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Improved convolutional neural network model for leukemia classification using EfficientNetV2M and bayesian optimization

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ABSTRACT

Leukemia is a health condition in which the body produces too many abnormal white blood cells or leukocytes. Leukemia can affect both children and adults. Early diagnosis of leukemia faces significant challenges, as diagnostic methods are time consuming, require experienced medical experts, and are expensive. Previous studies have been conducted using deep learning approaches, but it is still rare to find a model that shows the best performance and uses optimization methods to classify leukemia diseases. Therefore, a Convolutional Neural Network (CNN) model with EfficientNetV2M architecture and Bayesian Optimization is proposed as the main method assisted by ImageDataGenerator in preprocessing. This study shows a significant impact of Bayesian optimization with good Accuracy, Precision, Recall and F1-Score results of 91.37%, 93.00%, 87.00%, 89.00%, respectively, which are expected to improve the performance of the model in previous studies in classifying leukemia diseases.

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1. INTRODUCTION

One of the leading causes of death in the world is cancer, which will claim an estimated 9.7 million lives by 2022 according to the World Health Organization (WHO) [1]. Leukemia is one of the cancers with the highest number of deaths among adolescents and children and has a higher risk in children up to the age of five years [2]. More specifically, leukemia is a malignant disease of white blood cells, usually of unknown origin, resulting in immature blood cells that undergo genetic mutations that transform them into cancer cells in leukemia. And its main characteristic is the accumulation of diseased cells in the bone marrow, which replace normal blood cells [3].

Early diagnosis of leukemia faces significant challenges as current diagnostic methods are limited, time consuming, and require experienced medical experts and expensive equipment. The techniques commonly used in its diagnosis are complete blood count (CBC), peripheral blood smear, bone marrow biopsy, and laboratory tests such as cytochemistry and flow cytometry [4]. Image classification with a deep learning approach has been a major technological tool adopted in the last decade to overcome such drawbacks [5]. Deep learning is the most advanced image classification technique; the use of the Convolutional Neural Network

(CNN) resulted in a decrease in the misclassification rate from approximately 25% in 2011 to 3.6% in 2015 [6], [7].

In previous research on leukemia classification, several studies have been performed, but there are still some loopholes that need to be improved. Dese et al. (2021) used a deep hybrid CNN combining MobileNetV2 and ResNet18 [8]. The MobileNetV2 component provided computational efficiency, while ResNet18 ensured high accuracy by addressing the problem through skip connections. The hybrid model employed a novel probability-based weight factor to balance the benefits of both networks. demonstrates significant advances in the automatic classification of ALL, combining efficiency and accuracy through a novel hybrid deep learning approach. Despite its strengths, future research could focus on reducing computational and data requirements to make such methods more accessible in various medical contexts. Anilkumar et al. (2021) conducted research on leukemia detection using pre-trained deep convolutional neural networks (CNNs) for peripheral blood image analysis [9]. They found that the use of pre-trained networks resulted in 100% classification accuracy for the ALL_IDB1 dataset and ALL_IDB2 dataset, except for AlexNet and VGG-16 on the ALL_IDB2 dataset. This study also compared the performance of several optimization algorithms, such as stochastic gradient descent with momentum (SGDM), root mean square propagation (RMSprop), and adaptive moment estimation (ADAM). The results show that the use of the ADAM algorithm results in a slightly longer training time compared to the SGDM and RMSprop algorithms. This research makes a significant contribution to the development of automated leukemia diagnostic methods. However, this research only considers leukemia detection in general; it has not considered the classification of leukemia into different types.

