Frontiers in Health Informatics
ISSN-Online: 2676-7104
www.healthinformaticsjournal.com
2024; Vol 13: Issue 2
Open Access

Leukemia Diagnosis using Transfer Learning: An Efficient Approach

Ratnamala Mantri (Paswan) [1], Dr. Rais Abdul Hamid Khan[2], Suramya Jadhav[3]

[1]PhD scholar, School of Computer Science and Engineering, Sandip University, Nashik, India

[1]Asst prof, Department of Computer Engineering, PICT, Pune.

rspaswan@pict.edu

[2]Professor, School of Computer Science and Engineering, Sandip University, Nashik, India

rais.khan@sandipuniversity.edu.in

[3]Computer Engineering Department, Pune Institute of Computer Technology, Pune, India

2018suramyajadhav@gmail.com

Article Info

Article type:

Research

Article History:

Received: 2024-04-01

Revised: 2024-05-30

Accepted: 2024-06-22

Keywords:

CNN, ALL, leukemia, machine learning, and microscopic photos.

A B S T R A C T

Leukemia, the most prevalent type of blood cancer, affects both adults and children. For effective intervention, this necessitates prompt detection. Nevertheless, the conventional manual diagnostic techniques have lengthy procedures and are subject to variances based on skill. We use transfer learning techniques in our work, which take advantage of knowledge from models trained on massively parallel datasets. This method greatly improves time and cost efficiency by lowering the quantity of labeled data and processing resources required for the particular task of identifying acute lymphoblastic leukemia (ALL). This paper presents an automated leukemia diagnostic approach that makes use of machine learning methods, such as transfer learning and deep learning-based convolutional neural networks (CNNs). We present a approach that integrates CNN layers within Transfer Learning Architectures. The model that used EfficientNetB3 performed the best out of all the CNN architectures that were previously tested on the C-NMC-2019 ALL Dataset. It had 100% training accuracy, 96.87% testing accuracy, 96.9% F1-Score, 96.24% recall, and 97.58% precision. This model is considered one of the most promising models. The solution under proposal tackles the critical requirement of diagnosing leukemia early. By effectively examining microscopic images, identifying crucial information, and using filtering algorithms to improve accuracy, it overcomes the shortcomings of manual methods. By giving physicians and other healthcare professionals an accurate tool, this automated technique promises to increase blood cancer identification and greatly improve patient care and management of ALL.

1. INTRODUCTION

The most common type of blood cancer is leukemia, which is particularly common among young people. Breast cancer is a kind of cancer that affects the body's blood-producing tissues, including the lymphatic and bone marrow systems. A condition known as leukemia is brought on by the rapid multiplication of aberrant white blood cells, which results in uncontrolled growth within the bone marrow, which is the location where the majority of the body's blood is created. As a result of this excessive multiplication of aberrant white blood cells, the bone marrow is unable to create red blood cells and platelets, which in turn inhibits the body's ability to fight against infections. In addition, they are unable to fight off infection. It is common for leukemia cells to be immature white blood cells that are still in the process of developing. The development of a mass (tumor) that can be observed on imaging tests such as CT or X-rays is extremely uncommon in leukemia, in contrast to other types of malignancy.

Although leukemia does not result in powerful tumors, it does cause a large number of aberrant white blood cells that displace healthy platelets [2]. The leukemia disease is a fatal condition that poses a significant risk to the lives of

a large number of people all over the world. Acute and chronic leukemia are the two categories of leukemia there are. The progression of chronic leukemia is slower than that of acute leukemia, which requires diagnosis and treatment right once. Acute leukemia is divided into two subtypes: acute lymphoblastic leukemia (ALL) and acute myelogenous leukemia (AML). Chronic leukemia, on the other hand, is divided into two subtypes: chronic lymphocytic leukemia (CLL) and chronic myelogenous leukemia (CML) [3]. Those who are get impacted by leukemia include both adults and children.

We study acute lymphoblastic leukemia, a kind of childhood cancer that is rather frequent. But this can even happen to adults, and there's little possibility that a cure will be discovered in the future [7]. Since it spreads quickly to many vital organs, it can be lethal if left untreated [4]. This type of lymphoid blood cell cancer starts in the bone marrow and quickly spreads throughout the body. As a result, it has a significant impact on the function of white blood cells throughout the body [4, 7]. The development of immature lymphocytes is indicative of it. Because of this, leukemic people have problems with their immune systems' capability to fight off infections. Rapid multiplication of ALL causes harm to lymphocytes and their conversion to lymphoblasts. When it affects the liver, spleen, and other organs, it can occasionally be fatal. It may present with symptoms such as vomiting, tiredness, fever, and stomach discomfort [4]. When seen through a microscope, it may be difficult to discriminate between normal cells and juvenile leukemic blasts due to the fact that both types of cells share comparable physically identical traits.

All blood cancers are referred to as leukemias, and they make up 8–10% of all cancer cases worldwide. Worldwide, more than 900,000 people receive a blood cancer diagnosis each year. However, leukemia is difficult to diagnose because many people don't realize they have it because the initial symptoms resemble a common fever and exhaustion, which has long been a source of confusion for medical professionals, researchers, and hematologists [1, 8]. Health conditions can be improved and lives can be saved with early disease detection and suitable treatment facilities [4]. Because cancer is highly resistant to therapy, early detection will increase patient survival rates [1]. Prompt and precise diagnosis has the potential to decrease treatment expenses, boost the likelihood of remission, or possibly extend patients' lives [2]. That’s why, for effective early therapy, accurate and dependable cancer detection tools must be developed.

The development of leukemia can be brought on by a number of different reasons, such as being exposed to radiation or particular chemicals, as well as having a family history of the disease. A specific dataset, which may include examinations, signs, symptoms, and medical imaging, is utilized by a clinician in order to facilitate the process of making a diagnosis in order to determine whether or not a patient is suffering from a particular ailment. An incorrect diagnosis can have detrimental repercussions on a patient's health, such as the prescription of medicines that have negative effects. An inaccurate diagnosis may increase the cost of treatment and complicate the therapeutic process. Numerous investigations, including blood testing, bone marrow biopsies, physical examinations, and blood counts, might be used to provide a diagnosis. Microscopical analysis is typically performed by hand by a person who may become exhausted from completing multiple tests in a single day. This is despite the fact that it is the method of establishing early diagnosis that is the least expensive. Furthermore, manual diagnoses are intrinsically unreliable due to the complexity, time, and susceptibility to variations in each individual's observation of the condition being diagnosed. It is consequently vital to develop low-cost, automated equipment that are capable of accurately and independently distinguishing between examples of healthy and sick blood smears [2].

