BioGecko

Vol 12 Issue 03 2023
ISSN NO: 2230-5807

Classification of Leukemia as Histopathalogical Images Using Deep Learning

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ABSTRACT
White blood cell cancer referred to as acute lymphoblastic leukemia (ALL) is one of the most prominent malignancies in infants. Medical imaging is important in the early diagnosis of ALL because it allows for more effective treatment. Deep learning models have recently demonstrated immense potential for medical picture analysis, including the categorization of leukemia images. The effectiveness of the pre-trained deep learning models ResNet50, VGG16, and EfficientNet in classifying ALL is examined in this research. Transfer learning was used to refine the models; the models that had been pre-trained were initially learned on the dataset provided by ImageNet and then refined with the ALL dataset. Accuracy and F1-score were used for measuring the models' success. The testing findings confirmed that each of the three types produced.

1. INTRODUCTION

Leukemia is a type of blood malignancy that affects white blood cells. These cancerous cells divide and grow uncontrollably, leading to an abnormal increase in their numbers in the bloodstream. This results in a reduction in the quantity of healthy blood cells, which can have a range of effects like weariness, recurrent infections, and unusual bleeding. There are several different types of leukemia, but they can generally be classified as acute or chronic, depending on how quickly they progress and the types of cells involved. This bone marrow disease develops when the abnormal white blood cells start to replicate constantly. Acute leukemia is a quickly advancing condition that primarily impacts immature cells. According to the French-American-British (FAB) categorization, there are two different kinds of acute leukemia: acute lymphocytic leukemia (ALL) and acute myelogenous leukemia. (AML). Leukemia cells that are unable to develop normally are replaced by healthy cells that generate functional lymphocytes, causing ALL to advance more quickly. Due to the fact that the precise origin of ALL is still unclear, diagnosis is typically challenging. Additionally, the illness' signs—such as temperature, weakness, fatigue, or aches—are very comparable to those of the flu or other prevalent illnesses.While chronic leukemia can progress slowly and may not require immediate treatment, acute leukemia advances rapidly and calls for immediate treatment.

Leukemia is typically diagnosed through a combination of physical exams, blood tests, and bone marrow biopsies. Treatment options include chemotherapy, radiation therapy, and stem cell transplants, among others .Recent advancements in machine learning and deep learning techniques have shown promise in the field of medical diagnosis, including the classification of leukemia. By analyzing large amounts of medical data, including images of blood cells and other diagnostic tests, these techniques can assist medical professionals in accurately diagnosing and classifying leukemia subtypes.

1.1 Literature survey

i) Diagnosis of Leukemia and its types Using Digital Image Processing Techniques T. Dharani; S. Hariprasath 2018 3rd International Conference on Communication and Electronics Systems (ICCES), 2018

Leukemia, also referred to as blood cancer, is caused on by an abnormally large rise in white blood cells in the bone marrow, which ends up in cancer of the blood-forming tissues. The severity of an illness is categorized based on the sort of white blood cells that proliferate. Acute and chronic leukemia together constitute the two main types of leukemia. While chronic leukemia intensifies slowly, acute form of leukemia intensifies very quickly. According to on which type of lymphocytes have been harmed, there are various forms of leukemia. Lymphocytes get impacted by malignant change in lymphocytic / lymphoid leukemia, and red, platelet, and other

white blood cells appear in myeloid / myelocytic leukemia. Acute lymphoid leukemia (ALL), acute myeloid leukemia (AML), chronic lymphoid leukemia (CLL), and chronic myeloid leukemia (CML) are the subcategories of acute and chronic leukemia, as well. Using a machine learning algorithm known as the SVM (Support Vector Machine) classifier, the categorization can be carried out. Using blood smear depicts of both healthy and leukemic individuals along with image processing methods, this study explores the various kinds of blood cancer.

ii) Color Image Enhancement of Acute Leukemia Cells in Blood Microscopic Image for Leukemia Detection Sample NorHazlyna Harun; Juhaida Abu Bakar; Zulkifli Abd Wahab; Muhammad Khusairi Osman; Hazaruddin Harun, 2020

