Classification of Pneumonia from Chest X-ray images using Support Vector Machine and Convolutional Neural Network

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Abstract—Pneumonia presents a global health challenge, especially in distinguishing bacterial and viral types via chest Xray diagnostics. This study focuses on deep learning models Convolutional Neural Networks (CNN) and Support Vector Machines (SVM) for pneumonia classification. Our findings highlight CNN's superior performance. It achieves 91% accuracy overall, outperforming SVM's 79% in differentiating normal lungs and pneumonia-affected lungs. Specifically, CNN excels in distinguishing between bacterial and viral pneumonia with 92% accuracy, compared to SVM's 88%. These results underscore deep learning models' potential to enhance diagnostic precision, improve treatment efficacy and reduce pneumonia-related mortality. In the context of Society 5.0, which integrates technology for societal well-being, deep learning in healthcare emerges as transformative. Enabling early and accurate pneumonia detection, this research aligns with the United Nations Sustainable Development Goals (SDGs). It supports Goal 3 (Good Health and Well-being) by advancing healthcare outcomes and Goal 9 (Industry, Innovation, and Infrastructure) through innovative medical diagnostics. Therefore, this study emphasizes deep learning's pivotal role in revolutionizing pneumonia diagnosis, offering efficient healthcare solutions aligned with current global health challenges.

Keywords—Pneumonia; chest X-ray; Support Vector Machine; Convolutional Neural Network; SDGs; Society 5.0

I. INTRODUCTION

Pneumonia is a severe respiratory infection in the lungs and is the leading cause of mortality among children globally [1]. When infected, the alveoli in the lungs fill with fluid and pus, causing painful breathing and restricting oxygen intake [2]. Despite extensive research over recent decades, pneumonia remains one of the primary causes of death worldwide [3]. The Covid-19 pandemic has exacerbated this issue, with pneumonia acting synergistically with the virus to increase mortality rates, particularly among children [4]. In Indonesia, pneumonia was responsible for 15% of toddler deaths, accounting for approximately 922,000 deaths in 2015. From 2015 to 2018, the number of confirmed pneumonia cases in children under five rose by around 500,000 each year [5]. Detecting pneumonia by conventional means is time-consuming and complex [6], resulting in many deaths due to delayed treatment. Therefore, integrating artificial intelligence, especially deep learning, in healthcare, especially for pneumonia detection, might be a novel solution and significantly advance the industry in the Era of Society 5.0 [7]. Deep learning-enhanced and timely pneumonia diagnosis can lead to more effective treatments and improved public health outcomes. This research is crucial because clinical symptoms of pneumonia are often ambiguous and visually similar, particularly in chest X-rays, as illustrated in Fig. 1.

Observing Fig. 1, it is evident that distinguishing between viral and bacterial pneumonia solely from a chest X-ray is challenging [8]. The underlying cause of pneumonia greatly influences the treatment approach. For bacterial pneumonia, prompt antibiotic treatment is essential. Conversely, viral pneumonia requires supportive care, such as rest, Paracetamol, and possibly antiviral medication [9]. This underscores the critical nature of this research, as delays or errors in identifying the pneumonia type can lead to incorrect treatments, with potentially fatal consequences.

Several prior studies have focused on pneumonia classification, including one titled "Classification of Pneumonia in Lung X-Ray Image Augmentation Using Convolution Neural Network Method" [10]. Hipzi's research (2023) achieved a classification accuracy of 95.36%, but it was limited to determining the presence of pneumonia. Another study by Imran et al. (2020) employed various approaches for classifying pneumonia, including logistic regression, SVM, decision tree, and random forest [11]. Although these methods achieved an average accuracy of over 90%, they were restricted to classifying two categories (normal and pneumonia) and were based on numerical data rather than images. Therefore, the novelty of this study lies in developing a model capable of not only identifying pneumonia but also differentiating between bacterial and viral types. Additionally, this research will compare two methods with strong classification capabilities: support vector machine (SVM) and convolutional neural network (CNN).



