# Detection and Classification of Acute Lymphoblastic Leukemia (ALL) from Blood Smear Microscopic Images

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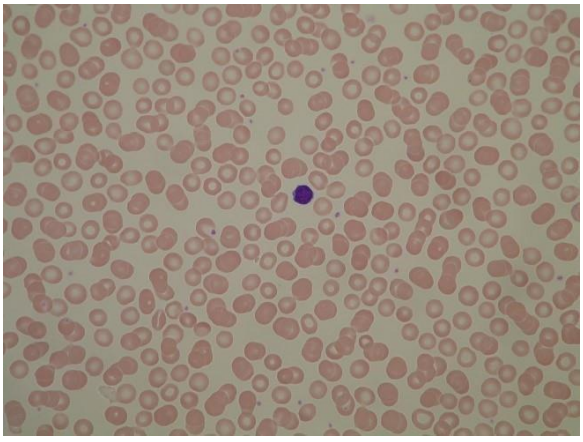
***Abstract*—White blood cells (WBC) which are also known as leukocytes, are a crucial part of the human body's immune system. Leukaemia is a haematological disorder that starts from the bone marrow and affects white blood cells (WBCs) due to mutations in DNA causing blood cell production to become out of control. This prevents the development of healthy blood cells. Acute lymphocytic leukemia (ALL) is a kind of cancer where the bone marrow forms many more lymphocytes. ALL can further be classified into L1, L2 and L3 based on the structure of nucleus and cytoplasm. Automatic detection of leukemia or detection of blood cancer is a tough job and it is very much essential in healthcare centres. ALL identification and interpretation using peripheral blood smear (PBS) pictures plays an important role in early identification in screening and treatment. Conventionally, the method was achieved manually by a skilled technician during a considerable amount of time however the examination of those PBS pictures by laboratory users typically contains diagnostic errors owing to the nonspecific nature of ALL signs and symptoms that usually results in misdiagnosis. So, to achieve more accurate classification results we use powerful segmentation and deep learning techniques to train the model on these images. Firstly, we pre-process the images to apply segmentation methods on them. The proposed model will attempt to eradicate the probability of errors in the manual process and it can be used as a supporting analysis tool for pathologists. So, various Artificial Intelligence-based ALL classification methods and approaches are analysed in a well-defined manner with advantages and disadvantages.**

***Keywords*—Acute Lymphoblastic Leukemia, Classification, Detection, Deep Learning Techniques.**

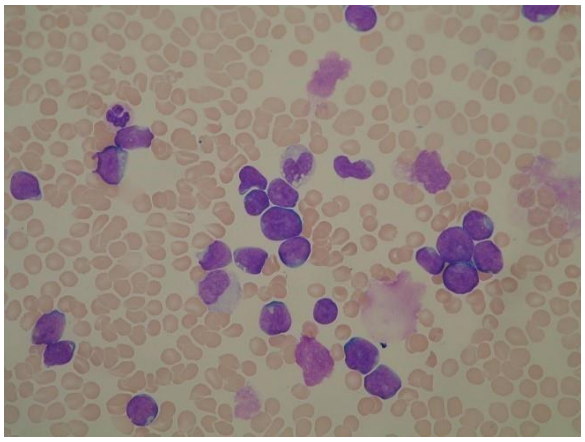
## I. INTRODUCTION

Cells that comprise of blood are of three types: platelets, white blood cells and red blood cells. The normal blood cell growth, hampered by the exponential growth of abnormal blood cells, is the main cause of blood cancer. There are three main types of blood cancers: Leukemia, Myeloma, and Lymphoma. [1][2] Leukemia is a production of abnormal leukocytes (WBCs) in the human body. Based on the rapidity of generation, they can be classified as chronic or acute, and based on the originator cell they can be further classified as Myeloid or Lymphoid.

Acute lymphocytic leukemia (ALL) is a type of cancer of the blood and bone marrow where the bone marrow creates a large number of lymphocytes. It is a rapidly growing blood-cancer that severely affects lymphoid progenitor cells in the bone marrow, blood, and extramedullary sites [4] "Acute" indicates the fast progress of the disease, and if it does not get treatedin the early stages, it might prove to be fatal within a short span [1], [2]. According to data reported in Ref. [7], in 2015, there were around 876,000 individuals who experienced ALL worldwide, and it triggered 111,000 deaths. According to the latest WHO data published in 2020, Leukemia deaths in India reached 33,383 or 0.39 percent of total deaths. According to French American British (FAB) classification, ALL is further categorized into 3 subtypes: L1, L2, and L3. L1 type cells are usually small in size and are of similar shape with little cytoplasm. Their nucleus is discoid and well structured. L2 type cells have shape variability and are oversized as compared to L1. Their nucleus is not regular and contains dissimilarities in their cytoplasm. L3 type cells are of identical shape and normal size with round or oval nuclei. They have a fair amount of cytoplasm which incorporates vacuoles. They are often larger than L1.[3]