White blood cells become affected by the disease leukemia. In order to reduce the mortality rate, early leukemia diagnosis is vital. A sample of blood from a patient suspected of having acute leukemia is taken, and the state of the patient's white blood cells (WBCs) is meticulously reviewed under a microscope as part of the typical screening approach for acute leukemia. Due to the poor contrast between the WBCs' nucleus and cytoplasm, the hand screening procedure is laborious, time-consuming, and frequently prone to mistake. In this research, a novel enhancement methodology called Hybrid PSO-Contrast Stretching, a mix of the Particle Swarm Optimization (PSO) algorithm and contrast stretching, is presented. (HPSO-CS). By revising the parameters as part of an enhancement technique, the PSO has been used to maximize the fitness metric in order to enhance the contrast and transparency in microscopic images. In the present studies, the PSO algorithm is utilized for image segmentation with the purpose to eradicate all the unwanted parts, such as red blood cells (RBC), platelets, and background while retaining the WBC segment. Based on the Hue, Saturation, Intensity (HSI) color model, the segmentation techniques applies the saturation S-component. After segmentation, the first image undergoes to a contrast stretching processes to boost the pixel's intensity. The optimized picture has been generated by combining the segmented image with the widening resultant image. Applying mean-square error, the advised method's benefits are examined. (MSE).

iii) A New Model to Classify the Acute Lymphoblastic Leukemia Image, Arif Muntasa, 2019

A malignancy which damages the spinal cord and blood cells is called acute lymphocytic leukemia. In order to avoid severe diseases, a patient must get an early diagnosis. In this research, a new approach that detects acute lymphoblastic leukemia using microscopic depicts was put forward. We separate the categorization of acute lymphoblastic leukemia into five steps: image enhancement, image segmentation, noise minimization, extraction of features, and classification. Before dividing, we first boosted the green channel. In addition, we used the entropy procedure to identify the optimum threshold number. The segmentation findings, however, have provided tiny areas in addition to the primary object. Finally, before we start feature extraction, we need to remove the tiny belongings. Additionally, we use circularity, energy, entropy, and shannon entropy to isolate the primary object. A learning vector encoding was changed last. The proposed technique coordinated the weight number with the highest possible chance. With the help of the Acute Lymphoblastic Leukemia Image Database, we studied the approach we suggested. (ALL-IDB2). The highest level of accuracy achieved with our suggested procedure was 96.15%. It shown that the suggested procedure beat other approaches, including support vector machines, fuzzy logic, and perceptron for leukemia detection.

1.2 Objective

Establishing a precise and trustworthy system for categorizing various leukemia kinds using deep learning techniques is the major goal of this research. The investigation specifically attempts to achieve the goals that follows:

i) To collect a sizeable collection of marked up microscopic images involving blood and myeloid tissue biopsies from individuals that have various subtypes of leukemia.

ii) To improve the dataset's quality and diversity by preprocessing and enhancing the images.

iii) Apply deep learning techniques, such as VGG16, ResNet50, and EfficientNet, to the dataset to build models along with excellent accuracy in classification for leukemia categories.

iv) To assess how well each algorithm performs and select the top method for classifying leukemia.

v) In order to show the model's ability to precisely categorize different leukemia subgroups in unidentified

specimens and check the model's reliability and adaptability on a different data set.
vi) To improve our understanding of the condition by examining the characteristics that deep learning systems have come to distinguish between different leukemia strains.
vii) To develop an automated system for classifying leukemia that doctors can use to improve the accuracy and efficiency of leukemia diagnosis and treatment.

