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A Systematic Review of Acute Leukemia Diagnosis by Using Deep Learning

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Abstract: Acute leukaemia, a malignancy that starts in the bone marrow, manifests as an unchecked, fast spread of white blood cells. Acute lymphoblastic leukaemia is more common in young kids under the age of 5 and older people over the age of 50. Automated diagnosis systems are increasingly using image analysis and Deep Learning techniques due to their great accuracy in a variety of health diagnostic sectors, such as the detection of Acute Lymphoblastic Leukemia from serum samples. The several automated techniques for identifying and categorising acute leukaemia are discussed in this systematic review research along with the challenges the authors faced. In this review, Sahlol, A.T. et al. employed ALL-IDB2 to performed segmentation using the Zack algorithm and achieved the highest segmentation accuracy (99.23%), sensitivity (100%) and uniqueness (97.1%). The study makes use of a number of methodologies, including thresholding, the Zack algorithm, the clustering-based technique, the fuzzy C-mean, the k-myeloid, and the k-means. In the domain of medical image analysis, deep learning worked remarkably well, and CNN made it extremely straightforward to build an end-to-end network. The numerous steps leading up to classification, including preprocessing, augmentation, segmentation, and feature extraction—all of which are discussed in this study.

Keywords: Leukemia; Deep Learning; Classification; CNN; ALL; Segmentation

1. Introduction

Doctors may diagnose a variety of disorders using microscopic blood cell imaging. White blood cells or leucocytes can be used in medical testing to identify leukemia, which is a kind of blood cancer. Two forms of leukemia —chronic and acute. Chronic is further divided into Chronic Myelogenous Leukemia (CML) and Chronic Lymphocytic Leukemia and acute is further divided into acute lymphoblastic leukemia (ALL) and acute myelogenous leukemia (AML) —were identified by the French-American-British (FAB) system (CLL) [1]. Figure 1, Shows cell structure of types of lymphoblastic leukemia.

The morphological identification of lymphoblast under a microscope, the immune-phenotypic evaluation of lineage commitment, and the developmental stage under a flow cytometer can all be used to diagnose acute lymphoblastic leukemia [2]. Doctors may examine and diagnose several disorders using blood samples. Any human-based diagnosis suffers from subpar accuracy since it mostly depends on the expertise of the doctor; it is also erroneous from a statistical perspective. Currently, a variety of devices exist that can count the quantity of blood cells by analyzing the physical and chemical characteristics of blood cells

to use a light sensor that distinguishes between different cell types using electrical impedance or fluorescence [3].

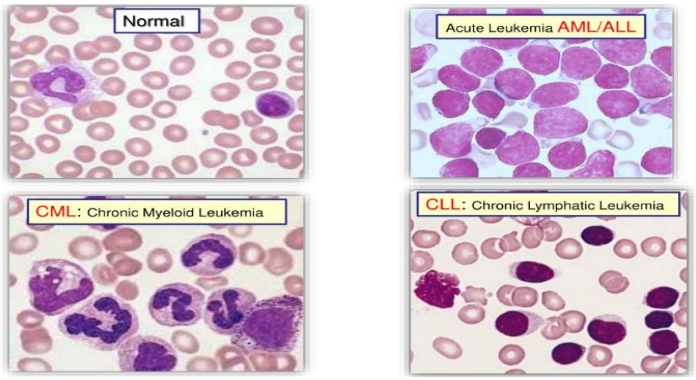

Figure 1. Types lymphoblastic leukemia

A supplemental blood study based on microscopic images is necessary since, despite the precision of the quantification data, it is expensive and does not identify cell morphological abnormalities. Image processing and its subsets such as image segmentation can offer methods for measuring the amount of blood cells and in return can offer useful details on the shape of the cells. Additionally, they are generalizable and statistically efficient. We shall also count and categorize the white blood cells (WBC) impacted by acute lymphoblastic leukemia. Red blood cells, platelets, and leucocytes are the three primary elements of a blood picture.

WBCs can be divided into two categories. Basophil, eosinophil, and neutrophil are all members of the first category, known as granulocytes. Since basophil granules have an uneven distribution and make up just 0-1% of all lymphocytes in human blood, they are responsible for allergic response and antigen [4]. Eosinophils, which make about 1-5% of human blood, are crucial for destroying parasites [5]. The blood stream contains the most neutrophils. It has multiple-lobed nuclei, which make up 50 to 70% of the nuclei in human blood [6]. The second category is a granulocytes, it contains lymphocyte and monocyte. The proportion of lymphocytes in human blood ranges from 20 to 45% [7]. The biggest WBCs are monocytes, which make about 3-9% of the leucocytes in circulation [8].

Lymphocytes contain a compact nucleus that is consistently formed and has continuous borders. On the opposite side, lymphoblast refers to lymphocytes that have been altered by ALL. They are amorphous, have tiny voids in the cytoplasm, and have spherical particles inside the nucleus; the more morphological alterations present, the more severe the illness is thought to be [9].

Although leukocytes are easily identifiable, the analysis and processing become highly challenging due to the numerous differences in their shapes, sizes, and edges. A group of cells that differ greatly from one another are collectively referred to as leucocytes. Therefore, these cells may be identified based on their size or form.

Medical and other areas have incorporated image analysis techniques [10-14]. For the early identification of acute lymphoblastic leukemia in blood microscopic pictures, Mohapatrain deployed an ensemble classifier system [15]. It was suggested a method to segment the pictures of acute leukemia cells by converting the RGB color space to C-Y color space. In the C-Y color space, the brightness component is utilized to segment [16]. After testing several classification models, it was shown that the support vector algorithm with a Gaussian radial basis kernel performed best in detecting acute lymphoblastic leukemia, with 93% accuracy and 98% sensitivity.

Figure 2, Shows normal blood cells and acute lymphoblastic leukemia.

