




CP_DeepNet: a novel automated system for COVID-19 and pneumonia detection through lung X-rays

Muhammad Hamza Mehmood¹ · Farman Hassan²  · Auliya Ur Rahman³ · Wasiat Khan⁴ · Samih M. Mostafa⁵ · Yazeed Yasin Ghadi⁶ · Abdulmohsen Algarni⁷ · Mudasser Ali⁸

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Abstract

In recent years, the COVID-19 outbreak has affected humanity across the globe. The frequent symptoms of COVID-19 are identical to the normal flu, such as fever and cough. COVID-19 disseminates rapidly, and it has become a prominent cause of mortality. Nowadays, the new wave of COVID-19 has created significant impacts in China. This virus can have detrimental effects on people of all ages, particularly the elderly, due to their weak immune systems. The real-time polymerase chain reaction (RT-PCR) examination is typically performed for the identification of coronavirus. RT-PCR is an expensive and time requiring method, accompanied by a significant rate of false negative detections. Therefore, it is mandatory to develop an inexpensive, fast, and reliable method to detect COVID-19. X-ray images are generally utilized to detect diverse respiratory conditions like pulmonary infections, breathlessness syndrome, lung cancer, air collection in spaces of the lungs, etc. This study has also utilized a chest X-ray dataset to identify COVID-19 and pneumonia. In this research work, we proposed a novel deep learning model CP_DeepNet, which is based on a pre-trained deep learning model such as SqueezeNet, and further added three blocks of convolutional layers to it for assessing the classification efficacy. Furthermore, we employed a data augmentation method for generating more images to overcome the problem of model overfitting. We utilized COVID-19 radiograph dataset for evaluating the performance of the proposed model. To elaborate further, we obtained significant results with accuracy of 99.32%, a precision of 100%, a recall of 99%, a specificity of 99.2%, an area under the curve of 99.78%, and an F1-score of 99.49% on CP_DeepNet for the binary classification of COVID-19 and normal class. We also employed CP_DeepNet for the multi-class classification of COVID-19, pneumonia, and normal person, in which CP_DeepNet achieved accuracy, precision, recall, specificity, area under curve, and F1-score of 99.62%, 99.79%, 99.52%, 99.69, 99.62, and 99.72%, respectively. Comparative analysis of experimental results with different preexisting techniques shows that the proposed model is more dependable as compared to RT-PCR and other prevailing modern techniques for the detection of COVID-19.

Keywords Pneumonia · COVID-19 · Deep Learning · Data Augmentation · SqueezeNet · Transfer Learning · Medical Imaging

