Leukemia Cancer Detection Using Transfer Learning

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***Abstract*—Leukemia is a blood cancer that begins in blood cells, especially the bone marrow, which produces lymphocytes and other blood cells. However, when a person develops leukemia, their bone marrow fails to function correctly, resulting in an abnormal production of both healthy and malignant cells. Detecting these abnormal cells accurately and reliably is critical for effective diagnosis and treatment. To achieve this, computer-aided diagnostic models that employ image processing techniques can be used to automate the detection of leukemia, reducing the workload on physicians while increasing the accuracy of diagnosis. In this paper, a thorough description of various approaches for automatic detection and classification of leukemia. The research focuses on the analysis of deep learning algorithms, specifically convolutional neural networks (CNN), visual geometry group 16 (VGG-16), Inception V3 and transfer learning algorithms, for classification and distribution of leukemia patients (including subtypes). In this paper a transfer learning model has been proposed to identify and classify leukemia , which achieves an overall accuracy of 95.74%. Additionally, a thorough analysis of several algorithms has been conducted in conjunction with the most up-to-date transfer learning approach, and all the experiments have been successfully implemented on Kaggle.**

***Keywords*— Leukemia, Cancer, WBC, Convolutional Neural Networks, Visual Geometry Group-16, ALL, CLL, AML, CML, Deep Learning, Transfer learning, Inception V3.**

1. INTRODUCTION

About Disease:

Human blood consists of three main components: red blood cells, which carry oxygen throughout the body; white blood cells, which play an important role in protecting the body from infection and platelets, which help blood clot. These blood cells are continually produced by the bone marrow, generating billions of cells each day. However, if the bone marrow begins to produce an excessive amount of white blood cells instead of red blood cells, it can lead to a type of blood cancer known as leukemia. Leukemia usually affects the blood and bones, the soft tissues that produce blood cells in the bones. Of all childhood cancers, leukemia is the most common, accounting for approximately one-third of cases. Acute Lymphoblastic Leukemia (ALL), Acute Myeloid Leukemia (AML), Chronic Lymphocytic Leukemia (CLL), and Chronic Myeloid Leukemia (CML), these are the four main types of leukeima. Symptoms of leukemia can vary but may include fatigue, fever, unexplained weight loss, frequent infections, easy bruising or bleeding, and swollen lymph nodes. Although the exact cause of leukemia is not fully understood, some factors, such as radiation exposure, certain medications, or certain diseases, can increase the risk of the disease.

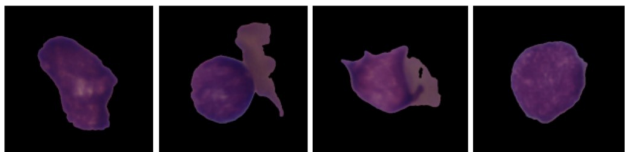

Fig. 1 Image of Blood Cells from the C-NMC-2019 dataset

Extensive research is indeed being conducted in the medical field to address the issue of leukemia, a type of blood cancer. Leukemia treatment varies depending on factors such as the stage of the cancer and the type of leukemia.

In this project, the focus is on developing an advanced image processing system to detect immature blood cells and determine their total count. The primary objective is to create a system that can accurately and efficiently identify specific forms of blood cells during critical situations, particularly in emergencies. Additionally, the system aims to differentiate immature cells and identify the presence of leukemia.

Traditionally, identifying leukemia cells from blood samples is a time-consuming process that requires expertise. To overcome this challenge, research in computer-aided diagnostic (CAD) systems. These systems analyze blood cell images or bone marrow biopsy samples using image processing techniques and machine learning algorithms to detect abnormal cells and assist in leukemia diagnosis. The implementation of CAD systems has the potential to alleviate the workload on physicians while improving the accuracy of diagnosis. However, it is crucial to address certain limitations of these methods, such as improving the accuracy of detection and refining the learning techniques utilized by the algorithms. By addressing these challenges, the development of an efficient and reliable CAD

system for leukemia detection can significantly aid in early diagnosis and treatment planning.