Das et al. (2021) proposed an efficient deep CNN-based framework to detect and classify acute lymphoblastic leukemia (ALL) [10]. Their approach utilized a novel hybrid of MobileNetV2 and ResNet18, using depth-wise separable convolutions, linear bottleneck architecture, inverted residuals, and skip connections. This method achieved remarkable precision on the ALLIDB1 and ALLIDB2 datasets, reaching up to 99.39% and 97.18% accuracy, respectively, with a 70-30 train-test split. The significant advantage of this approach lies in its computational efficiency and high accuracy. However, it still requires substantial computational resources and large datasets for training, which can be a limitation for practical applications in resource-constrained environments. Abhishek et al. (2022) conducted research on the automatic classification of acute leukemia using machine learning and deep learning techniques [11]. They proposed a new data set consisting of peripheral blood images that feature normal cases, acute myeloid leukemia (AML), and acute lymphoblastic leukemia (ALL). The methods used included feature extraction using Local Binary Patterns (LBP) and Histogram of Oriented Gradients (HOG), as well as the use of transfer learning techniques using various pre-trained artificial neural network architectures, such as VGG16, VGG19, and others. The results showed that, by using these techniques, the classification accuracy reached 98%. However, this research still needs improvement in terms of using a larger data set and using normalization and color standardization techniques in images.

This research aims to apply the convolutional neural network (CNN) technique in the peripheral blood image data set for the classification of leukemia. Using CNN, it is expected to obtain a more in-depth and representative feature extraction from blood images, thus improving the model's ability to distinguish between leukemia classes. The aim also is to improve the accuracy of leukemia classification, which is a major challenge in the effort to improve the accuracy of diagnosis. Although many studies have been conducted in this field, as mentioned earlier, improving classification accuracy remains a major focus to achieve more precise and rapid diagnosis results. In addition, this research is expected to have important implications in the fields of healthcare and technology. The ability to identify leukemia with higher accuracy can speed up the diagnosis process, improve treatment outcomes, and enable the development of more sophisticated decision support systems in clinical practice.

To achieve the expected goals and provide improvements from previous studies, this research proposes the convolutional neural network method using the EfficientNetV2M CNN architecture and Bayes optimization. EfficientNetV2M is an improved and faster version of the original EfficientNet. The original EfficientNet architecture is based on a new scaling method to increase the capacity of the model by scaling the width, depth and resolution dimensions of the model using simple compound coefficients [12]. Therefore, the use of CNN model with EfficientNetV2M architecture and Bayes optimization in this study is expected to achieve the expected goals as mentioned earlier.

2. METHOD

A method is proposed using the EfficientNetV2M CNN architecture and Bayes optimization. First, preprocessing is done for the dataset with ImageDataGenerator. After that, it is divided into training data and test data to facilitate the training and testing process. Next, training and testing are performed using the proposed method, and its performance can be seen from the evaluation metrics and confusion matrix generated.

Figure 1 illustrates a flow chart showing the step-by-step process used in this research, and a more detailed explanation will be explained in the next section.

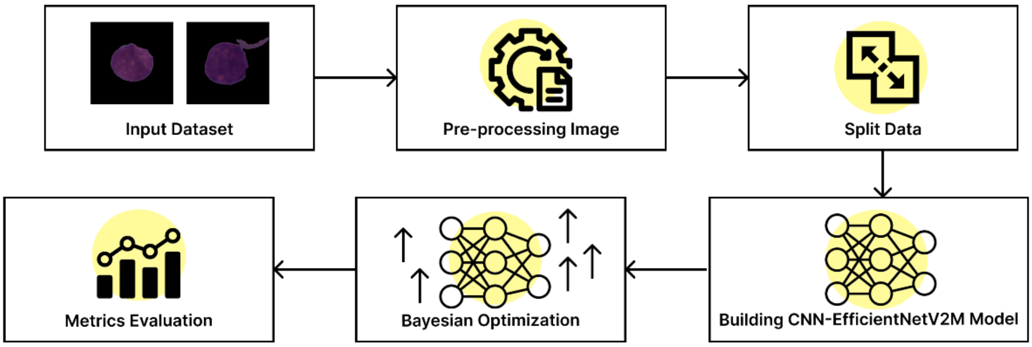

Figure 1. Flowchart of the proposed method using EfficientNetV2M and bayes optimization

Input Dataset

The dataset contains images of normal and leukemia blood cells obtained from peripheral blood smear examination. The data set sourced from Kaggle https://www.kaggle.com/datasets/andrewmvd/leukemia-classification/data was published in March 2019 and to date has been downloaded almost 12,000 times [13]. However, it is also available at the cancer imaging archive (TCIA) and is collected by the All India Institute of Medical Sciences (AIIMS) in Delhi, India [14], [15]. The dataset consists of 15,135 images with two classes, normal cell and leukemia.