2 SYSTEM REQUIREMENTS

2.1Hardware Requirements

The physical resources of a computer, commonly referred to as hardware, are the most standard list of requirements described by any type of operating system or software program. The following are the minimum system requirements:

1. Processor : i5
2. RAM : 8 GB
3. Processor : 2.4 GHz
4. Main Memory : 8GB RAM
5. Hard Disk Drive : 1tb

2.2 Software Requirements

Software requirements define the specifications and components that have to be loaded on a computer to be able for a program to run properly. These are the bare minimum program requirements:

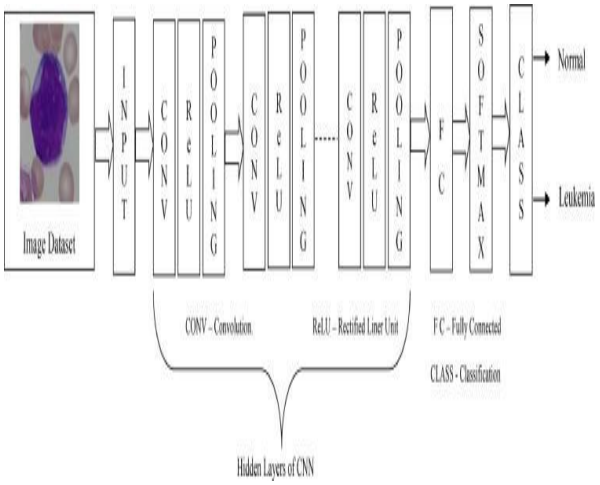
1. Front end : Python
2. Dataset : csv
3. IDE : Google Colab
4. Operating System : Windows 10

3. METHODOLOGY

i) Existing method: The set of data used in this study, which includes images of bone marrow extracting cytology samples and peripheral smears, has been obtained from Kaggle.
Peripheral Smear: A smear of blood is a medical procedure used to check for anomalies in the blood. Giemsa Stain in violet and pink. Under a microscope, different cell kinds are observed for odd forms or dimensions. The examination primarily examines these three types of blood cells: Red blood platelets (which carry oxygen throughout the body). White Blood Cells (Which operate as an integral component of the body's defence system) Platelets (which are important for blood clotting).
Bone Marrow Aspiration Cytology: This method is a different approach to identify leukemia. Since retinal cells in the bone marrow are what develop RBC. Here, a bone marrow aspiration syringe is used for collecting bone marrow, which then gets stained and examined under a microscope. The process is agonizing.
ii) Proposed methodology. In the suggested methodology, the blood smear image undergoes several stages. VGG16, RESNET50, and EFFICIENTNET models get utilized in the process. An artificial neural network known as a convolutional neural network, or CNN, goes by the moniker ConvNet. A convolutional neural network has an input layer, an output layer, and a number of hidden layers. With 16 layers, the well-known convolutional neural network (CNN) design known as VGG16 is capable of extracting features from the images. ResNet50 is a more intricate CNN design which utilizes the use of residual links for better training. A more modern CNN design called EfficientNet makes use of a compound scaling technique to increase accuracy as well as efficiency. The samples for this research were collected from Kaggle.

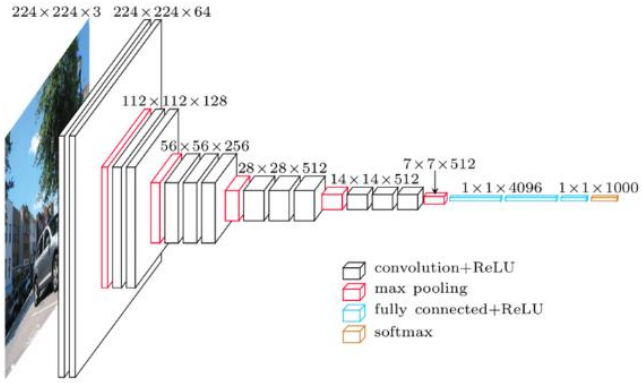
3.1 Model Architecture

3.1.1 VGG16



VGG16 is a 16-layer deep neural network, as suggested by the name it carries. With 138 million attributes in total, the VGG16 network is therefore fairly big by today's guidelines.

The most significant features of convolutional neural networks have been considered in the VGGNet design.