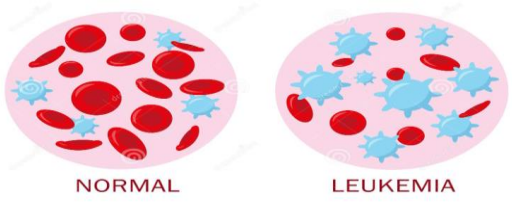

Figure 2. Normal to effected cells of blood

This paper exclusively addresses acute leukemia, which is well-known for mostly affecting children and older individuals. Acute lymphoblastic leukemia is more common in children under 5 year old and older individuals over 50 years old. If it isn't treated early, it can be deadly because it spreads quickly to several key organs including the blood circulation [17]. A completely automated diagnosis system is being developed for the detection, segmentation, feature extraction, and categorization of WBCs impacted by acute leukemia since early identification considerably benefits in giving the right therapy for acute leukemia.

The main objective of this study is to investigate how acute leukemia disease classification techniques have evolved through time. The primary contribution of the current study are;

1. To determine the practical applicability of the acute leukemia classification systems.
2. To give a summary of the existing research studies based on the benefits of acute leukemia classification and the course of future research.
3. Determine the current research trends and publishing interests based on the categorization of acute leukemia disease.

In the corresponding sections, Section 2 provides an overview of the techniques and findings that have been utilized by different researchers to diagnose acute leukemia, Section 3 includes the current methodologies, their benefits and drawbacks, and Section 4 offers a conclusion.

2. Literature Review

Leukemia, a blood cancer has an impact on the white blood cells that line the bone marrow. Acute leukemia must be distinguished by counting the proportion of white blood cells in blood plasma. Cancer of this kind has the potential to be lethal if it is not discovered in its early stages. In fact, manual microscopic examination methods are used to detect acute leukemia. But these manual procedures are inaccurate, prone to errors, and time-consuming due to human limitations including fatigue, stress, and inexperience. Algorithms for image processing have been developed to replace various human approaches. In this section, we discuss various computer-assisted methods for diagnosing acute leukemia, such as picture capture, pre-processing, segmentation, feature extraction, and classification. Using imaging techniques, leukemia may be promptly and easily detected, improving the possibility that patients will recover and receive the proper care.

When determining a leukemia diagnosis and classification, image analysis and machine learning techniques may be able to replace blood analysis specialists in regards to speed and accuracy [18]. Manual diagnostic methods need more duration, are less precise, and frequently produce errors due to a variety of human variables, such as stress, fatigue, and so on [19]. Segmentation using image processing is among the early methods for leukemia detection. To detect blood cancer leukemia, many algorithms, approaches, and procedures have been developed. Image segmentation presents essential difficulties in automated hematology analysis, necessitating precise execution.

In order to analyze data and distinguish between the various types of leukemia, V P. Jagadev and H. G. Virani used three algorithms: k means, HSV color-based segmentation, and Marker controlled watershed, in addition to the SVM classifier [20]. Incorporating socio-demographic, clinical, immunological, and cytogenetic factors with cross-validation segmentation nested by ten folds allowed Pan, L. et al. to discover the risk factor of acute lymphoblastic leukemia in children [21]. Sahlol, A.T. et al. used ALL-IDB2 by implementing the social spider algorithm (SSOA) for such identification of abnormal white blood cells. They first converted the image RGB into color space (CMYK) and performed segmentation using the Zack Algorithm. After that, some features (shape, color, and texture) were chosen and the best one was used for SSOA, obtaining segmentation accuracy of 99.23%, 100% sensitivity, and 97.1 % uniqueness [20]. Rehman et al. Utilized deep learning approaches for the categorization of ALL and a proposed automated segmentation algorithm to detect leukemia kinds are regarded as innovative. In order to properly identify L3 and L2 blast cells through extraction of features, they segmented the complete cell's nucleus. However, it still needs some adjustments to increase the precision of the classifier results and the capacity to examine overlapped cells [22]. When harmful cells are still found in a person's body after treatment and diagnosis for a malignant disease, the state is referred to as having "minimal residual diseases." Multi-color flow cytometry study assures that machine learning tool’s clinical assessment has a substantial advantage due to its capacity to combine with other diagnostic and therapeutic approaches by applying a computerized MFC

analysis using MRD identification in AML and MDS [23]. Medical experts have been manually identifying leukemia for the past several years by microscopically studying the bone marrow and blood samples of the patients. However, this technique has a 30–40% error rate and reduces the accuracy of the diagnosis since it takes into account human variability. Any endeavor that includes people has some degree of danger. In order to avoid these issues, Abdulsalami et al. assessed a machine learning algorithm called deep convolutional neural networks (CNNs), which is utilized in computer-aided systems that use microscopic images to diagnose leukemia [24]. Machine learning (ML) has made it feasible to improve pathological diagnosis, especially with the growing trend of digitizing microscopic images. In many places throughout the world, leukemia diagnosis is time-consuming and challenging, and there is a growing tendency to apply ML techniques for its diagnosis [25].

Deep learning must be used to enhance oncologic therapy and systems due to the rise in the number of blood cancer patients and the number of records gathered throughout the therapy process [26]. The prognosis for acute leukemia can aid in lowering death rates. The dataset underwent many phases before being classified as leukemia in order to facilitate better analysis [27]. This procedure enables us to eliminate undesirable distortion and reinforce the desired characteristic, both of which are essential for the particular application we are working on [28]. Resizing, Normalization, RGB Model, HSV, Histogram Equalization and Image Registration are some of the several image processing methods utilized [29] which shows in Figure 3.