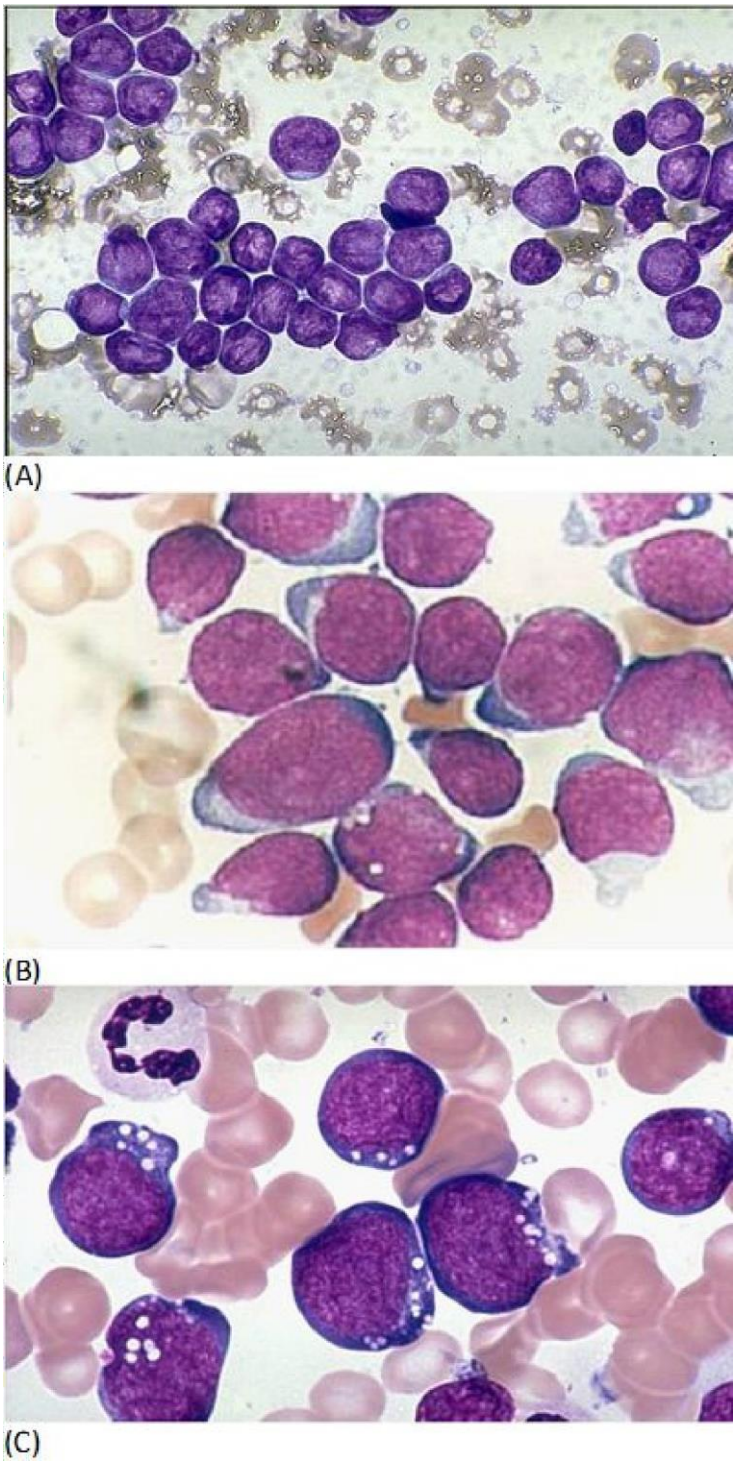


Non-ALL [18]



ALL [18]