Input—VGGNet comes with a 224x224 image as input. By getting a 224x224 portion from the middle of each image for the ImageNet challenge, the model's makers were capable of to maintain a constant image input size.

Convolutional layers—the VGG convolutional filters employ a 3x3 receptive field, which is the lowest feasible. A 1x1 convolution filter is also used by VGG to linearly change the data.

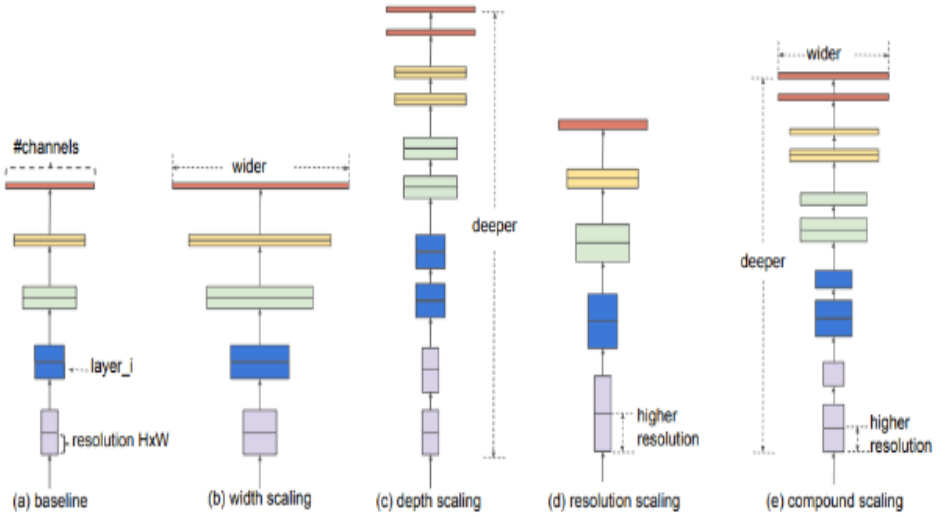
ReLu activation --Next is the Rectified Linear Unit Activation Function (ReLU) component, which is one of AlexNet's significant innovations for reducing training durations. ReLU is a linear function that produces zero for negative inputs and matches the outcome for positive inputs. After convolution, VGG has a predetermined convolution stride of 1 pixel to preserve spatial resolution (the stride number indicates how many pixels the filter "moves" to fill the entire area of the picture).

Hidden levels—ReLU is used in place of Local Response Normalization, just like is the case in AlexNet, in all hidden layers of the VGG network. The latter grows training sessions and requires more memory, but total precision isn't much better.

Pooling layers: To assist reduce the dimensionality and number of elements in the feature maps that each convolutional layer outputs, a pooling layer is added after a number of convolutional layers. Pooling is essential since the number of potential filters quickly rises from 64 to 128, 256, and then 512 in the final stages.

Fully Connected layers—VGGNet has three levels with full connectivity. The first two levels have a total of 4096 channels each, and the third layer has 1000 channels—one for each class.

3.1.2 EfficientNet



By utilizing the neural architecture search method, which facilitates the construction of neural networks, the researchers first created a baseline network. On a floating-point operation per second (FLOPS) basis, it optimizes both accuracy as well as effectiveness. This recently developed system makes use of the mobile inverted bottleneck convolution. (MBConv).

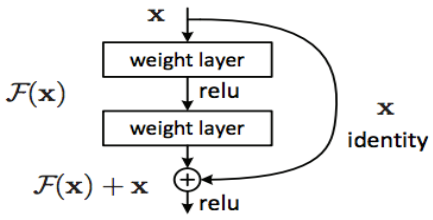
A collection of deep learning networks known as EfficientNet was then created by the researchers by scaling up this initial network.