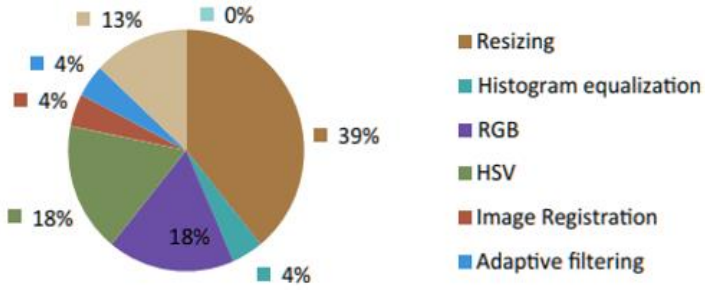

Figure 3. Processing methods used by researchers

The second phase is data augmentation after preprocessing. It is a method for producing artificial datasets or expanding the dataset. It is a method for expanding the dataset or producing artificial datasets [30]. A quantity of training data was needed for the deep learning model, but this data is not always readily available, particularly in the medical field [31]. To make a more generic model work, current data is therefore augmented using a variety of methods such as scaling, cropping, flipping, padding, rotation, translation, etc. [32]. Figure 4, shows different argumentation techniques used by researchers.

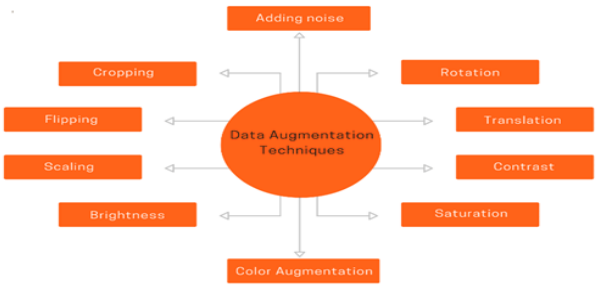

Figure 4. Argumentation techniques used by researchers

Finding the nucleus and cytoplasm inside the blood smear pictures is one of the most crucial tasks after preprocessing & augmentation procedures [33]. As a result of the fact that this step serves as the foundation for other procedures involving feature extraction and classification [34]. Image segmentation is a key component of automated cancer identification. To recover the region of interest (ROI), the image is divided into several sections or segments [35]. The problem that has to be solved determines how much segmentation or subdivision is done. For example, the ROI, cytoplasmic or nuclear detection may be used to diagnose acute leukemia. The subdivision is carried out in accordance with predetermined parameters, and several approaches including thresholding, the Zack algorithm, the clustering-based method, the fuzzy C-mean, the k-myeloid, and the k-means are employed in the study [36].

Features play a critical role in image processing. Several methods of image processing, including edge detection, bannering, zooming and normalization are applied to the sampled image prior to the acquisition of features [37]. Then, characteristics that may be used to categorize and recognize images are retrieved using feature extraction algorithms [38]. In a variety of image-processing applications, such as the classification of leukemia, feature extraction approaches are crucial. The primary advantage of extracting features is to make less fitting as fewer data redundancy reduces the chances of estimations based on noise. This results a reduction in training period because there is less data available to train on, an increase in accuracy as misguiding information and outliers are eliminated, and a decrease in training time overall [39]. Features, which reflect an image's behavior, the amount of storage needed to save a picture, categorization effectiveness & obviously time consumption [40]. The literatures make use of a wide variety of characteristics, including histogram features, form features, color histogram, geometrical and morphological aspects. Figure 5, shows WBCs feature extraction methods used by researchers.

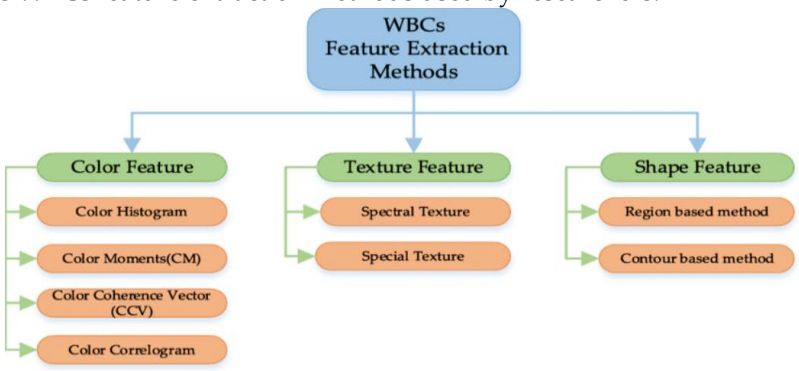

Figure 5. WBCs feature extraction methods

Instead of being developed by human engineers, we can measure the surroundings via deep learning. It makes use of data to enable feature extraction [41]. In the field of medical image processing, deep learning excelled, and CNN made it incredibly easy to build an end-to-end network [42]. Either manually extracted features are used to train machine learning models or using characteristics to execute a variety of categorization tasks using more basic machine learning algorithms[38]. The use of deep learning methods has gradually increased over the past five years as researcher's transition to deep learning from machine learning because of its automated extraction of features technique and the little human involvement. The use of machine learning methods and deep learning differed slightly in the years 2015, 2016, & 2017 as see in Figure 6, but as shows there is a clear trend over to using deep learning techniques in the years 2018, 2019, and 2020.

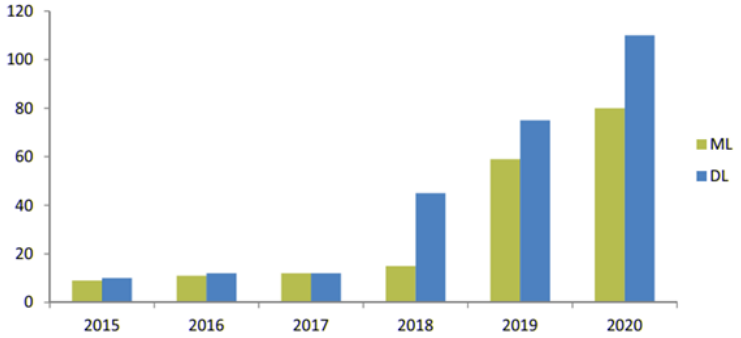

Figure 6. Graph of the machine learning and deep learning methods used to categorize leukemia (2015–2020)

Consequently, Researchers are now eager to investigate the benefits of DL in the categorization of acute leukemia after DL approaches caught their interest [43]. The use of deep Learning as a pattern identification technique in the field of medical image analysis is becoming more and more crucial [44]. According to a latest review of DL-based MIA, DL techniques, specifically convolutional networks have gained popularity as an option for evaluating medical data [45]. These methods are particularly suitable for scenarios demanding the processing of large volumes of data with humanlike intelligence [40].

