identified as malignant or non-cancerous based on the retrieved attributes.

Abu Daqqa et al.,[10]Three blood cancer classifiers have been discovered for this study: the decision tree (DS), the support vector machine (SVM), and the k-nearest neighbour (k-NN). The three classifiers were carefully applied and examined in terms of F-Measure and classification accuracy. Due to its ease of use in analysing outputs and results, DT is particularly popular in the medical industry . Popular for creating classification models from input data is the K-NN classifier. The three classifiers (SVM, Decision Tree, and K-NN) are utilised and compared in Rapid Miner 7.0.001 as the application environment.

Subhash Rajpurohit et al.,[11] In order to increase accuracy and enable early diagnosis compared to a human technique, the author of this research has created an automated system that can identify ALL from microscopic blood pictures. The microscopic blood picture is processed in order to retrieve the necessary properties. Finally, a comparison of the speed and accuracy of SVM, neural networks, and K-nearest Neighbor is shown.

Nizar Ahmed et al., [12] Using a CNN architecture that can distinguish between the four leukemia subtypes, the authors of this work offer a novel method for categorising the kind of leukemia shown in microscopic blood pictures. Their algorithm demonstrated its ability to work with the few available picture samples by using data enhancement strategies that helped cope with the overfitting issue. They used better samples to get the best results in the categorical categorization of ALL and HEALTHY categories. The categorization of the four leukemia subtypes into many categories received the second-highest score. The multi-classification problem is overcome by binary classification, though, because the algorithm can discriminate between categories with greater accuracy as more classes are adhering to and included in the method of classification. In terms of accuracy and loss measures, they found that SGD optimizer performs significantly better than ADAM optimizer. Additionally, they noticed that Exp#3a provided a better result than Exp#3b, indicating that longer epoch iterations do not improve the model's performance.

Kokeb Dese Gebremeskel et al., [13] In this paper author used blood cell pictures from the Nottingham University Hospital, Jimma University Specialized Hospital, and ALL_DB online database. Three haematologists who participated in this study as clinical collaborators labelled the images taken in the laboratory environment. First, preprocessing was performed on the stained blood image to remove noise generated during acquisition. As the method was being developed, the preprocessed image was segmented using k-means segmentation and indicator-controlled segmentation. Well-segmented leukemic blood images also improve the sensitivity and specificity of blood cancer detection and species identification. This shows the potential of employing digital image analysis to identify leukemia diseases since it is less time-consuming, labor-intensive, mistake-prone, and specialist knowledge-required than the manual approach. This will benefit today's fast evolving healthcare system since leukemia will be identified and classified earlier, which will improve patient outcomes.

Krishna Kumar Jha et al., [14] This paper describes a technology termed leukaemia identification and segmentation, which analyses individual blood cells from a smear accurately. This technique employs two distinct approaches: leukaemia cell segmentation and classification, which are carried out independently. The first step is to pre-process and segment the blood smear pictures to distinguish the cell's core from the surrounding region. Using shared information, the hybrid MI model is then utilised to partition the population. For classification, a limited subset of statistical characteristics is taken from the partitioned areas and fed into the proposed Chronological SCA-based Deep CNN. To choose the appropriate weights for the Deep CNN algorithm, the Chronological SCA technique, a modified form of SCA, is employed.On the basis of accuracy, the proposed Chronological SCA-based Deep CNN classifier is assessed and compared to current state-of-the-art techniques.

Arbab Muhammad Qasim et al., [15] In this paper the main goal of author's work is to identify lymphocytes, extract CNN properties, and categorise them. First, the location of lymphocytes, a subclass of WBCs, may be seen in a blood smear picture. Then, a number of CNN characteristics are extracted from the lymphocyte picture. Based on the obtained characteristics, the SVM classifier is trained to make classifications. According to experimental findings, the suggested strategy outperforms other cutting-edge classification techniques in terms of classification performance.

Angelo Genovese et al., [16] This research introduces a new machine learning approach based on Deep Learning (DL) to classify blood samples as either normal or lymphoblast. The proposed method utilizes advanced adaptive image processing techniques to improve image sharpness prior to training. Deep Convolutional Neural Networks (CNNs) are used to modify the parameters of the unsharpening algorithm. This technique enhances image details by estimating image focus quality and adaptively correcting data bias between image quality and classification. Results from experiments using open-access ALL datasets demonstrate that deep CNNs trained on unsharpened images using the proposed method improves lymphoblast detection accuracy, regardless of the CNN used.

Table1:.Algorithm and accuracy

Year	Author	Algorithm	Accuracy
2020	Kumar et al.,	CNN	97.25%
2020	Pradeep Kumar Das et al.,	SVM	96.00%
2021	Ranjitha P et al.,	K-means	90%
2019	Sarmad Shafique et al.	SVM	93.7%
2017	Preetham Kumar et al.,	Support Vector Machine	95%
2021	Kokeb Dese Gebremeskel et al.,	SVM	94.62%
2021	Angelo Genovese et al.,	CNN VGG-16	96.84%
2022	Arbab Muhammad Qasim et al.,	SVM CNN	98%
2017	Abu Daqqa et al.,	Support Vector Machine(SVM), K Nearest Neighbors (KNN) and Decision Tree	76.82% 72.15% 77.30%

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2018	Subhash Rajpurohit et al.,	CNN FNN KNN SVM	98.33% 95.40% 93.30% 91.21%
2019	Nizar Ahmed et al.,	CNN Naive Bayes Decision Tree KNN SVM	81.74% 52.68% 45.92% 43.51% 20.84%
2019	Krishna Kumar Jha et al.,	Hybrid segmentation + Chrono-SCA-DCNN	98%

III. CONCLUSION

This study examines several machine learning, image processing, and deep learning-based leukemia cancer diagnostic methods. Combining deep learning and image processing can expedite leukemia diagnosis and increase the likelihood that patients will be saved from further harm. An image processing strategy can take away the subjectivity of the job done by the microscopist when the involvement of a witness and their health have an influence on the outcomes.

IV. FUTURE WORK

To classify leukemia cells and identify their sub types in order to define the kind of leukemia, we want to use the hybrid model in future research.

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