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Infolitika Journal of Data Science

Vol. 1, No. 1, 2023

An Implementation of Hybrid CNN-XGBoost Method for Leukemia Detection

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Article History

Received 14 August 2023
Revised 12 September 2023
Accepted 20 September 2023
Available Online 24 September 2023

Keywords:
Leukemia
Classification
Hybrid method
XGBoost
Image detection

Abstract

Leukemia is a blood cancer in which blood cells become malignant and uncontrolled. It can cause damage to the function of the body's organs. Several machine learning methods have been used to automatically detect biomedical images, including blood cell images. In this study, we utilized a hybrid machine learning method, called a hybrid Convolutional Neural Network-eXtreme Gradient Boosting (CNN-XGBoost) method to detect leukemia in blood cells. The hybrid method combines two machine learning methods. We use CNN as the basic classifier and XGBoost as the main classification method. The aim of this methodology was to assess whether incorporating the basic classification method would lead to an enhancement in the performance of the main classification model. The experimental findings demonstrated that the utilization of XGBoost as the main classifier led to a marginal increase in accuracy, elevating it from 85.32% to 85.43% compared to the basic CNN classification. This research highlights the potential of hybrid machine learning approaches in biomedical image analysis and their role in advancing the early diagnosis of leukemia and potentially other medical conditions.

1. Introduction

Leukemia is a cancer that occurs in blood-forming tissues. It is caused by mutations in genetic material (DNA). Under normal circumstances, DNA dictates when blood cells should grow and when they should die. When leukemia occurs, DNA continuously orders the production of blood cells. As a result, blood cell production becomes uncontrolled. This causes the abnormal blood cells to crowd out healthy blood cells. Generally, leukemia occurs in white blood cells, where the number of white blood cells formed by the bone marrow is outside normal limits. This excessive number of white blood cells produced makes them unable to function normally and endangers the function of the body's organs [1].

In recent years, the Convolutional Neural Network (CNN) algorithm has been widely used to detect abnormalities in various images, including biomedical images. CNN has the ability to maintain spatial information in images. This capability is not shared by other machine learning algorithms, most of which only work well on tabular data, but cannot maintain spatial information in images [2].

Therefore, CNN is the most appropriate machine learning algorithm for solving problems involving images [3].

In recent years, many researchers have conducted studies and concurred them by using CNN. Kido et al. [4] designed an image-based computer-aided detection (CADe) algorithm by using areas with CNN features for detecting lung abnormalities. Lee et al. [5] demonstrated the values of sparsity increase by CNN with six CNN networks such as a well-known localization CNN network. They also showed comparative analysis results by implementing the compressed CNN networks to a CNN HW accelerator model. Yanagisawa et al. [6] examined the effectiveness of manga object detection by comparing Fast CNN, Faster CNN, and Single Shot MultiBox Detector models. Juyal and Kundaliya [7] developed a dual-channel convolutional neural network (DC-CNN) algorithm to improve the efficiency of automatic labeling. Two different CNN models are provided in the model of CNN.

Nurdin et al. [8] compared CNN-Extreme Gradient Boosting and CNN-Light Gradient Boosting to detect Pneumonia. Berdos et al. [9] used CNN to propose a model for recognizing speech emotion by using the natural database. Montaha et al. [10] utilized CNN to develop an optimal configuration for layer architecture and hyper-parameters in brain tumor classification. Altaf and Wahid [11] designed a CNN architecture for classifying hand gesture images. They yielded a significant improvement in accuracy values either in datasets using the dilated CNN or the standardized CNN. In general, the mentioned studies were focused on the use of CNN for dealing with their object studies but a lack of cases for investigating and integrating CNN with other classification methods.

Leukemia is a malignant disease and is characterized by a very rapid, deadly, and worsening disease course [12]. If patients are not treated immediately, they can die in a matter of weeks to days. One way that can be done to detect this disease is through a physical examination (including the symptoms experienced). To determine the diagnosis, supporting examinations in the form of blood test images are needed [13]. Therefore, it is necessary to have an expert system for leukemia in blood cell images using a classification technique based on machine learning.

One of the techniques used to classify the images is by integrating CNN and eXtreme Gradient Boosting (XGBoost) methods. In the beginning, blood test images are classified by using CNN. This classification process is called a basic classification. Then it continues to do a classification process using XGBoost, later on, it is called a main classification.