For the purpose of diagnosing Acute Myeloid Leukemia (AML), Maneela Shaheen et al. suggested Alex Net based model of classification, and the results were contrasted with a model based on LeNet-5 [46]. Based on database information from 4,000 blood smears, the investigations were conducted. LeNet-5,

however, correctly recognized 85.3% of the photos with 83.6% clarity and 96.25% accuracy, with an accuracy rate of 87.4%, Alex Net successfully recognized 88.9% of the photos. As per a system proposed using the Modified Convolution Neural Network (CNN) design, Kalaveseri et al. suggested that the classification process be optimized [47]. A CNN model with several kernel functions was used to extract the features from the pixel values based on an enhanced feature space. The input picture is 200x200 pixels and is in the RGB color space. The filters provided in our function declaration are used to transport the input layer to a convolution layer, a layer known as the Batch Normalization layer, and an activation method known as ReLU, and lastly, there is an additional convolution layer added. The input is fattened after repeating this output layer's process. The input is fattened after repeating this procedure for the output layer. To ensure that the two layers which will be converged have the same layer sizes, this phase must be accomplished. To avoid any network overfitting, a max-pooling layer and a dropout layer are added as additional layers. There are a total of 6 tiers in this complicated model's structure. Each of these layers has many levels, including convolution, activation, drop-out and a pooling layer. The images are analyzed and given labels by a fully linked dense layer that is created by combining these layers.

After feature extraction with HCNN IASO, a CNN layer with an attention-based architecture is added for fusion, Fredric suggested a data augmentation technique to handle a huge number of leukemia photos [48]. In their research, Kumar et al. developed an optimized DCNN for classifying leukemia using the recommended model, which had a 97.8 accuracy rate. Afterwards, the authors compared their findings to more established machine learning techniques, and the suggested model outperformed the benchmark approaches [49]. In order to identify leukemia, Bibi et al. introduced the DenseNet and ResNet systems. It has been found that ResNet-34 and DenseNet-121 have superior diagnostic capabilities than all other methods [50]. For the classification of microscopic pictures of leukemia-free and leukemia-infected blood, Loey et al. recommended using transfer learning in two different models [51]. DT, LD, SVM, and KNN are among the well-known classifiers that are used to classify the discriminant characteristics in the initial model, it furthermore uses a trained CNN named Alex Net. The SVM classifier is superior, according to experiments. The second model successfully performs feature extraction as well as classification using Alex Net. In their two-stage method, Liu et al. used two Inception ResNets, each of which had initial pre trained ImageNet weights, to train on the training sets A and B in the first stage. For the second step, the whole training set of ALL and HEM cells was used to "combine" and fine-tune the models created in the first stage [31]. Three models: AlexNet, CafeNet & VGG 16 are used in the strategy that Vogado et al. recommended. The convolutional layer's filters and the fully connected layer's number of neurons serve as the basis for differentiating these models from one another [52].

Angelo Genovese and others the authors describe the first histopathological transfer learning approach for identifying ALL. The technique is based on a CNN called HistoTNet1, which was fine-tuned for ALL identification after being trained on a pathology database to classify tissues. The results show that in terms of lymphoblast identification accuracy, their histopathology transfer learning approach works better than CNN's pre trained on the ImageNet database [32]. For the purpose of detecting acute lymphoblastic leukemia, Das et al. suggested a unique hybrid Deep CNN-based model. Here, MobileV2 and ResNet18 have been utilized in combination, and it is proposed to merge MobileNetV2 with ResNet18 using a unique probability-based weight factor [53]. In their study, Genovese et al. categories ALL data using image processing and deep learning [32]. Prior to classifier training, the approach evaluates focus quality and enhances picture sharpness using special adaptive image processing algorithms. An initial thin CNN called the VAR-PCANet that was trained to employ an unsupervised procedure and was constructed on some kind of feed-forward architecture, utilized to define the characteristics of the un-sharpening technique. The method's results demonstrate that their methodology can increase the accuracy of lymphoblast detection irrespective which intense CNN is utilized in the classification process in the end. It processes unsharpened images using cutting-edge deep CNNs to divide WBCs into 2 groups: healthy and lymphoblast. Muhammad Omer Aftab used two approaches in his study, the first of which was transfer learning [54]. BigDL's library and Apache Spark's framework were used for transfer learning, and validation and training accuracy were 94.78% and 97.33%, respectively. In the second way, a customized CNN deep learning algorithm using Keras was created, with validation and training accuracy of 92.69% and 96.42%, respectively. Both models used the exact same preprocessing techniques and dataset. When the outcomes from the two models were thoroughly compared, the BigDL model outperformed the Keras model.

In their work, Zouh et al. suggested two phases for the classification module [55]. In the first step of the process, they separated the many cells, such as damaged, crushed, and some other cells that weren't necessary for the diagnosis of leukemia. The calculable WBCs were subsequently sent for multiclass separation using RetinaNet, VGG and also the Feature Pyramid Networks in the second stage for cell identification. Stage one uses ResNext101 328d, ResNext50 324d & ResNet50; stage two uses ResNext101 328d, ResNext50 324d & ResNet50. Three picture sets, representing 70% training, 10% validation, and 20% test, were created from the whole dataset. Using the training set, the detection and classification models were developed. The best parameter for each model was determined using the validation set. Utilizing the test set, the trained model was assessed. In each stage, the same data division was applied. In their research, Eckardt suggested two classification models: one classifies cells at the cell level using an exception CNN, and the other classifies pictures at the image level using a fully connected layer without the use of dropout to create Ensemble Neural Nets (ENN). Finally, binary classification was used to categorize ALL and unhealthy cells.

