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RESEARCH ARTICLE

Leukemia Classification using a Convolutional Neural Network of AML Images

Karrar A. Kadhim[a,b*], Fallah H Najjar[c], Ali Abdulhussein Waad[a,b], Ibrahim H Al-Kharsan[d], Zaid Nidhal Khudhair[a,b], Ali Aqeel Salim[e]

[a]School of Computing, Faculty of Engineering, Universiti Teknologi Malaysia, 81310 UTM Johor Bahru, Johor, Malaysia; [b]Computer Techniques Engineering Department, Faculty of Information Technology, Imam Ja'afar Al-Sadiq University, Baghdad, Iraq; [c]Department of Computer Systems Techniques, Technical Institute of Najaf, Al-Furat Al-Awsat Technical University, Iraq; [d]Department of Computer Technical Engineering, College of Technical Engineering, Islamic University, Najaf 54001, Iraq; [e]Laser Center and Physics Department, Faculty of Science, Universiti Teknologi Malaysia, 81310 UTM Johor Bahru, Johor, Malaysia

Abstract Among the most pressing issues in the field of illness diagnostics is identifying and diagnosing leukemia at its earliest stages, which requires accurate distinction of malignant leukocytes at a low cost. Leukemia is quite common, yet laboratory diagnostic centres often lack the necessary technology to diagnose the disease properly, and the available procedures take a long time. They are considering the efficacy of machine learning (ML) in illness diagnostics and that deep learning as a machine learning method is becoming critical. This study proposes a convolutional neural network (CNN) deep learning model for leukemia diagnosis utilizing the AML (acute myeloid leukemia) dataset. The classification using the proposed method achieved results that exceeded 98% accuracy, the sensitivity of 94.73% and specificity of 98.87%.

Keywords: Leukemia, classification, CNN, AML, ALL-ADB1.

Introduction

Due to the absence of effective treatment options, leukemia has been ranked as the main cause of mortality among different types of cancers in most nations. Leukemia begins in the organs that produce blood and spreads to other tissues via the blood [1, 2]. For this reason, early detection of the tumor is crucial, as leukemia has a high potential for rapid dissemination [3]. Electric magnetic field exposure, hereditary abnormalities, extremely high levels of radiation, and exposure to certain chemical solvents are the most common causes of leukemia [4]. There is considerable variation in prognosis estimates between different age groups, sexes, races, and subtypes of leukemia [5]. Given its ability to invade and ultimately destroy the White Blood Cells (WBCs) and ultimately spread throughout the body's circulatory system, leukemia is widely regarded as one of the most lethal forms of cancer [6]. It is the bone marrow that leukemia tumors most often begin, and it is the blood stream where they eventually cause irreparable harm to the host [7]. Even when a specialist in the area makes the diagnosis of leukemia, there is room for error owing to insufficient training or misleading data in the microscopic image [8]. To improve detection accuracy in this area, computer-based algorithms can be highly useful. Leukemia is defined as myelogenous when it affects one of the two kinds of white blood cells (WBCs) found in human blood: monocytes or granulocytes [9-12].

Since the exact origin of AML is yet unclear, a proper diagnosis of AML is typically challenging [13]. It also has many symptoms with the flu and other common illnesses, including high temperature, extreme fatigue, and joint and muscle pain. A thorough blood count, renal function and electrolytes, and a liver

***For correspondence:**
ameer1986@graduate.utm.my

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enzyme and blood count should all be performed if the mentioned symptoms are present. Chemotherapy, radiation therapy, a bone marrow transplant, or biological therapy are all viable options for treating AML because the disease is not staged [14]. Figure 1 demonstrate the contrast between normal cells from AML patients and those from non-AML patients.

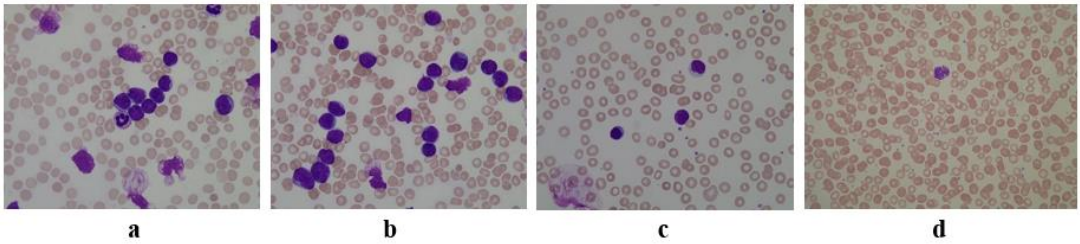

Figure 1. Microscopic Images: a, b Myeloblasts from AML patients. c, d Healthy cells from non-AML patients

Several research over the past two decades have used machine learning (ML) and computer-aided diagnostic techniques for laboratory image analysis to overcome the difficulties of a late diagnosis of leukemia and classify the disease into distinct subtypes [15]. These studies have examined blood smear image for the purposes of identifying and quantifying different forms of leukemia.