Extended author information available on the last page of the article

1 Introduction

In the year of 2019, COVID-19 pandemic originated from Wuhan, a prominent city situated in the People's Republic of China. In China, another new wave of COVID-19 has abruptly again in 2023, which has increased the chaos amongst the public. The numbers of COVID-19 cases are increasing on a daily basis, which can cause a shortage of various daily life necessities [1]. The dissemination of COVID-19 increases due to the avoidance of social distancing protocols. Therefore, there are several standard operating procedures (SOPs) imposed by different governments to reduce the spread of the virus. These SOPs are comprised of social distance, face cover, frequent hand washing, etc. The generic symptoms of COVID-19 encompass high fever, dry-cough, diminished breath capacity, weariness, cephalalgia, bodily discomfort, etc. COVID-19 has still a high death rate, 657 million total cases have been reported with 6.67 million deaths across 228 countries and territories. Most of the COVID-19 cases have been identified from the USA, India, France, Germany, Brazil, South Korea, and Italy. The highest number of mortalities has been recorded in Europe due to COVID-19, whereas the smallest number of mortalities has been proclaimed in Africa. In Europe, 241,462,209 cases of COVID-19 have been identified, and 1,973,182 people died from Covid so far. In Africa, 258,284 deaths have been confirmed until now, which is significantly lower compared to Europe. The other continents have also declared a high number of COVID-19 cases as well as mortalities. Asia has reported 203,451,005 cases of COVID-19 and 1,505,407 mortalities [2]. Different countries have developed digital apps for controlling and monitoring the situation of COVID-19. In Pakistan, the government has developed the "COVID-19 Gov PK" application for providing alerts and updates on COVID-19 to its citizens. This app provides the details of COVID-19 cases and the death count across the provinces and the whole country. It also offers other features such as radius alert, report SOP violations, corona chatbot, and awareness videos [3]. As we know that COVID-19 was started in Wuhan, but it disseminated across the globe within a short time-period. The study shows that half of the people who come in contact with Covid patients have a strong chance of getting infected by the virus [4]. Therefore, the COVID-19 virus spreads faster as compared to the flu or other previous viruses. This fast spread of the virus increases the chances of mortality rate that is 3.5% across the world. The weak immunity of elderly people causes a higher mortality rate as compared to other age groups. According to Worldometers reports, the highest mortality rate is 14.8% in 80+ years old people. This mortality rate decreases as the age decreases. The 70–79 years old people have an 8.0% mortality rate, 60–69 years old people have a 3.6% mortality rate, 50–59 years old people have a 1.3% mortality rate, 40–49 years old people have a 0.4% mortality rate, and 10–40 years old people have just 0.2% mortality rate with respect to each decade. Children below 10 years of age have no fatalities [2]. A recent study shows that an average of 4.7 to 6.6 people are infected by one covid positive person [5]. As a result, the virus can affect a large number of individuals in a short time period unless some countermeasures are employed. The conventional method utilized for the detection of COVID-19 is RT-PCR. In the RT-PCR test, the specimen is collected from the upper respiratory tract of the infected person. RT-PCR test machine uses chemical solutions to remove certain substances such as fats and proteins and extracts ribonucleic acid (RNA) from the sample. Reverse Transcription is applied to convert RNA into Deoxyribonucleic acid (DNA), which is then followed by the PCR process. The level of fluorescent dye indicates the signal of the presence of a virus in the DNA. Despite the fact that RT-PCR has the ability to detect variants of COVID-19, still it detected a few cases as

negative which proved positive on further investigation using CT scans [6]. The research community has used X-rays and computed tomography (CT) scans [6–9] instead of RT-PCR because RT-PCR is an expensive and very slow technique to identify COVID-19, and it also gives a significant number of false detections.

2 Related work

The authors have examined several deep-learning techniques [7, 10–12] to identify COVID-19 by utilizing X-ray images. X-ray images have been popularly utilized for the detection of multiple conditions such as accidental injuries, chest diseases, bone or joint dislocations, and cancer, etc. Many of the research studies have also used CT scans as X-ray images for various detections in soft tissues of human body, like the heart, lungs, and kidneys [10]. X-rays are considered more convenient, rapid, and less detrimental in contrary to CT scans for the detection of COVID-19 [7, 10]. The study in [7] used multiple pre-trained models to identify COVID-19 including Inception and ResNet models. The author also used five-fold cross-validation for achieving more accurate and reliable results. The developed system faced the issue of overfitting because of the small amount of dataset used in the study. In [11], the author used thirteen different convolutional models for extracting various attributes of the dataset. The author utilized support vector machine (SVM) for classifying data. SVM worked better with ResNet50 and achieved the highest accuracy of 95.33%. The other pre-trained models that were used for extracting features include AlexNet, ResNet101, GoogleNet, VGG16, VGG19, ResNet101, DenseNet, XceptionNet, ShuffleNet, and MobileNetv2 [12], etc. Furthermore, COVIDX-NET [13] was introduced for assisting practitioners to identify COVID-19 patients by utilizing their lung X-ray images. This research employed seven pre-trained models, but a very small number of X-ray data was utilized for training and testing purposes. This lack of data caused the problem of overfitting in the framework. VGG19 and DenseNet obtained an F1-score of 91%, which was the highest as compared to the other models.