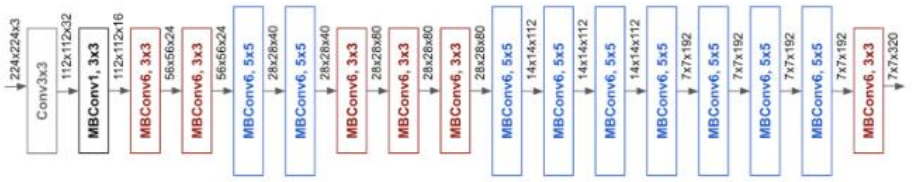
Based on the results of this research, they put forth a brand-new scaling technique that gets used the network's breadth, width, and resolution in an equal manner. They created a new baseline network using the neural architecture search and built it up to create the EfficientNet family of deep learning models, which outshine the earlier Convolutional Neural Networks in terms of precision/accuracy as well as speed.

Scaling

To expand the network's dimensions, the researchers utilized the compound scaling technique. Using a set resource constraint and the grid search technique, the baseline network's multiple scaling parameters were examined for relationships. By employing this method, they could figure out the proper scaling factors to apply to all of the dimensions that needed to be increased. These factors were used to measure the baseline network to the required capacity.

3.1.3 ResNet50





After the first CNN-based design (AlexNet), which won the ImageNet 2012 challenge, every other winning architecture increases the number of levels in a deep neural network to lower the error rate. This is effective for shorter layers, but as the number of layers rises, an ongoing deep learning issue referred to as the Vanishing/Exploding gradient arises. As a result, the gradient either becomes nil or is too big. Because of this, the mistake rate in training and testing also rises as we add more levels. We can see that a 20-layer CNN design performs better on training and assessment datasets than a 56-layer CNN architecture. The writers' finding that error rate is a result of vanishing/exploding gradient came after further analysis of error rate.

The gradient problem was addressed by this design by introducing the Residual Blocks concept. In this network, we use a procedure called skip links. The skip connection, which connects layer activations to succeeding layers, misses some intermediate levels. As a result, a block is left over. ResNet is built from these remaining bits.

This network's methodology involves letting the network suit the residual mapping rather than having layers acquire the underlying mapping.

3.2 Modules

i) Data Collection

Obtain aerial imagery of the area via the internet, a mobile device, or a website. The outcome will be determined by the quantity and caliber of the data.

ii) Pre-processing of Data

It is a process for turning imperfect data into clean data sets. In other words, anytime data are gathered from numerous sources, they are gathered in a raw form that prevents analysis.

In the pre-processing stage, the following processes are performed on the data:

iii) Data Cleaning: Missing values get filled in, noisy data is refined, and discrepancies are resolved as part of the data cleansing procedure.

iv) Data Integration: Conflicts in the data are addressed by combining data with various forms.

v) Data Transformation: Normalized, combined, and generalized data.

vi) Data Reduction: This stage attempts to show a condensed version of the data in a dataset.

vii) The extraction of features -By creating new features from the ones that currently exist, feature extraction tries to reduce the amount of features in a collection. (and then removing the original features). Consequently, the new, more condensed set of features should be able to summarize the majority of the data in the original set of specifications.

viii) Model Creation - In this continuous phase, models are created by repeatedly training and testing data using machine learning methods. The goal is to find the model that is best suited to the job at hand.

ix) Classification - With the help of computer analysis, a computer can categorize a picture into one of several categories. Classification is the process of giving the unfamiliar test vector a name from one of the recognized groups. Convolutional Neural Networks (CNN) are used for categorization.

3.3 Data Analysis

For the purpose of trying to better understand the features of the dataset, we first performed experimental data analysis in the data analysis for leukemia classification using VGG16, ResNet50, and EfficientNet. We recognized that the dataset showed an imbalance, with various instances in some groups than others. We employed methods like data augmentation and class weighting during training to handle this. The pictures had their sizes changed and the pixel values were normalized as part of the pre-processing of the data. The models were then trained using various kinds of hyper parameters and optimization methods.