The hybrid approach combines the advantages of basic classification algorithms as an initial stage in modeling. After this stage, the classification process continues using the main classification method. This approach has the potential to overcome prediction errors that may occur at the basic classification stage, with the objective of improving the accuracy of leukemia detection [14].

The rest of this paper is organized as follows. Section 2 presents the materials and methods used in this study. Section 3 explains experimental results and discussions. Section 4 summarizes some conclusions and future studies.

2. Materials and Methods

This research consists of two stages, which are training and testing. At the training stage, the data undergoes preprocessing first. There are two preprocessing applied, which are image resizing and rescaling. Image resizing is carried out to equalize the dimensions of all images so that they can be processed at the next stage. Image resizing is also carried out to reduce the computational complexity of images and memory efficiency so that the training process becomes faster. It was carried out by changing all dimensions to 180×180. Meanwhile, image rescaling is preprocessing used to change pixel values to a certain scale. This image rescaling is done so that the feature scale is consistent. Thus, it makes the training process more stable and speeds up the achievement of convergence. It changes the pixel value of each image into the range 0 and 1.

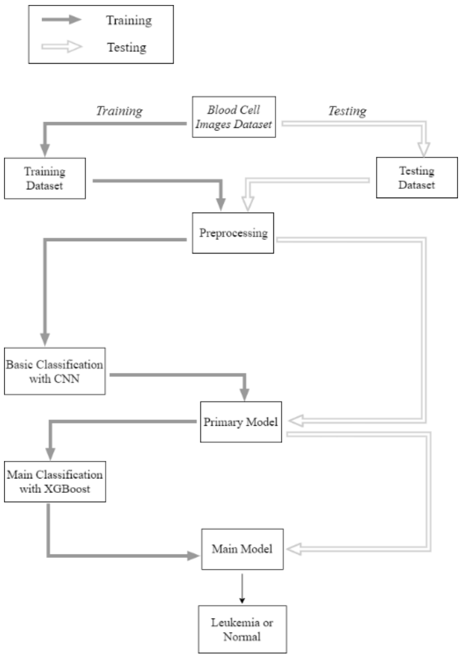

Figure 1. The methodology of this study

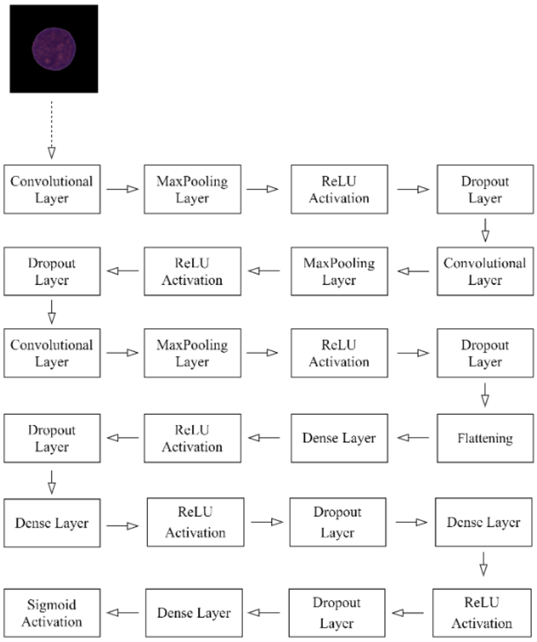

Figure 2. The CNN architecture

Table 1. The dataset used in this study

	Leukemia	Normal	Total
Training	5943	2826	8769
Validation	1274	605	1879
Testing	1274	606	1880
Total	8491	4037	12528

After the preprocessing stage, the next stage is to train the model using the basic CNN classification method. Model training using CNN was carried out for 10 epochs. One epoch is one phase for feedforward and backpropagation in a neural network. After the training process uses basic CNN classification, then it continues with the main classification process using XGBoost. This classification was conducted by using features in the form of the last hidden layer neuron values contained in the fully connected layer of the CNN. After training the main classifier, XGBoost produced a new model that could also be used to make prediction.

The final stage is model testing to measure the performance of the classification method. The testing data also undergoes preprocessing like in the training stage. After that, the testing data is directly passed to the basic CNN classification model produced in the training stage. Then, using the hidden layer fully connected layer CNN neuron values as features, testing was carried out on the XGBoost model. All the mentioned stages are depicted in Figure 1.