Two different types of dataset have been utilized in 60 studies; one is a real scenario dataset that was self-acquired, while the other is a publicly accessible dataset. Both the ALL IDB and the CNMC datasets have been utilized as the benchmark datasets in the publicly accessible dataset. There are two versions of the ALL IDB (Acute Lymphoblastic Image Dataset), referred to as ALL-IDB1 and ALL-IDB2. About 39,000 blood components, including lymphocytes identified by oncologists, are present. ALL-IDB2 is a subset of the ALL-IDB1 datasets that comprises clipped areas of focus of normal and blast cells. The pictures were taken using a microscope at magnifications varying from 300 to 500. The only difference between ALL-IDB2 and ALL-IDB1 photos is the image size. The ISBI 2019 CNMC dataset is the second publicly accessible dataset [56]. In this study, there are 76 people, 47 of them have ALL, while the remaining ones are healthy. 10,661 cells are present in total, of which 7272 are classified as ALL and 3389 as HEM and the self-acquired dataset, which is compiled by the researcher, is the second group. Figure 7, Exemplifies the self-gathered datasets that the researchers used in the study.

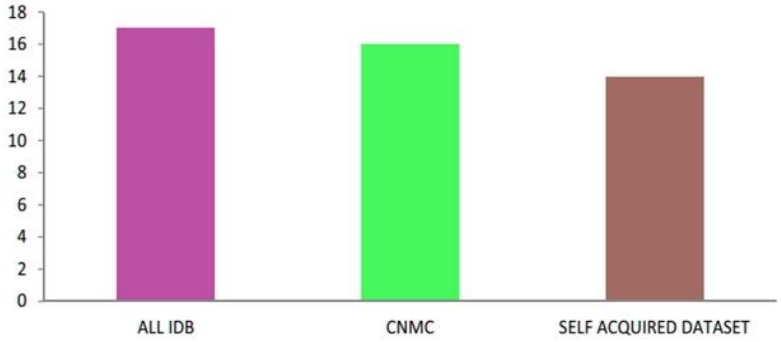

Figure 7. Self-acquired datasets that the researchers utilized in the literature

3. Methodology

The intended systematic review study used digital libraries to conduct a formal research approach, which is covered in this section. A prepared search technique and literature that satisfies this search criterion are needed in order to utilize the accessible digital resources with purpose. The Web of Science, Science Direct & IEEE were three of the internet databases I utilized to efficiently search for research publications. The phrases used in each search are predefined, and they are all done automatically.

3.1. Preprocessing

The preprocessing stage involves the first noise reduction of the microscopic images. There are several noise-reduction filters available, such as wiener and median filters. The preprocessing steps change the image's pixel values to reduce random noise. Another method of reducing noise is thresholding, in which pixels inside of a range are handled as images while pixels outside of that range are handled as noise.

3.2. Feature Extraction

By grouping together the grey values that are comparable, features may be extracted. The extraction of texture, edge, and form, as well as color, characteristics is another method of feature extraction.

3.2.1. Textural Feature

The inter-pixel connection between the pixels present in a picture is essentially defined by the texture characteristic. The texture function pulls out the inner details of a picture, such as its smoothness, roughness, sharpness, and textures.

3.2.2. Morphological Feature

The characteristics that were taken from binary pictures are contained in the morphological feature. Shape characteristics, edge features, the number of linked components, the size, and the perimeters of the picture make up the principal morphological feature.

3.2.3. Morphological Feature

Gray Level Correlation relation Matrix features, which are essentially texture features, are extremely effective for image processing's detection and classification. Contrast, homogeneity, entropy, and pixel correlation are a few of the key characteristics of GLCM.

3.3. Deep Learning Techniques For Classification

3.3.1. Artificial Neural Network (ANN)

The neural network model closely resembles the human brain, which connects many neurons to form a very complicated pattern. The artificial neural network is made up of a number of notes connected by several additional roadways using connecting threads. When a node's information crosses a certain threshold, the information moves on to the next node. Using a neural network there are two steps that must be completed: the training phase, which prepares the model, and the testing phase, which evaluates the model's effectiveness. In order to train the neural network, which can be done using the extracted features from the MRI images, we can use these images. Then, when it comes time to test the model, we can use the features of people who are still alive. This is why many authors suggest using artificial neural networks to detect leukemia. An ANN has been cited by several writers as a very excellent alternative for classifying leukemia disease. The sorts of diseases that might cause leukemia are mostly separated into four categories, therefore we can suggest using a neural network model that has two neurons in the O/P levels and a similar number of neurons as characteristics in the I/P levels to appropriately classify the condition.

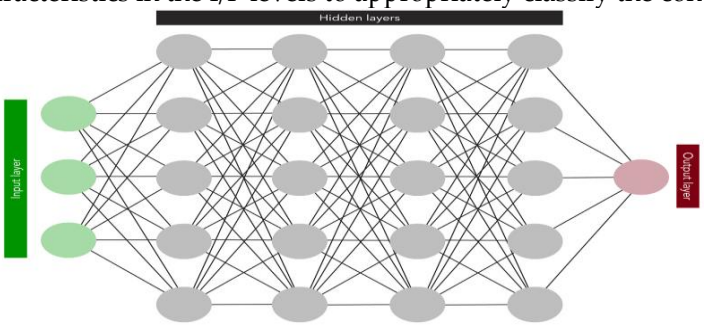

Figure 8. Artificial Neural Network Model

3.3.2. Support Vector Machine (SVM)

SVM is a recognized, extensively used classification technique that is typically used for linear classification. It is excellent for binary classification, but it is increasingly used for multiclass classification as well these days. Data belonging to the same space are categorized as belonging to the same class by the support vector machine's hyper plane, which it uses to partition the data into particular categories.

