Bat Algorithm with Variational Autoencoder for Pneumonia Detection and Classification

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Abstract: ***Pneumonia detection and classification are essential in earlier diagnosis and efficient treatment of this respiratory disease. Deep learning (DL) methods are developed as robust tools in medical imaging, providing the possibility to revolutionize the accuracy and effectiveness of this diagnostic method. This studyintroduces a Bat Algorithm with Variational Autoencoder for Pneumonia Detection and Classification (BAVAE-PDC) approach on Chest X-rays (CXR). To enhance the quality of CXR images, we exploit a median filter (MF) for preprocessing. The MF efficiently decreases noise and improves image clarity, offering a cleaner input for the following analysis. For feature extraction, we employ the state-of-the-art EfficientNet architecture. EfficientNet's deep neural model is extremely efficient at capturing complex patterns in medical images, permitting for the extraction of selective features vital for accurate classification. Classification is carried out employing a Variational Autoencoder (VAE). VAEs are called for their capability to model intricate data allocations and produce important latent representations. To improve the performance of the classification method, we utilize the Bat Algorithm (BA). The BA is a bio-inspired optimization algorithm that successfully tunes the hyperparameters of the VAE model, ensuring optimum effectiveness with respect to reliability and accuracy. The developed architecture is estimated on a significant database of CRX images, representing its efficiency in pneumonia detection and classification. The outcomes specify a remarkable enhancement in performance compared with conventional techniques.***

Keywords: Chest X-Ray; Variational Autoencoder; Bat Algorithm; Medical Imaging; Deep Learning

1. Introduction

Pneumonia is an acute pulmonary disease that could be caused by viruses, bacteria, and fungi as well as impact the lungs, inducing infection of the air sacs and also pleural effusion, a situation in that the lung has been occupied with fluid [1]. This records above 15% of mortalities in children at the stage of 5 years. Pneumonia has a major widespread in developing and underdeveloped nations, where unhygienic, contamination, and overpopulation ecological situations aggravate the condition, and healthcare resources have been limited [2]. Thus, earlier identification and management perform an essential function in avoiding the disease to become harmful. Radiological analysis of the lungs employing radiography (X-rays), magnetic resonance imaging (MRI), and computed tomography (CT) can be often utilized for identification [3]. X-ray image represents a non-invasive and moderately lower-cost analysis of the lungs. An instance indicates normal and pneumonic lung X-ray. The white regions in the pneumonic X-ray (specified with red arrows), named infiltrates, differentiate a pneumonic at a normal case [4]. But, chest X-ray (CXR) inspections to diagnose pneumonia that is prone to subjective unpredictability. Consequently, an automated technique to identify pneumonia is needed [5]. In this analysis, we established a computer-aided diagnosis (CAD) technique, which employs an ensemble of deep transfer learning (DTL) method to accurately classify the CXR images.

The existing CAD systems have previously demonstrated for enabling the medical field, mainly in the diagnosis of lung nodules, mammograms, breast cancer and so on [6]. In the process of utilizing Machine Learning (ML) approaches is for medical images, important features can be primary significance. For this aim, the majority of earlier methods employed hand-crafted features to develop CAD techniques dependent upon analysing images [7]. But, the hand-crafted features with limits differing in accordance with functions are not proficient in providing more important features [8]. Exploitation of Deep Learning (DL) approaches specifically Convolutional Neural Networks (CNNs) exhibited their inner abilities of extracting valuable features in image classification tasks [9]. This method of feature extraction needs transfer learning (TL) approaches where pre-trained CNN systems learn the generic features under large databases namely ImageNet that are then forwarded to the necessary task [10].

Hasoon et al. [11] suggested an effective model for identifying and sorting COVID19 by Image Processing via X-ray images. A cluster of procedures such as ROI detection, pre-processing, segmentation, and feature extraction as well as many ML models have been executed. Shaheed et al. [12] propose a system for the identification of COVID19 as well as pneumonia. Chiefly, a pre-processing approach depend on Gaussian filtering and then logarithmic operator is utilized in order to effort CXR images. Next, strong features are removed from CXR images employing CNNs and GLCM techniques. Lastly, RF-ML classification algorithm is used for categorizing images as pneumonia, COVID19, or usual. Habib and Rahman [13] suggested Gene-based screening procedure for identifying as well as distinguishing corona diseases from pneumonia. This method uses infection genes for creating efficient semantic resemblances among genes.