2.1. Dataset

The research utilizes a dataset of 12,528 blood cell images, which includes 8,491 images of leukemia blood cells and 4,037 images of normal blood cells [15]. The image is divided into three distinct sets: a training dataset, a validation dataset, and a testing dataset. The training dataset, comprising 70% of the total images (8,769 images), is employed to train the model. Subsequently, the validation dataset, consisting of 15% of the total images (1,879 images), is employed to monitor the model's performance during training. Finally, the testing dataset, also comprising 15% of the total images (1,880 images), is used to evaluate and assess the model's performance. Table 1 provides an overview of the leukemia dataset split into training, validation, and testing subsets for this study.

2.2. Basic Classification

In this stage, we utilize the CNN method to classify chest X-ray images. The number of batches used in CNN training is 32. This classification process consists of the stages of convolutional layer, max pooling layer, ReLU activation, dropout layer, and fully connected layer. In the convolution stage, 64 filters are used, with a filter matrix size of 3×3. The number of convolution layers applied is three layers. Each convolution layer contains a max pooling layer used to reduce convolution results using a 2×2 matrix and a dropout layer used to control data overfitting by deactivating several neurons at each epoch. The final stage of convolution is flattening the entire matrix into a one-dimensional form (flattening). The features that have been flattened are then forwarded to the dense layer or fully connected layer. The fully connected layer also consists of three layers, in which each layer consists of 256 nodes. The last hidden layer prediction in the fully connected layer is used as a feature passed to the main classification. The CNN architecture can be seen in Figure 2.

During CNN model training, the hyperparameters that are tuned are the dropout layers. Meanwhile, during the tuning process, the best selected model is the model that produces the best F-score of training accuracy and validation accuracy. Equation 1 is the F-score formula for training accuracy and validation accuracy:

$$F-score = \frac{2 \times\ Precision \times Recall}{Precision + Recall} \tag{1}$$

2.3. Main Classification

XGBoost is an ensemble learning algorithm that is renowned for its performance and has consistently delivered impressive results, as demonstrated in numerous studies [16–18]. The XGBoost algorithm is used in this study to be the main classification feature. This classification is carried out by using features produced by the last hidden layer of the CNN. During

Table 2. The CNN tuning results.

Dropout layer	F-score for every epoch (in %)									
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
5%	81.93	83.51	83.68	84.92	84.07	85.05	85.72	85.51	86.45	86.62
10%	81.46	83.46	82.68	84.61	84.90	85.17	85.14	83.14	86.37	**86.87**
15%	81.02	82.83	81.76	83.74	84.41	83.38	85.24	85.07	85.79	86.28
20%	81.43	82.71	83.47	84.39	84.93	84.96	84.61	85.71	85.96	86.37
25%	80.69	82.48	83.02	83.85	83.59	85.76	84.81	85.60	86.10	86.78
30%	81.52	83.48	83.65	84.42	84.19	84.55	86.01	86.08	84.57	82.20
35%	81.09	82.05	83.55	84.01	84.86	84.72	84.81	85.24	86.16	85.30
40%	81.22	83.40	84.15	84.47	84.10	84.71	84.36	85.13	85.44	85.43
45%	79.03	82.12	82.75	83.12	82.92	84.10	84.71	84.35	85.08	84.74
50%	76.63	82.30	83.10	82.79	83.35	83.60	84.79	84.68	84.23	84.42

Table 3. The CNN confusion matrix

	Predicted Leukemia	Predicted Normal	Total
Actual Leukemia	1143	145	1288
Actual Normal	131	461	592
Total	1274	606	1880

Table 4. The performance of basic classification.

Metric	Value
Accuracy	85.32%
Precision	89.72%
Recall	88.74%

training, the hyperparameters that are tuned for both main classifiers are learning rate and maximum tree depth.

2.4. Model Evaluation

The experimental results from the model were evaluated using accuracy, recall, precision, and Area Under ROC Curve (AUC) values. Accuracy measured how well the model made predictions correctly. Precision served as a metric to assess the relevance of the positive class or the model's ability to predict the leukemia class, while recall gauged the model's ability to correctly identify the positive class or leukemia label class. These metrics were calculated using Equations 2, 3, and 4 [13, 19].

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{2}$$

$$Precision = \frac{TP}{TP + FP} \tag{3}$$

$$Recall = \frac{TP}{TP + FN} \tag{4}$$

Finally, we utilized an AUC metric to measure the ability of model to differentiate between two classes. The AUC value can be obtained by calculating the area under the ROC (receiver operating characteristic) curve area.

