

Optimized double transformer residual super-resolution network-based X-ray images for classification of pneumonia identification

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ABSTRACT

Pneumonia is an infectious disease characterized by inflammation of the lungs' air sacs, which results in the accumulation of fluid or pus. Medical images is important for the timely identification and precise diagnosis of illnesses; chest X-rays are a commonly utilized modality for respiratory disorders including pneumonia. In this research, optimized double transformer residual super-resolution network-related chest x-ray imageries for the classification of pneumonia identification (DTRSN-XRI-CPI). The procedure involves pre-processing the input image using region-aware neural graph collaborative filtering (RNGCF) to reduce noise, enhance contrast, and eliminate high and low frequencies from the collected dataset. Next, the Synchro-squeezed fractional wavelet transform (SFWT) is utilized for the feature extraction to extract color features such as color, shape, spatial, texture, and relation from the image. Hence, the weight parameters for DTRSN are optimized using the Hunter Prey Optimization Algorithms (HPOA). Then the DTRSN-XRI-CPI is implemented in Python and the performance metrics like precision, accuracy, recall, specificity, F1-score, and ROC are analysed. The performance of the DTRSN-XRI-CPI approach attains 20.7 %, 22.6 % and 30.5 % higher accuracy; 21.8 %, 29.3 % and 30.5 % higher precision and 21.8 %, 29.5 % and 32.6 % higher recall when analysed through existing an intelligent computational framework based on deep learning for the identification and classification of pneumonia illness (ICPD-DL-ICF), an adaptive and altruistic deep feature selection approach based on PSO for pneumonia detection from chest X-rays (APSO-DFSM-PDCX) and a deep learning system that uses explainable AI (DLAIB-PI-EAI) techniques respectively.

1. Introduction

Bacteria, viruses, fungi, and germs can all cause pneumonia. If not treated promptly, pneumonia can be extremely dangerous and fatal because it irritates the lungs' air sacs [1]. Patient health rapidly deteriorates as a result of lung infection affecting the pulmonary alveoli. There are several different kinds of pneumonia, including mycoplasma, bacterial, and viral pneumonia [2]. Bacteria or fungi can cause bacterial pneumonia, but viruses like the flu are responsible for around one-third of cases. Atypical pneumonia sometimes referred to as mycoplasma pneumonia, which is a bacterial infection that often affects individuals of all ages [3]. However, individuals with weaker immune systems, recent surgery patients, smokers, alcoholics, and asthma are at an increased risk of developing mycoplasma pneumonia. Viral pneumonia

is thought to be very dangerous; bacterial pneumonia is more likely to attack than viral pneumonia. A number of symptoms can indicate pneumonia, such as fever, coughing, tiredness, sweating excessively, chest pain, shaking, difficulty of breath appetite loss, confusion, and blue lips and nails [4]. It is regarded as a dangerous disease that can be dangerous everywhere, but especially in China. Deaths from this disease are particularly high in South Asia and Sub-Saharan Africa. This illness claimed the lives of almost 0.9 million individuals in 2017, according to a report. An estimated one million individuals have been identified with pneumonia, and in a nation such as the United States (US), the disease takes the lives of generally fifty thousand people per year [5]. Considered the "ultimate disease of poverty," the death ratio from childhood pneumonia was >50 % in India, Pakistan, Ethiopia, Nigeria, and the Republic of Congo [6–8]. In Portugal, pneumonia ranks as the second

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most prevalent cause of death, behind lung cancer, which can cause breathing difficulties [9,10]. One of the top three deadliest illnesses in Japan is pneumonia, which kills a disproportionate number of individuals, especially the elderly (over 75). Pneumonia is a treatable illness that cannot spread over national borders; instead, it usually spreads within local populations and may be controlled with common sense measures [11]. It can be managed by often washing your hands, performing healthy activities, getting enough sleep, quitting smoking, eating a diet high in vegetables, etc. One of the worst illnesses in the world, pneumonia is the primary cause of death for both children and the elderly [12,13]. Pneumonia is detected by a number of techniques, including bronchoscopy, pulse oximetry, chest X-ray imaging, blood culture and sputum culture.

A chest X-ray is the most crucial and commonly used technique for diagnosing pneumonia worldwide. A radiologist with specialized knowledge in the field is necessary for an accurate and effective analysis of the X-ray images [14]. Two-thirds of people worldwide do not have access to radiologists, according to a research. Analyzing X-ray images to identify pneumonia can also be a time-consuming and inefficient procedure. This is because a lot of other illnesses, such as lung cancer, have comparable visual opaqueness [15]. Therefore, it is crucial to read these images with precision and consistency. The impact of computational models is acknowledged globally [16]. The development of a diagnosis model can aid in the precise and efficient analysis of X-ray images by identifying the causes of pneumonia in clinical imaging. Of all the techniques, medical image analysis seems the most promising and is used to diagnose a number of diseases, including pneumonia, MERS, Covid-19, and others [17,18]. As a result, different medical experts use chest x-ray images to detect pneumonia. Analyzing X-ray images accurately and efficiently is seen as a crucial responsibility for radiologists [19]. Several scientists have put forth several algorithms for X-ray picture analysis. To provide insights into the X-ray pictures, researchers have developed a variety of computer-guided diagnostic approaches. However, these instruments and methods fell short in providing doctors with relevant data regarding medical images so they may make informed decisions. ML is becoming a major aid in the identification of many diseases. These techniques have been applied extensively in the diagnosis of chest and lung conditions. While exhibiting strong performance, machine learning techniques fell short in achieving high accuracy, low error rate, and minimal computational power [20,21]. With its increased accuracy, deep learning (DL) has already shown its worth and is being applied to a count of tasks, like object detection, segmentation, text and imager categorization, and more. The deep learning has proven to be capable of target segmentation and recognition in medical-image-process, including radiology image analyses, which allows for the investigation of abnormal or biological human body shapes. Additionally, compared to traditional state-of-the-art machine learning algorithms and methodologies, deep learning approaches and algorithms offer superior accuracy [22,23].

Several studies were conducted in the works based on the identification of pneumonia using deep learning. A few of the current works are reviewed here,

Yi, et al. [24], have suggested a scalable and interpretable deep convolutional neural network (DCNN) for detecting pneumonia from chest X-ray images. The suggested modified DCNN model first collects relevant image features before classifying the images into normal and pneumonia classes. To train and test the suggested method, the chest X-ray image dataset was utilised.

Pramanik, et al. [25], have introduced a computer-aided diagnosis (CAD) system that recognises pneumonia from chest X-rays using a meta-heuristic algorithm and deep learning principles. Deep features were extracted using the pre-trained ResNet50, which was optimised on a target pneumonia dataset. A particle swarm optimisation (PSO)-based feature selection method was enhanced by adding an altruistic behaviour to the agents and changed by a memory-based adaption parameter. The feature selection method is known as Adaptive and Altruistic PSO

(AAPSO). By effectively removing non-informative features derived from the ResNet50 model, the suggested approach enhances the framework's overall capacity to diagnose pneumonia.

Yang, et al. [26], have suggested a DL method that takes into account the background information of images and evaluates their explainability using explainable deep learning. The suggested method consists of the following steps: (1) developing initial DL models to identify X-ray images of pneumonia without accounting for background; (2) developing DL models that take background information into account when identifying pneumonia X-ray images to improve the identification accuracy; and (3) using explainability analysis with the Grad-CAM method.