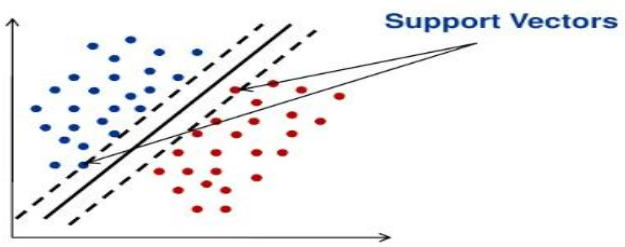

Figure 9. Support Vector Machine

3.3.3. Linear Discriminant Analysis (LDA)

The preprocessing technique linear discriminant analysis has been used in several publications. The controlled linear discriminants that are determined by the linear discriminant analysis will be quite helpful for categorizing segments into multiple types.

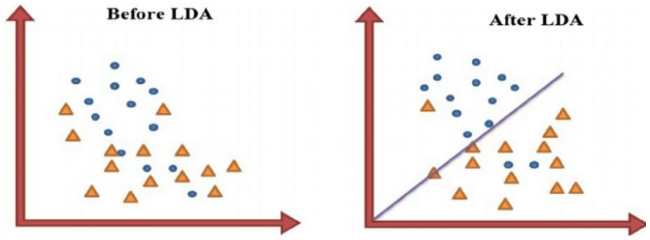

Figure 10. Linear Discriminant Analysis

3.4. Deep Learning Techniques For Classification

The use of deep learning algorithms for classification and identification is very common nowadays. The classification accuracy of the deep learning approach is always better than that of the earlier classifiers, which is one of its most noticeable features. If the input is in the form of a picture or sequence of photos, CNN model may be used for feature extraction in the case of leukemia categorization. As RNN models are appropriate for series inputs, we may utilize them if we've identified features from text or excel files.

3.5. Pros Of Current Methods

Use the extraction of morphological characteristics, whereas the combined methods classify leukemia using color, texture, and other microscopy aspects. A good degree of categorization may be obtained using well-chosen image processing techniques that result in effective feature extraction.

3.6. Cons Of Current Methods

The accuracy of categorization is the issue with the current technique that has been identified. Most methods have classification accuracy that varies from 75% to 95%, however employing deep learning models like convolutional neural networks and other comparable models, this accuracy may increase to 97% or higher.

4. Conclusions

A total of 34 studies on the automated detection and classification of acute leukemia using deep learning approaches are included in this systematic review. The article provided a summary of the many methods suggested for finding acute lymphoblastic leukemia. Different procedures were utilized in the different datasets before classification of acute leukemia. The many difficulties and barriers that the writers experienced when trying to identify and classify. In order to improve the outcomes of classification and detection, researchers who wish to study in the same field might investigate the approach for further classification. We come to the conclusion that several of the most recent machine learning algorithms can classify the leukemia disease. However, it is preferable to employ deep learning architectures for classifications when we have a huge collection of pictures.