Pre-processing Image

ImageDataGenerator is used at this stage to help preprocessing and image augmentation. During the testing process, the incoming images are not all perfect and ideal, so preprocessing and also image augmentation, which uses parameters that horizontal flip and fill mode in assisting this stage, details of the value which are shown in Table 1.

Table 1. Parameters used for 'ImageDataGenerator'

Parameter	Value
horizontal_flip	True
fill_mode	nearest

To train deep learning models well, a large number of images in any state are required. The size of the training data set has a great impact on the performance of deep learning models in image processing, as the more data learned, the better the model performs [16]. Horizontal flip adds variety to the dataset, ensuring that the model can recognize objects that are out of orientation. The 'nearest' filling mode was deliberately chosen to preserve semantic content by filling pixels outside the image boundary with values from the nearest edge [17].

Split Data

Data division is done to help the training and testing process. In this research, train_test_split is used to help the dataset division process. The results of dividing the dataset consisting of 2 classes are 70% for training data as many as 7462 images, 15% for validation data as many as 1599 images, and 15% for testing data as many as 1600 images.

Building CNN-EfficientNetV2M Model

The method proposed in this research is to use a deep learning model approach, CNN with EfficientNetV2M architecture. Figure 2 shows the details of the EfficientNetV2M architecture [18].

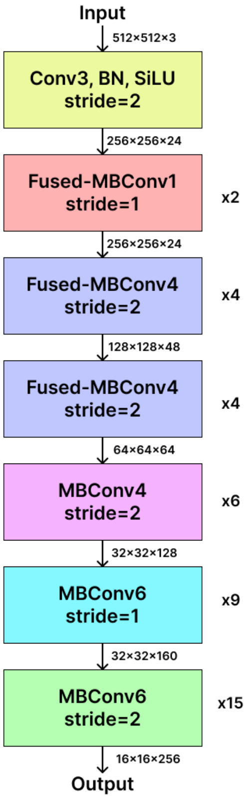

Figure 2. The architecture of EfficientNetV2M [18]

EfficientNetV2M is a neural network architecture built on the EfficientNet model, aiming to optimize model size and performance. The architecture combines the adjustment of compound scaling, depth, width, and resolution in a balanced manner to achieve superior efficiency. Equations (1), (2), and (3) are used to calculate the scaling where the depth, width, and resolution of the network are then used in EfficientNetV2M calculations [19], [20].

$$Width_{new} = Width_{old} \times \emptyset^{\alpha} \tag{1}$$

$$Depth_{new} = Depth_{old} \times \emptyset^{\beta} \tag{2}$$

$$Resolution_{new} = Resolution_{old} \times \emptyset^{\gamma} \tag{3}$$

$\emptyset$ is the scaling vector, α, β and γ is a coefficient to determine how many aspects should be scaled [19].