3. Results and Discussion

3.1. Result of Basic Classification

Basic CNN classification was carried out by setting dropout layer hyperparameters of 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, and 50%. The use of dropout layers was done to prevent excessive co-adapting, thereby reducing the opportunity for overfitting. Meanwhile, the number of epochs used was 10 epochs, where at each epoch training was carried out using a batch size of 32. Based on the hyperparameter tuning results, Table 2 is the basic classification results obtained from this study.

From the CNN parameter tuning results from Table 2, it can be seen that the highest F-score was yielded using a dropout layer of 10% at the 10th epoch. Dropout is a neural network regularization technique in which some neurons are randomly selected and not used during training. It can prevent overfitting and also speed up the learning process. Additionally, it refers to removing neurons in the form of hidden or visible layers in the network. Therefore, the model uses this dropout layer and selects this epoch in order to test the dataset and apply it for subsequent classification.

By using the model that produces the highest epoch, Table 3 is the confusion matrix of testing results for basic CNN classification. Based on the confusion matrix, the performance of the model is calculated and presented in Table 4. The basic CNN classification method yields an AUC value of 92.13%, as depicted in Figure 3.

3.2. Result of Main Classification

The main classification of XGBoost was conducted by applying alpha and lambda regularization. Meanwhile, the learning rate parameters and maximum tree depth

Table 5. The XGBoost tunning result

Learning rate	F-score for every maximum tree depth (in %)									
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
0.05	88.19	88.17	88.32	88.46	88.78	89.20	89.63	90.20	90.43	90.65
0.06	88.30	88.18	88.27	88.78	88.96	89.66	89.80	90.43	90.56	91.05
0.07	88.33	88.28	88.37	88.76	89.36	89.64	90.33	90.65	91.07	91.29
0.08	88.23	88.28	88.38	88.96	89.61	90.18	90.41	90.72	91.18	91.60
0.09	88.11	88.32	88.48	89.18	89.77	90.24	90.64	91.05	91.12	91.43
0.1	88.25	88.23	88.81	89.11	89.88	90.16	90.95	91.27	91.26	91.69
0.2	88.31	88.78	89.19	90.00	90.32	91.13	91.47	91.94	**92.17**	92.08
0.3	88.50	88.89	89.53	90.45	91.27	91.51	91.55	91.89	92.01	91.64
0.4	88.59	88.87	89.90	90.76	91.07	91.29	91.31	91.85	91.69	91.67
0.5	88.59	88.76	89.54	91.15	91.57	91.57	91.67	91.86	91.81	91.20

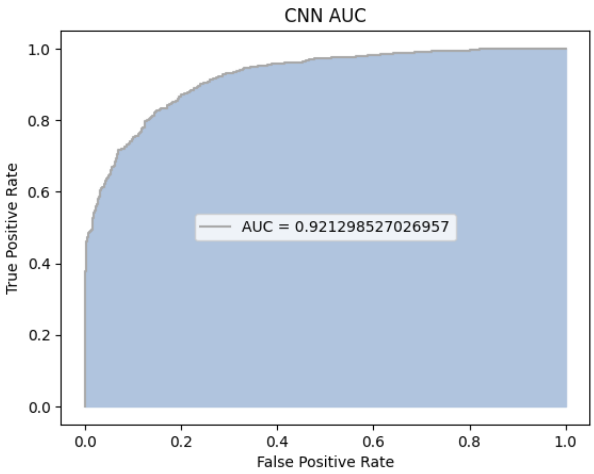

Figure 3. CNN AUC.

Table 6. The XGBoost confusion matrix

	Predicted Leukemia	Predicted Normal	Total
Actual Leukemia	1152	122	1274
Actual Normal	152	454	606
Total	1304	576	1880

Table 7. The performance of basic classification.

Metric	Value
Accuracy	85.43%
Precision	88.34%
Recall	90.42%

were the tuned parameters, which were 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, and 0.5. Meanwhile, the tree depths used in this study were 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. Based on the hyperparameter tuning results, Table 5 demonstrates the obtained results for the main classification of the XGBoost algorithm.

From Table 5, it can be seen that the best F-score results were produced at a learning rate of 0.2 and a maximum tree depth of 9. Therefore, the model with the specified learning rate and tree depth was used to test the testing dataset.