There are multiple studies [4, 7, 14–16] performed for the identification of Covid19, that have utilized CT scans. The researchers [4, 17] have stressed the significantly low true positive and true negative rates of the RT-PCR for the detection of COVID-19. We know that the conventional method for the detection of coronaviruses is RT-PCR, but it gives a high false negative rate because of different factors such as sample collection technique, disease phases, and apparatus deficiencies. This drawback of RT-PCR can hinder the timely diagnosis of COVID-19. Consequently, it is not reliable to use RT-PCR for evaluating the presence of COVID-19. It is possible to use CT-scan technique for covid detection but it has higher expenditures as compared to the x-ray method. Another research [14] has shown that the DNA and RNA test is ineffective and untrustworthy because it achieves an accuracy of less than 50%. The study [4] has performed a comparative analysis of CT scans and RT-PCR for the identification of COVID-19 in a total of 51 people who had symptoms of the disease and had traveled to disease-affected areas. In this comparison, RT-PCR showed a sensitivity of 71%, whereas CT-scan achieved a sensitivity of 98% for detecting COVID-19 cases. Moreover, RT-PCR kits are quite expensive and finite for a substantial number of COVID-19 patients, therefore, it is necessary to develop a computerized framework as a replacement for RT-PCR tests to avoid the fast spread as well as cost-effective detection of COVID-19 [7]. In [14], a pre-trained deep learning model was improvised to identify COVID-19 disease utilizing 453 thoracic CT scans of 99 people. The enhanced

inception model achieved significant results with an 89.5% accuracy for internal validation and an accuracy of 79.3% for external testing datasets. In [15], the author suggested a model that consisted of multiple two-dimensional and three-dimensional deep neural architectures to diagnose COVID-19 by utilizing chest CT scans. These deep learning algorithms were employed on a small dataset that contained CT scans of 157 people. In [16], another deep learning-based model named ResNet-50 was used for identifying different lung infectious diseases including COVID-19, bacterial pneumonia, tuberculosis, and normal lungs. The dataset contained 31,554 CT scans gathered from 618 patients of different diseases, and 28,873 CT scans gathered from 300 normal people. In [18], the author described that RT-PCR is not a very reliable technique for the identification of COVID-19 during its early phase. Therefore, ResNet18 deep model was applied for extracting features in CT scans. The classification was performed using the Bayesian function and achieved 86.7% accuracy.

All of the above-mentioned studies have contributed to the identification of Alzheimer. However, certain critical research gaps persist within the existing literature. A prevalent limitation in prior studies pertains to the utilization of imbalanced datasets, where an unequal distribution of samples across classes may compromise model generalization. In this study, we addressed this gap by adopting a balanced dataset, ensuring equitable representation of all classes of dataset. Additionally, the exploration of data augmentation techniques in prior research efforts has often been limited. Our study goes further by emphasizing how the strategic use of data augmentation greatly enhances both the robustness and performance of our model. In previous studies, a significant issue was the choice of basic models, often neglecting the benefits of lightweight designs. In our research, we deliberately tackle this problem by using SqueezeNet as the main model. SqueezeNet prioritizes efficiency without sacrificing performance, which differentiates it from the commonly used models. This deliberate decision is aimed at creating models that use fewer resources, which is crucial for practical use in real-world clinical settings with limited computational capacity. By making SqueezeNet the foundation of our novel model, we not only contribute to better understanding Alzheimer's disease detection but also encourage exploring and using alternative model designs that meet the practical needs of clinical applications.

2.1 Main contributions

In this study, we introduce CP_DeepNet, an innovative deep learning model built upon the SqueezeNet architecture to address the binary classification of COVID-19 patients and the multiclass classification of individuals into COVID-19, pneumonia, and normal categories. SqueezeNet, developed by Landola et al. [19], leverages the unique "squeeze" and "expand" convolutional layers technique, and our work extends this by customizing the SqueezeNet model specifically for the accurate identification of COVID-19 cases. Our CP_DeepNet model not only outperforms existing approaches but also brings forth several key contributions, emphasizing its significance in the field:

1. We present a novel deep-learning methodology tailored for automated detection of COVID-19 and pneumonia from lung X-rays.
2. Our approach exhibits robust performance in simultaneously detecting three distinct classes: normal, COVID-19, and pneumonia cases. This versatility enhances its applicability in diverse clinical scenarios.