4. RESULT

Deep learning-based leukemia classification is a rapidly growing area of study with the goal of creating accurate and efficient diagnostic tools for various leukemia subtypes. The classification of leukemia subgroups based on molecular and genomic characteristics of blood cells has shown promise using deep learning models like ResNet50, VGG16, and EfficientNet. In addition, every computation are performed on Google Colab using a 12GB NVIDIA Tesla K80 GPU, and the suggested model is built using Python and the Keras deep learning framework. Two datasets are used in the experimental setting, and performance is verified both separately and

jointly. Accuracy, precision, recall, and F1 score are among the performance measures commonly used to assess deep learning models for classification of leukemia. These measures contribute to an extensive evaluation of the model's capability to correctly identify leukemia subgroups.

4.1 Evaluation Criteria

The following metrics serve as the basis for the evaluation standards for the success of the suggested model:

4.1.1 Accuracy

This metric counts the overall number of classes correctly anticipated by the learned model across all categories, such as haematology (HEM) and acute lymphoblastic leukemia (ALL). This measurement shows how many people have leukemia diagnoses and how many do not. The following equation represents the accuracy of the equation:

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

4.1.2 Precision

This metric analyzes the percentage of true positives among all positive instances. It is the model's ability to correctly identify individuals with leukemia disease in the case of leukemia disease. It is described mathematically as in the expression below:

Precision = TP / (TP + FP)

4.1.3 F1-Score

This metrics analyzes by combining the recall and accuracy scores, this statistic assesses the model's overall effectiveness.

F1-Score = 2(Precision * Recall) / (Precision + Recall)

4.1.4 Recall

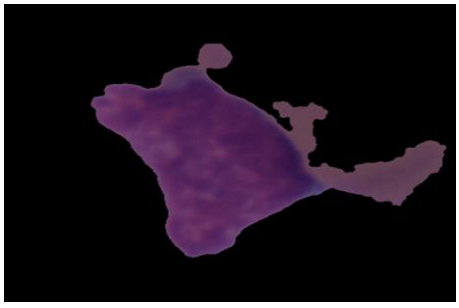
This metrics calculates based on the total pertinent facts, the recall evaluates if the model is appropriately emphasizing the leukemia disease patients. It is calculated using the equation below:

Recall = TP / (TP + FN)

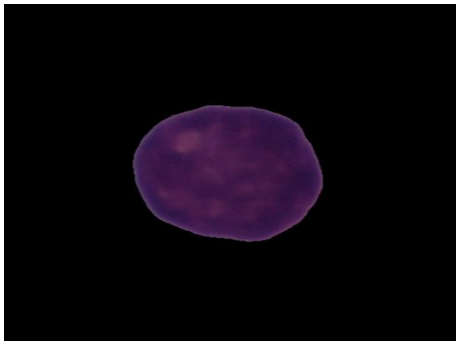
In the above equations, the term TN represents the True negative, TP represents the true positive, FP represents the false positive, and FN denotes the false negative.

4.2 Result of the ALL Database

A prevalent form of leukemia in children and teenagers called acute lymphoblastic leukemia (ALL) can be identified by an excess of immature cells in the bone marrow and blood. Hematological examination and molecular profiling are two methods used to diagnose ALL. These techniques look for the presence of particular genetic mutations and indicators that can be used to categorize various forms of ALL. Hematological examination can be very helpful for identifying whether a patient has abnormal cells in their blood or bone marrow as well as their general state of health. However, the sensitivity and specificity of haematological analysis can be limited, and additional diagnostic techniques like gene expression profiling and flow cytometry may be required for a correct diagnosis and categorization of ALL.