2. Related work

This section presents the existing methods, which mainly cover leukemia detection, segmentation, deep feature classification, and hand-crafted feature extraction methods [1,2,3,4]. The pre-processing stage increases the ROI, which directly affects the segmentation results [5,6,7,8,9]. A Wiener filter [10] based on a curvelet transform was used to enhance the input images to avoid spurious noise edges. He proposed three consecutive preprocessing techniques, namely colour distortion, image flip-mirror, and border distortion [11]. To improve

image quality for segmentation, [12] proposed a preprocessing algorithm using partial contrast

stretching, k-means clustering, subtractive clustering, and median filter. The three colour components (C and M of CMYK colour space, S of HSV colour space) are pre-processed to form new image components named Cn, Mn, and Sn to select the best PCA-fused features for white blood cell nuclei segmentation [13]. RGB to HSV color space transformation method with weighted cross-entropy loss function for white blood cell segmentation proposed by [14]. Deep convolutional generative adversarial networks (DCGANs) are a famous method for increasing the number of image samples [15], which is done by preprocessing matrix transformations (horizontal and vertical flips) and DCGANs [16] to increase the robustness of

the training model, DCGAN. then combined with ResNet classification for WBCs. Deep

learning methods [5,6,18,19,20,21] are pre-trained models such as AlexNet, GoogleNet [22] , ResNet

[23], VGG-16 [17], Inception V3 [24] and many others are used such as feature extractors and feature selectors. Ahmed et al. proposed a WBC feature extraction method using the powerful CNN VGGNet architecture, the extracted features are then filtered by electron spectra simulation for surface analysis algorithm (SESSA) [25]

3. Data set

The authors used the C-NMC-2019 dataset in

their study, which included 118 studies involving 49 Hem patients. Details on the data can be found in Table 1.In their proposed model, they categorized the training database into two subsets: the train set and the validation set. Additionally, they had a separate test set for evaluation purposes. The images in the file are converted to a resolution of 128×128 pixels.

Dataset Source:
https://www.kaggle.com/datasets/avk256/cnmc-leukemia

Table 1 a: C-NMC-2019 database

States	Dataset Categories		Subjects	
			ALL (Cancerous)	Hem (Normal)
1st	Training Set	Training	32	19
		Validation	15	7
2nd	Test set	-	13	15
3rd	Final Test set	-	9	8
Total			69	49

Table 1 b: C-NMC-2019 database

States	Dataset Categories		Images	
			ALL (Cancerous)	Hem (Normal)
1st	Training Set	Training	5822	2703
		Validation	1450	686
2nd	Test set	-	1219	648
3rd	Final Test set	-	1716	825
Total			10252	4862

According to the findings presented in Table 1, the database exhibits inconsistency, with a higher number of training images for cancer cells compared to normal cell images, resulting in a slight bias in the ALL categories. To address this bias caused by data inequality, the proposed framework incorporates two strategies aimed at reducing the bias

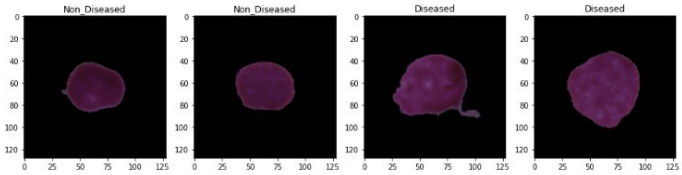

Fig. 2 Sample images from the C-NMC-2019 dataset reveal the presence of unnecessary black regions surrounding the region of interest

4. METHODOLOGY

The proposed model followed a series of steps starting with the download of two image datasets. These datasets underwent image preprocessing, which involved normalization, contrast processing, resizing, and artifact removal. It is very important to perform these preliminary steps to obtain accurate results. The data is then divided into training set (70%), validation set (10%) and testing set (20%).In the next step, transfer learning was employed using the EfficientNet-B3 model. The first phase of transfer learning involved supervised pre-training, where a pre-trained ImageNet neural network with pre-trained parameters from a large dataset was utilized. The second phase of transfer learning involved fine-tuning the EfficientNet-B3 network using the C-NMC_Leukemia and NIH datasets. Evaluate the model's performance by calculating the error in the training data. If the error was not sufficiently low, the model was retrained. Conversely, if the error on the training dataset was low, the error on the test dataset was calculated. If the error on the test dataset was not low, the model was retrained.

Training a model from scratch requires a huge

amount of data to be fed to the network for a specific task. This requires a lot of time and resources due to the number of parameters the network is learning. Sometimes we may not have enough data to train our classifier from scratch. This is where transfer learning comes in with techniques namely feature extraction and fine tuning to help transfer knowledge gained on one dataset to another dataset.