Usually, the dark-purple color of those WBC cells makes it straightforward to spot them, however the assessment and processing become very tough due to the pattern and texture-based variations. Leukocytes may well be recognized by their form or size; however, one problematic issue is that they are flanked by other parts of the blood which include red blood cells and platelets. The shape of lymphocytes is somewhat regular, and their nuclei have uniform and flat borders. The lymphocytes have the same border and small cavities within the protoplasm, referred to as vacuoles similarly, as within the nuclei spherical particles named as nucleoli. On the contrary, the visual look of cancer cells is somewhat kind of like traditional cells in microscopic pictures, that makes it onerous to differentiate between them. The screening of malignant neoplastic disease by a specialist through human blood samples could be a crucial and long task.[5] It is extremely crucial for the specialists to diagnose the presence of leukemia beside its specific type to stop medical issues and confirm the best treatment of malignant neoplastic disease. It would end in premature death if the intervention is neglected and if diagnosing is completed later within the disease's progression. The survival rate of patients has inflated up to 70% with early assessment and intervention [8]. Hence, at the sooner stages of acute lymphoblastic leukemia, its diagnosing and effective treatment are essential.




FAB (French American and British) morphological classification of lymphoblasts. (A) L1 lymphoblasts. (B) L2 lymphoblasts. (C) L3 lymphoblasts.[4]

Manual detection of medicine disorders like leukemia needsa well-experienced skilled physician or doctor for the correct early detection. Additionally, the complicated nature of blood cells, intensity irregularity, blurring, weak edges, presence of noise, cell overlapping makes the task of manual detection using microscopic analysis of blood cells quite tough. Manual detection of leukemia may be a time consuming and error prone method. On the other hand, recent advancements in AI techniques like machine learning and deep learning facilitate correcting systems for detecting medicine disorders. Additionally, in pre-processing and segmentation steps, special care ought to be taken to suppress the preceding problems. However, in deep learning approaches, the extraction of more substantial deep features in addition to efficient classification is performed among a neural network system for achieving further precise detection by nullifying the results of noise, intensity irregularity, weak edges, blurring, and cell overlapping to a great extent. Hence, more efficient computer aided detection (CAD) systems facilitate in additional correct early detection of diseases like leukemia. It helps the doctor in correct diagnosis and treatment to save precious lives. Computer vision-based systems have been already developed within the past to notice such medical disorders. Machine Learning and Deep Learning have emerged as a most popular medical image analysis approach for more correct disease detection and diagnosis.

## II. RELATED WORKS

Researchers applied various methods which incorporate Deep Learning (DL), Deep Neural Networks (DNN), and Medical Image Processing to detect leukemia cells from blood smear images and bone marrow images. ALL can be classified further into three types. Thus, identifying the type of ALL (L1, L2, L3) is necessary.

M. Bennet Rajesh and S. Sathiamoorthy [12] have proposed a GkNN method for classification of leukemia images and the features are extracted using the graylevel co-occurrence matrix, and for pre-processing, median filter is employed. The accuracy of 96.57 percent was obtained, which was better than SVM and MLPNN techniques. Niranjana Sampathila et al [14] proposed an intelligent deep learning algorithm that uses the microscopic images of blood smears as the input data. This algorithm implemented a convolutional neural network (CNN) to predict the leukemic cells from the healthy blood cells. The custom model was trained and tested using the microscopic images available as open-source data. Maximum accuracy of 95.54 percent, specificity of 95.81 percent, sensitivity of 95.91 percent, F1-score of 95.43 percent, and precision of 96 percent were obtained. Deepika Kumar el al [11] proposed a model that first pre-processes the images to extract its best features required for training the DCNN (Dense Convolutional neural network) framework to predict the type of cancer cells present. Overall accuracy achieved was 97.2 percent.

Amjad Rehman et al [13] proposed a method to classify ALL into its subtypes using stained bone marrow images. A robust segmentation and deep learning techniques with the convolutional neural network was used to train the model on the bone marrow images. Experimental results revealed that the proposed method achieved 97.78 percent accuracy. M. A. Hossain el al [15] have employed Apriori algorithm for generating explainable rules for leukemia prediction. The decision tree model proposed in their experiments has achieved 0.63 of Mathew's Correlation Coefficient (MCC) and 0.783 of area under Receiver Operating Characteristic (ROC) curve on the test set.

The research about leukemia classification in recent years is based on computer vision. The most common algorithm in this approach consists of several rigid steps: image pre-processing, clustering, morphological filtering, segmentation, feature selection or extraction, classification, and evaluation [14]. Almost all authors have used machine learning techniques to detect blood cells in images and to classify cells in images. They extract features representing points, regions, or objects of interest and then use those features to train a model to classify or learn patterns in the image data. Feature extraction usually involves processing each image with some image processing operations, such as calculating gradients to extract the discriminative information from each image. In this paper, we used the method of deep learning to learn characteristics of leukemia shape to classify normal and abnormal cell images.