Alshmrani, et al. [27], have investigated a deep learning (DL) design for the multi-class categorization of lung cancer, lung opacity, pneumonia, TB, and most recently COVID-19. To meet the DL requirements, 10,192 normal images, 6012 lung opacity, 5870 pneumonia, 20,000 lung cancers, 1400 tuberculosis, and 3615 COVID-19 were shrunk, normalized and randomly split. Three convolutional neural network (CNN) blocks were utilized as a feature extraction and fully linked network during the classification phase, along with a pre-trained model called VGG19.

Zhang, et al. [28], have suggested an improved Harris Hawk's optimisation (GSHHO) based on the simulated annealing method and Gaussian mutation mechanism to detect two distinctive CT phenomena of influenza pneumonia: the bronchovascular bundle and ground glass opacity (GGO). Next, GSHHO and fuzzy k-nearest neighbor (FKNN) were combined to create a GSHHO-FKNN machine learning model.

Salama, and M.H. Aly [29], have investigated numerous approaches for the categorization task. CT lung images were classified as either COVID-19 positive or negative using the ResNet50 and VGG16 models. To improve system performance, CT lung images were segmented before the classification process using VGG16 and ReNet50 in conjunction with U-Net, one of the most used designs in deep learning for image segmentation. To enhance images and lower noise, preprocessing techniques such as the Wiener filters and image size-dependent normalisation technique (ISDNT) were applied. Transfer learning and data augmentation methods were also used to address the problem of COVID-19 CT lung image deficiencies; consequently, over-fitting of deep models can be avoided.

Ravi, et al., [30] have presented a multichannel deep learning technique for using chest X-rays to identify lung disease. The pretrained EfficientNetB0, EfficientNetB1 and EfficientNetB2 multichannel models were employed. The EfficientNet models' features were combined. The fused features were then sent into many completely connected non-linear layers. To diagnose lung diseases, the features were then fed into a stacked ensemble learning classifier. In order to detect lung diseases, the stacked ensemble learning classifier employs random forest and SVM in the first stage and logistic regression in the second. The effectiveness of the suggested approach was thoroughly examined for several pulmonary conditions, including tuberculosis (TB), pneumonia, and COVID-19.

The reviewed deep learning methods for pneumonia detection exhibit several limitations. Many techniques rely heavily on pre-trained models like ResNet50, VGG16, and U-Net, which, despite their effectiveness lead to over fitting on small or imbalanced datasets, limiting generalizability. The use of computationally intensive architectures also increases processing time and resource requirements, making real-time or resource-constrained deployment challenging. Feature selection approaches that depend on meta-heuristic algorithms, such as PSO or Harris Hawk Optimization, often require extensive parameter tuning, which are time-consuming and not guarantee optimal feature subsets across different datasets. Some methods overlook critical aspects like image background context, which lead to suboptimal model performance in scenarios where background artifacts influence pneumonia detection. The focus on binary classification in many models restricts their utility for multi-class lung disease detection, which is vital for

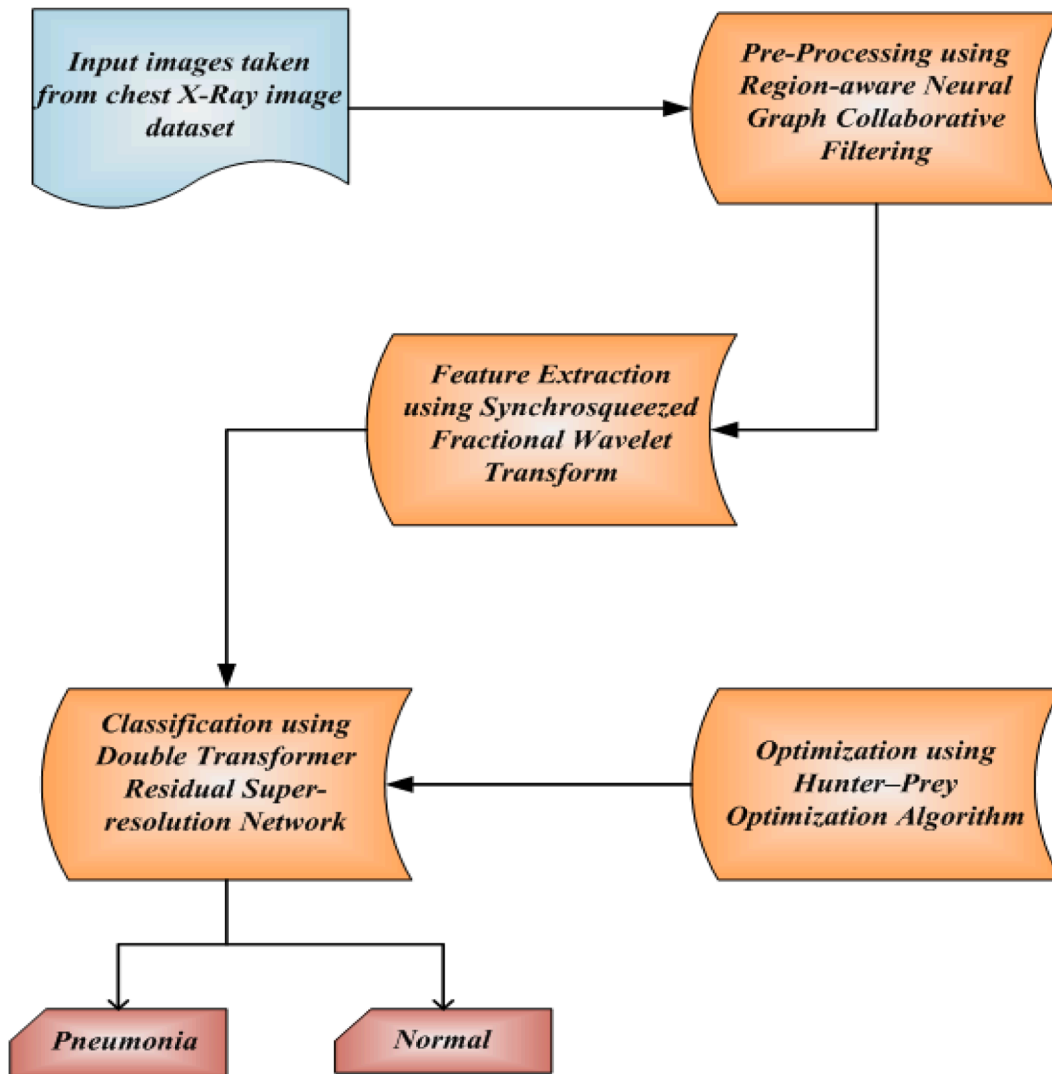


Fig. 1. Block diagram for proposed DTRSN-XRI-CPI Method.

accurate differential diagnosis. Explainable AI (XAI) techniques are often limited in interpretability, reducing their acceptance in clinical settings where transparent decision-making is crucial for trust and reliability. Variations in dataset quality, pre-processing techniques and the absence of cross-validation across diverse populations reduce the robustness and scalability of these models for real-world clinical applications. These drawbacks have motivated to do this work.