Fig. 1. Chest X-Rays based on pneumonia status.

In summary, pneumonia remains a major global health challenge, exacerbated by the Covid-19 pandemic and the limitations of current diagnostic methods. Integrating deep learning into healthcare, specifically for pneumonia detection, offers a promising solution. This research aims to develop a model that classify pneumonia types with using of advanced classification methods. By improving diagnostic accuracy and timeliness, this study supports the United Nations Sustainable Development Goals (SDGs), particularly Goal 3 (Good Health and Well-being) and Goal 9 (Industry, Innovation, and Infrastructure). Enhancing healthcare technology through deep learning aligns with these goals by promoting better health outcomes and fostering innovation in medical diagnostics.

II. RELATED WORK AND DATASET

A. Related Work

The methods used in this research are Support Vector Machine (SVM) and Convolutional Neural Network (CNN). SVM has been applied in various image classification tasks, such as Setiawan and Putra (2018), who achieved an accuracy rate of 80% in their study for breast cancer classification [12], and Purnajaya (2021), who obtained a 99% accuracy rate in their study for classifying Covid-19 patients using chest X-ray data [13]. Additionally, the CNN method was chosen for comparison because of its advantages in image classification [14]. This is possible because CNN can process data with grid-like patterns and is designed to automatically learn spatial hierarchies [15]. Through this research, it is hoped that the healthcare industry can leverage artificial intelligence-based technologies such as SVM and CNN to enhance efficiency in pneumonia diagnosis. Additionally, this research can contribute to accelerating the achievement of Sustainable Development Goal 3 on Good Health and Well-being by helping improve public health, particularly by reducing pneumonia-related mortality [16].

Through this research, it is hoped that the healthcare industry can leverage artificial intelligence-based technologies such as SVM and CNN to enhance efficiency in pneumonia diagnosis. Additionally, this research can contribute to accelerating the achievement of Sustainable Development Goal 3 on Good Health and Well-being by helping improve public health, particularly by reducing pneumonia-related mortality [17].

B. Dataset

This research is primarily focused on the classification of pneumonia diseases utilizing secondary data obtained from the Kaggle platform [18]. The dataset comprises 6,140 X-ray images of human lungs categorized into three distinct classes namely normal, viral pneumonia patients, and bacterial pneumonia patients. The dataset was collected from a healthcare facility in Guangzhou, China, and has been rigorously verified by three expert radiologists. In the international medical field, there is an independent organization known as the International Commission on Radiological Protection (ICRP), which focuses on providing recommendations and guidelines on all aspects of radiological protection. One of the recommendations from the ICRP that serves as a reference for the entire world pertains to the acquisition and use of X-ray images, as found in the "Occupational Radiological publication Protection in Interventional Procedures" [19]. Therefore, it can be concluded

that the techniques for obtaining and interpreting X-ray images are universal and can be applied worldwide. This suggests that the use of X-ray image datasets originating from China can also be applied in Indonesia.

III. METHOD

To conduct this study, several methodological steps were undertaken, including a literature review, data collection, and data pre-processing. These methods culminated in the creation of a final dataset, which was subsequently split before entering the classification phase. Based on experiments performed by Montesinos-López (2023), the optimal dataset split was determined to be 85% for training data and 15% for testing data. As such, this same split ratio was applied in the present research [20].

A. Data Standardization

The dataset used must go through a standardization process involving pre-processing. In this study, images are read in grayscale, then resized to 150×150 pixels and normalized with Min-Max Normalization with the lower bound of 0 and upper bound of 1, so that pixel values fall within the range of 0 to 1 to ensure efficient training [16]. In the CNN, the data is obtained in the form of a 150×150 array for each image. However, in the SVM, each image is further processed from a 150×150 array into a $1 \times 22,500$ array for one image. This is due to the limitation of SVM, which cannot handle multi-dimensional array data.