Proposed Technique CNN Classifier for Leukemia

This section, we discuss the proposed approach for detecting Leukemia from a single blood smear. In this work, we offer a system for detecting leukemia, and its components are shown in Figure 2. This system makes use of a new hybrid segmentation model and a classifier.

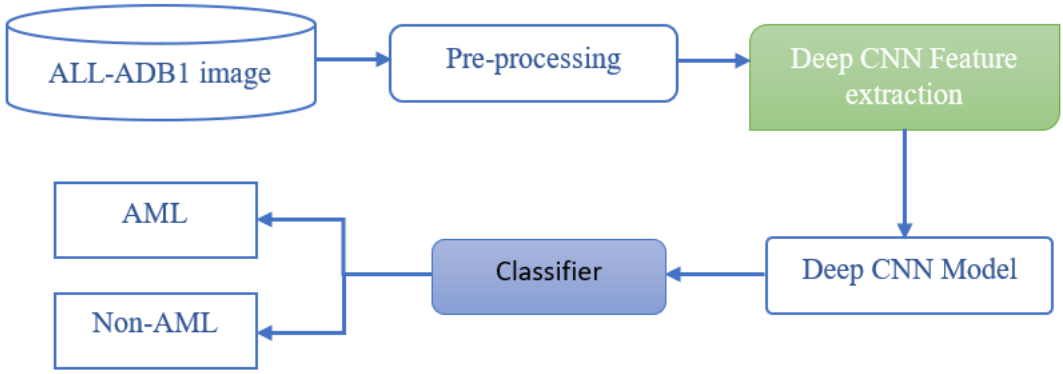

Figure 2. The proposed CNN method for classifier

Pre-processing

Consider about the repository of single-cell blood smear photographs. Pre-processing is applied to the images already in the database to enhance categorization outcomes. Images are resized in pre-processing to ensure they are of an appropriate size for use in controlling the segmentation job. Reducing the size of an image makes segmentation easier [16]. After that the filters are applied to images based on the image's denoise filter [17,18]. A convolutional neural network technique is then used to train the images, which aids in extracting the images' features. A variety of techniques, including the CNN model, are utilized for medical image categorization. Figure 3 illustrates a set of images of ALL-ADB1 datasets are used in this article.

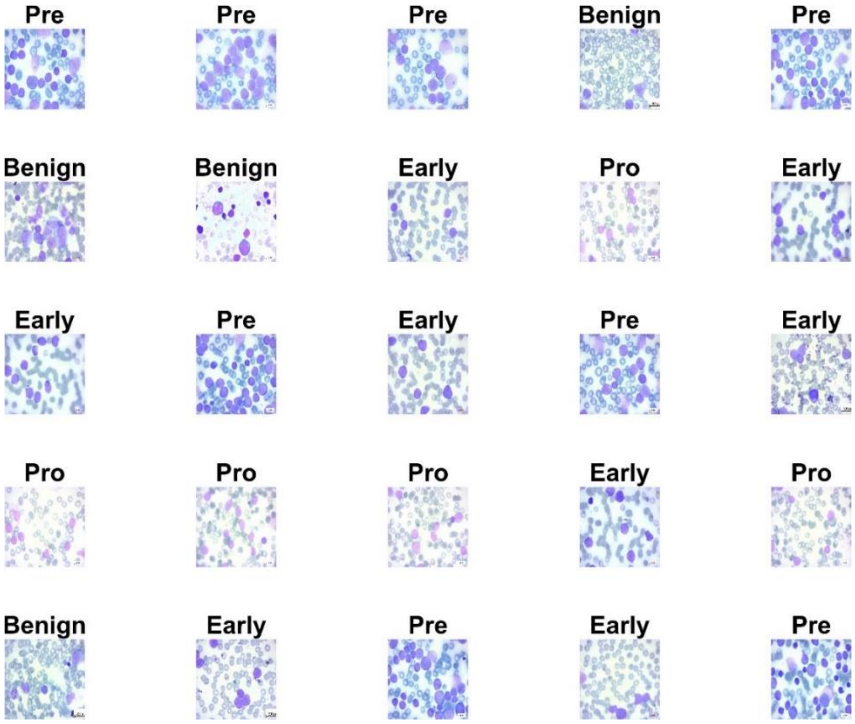

Figure 3. A collection of datasets images illustrates types of leukemia

Proposed CNN to Diagnosis Leukemia Cancer

The model of the convolutional neural network is given features that have been retrieved from an application for the aim of classification. Following that, the CNN model performs the categorization based on the extracted characteristics [19].