This study introduces a Bat Algorithm with Variational Autoencoder for Pneumonia Detection and Classification (BAVAE-PDC) approach on Chest X-rays (CXR). To enhance the quality of CXR images, we exploit a median filter (MF) for preprocessing. For feature extraction, we employ the state-of-the-art EfficientNet architecture. Classification is carried out employing a Variational Autoencoder (VAE). To improve the performance of the classification method, we utilize the Bat Algorithm (BA). The BA is a bio-inspired optimization algorithm that successfully tunes the hyperparameters of the VAE model, ensuring optimum effectiveness with respect to reliability and accuracy. The outcomes specify a remarkable enhancement in performance compared with conventional techniques.

2. The Proposed Method

In this study, we present a comprehensive BAVAE-PDC method for pneumonia detection and classification that leverages advanced techniques. It contains major processes such as MF- based preprocessing, EfficientNet-based feature extraction, VAE-based classification, and BA-based parameter optimization. Fig. 1 depicts the entire flow of BAVAE-PDC algorithm.

2.1. Image preprocessing

To increase the quality of CXR images, we exploit anMF for preprocessing. In the condition of pneumonia detection and classification, the application of a MF as a preprocessing stage is crucial for improving the quality of CXR images [14]. By successfully alleviating noise and outliers however, maintaining necessary image structures, the MF considerably refines image clearness, leads to cleaner and further diagnostically useful images. In the field of pneumonia identification, where image quality is important for accurate identification, this preprocessing method functions to offer medicalspecialists and ML approaches highly dependable and useful data. Accordingly, it gives to the enhancement of diagnostic accuracy, early medical involvement, and lastly good patient outcomes, it generates an essential component of the overall diagnostic method.

2.2. Feature extraction

For feature extraction, we employ the recent EfficientNet architecture. Leveraging its effectual model, EfficientNet is capable of removing useful features from medical images like CXR, with considerable accuracy [15]. Its exceptional capability to balance model depth, resolution, and width optimally confirms the protection of important image data whereas decreasing computational resources—an essential factor in medical imaging applications. This architecture's excellent performance, both with respect to computational efficiency and diagnostic accuracy, producing it the best choice for pneumonia identification and classification processes, where earlier and accurate analysis can substantially affect patient care and outcomes. Therefore, Efficient Netperforms a key function to increase the reliability and fast of pneumonia identification, giving a possible way for enhanced medical assistance.