References

1. Bennett, J., Catovsky, D., Daniel, M., Flandrin, G., Galton, D.A., Gralnick, H.R., & Sultan, C. (1976). Proposals for the Classification of the Acute Leukaemias French-American-British (FAB) Co-operative Group. British Journal of Haematology, 33.Inaba, H., Greaves, M., Mullighan, C.G.: Acute lymphoblastic leukaemia. Lancet 381, 1943– 1955 (2013)
2. Putzu, L., Caocci, G., & Ruberto, C.D. (2014). Leucocyte classification for leukaemia detection using image processing techniques. *Artificial intelligence in medicine, 62 3*, 179-91 .
3. Wong, C. K., Lam, C. W., Wu, A. K., Ip, W. K., Lee, N. L., Chan, I. H., Lit, L. C., Hui, D. S., Chan, M. H., Chung, S. S., & Sung, J. J. (2004). Plasma inflammatory cytokines and chemokines in severe acute respiratory syndrome. Clinical and experimental immunology, 136(1), 95–103. https://doi.org/10.1111/j.1365-2249.2004.02415.x
4. Meeusen, E. N., & Balic, A. (2000). Do eosinophils have a role in the killing of helminth parasites?. Parasitology today (Personal ed.), 16(3), 95–101. https://doi.org/10.1016/s0169-4758(99)01607-5
5. Kolaczkowska, E., & Kubes, P. (2013). Neutrophil recruitment and function in health and inflammation. Nature reviews. Immunology, 13(3), 159–175. https://doi.org/10.1038/nri3399
6. Thompson, S.C., Bowen, K.M., & Burton, R.C. (1986). Sequential monitoring of peripheral blood lymphocyte subsets in rats. *Cytometry, 7 2*, 184-93 .
7. Brown, A. L., Zhu, X., Rong, S., Shewale, S., Seo, J., Boudyguina, E., ... & Parks, J. S. (2012). Omega-3 fatty acids ameliorate atherosclerosis by favorably altering monocyte subsets and limiting monocyte recruitment to aortic lesions. Arteriosclerosis, thrombosis, and vascular biology, 32(9), 2122-2130.
8. Labati, R. D., Piuri, V., & Scotti, F. (2011, September). All-IDB: The acute lymphoblastic leukemia image database for image processing. In 2011 18th IEEE international conference on image processing (pp. 2045-2048). IEEE.
9. Mostafa, A., Fouad, A., Abd Elfattah, M., Hassanien, A. E., Hefny, H., Zhu, S. Y., & Schaefer, G. (2015). CT liver segmentation using artificial bee colony optimisation. Procedia Computer Science, 60, 1622-1630.
10. Zidan, A., Ghali, N. I., Hassanien, A. E., Hefny, H., & Hemanth, J. (2013). Level set-based CT liver computer aided diagnosis system. Int. J. Imaging Robot, 9, 26-36.
11. Anter, A. M., Hassanien, A. E., ElSoud, M. A. A., & Tolba, M. F. (2014). Neutrosophic sets and fuzzy c-means clustering for improving ct liver image segmentation. In Proceedings of the Fifth International Conference on Innovations in Bio-Inspired Computing and Applications IBICA 2014 (pp. 193-203). Springer, Cham.
12. Sahlol, A. T., Suen, C. Y., Zawbaa, H. M., Hassanien, A. E., & Abd Elfattah, M. (2016, July). Bio-inspired bat optimization algorithm for handwritten arabic characters recognition. In 2016 IEEE Congress on Evolutionary Computation (CEC) (pp. 1749-1756). IEEE.
13. Elhoseny, M., Farouk, A., Batle, J., Shehab, A., & Hassanien, A. E. (2020). Secure image processing and transmission schema in cluster-based wireless sensor network. In Sensor Technology: Concepts, Methodologies, Tools, and Applications (pp. 698-715). IGI Global.
14. Mohapatra, S., Patra, D., & Satpathy, S. (2014). An ensemble classifier system for early diagnosis of acute lymphoblastic leukemia in blood microscopic images. Neural Computing and Applications, 24(7), 1887-1904.
15. Mohammed, R., Nomir, O., & Khalifa, I. (2014). Segmentation of acute lymphoblastic leukemia using CY color space. International Journal of Advanced Computer Science and Applications, 5(11).
16. Biondi, A., Cimino, G., Pieters, R., & Pui, C. H. (2000). Biological and therapeutic aspects of infant leukemia. Blood, The Journal of the American Society of Hematology, 96(1), 24-33.
17. Aljaboriy, S., Sjarif, N., & Chuprat, S. (2019). Segmentation and detection of acute leukemia using image processing and machine learning techniques: a review. AUS, 26, 511-531.
18. Parthvi, A., Rawal, K., & Choubey, D.K. (2020). A Comparative study using Machine Learning and Data Mining Approach for Leukemia. *2020 International Conference on Communication and Signal Processing (ICCSP)*, 0672-0677.
19. Sahlol, A. T., Abdeldaim, A. M., & Hassanien, A. E. (2019). Automatic acute lymphoblastic leukemia classification model using social spider optimization algorithm. Soft Computing, 23(15), 6345-6360.
20. Pan, L., Liu, G., Lin, F., Zhong, S., Xia, H., Sun, X., & Liang, H. (2017). Machine learning applications for prediction of relapse in childhood acute lymphoblastic leukemia. Scientific reports, 7(1), 1-9.
21. Rehman, A., Abbas, N., Saba, T., Rahman, S. I. U., Mehmood, Z., & Kolivand, H. (2018). Classification of acute lymphoblastic leukemia using deep learning. Microscopy Research and Technique, 81(11), 1310-1317.
22. Ko, B. S., Wang, Y. F., Li, J. L., Li, C. C., Weng, P. F., Hsu, S. C., ... & Tang, J. L. (2018). Clinically validated machine learning algorithm for detecting residual diseases with multicolor flow cytometry analysis in acute myeloid leukemia and myelodysplastic syndrome. EBioMedicine, 37, 91-100.
23. Abdelsalam, E. M. N., Hussain, K. F., Omar, N. M., & Ali, Q. T. (2018). Computer Aided Leukemia Detection using Microscopic Blood Image Based Machine Learning" Convolutional Neural Network". Clinical Lymphoma, Myeloma and Leukemia, 18, S297.
24. Li, H., Xu, C., Xin, B., Zheng, C., Zhao, Y., Hao, K., ... & Zhou, Y. (2019). 18F-FDG PET/CT radiomic analysis with machine learning for identifying bone marrow involvement in the patients with suspected relapsed acute leukemia. Theranostics, 9(16), 4730.