Table 6. Comparison between basic and main classification

Metric	Basic classification (CNN)	Main classification (CNN-XGBoost)
Accuracy	85.32%	**85.43%**
Precision	**89.72%**	88.34%
Recall	88.74%	**90.42%**
AUC	**92.13%**	91.63%

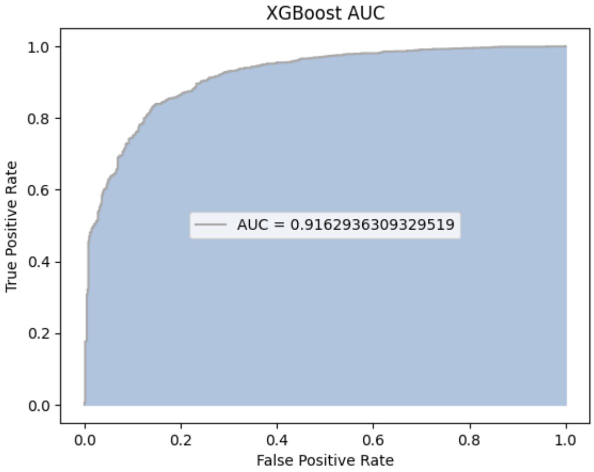

Figure 4. XGBoost AUC

Table 6 is the confusion matrix for the main classification test of XGBoost. Based on the confusion matrix, the performance of the model is calculated and presented in Table 7. The basic CNN classification method yields an AUC value of 91.63%, as depicted in Figure 4.

Furthermore, we compared the results between the basic and main classification tests, as presented in Table 7. The results indicates that the proposed hybrid CNN-XGBoost performed better results, especially for accuracy and recall values, compared to CNN. Meanwhile, the CNN method is superior for precision and AUC values.

To be more specific, according to the accuracy results, the main classification of XGBoost was able to increase the accuracy of the basic CNN classification from 85.32% to 85.43%. In addition, if we look at the precision value, the basic CNN classification is still better at predicting images of leukemia blood cells or the positive class. The precision of CNN's basic classification, which is 89.72%, is still better than the main classification of XGBoost, which is 88.34%. Whereas, the recall values indicate that the XGBoost main classification method is able to increase the model's ability to re-recognize leukemia images or positive classes, from 88.74% in the basic CNN classification to 90.42% in the XGBoost main classification. Finally, the AUC value demonstrates that the basic CNN classification method is still better in its ability to differentiate between leukemia cell images and normal cell images. The AUC value calculated by the basic CNN classification method is 92.13%, still better than the main classification of XGBoost, which is 91.63%.

4. Conclusions

A leukemia detection study using the hybrid CNN-XGBoost algorithm has been carried out. Based on experimental results from 12528 image datasets, comparing the performance of CNN basic classification and main classification summarizes several conclusions. Firstly, based on the resulting accuracy values, the main classification of XGBoost was able to increase the accuracy of the basic CNN classification from 85.32% to 85.43%. Secondly, the precision values show that the basic CNN classification is still better at predicting images of leukemia blood cells or the positive class. The precision of CNN's basic classification, which is 89.72%, is still better than the main classification of XGBoost, which is 88.34%. Thirdly, the recall values confirm that the XGBoost main classification method is able to increase the model's ability to re-recognize leukemia images or positive classes, from 88.74% in the basic CNN classification to 90.42% in the XGBoost main classification. Finally, based on the resulting AUC value, the basic CNN classification method is still better in its ability to differentiate between images of leukemia cells and images of normal cells. The AUC value produced by the basic CNN classification method is 92.13%, still better than the main classification of XGBoost, which is 91.63%.

We realize that this study still has weaknesses. Among the weaknesses are the inability of this hybrid algorithm to accurately detect images with irregular object positions, and the lack of the number of images in the dataset, which causes overfitting, which was overcome by the data augmentation technique. Therefore, further research is focused on the initial image processing process using other image processing methods.

Author Contributions: Conceptualization, T.H. and I.I.; methodology, T.H.; software, T.H., E.H, I.S.D; validation, T.H., I.I. and Z.V.; formal analysis, T.H.; investigation, Z.V.; resources, T.H, E.H.; data curation, T.H, I.S.D; writing—original draft preparation, T.H. and I.I; writing—review and editing, T.H. and I.I; visualization, E.H.; supervision, I.I.; project administration, Z.V. All authors have read and agreed to the published version of the manuscript.

Funding: This study does not receive external funding.

Ethical Clearance: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data used in this study available at C_NMC_2019 Dataset: ALL Challenge dataset of ISBI 2019 (C-NMC 2019) on Cancer Imaging Archive. Link: https://wiki.cancerimagingarchive.net/pages/viewpage.action?pageId=52758223.

Conflicts of Interest: All the authors declare that there are no conflicts of interest.

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