3. To address dataset limitations and mitigate overfitting concerns, we incorporate familiar data augmentation techniques. This augmentation not only enlarges the dataset but also enhances the model's generalization capabilities.
4. We conduct comprehensive experiments to rigorously validate the proposed approach, evaluating its performance in both two-class (COVID-19 vs. normal) and three-class (COVID-19 vs. pneumonia vs. normal) scenarios. This thorough validation ensures the reliability and effectiveness of our model.
5. Through a meticulous comparative analysis against prevailing methods, our proposed approach demonstrates superior capabilities in identifying COVID-19 and pneumonia patients. This positions our model as a viable and efficient tool for deployment in clinical centers, offering valuable support in disease diagnosis.

This research introduces CP_DeepNet as a cutting-edge solution for automated COVID-19 and pneumonia detection, with a particular focus on its robustness, innovative methodology, data augmentation strategies, rigorous validation, and comparative efficiency. These contributions collectively underscore the potential impact of our model in advancing diagnostic capabilities in healthcare settings.

The subsequent manuscript is structured as follows: Section 2 elaborates on the particulars related to the CP_DeepNet model, whereas Section 3 comprehensively presents the specifics pertaining to the exploratory findings. Ultimately, our conclusions are summarized in Section 4.

3 Proposed system

The primary objective of this investigation is to formulate a robust system to identify COVID-19 through chest X-rays dataset. There are three main stages involved in this proposed system, i.e., pre-processing, data augmentation, fine-tuning of the model, and evaluation of the model. Initially, we applied the data pre-processing to remove all kinds of flaws from the utilized data, and then the data augmentation method for increasing the number of images in the dataset to avoid the issue of overfitting. Next, we enhanced the SqueezeNet model to improve its performance in detecting COVID-19 and pneumonia patients. Finally, we performed experimentation to evaluate the validation and significance of the proposed model. The comprehensive working mechanism of our developed approach is given in Fig. 1.

3.1 Data pre-processing and augmentation

The data pre-processing was applied to the radiography dataset [20] to eliminate its flaws. The pre-processing was conducted on the basis of the input size of the SqueezeNet model. Normalization and resizing methods were applied in the pre-processing stage. All images of the dataset were resized to 227×227 for the SqueezeNet model. We applied normalization on a dataset in accordance with the framework of the proposed model. Normalization provides the advantages of common scale data, rapid convergence, and a faster learning rate.

In order to overcome the issue of model overfitting and improper training, it is necessary to train deep-learning models using an extensive dataset. Data augmentation is used for this purpose, in which multiple augmentation techniques are applied for enlarging the available dataset. Different data augmentation techniques are comprised of rotation, translation, scaling, cropping, flipping, zooming, etc. In this study, we used a

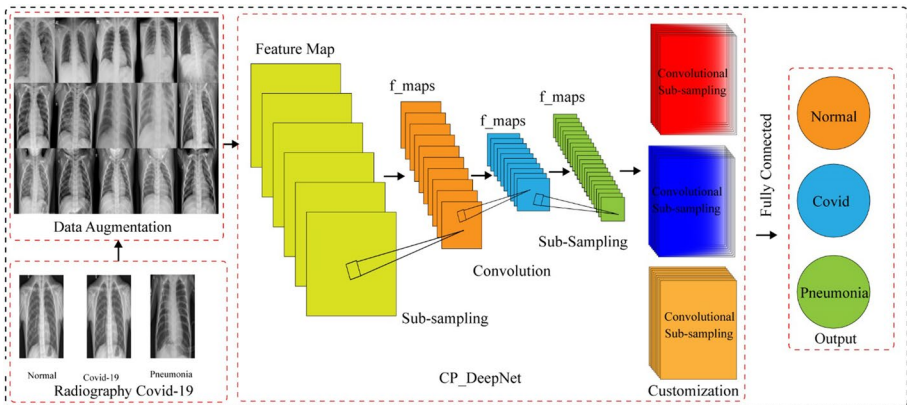


Fig. 1 Architecture of Proposed System

balanced dataset that contained overall 1000 X-ray images, 500 samples of COVID-19 patients, and 500 samples of normal people. We used four data augmentation techniques including rotation, translation, shearing, and scaling as given in Table 1. After applying these data augmentation techniques, the total count of X-ray images reached 7000, with 3500 samples of COVID-19 and 3500 samples of normal people. Figure 2. shows the data augmentation.