The novelty of the proposed DTRSN-XRI-CPI framework lies in its innovative integration of advanced methods such as RNGCF for context-sensitive noise reduction and contrast enhancement, preserving critical diagnostic features. The SSFWT enhances feature extraction by improving time-frequency concentration and capturing complex patterns such as color, shape, texture, and spatial relationships. DTRSN optimized with HPOA enhances the classification of pneumonia identification, preventing over fitting and improving generalization. The proposed DTRSN-XRI-CPI framework addresses key challenges like feature overlap, noise interference, and model interpretability, offering significant advancement over prior methods that often rely on pre-trained which are prone to over fitting, lack adaptability, and offer limited interpretability in clinical settings.

The major contribution of this paper includes,

- Image Gathered from a varied and extensive dataset of imageries from chest CT scans or X-rays, encompassing instances with and without pneumonia.
- RNGCF dynamically adapts noise reduction based on contextual importance, preserving critical diagnostic features and improving image quality.
- SSFWT provides a more comprehensive feature representation by capturing complex, non-stationary patterns in medical images
- The DTRSN enhances Identification and Classification of pneumonia such as normal and Pneumonia.
- HPOA fine-tunes DTRSN's parameters, ensuring better generalization, faster convergence, and reduced computational burden
- The optimized DTRSN makes a substantial contribution to the field of pneumonia identification through X-ray images.

The last part of the manuscript is organized as follows: The proposed approach is shown in Part 2, results are shown with discussions in Part 3, and the manuscript is concluded in Part 4.

2. Proposed methodology

In the proposed methodology, the DTRSN-XRI-CPI method is discussed for chest X-ray imageries classification of pneumonia identification. This model is composed of two types of pneumonia

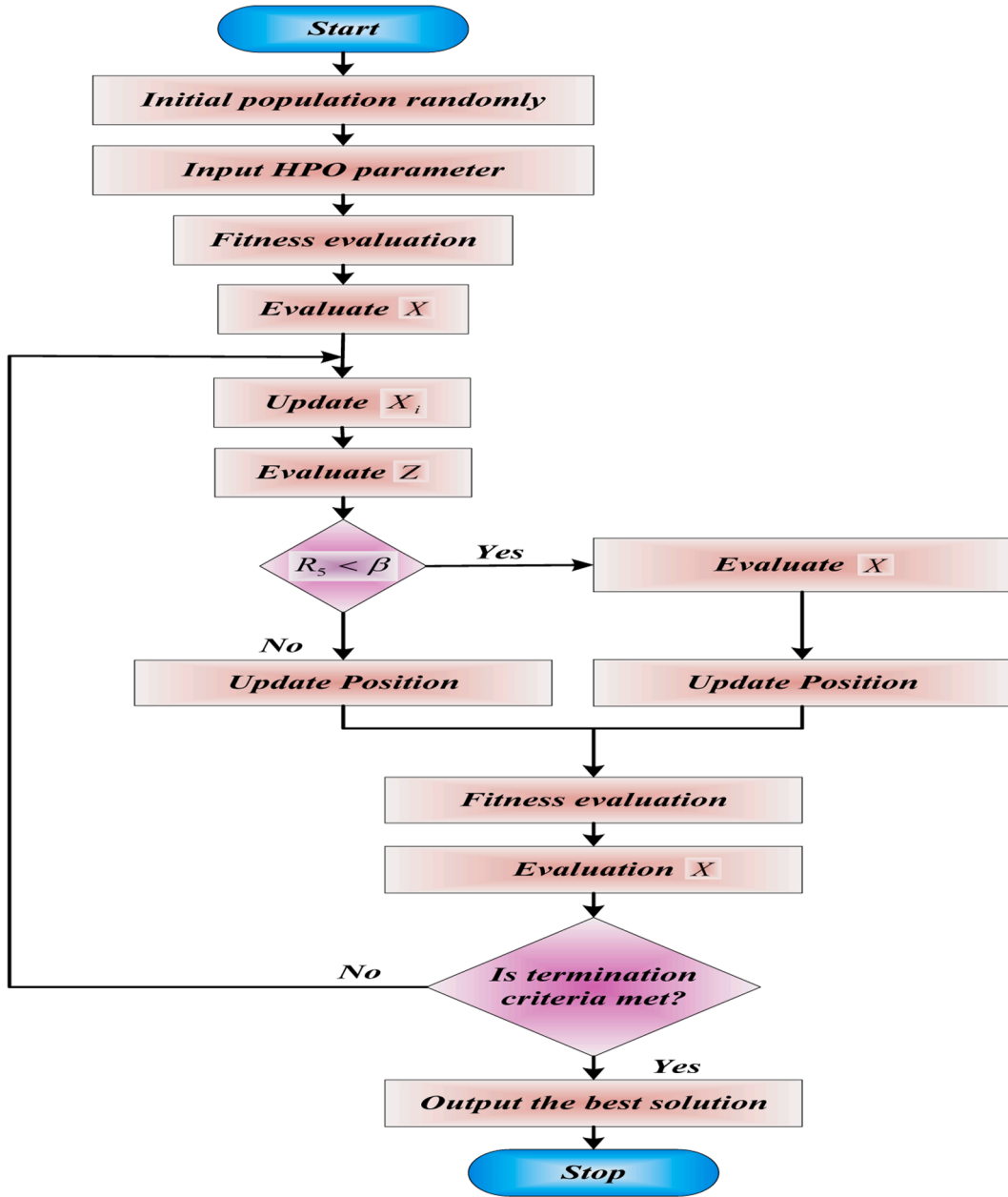


Fig. 2. Flow chart of HPOA for optimizing DTRSN.

classifications, such as pneumonia and normal. After accurately determining the presence, location, and features of pneumonia during the first image collection, the model is sent for additional processing. Pre-processing, feature extraction, and classification are the three main processes that these phases endure in subsequent sectors. Block diagram of DTRSN-XRI-CPI is depicted in Fig. 1.

2.1. Image acquisition

The images in this section are from the set of X-ray images of the chest [31]. The testing and training sets of images from CXR make up the dataset. The 5863 X-ray images are divided into two groups, such as normal and pneumonia. Using the retrospective cohorts of pediatric patients, aged one to five, from the Guangzhou Women and Children's Medical Centre, the chest X-ray pictures were selected. Each patient's chest X-ray was obtained as part of a routine clinical procedure. In order to ensure quality control, all chest radiographs had any low-quality or invisible images removed before they were evaluated.