Bayesian Optimization

Bayesian optimization is a popular optimization technique that is commonly used to optimize the performance of deep learning and machine learning [21]. The Bayesian optimization method uses Bayes' theorem to find a combination of the minimum and maximum values of a predefined objective function to find the optimal value to improve model performance [22]. Equation (4) is used to calculate Bayesian optimization [23].

$$z^{+} = arg_{z \in S}^{\max f(z)} \tag{4}$$

Where, S represents the search space z. Bayesian Optimization is extended from Bayes' theorem given sample data D representing the observed set. Equation (5) to calculate the probability of the sample data and the model. In Equation (5) D is the sample data and y is the model.

$$p(y|D) = \frac{p(D|y)p(y)}{p(D)} \tag{5}$$

Metrics Evaluation

The confusion matrix can present the predictions and actual conditions on the data generated by deep learning models. In the confusion matrix, true positives (TP), true negatives (TN), false positives (FP) and false negatives (FN) are classes commonly used in the confusion matrix [24]. Equations (6) is used to calculate Accuracy [25]. Accuracy indicates the ratio of correctly classified data to the total number of data sets [26].

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{6}$$

Precision is the ratio of true positive observations to the total predicted positive observations. Equation (7) is used to calculate precision [27].

$$Precision = \frac{TP}{TP + FP} \tag{7}$$

Recall measures the ratio of true positive predictions (TP) to all true positive events. Equation (8) is used to calculate Recall [28].

$$Recall = \frac{TP}{TP + FN} \tag{8}$$

The F1 score is a weighted average of recall and precision, which aims to validate when the target distribution is irregular by using the positive and negative functions shown. Equation (9) is used to calculate the F1 score [29].

$$f1\,score = \frac{2 \times precision \times recall}{precision + recall} \tag{9}$$

3. RESULTS AND DISCUSSIONS

Previously, several tests have been carried out using other methods, but in the process of experimentation and testing this research, the use of CNN with EfficientNetV2M and Bayes optimization architecture provides the best performance compared to testing using other methods.

Result of CNN Model Without Using VGG16 and VGG19

In this test, 3 convolutional layers, 3 max pooling layers, 1 fully connected layer, and 1 output layer were used, the arrangement of which can be seen in Figure 3.

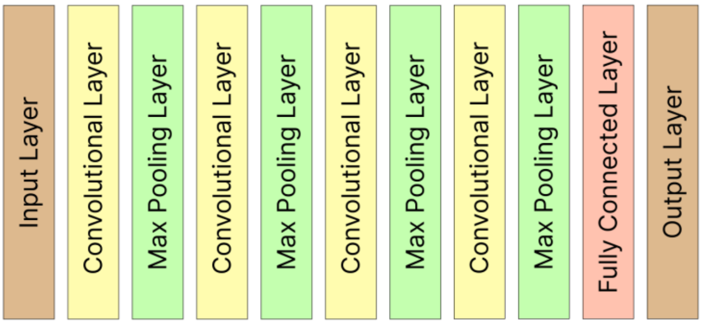

Figure 3. CNN Layer without using VGG16 and VGG19

In addition to the layers listed in Figure 3. In this experiment, the Adam optimizer is used to help model performance, and a sigmoid activation function is used in the output layer because the class to be classified is 2 classes or binary. Then the performance results can be seen in Table 2.

Table 2. Result CNN Model without using VGG16 and VGG19

Parameter	Value
Accuracy	82.72%

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Result of CNN Model Using VGG16

VGG16 consists of 13 convolution layers followed by 3 fully connected layers. The first two convolution blocks consist of two convolution layers followed by a maximum pooling layer, and the next three convolution blocks consist of three convolution layers followed by a maximum pooling layer. The pooling layer helps to reduce the number of trainable parameters [30]. The layer arrangement can be seen in Figure 4.

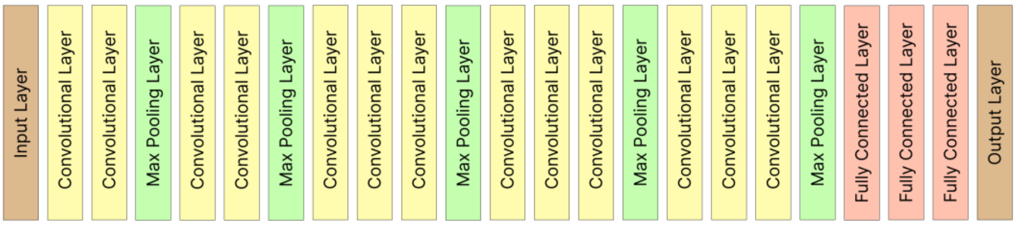

Figure 4. The architecture of VGG16

The VGG16 model has been trained on ImageNet [31]. Previously trained weights can be reused for various computer vision tasks [32]. Table 3 shows the results of the experiments using VGG16 as the main architecture with a data set split that has a ratio of 80:20.