Table 1 Data Augmentation Techniques

Techniques	Values
Rotational	20, -20
X-translation	12, -12
Y-translation	0.5, -0.5
X-scale	0.7, -0.7
Y-scale	0.5, -0.5
X-shear	0.5, -0.5
Y-shear	0.5, -0.5

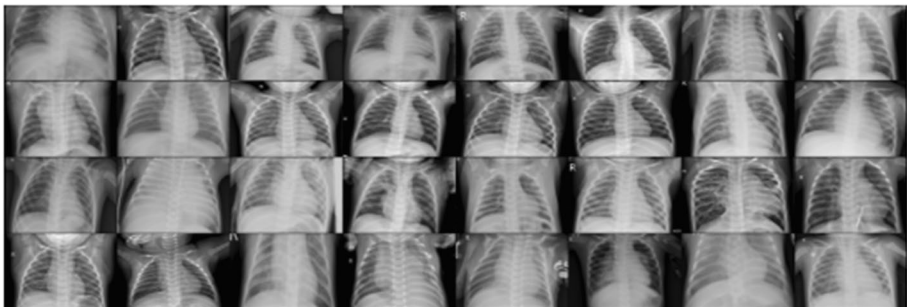


Fig. 2 X-rays Images After Data Augmentation

3.2 Pretrained models

Pre-trained models are the deep learning model that have already been trained on large sets of data. In the proposed work, a pre-trained model, namely SqueezeNet, was utilized to identify COVID-19. We explained the details of that model in the following section.

3.3 SqueezeNet

SqueezeNet [19] is a smaller convolutional neural network (CNN) based model that contains overall 18 deep layers. There are over one million of the ImageNet [21] dataset used for the training of this model. SqueezeNet has the ability to perform the classification of 1000 classes of objects such as mice, fruits, keyboards, etc. The training on large datasets has enabled the model to collect abundant information on features across the majority of image categories. The input image dimensions for the model are 227×227 .

The advantage of SqueezeNet is that it has 50 times fewer parameters as compared to the AlexNet, but it gives the same results as the AlexNet model. There are a few design strategies used by SqueezeNet for parameters reduction. The first strategy is to replace the 3×3 filters with 1×1 filters. In order to meet the budget requirements, SqueezeNet implemented the usage of 1×1 filters as against the conventional 3×3 filters. This strategy has decreased the parameters up to 9 times than a conventional filter. The second strategy is important in which the number of input channels is decreased to 3×3 filters. The smaller 1×1 filter size makes necessary to reduce the number of input channels. The squeeze layer is used for this purpose. The last strategy used by SqueezeNet is downsampling later in the network. This strategy enables to achieve larger activation maps for the convolutional layers. The convolutional layer of CNN generates an output activation map having spatial resolution starting from 1×1 to a very large value. The dimension (height and width) of these activation maps depends upon two aspects such as the dimension of input data and downsampling in the convolutional network architecture.

At the start of SqueezeNet architecture, there was an autonomous convolutional layer named conv1, which succeeded with 8 fire modules named fire2 to fire9 and finished with the final convolutional layer named conv10. The quantity of filters for each module is slowly incremented from the start to the finish of the network. In the SqueezeNet model, max-pooling is carried out with a stride of 2 after conv1, fire4, fire8, and conv10 layers. These comparatively late deployments of max-pooling are based on the third strategy of SqueezeNet. The whole architecture of the SqueezeNet model is shown in Fig. 3. SqueezeNet is on the left, SqueezeNet employing simple bypass is in the middle, and SqueezeNet featuring intricate bypass is on the right.

In order to make the same size (height and width) of both 3×3 and 1×1 filters of SqueezeNet, the 3×3 filters of the expansion module are filled with a 1-pixel border of zero-padding. SqueezeNet has used rectified linear unit (ReLU) for the activation of both squeeze and expand layers. The dropout layer added 50% of drop dropout regularization following the fire9 module. SqueezeNet has not used the fully connected layers as influenced by the NiN architecture. The learning rate when training SqueezeNet begins at 0.04 and gradually decreases over the training process.