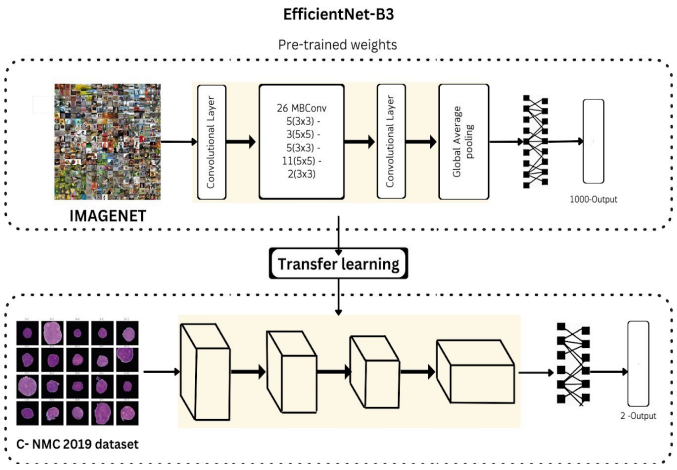

Fig. 3 Flow Diagram Of The Proposed Methodology

4.1 Image Preprocessing

To enhance the ALL-prediction system, several key preprocessing strategies were implemented. Since most database images contained a main region of interest against a dark background, a strategy was employed to extract the central 10 images with a size of 128 × 128 pixels. This approach reduced input data size, accelerated training, and focused on the region of interest. Addressing class inequality in medical imaging can be challenging due to complex annotations and limited accessibility. To mitigate class imbalance, random resampling was employed by duplicating samples from the minority class and augmenting the training dataset. In the proposed model, the Hem group has 5822 images to be modeled and is trained from a total of 11,644 images. In the proposed model, the Hem group has 5822 images to be modeled and is trained from a total of 11,644 images. To improve model performance, data optimization techniques such as scaling, rotation, horizontal and vertical flipping are used during training**.** To address the issue of image contrast, a normalization process was implemented during training by normalizing the contrasts of the training images. Additionally, noise was removed from the images through a filtering process. To improve the quality and clarity of the image, each pixel in the image is subtracted from the average of the three primary colors (red, green and blue).

$$Mask\,(m,n) = \begin{cases} \max_i \ , i\,(m,n) \geq \min_i \\ 0\ otherwise. \end{cases}$$

4.2 Implementation

Efficient Net is a widely recognized architecture that has achieved remarkable performance in various machine learning tasks. It introduces a novel scaling method, known as the compound coefficient, which uniformly scales dimensions such as depth, width, and resolution using a set of efficient scaling factors. This approach ensures that the model's parameters are adjusted in a balanced and effective manner.

Among the Efficient Net variants, EfficientNet-B3 has demonstrated notable success in image classification. In this study, the main objective is to develop an automated system for analyzing C-NMC_Leukemia images and accurately identifying the presence of ALL-cell disease. The proposed model encompasses several key steps, as depicted in Figure 3:

1. Image preprocessing: This step involves preparing the input images by applying necessary transformations or cropping to extract the relevant region of interest.
2. Dataset normalization: To ensure

consistency and comparability, the dataset is normalized, typically by adjusting the pixel values or applying standardization techniques.

3. Model training: The EfficientNet-B3 model is trained using the preprocessed and normalized dataset. During this stage, the model learns to extract relevant features and make predictions based on the provided training examples.
4. Training evaluation: Evaluate the effectiveness of the training model using appropriate metrics to measure its accuracy, precision, recall, or other metrics. This evaluation helps to gauge the effectiveness of the model in capturing the desired disease characteristics.
5. Test evaluation: Finally, the trained model is tested on a separate test dataset to assess its generalization ability and performance on unseen data. This evaluation provides insights into how well the model can perform in real-world scenarios.

By following these steps, the proposed model aims to develop an efficient and accurate system for automated ALL-cell disease identification based on the analysis of C-NMC_Leukemia images.

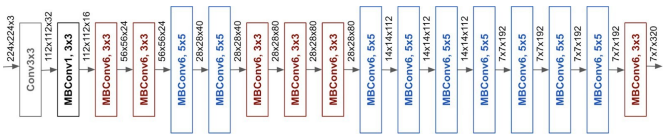

Fig. 4 Structure of the EfficientNet-B3 model

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4.3 Setup for Experiment

The experimental work of this project was done using the Python programming language, Keras package and TensorFlow deep learning. The breach will take place on an online site called Kaggle, which provides a convenient and customizable Jupyter Notebooks environment without the need for installation locally. Kaggle offers ample computational resources, including approximately 16GB of GPU, around 14GB of RAM, and approximately 80GB of disk space, facilitating efficient model training and evaluation.

