Detection and Classification of Leukemia using Machine Learning

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***Abstract*—Leukemia is a haematological malignancy characterized by the abnormal proliferation of cancerous cells inside the bone marrow, resulting in the disruption of normal blood cell production. It induces a rise in the number of leukocytes. Leukemia is characterized by an aberrant proliferation of white blood cells. Leukemia is a heterogeneous disease characterized by the presence of several subtypes. Certain forms of leukemia have been observed to impact the paediatric population. Adults can be affected by several forms of leukemia. Leukemia is categorized according to the progressive elevation of white blood cell counts. There are two main classifications of leukemia, namely Acute leukemia and Chronic leukemia. When the rate of progression is gradual, individuals are diagnosed with chronic leukemia. Acute leukemia is characterized by a rapid proliferation of white blood cells. These two categories are further subdivided into two distinct subtypes for each form of leukemia. Our models were constructed using a customized version of the VGG13 architecture. The VGG13 architecture is a widely used Convolutional Neural Network (CNN) model that consists of many layers. The object recognition model is considered to be innovative. The models are utilized to categorize the microscopic blood smear images provided as input into three distinct categories: Acute Lymphocytic Leukemia or normal cells. The model achieves 92% accuracy in classifying ALL cells assisting automated identification of leukemic cells.**

Keywords— leukemia detection, leukemia classification, VGG, CNN, Acute leukemia

I. INTRODUCTION

Leukemia is a haematological malignancy characterized by the infiltration of abnormal white blood cells, leading to the development of Myelodysplastic Syndrome and Myeloproliferative disorders. This pathological condition gives rise to a disturbance in the functionality of stem cells, resulting in an abnormal proliferation of immature neutrophils. The types of white blood cells are characterized by their immaturity, indicating that they have not reached full maturation. The most prevalent kind of white blood cells is the condition known as Leukemia, specifically characterized by the presence of immature neutrophils. Newly generated tissues are linked to the process of combating infections or repairing damaged tissues. The proliferation of leukemia disorders within the bone marrow exhibits unregulated growth. Leukemia cells exhibit ongoing proliferation of white blood cells, with a higher incidence observed in paediatric populations, but it predominantly manifests in adult individuals. The treatment of leukemia, a group of disorders that adversely affect the bone marrow, poses a significant challenge due to its intricate nature. However, the administration of medication can be determined according to the severity of the infection resulting from leukemia. Leukemia encompasses various disease subtypes that are differentiated by distinct white blood cell populations and their respective rates of proliferation. Leukemia is categorized into two main types: Acute Leukemia and Chronic Leukemia. These two classifications encompass other subcategories, including lymphocytic and myeloid. Additionally, these classifications are determined by the proliferation of leukocytes. Acute Leukemia exhibits a notable rate of expansion and is categorized into two main subtypes: Acute Lymphocytic Leukemia (ALL) and Acute Myelogenous Leukemia (AML). In contrast to Acute Leukemia, Chronic Leukemia is characterized by a gradual progression of the disease. It is further categorized into Chronic Lymphocytic Leukemia (CLL), Chronic Myelogenous Leukemia (CML), and Chronic Myelomonocytic Leukemia (CMML). The manifestation of symptoms in leukemia exhibits variability due to the existence of many subtypes of the disease. Common symptoms observed in individuals diagnosed with various forms of leukemia include high fever, feelings of nausea leading to vomiting, nocturnal perspiration, and general bodily weakness. Additional symptoms of leukemia include rapid and unexplained weight loss, persistent and excessive bleeding, intense headaches, respiratory difficulties, sensations of coldness, frequent episodes of fever, and discomfort in the bones, among others.

II. LITERATURE SURVEY

Zakir Ullah et al. [1] introduced a Convolutional Neural Network (CNN) model incorporating an attention module known as Efficient Channel Attention (ECA). This attention module is designed to extract profound information from images, hence enhancing the quality of feature representation and improving classification outcomes. The C-NMC dataset is commonly employed for the purpose of distinguishing between normal and acute lymphoblastic leukaemia (ALL) cells through classification techniques. To address the issue of a restricted dataset size and class imbalance, researchers have

implemented data augmentation techniques. The utilisation of ECA has been implemented subsequent to each VGG16 block in order to enhance the process of feature extraction. The model is evaluated for the purpose of binary class classification, namely distinguishing between normal cells and ALL cells. However, it should be noted that the model has not been tested for identifying different forms of leukaemia.