B. Support Vector Machine

Support Vector Machine (SVM) is a machine learning algorithm that operates based on the principles of Structural Risk Minimization and optimization theory by determining the optimal hyperplane capable of separating specific classes [21]. A hyperplane represents a linear boundary between one class and the others. The best hyperplane is chosen when the distance between the separation line and the nearest feature point (margin) is maximized [22]. Maximizing the margin yields an SVM structure that minimizes the risk of classification errors. The concepts of the hyperplane and margin are visually depicted in Fig. 2.



Fig. 2. Hyperplane and margin illustration.

Not all feature data can be straightforwardly separated by a linear boundary. In cases where feature data cannot be linearly separated, SVM hyperplanes employ kernel tricks. Kernel tricks are techniques that transform data into higher-dimensional spaces based on mathematical functions to facilitate linear separation of classes [23]. An illustration of kernel tricks is provided in Fig. 3.



Fig. 3. Kernel tricks illustration.

In Fig. 3, it is evident that what initially could not be represented as a hyperplane can be transformed into a flat, linear hyperplane in a 3-dimensional space. The variable ϕ represents the transformation function variable utilized within the kernel function.

In summary, there are three parameters involved in SVM calculations such as, C value, gamma, and the kernel function. The C value serves as a penalty for errors, and if it is too low, it may lead to misclassifications; conversely, if it is too high, it may result in bias [24]. Therefore, in this research, the iterated C values range from 0.1 to 10. Gamma represents the influence of one data point on another [25]. Generally, the gamma parameter is standardized and frequently used in SVM parameters [26]. As for the last parameter, this study compares three kernel functions: RBF, polynomial, and sigmoid, as all three can be applied to datasets with numerous numerical features [27]. In this research, the classification is divided into two stages: the first model classifies detected pneumonia and normal cases, while the second model differentiates between bacterial and viral pneumonia. This division is made because SVM is particularly suited for binary classification tasks [28].

C. Convolutional Neural Network

With the advancement of technology, CNN models have demonstrated superior performance in image classification when compared to traditional classification methods. CNN leverages spatial structures through convolutional operations to enhance efficiency and effectiveness in the training process. This model has been widely employed in classifying various image types, including pneumonia images [29]. This research also adopts a CNN approach employing two models to classify pneumonia diseases, thereby minimizing classification errors.

Convolutional Neural Networks (CNN) are machine learning models commonly used for image classification. They leverage the concept of Artificial Neural Networks (ANN) to process data with grid-like topologies [30]. For example, time series data can be viewed as a one-dimensional grid by sampling at fixed time intervals, and image data is considered a twodimensional grid of pixels. CNN makes use of the spatial structure of images through convolution operations to enhance the efficiency and effectiveness of the learning process. Convolution is a specific type of linear operation. CNN consists of several layers, including convolutional layers, pooling layers, and fully connected layers.

The convolutional layers in CNN are responsible for performing convolution operations on input data with specific filters or kernels. These filters extract portions of the input data and generate feature maps that represent features within the input. Each filter in the convolutional layer produces a different feature map, so the more filters you use, the more features can be identified in the input [31].

The pooling layers in CNN are responsible for reducing the dimensions of the feature maps generated by the convolutional layers. This is done to decrease the number of parameters in the model and speed up the training process. Several common types of pooling are used, such as max pooling and average pooling. Max pooling selects the maximum value from a group of values in the feature map, while average pooling calculates the average value from a group of values in the feature map [32].

The fully connected or dense layers in CNN are responsible for connecting the output from the previous layers to the final output. These layers consist of multiple neurons, each of which is connected to all the neurons in the previous layer. The fully connected layers will produce output in the form of probabilities for each class in the data. This output is then used to determine the predicted class of the input data [33].

D. Confusion Matrix

The confusion matrix is an evaluation method used in classification systems to measure the performance of a developed classification model [34]. It contains information comparing actual and predicted values to determine the model's accuracy. The confusion matrix has a size of $n \times n$, where n represents the number of classes to be predicted. In evaluating model performance using a confusion matrix, there are four terms that represent the classification results: TP (true positive) is the number of positive class data correctly predicted as positive, FP (false positive) is the number of negative class data incorrectly predicted as positive, and TN (true negative) is the number of negative class data correctly predicted as negative, and TN (true negative) is the number of negative class data correctly predicted as negative [35]. The basic structure of a confusion matrix is shown in Fig. 4.



