ALLD: Acute Lymphoblastic Leukemia Detector

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Abstract. Acute Lymphoblastic Leukemia (ALL) is a life-threatening type of cancer wherein mortality rate is unquestionably high. Early detection of ALL can reduce both the rate of fatality as well as improve the diagnosis plan for patients. In this study, we developed the ALL Detector (ALLD), which is a deep learning-based network to distinguish ALL patients from healthy individuals based on blast cell microscopic images. We evaluated multiple DL-based models and the ResNet-based model performed the best with 98% accuracy in the classification task. We also compared the performance of ALLD against state-of-the-art tools utilized for the same purpose, and ALLD outperformed them all. We believe that ALLD will support pathologists to explicitly diagnose ALL in the early stages and reduce the burden on clinical practice overall.

Keywords. Leukemia, Acute lymphoblastic leukemia, Deep learning, Computer aided diagnosis (CAD).

1. Introduction

Leukemia is a malignant, progressive deadly health condition in which abnormal, distorted proliferation of leukocytes and its precursor occur due to error in blood-forming organs. Subsequently, normal blood cell production will cease. The principal type of cell involved in this malignancy is commonly classified as lymphoid or myeloid, and chronic or acute, according to percentage or degree of leukemic cell differentiation in the bone marrow. The environmental risk factors have been well studied; however, the exact cause of leukemia is still unknown [1]. There are four main types of Leukemia classified based on severity level and affected cells type: chronic lymphocytic leukemia, chronic myeloid leukemia, acute myeloid leukemia, and acute lymphoblastic leukemia (ALL). ALL is one of the two classes of acute leukemia that develops from immature forms of lymphocytes cells in the bone marrow. ALL is recorded as the most common type of leukemia among children but the least common type in adults [2]. However, the fatality rate for ALL in adults is relatively higher than other types of acute leukemia. In most

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leukemia-affected white blood cells, the average cell often changes to about two times the size of the red blood cells surrounding them. In most ALL affected cells, the nucleus area occupies almost 80-90% of the whole cell and leaves about 20-30% of cell area for the cytoplasm [2]. One of the diagnostic approaches for ALL is the microscopic inspection of blood cells. Both the malformed white blood cells as well outnumbered lymphoblasts may hint at the early onset of ALL and requires the assessment by an 0experienced pathologist [3]. Detecting ALL based on pathological images is tedious work and subjective by nature as it depends upon the evaluation by the pathologist. In some cases, this kind of individual and subjective interpretation may lead to a delay in the proper diagnosis plan for ALL patients.

To overcome these challenges and to support the pathologists, Computer Aided Diagnosis (CAD) systems may play a crucial role in detecting ALL in a precise manner. Many of the included studies focused on the classification of the images of lymphoblast cells from healthy individuals and leukemia patients. Sahlol et al. proposed an automatic ALL classification model using a social spider optimization algorithm. The proposed kNN-based model achieved 95.67% classification accuracy [3]. While Neoh et al. proposed an intelligent decision support system for leukemia diagnosis using microscopic blood cell images. Their Support Vector Machine (SVM)-based model systems attained the highest 96.67% accuracy [4]. Singhal and Singh have used the local binary pattern-based texture features to detect ALL, and the proposed SVM classifier was 93.84% reliable [5]. Recently, deep learning (DL)-based models have gained huge attention for the same task. In 2021, Genovese et al. used the transfer learning-based ResNet18 model to achieve 97.92% accuracy [6]. The same group has used adaptive unsharpening image processing on the images dataset to develop a VGG16-based model achieving 96.84% accuracy [7]. Table 1 summarizes the list of recent publications based on ML models for ALL detection.

Table 1 Existing Tools for the classification of classification of ALL-IDB2 dataset

Reference	Model	Accuracy	Remarks
[5] (2016)	SVM	93.84	Local binary pattern-based texturing
[3] (2020)	kNN	95.67	Social spider optimization
[4] (2015)	SVM	96.67	Texture, color, shape of nucleus and cytoplasm
[7] (2021)	VGG	96.84	Unsharpening of image
[6] (2021)	**ResNet**	**97.92**	Transfer learning based on histopathology database

In this study, we introduce the ALL Detector (ALLD), a deep learning-based model to distinguish ALL patients from healthy persons based on the image of peripheral blood samples.