Table 3. Result CNN model using VGG16

Parameter	Value
Accuracy	80.28%

Result of CNN Model Using VGG19

Therefore, based on previous experiments, an evaluation was conducted in which VGG19 was proposed as CNN architecture and dataset division with a ratio of 80:20. VGG-19 is a trained artificial neural network with 19 layers consisting of 16 convolution layers and 3 fully connected layers invented by the Visual Geometry Group of Oxford University [33]. As well as the use of Adam as optimizers and Sigmoid in the output layer because it is in accordance with the class you want to classify, namely 2 classes or binary whose results can be seen in Table 4.

Table 4. Result CNN model using VGG19

Parameter	Value
Accuracy	83.66%

Result of CNN Model Using EfficientNetV2M

In contrast to previous experiments that used the VGG approach as the CNN architecture and the dataset sharing, which has a ratio of 80:20. In this experiment, EfficientNetV2M based on EfficientNet is used as the main CNN architecture and the dataset has a ratio of 70:15:15 to perform leukemia classification, the results of which are shown in Table 5.

Table 5. CNN result model using EfficientNetV2M

Parameter	Value
Accuracy	87.61%

Result of CNN Model Using EfficientNetV2M and Bayes Optimization

In this experiment, EfficientNetV2M is used as the main architecture for CNN and Bayes optimization to improve CNN performance. The parameters used by bayes optimization to improve CNN performance are Units of fully connected layer and dropout rate of dropout layer.

which in the units of the Fully Connected layer has a minimum limit of 64 and a maximum limit of 256. While the dropout rate of the Dropout layer has a minimum limit of 0.2 and a maximum limit of 0.5. After training and testing using this model, the most optimal parameters for the fully connected layer are 66 and the dropout rate for the dropout layer is 0.39. Thus, these parameters can be used to find the optimal performance of the model, and the results show significant results as shown in Table 6.

Table 6. Result CNN model using EfficientNetV2M and Bayes optimization

Parameter	Value
Accuracy	91.37%
Precision	93.00%
Recall	87.00%
F1-Score	89.00%

After considering the experimental results, it is concluded that EfficientNetV2M and Bayes optimization show the best performance in detecting leukemia using blood edge images. This can be seen in Table 7 which is a comparison table between previous research and experiments with the proposed method.

Table 7. Comparison of results from previous models

Author	Algorithm	Objective	Result
B. P. Amiruddin et al. [34]	CNN-(VGG-16, MobileNetV2, EfficientNet-B1, NASNetMobile)	Classification of mosquitoes in Indonesia	Highest Accuracy MobilenetV2 80.00%
M. Akay et al. [35]	CNN-MobileNetV2	Classification of Systemic Sclerosis Skin	82.90%
Result of Experiments	CNN without using VGG16 and VGG19	Classification Leukemia	82.72%
Result of Experiments	CNN-VGG16	Classification Leukemia	80.28%
Result of Experiments	CNN-VGG19	Classification Leukemia	83.66%
Result of Experiments	EfficientNetV2M	Classification Leukemia	87.61%
Proposed Method	EfficientNetV2M and Bayes optimization	Classification Leukemia	91.37%

Table 7 shows a comparison of the results from previous models. Where in the research that has been done using CNN architecture such as in research conducted by B. P. Amiruddin et al. [34]using mosquito image datasets in Indonesia by conducting various experiments using CNN models with VGG-16, MobilenetV2, EfficientNet-B1, and NasNetMobile architectures. The results obtained were less than optimal for mosquito image classification due to the lack of datasets, and testing only several CNN architectures. Then in the research conducted by Akay et al. [35] which uses the Systemic Sclerosis Skin image dataset and the CNN model of the MobileNetV2 architecture. This research still shows poor results because the number of datasets used is only a few, while the number of datasets affects CNN performance.