In this part, we will quickly go through the fundamentals of the Deep CNN's structure. In the past, CNNs were not set up in a staged fashion as they are now, which is why the introduction of Deep CNN has been so beneficial. Convolutional layers, or conv layers, pooling layers, or Max-pooling layers, and Fully Connected (FC) layers make up a deep convolutional neural network [20]. Since the convolutional layer is the most important layer, it receives the D features extracted from the segmented image samples. The goal of the convolutional layer is to generate the feature map used in the classification process. Next, the POOL layer conducts subsampling on the feature maps before passing them on to the FC layer for classification. The output compilation is performed by feeding the weight parameters depending on the kernel to each layer [21].

The convolutional layer then uses those characteristics to further analyze the images. There are several convolutional layers in the Deep CNN, all interconnected by weight parameters. The Convolutional layer creates a feature map by fusing the learned weights with the feature vector. When the activation function is applied to the data in the Convolutional layer, the data is sent to the subsequent layer. When using a Deep Neural Network (CNN), the feature vector that makes its way to the network's convolutional layer is represented [22]. As seen in Figure 4, the proposed technique employs a deep CNN model.

The Rectified Linear Unit (ReLU) and Pooling (Max-pooling) layer is responsible for controlling the Convolutional layer's outputs through its activation function [23]. In addition, the ReLU layer guarantees efficiency, which facilitates the management of massive networks. Fully Connected layers: Once the output of the pooling layer has been obtained, the information is then passed to the FC layer. To carry out the categorization, the inputs that have been sent to the FC layer are placed via high-level reasoning [24].

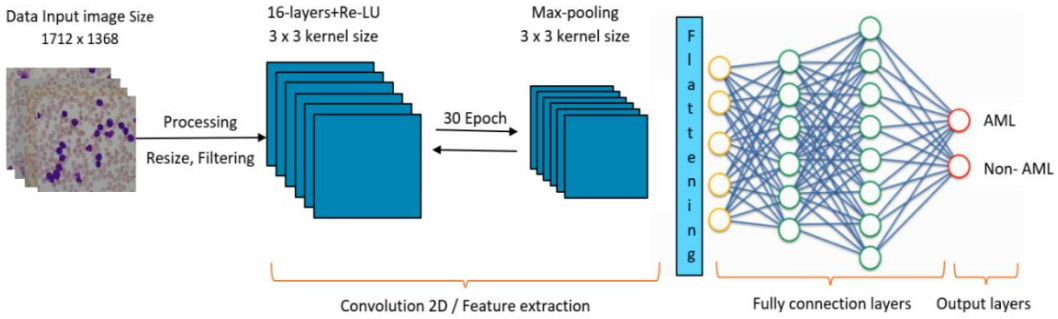

Figure 4. Convolution Neural Network in the proposed method

The Experiment Setup

All work on the proposed Deep CNN classifier is carried out within the MATLAB environment, with the following system requirements for the experiments being taken into account: personal computer running Windows 11; 16 GB of RAM; Intel I7 processor; and 6 GB of graphics processing unit.

Description of the Database

In order to put the suggested strategy into action, images of white blood cells at the microscopic level are taken from the ALL-ADB1 Database. There are a total of 100 photos in this collection. 45 of these photos depict blast cells, whereas the remaining 55 depict non-blast cells. It's estimated that there are 35,000 different blood components in there. In this data collection, lymphocytes have been categorized by oncology specialists [26-28].

Performance Metrics

The evaluation criterion is a primary component in assessing the classification methods [27], and it serves as a guide for developing and improving the classification models. All measurements are derived from these four-factor values: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) [28,29]. See Table 1: Definition of the measuring parameters.
The following common measurements are the most used in the classification field: PPV (predictive power) and sensitivity (recall) are the other two metrics that are used for quantitative assessment and comparison. The harmonic mean of these two metrics is also utilized (f1-score). True positive, true negative, false positive, and false negative are referred to as TP, TN, FP, and FN. the evaluation metrics are outlined as follows:

$$accuracy = ((TP + TN))/ ((TP + FP + FN + TN))$$

$$precision=TP/ ((TP + FP))$$

$$recall= TP/ ((TP + FN))$$

$$f\ 1\text{-}score= ((2TP))/ ((2TP + FP + FN))$$

Table 1. Definition of the measuring parameters

Parameter	Definition
TP	Pattern correctly classified as positive.
FN	Pattern incorrectly classified as negative.
FP	pattern incorrectly classified as positive
TN	Pattern correctly classified as negative.