In the beginning, scientists developed a few different diagnosis systems, the majority of which relied on conventional machine approaches. In most cases, the approach for the system begins with the preprocessing of the input image, then moves on to segmentation, extracting feature, and finally grouping. In spite of this, convolutional neural networks, also known as CNNs, are utilized in modern times in order to improve the effectiveness of the system. Traditional algorithms that are based on machine learning often make use of features that are established manually in order to do categorization. On the other hand, deep features are determined by employing modern CNN-based algorithms to directly extract them from the raw input photos. The CNN is one of the most fascinating developments in the field of computer vision. CNN finds extensive use in various real-world applications, including disease detection, item identification, visual search, face recognition, and photo categorization [4]. When treating leukemia, deep learning algorithms are frequently utilized to diagnose the disease. The increased accuracy of deep learning and image analysis techniques in several health diagnostic areas has led to their increasing application in automated diagnosis systems.

Numerous automated techniques for ALL diagnosis have been introduced in recent years. Attaining a dependable and effective computerized diagnosis requires the capacity to distinguish between the features of healthy and blast cells [2]. A very accurate classification system that is based on transfer learning is proposed in this collection of contributions. The method is intended to differentiate between normal and abnormal blood smear images. This lack of data for particular jobs is one of the primary motivations for adopting transfer learning. Labeling and data collecting can be time-consuming and expensive, thus this is one of the key reasons why transfer learning is used. In addition, the utilization of actual user data is becoming increasingly difficult as a result of the growing concerns around privacy. Investigating the automatic diagnosis of leukemia in medical images is the focus of this work, which makes use of deep learning, more especially the EfficientNetB3 architecture. In the ImageNet classification test, Google's EfficientNet design recently exceeded prior state-of-the-art architectures like as DenseNet and ResNet. By requiring fewer parameters and epochs to converge, EfficientNet was ultimately successful [6]. There are 15,135 photos from 118 different people that are included in the C-NMC 2019 dataset, which can be found on Kaggle. These pictures are separated into two labeled categories: leukemia blast cells and normal cells. We started by preparing the pictures, which included augmentation of the data. Additionally, we extracted features using a pre-trained deep learning model called EfficientNetB3. The underlying model is then fine-tuned for the leukemia detection job using batch normalization, thick layers, and dropout. In addition, we have contrasted EfficientNetB3's performance with that of other architectures, such as MobileNet and VGG16. Our findings demonstrate that EfficientNetB3 can outperform other models and converge more quickly under similar training settings, resulting in 96.87% test accuracy. During the pre-screening stage, complete blood counts (CBCs) and peripheral blood tests may be used to detect leukemia cells [7].

2. RELATED WORK

As medical technology has advanced, the capacity to detect white blood cells with greater precision has become increasingly important for properly diagnosing illnesses and administering additional treatment. An immense amount of ALL cell image datasets have been employed by a number of machine learning projects over the years, including the ALL-IDB, the ASH image bank, and the ISBI 2019 C-NMC challenge dataset. These initiatives have been undertaken in order to solve the difficulty of picture categorization. In the present moment, the CNMC dataset is among the most extensive single-cell ALL picture sets that are accessible. Because of this, it is particularly well-suited for applications that include machine learning. This is because larger datasets allow for greater variance in patient instances, which ultimately results in improved diagnostic accuracy.

For each kind, there are different amounts of data in the CNMC dataset. Using image augmentation techniques, one of the classes can have more photographs added to it.

It was suggested by E. Mauricio de Oliveira and D. O. Dantas [9] that in order to increase the number of photos that belong to the healthy cell class, it would be beneficial to adopt the following methods: vertical and horizontal reflections, sixty-degree rotations, 17 x 17-pixel Gaussian blurred images, salt and pepper noise, and a shear factor of 0.3.

Kasani et al. [10] added brightness, intensity, and flips to the data and scaled it to 380 × 380 pixels in order to enhance the information. The original 450 × 450 p pixels of the image are adjusted to remove extraneous black borders.

Large training datasets are not necessary using transfer learning, which uses a neural network for either immediate discovery of features or refining on a fresh dataset. Pretrained AlexNet is utilized in [11] and [12] to classify various ALL subtypes. B-ALL is diagnosed in [13] via feature extraction, feature selection, and assembling. For feature extraction, a trained VGG-F architecture is employed. The last step is to do an analysis of principal components in order to choose the characteristics that will be utilized by a group of classifiers (an ensemble).

Neural networks' early success in classifying images led to the development of other CNN variants. The most often used CNN types are ResNet, AlexNet, and GoogLeNet [14]. Two instances of more conventional neural networks that J. E. Mauricio de Oliveira and D. O. Dantas [9] tried to employ an overly complicated design in order to attain high accuracy are Xception and VGG16. Kasani et al. [10] used a number of ensemble model combinations to get the exact forecast.

A total of one thousand neurons are generated by the output layer of VGGNet models by the application of the softmax approach. Through the use of repaired linear units (ReLU), Oliveira and Dantas [9] were able to replace the global average pooling layer for neurons. Following that, the softmax function was utilized in order to establish a connection between two fully connected layers, each of which contained 512 neurons, and a prediction layer that contained two neurons. In addition, a dropout layer was implemented in order to significantly lessen the likelihood of the data being over fit.

An average pooling layer application was made to the five layers that were eliminated from the MobileNet by Kasani et al. [10]. Overall, they received a rating of 96.17% for their correctness.

For the purpose of spatial downsampling, Prellburg and Kramer [15] utilized a factor of two in their model. This was done between each of the five convolutional layers used in the model. Using a linear classifier and global pooling, this model achieved 89.91% accuracy. In their study, Honnalgere and Nayak [16] utilized a mixed-model architecture, training each stage with two Inception ResNets that had been trained on ImageNet in the past. For the purpose of data categorization, the outputs from each model were combined and then fed into a pair of neurons and processed.

As part of their research, Yarlagadda and colleagues utilized the ResNet and Inception-v3 models in conjunction with R-MAC global descriptors. [17] were able to accurately capture the attributes of the CNN layer. Increased efficiency is achieved by the utilization of less expensive inception blocks and residual connections in the Inception-ResNet model; however, this comes at the expense of accuracy. When the R-MAC global descriptors are applied, spatial areas are exploited in order to build an image representation of the CNN features. A total of 940 epochs were utilized in the training of CNN using the dataset. They looked to their immediate neighbors in order to determine the characteristic that was most similar to them. They achieved a 94.6% success rate with this particular method.

The capacity to correctly identify white blood cells has grown in significance for diagnosis as medical understanding has progressed. WBCs were segmented and classified using the UNET architecture of a convolutional neural network (CNN) by Alharbi et al. [18].

Yentrapragada [19] uses a hybrid method that combines CNN and deep learning to identify WBC from blood smears. A selection of 12,500 photographs was made from the Kaggle image library. CNN combined with LSTM is utilized as a classifier, while the hybrid optimization method is used as a feature extractor.

Munir et al. [20] classified photos related to breast cancer using an auto-encoder. The Wisconsin Diagnostic Data Collection yielded a total of 569 samples, of which 212 had malignant characteristics and 357 had benign characteristics. The suggested work was then completed using the MATLAB R2017 platform.

Several scholars also attempted to address image categorization tasks by the application of machine learning techniques.