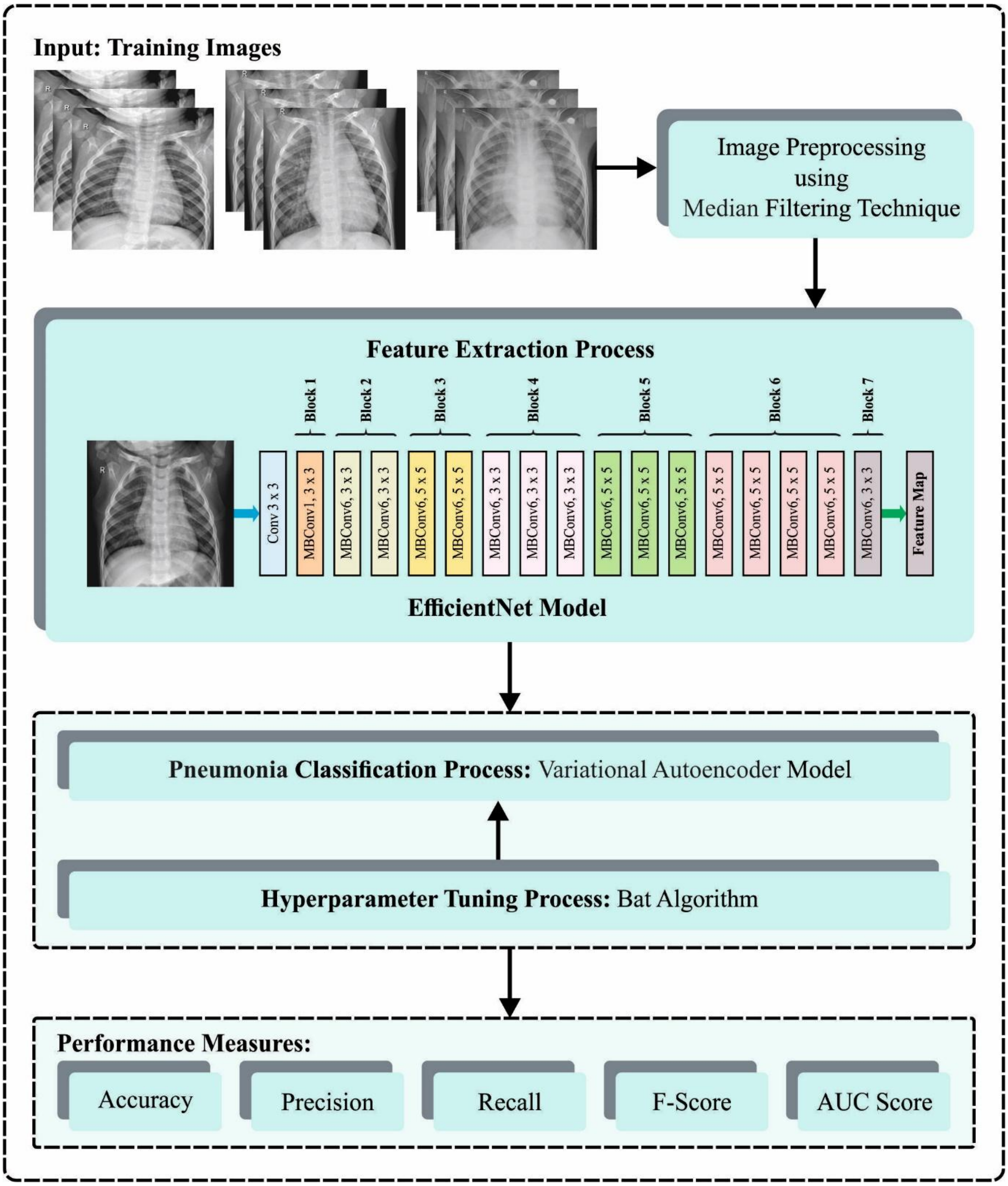


Figure 1: Overall flow of BAVAE-PDC algorithm

2.3 Image classification

To optimize the performance of the classification model, we employ VAE model. VAE almost enhances sign [16]. The VAEs is also known as Auto-Encoders because training objective look like an encoder-decoder grouping. Regrouping the description of KL deviation (renaming estimated later as $q_\phi(z|x)$) that get

$$KL(q_\phi(z|x)||\, p(z|x)) = \mathbb{E}_{q_\phi(z|x)}\left[\log q_\phi(z|x) - \log p_\theta(x|z) - \log p_\theta(z)\right] + \log p_\theta(x) \quad (1)$$

where ϕ and θ are function parameters p and q that map X to Z is called as encoder and Z to X is known as decoder correspondingly. Employing KL deviation description gives one more chance for Eq. (1) to

$$\log p_\theta(x) - KL\left(q_\phi(z|x)||\left(p(z|x)\right)\right)$$
$$= \mathbb{E}_{q_\phi(z|x)}[\log p_\theta(x|z)] - KL\left(q_\phi(z|x)||\left(p_\theta(z)\right)\right) \quad (2)$$

Paper ID: SR231025120314 DOI: 10.21275/SR231025120314

Eq. (2) is an important calculation in a part of VAEs: The term left side like to enhance that is entire of log -likelihood of information, $x \in X$, detriment the error in resembling the true posterior $p_\theta(z|x)$ with estimated one $q_\phi(z|x)$. The right side of calculation is equal to explanation of ELBO as well as enhance utilizing stochastic gradient descent (SGD) assuming correct choice of q. Hence, the main utility of VAE is determined as:

$$\mathcal{L}(\theta, \phi; x) = \mathbb{E}_{q_\phi(z|x)}[\log p_\theta(x|z)] - KL\left(q_\phi(z|x)||(p_\theta(z))\right) \tag{3}$$

But, taking gradient of $\mathcal{L}(\theta, \phi; x)$ respect to ϕ is difficult, particularly for primary term. Kingma and Welling recommend an optimal solution known as re-parameterization that presents variable $e \sim \mathcal{N}(0, I)$, then re-formulates main role so that prospect must be fixed with respect to x and e. This safeguards major functions to be determined as well as nonstop in θ andϕ, that creates back propagation with SGD probable.