2.2. Pre-processing using region-aware neural graph collaborative filtering (RNGCF)

Here, the RNGCF [32] technique is utilized which used increase quality through an improving contrast, removal of noise and deletion of low and high frequencies from the input imageries from the collected dataset. Traditional pre-processing methods often struggle to balance noise reduction with feature preservation, leading to a loss of important details. RNGCF offers significant advantages over conventional image preprocessing methods by leveraging graph-based relationships between different regions of chest X-ray images. Unlike conventional filtering techniques, which apply uniform noise reduction across the image, RNGCF dynamically adapts its filtering process based on the contextual importance of each region. This ensures that critical diagnostic features are preserved while irrelevant noise and artifacts are suppressed. The first specification of regions is,

$$E_r = [e_1, e_2 \dots e_{o-1}, e_o] \quad (1)$$

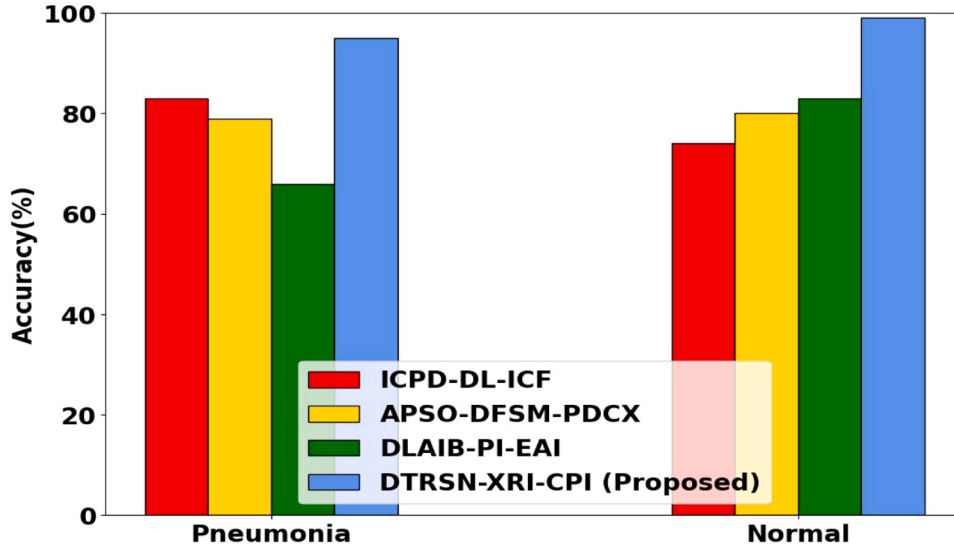


Fig. 3. Analyses of performance accuracy.

where, e denote the elements of the sequence, E_r denote the vector sets of regions, and e_o denote the last element of region. One specific type of vector is shared by region aggregator. The update process used for item vectors is almost identical in the updating process of region vectors. The regions vectors that collect information is defined as Eq. (2),

$$m_{u \leftarrow i} = \frac{1}{\sqrt{|N_u|}|N_i|}} (W_1 e_i + W_2 (e_i \otimes e_u)) \quad (2)$$

here, $m_{u \leftarrow i}$ denotes a vector that region collected from their neighbor vector; N_u and N_i denotes the amount of direct connect neighbour vector of region; W_1 and W_2 denotes the two training parameter matrices and items and $e_i \otimes e_u$ indicates the details of the interaction between the object and the area. Then, (3) is the definition of the aggregation process.

$$e_u^{(1)} = \text{LeakyReLU} \left(m_{u \leftarrow u} + \sum_{i \in N_u} m_{u \leftarrow i} \right) \quad (3)$$

here, $e_u^{(1)}$ denotes the region vector's representation vectors;

LeakyReLU denotes the activation function; $m_{u \leftarrow u}$ denotes the preserved feature information and $m_{u \leftarrow i}$ denotes the data that area gathered from its neighboring vector. In order to complete the fusing process, use Eq. (4).

$$e_{i-r}^* = e_i^* \oplus e_r^* \quad (4)$$

here, $\oplus$ indicates the element wise addition of vectors, e_{i-r}^* implies the objects' fused vector representation. Then, the similarity between the region and item vectors is then evaluated by computing the dot product of the vectors, which is given by Eq. (5).

$$\hat{y}_{(u,i-r)} = e_u^{*T} e_{i-r}^* \quad (5)$$

where as, e_u^{*T} denotes the region vector; $\hat{y}_{(u,i-r)}$ denotes the last preference score for the region u to item i ; e_i^* denotes the item vector and r is a constant term. Through the use of the RNGCF processing method, noise is eliminated, and quality is enhanced by boosting contrast and removing high and low frequencies from the input imageries is obtained from the dataset. The pre-processed data are then used in the feature extraction stage.

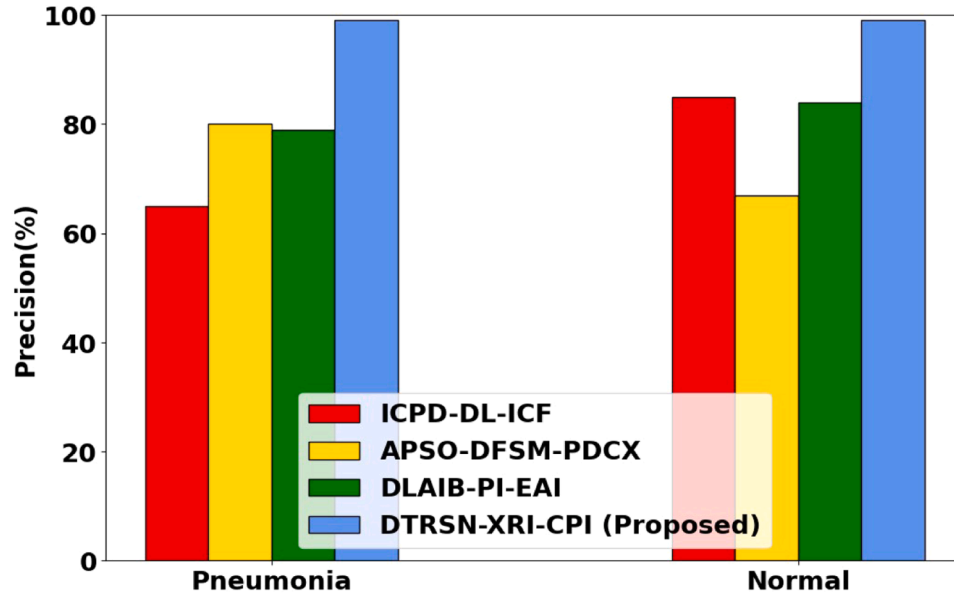


Fig. 4. Analyses the performance of the precision.

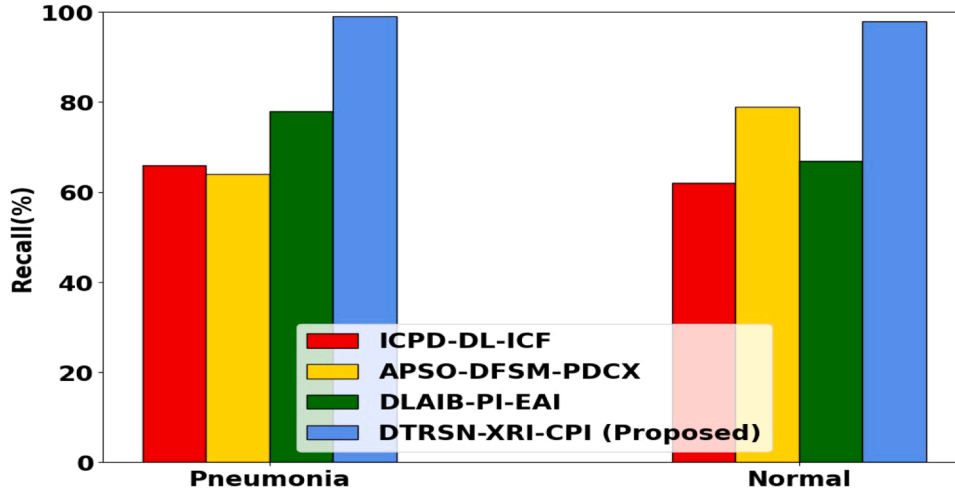


Fig. 5. Performance analyses of recall.