## III. METHODOLOGY

### *A. Dataset:*

We have used the ALL-IDB1 dataset created by Fabio Scotti, Associate Professor Dipartimento di Informatica, Universita degli Studi di Milano. This dataset is composed of` 108 images collected during September, 2005. It contains about 39000 blood elements, where the lymphocytes have been labelled by expert oncologists. The images are taken with different magnifications of the microscope ranging from 300 to 500. Out of the 108 images, 59 are healthy and 49 are ALL-affected images.

Link:
https://www.kaggle.com/datasets/nikhilsharma00/leukemiadat aset

### *B. Architecture of CNN*

In this work we have created and trained a Convolutional Neural Network, to detect Acute Lymphoblastic Leukemia (ALL) using Keras and TensorFlow. The architecture created

is based on the network proposed in the Acute Leukemia Classification Using Convolutional Neural Network in Clinical Decision Support System paper by Thanh.TTP, Giao

N. Pham, Jin-Hyeok Park, Kwang-Seok Moon, Suk-Hwan Lee, and KiRyong Kwon. We tend to project a network containing four layers. The primary three layers are for detection work and the alternative two layers (Fully connected and Softmax) are for classifying the features. The input image has the scale 50x50x3. The receptive field (or the filter size) is 5x5. The stride is 1, that is we tend to move the filters one pixel at a time. The zero-padding is 2. It enables us to regulate the spatial size of the output image (we will use it to precisely preserve the spatial size of the input volume so that the input and output breadth and height are the same). Throughout the experiment, we tendto find that in our case, changing the size of the first image throughout the convolution decreases the accuracy by about 40 percent. So, the output image after convolution layer 1 has a similar size with the input image. The second convolution layer has a similar structure as the first convolution layer. The size of the filter is 5x5, the stride is 1 and also the zero-padding is 2. The quantity of feature maps (the channel or the depth) in our case is 30. If the quantity of feature maps is less than or more than 30, the accuracy can decrease by half. By experiment, we tend to find a 50 percent decrease in accuracy if we try to take away Convolution layer 2. The Filter size of Max-Pooling layer (25x25) is 2 and its stride is also 2. The fully connected layerhas a pair of neurons. At the end for the classification, the Softmax layer is used.

*C. Proposed model*

Medical image analysis with deep learning ways is obtaining outstanding attention attributable to its excellent performance. Here, we have discussed the deep learning-based classification method: Convolutional Neural Network (CNN). The main accomplishment about CNN compared to its predecessors is thatit mechanically identifies the relevant options with non-human supervision. The structure of CNNs was impressed by neurons in human and animal brains, just like a standard neural network. Especially, a complex sequence of cells in a cat's brain forms the visual cortex. This sequence is simulated by CNN. Goodfellow et al. know 3 key edges of the CNN: equivalent representations, distributed interactions, and parameter sharing. CNNs are used to create full use of 2nd input-data structures like image signals. This operation utilizes a particularly tiny range of parameters that simplifies the coaching method and speeds up the network. This is often similar to the visual cortex cells. Notably, tiny regions of a scene are detected by these cells instead of the entire scene (i.e., these cells spatially extract the native correlation within theinput, like local filters over the input).

In comparison to different image classification algorithms, they use a bit of pre-processing. CNN works better for correlated multidimensional data inputs like images and thus helps to get the most relevant features out of it without correlation. [17] A CNN model consists of an input layer, an output layer, and multiple hidden layers.

- Convolution Layer

A convolution layer may be a basic part of the CNN design that performs feature extraction, which generally consists of a mix of linear and nonlinear operations, i.e., convolution operation and activation operation. This layer is employed for extracting numerous options from the input pictures. The operation of convolution is performed during this layerbetween the input image and a filter of a specific size. By slippery this filter over the input image and taking the real between the filter and the elements of the input image withrelevancy the dimensions of the filter the Feature map is obtained. Feature map is the output which provides US info concerning the image like the corners and edges. Later, this feature map is then given as the input to different layers to find out many different options of the input image. The convolution layer in CNN passes the result to the following layer once applying the convolution operation within the input. Convolutional layers in CNN profit loads as they makesure the spatial relationship between the pixels is unbroken. This layer is used for extracting varied choices from the input photos. The computation of convolution is performed throughout this layer between the input image and a filter of a specific size. This filter is slided over the input image and taking the real between the filter and the elements of the input image with respect to the size of the filter the Feature map is obtained. Feature map is the output that provides USinfo regarding the image just like the corners and edges. Later, this feature map is fed to the additional layers to spot different options of the input image.

