



White Blood Cell Cancer (Acute Lymphoblastic Leukemia) Detection using Deep Learning

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ABSTRACT

Cancer, a term encompassing various diseases, has the potential to impact any part of the body. Acute lymphoblastic leukemia's (ALL) main target is white blood cells. It is a malignancy that is extremely dangerous and potentially fatal. Improved patient outcomes and an efficient course of therapy depend on the early and precise identification of ALL. The advances in using deep learning algorithms for automated ALL identification from minuscule white blood cell pictures are examined in this review study. We examine the drawbacks of conventional diagnostic techniques and emphasize how deep learning algorithms may improve diagnostic precision. This study gives insights into the present status of ALL detection using deep learning, reviews recent research initiatives, and examines several deep learning architectures, datasets, and assessment metrics typically utilized in the area. Additionally, we discuss the limitations and prospects of this technology in the context of improving the diagnosis and prognosis of ALL.

Keywords: ALL detection, Blood Cancer Detection, Acute Lymphoblastic Leukemia Detection, Deep Learning

Introduction

Blood cells play a critical role in human body's circulatory system as they carry vital materials including oxygen, nutrition, hormones, and waste products. These blood cells are produced in the bone marrow, which include the differentiating and hematopoietic maturation of stem cells into different kinds of blood cells. This process is called as hematopoiesis.

The three primary types of blood cells are:

- **Red Blood Cells (Erythrocytes):** Hemoglobin is a special protein that is found in red blood cells. It binds oxygen in the lungs so that they can transport them where it's needed. Moreover, they also help in getting rid of carbon dioxide from our body by transporting it back to the lungs, where it is exhaled, from the tissues.
- **White Blood Cells (Leukocytes):** WBCs are essential to humans because the immune system depends on them as they protect our bodies from pathogens and external invaders. They play a role in several immunological responses, such as the release of cytokines, the generation of antibodies, and phagocytosis.
- **Platelets (Thrombocytes):** Platelets consist of small cell fragments that help in wound healing and the clotting of blood. They prevent excessive bleeding by clinging to damaged blood vessel walls and release chemicals that stimulate clot formation.

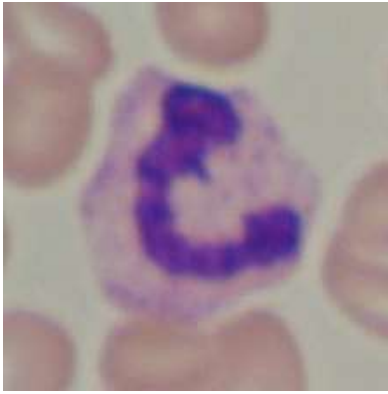


Figure 1: Normal Blood Image

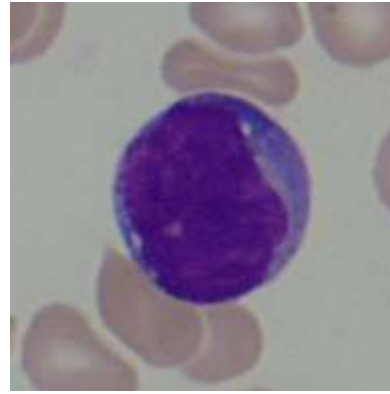


Figure 2: Image with Leukemia

Blood cancers are of several types; generally they are classified into three main groups:

- **Leukemia:** Leukemia is a kind of cancer that affects the blood and bone marrow. It arises when aberrant WBCs grow uncontrollably and push out healthy blood cells. Reduced production of platelets, red blood cells, and healthy white blood cells hinders the body's ability to fight infections and form blood clots. Fatigue, bruising easily, weight loss, and recurring infections are some of the signs of leukemia. It may be chronic or acute.
- **Lymphoma:** It is a type of cancer that starts in the lymphatic system, a crucial part of the human immune system that helps us fight off infections and diseases. When someone has lymphoma, the cells in their lymph nodes start to proliferate abnormally, which leads to the formation of tumors.
- **Myeloma:** Multiple myeloma is a form of cancer that targets plasma cells, a particular kind of white blood cell. These cells can be found in the bone marrow and are vital to the immune system. When someone has multiple myeloma, these plasma cells start to grow abnormally and produce too many harmful proteins. This can weaken the bones and lead to various complications. Multiple myeloma is more commonly diagnosed in older adults, who may experience symptoms like bone pain, fatigue, and increased infections.