Fatma M. Talaat et al. [2] employ a classification model to differentiate between cells that are healthy and those that are impacted by leukaemia. The methodology encompasses the stages of picture pre-processing, feature extraction, and classification. The image preprocessing phase encompasses several data augmentation techniques, including but not limited to reflection, rotation, mirroring, Gaussian blurring, and translation. The process of feature extraction is performed via Convolutional Neural Networks (CNN), while the classification task is accomplished using an optimised version of CNN. The model is capable of categorising the images into two distinct groups: normal cells and aberrant cells. Fuzzy logic optimisation is employed in the optimisation of a convolutional neural network (CNN) classifier. The optimised convolutional neural network (CNN) has been determined to be a superior model compared to the conventional CNN. In their study, Abuared et al. [3] employed the Transfer Learning technique on the VGG19 model for the purpose of classifying photos related to skin cancer. In their study, Batool et al. [6] introduced a tailored model utilising EfficientNet-B3 architecture for the purpose of classifying white blood cell pictures into two categories: acute lymphoblastic leukaemia (ALL) cells and normal cells. The proposed model employs a reduced number of trainable parameters in order to improve the performance and efficiency of leukaemia classification.

Ratley et al. [5] conducted a comprehensive analysis of published research studies pertaining to the diagnosis of leukaemia, employing a range of machine learning and deep learning methodologies. The data preprocessing stage involved the examination of many characteristics of the input image, including morphological, textural, and GLCM features. Additionally, various models, such as Artificial Neural Networks (ANN), Support Vector Machines (SVM), Linear Discriminant Analysis (LDA), and Convolutional Neural Networks (CNN), were evaluated. A tabular representation was provided, encompassing a comprehensive description of diverse datasets and models, along by an evaluation of their respective performance. In their study, Das et al. [7] provided an extensive analysis of several approaches in preprocessing, feature extraction, segmentation techniques, machine learning (ML) and deep learning (DL) models, available datasets, and the inherent obstacles associated with improving the accuracy of leukaemia detection models.

Hossain et al. [16] conducted an evaluation of different supervised machine-learning methodologies in order to predict leukaemia at an early stage. The data was obtained from a diverse group of patients, including those diagnosed with Leukaemia and those without Leukaemia, who underwent regular check-ups at various hospitals. The researchers primarily focus on 17 symptoms in order to forecast the likelihood of leukaemia in a patient. The objective is to categorise individuals diagnosed with leukaemia and those who are in good health by utilising the identified characteristics. The Naive Bayes (NB), K-Nearest Neighbour (KNN), Random Forest (RF), Linear Regression (LR), Adaboost, and other machine learning methods are commonly employed to evaluate the performance of a model. The Random Forest classifier and the Decision Tree exhibit superior performance compared to other classifiers. In their study, Nizar Ahmed et al. [17] conducted experiments on the architecture of Convolutional Neural Networks (CNN) as well as other machine learning algorithms, including naive Bayes, support vector machine, k-nearest neighbour, and decision tree. The objective was to perform binary classification of one leukaemia type (ALL and healthy samples) and to classify all leukaemia subtypes. The findings of the study indicated that CNN exhibited superior performance compared to the other machine learning algorithms, achieving high accuracy. The utilisation of convolutional neural networks (CNN) for the diagnosis of various subtypes of leukaemia through the analysis of microscopic blood cell pictures necessitates a substantial training dataset. Given the relatively modest size of the dataset, data augmentation is employed to artificially generate additional training examples. The CNN model demonstrates superior performance in accurately distinguishing healthy and leukaemia cells, namely Acute Lymphoblastic Leukaemia (ALL).

The field of transfer learning has experienced significant growth and is increasingly recognized as a superior methodology for medical imaging analysis, owing to its exceptional performance. Transfer learning is a commonly utilized approach in the classification of acute leukemic cells and normal cells. This method effectively extracts more meaningful features and does not necessitate a large dataset of images for training. It achieves this by leveraging a pre-trained network and transferring its weights to the classification task. In their study, P. K. Das et al. [12] introduced a novel transfer-learning approach utilizing SqueezeNet for the purpose of classifying malignant and benign cases. The researchers incorporated channel shuffling and pointwise-group convolution techniques to enhance the model's performance. In their study, A. Abhishek et al. [11] introduced a multilevel classification approach for Acute Lymphoblastic Leukemia (ALL) utilizing the transfer learning technique. ResNet50 and MobileNet are commonly employed for the purpose of feature extraction. The recovered features are subsequently fed into supervised models, such as support vector machine and logistic regression, as well as an unsupervised model known as the k-Nearest Neighbor classifier. This approach has been observed to generate favorable levels of accuracy. In a separate study, the researchers employed transfer learning techniques to classify leukemia by utilizing a dataset consisting of 1358 microscopic blood smear images. The VGG16 model, which has been pre-trained, is further refined using the leukemic dataset to accurately categorize images into three distinct classes: acute, chronic, and healthy cells.