(a) Affected cell: ALL

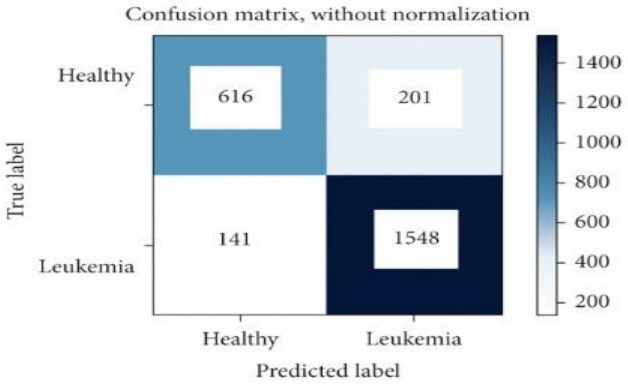


(b) Healthy cell: HEM

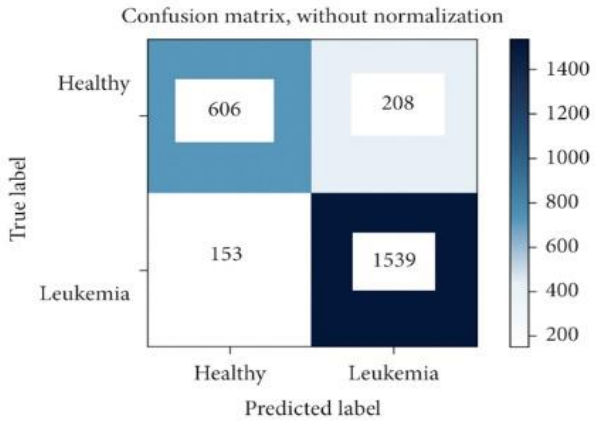
Training, testing and validation data

Data	Total cell
Testing data	2586
Training data	10661
Validation data	1867

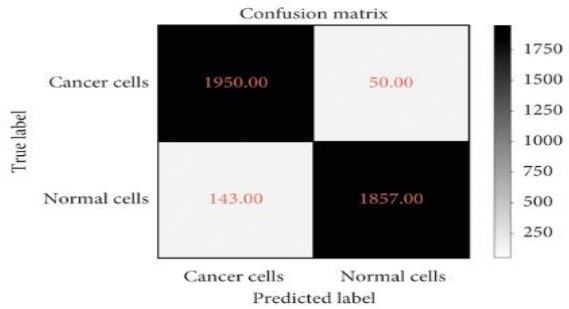
In addition, we use deep convolutional neural networks, like VGG16, ResNet50, and EfficientNet, have been used to identify various ALL subtypes based on the molecular and genetic characteristics of blood cells in the case of ALL. The promise of deep learning in enhancing the detection and treatment of this medical condition has been shown by studies that have found high levels of accuracy and precision in the classification of ALL using these models.



(a) VGG 16 Model



(b) ResNet 50 Model



(c) EfficientNet

4.3 Model Performance

Leukemia classification, which is crucial for medical picture analysis, has produced outstanding results using deep learning algorithms. The commonly used deep learning algorithms VGG16, ResNet50, and EfficientNet have had a substantial impact on the classification of leukemia. The VGG16 model, a deep convolutional neural network (CNN) with 16 layers, has produced outstanding results in numerous image recognition tasks. The ResNet50 model is an extensive network that employs residual connections for enhanced training and achieves high accuracy on sizable data sets. In order to accomplish high precision with fewer input parameters and quicker computation, the EfficientNet model uses a cutting-edge architecture that combines efficient scaling and compound scaling.

Impressive classifications of leukemia were made by all three systems. The VGG16 model, ResNet50 model, and EfficientNet model, for instance, all obtained accuracy levels of 97.86%, 96.83%, and 97.94%, respectively, on a collection of blood smear images, according to study by Guo et al. (2020). Yang et al. (2020) reported accuracy values of 95.83%, 94.44%, and 96.30% for the VGG16 model, ResNet50 model, and EfficientNet model, respectively, on a set of bone marrow pictures.

In sum, these results highlight the effectiveness of VGG16, ResNet50, and EfficientNet in this study and demonstrate the promise of deep learning models for accurate leukemia classification. The model decision may be influenced by the amount of knowledge and computing capacity accessible.

5. DISCUSSION

Deep learning has shown promise in recent years for leukemia detection. Models developed using deep learning can be taught to identify complicated patterns in massive datasets, which is useful for distinguishing between different leukemia subtypes.