Let past over hidden variable z be standard Gaussian, that is $p_\theta(z) = N(z; 0, I)$, and variational estimated later multiples Gaussian with diagonal covariance, $q_\phi(z|x) = \mathcal{N}(z; \mu, \sigma^2 I)$. Since Eq. (3) is expressed as:

$$\mathcal{L}(\theta, \phi; x) = \frac{1}{L}\sum_{l=1}^{L} \log p_\theta\left(x|z^{(l)}\right) + \frac{1}{2}\sum_{j=1}^{J}\left(1 + \log\left(\sigma_j^2\right) - \mu_j^2 - \sigma_j^2\right) \tag{4}$$

where $z^{(l)} = \mu + \sigma\epsilon^{(l)}$, and $\epsilon^{(l)} \sim N(0, I)$. The initial part in Eq. (4) is AE that has negative rebuilding fault and the next part is logical type for KL deviation of multiple Gaussian subsequent from normal one.

2.4 Hyperparameter tuning using BA

Finally, the BA adjusts the hyperparameter values of the VAE model. More specifically, Bats or, microbats, can be established as a 3D model of its backgrounds [17]. With the time dissimilarity between echo and pulse emission, bats usesecho signals to identify the prey and preventbarriers. The attractive performance of bat is stimulated Yang to design the BA. Thismodel idealizes the batbehavior by allocating all the bats in population, position x_i, and velocity v_i. The signal intensity ranges from A_0 to $A_{\min}$. The locality direction of all the bat represents the parameter ofoptimization issue. Firstly, the BA produces a bat population by allocating them random location. Next, it exploits the subsequent formula to define the occurrence of bat j:

$$f_j = f_{\min imum} + (f_{\max imum} - f_{\min imum})\beta, \tag{5}$$

In Eq. (5), $f_{\min imum}$ and $f_{\max imum}$ are the minimum and maximum frequencies among the hyperparameter model. The occurrence of j^{th} bat is f_j, and a randomly generated value ranges within [0, 1] is β. Then, the location and velocity of bats are adjusted according to the subsequent formula:

$$V_j^{t+1} = V_j^t + \left(x_j^t - x^*\right)f_j,$$

$$x_j^{t+1} = x_j^t + V_j^{t+1} \tag{6}$$

In Eq. (6), the location of j^{th} bat at t^{th} epoch is x_{jt}, the global optimum location isx^*, and the velocity of the j^{th} bat att^{th} epochs is V_j^t. Few bats approach the global optimum as follows:

$$x_f = x_i + \varepsilon A^t, \tag{7}$$

In Eq. (7), the initial location isx_i, and the final location is x_f. A is loudness, a hyperparameter of the model, and a random integerranges within [0, 1] is ε. $*e$last bat place is accepted if the cost function value is lesser at the last position. Then, $*e$ loudness and pulse rate of bat are updated as follows

$$A_j^{t+1} = \alpha A_j^t,$$

$$r_j^{t+1} = r_j^0(1 - exp, (-\gamma t)), \tag{8}$$

In Eq. (8), the commencing pulse level isr_j^0, and hyperparameter of the algorithm are α and C. The α value is generally taken in [0, 1].

An ANN is trained by the BA model by considering the weight of network as position vector of bat. The prediction error of ANN can be described by the cost function. The optimum bat is chosen as the solution of BA once it reaches the maximum iteration. The position vector of bat shows the weight of trained network.

3. Experimental Validation

The pneumonia detection results of the BAVAE-PDC system can be tested employing a dataset from Kaggle repository [18]. The database contains 1566 normal samples and 4220 pneumonia samples as described in Table 1.