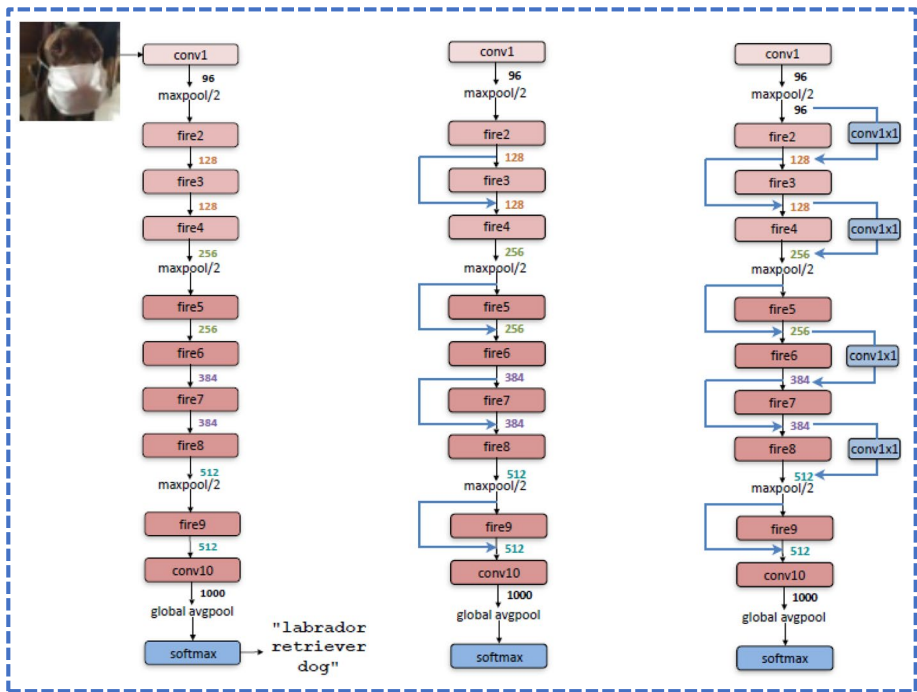


Fig. 3 Conventional SqueezeNet Architecture

3.4 Architecture of proposed CP_DeepNet

Transfer learning is a method of training deep learning models in which feature information collected from a particular task can be utilized for any other task. The type of data utilized in the second task needs to be identical to the first task. In this way, the prior trained model can be used as an initial point for solving another task by making adjustments to the structure of the model. Therefore, researchers use pre-trained models as their initial point rather than developing the model from the start and random initialization of weights for the model which will take more energy, time, and cost. More precisely, the key benefit of transfer learning is that it assists in the quick training of datasets with low computational resources. For that reason, we also used a pre-trained CNN model, named as SqueezeNet, and finetuned the deep-layers of the model when training with fresh COVID-19 data to identify the COVID-19 and pneumonia cases. SqueezeNet pre-trained model has rich information about the multiple classes of images, and after fine-tuning the model, it surpassed the other modern methods. SqueezeNet is comprised of a total of 18 layers, and we further added three distinct layers convolutional layers, max-pooling layers, and at last dense layer. We added 3 convolutional layers, and every layer is accompanied by a batch normalization, a dropout layer, and a max-pooling layer. The first 2 convolutional layers have hidden unit length and width (size) of 64×64 , and kernel size of 5×5 . Whereas the third convolutional has a size of 128 with a kernel size of 9. The following layers of convolutional layers are batch normalization, dropout layer, and max-pooling layers that have a size (length and width) of 2×2 . The dropout layer of 0.5 is used for reducing overfitting. In

Table 2 Detail of proposed CP_DeepNet Layers

Layer Type	Output Size	Details
Input	$227 \times 227 \times 3$	Input image size of 227×227
18 Layers of SqueezeNet model		
Convolution	$64 \times 64 \times 64$	Kernel size: 5×5
Batch Normalization	$64 \times 64 \times 64$	Batch normalization after the first convolution layer
Dropout	$64 \times 64 \times 64$	Dropout rate: 0.5
Max-Pooling	$32 \times 32 \times 64$	Pooling size: 2×2
Convolution	$32 \times 32 \times 64$	Kernel size: 5×5
Batch Normalization	$32 \times 32 \times 64$	Batch normalization after the second convolution layer
Dropout	$32 \times 32 \times 64$	Dropout rate: 0.5
Max-Pooling	$16 \times 16 \times 64$	Pooling size: 2×2
Convolution	$16 \times 16 \times 128$	Kernel size: 9×9
Batch Normalization	$16 \times 16 \times 128$	Batch normalization after the third convolution layer
Dropout	$16 \times 16 \times 128$	Dropout rate: 0.5
Max-Pooling	$8 \times 8 \times 128$	Pooling size: 2×2
Dense	$1 \times 1 \times \text{num_classes}$	Dense layer for binary/multi-class classification