2.3. Feature extraction using synchrosqueezed fractional wavelet transform (SSFWT)

In this segment, SSFWT [33] is discussed to improve the structures, like shape, colour, spatial and texture relation, from the pre-processed image. The use of SSFWT for the classification of pneumonia from chest X-ray images has several theoretical and practical benefits. Traditional wavelet transforms often struggle with overlapping features and noise interference, hindering the identification of subtle differences between pneumonia-affected and healthy tissue. SSFWT enhances time-frequency concentration, enabling better separation of overlapping features. SSFWT fractional order flexibility allows for more precise extraction of complex patterns, improving feature capture in non-stationary medical signals. SSFWT synchro squeezing property effectively reduces noise interference, preserving essential diagnostic features like texture, shape, and spatial relationships. This makes it more resilient to background artifacts, a common challenge in medical imaging. By extracting diverse features such as color, shape, spatial and texture, SSFWT provides a comprehensive feature representation, overcoming the limitations of previous methods that only capture a subset of relevant features. These enhancements greatly improve deep learning models' performance by resolving issues with noise interference, feature overlap, and limited feature extraction. Eq. (6) is used to initiate the feature extraction process from the preprocessed images.

$$T_f(\omega, t) = \int_f W_f(a, t) a^{-\frac{3}{2}} \delta(\omega_f(a, t) - \omega) da \quad (6)$$

where, $T_f(\omega, t)$ denotes the kernel function; $W_f(a, t)$ denotes a transmissions; δ specifies the Dirac delta; a and t provide the settings for scale and translation; $\omega_f(a, t)$ denotes a phase transform and ω denote the modulation rate. A transmissions of Fractional Wavelet Transform (FRWT) is defined as (7),

$$f(t) = \frac{1}{C_\psi} \int_{\mathbb{R}} T_f^a(\omega, t) d\omega \quad (7)$$

where, $f(t)$ denotes linear chirp transmissions; C_ψ denotes the admissibility constant of the FRWT; ω implies the modulation rate; t implies the translation parameters, and T_f^a denotes the FRWT of a transmissions. Then, the inverse synchro-squeezed fractional wavelet transform is defined as (8),

$$\int_{\mathbb{R}} T_f^a(\omega, t) d\omega = C_\psi f(t) \quad (8)$$

where, T_f^a denotes the transmission of FRWT; ω, t denotes the modula-

tion rate and translation parameters; C_ψ denotes the admissibility constant of the FRWT and $f(t)$ denotes linear chirp signal. The basic properties of SSFWT complex conjugate is defined as Eq. (9),

$$T_g^a(\omega, t) = \left(T_f^a(-\omega, t) \right)^* \quad (9)$$

where, $T_g^a(\omega, t)$ denotes linear chirp transmissions; T_f^a denotes the FRWT of a transmissions and $(-\omega, t)$ denotes the modulation rate and translation parameters. The scaling characteristics of FRWT is defined as Eq. (10),

$$\omega_g^a(a, t) = ct + \omega_f^a(a, t) \quad (10)$$

where as, $\omega_g^a(a, t)$ implies the variables of linear combination; c and t denotes the constant and variable and $\omega_f^a(a, t)$ denotes the real function of SSFWT. Shape defines the general shape or form of an object in a picture. Various shape descriptors exist, such as Hu moments, Fourier descriptors, or geometric moments. These methods capture the essential characteristics of the shape. The shape is defined as Eq. (11),

$$Shape = \sqrt{\frac{Area}{(\pi * MaxRadius^2)}} \quad (11)$$

where, $Area$ denotes calculate area of the shape; π denotes index values and $MaxRadius$ denotes maximum radius of the feature. The colour model is primarily used in electronic systems for image sensing, representation, and display. The colour is defined as Eq. (12),

$$Colour = \sqrt{(R)^2 + (G)^2 + (B)^2} \quad (12)$$

where, R denotes the mediums emit colour red; G denotes the mediums emit colour green and B denotes the mediums emit colour blue. The arrangement of items in a space with respect to one another is referred to as spatial relations. The special relation is defined as Eq. (13),

$$X \in R^{C \times S} \quad (13)$$

here, X denotes the special relation channel; C and S denotes the count of channels and samples, and R denotes the electroencephalogram trial. The distribution of a polycrystalline sample's crystallographic orientations is known as its texture. The texture is defined as Eq. (14),

$$T = (f(x, y)) \quad (14)$$

where, T denotes the texture; f denotes the value of the texture function and x and y denotes the image position. Finally, features such as shape,

colour, spatial relation, and texture are extracted with SSFWT. Then these extracted features are fed to DTRSN to identifying and classifying pneumonia.

2.4. Pneumonia identification and classification using double transformer residual super-resolution network (DTRSN)

In this section, Identification and Classification of pneumonia using DTRSN [34] is discussed. DTRSN is classified into two types such as, pneumonia and normal. Traditional models often struggle with low-resolution images and image quality variations, which hinder the detection of subtle pneumonia features. DTRSN addresses these challenges by enhancing image resolution, improving the visibility of pneumonia indicators such as infiltrates and consolidations, and distinguishing between pneumonia and normal lung tissue. DTRSN dual transformer architecture captures both spatial and contextual relationships, enabling accurate classification of pneumonia-affected regions. The ability to model long-range dependencies ensures the detection of subtle pneumonia patterns with greater precision. DTRSN's robustness to variations in image quality guarantees consistent performance across diverse datasets and clinical settings, and its cross-resolution analysis capability allows it to effectively handle images from different devices, improving classification accuracy in clinical practice. The mapping function is,

$$I_{SR}(i, j) = f(F_{LR}(\tilde{i}, \tilde{j}), W(i, j)) \quad (15)$$

In this case, $W(i, j)$ stands for the weight prediction module at i, j , the super-resolution image's pixel value at (i, j) , and $F_{LR}(\tilde{i}, \tilde{j})$ stands for the feature vectors for matching pixels in low-resolution images. Imageries that have been upgraded to have a greater resolution than their original version are referred to as super-resolution images. The super-resolution images are defined as the following Eq. (16),

$$W(i, j) = \phi(v_{ij}, \theta) \quad (16)$$

where, ϕ denotes the weight prediction network; $W(i, j)$ denotes the convolutional kernel weight; and v_{ij} denotes the vector associated with that particular pixel. A visual pattern that is unique from its immediate

where, *avgpooling* denotes the global average pooling; y_i denotes the detection probability; f_l^i denotes the local feature, and $R(i, i)$ denotes the final relational feature. The last and most significant component of a system or product is its last feature. The final feature can be defined as Eq. (19),

$$v = \text{conv} \left[D(f_l^1, \dots, f_l^N) + f_g \right] \quad (19)$$

where, v denotes the final feature; D denotes the affinity matrix; f_l^1 and f_l^N denotes the functions of pixel and f_g denotes the embedded function. Finally, DTRSN have accurately classified the pneumonia identification such as pneumonia and normal. Then the HPOA is used to improve the DTRSN. HPOA is used to adjust the weight and bias parameters of DTRSN.