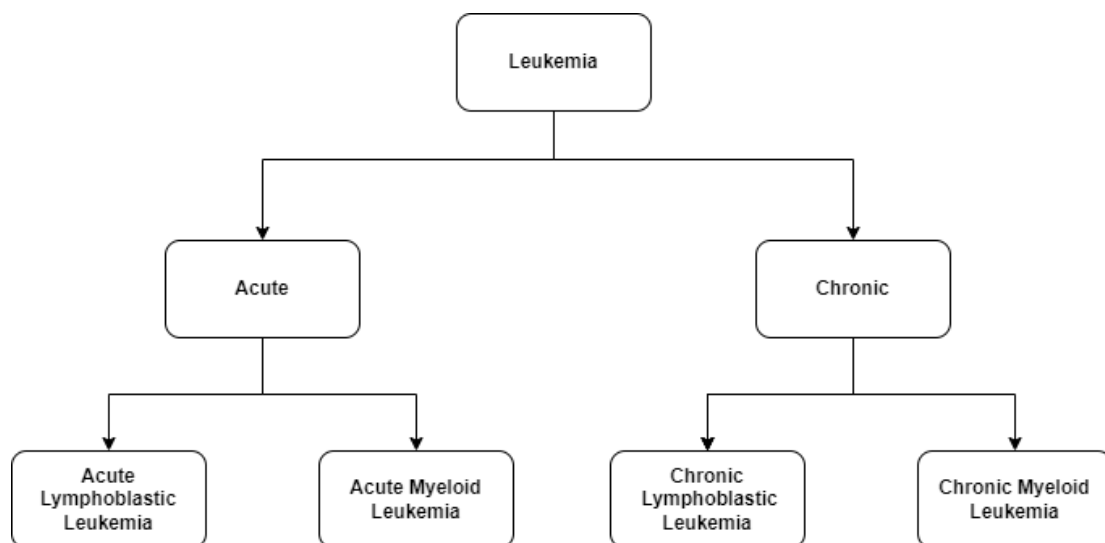


Fig 3. Types of Leukemia

Acute lymphoblastic leukemia is a type of cancer that primarily impacts white blood cells in children. Proper diagnosis and early identification are essential for successful treatment and better patient outcomes. The manual examination of blood samples under a microscope as part of conventional approaches for leukemia detection is tedious, time-consuming, and prone to human error. In addition, differences in the diagnosis made by medical professionals might arise from the subjective nature of visual assessment. The discipline of image analysis in medicine has been significantly revolutionized with the development of deep learning techniques, namely new convolutional neural networks (NCNNs), which have made it possible to accurately and automatically identify anomalies in medical pictures. Our study seeks to develop a dependable and efficient method for identifying ALL cells from tiny blood cell pictures by utilizing the power of deep learning. We want to improve ALL detection accuracy, speed, and reliability by utilizing NCNNs and novel data augmentation approaches. This will help patients with Acute Lymphoblastic Leukemia receive prompt diagnosis and treatment. This research has great potential to impact both the development of medical technology and the quality of cancer patient care.

Literature Survey

Several techniques for automatically detecting leukemia in microscopic images are being developed over time and documented in the literature. Traditional machine learning classifiers and deep learning algorithms are two examples of these methodologies. However, hybrid deep learning techniques and ensemble machine learning have been used in several ways for leukemia cancer detection. When analyzing images of infected blood cells, three phases are often involved: pretreatment procedures, extraction, feature selection, and classification. Research on several cancers, including myeloma, lymphoma, and leukemia, has been extensive.