5. Result And Analysis

The proposed work involves the implementation of a transfer learning model for the detection and classification of leukemia. The model achieves an impressive overall accuracy of 95.74%. In order to assess the effectiveness of the proposed model, a comprehensive comparative analysis has been conducted, comparing it with previous works in the field. Various performance metrics including precision, F1 score, and sensitivity have been evaluated to provide a thorough analysis of the model's performance. This ensures a comprehensive assessment of the proposed model's capabilities and its superiority overexisting approaches

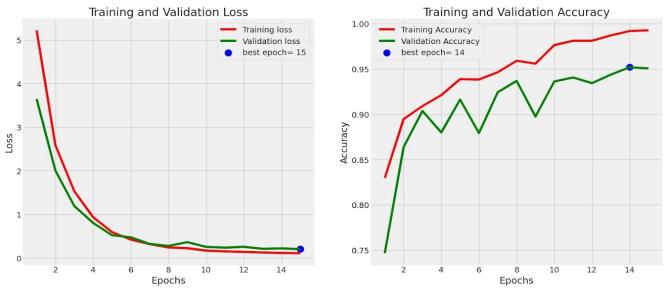

Fig 5. Displaying Model Performance

	precision	recall	f1-score	support
all	0.98	0.96	0.97	1091
hem	0.92	0.95	0.93	509
accuracy			0.96	1600
macro avg	0.95	0.96	0.95	1600
weighted avg	0.96	0.96	0.96	1600

Fig. 6 Different Performance Metrics

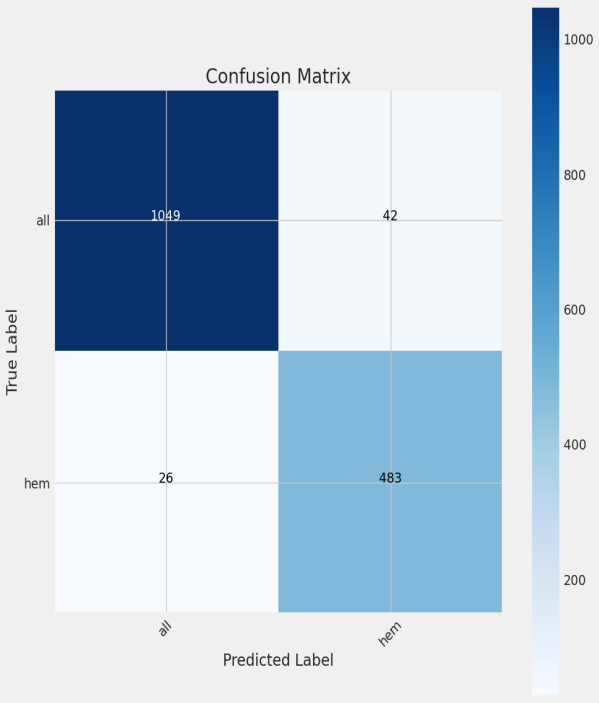

Fig. 7 Confusion Matrix

Table 2 Comparison of different methods

Method Used	Accuracy (%)	Val_accuracy(%)	F1_score (%)
VGG-16	76.8%	72.7%	74.8%
CNN	82.3%	76.8%	80%
Inception v3	90.6%	88.2%	90.7%
Transfer Learning	95.7%	94.8%	96%

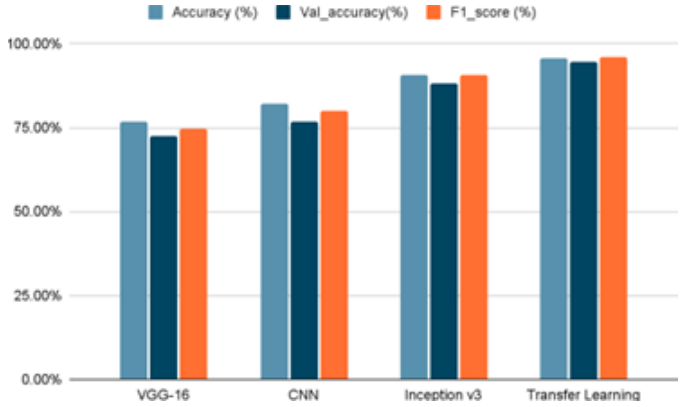

Fig 8. Bar chart displaying accuracy val_accuracy & F1_score of different methods

6. Conclusion

In this proposed paper, a comparative analysis has been conducted to evaluate various methods previously proposed for the detection and prediction of leukemia. The focus of the paper is on the utilization of transfer learning, which has shown exceptional performance with an overall accuracy of 95.7%. When compared to other methods, such as VGG-16, Convolutional Neural Network (CNN), and Inception V3, the recent transfer learning technique outperforms them significantly. Specifically, VGG-16 achieves an overall accuracy of 76.8%, while CNN achieves 82.3% accuracy. Inception V3 demonstrates better performance than VGG-16 and CNN, with an accuracy of 90.6%.

Transfer learning is described as a method of leveraging a pretrained model that has been trained on a large dataset and applying that knowledge to solve a new problem related to it. By employing transfer learning, the proposed model exhibits a significant increase in performance while requiring fewer computational resources and time. It is concluded that the recent implementation of transfer

learning offers superior results for the detection and prediction of leukemia compared to earlier proposed methods.

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