The Support Vector Machine (SVM) was employed by the authors, T.S. Furey [21], to ascertain whether leukemia was present in the blood cells. Leukocyte nuclei were recovered using segmentation using k-means clustering (KMC) and color-based clustering. Several characteristics, including fractal dimension and shape, were extracted from the segmented images. They also employed cross-validation methods using the SVM classifier.

A number of machine learning methods were proposed by Kashef [22], with XGBoost exhibiting the greatest results. The decision tree, the gradient boosting machine (RF), the support vector machine (SVM), the linear discriminant analysis, and the multinomial linear regression stood out among these methods. The classification of leukemia is another area that frequently makes use of deep learning techniques.

[16] Honnalgere and Nayak put forward the idea of a VGG-16 network. Following the completion of the pre-training process on the ImageNet dataset, batch normalization was utilized in order to enhance the dataset. In order to develop a DL-based framework, Marzahl et al. [23] integrated many augmentation techniques with a pre-processing stage that was based on normalization. In order to forecast the bounding box for classification made with the ResNet-18 network, they incorporated an additional regression head into the system.

In order to discriminate malignant cells from normal cells, the authors of report [24] created an ensemble model that was based on DCT. Recurrent neural networks and convolutional neural networks were merged to create CNN-

RNN. For the purpose of extracting features from the dynamic spectral domain, their hybrid model utilized both a CNN that had been pre-trained and an RNN.

Inception-V3 [26], InceptionResNet-V2 [28], and DenseNet-121 [27] are the three independent deep learning-based architectures that were presented by Ding et al. [25] for the purpose of classifying microscopic images of white blood cell malignancies with regard to classification. In addition, they suggested an ensemble neural network design, which helped them demonstrate that their one-of-a-kind layered model performed much better than a great deal of other single-class models.

AlexNet, VGG, and GoogleNet were the three independent deep learning-based algorithms that were investigated by the authors of [29] in order to be able to classify lymphocytic cells.

Our proposed model makes use of this well-known image classification tool, which is EfficientNetB3, which is designed to strike a compromise between the efficiency and accuracy of convolutional neural networks (CNNs) by employing a method known as compound scaling.

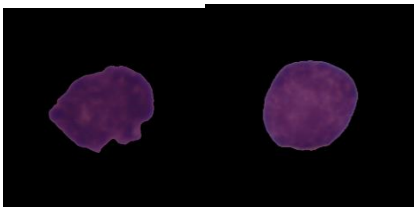
The results of Ahmed Adil Nafea's [31] use of EfficientNetB3 to diagnose lung cancer were 2.13% more accurate than those obtained by the classifier with the highest level of training. With the use of the EfficientNet model, Ahmad Huri [32] was able to improve and increase the classification accuracy of magnetic resonance imaging (MRI) pictures of brain malignancies. The system that has been suggested is comprised of two basic phases. CNN is utilized for the purpose of classifying the preprocessed images after they have been initially produced through the utilization of a variety of approaches. Using a dataset of 3,064 photos, the study concentrated on differentiating between three different forms of brain cancers: meningiomas, pituitary tumors, and gliomas. Utilizing the model that the researchers had put in place, the experiment produced remarkable results: 98.00% accuracy, 96.00% precision, and 97.00% average recall. These outcomes demonstrate how well the model performs when it comes to correctly categorizing brain tumors from medical photos. Furthermore, an enhanced version of the EfficientNetB3 model specifically created for the classification of skin lesions that are malignant is offered by [33]. Developed by Sudhir D. and his co-authors, this improved approach is based on the idea of fine-tuning transfer learning. The pre-trained model's performance was further enhanced by the researchers by tailoring it to this particular task, which allowed it to identify between benign and malignant skin lesions with remarkable accuracy.

The promise of these models in medical diagnostics is showcased by the application of sophisticated deep learning algorithms, such the ones presented in this paper. The models for classifying skin lesions and brain tumors both demonstrated exceptional recall, accuracy, and precision, highlighting the crucial role that transfer learning and fine-tuning play in improving model performance for challenging medical imaging tasks. Deep learning models that have already been pre-trained have been compared. These models include ResNet50, InceptionV3, InceptionResNetV2, EfficientNet B0-B2 models, and InceptionV3. With regard to the development of computer-aided diagnostic systems and the diagnosis of melanoma, the findings of the experiment suggest that an enhanced version of EfficientNetB3 may be of use.

3. METHODS

A. Dataset Description

The IEEE International Symposium on Biomedical Imaging (ISBI) hosted the C-NMC 2019 medical imaging competition [19], which used a dataset comprising 118 distinct individuals..Out of these, 69 had an ALL diagnosis and 49 had a Hem diagnosis. A detailed overview of the dataset's details is given in Table 1.



I II

Fig 1. ALL (I) and Hem (II) image

Data Categories	Subjects-Cancerous (ALL)	Subjects-Normal (Hem)	Subjects-Total	Images (ALL)	Images (Normal)	Images (Total)
Train Set	47	26	73	7272	3389	10661
Preliminary Test Set	13	15	28	1219	648	1867
Final Test Set	9	8	17	1761	825	2586

TABLE I

B. Methodology

1) Data Augmentation:

Training the network on a lot of data is a key strategy to increase the neural network technique's efficiency. Most computer vision tasks use small datasets, which leads to subpar classification models. Large-scale datasets like ImageNet can be used to train deep learning models beforehand, which can result in notable performance gains. We apply the data augmentation technique to generate an effective leukemia grouping model by improving the amount of training data. A method called data augmentation [23] entails purposely increasing the sum by making small changes to the current information. The Training the network on a lot of data is a key strategy to increase the neural network technique's efficiency. Most computer vision tasks use small datasets, which leads to subpar classification models. In order to train deep learning models in advance, large-scale datasets such as ImageNet can be utilized. This allows for significant performance improvements to be achieved. The training dataset is expanded through the utilization of data augmentation techniques in order to facilitate the development of an effective leukemia classification model. The process of data augmentation [23] entails making minor adjustments to the data that is already available, with the goal of purposefully expanding the number of training data copies without going through the process of collecting new data.

Augmentation Technique	Parameters
Horizontal Flip	True
Vertical Flip	True
Rotation angle	30 degrees
Width Shift	25%
Height Shift	25%
Zoom	30%
Shear	20%
Fill Mode	Nearest
Channel Shift Range	10

TABLE II

One of the most popular methods for enhancing deep learning model performance and minimizing over-fitting issues is image augmentation.

As shown in Table II, we used a variety of data augmentation strategies in our study, such as fill mode, channel shift range, shear, zoom, rotation range, width shift, height shift, and flip vertically.

2) Transfer Learning:

Transfer learning is a machine learning technique that applies knowledge from task- or field-specific training to problem-based training [24, 25]. To learn and specify the image properties in this procedure, the first few layers of deep learning are used. The pre-trained network's last layers can be eliminated during transfer learning, enabling the network to be retrained with a new layer customized for the target image. When opposed to training a model from scratch, which would necessitate substantial visual input and previous network data, this approach greatly improves efficiency and precision. Transfer learning makes model creation more successful and resource-efficient by utilizing previously acquired knowledge.