“Y. Liu and F. Long [1]” utilized a deep bagging ensemble learning approach for ALL cell analysis in microscopic images, showcasing revolutionary deep-learning methods for precise leukemia cell classification [1]: ‘Classification in Cancer Cell Imaging,’ where they employed a deep bagging ensemble learning approach to analyze ALL cells in microscopic images. This paper shows how advanced deep learning methods are utilized to accurately classify leukemia cells.

“Jasmine Begum, A.R., and Abdul Razak [2]” emphasized the significance of computer-based image analysis in improving leukemia diagnosis accuracy through image analysis and processing techniques [2]. In a similar vein, leukemia is diagnosed from microscopic images using image analysis and processing techniques. Their work emphasized the significance of computer-based image analysis in improving leukemia diagnosis accuracy.

“S. Mandal, V. Daivajna, S. Kalsangra, V. Rajagopalan, and A. Kuchlous [3]” proposed a computer-assisted system for automatically identifying and labeling nuclei in leukemia cell images, contributing to the development of automated systems for leukemia cell identification [3]: They developed a computerized system to automatically find and label nuclei in images of leukemia cells, which helps medical professionals identify leukemia cells more easily.

“S. Mourya, S. Kant, P. Kumar, A. Gupta, and R. Gupta [4]” provided the “ALL Challenge dataset of ISBI 2019,” serving as a valuable resource for the development and evaluation of leukemia cell detection algorithms [4].

“Namayandeh SM, Khazaei Z, LariNajafi M, Goodarzi E, Moslem A [5]” examined the global incidence and fatality rate of leukemia in children between the ages of 0 to 14, incorporating data on human development indices and providing valuable insights into the epidemiological aspects of leukemia, adding a crucial global perspective to the literature survey [5].

At the “16th International Joint Conference on Computer Vision, Imaging, and Computer Graphics Theory and Applications (VISIGRAPP 2021), Maurício de Oliveira J and Dantas D [6]” explored the use of data augmentation and CNNs to study the classification of normal versus leukemic cells. They demonstrated how CNNs and data augmentation techniques can improve leukemia cell classification [6].

An IEEE Conference Publication focused on the “Classification of Blasts in Acute Leukemia Blood Samples Using k-Nearest Neighbors,” highlighting the role of traditional machine learning methods, such as k-NN, in leukemia cell classification [7].

“Raje, C., & Rangole, J. (2014). Detection of Leukemia in microscopic images using image processing. In International Conference on Communication and Signal Processing, ICCSP 2014 - Proceedings (pp. 255–259). Institute of Electrical and Electronics Engineers Inc. [8]

“A. B. Kulchynskiy, V. M. Kyjenko, W. Zukow, and I. L. Popovych [9]” In this paper they have researched about how EEG readings, heart rate variability, and white blood cell count are connected. It helps us understand how the brain and immune system interact in chronic inflammatory conditions like pyelonephritis and cholecystitis.

“J. Zhao, M. Zhang, Z. Zhou, J. Chu, and F. Cao [10]” The study introduces a novel approach to efficiently analyze and categorize leukocytes in medical images. This research contributes to the development of automated systems for diagnosing leukocyte-related conditions, offering potential improvements in medical diagnostics and treatment.

“S. Kant [11]”, “Leukonet Dct-based cnn architecture for the classification of normal versus leukemic blasts in b-all cancer [11]”. This paper presents a DL framework for differentiating between leukemic and normal blasts in B-ALL cancer. To create a reliable classifier, the model combines Optical Density (OD) space characteristics with Discrete Cosine Transform (DCT) domain data that are extracted using CNN. This research represents a novel approach to leukemia classification, potentially aiding in more accurate diagnosis and treatment planning for B-ALL cancer patients. Comprehensive tests have been carried out to validate the suggested LeukoNet classifier.