Fig. 4. Confusion matrix structure.

Based on the values obtained from TP, FP, FN, and TN in the confusion matrix, several evaluation metrics such as accuracy, precision, recall, and F1-score can be calculated to assess the model's performance [36]. Accuracy indicates how accurately the model's predictions match the overall data. The accuracy value can be determined using the following Eq. (1).

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN}$$
(1)

Precision measures the accuracy between the given data and the model's predicted results. The precision value can be calculated using Eq. (2).

$$Precision = \frac{TP}{TP + FP}$$
(2)

Recall measures the model's success rate in retrieving relevant information. It is the ratio of true positive data to the total positive data. The recall value can be calculated using Eq. (3).

$$Recall = \frac{TP}{TP + FN}$$
(3)

Finally, F1-score, or F-measure, is derived from the precision and recall values. The F1-score can be calculated using Eq. (4).

$$F1 = \frac{2 \times recall \times precision}{recall + precision}$$
(4)

IV. EXPERIMENTAL RESULT

A. Experimental Setup

The utilized dataset underwent a standardization process involving pre-processing procedures. In this study, the images were initially read in grayscale, scaled down to 150×150 pixels, and normalized to ensure pixel values fall within the range of 0 to 1, facilitating an efficient training process. In the Convolutional Neural Network (CNN), the input is obtained in the form of an array of dimensions 150×150 for each image. However, in the case of Support Vector Machine (SVM), further data transformation is applied, converting the initial 150×150 input array into a $1 \times 22,500$ array for each image. This adaptation is necessitated by the inherent limitation of SVM in processing multidimensional input arrays.

B. Support Vector Machine Training Process

Before performing classification, it is essential to consider the balance of the utilized data. There are 1,341 instances of healthy lung data and 3,875 instances of pneumonia detection. Therefore, balancing needs to be carried out to ensure equilibrium in the training data between healthy lungs and pneumonia cases. The objective of balanced data is to enable the model to recognize data patterns more effectively and avoid anomalies in the dataset [37]. One approach to achieving balance is through the Synthetic Minority Oversampling Technique (SMOTE) algorithm, which generates synthetic data for the minority class based on the nearest distance [38]. Following the application of SMOTE, a total of 3,875 instances of both healthy lungs and pneumonia cases were obtained.

Subsequently, the data will be trained, and the bestperforming SVM Model 1 will be applied to a test dataset comprising 624 instances. Table I illustrates the performance of SVM Model 1.

Therefore, the optimal SVM Model 1 utilizes the RBF kernel function with a C value of 0.1. Next, Model 2 will analyze bacterial and viral pneumonia diseases using 2,530 training instances that have undergone the SMOTE process. Subsequently, the best-performing model will be applied to a test dataset consisting of 390 instances. Table II below displays the performance of SVM Model 2.

 TABLE I.
 CLASSIFICATION PERFORMANCE OF SVM METHOD FROM MODEL 1

Kenel Function	Cost (C) Parameter	Accuracy
Radial Basis Function (RBF)	0.1	84%
	1	88%
	10	85%
Polynomial	0.1	87%
	1	86%
	10	83%
Sigmoid	0.1	61%
	1	43%
	10	67%

 TABLE II.
 CLASSIFICATION PERFORMANCE OF SVM METHOD FROM MODEL 2

Kenel Function	Cost (C) Parameter	Accuracy
Radial Basis Function (RBF)	0.1	84%
	1	88%
	10	85%
Polynomial	0.1	87%
	1	86%
	10	83%
Sigmoid	0.1	61%
	1	43%
	10	67%

Based on Table II, the optimal SVM Model 2 is identified, utilizing the RBF kernel function with a C value of 1 for the classification between bacterial and viral pneumonia. In greater detail, the number of classification errors along with metrics from the best performing SVM Models 1 and 2 presented in Table III and Fig. 5.