3) Proposed Framework:

Following the use of data augmentation to the leukemia cell image dataset, the transfer learning model is implemented after certain parameters are specified in Table II. We used a variety of models, including ResNet, VGG16, and MobileNet, but the EfficientNetB3 model produced the greatest results for us.

We suggest the EfficientNetB3 version as a middle ground between exceptional performance and running time. EfficientNet is a class of convolutional neural network designs that was developed by Google Research. Within this family, which is well-known for its effectiveness and equilibrium, the EfficientNet-B3 remains one of the models that stands out as being representative.

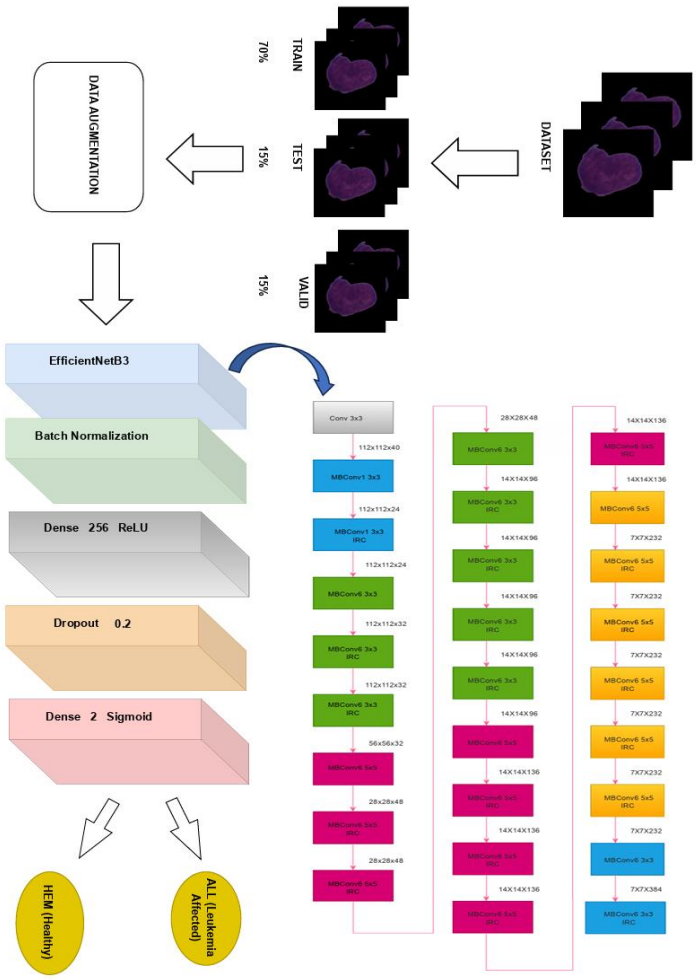


Fig 2. Methodology and Model Architecture

EfficientNet-B3 is distinguished by its automated architectural scaling, which adjusts itself according to the resolution of the images that are input. This is one of the most important characteristics of the network. This scaling makes it possible to add additional layers and filters, which in turn increase the depth and width of each layer they are included within. The EfficientNet-B3 model has a resolution that is 1.3 times larger and 1.2 times broader than the EfficientNet-B0 model, which is the third model in the family. However, the depth of the image remains the same. This makes it possible for the model to extract more detailed information from images, which is made possible by the increasing spatial resolution and additional filters that are present in each layer.

Batch normalization, a dense layer, a dropout layer, and an additional dense layer are some of the new components that we have incorporated into the EfficientNet-B3 architecture. These additions have significantly improved the performance of the system.

Batch normalization is used to equalize the outputs of a layer inside each mini-batch. When normalized inputs stabilize the learning process, higher learning rates and faster convergence can be achieved. Batch normalization reduces overfitting and improves generalization performance. Batch normalization facilitates hyperparameter adjustment by lessening the network's sensitivity to weight initialization settings. For these reasons, batch normalization is crucial to our suggested architecture.

Next, a dense layer of L1 and L2 regularizers was applied. An L2 regularizer has been applied to the kernel weights of this dense layer. To create a smoother decision boundary during training, it tends to lower all weights to zero and penalizes the sum of squares of these weights. By lessening sensitivity to noise or outliers, this tends to increase resilience. The L1 regularizer was applied to the activations and biases of this dense layer. The L1 regularizer penalizes the total absolute value of these items. It tends to set some weights to zero in order to do feature selection as efficiently as possible. This removes less significant elements from our model, improving its interpretability.

Because it causes a specific percentage of neurons in each hidden layer to become zero during training, the dropout layer is included. This essentially removes those neurons, enabling the neurons that remain to develop stronger, more autonomous properties. The network is less likely to memorize training input and is better equipped to construct generalization representations by keeping each neuron from becoming dependent on a subset of characteristics. Complex interactions and feature extraction are made possible by the dense layer's creation of a dense connection structure. Each input connection to a neuron in this layer is given a weight value. During the training process, the learning algorithm makes adjustments to these weights in order to improve the accuracy of the network's predicting. Table III presents the hyperparameters that are associated with the model that we have suggested.

Layers	**Hyperparameters and Value**
Base Model-- EfficientNetB3	Input Dimensions= (224,224,3)
Batch Normalization	Axis:1
Dense Layer 1	Units: 256 Kernel Regularizer: L2 (λ = 0.016) Activity Regularizer: L1 (λ = 0.006) Bias Regularizer: L1 (λ = 0.006) Activation Function: ReLU
Dropout Layer	Dropout Rate: 20%
Dense Layer 2	Units: 2 Activation Function: Sigmoid
Compiler	Optimizer: Adamax (Learning Rate = 0.003) Loss: Binary Crossentropy Metrics: Accuracy
Batch size	40

TABLE III

4. RESULTS AND MODEL EVALUATION

We employed a number of performance measures, such as precision, accuracy, F1-score, and recall, to evaluate the suggested model's efficacy prior to validating its performance.

The analysis metric calculates the following parameters:

- True Positive (TP): The total count in which ALL (cancer) is indicated by both the actual and anticipated values.
- True Negative (TN): The total count in which Hem (normal) is shown by both the actual and anticipated values.
- False Positive (FP): The total count in which Hem is the actual value and ALL is the predicted value.
- False Negative (FN): The total count in where ALL is the actual value and Hem is the predicted value.

Observe	Equations	Description
Accuracy	TP+TN/TP+TN+FP+FN	The classifier's accuracy in classifying the class label.
Precision	TP /TP+FP	The number of positive classes with accurate answers is indicated by this measure.
Recall	TP /TP+FN	The percentage of all positive classes that were correctly classified is displayed by this measure.
F1-Score	2*(Precision*Recall) /(Precision+Recall)	This measure employs a percentage of the recall-precision trade-off.

TABLE IV

One of the most promising models is our suggested one, which has a precision of 97.58%, a recall of 96.24%, an F1-score of 96.9%, and an accuracy of 96.87%. Table V lists the common CNN architectures that we tested with. The term "modified architecture" in this table refers to adopting the same suggested architecture with only the basic model altered (e.g., Modified MobileNet).