In the tests carried out previously in this study, it was started by using a fine tuning CNN, which showed poor results because the model used was not complex enough to classify leukemia. Then the next test used the VGG16 and VGG19 architectures, this time the test also showed less than optimal results, this is not commensurate with the amount of time required for training this model. Furthermore, testing began using the EfficientNetV2M architecture CNN model, this model showed pretty good results compared to previous tests. So, it is proposed to use an optimization method in the form of Bayes optimization which is expected to be able to significantly improve the performance of CNN with the EfficientNetV2M architecture. And this model shows a significant increase in accuracy so that the proposed model has good performance in classifying leukemia.

4. CONCLUSION

On the basis of the results of experiments and tests using several methods, it can be concluded that the proposed method can classify leukemia quite well. As well as the impact of using bayes optimization, it can significantly improve the performance of deep learning. This can be seen by the accuracy before and after the use of Bayes optimization, which is 87.61% before use and 91.37% after use. This model can be expected to contribute to the world of research, especially in health and education. However, more research is needed to improve the performance of deep learning in classifying leukemia diseases using other methods as well.

REFERENCES

[1] O. Attallah, "Acute lymphocytic leukemia detection and subtype classification via extended wavelet pooling based-CNNs and statistical-texture features," *Image Vis Comput*, vol. 147, Jul. 2024, doi: 10.1016/j.imavis.2024.105064.

[2] L. H. S. Vogado, R. M. S. Veras, F. H. D. Araujo, R. R. V. Silva, and K. R. T. Aires, "Leukemia diagnosis in blood slides using transfer learning in CNNs and SVM for classification," *Eng Appl Artif Intell*, vol. 72, pp. 415–422, Jun. 2018, doi: 10.1016/j.engappai.2018.04.024.

[3] M. L. Claro *et al.*, "Assessing the impact of data augmentation and a combination of CNNs on leukemia classification," *Inf Sci (N Y)*, vol. 609, pp. 1010–1029, Sep. 2022, doi: 10.1016/j.ins.2022.07.059.

[4] M. T. Aziz, S. M. H. Mahmud, K. O. M. Goh, and D. Nandi, “Addressing label noise in leukemia image classification using small loss approach and pLOF with weighted-average ensemble,” *Egyptian Informatics Journal*, vol. 26, Jun. 2024, doi: 10.1016/j.eij.2024.100479.

[5] L. Boldú, A. Merino, A. Acevedo, A. Molina, and J. Rodellar, “A deep learning model (ALNet) for the diagnosis of acute leukaemia lineage using peripheral blood cell images,” *Comput Methods Programs Biomed*, vol. 202, Apr. 2021, doi: 10.1016/j.cmpb.2021.105999.

[6] N. Ouyang *et al.*, “Diagnosing acute promyelocytic leukemia by using convolutional neural network,” *Clinica Chimica Acta*, vol. 512, pp. 1–6, Jan. 2021, doi: 10.1016/j.cca.2020.10.039.

[7] K. A. H. Wibowo and A. Alamsyah, “Klasifikasi Diabetic Retinopathy Menggunakan CNN dengan Arsitektur yang Dimodifikasi,” *Indones. J. Math. Nat. Sci*, vol. 46, no. 1, p. 2023, [Online]. Available: http://journal.unnes.ac.id/nju/index.php/JM

[8] K. Dese *et al.*, “Accurate Machine-Learning-Based classification of Leukemia from Blood Smear Images,” *Clin Lymphoma Myeloma Leuk*, vol. 21, no. 11, pp. e903–e914, Nov. 2021, doi: 10.1016/j.clml.2021.06.025.