2.5. Optimization using hunter-prey optimization algorithm (HPOA)

The proposed HPOA [35] is utilized to enhance weights parameter- v_{ij} and θ of proposed DTRSN. HPOA is a type of computational optimization method inspired by the hunting behaviour observed in nature. HPOA improves the performance of DTRSN by optimizing its parameters, helping the model avoid over fitting, speed up convergence, and handle the complex, high-dimensional nature of the parameter space more efficiently. This optimization process ensures better generalization on small or imbalanced datasets and reduces the computational burden. By optimizing the DTRSN, HPOA contributes to more accurate and reliable pneumonia classification. The combination of HPOA with DTRSN improves the overall robustness, efficiency, and scalability of the pneumonia detection system in clinical environments. Here, a thorough procedure for utilizing HPOA to get the appropriate DTRSN values is described. In order to optimize the finest DTRSN factors, a uniformly distributed population is created. Next, the full step technique is shown below.

Step 1: Initiation

Randomness is used to create the initial population of HPOA. Eq. (20) is then used to derive the initialization.

$$X = \begin{bmatrix} X_1 \\ \vdots \\ X_i \\ \vdots \\ X_N \end{bmatrix}_{N \times m} = \begin{bmatrix} x_{1,1} & \cdots & x_{1,d} & \cdots & x_{1,m} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ x_{i,1} & \cdots & x_{i,d} & \cdots & x_{i,m} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ x_{N,1} & \cdots & x_{N,d} & \cdots & x_{N,m} \end{bmatrix}_{N \times m} \quad (20)$$

surroundings is called a local feature. It is typically linked to alterations in one or more picture attributes at the same time; however, it is not always precisely focused on these modifications. The local feature is defined as Eq. (17),

$$f_l^n = f_g \otimes m_n \quad (17)$$

where, f_l^n denotes the local feature; f_g denotes the global feature; and m_n denotes the key point. A local feature is a pattern or unique structure found in the imageries, like a small picture patch, edge, or point. The weight information of i^{th} local-feature is defined Eq. (18).

$$y_i = \text{avgpooling} \left(f_l^i \right) \cdot R(i, i) \quad (18)$$

here, X_i specifies the i^{th} population member; X denotes the population matrix; N and m denotes the count of population member and variables; and $x_{i,d}$ denotes the d^{th} variable's value for i^{th} population member.

Step 2: Generating in random

The input-weight v_{ij} and θ parameter is developed randomness via HPOA method.

Step 3: Fitness function

The arbitrary solution is generated using the initialised values. It is expressed in Eq. (21),

$$\text{Fitness function} = [\text{optimizing}(v_{ij}, \theta)] \quad (21)$$

where, v_{ij} is used for increasing accuracy and θ is used to increasing the

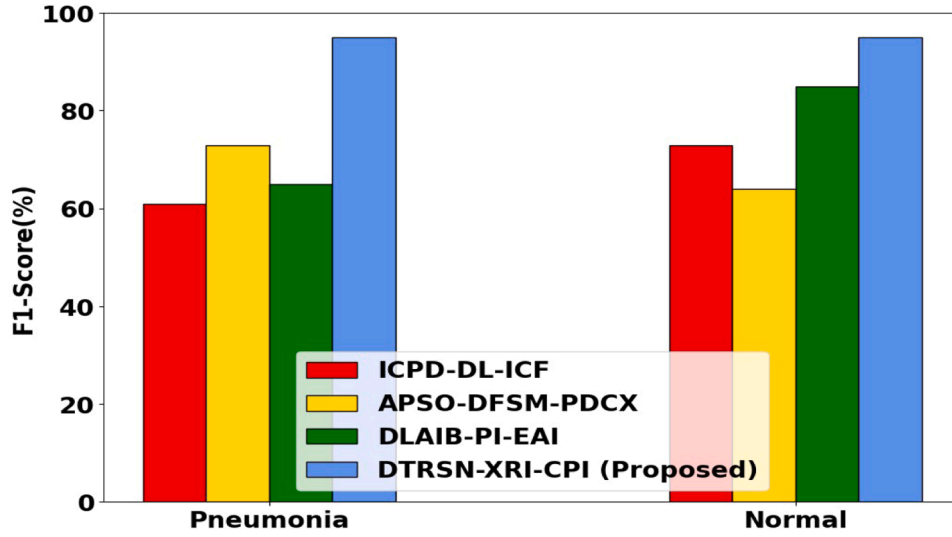


Fig. 6. Analyses the performance of F1-Score.

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Step 4: Exploration phase for optimizing v_{ij}

A collection of guidelines and approaches generated by the algorithm under consideration enable the control and direction of the population inside the search space; this cycle continues until the algorithm breaks. Each person's place within the population undergoes adjustments based on the specified rules algorithm, followed by an evaluation of the new position by an objective function. As can be seen from Eq. (22) each member of the initial population is given a random location in the search space.

$$x_i = rand(1, d) * (ub - lb) + lb \quad (22)$$

whereas, x_i denotes the prey or the hunter's position; lb denotes the lowest possible number for the variables in issue; d specifies the count of variables, and ub specifies the problem variables' maximum value. It is necessary to design and execute a search mechanism multiple times in order to guide the search agents to the most appropriate location. The significant modifications in solutions are rapid additional investigation of the search-space to identify its possible locations. Adaptive methods

are schedule-based procedures to alter certain model parameters during training. The adaptive parameter are defined as Eq. (23),

$$Z = R_2 \otimes IDX + \vec{R}_3 \otimes (\sim IDX) \quad (23)$$

where, R_2 and $\vec{R}_3$ implies the random number; Z denotes the adaptive parameter; IDX specifies the vector's index numbers, $\otimes$ denotes the element-wise multiplication, and R_2 and $\vec{R}_3$ implies a random number. Fig. 2 shows the flow chart of HPOA for optimizing DTRSN.

Step 5: Exploitation phase for optimizing θ

If the approach consistently prefers the search agent that is situated farthest from the center of the average it will exhibit delayed convergence. To compare it to hunting, once the hunter kills and catches the prey, the hunter must move on to a new target in order to continue the cycle. The hunter selects the last search agents, whose position assaults the search agents and deviates from their average. Eq. (24), which defines the prey's positions,

$$\mu = \frac{1}{n} \sum_{i=1}^n \vec{x}_i \quad (24)$$

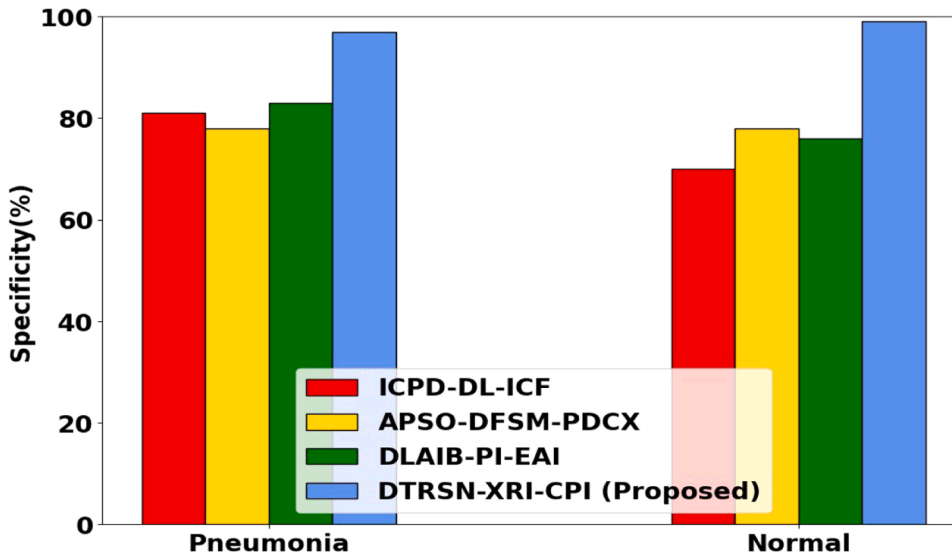


Fig. 7. Analysis the performance of specificity.