CNN Architectures	Accuracy
VGG-16	83.78
InceptionV3	84
EfficientNet	84.5
MobileNetV2	88.89
DenseNet121	89
ResNet18	89.33
ResNet50	90
Modified VGG-16	93.46
Modified MobileNet	95.87
Modified EfficientNetB3 without L1 and L2 regularizers	94.43
Proposed EfficientNetB3	96.87

TABLE V: The performance of the proposed modified architecture vs. common CNN architectures.

Model	F1 Score (%)
Kaiqiang Ma & Lingling Sun (2019) [34]	85.80
Yongsheng Pan & Mingxia Liu (2019) [35]	91.0
Ekansh Verma & Vijendra Singh (2019) [36]	89.4
Jonas Prellberg & Oliver Kramer (2019) [37]	88.9
Fenrui Xiao & Ruifeng Kuang (2019) [38]	88.5
Ying Liu & Feixiao Long (2019) [39]	87.6
Yifan Ding & Yujia Yang (2019) [40]	85.5
Atmika Hinnalgere & Gaurav Nayak (2019 [41]	91.7
Puneet Mathur & Mehak Piplani (2020) [42]	91.89
Shiv Gehlot & Anubha Gupta (2020) [43]	94.86
Shubham Goswami & Suril Mehta (2020) [44]	95.26
Jose de Oliveria & Daniel Dantas (2021) [9]	92.60
William Lamberti (2022) [45]	90.10
Pradeep Das & Biswajeet Sahoo (2022) [46]	91.48
Adel Sulaiman & Sheifali Gupta (2023) [47]	92.90
Proposed	96.90