[9] K. K. Anilkumar, V. J. Manoj, and T. M. Sagi, “Automated detection of leukemia by pretrained deep neural networks and transfer learning: A comparison,” *Med Eng Phys*, vol. 98, pp. 8–19, Dec. 2021, doi: 10.1016/j.medengphy.2021.10.006.

[10] P. K. Das and S. Meher, “An efficient deep Convolutional Neural Network based detection and classification of Acute Lymphoblastic Leukemia,” *Expert Syst Appl*, vol. 183, Nov. 2021, doi: 10.1016/j.eswa.2021.115311.

[11] A. Abhishek, R. K. Jha, R. Sinha, and K. Jha, “Automated classification of acute leukemia on a heterogeneous dataset using machine learning and deep learning techniques,” *Biomed Signal Process Control*, vol. 72, Feb. 2022, doi: 10.1016/j.bspc.2021.103341.

[12] M. M. Ahsan, S. Raman, Y. Liu, and Z. Siddique, “Defect analysis of 3D printed object using transfer learning approaches,” *Expert Syst Appl*, vol. 253, Nov. 2024, doi: 10.1016/j.eswa.2024.124293.

[13] C. Mondal *et al.*, “Ensemble of Convolutional Neural Networks to diagnose Acute Lymphoblastic Leukemia from microscopic images,” *Inform Med Unlocked*, vol. 27, Jan. 2021, doi: 10.1016/j.imu.2021.100794.

[14] M. T. Aziz, S. M. H. Mahmud, K. O. M. Goh, and D. Nandi, “Addressing label noise in leukemia image classification using small loss approach and pLOF with weighted-average ensemble,” *Egyptian Informatics Journal*, vol. 26, Jun. 2024, doi: 10.1016/j.eij.2024.100479.

[15] C. Mondal *et al.*, “Ensemble of Convolutional Neural Networks to diagnose Acute Lymphoblastic Leukemia from microscopic images,” *Inform Med Unlocked*, vol. 27, Jan. 2021, doi: 10.1016/j.imu.2021.100794.

[16] M. Ahmad *et al.*, “Industry 4.0 technologies and their applications in fighting COVID-19 pandemic using deep learning techniques,” *Comput Biol Med*, vol. 145, Jun. 2022, doi: 10.1016/j.compbiomed.2022.105418.

[17] V. Singla, S. Bawa, and J. Singh, “Enhancing Indian sign language recognition through data augmentation and visual transformer,” *Neural Comput Appl*, 2024, doi: 10.1007/s00521-024-09845-1.

[18] N. H. Shabrina, R. A. Lika, and S. Indarti, “Deep learning models for automatic identification of plant-parasitic nematode,” *Artificial Intelligence in Agriculture*, vol. 7, pp. 1–12, Mar. 2023, doi: 10.1016/j.aiia.2022.12.002.

[19] A. Koul, R. K. Bawa, and Y. Kumar, “Enhancing the detection of airway disease by applying deep learning and explainable artificial intelligence,” *Multimed Tools Appl*, 2024, doi: 10.1007/s11042-024-18381-y.

[20] H. Syamsudin, S. Khalidah, and J. Unjung, “Lepidoptera Classification Using Convolutional Neural Network EfficientNet-B0,” *Indonesian Journal of Artificial Intelligence and Data Mining*, vol. 7, no. 1, Nov. 2023, doi: 10.24014/ijaidm.v7i1.24586.

[21] R. Guo *et al.*, “Machine learning-based prediction of outdoor thermal comfort: Combining Bayesian optimization and the SHAP model,” *Build Environ*, vol. 254, Apr. 2024, doi: 10.1016/j.buildenv.2024.111301.

[22] G. Ye *et al.*, “Prediction of effluent total nitrogen and energy consumption in wastewater treatment plants: Bayesian optimization machine learning methods,” *Bioresour Technol*, vol. 395, Mar. 2024, doi: 10.1016/j.biortech.2024.130361.