TABLE III. EVALUATION METRICS BETWEEN MODEL 1 AND MODEL 2 WITH SVM METHOD

Model	Model 1		Model 2	
Class Classification	Normal	Pneumonia	Viral	Bacterial
Precision	0.91	0.77	0.89	0.88
Recall	0.5	0.97	0.78	0.94
F1	0.65	0.86	0.83	0.91
Accuracy	79.00%		88.00%	

In conclusion, SVM Model 1, with an accuracy of 79%, exhibits numerous classification errors in healthy lung data. On the other hand, Model 2 performs well in predicting bacterial and viral pneumonia data with an accuracy of 88%. Overall, SVM Model 1 proves to be excellent and effective when used to differentiate between bacterial and viral pneumonia. However, in the classification of healthy lungs and pneumonia cases, the performance of SVM Model 2 can be considered satisfactory.





Fig. 5. Confusion matrix for SVM method: (up) Model 1, (below) Model 2.

C. Convolutional Neural Network Training Process

In CNN modeling, data augmentation is performed to address imbalances in the dataset. Data augmentation is carried out by applying random transformations to images, such as rotation, zoom, and shifts, both horizontally and vertically. The purpose of this data augmentation is to expand the variation in the dataset and prevent overfitting [39].

After the images had undergone augmentation, the researchers constructed a CNN model with an architecture consisting of several layers. The first layer is a convolutional layer with 32 filters, followed by a batch normalization layer and a maximum pooling layer. This process is repeated several times with a different number of filters for each convolutional layer. After that, the images are transformed into one-dimensional vectors using a flattened layer before passing through two dense layers. Dropout layers are also used after several convolutional layers and before the dense layers to prevent overfitting. The output layer has one neuron and the goal of the CNN model in this study is binary classification that is, predicting whether X-ray images of the lungs show pneumonia or not [40]. To facilitate understanding of the model architecture, Fig. 6 below is a visualization of the CNN model architecture.

Based on Fig. 6, the Conv2D layer performs convolution to extract image features, while the MaxPooling2D layer reduces data dimensions [41]. Then, the BatchNormalization layer accelerates training and stabilizes the model [42], which is

assisted by the Dropout layer to prevent overfitting [43]. After that, the flattened layer transforms the data into a onedimensional vector, and the Dense layer is used as the output layer in the CNN model.



Fig. 6. Architecture of CNN model to classify pneumonia.

To train the model, the researchers used data generated from data augmentation to obtain a greater variation of training data. The researchers used a batch size of 32 and trained the model for 36 epochs, which were chosen based on the model's performance during the learning process. In each epoch, there are evaluation metrics such as accuracy, loss, or other metrics appropriate to the model's objectives as performance indicators. The number of epochs was chosen at the point where the model's performance was stable or there was no significant improvement in evaluation metrics. In addition, to minimize the symptoms of overfitting, the researchers used callbacks to reduce the learning rate if there was no improvement in validation accuracy after several epochs.

In this stage, the researchers conducted model learning on the two CNN models they had previously created. The first model (Model 1) was intended to classify the occurrence of pneumonia, and the second model (Model 2) was intended to classify the type of pneumonia. Thus, the first model was trained using several X-ray images of lungs consisting of healthy lungs and lungs with pneumonia, and the second model was trained using several X-ray images of lungs with pneumonia consisting of viral pneumonia and bacterial pneumonia.