TABLE VI: The performance of the proposed method vs. previous methods

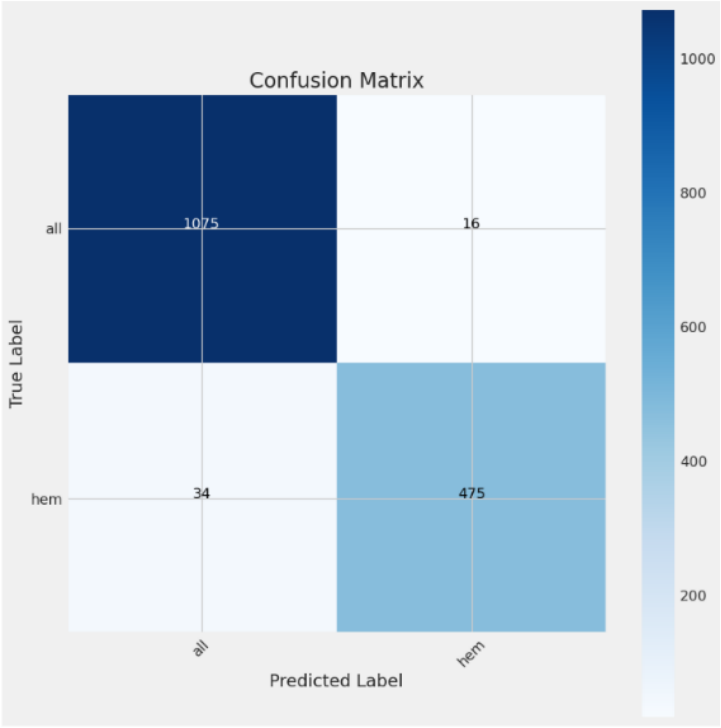


Fig. 3. Confusion Matrix of Proposed Architecture for 1600 unseen test samples

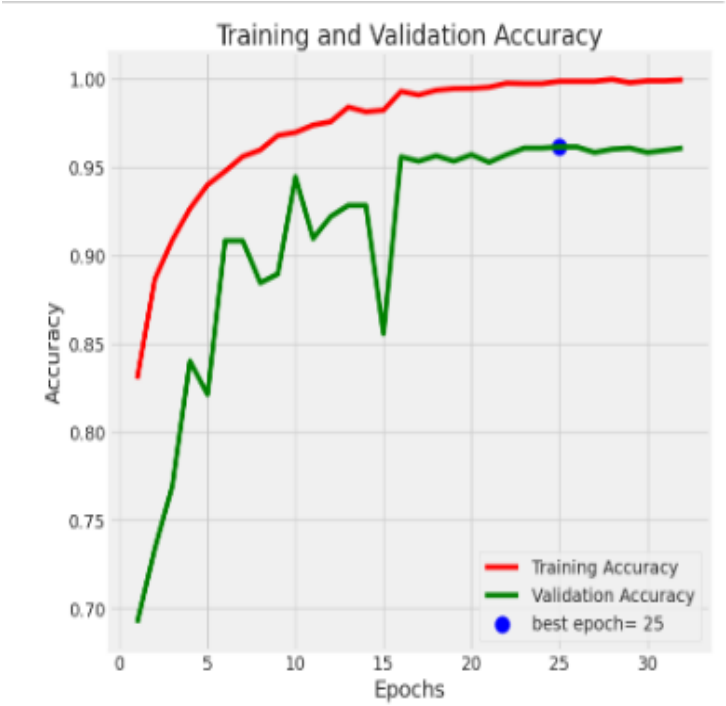


Fig. 4. Accuracy Curve of Proposed Architecture

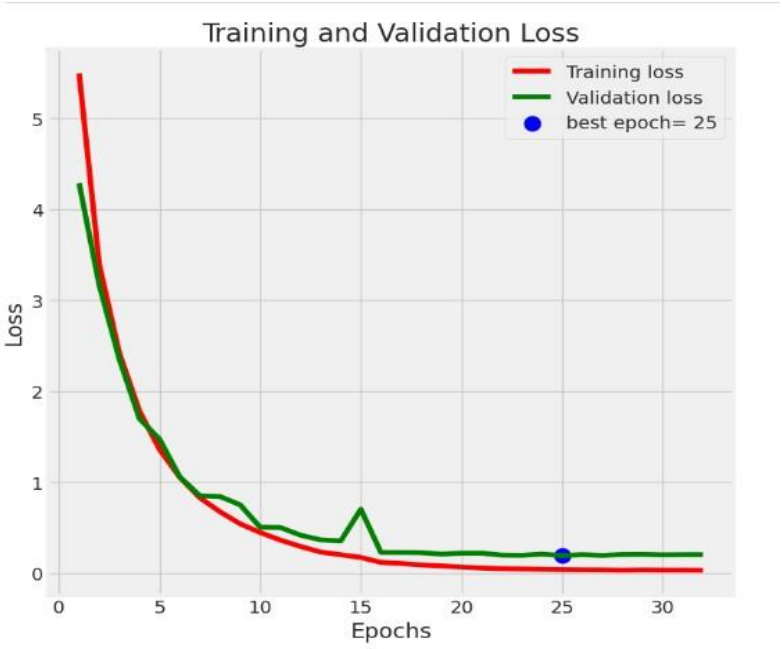


Fig. 5. Loss Function Curve of Proposed Architecture

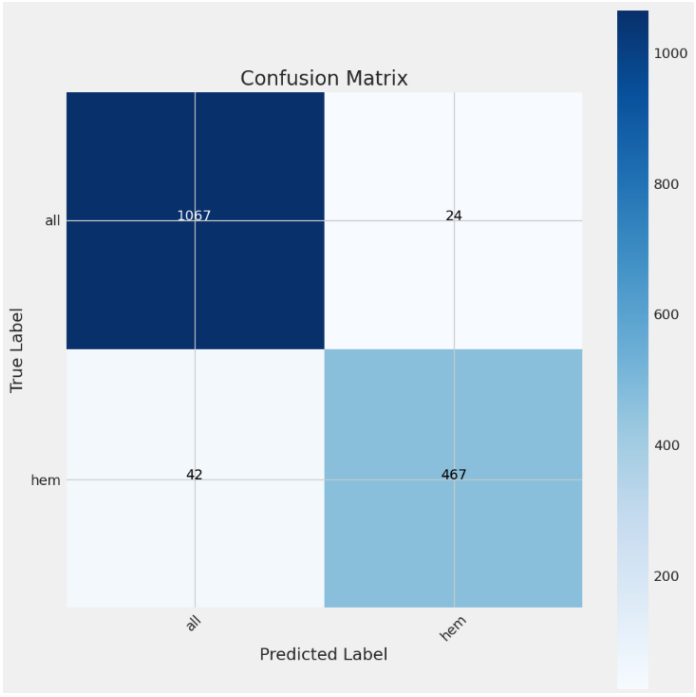


Fig. 6. Confusion Matrix of modified MobileNet Architecture for 1600 unseen test samples

Fig. 7. Accuracy Curve of modified MobileNet Architecture

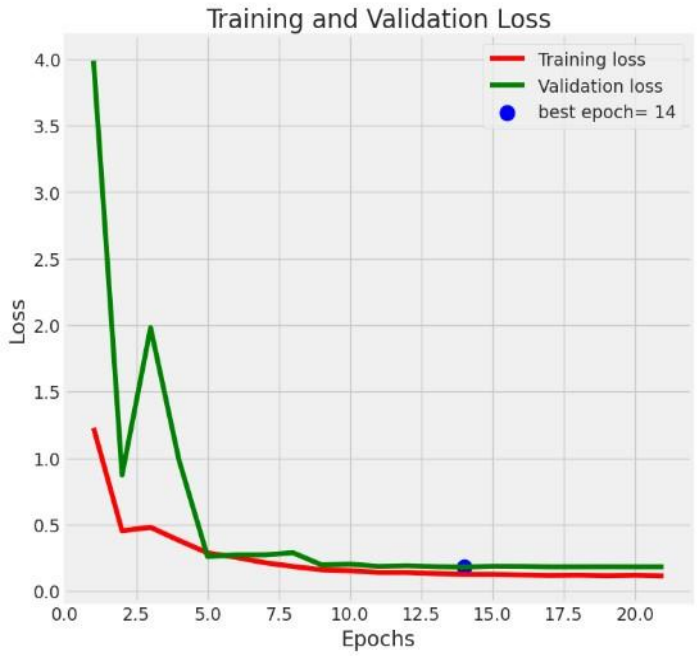


Fig. 8. Loss Function Curve of modified MobileNet Architecture

5. CONCLUSION

Early leukemia diagnosis and detection as well as the precise and economical identification of malignant leukocytes in the early stages of the disease are the primary concerns in the field of sickness diagnostics. Laboratory diagnosis institutes have inadequate flow cytometer equipment and labor-intensive processes, even with the high incidence of leukemia. Early detection can lead to more successful treatment for leukemia. We present a competitive and effective method for classifying leukemia-affected cells from healthy cells that may be applied even in the absence of data. In our research, we suggest an improved CNN architecture that includes L1 and L2 regularizations in the dense layer, as well as additional relevant layers at the end of the network. These additional layers, as indicated by the results of the experiments, make it possible for the model to differentiate between malignant cells and normal cells more accurately than earlier models that utilized simple CNN designs. We find that the proposed method outperforms on unobserved data and efficiently handles complex images. As a result, the suggested updated design improves its efficacy in a variety of picture classification applications.

REFERENCES

[1] J. Sheet, C. Ghosh and B. K. Das, "Deep Learning-Based Transfer Learning for the Detection of Leukemia," 2023 International Conference on Intelligent Systems, Advanced Computing and Communication (ISACC), Silchar, India, 2023, pp. 1-6, doi: 10.1109/ISACC56298.2023.10084138.

[2] Gundepudi, Surya & Jain, Charu & Narasimhan, Venkateswaran. (2021). Detection of Acute Lymphoblastic Leukemia by Utilizing Deep Learning methods.

[3] Raina, Rohini & Gondhi, Naveen Kumar & Chaahat, & Singh, Dilbag & Kaur, Manjit & Lee, Heung-No. (2022). A Systematic Review on Acute Leukemia Detection Using Deep Learning Techniques. Archives of Computational Methods in Engineering. 30. 10.1007/s11831-022-09796-7.

[4] P. Das, B. Sahoo and S. Meher, "An Efficient Detection and Classification of Acute Leukemia Using Transfer Learning and Orthogonal Softmax Layer-Based Model" in IEEE/ACM Transactions on Computational Biology and Bioinformatics, vol. 20, no. 03, pp. 1817-1828, 2023.

[5] R. Ribani and M. Marengoni, "A Survey of Transfer Learning for Convolutional Neural Networks," 2019 32nd SIBGRAPI Conference on Graphics, Patterns and Images Tutorials (SIBGRAPI-T), Rio de Janeiro, Brazil, 2019, pp. 47-57, doi: 10.1109/SIBGRAPI-T.2019.00010.

[6] M. Chandrasekar, M. Ganesh, B. Saleena and P. Balasubramanian, "Breast Cancer Histopathological Image Classification using EfficientNet Architecture," 2020 IEEE International Conference on Technology, Engineering, Management for Societal impact using Marketing, Entrepreneurship and Talent (TEMSMET), Bengaluru, India, 2020, pp. 1-5, doi: 10.1109/TEMSMET51618.2020.9557441.

[7]] Sampathila, N.; Chadaga, K.; Goswami, N.; Chadaga, R.P.; Pandya, M.; Prabhu, S.; Bairy, M.G.; Katta, S.S.; Bhat, D.; Upadya, S.P. Customized Deep Learning Classifier for Detection of Acute Lymphoblastic Leukemia Using Blood Smear Images. Healthcare 2022, 10, 1812. https://doi.org/10.3390/healthcare10101812.

[8]] M. O. Aftab, M. Javed Awan, S. Khalid, R. Javed and H. Shabir, "Executing Spark BigDL for Leukemia Detection from Microscopic Images using Transfer Learning," 2021 1st International Conference on Artificial Intelligence and Data Analytics (CAIDA), Riyadh, Saudi Arabia, 2021, pp. 216-220, doi: 10.1109/CAIDA51941.2021.9425264.