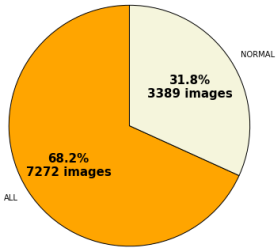
In recent times, there has been an increasing interest in utilizing quicker convolutional neural network (CNN) models, such as YOLO and its several iterations, for the purpose of classifying medical images. The You Only Live Once (YOLO) model has undergone several iterations, namely YOLO, YOLOv2, YOLOv3 [10], and YOLOv4 [14]. These versions represent advancements in the field of

convolutional neural networks (CNNs) and are designed to enhance the speed and efficiency of object detection tasks. The object identification model utilize a Convolutional Neural Network (CNN) architecture to effectively carry out both localization and classification tasks. Additionally, it incorporates a convolutional layer to accurately forecast the precise location of a bounding box. Magpantay et al. [10] conducted an experiment utilizing the YOLOv3 model for the purpose of classifying both ALL and normal cells. The model yielded favorable outcomes in terms of training accuracy. In their study, Fatichah et al. [14] conducted a comparative analysis of the YOLO and Mask R-CNN models in terms of their efficacy in detecting and classifying subtypes of acute leukemic cells. The researchers employed multiple evaluation metrics to assess the performance of these models. Based on their findings, it was determined that YOLOv4 exhibited superior performance compared to YOLOv5 and Mask R-CNN specifically in the identification of all subtypes of acute leukemic cells. In their study, Chen et al. [13] examined the efficacy of convolutional neural network and YOLO models in the real-time detection of leukemic cells. In the study, many models were employed, including CNN and three iterations of YOLO (versions 5, 6, and 7). Notably, the YOLO version 5 smaller model shown favorable performance in detecting both leukemic and healthy cells.

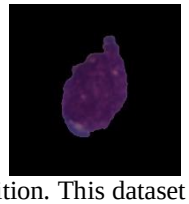
III. METHODOLOGY

A. *Dataset preparation*

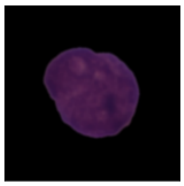
The initial stage of the process involves the acquisition of the dataset. The objective of this phase is to acquire a collection of image data characterized by high resolution and excellent clarity. This study utilizes the C-NMC 2019 dataset, which comprises micrographic images of leukemic cells and normal cells. The dataset was obtained from a sample of 26 individuals who were in good health and a total of 47 people



diagnosed with leukemia. The Cancer Imaging Archive (TCIA) has made available the C-NMC dataset for the ALL



Disease Diagnostics Competition. This dataset is specifically designed to facilitate the development of an automated and efficient solution for the detection of leukemic cells in contrast to normal cells. The dataset has approximately 7200 photos depicting Acute leukemic cells and 3300 images representing healthy or normal cells. The dimensions of the RGB images are 450 × 450 pixels. The dataset consists of a total of 10,600 photos, with 80% of the images allocated for the training phase and the remaining 20% designated for the test phase.



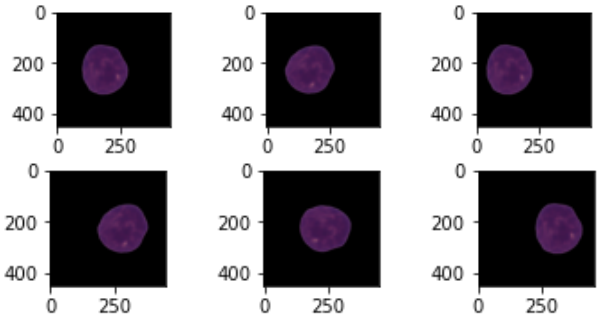
(a) (b)

(c)