Experimental Results

The experimental findings of the deep CNN model are shown in this section. The samples from the ALL-ADB1 database are supplied here, reflecting the blood smear input samples utilized in this work. Table 2 shows the work outputs from this work.

The results of the proposed model showed classification accuracy at a rate exceeding 98% as shown in Figure 5 that showing the results of proposed deep CNN. While Figure 6 also shows the results of the training phase and the number of epochs of implementation, as well as the results of accuracy and losses for deep CNN model.

Table 2. Experimental results of the Deep CNN Proposed

Class	TP	TN	FP	FN	ACC	PRE	SEN	F1	SP
Benign	41	271	3	9	0.9630	0.9318	0.8200	0.8723	0.9679
Early	96	220	6	2	0.9753	0.9412	0.9796	0.9600	0.9910
Pre	96	226	2	0	0.9938	0.9796	1.0000	0.9897	1.0000
Pro	79	243	1	1	0.9938	0.9875	0.9875	0.9875	0.9959

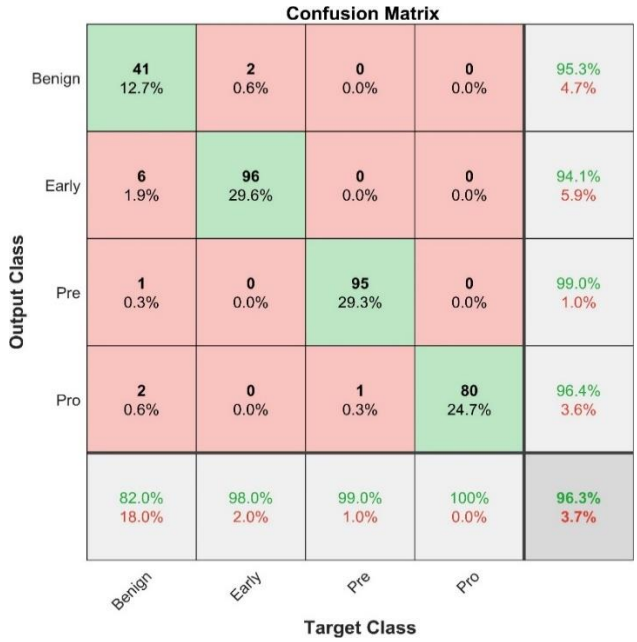

Figure 5. Classification results of leukemia by types of disease

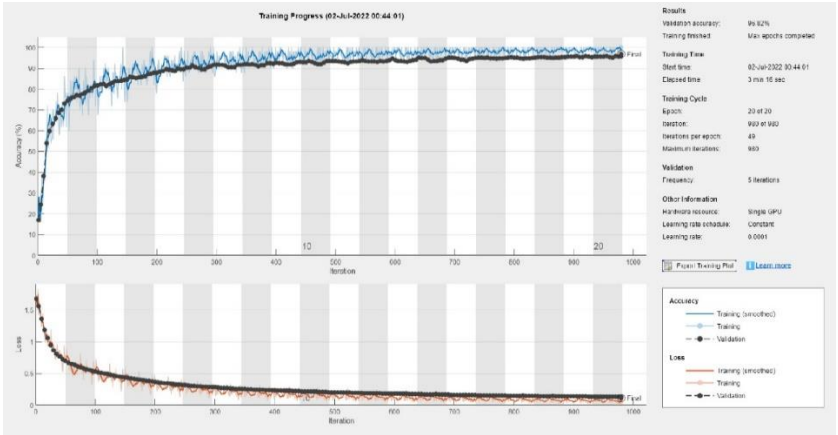

Figure 6. Illustrate the results of the training for deep CNN model

Conclusion

In this study, we present the methodology behind our automated AML screening system, which uses microscopic images of blood samples to detect the presence of the disease. The American Society of Hematology provided the 100 high-resolution photos used in this study. The provided system is capable of performing a variety of automated processing tasks, such as colour correlation, segmentation of the nucleated cells, and efficient validation and categorization. To effectively classify cells, we build a feature set that makes use of the cell's shape, colour, and texture properties. According to the findings, this characteristic reliably distinguishes cancerous from normal cells. More samples will need to be collected in order to improve performance, and an overall system for cancer categorization will need to be constructed.

Conflicts of Interest

The author(s) declare(s) that there is no conflict of interest regarding the publication of this paper.

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