“I. Arel, D. C. Rose, and T. P. Karnowski [12]”, “Deep machine Learning” A new frontier in artificial intelligence research,” IEEE Computer Intell. Mag., vol. 5, no. 4, pp. 13–18, Nov. 2010 [12]: It discusses how deep learning techniques have become a significant area of focus in artificial intelligence research, offering new opportunities and challenges for advancing intelligent systems. This paper sheds light on the potential applications and implications of deep machine learning across various domains, highlighting its significance in shaping the future of artificial intelligence.

“R. Duggal, A. Gupta, R. Gupta, and P. Mallick [13]” presented the “Sd-layer, a stain deconvolutional layer for convolutional neural networks (CNNs) in medical microscopic imaging. [13].”

“L. Zhang, L. Lu, I. Noguez, R. M. Summers, S. Liu, and J. Yao [14]” looked at the application of deep CNNs for categorization of cervical cell. They introduced “DeepPap,” an advanced deep learning method for automating the categorization of cervical cells [14].

In their paper, “R. Gad, M. Talha, A. A. A. El-Latif et al. [15]” highlighted multi-algorithmic techniques in iris identification inside the “Cognitive Internet of Things (CIoT) framework [15].”

A. Rehman, "N. Abbas, T. Saba, S. I. u. Rahman, Z. Mehmood, and H. Kolivand [16]" emphasis on the precise and systematic categorization of ALL employing DL techniques, published in "Microscopy Research and Technique" [16].

“T. Tran, O.-H. Kwon, K.-R. Kwon, S.-H. Lee, and K.-W. Kang [17]”, in their conference paper in IEEE, Xi'an, China, December 2018, [17]: They discussed about the ability to distinguish between WBCs and RBCs in peripheral blood smear pictures is critical for the assessment and detection of number of illnesses, such as infection, leukemia, and some cancers. Prior to the segmentation stage, images are often improved in quality using a variety of image processing techniques. As a result, segmenting blood cells remains difficult. However, in this study, RBCs and WBCs are separated from blood smear images using DL semantic segmentation, an emerging technique. The outcome of the trial demonstrates that the model's global accuracy produced 89.45%. In addition, the precision with which WBCs and RBCs are divided.

In "Automated screening system for acute myelogenous leukemia detection in blood microscopic images [18]", “S. Agaian, M. Madhukar, and A. T. Chronopoulos [18]”, used a simple technique for classifying and automatically identifying AML in blood smears is offered. Unlike previous approaches, the proposed system classifies whole blood smear photos using a simple methodology instead of subimages. Nucleated cells are then identified and segmented using these techniques. The following tests were carried out using computer simulation: comparing results of certain current systems with proposed system; comparing effect of the Hausdorff dimension on the system before and after local binary pattern influence; and evaluating the efficacy of the suggested algorithms on both sub and full images. Analysis was done on eighty small blood pictures [18].

“S. Shafique and S. Tehsin [20]”, “Acute lymphoblastic leukemia detection and classification of its subtypes using pre-trained deep convolutional neural networks,” Technological innovation in cancer therapy Research & treatment [19].

Proposed Methodology

A step-by-step detailed explanation of proposed methodology is outlined throughout this section.

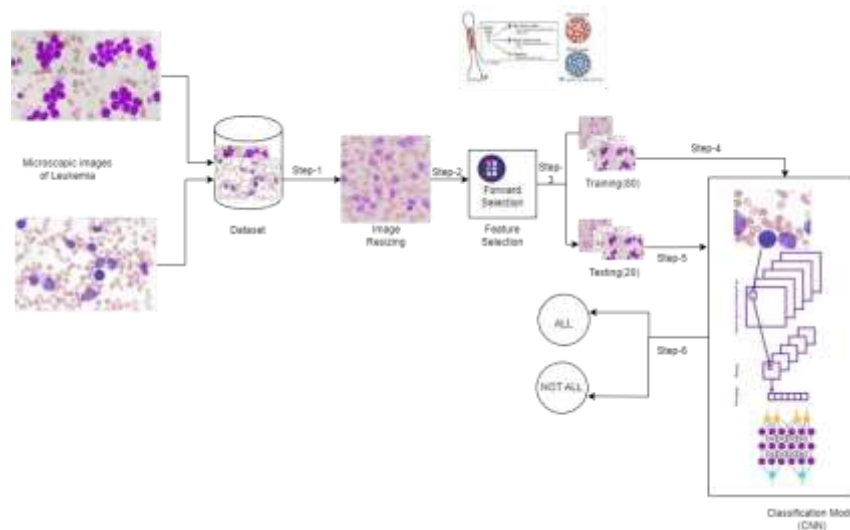


Fig 4 System Architecture

➤ Dataset:

To predict leukemia cancer, a model's performance is evaluated using various datasets such as CNMC leukemia, IDB, and SN-AM. Users have the flexibility to collaborate with other machine learning and deep learning experts, access different datasets on platforms like Kaggle, and create and analyze different models in diverse data science scenarios. The dataset sourced from the Kaggle repository is openly available for use. This approach allows for comprehensive evaluation and comparison of models in predicting leukemia cancer, enabling researchers to make informed decisions based on the data at hand.

➤ Data Collection and Preprocessing-

The dataset for the intended study is obtained from the Kaggle dataset, which is publicly available. The purpose of data preprocessing is to prepare the data in a clean, structured, and suitable format that facilitates accurate and efficient analysis. Data often contains errors, inconsistencies, and missing values. Data cleaning involves identifying and handling these issues. It may include removing duplicate records, filling in missing values, and correcting data entry errors.

- **Augmentation-** It's a method for making artificial datasets or growing existing datasets. Many training data points are needed for the deep learning model, and these are not usually available to the public, particularly in the medical field. In order to create a more accurate and widely applicable model, the existing data is therefore supplemented using various techniques, such as scaling, cropping, flipping, padding, rotation, translation, etc.
- **Feature Selection-** A major part of the preprocessing phase of data analysis is feature selection. In intelligent systems, features must provide enough attributes to classify the data or classes for subsequent analysis and decision-making to attain high accuracy. The outcomes won't be adequate if only a few parts are utilized. When numerous features are selected, performance becomes an issue. To improve accuracy, more features that are necessary can be added. Three feature selection methods were used in this study: Random Forest (RF), Recursive Feature Elimination (RFE), and ANOVA.

➤ **Use of Deep Learning Over Traditional Machine Learning:**

➤ **Traditional Machine Learning:** Conventional Machine Learning need manually designed features. Experts identify these characteristics based on their understanding of leukemia cells. Models produced by using these predetermined characteristics may be less accurate since they may not fully represent the complexity of the data.

➤ **Deep Learning (specifically Convolutional Neural Networks - CNNs):**

Specifically, deep learning (using CNNs, or convolutional neural networks): Automatic feature extraction: CNNs in particular, which are deep learning models, are capable of automatically extracting features from the data, in this example, blood stain photos.

Captures intricate patterns: CNNs are able to recognize minute patterns in the pictures that could be challenging for people to manually characterize. They can now acquire characteristics that are more useful in distinguishing between leukemic and healthy cells as a result.

Deep learning is changing the game when it comes to analyzing data, especially in medical imaging. Unlike traditional methods that rely on hand-crafted features, deep learning allows us to let the computer itself learn from the environment where the data is used. In medical image processing, deep learning has shown remarkable results, making it a breeze to create end-to-end networks with tools like CNN. Instead of manually extracting features for different tasks, machine learning models can now simply learn these features on their own, thanks to deep learning techniques. This shift towards more automated and adaptive methods is revolutionizing the field, making complex tasks much easier to tackle.

➤ **Classification Using Convolutional Neural Network (CNN):**

CNNs are a kind of deep neural network that is designed to detect complex features of data, especially for tasks like image classification. It is made up of neurons that work together to select and recognize important features in the input data. This specialized network structure allows CNNs to effectively process visual information, making them a powerful tool in computer vision and image analysis. By breaking down input images into smaller, more manageable pieces, CNNs can identify patterns and features that help to accurately classify and categorize images with remarkable precision.