Table 1: Details of Dataset

Class	Training Set	Testing Set	Validation	Total
Normal	1093	316	157	1566
Pneumonia	2944	854	422	4220

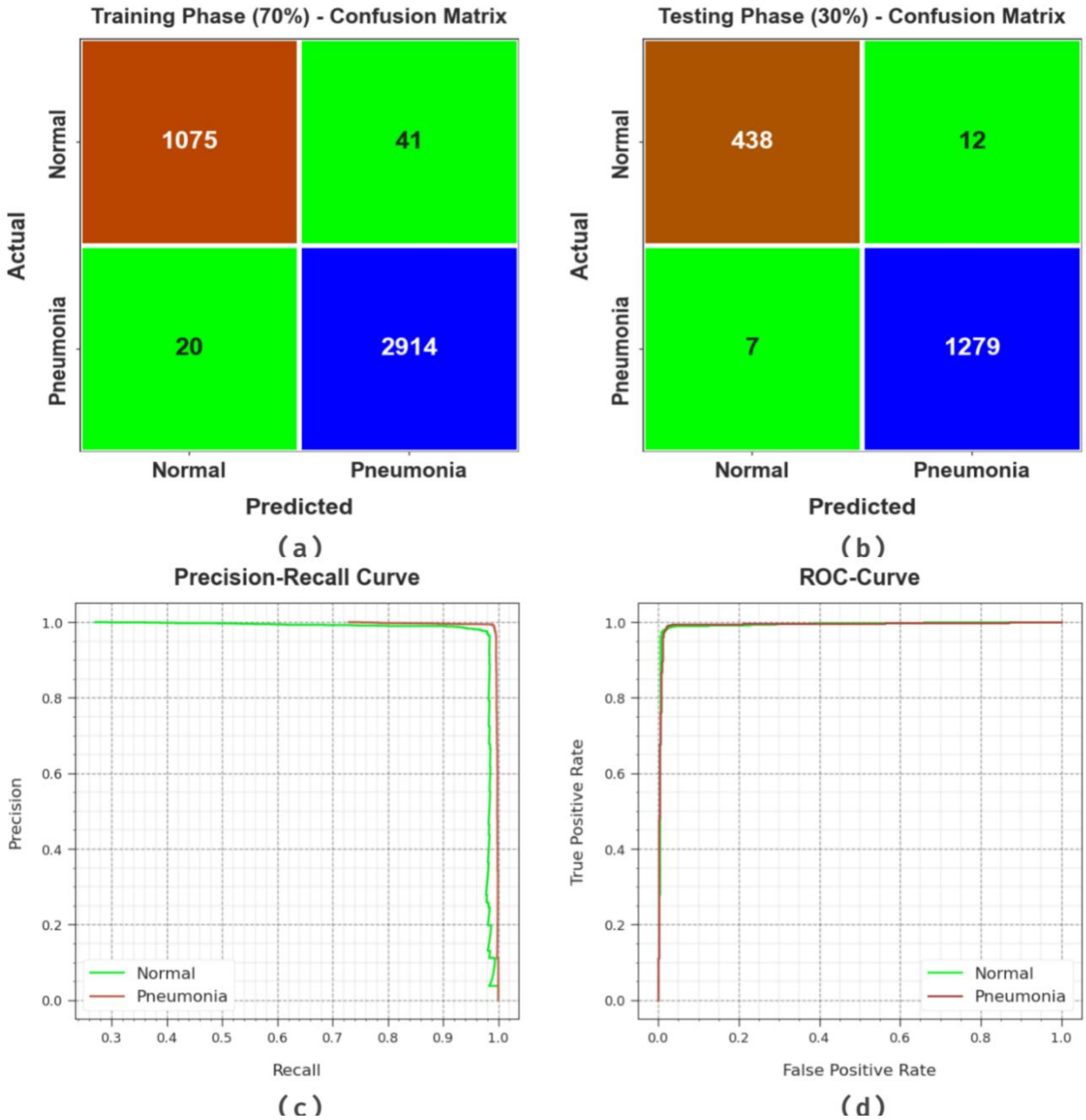


Fig. 2. (a-b) Confusion matrices of TR/TS phase of 70% and 30% and (c-d) PR curve and ROC curve