[9] Oliveira, José & Dantas, Daniel. (2021). Classification of Normal versus Leukemic Cells with Data Augmentation and Convolutional Neural Networks. 685-692. 10.5220/0010257406850692.

[10] Kasani PH, Park SW, Jang JW. An Aggregated-Based Deep Learning Method for Leukemic B-lymphoblast Classification. Diagnostics (Basel). 2020 Dec 8;10(12):1064. doi: 10.3390/diagnostics10121064. PMID: 33302591; PMCID: PMC7763941.

[11] Rehman A, Abbas N, Saba T, Rahman Syed Ijaz ur, Mehmood Z, Kolivand H. Classification of acute lymphoblastic leukemia using deep learning. Microsc Res Tech. 2018; 81: 1310–1317. https://doi.org/10.1002/jemt.23139

[12] Shafique S, Tehsin S. Acute Lymphoblastic Leukemia Detection and Classification of Its Subtypes Using Pretrained Deep Convolutional Neural Networks. Technology in Cancer Research & Treatment. 2018;17. doi:10.1177/1533033818802789

[13] Vogado, Luis Henrique & Veras, Rodrigo & Andrade, Alan & Araújo, Flávio Henrique & Silva, Romuere & Aires, Kelson. (2017). Diagnosing Leukemia in Blood Smear Images Using an Ensemble of Classifiers and Pre-Trained Convolutional Neural Networks. 10.1109/SIBGRAPI.2017.55.

[14] W., Wang, Z., Liu, X., Zeng, N., Liu, Y., & Alsaadi, F. E. (2017). A survey of deep neural network architectures and their applications. Neurocomputing, 234, 11–26. https://doi.org/10.1016/j.neucom.2016.12.038.

[15] Prellberg, J., Kramer, O. (2019). Acute Lymphoblastic Leukemia Classification from Microscopic Images Using Convolutional Neural Networks. In: Gupta, A., Gupta, R. (eds) ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging. Lecture Notes in Bioengineering. Springer, Singapore. https://doi.org/10.1007/978-981-15-0798-4_6.

[16] Honnalgere, A., Nayak, G. (2019). Classification of Normal Versus Malignant Cells in B-ALL White Blood Cancer Microscopic Images. In: Gupta, A., Gupta, R. (eds) ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging. Lecture Notes in Bioengineering. Springer, Singapore. https://doi.org/10.1007/978-981-15-0798-4_1.

[17] Dig Vijay Kumar Yarlagadda, Praveen Rao, Deepthi Rao, and Ossama Tawfik "A system for one-shot learning of cervical cancer cell classification in histopathology images", Proc. SPIE 10956, Medical Imaging 2019: Digital Pathology, 1095611 (18 March 2019); https://doi.org/10.1117/12.2512963.

[18] Alharbi AH, Aravinda CV, Lin M, Venugopala PS, Reddicherla P, Shah MA. Segmentation and Classification of White Blood Cells Using the UNet. Contrast Media Mol Imaging. 2022 Jul 11;2022:5913905. doi: 10.1155/2022/5913905. PMID: 35919503; PMCID: PMC9293541.

[19] Yentrapragada, D. Deep features based convolutional neural network to detect and automatic classification of white blood cells. J Ambient Intell Human Comput 14, 9191–9205 (2023). https://doi.org/10.1007/s12652-022-04422-7.

[20] Munir, Muhammad Asif & Aslam, Muhammad & Shafique, Muhammad & Ahmed, Rauf & Mehmood, Zafar. (2021). Deep Stacked Sparse Autoencoders -A Breast Cancer Classifier. Mehran University Research Journal of Engineering and Technology. Vol 41 No 1 (2022). 2413-7219. 10.22581/muet1982.2201.05.

[21] Furey TS, Cristianini N, Duffy N, Bednarski DW, Schummer M, Haussler D. Support vector machine classification and validation of cancer tissue samples using microarray expression data. Bioinformatics. 2000 Oct;16(10):906-14. doi: 10.1093/bioinformatics/16.10.906. PMID: 11120680.

[22] Kashef, Amirarash & Khatibi, Toktam & (M.D, Azim. (2020). Treatment outcome classification of pediatric Acute Lymphoblastic Leukemia patients with clinical and medical data using machine learning: A case study at MAHAK hospital. Informatics in Medicine Unlocked. 20. 100399. 10.1016/j.imu.2020.100399.

[23] Marzahl, C., Aubreville, M., Voigt, J., Maier, A. (2019). Classification of Leukemic B-Lymphoblast Cells from Blood Smear Microscopic Images with an Attention-Based Deep Learning Method and Advanced Augmentation Techniques. In: Gupta, A., Gupta, R. (eds) ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging. Lecture Notes in Bioengineering. Springer, Singapore. https://doi.org/10.1007/978-981-15-0798-4_2.

[24] de Sant'Anna, Y.F.D.; de Oliveira, J.E.M.; Dantas, D.O. Interpretable Lightweight Ensemble Classification of Normal versus Leukemic Cells. Computers 2022, 11, 125. https://doi.org/10.3390/computers11080125.

[25] Ding, Yifan & Yang, Yujia & Cui, Yan. (2019). Deep Learning for Classifying of White Blood Cancer. 10.1007/978-981-15-0798-4_4. Gupta A, Gupta R, editors. ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging. Springer Singapore; 2019. p. 33–41.

[26] C. Szegedy, V. Vanhoucke, S. Ioffe, J. Shlens and Z. Wojna, "Rethinking the Inception Architecture for Computer Vision," 2016 IEEE Conference on Computer Vision and Pattern Recognition (CVPR), Las Vegas, NV, USA, 2016, pp. 2818-2826, doi: 10.1109/CVPR.2016.308.

[27] G. Huang, Z. Liu, L. Van Der Maaten and K. Q. Weinberger, "Densely Connected Convolutional Networks," 2017 IEEE Conference on Computer Vision and Pattern Recognition (CVPR), Honolulu, HI, USA, 2017, pp. 2261-2269, doi: 10.1109/CVPR.2017.243.

[28] Szegedy, C., Ioffe, S., Vanhoucke, V., & Alemi, A. (2017). Inception-v4, Inception-ResNet and the Impact of Residual Connections on Learning. Proceedings of the AAAI Conference on Artificial Intelligence, 31(1). https://doi.org/10.1609/aaai.v31i1.11231.

[29] Safuan, Syadia & Tomari, Razali & Wan Zakaria, W.N & Mohd, Mohd & Hani Suriani, Nor Suraya. (2020). Investigation of white blood cell biomaker model for acute lymphoblastic leukemia detection based on convolutional neural network. Bulletin of Electrical Engineering and Informatics. 9. 10.11591/eei.v9i2.1857.

[30] Raju, Anand & Shanthi, T. & Nithish, M. & Lakshman, S.. (2020). Face Recognition and Classification Using GoogleNET Architecture. 10.1007/978-981-15-0035-0_20.