the end, we added a dense layer for binary classification and multi-class classification. We utilized the subsequent parameters for the proposed model such as sqdm optimizer, learning rate $3e-4$, maximum epoch equals 10, minibatch size equals 64, and randomize the data at each epoch. All images of the dataset were reduced to 227×227 size for the SqueezeNet model. The detail of the proposed CP_DeepNet Layers is given in Table 2.

The proposed CP_DeepNet framework, based on the SqueezeNet model, establishes a clear advantage in terms of computational complexity when compared to the original model. We measured the computational complexity of our proposed CP_DeepNet model in terms of G-FLOPs, representing the capability of system to perform billions of floating-point operations per second, especially relevant for tasks involving extensive numerical calculations. Our research indicates that our proposed model exhibits a computational complexity ranging between 4 to 5 G-FLOPs, underscoring its efficiency and suitability for numerical computation-intensive tasks. This efficiency is attained through a thoughtfully designed architecture featuring fewer parameters, resulting in a more streamlined structure with reduced computational complexity. In practical terms, the proposed model processes information with fewer computational operations, leading to quicker inference times and lower resource requirements. Despite its enhanced computational efficiency, the framework maintains competitive or superior performance, as demonstrated by comparable accuracy and other key metrics. These qualities position the model as a promising solution for efficient and accurate COVID detection, particularly in scenarios with limited computing resources.

3.4.1 Convolutional layer

The convolutional layer is the primary component of any convolutional neural network. This layer is comprised of smaller-size filters and parameters. The proposed architecture

has applied one of these filters on the input images with a stride of 2. These filters are convolved with the input image for the creation of an activation map.

$$x_{ij}^l = \sum_{a=0}^{m-1} \sum_{b=0}^{m-1} w_{ab} y_{(i+a)(j+b)}^{l-1} \quad (1)$$

The above equation is the convolution, in which output x_{ij}^l is calculated by the sum up of all the previous weights and targeted values.

3.4.2 Batch normalization

Batch normalization is used for multiple purposes such as dealing with unstable gradients, faster model learning, and also addressing the overfitting problem. In batch normalization, we normalize all the outputs of all the layers of the proposed network.

$$x^* = \frac{x - E[x]}{\text{sqrt}(\text{var}(x))} \quad (2)$$

In the above equation, x^* denotes the new value, $E[x]$ denotes the means value of x with a batch, $(\text{var}(x))$ denotes the variance of x with a batch.

3.4.3 Dropout layer

The primary reason of the dropout layer is to avoid the model from overfitting by randomly dropping a few of the output neurons based on the dropout rate. The dropout rate is basically the probability ρ of any neuron being inactive in any training circle. The proposed model has utilized a dropout rate of 0.5 in the dropout layer.

3.4.4 Max pooling layer

Max-pooling layer also referred to as sub-sampling that is used for downsampling of the images and dimensionality reduction, which results in lowering overall costs and computational efforts. The output of a convolutional layer undergoes a max pooling operation, and it works by choosing the highest value within a set of contiguous input values.

4 Experimental results and discussions

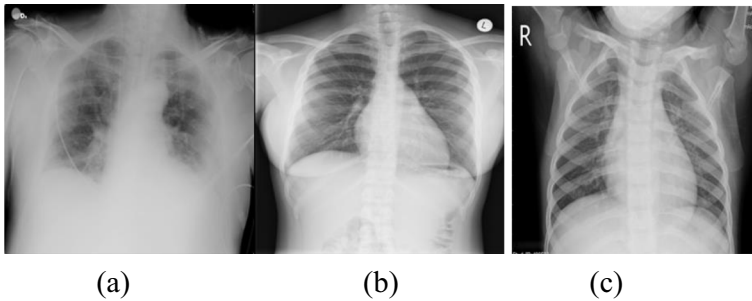
This segment provides an exposition regarding the experimental outcomes and assessment criteria employed in this research study to check the performance and significance of our proposed model in the identification of individuals afflicted by COVID-19 and pneumonia. We used four performance metrics for this purpose such as accuracy, recall, precision, and F1-score. The details are given as follows.