*Convolution*

Convolution could be a specialized kind of linear operation used for feature extraction, where a little array of numbers, referred to as a kernel, is applied across the input, that is an array of numbers, referred to as a tensor. Element-wise product between every element of the kernel and the input tensor is calculated at every location of the tensor and summed to get the output worth within the corresponding position of the output tensor, referred to as a feature map

*Nonlinear activation function*

The outputs of a linear operation like convolution are then passed through a nonlinear activation function. Although smooth nonlinear functions, like sigmoid or hyperbolic

tangent (tanh) function, were used antecedently as they are a result of mathematical representations of a biological neuron behaviour, the most common nonlinear activation function used presently is the rectified linear unit (ReLU), that merely computes the function: f(x)=max (0,x).

*Pooling layer*

A pooling layer provides a typical down sampling operation that reduces the in-plane spatial property of the feature maps to introduce a translation independent to the tiny shifts and distortions, and reduce the quantity of resulting learnable parameters. It is of note that there is no learnable parameter in any of the pooling layers, whereas filter size, stride, and padding are hyperparameters in pooling operations, kind of like convolution operations.

*Max pooling*

It is the most popular form of pooling operation, that extracts patches from the input feature maps, outputs the maximum value in every patch, and discards all the remaining values. A filter of size 2×2 with a stride of 2 is usually employed in this max pooling layer. This down samples the in-plane dimension of feature maps by a factor of two. In contrast to height and width, the depth dimension of feature maps remains unchanged.

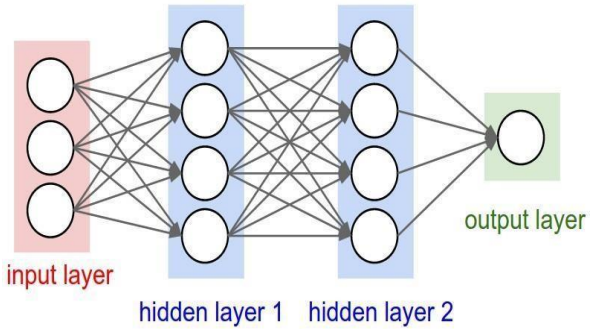



Fig. Fully-Connected-Layer [19]

*Fully connected layer*

The output feature maps of the ultimate convolution or pooling layer is usually planate, i.e., reworked into a one-dimensional (1D) array of numbers (or vector), and connected to at least one or more fully connected layers, additionally called dense layers, wherein each input is connected to each output by a learnable weight. Once the features are extracted by the convolution layers and down sampled by the pooling layers are created, they are mapped by a set of fully connected layers to the ultimate outputs of the network, like the chances for every category in classification tasks. The final fully connected layer generally has a constant number of output nodes as the number of categories. Every fully connected layer is followed by a nonlinear operation, like ReLU, as described above.

*Last layer activation function*

The activation function applied to the last fully connected layer is typically completely different from the others. An applicable activation operation must be chosen per task. An activation function applied to the multiclass categorification task could be a softmax function that normalizes output real values from the last fully connected layer to focus on class probabilities, wherever every value ranges between zero and one and all values add to one.

In this paper, we are going to use a Convolution Neural Network (CNN) to perform classification and extract features from raw images.

## IV. RESULT

We have used the ALL-IDB1 dataset which is composed of 108 cell images (59 normal cell images, 49 abnormal cell images). The accuracy rate of the recognition of Acute Lymphoblastic Leukemia by our proposed CNN model achieved is 92.8 percent.

## V. CONCLUSION AND FUTURE SCOPE

In this paper we have been given a Convolutional Neural Network model which will facilitate in classifying leukemia from alternative WBCs. The dataset used is Acute lymphocytic leukemia Image information for Image process by Fabio Scotti from Department of Information Technology - University of Milan. We have applied CNN to the construction modules with four layers consisting of feature detection and classification. In future, the accuracy of this model may be improved by implementing feature extraction before applying the CNN model. Additionally, the CNN layers may be increased to produce an improved result. Classification of ALL into its subtypes like L1, L2, and L3 may be done to assist in increasing the survival rates by eliminating human errors. We powerfully believe this model can facilitate building an enhanced dataset which in turn will help strengthen the model after further analysis and model building.

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