[23] M. A. Khan *et al.*, “HGRBOL2: Human gait recognition for biometric application using Bayesian optimization and extreme learning machine,” *Future Generation Computer Systems*, vol. 143, pp. 337–348, Jun. 2023, doi: 10.1016/j.future.2023.02.005.

[24] K. A. H. Wibowo, S. A. H. Putri, J. Jumanto, and M. A. Muslim, “Random State Initialized Logistic Regression for Improved Heart Attack Prediction,” *Jurnal ELTIKOM*, vol. 7, no. 2, pp. 116–124, Dec. 2023, doi: 10.31961/eltikom.v7i2.822.

[25] M. A. Muslim *et al.*, “New model combination meta-learner to improve accuracy prediction P2P lending with stacking ensemble learning,” *Intelligent Systems with Applications*, vol. 18, May 2023, doi: 10.1016/j.iswa.2023.200204.

[26] Y. Fu, L. Guo, and F. Huang, “A lightweight CNN model for pepper leaf disease recognition in a human palm background,” *Heliyon*, vol. 10, no. 12, p. e33447, Jun. 2024, doi: 10.1016/j.heliyon.2024.e33447.

[27] A. G. Argho, M. M. S. Maswood, M. I. Mahmood, and N. Mondol, “EfficientCovNet: A CNN-based approach to detect various pulmonary diseases including COVID-19 using modified EfficientNet,” *Intelligent Systems with Applications*, vol. 21, Mar. 2024, doi: 10.1016/j.iswa.2023.200315.

[28] D. K. Saha, A. M. Joy, and A. Majumder, “YoTransViT: A transformer and CNN method for predicting and classifying skin diseases using segmentation techniques,” *Inform Med Unlocked*, vol. 47, Jan. 2024, doi: 10.1016/j.imu.2024.101495.

[29] C. Ashwini and V. Sellam, “An optimal model for identification and classification of corn leaf disease using hybrid 3D-CNN and LSTM,” *Biomed Signal Process Control*, vol. 92, Jun. 2024, doi: 10.1016/j.bspc.2024.106089.

[30] A. Abhishek, R. K. Jha, R. Sinha, and K. Jha, “Automated detection and classification of leukemia on a subject-independent test dataset using deep transfer learning supported by Grad-CAM visualization,” *Biomed Signal Process Control*, vol. 83, May 2023, doi: 10.1016/j.bspc.2023.104722.

[31] P. Rastogi, K. Khanna, and V. Singh, “LeuFeatx: Deep learning–based feature extractor for the diagnosis of acute leukemia from microscopic images of peripheral blood smear,” *Comput Biol Med*, vol. 142, Mar. 2022, doi: 10.1016/j.compbiomed.2022.105236.

[32] M. Subramanian, J. Cho, V. E. Sathishkumar, and O. S. Naren, “Multiple Types of Cancer Classification Using CT/MRI Images Based on Learning Without Forgetting Powered Deep Learning Models,” *IEEE Access*, vol. 11, pp. 10336–10354, 2023, doi: 10.1109/ACCESS.2023.3240443.

[33] J. Unjung and M. R. Ningsih, “Optimized Handwriting-based Parkinson’s Disease Classification Using Ensemble Modeling and VGG19 Feature Extraction,” *Scientific Journal of Informatics*, vol. 10, no. 4, p. 489, 2023, doi: 10.15294/sji.v10i4.47108.

[34] B. P. Amiruddin and R. E. A. Kadir, “CNN Architectures Performance Evaluation for Image Classification of Mosquito in Indonesia,” *IEEE*, pp. 223–227, 2020.

[35] M. Akay *et al.*, “Deep Learning Classification of Systemic Sclerosis Skin Using the MobileNetV2 Model,” *IEEE Open J Eng Med Biol*, vol. 2, pp. 104–110, 2021, doi: 10.1109/OJEMB.2021.3066097.