The information technology sector has seen a significant rise in the need for a specific set of abilities in recent years: deep learning. The domain of deep learning is a subfield of machine learning where it utilizes algorithms influenced by neural networks or the structure of the human brain.

Neural networks are a term used to describe these structures. It instructs machines to do things that come naturally to people. Reinforcement learning, autoencoders, recurrent neural networks (RNN), and artificial neural networks (ANN) are examples of DL models. However, a single model—Convolutional Neural Networks (CNN), also referred to as ConvNets—has significantly advanced computer vision and image processing. CNNs are frequently used for visual image analysis. They are able to recognize and classify particular elements in pictures. Natural language processing, computer vision, medical image analysis, classification, and image and video recognition are some of their possible applications.

CNN uses the term "convolution" to refer to the mathematical function that is called convolution. Convolution is a special kind of linear operation where two functions are added together to produce a new function that describes how the other function modifies the first function's form. To put it simply, multiplying two matrices-representable pictures yields a result that may be utilized to extract characteristics from the image.

CNN consists of three layers:

- **Convolutional layer:**

It is the first layer of a CNN and is responsible for extracting features from an input image. This layer scans the input picture with convolutional filters, often referred to as kernels, in order to find patterns or features. These characteristics might be as basic as textures and edges or as intricate as forms.

- **Pooling layer:**

Often, a pooling layer comes after the convolutional layer. By down sampling the feature maps while keeping the most crucial data, a process known as pooling lowers their spatial dimensions.

A popular pooling method called "max-pooling" removes all other values apart from the maximum value and keeps it in a small area of the feature map. This lessens the workload on the computer and facilitates the creation of translation-invariant features.

- **Fully connected layer:**

This is the last layer of the architecture. It is used for making decisions based on the features learned in the previous layers. This layer may be used to classify the detected object or to predict its position.

First, we will train the convolution layer using the training dataset. We repeat the training of the convolution network until 10 epochs and then evaluate the network using the testing dataset.

4. Conclusion

This review focuses on the automated identification and categorization of ALL by deep learning methods. In summary, the application of Convolutional Neural Networks (CNNs) for Acute Lymphoblastic Leukemia (ALL) detection demonstrates significant progress in the field of medical image analysis. CNNs have shown the potential to enhance the accuracy and improve the efficacy of ALL diagnoses by automatically extracting vital features. These models, supported by techniques like data preprocessing, feature selection, and transfer learning, have shown remarkable success in recognizing patterns and abnormalities in cell morphology, texture, and color information performing the preprocessing on the data set which is split into two halves in a ratio 80:20. The 80 % of data will be sent to the CNN, classification model for classification. CNN can learn automatically from the raw data. Through numerous layers of convolutions, activations, and pooling, the network gains the capability to differentiate features. After training the model, 20% data will be given to the trained model for testing.

In conclusion, CNNs offer promising results for advancing the early detection of ALL. Their ability to uncover critical information in medical images holds the potential to make a meaningful impact in the fight against this disease.

5. Future Scope

There is a bright future ahead of us for applying deep learning to identify acute lymphoblastic leukemia (ALL). Artificial intelligence (AI)'s deep learning subgroup has demonstrated impressive skills in medical picture analysis, including the identification and categorization of several illnesses, including leukemia. To increase the accuracy rates of identifying leukemia cells from blood smears or bone marrow samples, deep learning models may be further improved and enhanced. Models that perform more accurately and efficiently than human specialists and conventional approaches can be created via continued study and improvement.

It is possible to create deep learning models that can constantly learn from fresh data and adjust to changing trends and patterns in the presentation and diagnosis of ALL. This flexibility makes sure that, even as the landscape of diseases shifts over time, the diagnostic algorithms continue to be applicable and efficient. Overall, there appears to be a bright future ahead for the application of deep learning in the detection of acute lymphoblastic leukemia, with potential uses in many areas of patient care, diagnosis, and therapy. Realizing the full potential of deep learning to improve outcomes for ALL patients will need multidisciplinary cooperation, ongoing research, and technical improvements.

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