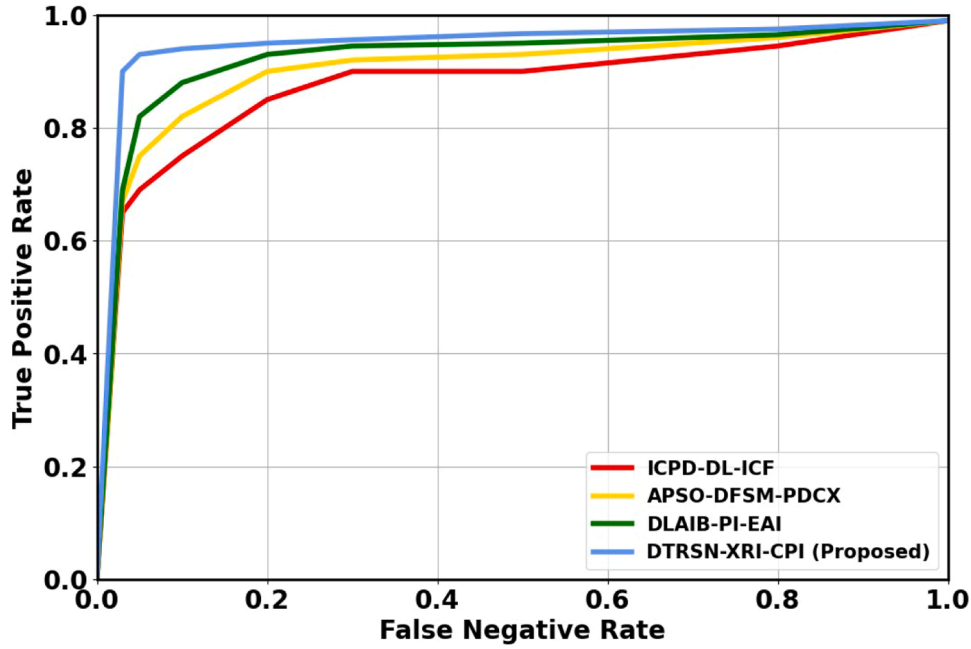


Fig. 8. Analyses the performance of ROC.

whereas, n implies the count of search agents; μ denotes the average position; i denotes a pixel value, and $\vec{x}_i$ denotes the random vector. They suggest that the best global position is the safest since it increases the chances that the prey will make it and may even lead the hunter to select a different target. The position of the prey is proposed to update the following Eq. (25),

$$x_{ij}(t+1) = T_{pos(j)} + CZ\cos(2\pi R_4) \times (T_{pos(j)} - x_{ij}(t)) \quad (25)$$

whereas, $x(t+1)$ and $x_{ij}(t)$ denotes the next and present position of the prey; R_4 denotes the range's random number; and CZ denotes the current position adaptive parameter.

Step 6: Termination

The weight parameter value of generator v_{ij} and θ from the double transformer residual super-resolution network is optimized by utilizing HPOA; and step 3 repeats till it obtains its halting criterion, $x = x + 1$. Next, the DTRSN-XRI-CPI defectively assesses the quality of early detection and classification of pneumonia by higher accuracy and higher ROC.

3. Results with discussion

The DTRSN-XRI-CPI method's experimental results are presented. The dataset of chest x-ray images is split into training (70 %) and testing (30 %), with 20 % going to testing and 10 % going to validation. Metrics such as recall, accuracy, precision, F1-score, specificity, and RoC are used to evaluate the performance. Using Python 3.8 and the PyTorch library, experiments were carried out on Google Colab with an NVIDIA

Tesla T4 GPU (16 GB RAM). The results of DTRSN-XRI-CPI are compared with existing techniques, including ICPD-DL-ICF [24], APSO-DFSM-PDCX [25] and DLAIB-PI-EAI [26] respectively.

The selection of ICPD-DL-ICF, APSO-DFSM-PDCX and DLAIB-PI-EAI as baseline models is based on their distinct methodologies and limitations in pneumonia detection from chest X-ray images, providing a comprehensive benchmark for evaluating the proposed DTRSN-XRI-CPI framework. ICPD-DL-ICF uses a DCNN to extract features and classify images into normal and pneumonia categories, exhibiting high accuracy but limited generalisability on small or imbalanced datasets, affecting its performance in diverse clinical environments. APSO-DFSM-PDCX combines deep learning with Adaptive and Altruistic Particle Swarm Optimization (AAPSO) to optimize feature selection and enhance diagnostic accuracy by removing non-informative features from ResNet50-extracted deep features. Its high computational complexity and extensive parameter tuning make it less suitable for real-time or resource-constrained applications. DLAIB-PI-EAI focuses on integrating background information for improved pneumonia classification and uses Grad-CAM to provide visual explanations, enhancing interpretability in clinical settings. It struggles with robustness to image quality variations and low-resolution data, limiting its scalability across diverse datasets.

3.1. Performance measures

This step is essential for deciding whether to explore optimization algorithms. Performance metrics such as recall, F1-score, specificity, accuracy, precision, and RoC are used to evaluate performance.

Table 1
Ablation study.

Configuration	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	Specificity (%)	RoC
Without RNGCF	98.45	97.12	96.87	98.25	97.32	0.953
Without SFWT	98.56	97.44	97.12	98.47	97.56	0.961
Without HPOA	98.32	96.89	96.43	98.05	97.21	0.948
Without RNGCF and SFWT	97.98	96.67	96.12	97.85	96.98	0.931
Without RNGCF and HPOA	97.88	96.34	96.01	97.75	97.02	0.923
Without SFWT and HPOA	97.56	95.76	95.44	97.34	96.75	0.917
DTRSN-XRI-CPI (Proposed)	99.67	98.82	98.61	99.84	98.57	0.972

3.1.1. Accuracy

It is a metric that calculates the total rightness of forecasts ready by the classification method. It defines the ratio of exact forecasts to total instances, and is expressed in Eq. (26),

$$\text{Accuracy} = \frac{TP + TN}{FN + TP + FP + TN} \quad (26)$$

here, TN and TP implies the true negative and positive; FP and FN implies false positive and negative.