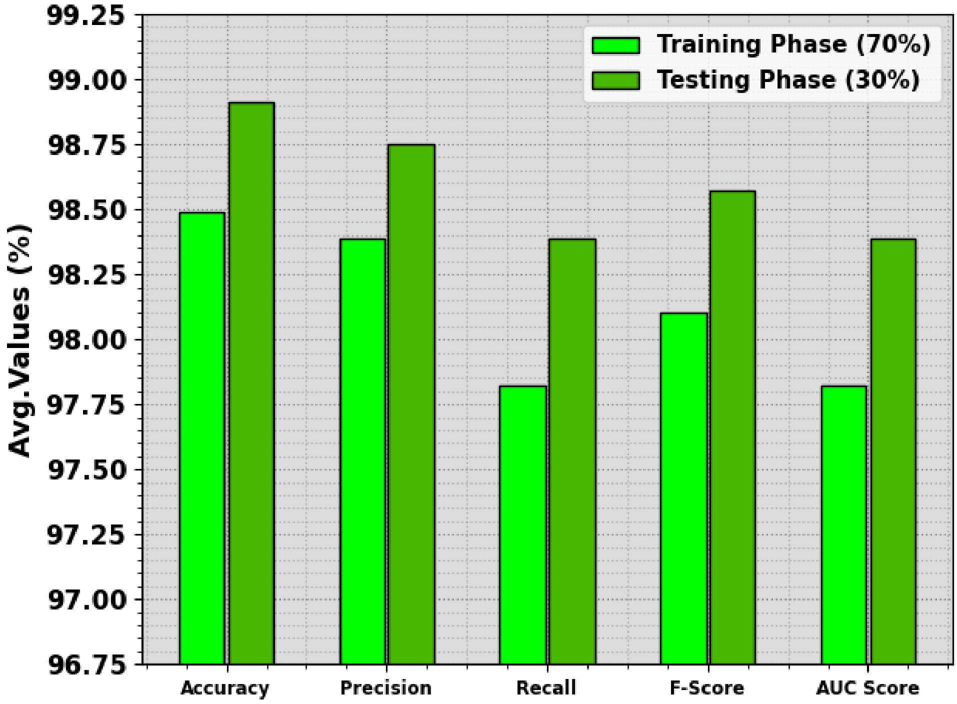
Fig. 2 demonstrates the classifier analysis of the BAVAE-PDC system at test database. Figs. 2a-2b illustrates the confusion matrix provided by the BAVAE-PDC methodolgoy with70:30 of TR Phase/TS Phase. The figure shown that the BAVAE-PDC approach is suitably recognized and categorized with normal and pneumonia classes. Moreover, Fig. 2c represents the PR performances of the BAVAE-PDCmodel. Then, this figure shows that the BAVAE-PDC system acquires excellent PR performance with two classes. Also, Fig. 2d shows the ROC outcome of the BAVAE-PDC methodology. The figure indicated that the BAVAE-PDC methodology accelerates effectual outcomes with superior ROC values with each class.

The pneumonia recognition analysiswith 70:30 of TR phase/TS phase is indicated in Table 2. The achived outcome show that the BAVAE-PDC methodology appropriately recognizes and catagoriestwo classes. Accoding to 70% of TR phase, the BAVAE-PDC technique attains an average $accu_y, prec_n, reca_l, F_{score}$, and AUC_{score} of 98.49%, 98.39%, 97.82%, 98.10%, and 97.82%. Besides, with 30% of TS phase, the BAVAE-PDC system achieves an average $accu_y, prec_n, reca_l, F_{score}$, and AUC_{score} of 98.91%, 98.75%, 98.39%, 98.57%, and 98.39% respectively.