25. Khalil, A. J., & Abu-Naser, S. S. (2022). Diagnosis of Blood Cells Using Deep Learning. International Journal of Academic Engineering Research (IJAER), 6(2).
26. Sahlol, A. T., Kollmannsberger, P., & Ewees, A. A. (2020). Efficient classification of white blood cell leukemia with improved swarm optimization of deep features. Scientific Reports, 10(1), 1-11.
27. Abas, S. M., & Abdulazeez, A. M. (2021). Detection and Classification of Leukocytes in Leukemia using YOLOv2 with CNN [J]. Asian Journal of Computer Science and Information Technology, 8(3), 64-75.
28. Sidhom, J. W., Siddarthan, I. J., Lai, B. S., Luo, A., Hambley, B. C., Bynum, J., ... & Shenderov, E. (2021). Deep learning for diagnosis of acute promyelocytic leukemia via recognition of genomically imprinted morphologic features. NPJ precision oncology, 5(1), 1-8.
29. Zolfaghari, M., & Sajedi, H. (2022). A survey on automated detection and classification of acute leukemia and WBCs in microscopic blood cells. Multimedia Tools and Applications, 81(5), 6723-6753.
30. Liu, Y., & Long, F. (2019). Acute lymphoblastic leukemia cells image analysis with deep bagging ensemble learning. In ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging (pp. 113-121). Springer, Singapore.
31. Das, P. K., & Meher, S. (2021). An efficient deep convolutional neural network based detection and classification of acute lymphoblastic leukemia. Expert Systems with Applications, 183, 115311.
32. Renuka, T. V., & Surekha, B. (2021). Acute-lymphoblastic leukemia detection through deep transfer learning approach of neural network. In Proceeding of First Doctoral Symposium on Natural Computing Research (pp. 163-170). Springer, Singapore.
33. Rawat, J., Singh, A., Bhadauria, H. S., Virmani, J., & Devgun, J. S. (2017). Classification of acute lymphoblastic leukaemia using hybrid hierarchical classifiers. Multimedia Tools and Applications, 76(18), 19057-19085.
34. Andrade, A. R., Vogado, L. H., de MS Veras, R., Silva, R. R., Araujo, F. H., & Medeiros, F. N. (2019). Recent computational methods for white blood cell nuclei segmentation: A comparative study. Computer methods and programs in biomedicine, 173, 1-14.
35. Karami, K., Akbari, M., Moradi, M. T., Soleymani, B., & Fallahi, H. (2021). Survival prognostic factors in patients with acute myeloid leukemia using machine learning techniques. PloS one, 16(7), e0254976.
36. Schouten, J. P., Matek, C., Jacobs, L. F., Buck, M. C., Bošnački, D., & Marr, C. (2021). Tens of images can suffice to train neural networks for malignant leukocyte detection. Scientific Reports, 11(1), 1-8.
37. Raina, R., Gondhi, N. K., Singh, D., Kaur, M., & Lee, H. N. (2022). A Systematic Review on Acute Leukemia Detection Using Deep Learning Techniques. Archives of Computational Methods in Engineering, 1-20.
38. Elhassan, T. A. M., Rahim, M. S. M., Swee, T. T., Hashim, S. Z. M., & Aljurf, M. (2022). Feature Extraction of White Blood Cells Using CMYK-Moment Localization and Deep Learning in Acute Myeloid Leukemia Blood Smear Microscopic Images. IEEE Access, 10, 16577-16591.
39. Jayavikash, K. P., Gopinath, P., Nandheeswaran, U., Sivabalan, R., & Bharathi, T. D. (2021, May). Detection of Leukemia Using Machine Learning Algorithms. In Journal of Physics: Conference Series (Vol. 1916, No. 1, p. 012220). IOP Publishing.
40. Arivuselvam, B., & Sudha, S. (2022). Leukemia classification using the deep learning method of CNN. *Journal of X-ray science and technology*, *30*(3), 567–585. https://doi.org/10.3233/XST-211055
41. Das, P. K., Nayak, B., & Meher, S. (2022). A lightweight deep learning system for automatic detection of blood cancer. Measurement, 191, 110762.
42. Rezayi, S., Mohammadzadeh, N., Bouraghi, H., Saeedi, S., & Mohammadpour, A. (2021). Timely Diagnosis of Acute Lymphoblastic Leukemia Using Artificial Intelligence-Oriented Deep Learning Methods. Computational Intelligence and Neuroscience, 2021.
43. Sashank, G. V. S., Jain, C., & Venkateswaran, N. (2021). Detection of Acute Lymphoblastic Leukemia by Utilizing Deep Learning Methods. Machine Vision and Augmented Intelligence—Theory and Applications: Select Proceedings of MAI 2021, 796, 453.
44. Bukhari, M., Yasmin, S., Sammad, S., El-Latif, A., & Ahmed, A. (2022). A Deep Learning Framework for Leukemia Cancer Detection in Microscopic Blood Samples Using Squeeze and Excitation Learning. Mathematical Problems in Engineering, 2022.
45. Shaheen M, Khan R, Biswal RR, Ullah M, Khan A, Uddin MI, Zareei M, Waheed A (2021) Acute myeloid leukemia (AML) detection using alexnet model. Complexity 2021:1–8
46. Kalaiselvi, D. T., Kumar, D. S., Subhashri, K. S., & Siddharth, S. M. (2020). Classification of leukemia using convolution neural network. Eur J Mol Clin Med, 7(4), 1286-1293.
47. Sakthiraj, F. S. K. (2022). Autonomous leukemia detection scheme based on hybrid convolutional neural network model using learning algorithm. Wireless Personal Communications, 126(3), 2191-2206.
48. Kumar, D., Jain, N., Khurana, A., Mittal, S., Satapathy, S. C., Senkerik, R., & Hemanth, J. D. (2020). Automatic detection of white blood cancer from bone marrow microscopic images using convolutional neural networks. IEEE Access, 8, 142521-142531.
49. Bibi, N., Sikandar, M., Ud Din, I., Almogren, A., & Ali, S. (2020). IoMT-based automated detection and classification of leukemia using deep learning. Journal of healthcare engineering, 2020.
50. Loey, M., Naman, M., & Zayed, H. (2020). Deep transfer learning in diagnosing leukemia in blood cells. Computers, 9(2), 29.
51. Vogado, L. H., Veras, R. M., Araujo, F. H., Silva, R. R., & Aires, K. R. (2018). Leukemia diagnosis in blood slides using transfer learning in CNNs and SVM for classification. Engineering Applications of Artificial Intelligence, 72, 415-422.

52. Genovese, A., Piuri, V., Scotti, F., & Vishwakarma, S. (2019). Touchless Palmprint and Finger Texture Recognition: A Deep Learning Fusion Approach. *2019 IEEE International Conference on Computational Intelligence and Virtual Environments for Measurement Systems and Applications (CIVEMSA)*, 1-6.
53. Aftab, M. O., Awan, M. J., Khalid, S., Javed, R., & Shabir, H. (2021, April). Executing spark BigDL for leukemia detection from microscopic images using transfer learning. In 2021 1st International Conference on Artificial Intelligence and Data Analytics (CAIDA) (pp. 216-220). IEEE.
54. Zhou, M., Wu, K., Yu, L., Xu, M., Yang, J., Shen, Q., ... & Zhao, L. (2021). Development and evaluation of a leukemia diagnosis system using deep learning in real clinical scenarios. Frontiers in Pediatrics, 616.
55. Eckardt, J. N., Schmittmann, T., Riechert, S., Kramer, M., Sulaiman, A. S., Sockel, K., ... & Middeke, J. M. (2022). Deep learning identifies Acute Promyelocytic Leukemia in bone marrow smears. BMC cancer, 22(1), 1-11.
56. Lin, G., Adiga, U., Olson, K., Guzowski, J. F., Barnes, C. A., & Roysam, B. (2003). A hybrid 3D watershed algorithm incorporating gradient cues and object models for automatic segmentation of nuclei in confocal image stacks. Cytometry Part A: the journal of the International Society for Analytical Cytology, 56(1), 23-36.