2. Materials and Methods

2.1. Dataset Collection

We collected microscopic blood cell images from the ALL-IDB2 database [2]. ALL-IDB2 dataset contains 260 images, each having 257*257 resolution. Out of these, half (n=130) of the images were from healthy individuals and the remaining images (n=130) were from leukemia patients. The image of lymphoblast cells was captured using a Canon PowerShot G5 camera. The images were shared in *.tif* format in the publicly available database. Figure 1 shows examples of images from healthy individuals (A-C) and leukemia patients (D-F).
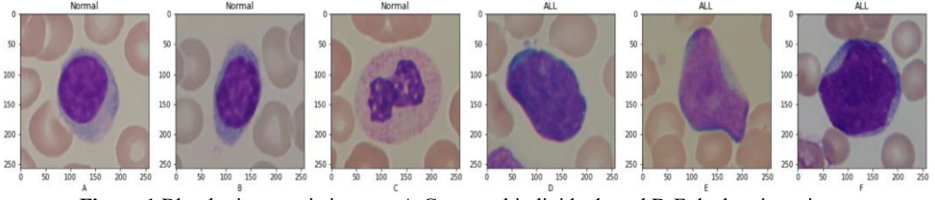
Figure 1 Blood microscopic images. A-C: normal individuals and D-F: leukemia patients.

2.2. Image Preprocessing

To increase the robustness of our experiment, we preprocessed the input images using a variety of image augmentation techniques: cropping, rotation, horizontal and vertical flipping, shearing, brightness and contrast perturbations, etc. Using image augmentation allows the network to become less sensitive to small changes in the inputs. This is possible because in each epoch, the input images undergo a subset of these operations parameterized with a random set of parameters. This forces the network to learn a general representation of the distribution rather than dataset-specific aspects, which reduces overfitting.

2.3. Development of Deep Learning Model ALLD

For the development of a deep learning-based model, we used fast.ai version 2.4.1. We split the data set in an 80-20 fashion. Twenty percent of the images were used for testing. The remaining 80% of images were used for training and validating the trained model. We considered ALL patients as the positive class and the healthy individuals as the negative class for the model. We used VGG16, VGG19, ResNet34, and ResNet50 for distinguishing ALL patients from healthy individuals. The Adam algorithm was used for the optimization of parameters. For momentum parameters ($\beta1$ and $\beta2$), we used default values of 0.9 and 0.99, respectively. We used a batch size of 64 in our experiments. Additionally, we used the one cycle policy for scheduling the learning rate with a maximum learning rate of 10^{-33} over a total of 20 epochs. The first 2 epochs updated the parameters of only the classification layer, whereas the last 18 updated all layers with differential learning rates. The experiments were carried out on a computer with a Ryzen 5800x CPU, 64 GB of DDR4 memory, and an Nvidia RTX 3090 GPU. For performance evaluation, we considered multiple standard performance evaluation metrics such as (i) Accuracy, (ii) Sensitivity, and (iii) Specificity to measure the effectiveness of the proposed ML models.

3. Results and Discussions

The performance of different DL-based models is highlighted in Table 2. Based on the performance results, we observed that ResNet-based models demonstrated the best performance in classifying the ALL group from the healthy group with the highest accuracy. As the ResNet-based model performed the best, we propose the ResNet-based model as the final ALLD model for ALL detection. ALLD outperformed all the existing machine learning models for the same purpose (Table 1 and Table 2).

Table 2 Machine Learning models performance for developing ALLD

Model	Accuracy	Sensitivity	Specificity
VGG16	94.230	95.652	93.103
VGG19	98.076	95.652	100.00
ResNet34	98.076	100.00	96.551
ResNet50	98.076	100.00	96.551

This study has some limitations worth mentioning. We worked on a relatively smaller-sized dataset of 260 images. In the future, we plan to evaluate the proposed model based on a larger dataset. Moreover, the participants' lifestyle, socio-demographic information, and genetic information were not available in the ALL-IDB2 database. Integrating such information, based on its availability, would provide more insight into ALL diagnoses.

4. Conclusions

Early detection, classification, and identification of ALL are very important for effective treatment to be provided in a timely manner, and, most importantly, on a person's survival. Automated detection and classification of acute leukemia is one of the emerging technology directions previously used. ALLD outperformed multiple existing tools utilized for the same purpose, and we believe it will also support pathologists in making a conclusive diagnosis plan in a treatment setting. We believe our tool ALLD will support both the early detection of ALL as well as the proper diagnosis plan for the patients.

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