3.1.2. Precision

It is a metric that computes the accuracy of positive forecasts created by classification method. It displays the ratio of true positives to all false positives and true positives. Thus, it is executed in Eq. (27),

$$\text{Precision} = \frac{TP}{FP + TP} \quad (27)$$

3.1.3. Recall

True positive rate, or sensitivity, is the term for it. It is the metric that quantifies the ability of the classification method to capture and properly detect relevant instance of the positive class. This can be found in Eq. (28).

$$\text{Recall} = \frac{TP}{FN + TP} \quad (28)$$

3.1.4. F1- Score

Recall and accuracy are combined into a single metric by the F1-Score. It is mainly valuable in situations where you want to balance both false positive and negative. Thus, it is given in Eq. (29),

$$F1 - \text{score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (29)$$

3.1.5. Specificity

In physics, chemistry, biology, economics, and many other fields, specificity can take many different forms and symbolize relationships. It is employed to assess the classification method's capacity to accurately identify negative instances. Consequently, it is provided in Eq. (30).

$$\text{Specificity} = \frac{TN}{TN + FP} \quad (30)$$

3.1.6. ROC

It is a graphical depiction of the classification method at numerous threshold settings. For various threshold values, it is formed by charting the real positive rate vs the rate of the false positive. The ROC is categorized as true and false positive rates in this instance. Thus, given in Eq. (31),

$$\text{False Positive Rate} = \frac{FP}{FP + TN} \quad (31)$$

3.2. Performance analysis

Figs. 3 to 8 shows simulation outcome of DTRSN-XRI-CPI technique. The DTRSN-XRI-CPI is analysed to the existing ICPD-DL-ICF [24], APSO-DFSM-PDCX [25] and DLAIB-PI-EAI [26] methods correspondingly.

Fig. 3 illustrated the analyses of performance accuracy. The DTRSN-XRI-CPI method attains 20.7 %, 22.6 %, 30.5 % higher accuracy for pneumonia; 19.6 %, 22.8 %, 32.5 % higher accuracy for normal; with existing ICPD-DL-ICF [24], APSO-DFSM-PDCX [25] and DLAIB-PI-EAI [26] methods correspondingly.

Fig. 4 depicts the analyses the performance of the precision. The DTRSN-XRI-CPI method attains 21.8 %, 29.3 % and 30.5 % higher precision for pneumonia; 21.8 %, 27.4 %, and 30.7 % higher precision

for normal; with existing ICPD-DL-ICF [24], APSO-DFSM-PDCX [25] and DLAIB-PI-EAI [26] methods correspondingly.

Fig. 5 shows the performance analyses of Recall. The DTRSN-XRI-CPI method attains 21.8 %, 29.5 % and 32.6 % higher recall for pneumonia; 20.7 %, 26.7 %, 31.1 % higher recall for normal; with existing ICPD-DL-ICF [24], APSO-DFSM-PDCX [25] and DLAIB-PI-EAI [26] approaches.

Fig. 6 portrays the analyses the performance of F1-Score. The DTRSN-XRI-CPI method attains 21.6 %, 26.4 %, 32.2 % higher F1 score for pneumonia; 19.7 %, 26.7 %, 30.1 % higher F1 score for normal; with existing ICPD-DL-ICF [24], APSO-DFSM-PDCX [25] and DLAIB-PI-EAI [26] methods.

Fig. 7 portrays the analysis the performance of specificity. The DTRSN-XRI-CPI method attains 21.8 %, 29.3 % and 30.5 % higher specificity for pneumonia; 20.7 %, 26.7 %, 31.1 % higher specificity for normal; analysed with existing like ICPD-DL-ICF [24], APSO-DFSM-PDCX [25] and DLAIB-PI-EAI [26] techniques respectively.

Fig. 8 depicts the analyses the performance of ROC. The proposed DTRSN-XRI-CPI method provides 5.622 %, 1.292 %, and 3.771 % greater ROC is analysed with existing like ICPD-DL-ICF [24], APSO-DFSM-PDCX [25] and DLAIB-PI-EAI [26] techniques respectively.

The ablation study in Table 1 presents the impact of removing key components (RNGCF, SFWT, and HPOA) from the proposed DTRSN-XRI-CPI framework on various performance metrics. With an specificity of 98.57 %, accuracy of 99.67 %, precision of 98.82 %, recall of 98.61 %, F1-score of 99.84 %, and RoC of 0.972, the full model performs best across all metrics, indicating the robustness of the proposed framework. When RNGCF is removed, accuracy drops to 98.45 %, and precision and recall decrease to 97.12 % and 96.87 %, respectively, highlighting its critical role in enhancing feature representation through noise reduction and contrast enhancement. Excluding SFWT, results in a slightly better accuracy of 98.56 % but impacts recall and F1-score, indicating its importance in extracting features. The absence of HPOA leads to an accuracy of 98.32 %, showing that optimization of weight parameters is essential for fine-tuning the model's performance. Combinations of omitted components result in more significant performance degradation. Removing both RNGCF and SFWT reduces accuracy to 97.98 %, precision to 96.67 %, and recall to 96.12 %, while excluding RNGCF and HPOA results in a further drop to 97.88 % accuracy. The worst performance is observed when both SFWT and HPOA are removed, leading to an accuracy of 97.56 %, precision of 95.76 %, and RoC of 0.917. The results demonstrate that each component such as RNGCF, SFWT, and HPOA plays a significant and complementary role in the overall performance of the framework. The highest accuracy and reliability of the proposed DTRSN-XRI-CPI framework emphasize the critical synergy between these components for effective pneumonia detection from chest X-rays.

3.3. Discussion

The proposed DTRSN-XRI-CPI framework demonstrates significant improvements in pneumonia detection from chest X-ray images contrasted to existing techniques. By integrating Region-Aware Neural Graph Collaborative Filtering (RNGCF) for context-sensitive noise reduction and contrast enhancement, the model preserves critical diagnostic features often lost in traditional pre-processing methods. The use of the Synchro-Squeezed Fractional Wavelet Transform (SSFWT) for feature extraction enhances the representation of complex, non-stationary patterns such as color, shape, texture, and spatial relationships, which are crucial for accurate classification. The optimization of the DTRSN using the Hunter Prey Optimization Algorithm (HPOA) ensures better generalization, reduced over fitting, and faster convergence, making it suitable for diverse and imbalanced datasets. Compared to baseline models like ICPD-DL-ICF, APSO-DFSM-PDCX, and DLAIB-PI-EAI, the proposed framework achieves higher accuracy, precision and recall, demonstrating its robustness and scalability across varying image quality and dataset conditions. The incorporation of explainability

through feature interpretability and the reduction of computational complexity enhance its potential for real-time clinical applications, addressing key challenges such as resource constraints and the need for transparent decision-making in medical diagnosis.

4. Conclusion

The Optimized Double Transformer Residual Super-resolution Network-related chest X-ray imageries for classification of Pneumonia Identification (DTRSN-XRI-CPI) is proposed and successfully implemented in the Python. The performance of DTRSN-XRI-CPI technique performed better when used with the Co-training than when used separately regards 21.6 %, 26.4 % and 32.2 % higher f1 score, 21.8 %, 29.3 % and 30.5 % higher specificity and provides 5.622 %, 1.292 %, and 3.771 % greater ROC when compared to existing ICPD-DL-ICF, APSO-DFSM-PDCX and DLAI-PI-EAI methods. In the future research projects, a deep learning (DL) framework will be utilised to identify and categorise pneumonia, which may concentrate on enhancing the interpretability of the model, incorporating various medical data sources, resolving issues with real-time diagnosis, and guaranteeing ethical considerations in data usage for reliable and useful clinical deployment. The study aims to develop a very precise and sensitive instrument for identifying pneumonia, which will ultimately help patients and medical professionals. Accordingly, the proposed approach to classification and identification of pneumonia depending on the CXR imageries method is more successfully implemented.

CRedit authorship contribution statement

Jerald Prasath G: Writing – original draft. **Prabu S:** Supervision. **V. Valli Mayil:** Supervision. **Sumit Saini:** Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper

Data availability

No data was used for the research described in the article.

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