Fig. 1. (a) Normal cell, (b) Leukemic cell, (c) Distribution of images in C-NMC dataset

B. *Data pre-processing*

Pre-processing techniques are employed to increase the quality of images through utilization of denoising, deblurring, and edge enhancement methods. The primary aim of segmentation is to extract specific cells and effectively separate cells that are overlapping with one another. Subsequently, pertinent characteristics are extracted, followed by the application of a classifier in order to get enhanced efficiency. Data augmentation techniques in the field of image processing encompass a set of methodologies employed to supplement the quantity of available data. The act of manipulating photos involves the incorporation of subtly modified replicas of pre-existing images or the creation of entirely new artificial images derived from existing ones. A variety of techniques can be employed to generate synthetic



images. Position augmentation techniques encompass a variety of operations such as vertical and horizontal rotation, flipping, padding, scaling, cropping, zooming, and others. The practice of augmenting picture data is commonly employed in deep learning models with the aim of mitigating and avoiding overfitting. Due to the limited quantity of single cell pictures of Acute Lymphoblastic Leukemia (ALL) present in the dataset, we are employing data augmentation approaches to address the imbalanced distribution of images across different classes. Given the inherent imbalance in the class photos, the application of image augmentation techniques has been employed to generate synthetic images.

Fig. 2. Image augmentation on normal cell images

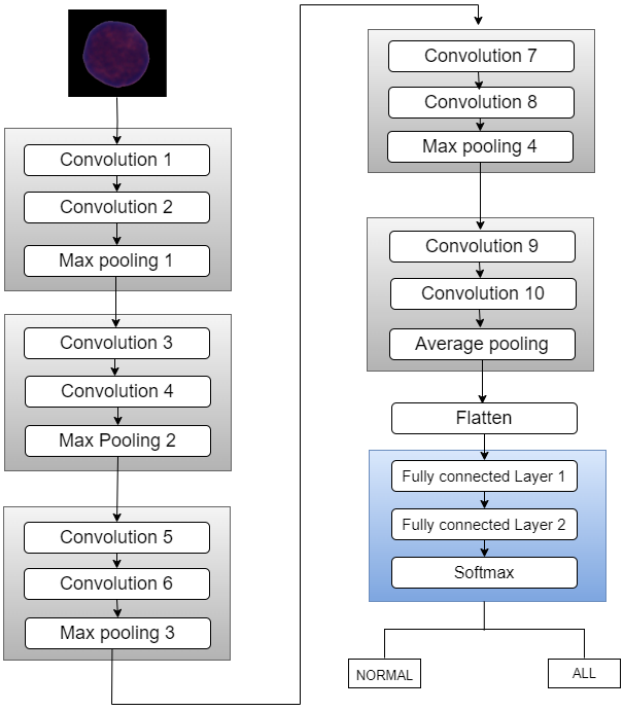
The Laplacian operator is employed in the context of image processing for the purposes of deblurring and enhancing edges. The Laplacian operation detects edges by identifying zero crossings, where the values transition from

negative to positive or vice versa. This method offers improved edge localization in comparison to the first-order derivative.

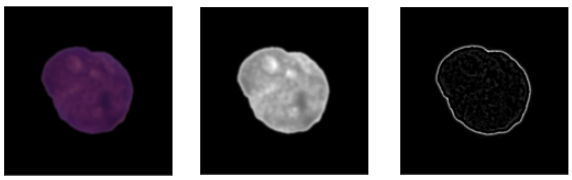
$$\nabla^2 = \frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2} \quad (1)$$

The Laplacian filter is commonly employed for the purpose of edge detection in images. However, it exhibits a drawback in comparison to the photographs with higher levels of noise.

$$LoG = -\frac{1}{\pi\sigma^4}\left[1 - \frac{x^2+y^2}{2\sigma^2}\right] e^{-\frac{x^2+y^2}{2\sigma^2}} \quad (2)$$



The Laplacian of Gaussian filter is a technique that involves the application of a Gaussian filter to reduce noise in a picture prior to doing the Laplacian operation. The initial phase in the process involves applying a Gaussian filter to the picture in order to achieve smoothing. Subsequently, the zero crossings are identified through the utilization of the Laplacian operator. This two-step procedure is commonly referred to as the Laplacian of Gaussian (LoG) operation.