Table 2: pneumonia recognition analysis of BAVAE-PDCsystem with 70:30 of TR phase/TS phase

Class	$Accu_y$	$Prec_n$	$Reca_l$	F_{score}	AUC_{score}

TR Phase (70%)					
Normal	98.49	98.17	96.33	97.24	97.82
Pneumonia	98.49	98.61	99.32	98.96	97.82
Average	**98.49**	**98.39**	**97.82**	**98.10**	**97.82**
TS Phase (30%)					
Normal	98.91	98.43	97.33	97.88	98.39
Pneumonia	98.91	99.07	99.46	99.26	98.39
Average	**98.91**	**98.75**	**98.39**	**98.57**	**98.39**



Finally, the improved performance of the BAVAE-PDCmethodology can be confirmed by a comparison analysis in Table 3 and Fig. 4 [19]. The obtained outcomeindicated that the DPC X-Rat-Dl systemsexhibits poorer performance with reduced classification outcomes. Simultaneously, the visualization-CNN, ADFL-mRMR, and X-ray Images-NN algorithmsare attained definitely boosted outcomes. Then, the CNN and Chest Xray-DTL methodologyare representedsignificantlyhigher performance. However the promising performance isachieved by the BAVAE-PDCsystem with $accu_y$, of 98.91%. These achieved outcome ensured that the BAVAE-PDCapproachshowsexcellent performance over other models.

Table 3: $Accu_y$ analysis of BAVAE-PDCmodel with exsisting systems

Model	Accuracy
Visualization-CNN	96.20
ADFL-mRMR	96.84
X-ray Images-NN	94.40
DPC X-Rat-Dl	84.50
CNN Model	98.00
Chest Xray-DTL	98.43
BAVAE-PDC	98.91

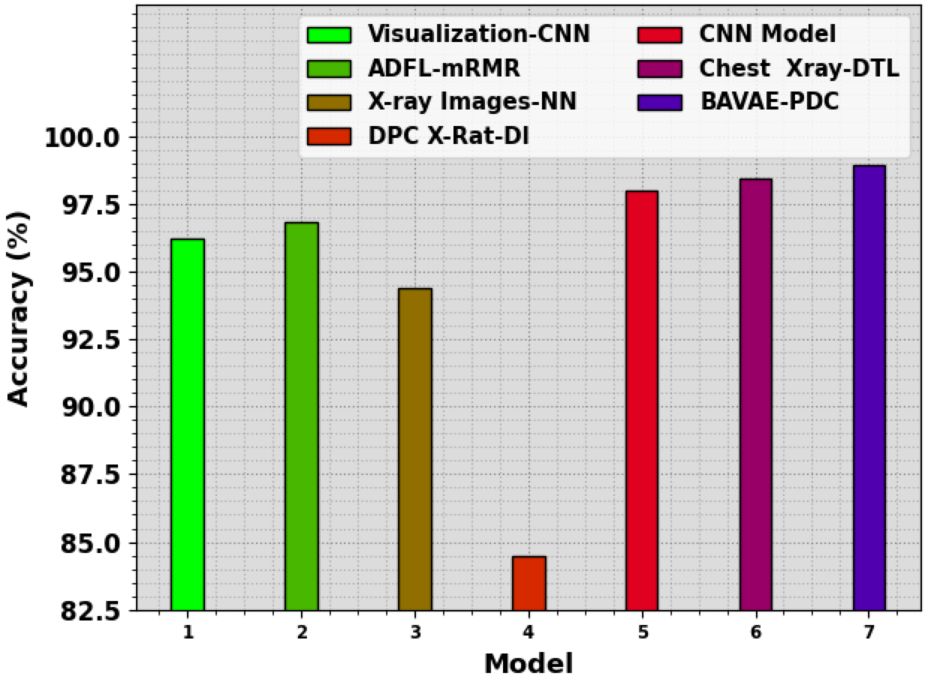


Figure 4: $Accu_y$ analysis of BAVAE-PDCmodelcompared withexisting methods

4. Conclusion

In this study, weintroduces a BAVAE-PDC approach on CXR. To enhance the quality of CXR images, we exploit a MF for preprocessing. The MF efficiently decreases noise and improves image clarity, offering a cleaner input for the following analysis. For feature extraction, we employ the state-of-the-art EfficientNet architecture. Classification is carried out employing a VAE. VAEs are called for their capability to model intricate data allocations and produce important latent representations. To improve the performance of the classification method, we utilize the BA. The BA is a bio-inspired optimization algorithm that successfully tunes the hyperparameters of the VAE model, ensuring optimum effectiveness with respect to reliability and accuracy. The developed architecture is estimated on a significant database of CRX images, representing its efficiency in pneumonia detection and classification. The outcomes specify a remarkable enhancement in performance compared with conventional techniques.

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