[31] "A Deep Learning Algorithm for Lung Cancer Detection Using EfficientNet-B3", WJCMS, vol. 2, no. 4, pp. 68–76, Dec. 2023, doi: 10.31185/wjcms.209.

[32] Swati ZNK, Zhao Q, Kabir M, Ali F, Ali Z, Ahmed S, Lu J. Brain tumor classification for MR images using transfer learning and fine-tuning. Comput Med Imaging Graph. 2019 Jul;75:34-46. doi: 10.1016/j.compmedimag.2019.05.001. Epub 2019 May 18. PMID: 31150950.

[33] Salian, Saumya & Sawarkar, Dr. (2022). MELANOMA SKIN LESION CLASSIFICATION USING IMPROVED EFFICIENTNETB3. Jordanian Journal of Computers and Information Technology. 8. 1. 10.5455/jjcit.71-1636005929.

[34] Kaiqiang Ma, Lingling Sun, Yaqi Wang, and Junchao Wang "Classification of blood cancer images using a convolutional neural networks ensemble", Proc. SPIE 11179, Eleventh International Conference on Digital Image Processing (ICDIP 2019), 1117903 (14 August 2019); https://doi.org/10.1117/12.2539605.

[35] Pan, Y., Liu, M., Xia, Y., & Shen, D. (2019). Neighborhood-correction algorithm for classification of normal and malignant cells. In Lecture Notes in Bioengineering (pp. 73-82). (Lecture Notes in Bioengineering). Springer. https://doi.org/10.1007/978-981-15-0798-4_8.

[36] Verma, Ekansh & Singh, Vijendra. (2019). ISBI Challenge 2019: Convolution Neural Networks for B-ALL Cell Classification. 10.1007/978-981-15-0798-4_14.

[37] Prellberg, Jonas & Kramer, Oliver. (2019). Acute Lymphoblastic Leukemia Classification from Microscopic Images Using Convolutional Neural Networks. 10.1007/978-981-15-0798-4_6.

[38] Xiao, F., Kuang, R., Ou, Z., Xiong, B. (2019). DeepMEN: Multi-model Ensemble Network for B-Lymphoblast Cell Classification. In: Gupta, A., Gupta, R. (eds) ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging. Lecture Notes in Bioengineering. Springer, Singapore. https://doi.org/10.1007/978-981-15-0798-4_9.

[39] Liu, Ying & Long, Feixiao. (2019). Acute Lymphoblastic Leukemia Cells Image Analysis with Deep Bagging Ensemble Learning. 10.1007/978-981-15-0798-4_12.

[40] Ding, Y., Yang, Y., Cui, Y. (2019). Deep Learning for Classifying of White Blood Cancer. In: Gupta, A., Gupta, R. (eds) ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging. Lecture Notes in Bioengineering. Springer, Singapore. https://doi.org/10.1007/978-981-15-0798-4_4.

[41] Honnalgere, A., Nayak, G. (2019). Classification of Normal Versus Malignant Cells in B-ALL White Blood Cancer Microscopic Images. In: Gupta, A., Gupta, R. (eds) ISBI 2019 C-NMC Challenge: Classification in Cancer Cell Imaging. Lecture Notes in Bioengineering. Springer, Singapore. https://doi.org/10.1007/978-981-15-0798-4_1.

[42] P. Mathur, M. Piplani, R. Sawhney, A. Jindal and R. R. Shah, "Mixup Multi-Attention Multi-Tasking Model for Early-Stage Leukemia Identification," ICASSP 2020 - 2020 IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP), Barcelona, Spain, 2020, pp. 1045-1049, doi: 10.1109/ICASSP40776.2020.9054672.

[43] Gehlot S, Gupta A, Gupta R. SDCT-AuxNetθ: DCT augmented stain deconvolutional CNN with auxiliary classifier for cancer diagnosis. Med Image Anal. 2020 Apr;61:101661. doi: 10.1016/j.media.2020.101661. Epub 2020 Feb 4. PMID: 32066066.

[44] Goswami, Shubham & Mehta, Suril & Sahrawat, Dhruva & Gupta, Anubha & Gupta, Ritu. (2020). Heterogeneity Loss to Handle Intersubject and Intrasubject Variability in Cancer.

[45] Lamberti, William. (2022). Classification of White Blood Cell Leukemia with Low Number of Interpretable and Explainable Features.

[46] Das, Pradeep & Nayak, Biswajit & Meher, Sukadev. (2022). A lightweight deep learning system for automatic detection of blood cancer. Measurement. 191. 110762. 10.1016/j.measurement.2022.110762.

[47] Sulaiman, Adel & Anand, Vatsala & Gupta, Sheifali & Asiri, Yousef & Elmagzoub, M. & Al Reshan, Mana & Shaikh, Asadullah. (2023). A Convolutional Neural Network Architecture for Segmentation of Lung Diseases Using Chest X-ray Images. Diagnostics. 13. 1651. 10.3390/diagnostics13091651.

[48] David A van Dyk & Xiao-Li Meng (2001) The Art of Data Augmentation, Journal of Computational and Graphical Statistics, 10:1, 1-50, DOI: 10.1198/10618600152418584.

[49] Abiwinanda, N., Hanif, M., Hesaputra, S.T., Handayani, A., Mengko, T.R. (2019). Brain Tumor Classification Using Convolutional Neural Network. In: Lhotska, L., Sukupova, L., Lacković, I., Ibbott, G.S. (eds) World Congress on Medical Physics and Biomedical Engineering 2018. IFMBE Proceedings, vol 68/1. Springer, Singapore. https://doi.org/10.1007/978-981-10-9035-6_33.

[50] B. Zoph, V. Vasudevan, J. Shlens and Q. V. Le, "Learning Transferable Architectures for Scalable Image Recognition," 2018 IEEE/CVF Conference on Computer Vision and Pattern Recognition, Salt Lake City, UT, USA, 2018, pp. 8697-8710, doi: 10.1109/CVPR.2018.00907.

[51] V. -T. Hoang and K. -H. Jo, "Practical Analysis on Architecture of EfficientNet," 2021 14th International Conference on Human System Interaction (HSI), Gdańsk, Poland, 2021, pp. 1-4, doi: 10.1109/HSI52170.2021.9538782.

[52] Ghodake, Sonali B., and R. S. Paswan. "Survey on recommender system using distributed frame work." *Int. J. Sci. Res.(IJSR)* 5.1 (2016).

[53] Shegokar, Pooja S., and R. S. Paswan. "Women Health Monitoring: A Survey." *International Journal of Advanced Research in Computer and Communication Engineering* 6.5 (2017).

[54] D. S. Wankhede, Nuvita Kalra, Ritika Dhabliya, Vinit Khetani, Tushar Waykole, and Aparna S. Shirkande. 2024. Enhancing Alzheimer's Disease Prediction with Bayesian Optimization and Ensemble Methods. In Proceedings of the 5th International Conference on Information Management & Machine Intelligence (ICIMMI '23). Association for Computing Machinery, New York, NY, USA, Article 108, 1–6. https://doi.org/10.1145/3647444.3647935