(a) (b) (c)

Fig. 3. Laplacian of Gaussian filter (a) Original Image (b) Gaussian filter (c) Laplacian filter

C. *Feature extraction and classification*

VGG16 architecture is comprised of 13 convolutional layers and three fully linked layers. The customized VGG13 architecture has ten convolutional layers and three fully linked layers. The network consists of 13 layers, each of which possesses adjustable parameters. The depth of the network has been decreased, resulting in a reduction in the number of parameters. The decrease in network depth serves as a preventive measure against the occurrence of both overfitting and underfitting issues during the training process.

The hidden layer architecture of VGG13 is composed of five blocks. The initial four blocks consist of a consecutive arrangement of two convolutional layers, succeeded by a max-pooling layer. The last block segment of the feature extraction comprises of two convolutional layers, succeeded by an average pooling layer. The pooling layer further decreased the size of the image, while the flattened layer transformed the feature maps into a one-dimensional representation. Subsequently, three fully connected layers were combined into a single fully connected output layer, which utilize a softmax activation function to assign features to one of two categories.

Fig. 3. VGG13 network

The input image undergoes a resizing operation, resulting in an image with dimensions of 128×128 pixels. The dimensions of the input image have been decreased to half the dimension followed by the use of max pooling subsequent to the initial block. The subsequent two blocks of VGG13 entail the execution of comparable operations on the image.

$$RELU(x) = \begin{cases} 0 \text{ if } x < 0 \\ x \text{ if } x >= 0 \end{cases} \quad (3)$$

$$\text{softmax}(z_j) = \frac{e^{z_j}}{\sum_{k=1}^{K} e^{z_k}} \text{ for j = 1,...,K} \quad (4)$$

The feature map is subsequently inputted into the fourth convolutional block, where average pooling is applied to compute the average representation of a feature. The recovered features are forwarded to two completely connected layers that utilise the Rectified Linear Unit (ReLu) activation function, followed by a final fully connected layer that employs the softmax activation function.

IV. RESULT AND DISCUSSION

The studies were conducted using a standard workstation PC equipped with an Intel Core i5-8600 CPU, 16 GB of RAM, and an Nvidia Graphics Card featuring 12 GB of graphic memory. The software environments utilised in this study are built upon the Windows 10 operating system. The training process is conducted using Tensorflow version 2.13.0.

Accuracy = TP+TN / TP+FP+TN+FN (5)

Sensitivity = TP / TP+FN (6)

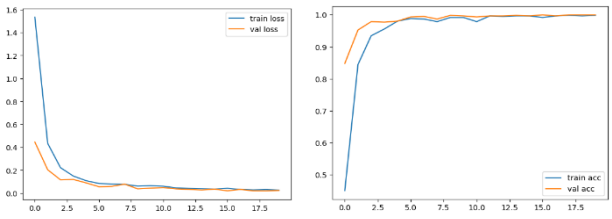
Specificity = TN / TN+FP (7)

TABLE I. Performance measure of various analyzed models

Classifier	Sensitivity %	Specificity %	Accuracy %
KNN	86.23	89.90	91.20
SVM	88.50	90.56	93.50

VGG19	92.64	96.00	96.00
VGG16	86.15	78.97	82.97
VGG16 + RF	87.53	86.05	86.92
VGG13	95.95	89.10	92.56

The collection was generated by amalgamating diverse photos obtained from multiple sources. The VGG13 model, which was tailored to suit specific requirements, underwent training using the provided dataset. The objective is to classify the input test image as either AML, ALL, or normal. The model's accuracy for the dataset is projected to be 92%. The model demonstrates strong performance throughout multiple iterations of the VGG model.



(a) (b)

Fig. 5. (a) Loss during training and validation of model (b)Mapping of accuracy during training and validation of model

V. CONCLUSION

This research introduces a methodology for the identification and classification of ALL and healthy cells. The collection was generated by merging photos of ALL and healthy cells that were collected from online sources. The utilization of data augmentation techniques serves the purpose of enhancing the quality of datasets and addressing the issue of image imbalance. In further research endeavours, it is recommended to enhance the performance by utilising more extensive datasets. The application of transfer learning has also been implemented on the VGG13 model, resulting in a reduction in training time. The topic of interest is the optimization of deep learning algorithms to achieve higher levels of efficiency.

The utilisation of a method that is based on transfer learning, particularly in the context of segmentation, has the potential to produce segmentation results that are more accurate. The utilization of ensemble or hybrid models can enhance the performance of the model

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