After going through the learning process, a visualization of the results and performance of the model for classifying normal lungs and pneumonia, or CNN Model 1, is provided. This is presented in Fig. 7 as follows:

Then, a visualization and performance results of the CNN model for classifying the type of viral or bacterial pneumonia, or CNN Model 2, is provided. This is presented in Figure 8 as follows:

After obtaining the best weights for the CNN model that has been trained with 36 epochs, the performance of which is represented in Fig. 6 and Fig. 7, and selecting the epoch with the best performance based on the highest accuracy, the classification results are obtained as shown in Table IV:



 TABLE IV.
 Evaluation Metrics between Model 1 and Model 2 with CNN Method

Model	Model 1		Model 2	
Class Classification	Normal	Pneumonia	Viral	Bacterial
Precision	0.88	0.93	0.88	0.94
Recall	0.88	0.93	0.89	0.93
F1	0.88	0.93	0.93	0.89
Accuracy	91.00%		92.00%	

Based on Table IV, the classification results can be visualized using a confusion matrix, which is presented in Fig. 9 as follows.

Based on Table IV and Fig. 9, the trained CNN model shows good performance in classifying X-ray images. For the pneumonia class, the model achieves a precision of 0.93, recall of 0.93, and F1-score of 0.93. For the normal class, the model achieves a precision of 0.88, recall of 0.88, and F1-score of 0.88. This indicates that the model can identify both classes with almost the same accuracy, with the overall CNN model for detecting pneumonia having an accuracy rate of 91%. The CNN model for detecting the type of pneumonia also shows good performance in classifying the type of pneumonia, with a precision value of 0.94 for bacterial pneumonia and 0.88 for viral pneumonia, overall having an accuracy rate of 92%. Based on the results of these models, it can be concluded that the Convolutional Neural Networks method is an effective method for classifying lung X-ray images to detect pneumonia and the type of pneumonia. With the application of appropriate preprocessing and data augmentation stages, as well as the correct selection of parameters for training the model, CNN can achieve good performance in classification.



Fig. 9. Confusion matrix for CNN method: (up) Model 1, (below) Model 2.

V. DISCUSSION

Based on the analysis presented, this research has the potential to offer new insights into how pneumonia detection can be performed. By implementing deep learning, the accuracy achieved in detecting normal lungs versus pneumonia, as well as distinguishing between bacterial and viral pneumonia, is very high. A study conducted in 2020 focused on classifying lung diseases [44]. This research used transfer learning with CNN to classify tuberculosis and pneumonia, achieving the highest accuracy of 90% with the ensemble transfer learning method. Another advanced study in 2020 detected normal lungs and Covid-19 infected lungs using a combination of DenseNet121 and SVM models [45]. However, the deep learning model results were implemented through a data pipeline and integrated into a web-based CAD using Flask RESTful. The findings of this current research can also be further implemented by deploying the obtained deep learning model through Flask service to be accessible to a wider audience.

Therefore, the modeling research for detecting normal lungs, bacterial pneumonia, and viral pneumonia holds significant potential for integrating technology with healthcare [46]. It is hoped that this discovery will contribute a leading pneumonia detection model that can be integrated into digital technology in the future, thereby enhancing public health in the era of Society 5.0 and supporting the global Sustainable Development Goals (SDGs).

VI. CONCLUSION

In this study, demonstrates that the CNN method outperforms the SVM method in accurately classifying pneumonia disease and distinguishing its specific types. The diagnostic challenge of pneumonia, particularly when relying solely on chest X-ray images, underscores the critical need for technology capable of swiftly, cost-effectively, and accurately diagnosing pneumonia. This capability is essential for improving treatment outcomes and reducing pneumonia-related mortality rates.

The integration of deep learning, particularly through CNN methods, holds significant promise in advancing the field of pneumonia classification. Such advancements align with the objectives of Society 5.0, where technological innovation is leveraged to enhance societal well-being through smart and efficient solutions in healthcare. By enabling early detection of pneumonia symptoms, this research not only contributes to Goal 3 (Good Health and Well-being) of the Sustainable Development Goals (SDGs) but also supports Goal 9 (Industry, Innovation, and Infrastructure). Goal 3 aims to ensure healthy lives and promote well-being for all at all ages, while Goal 9 focuses on building resilient infrastructure, promoting inclusive and sustainable industrialization, and fostering innovation.

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