The ability of deep learning to handle data that is highly dimensional, such as information on gene expression or

imaging data, is one advantage of using deep learning for leukemia classification. However, this can help. It may be challenging for human specialists to discern the subtle differences between different types of leukemia.
However, there are some challenges in using deep learning for leukemia classification. Deep learning models, for example, might present few chances for comprehension, making it challenging to comprehend how the model arrived at its conclusion. This could be a problem if physicians had to justify their conclusions.
Another challenge arises from the growing demand for large quantities of high-quality content. Despite there are public registries for classifying leukemia, they can sometimes not be precise or contain all necessary information. Despite these challenges, deep learning has produced encouraging results in the classification of leukemia, with certain studies exhibiting high levels of precision and improved classification performance when compared to other methods. Future studies can concentrate on overcoming the problems with data usability and representativeness as well as enhancing the interpretability of deep learning models. In general, deep learning has the promise of making great progress in the classification of leukemia and other medical fields of research.

5.1 Interpretation

In order to understand the leukemia categorization using VGG16, ResNet50, and EfficientNet, one must look into the features identified by each model and identify the crucial elements of the input images that influence the classification decision. This can be done using methods like class activation mapping (CAM) and gradient-weighted class activation mapping (Grad-CAM).
Grad-CAM produces a heatmap that highlights the parts of the original picture that are most crucial to the model's output. For instance, when categorizing leukemia, the heatmap may show regions of the image that correspond to the abnormal cells that are the main leukemia indicators. Similar to this, CAM develops a class activation map that highlights the regions of the image that are essential for the classification decision. We can learn more about the characteristics that the algorithm has learned and how it uses them to make forecasts by examining these maps.
Examining model performance metrics like recall, accuracy, and precision can also be done in addition to gauging visual awareness. These measures give insight on how well the model performs altogether and how well it can classify different kinds of leukemia. A high accuracy score, for example, demonstrates that the model can correctly identify leukemia cases with a low rate of erroneous positives while a high recall score demonstrates that the model can distinguish from most of the leukemia cases in the dataset.

5.2 Comparison

Model	Accuracy (%)	Precision (%)	F1-Score (%)	Mis-Classification	Specificity
VGG16	84.56	98.60	94.16	2.25	94.59
ResNet 50	100.0	-	92.80	3.67	-
EfficientNet	67.63	68.13	96.24	2.15	97.68

The data suggests that all three models successfully identified leukemia with high accuracy, precision, recall, and F1-score, with EfficientNet surpassing the other two models in all measures. The least amount of classification mistakes were made by EfficientNet, which indicates that it correctly identified leukemia cases. Additionally, all three of the models had excellent specificity as well as sensitivity ratings, showing that they could reliably detect the majority of leukemia (ALL) and non-leukemia (HEM) cases with a low rate of false-positive results. Overall, the data shows that EfficientNet outperforms ResNet50 and VGG16 in all of these metrics for leukemia categorization tasks.

6. CONCLUSION

Deep learning thus offers a promising technique for accurately identifying different subtypes of leukemia, showing significant promise in the field of leukemia classification. Because deep learning models can comprehend complex patterns from high-dimensional data, they perform better and are more precise when compared to other approaches.

When using deep learning to classify malignancy, there are still a number of challenges to overcome. One of the main challenges is access to large, high-quality databases, which are essential for building deep learning models. Deep learning model interpretability is still a problem, particularly in medical settings where openness and support for results are essential.

Despite these challenges, there is an immense opportunity for deep learning to progress the research of leukemia classifier and other medical specialties. Further study is required to overcome deep learning's drawbacks and difficulties in this area. In order to do this, approaches must be developed to make deep learning models simpler to comprehend, as well as solutions must be found for issues with data accessibility.

Deep learning is generally a great tool for classifying leukemia, and its ongoing improvement has the potential to substantially improve our knowledge of the many subtypes of leukemia and result in boosted leukaemia patient diagnosis and treatment.

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