4.1 Dataset

In this work, we utilized the COVID-19 pulmonary X-rays dataset [20], which is freely accessible to everyone. Professionals from 4 countries of Asia and Middle-East

Table 3 Dataset Details Pre- and Post-Data Augmentation

Data Augmentation	COVID-19 images	Pneumonia images	Normal images
Before	500	500	500
After	3500	3500	3500

**Fig. 4** COVID-19 (a), Normal (b), and Pneumonia (c)

collaborated to create a novel database of chest x-ray images for pulmonary diseases, in which they collected patient data of three classes, such as, COVID-19, Pneumonia, and Normal classes. Initially, they published overall 2905 x-rays images, in which 219 chest X-ray (CXR) images depicted COVID-19 cases, 1341 showcased normal conditions, and 1345 featured instances of viral pneumonia. In the first revision, the instances of COVID-19 class were enlarged to the number of 1200 images. Currently, this database contains 3616 positive COVID-19 cases, in addition to 10,192 normal cases, and 1345 images illustrating viral pneumonia. The real size of images in the dataset was 299×299 , which was reduced to 227×227 in SqueezeNet model. In this study, we performed 2 distinct experiments to detect COVID-19, Pneumonia, and Normal cases. In 1st experiment, we utilized COVID-19 and Normal classes, whereas, we used all three classes of dataset in 2nd experiment, such as COVID-19, Pneumonia, and Normal. Table 3 provides the specifics of the datasets employed in this study, both pre- and post-data augmentation.

In Fig. 4, chest X-ray images for normal individuals, patients with COVID-19, and patients with pneumonia are depicted.

4.2 Performance of the proposed CP_DeepNet on Covid and normal

This experimentation is performed for assessing the efficacy of the developed framework for the identification of COVID-19 patients. All of these experiments were repeated 5 times and achieved similar results. In order to perform the experiments, we used an overall 1000 images from two classes of dataset. 500 images were part of the COVID-19 patient class, whereas the other 500 were of the normal people class. The data augmentation technique enlarged the dataset by 7 times. We randomly allocated 80% and 20% of the data for the training and testing sets, respectively. In our ablation study, we initiated the training of the SqueezeNet model on the provided dataset, yielding impressive accuracy and precision rates of 96.2% and 96.8%, respectively. Seeking optimization, we tailored

the architecture of model by incorporating three additional layers at the conclusion of its structure. Specifically, the notation "32×32×64" in the second convolutional layer of our proposed model signifies a feature map with spatial dimensions of 32×32 and 64 channels. Recognizing the task-specific nature of convolutional layer efficiency, we initially utilized a size of "64×64×64" in the second convolutional layer, observing minimal impact on results. Consequently, we conducted downsampling, reducing the spatial dimensions to "32×32," resulting in enhanced performance for the CP_DeepNet model. The refined model demonstrated outstanding metrics, boasting accuracy and precision of 99.32% and 100% respectively.

The detailed results of all the performance metrics are provided in Fig. 5. As depicted in Fig. 5, it is discernible that the tailored SqueezeNet obtained 99.32% accuracy, 100% precision, 99% recall, 99.2% specificity, 99.78% area under the curve, and 99.49% f1-score. These results validated that the proposed CP_DeepNet framework has the ability to identify COVID-19 patients efficiently. The tailored SqueezeNet can dependably be utilized for the identification of COVID-19 patients for obstructing rapid dissemination of the COVID-19 epidemic. The higher accuracy and precision of SqueezeNet demonstrate that the proposed framework can be used in healthcare and diagnostic center. The proposed framework also has low false-positive as compared to the conventional RT-PCR technique. These significant outcomes ensure the efficiency of developed framework for identification of COVID-19 patients.

4.3 Performance of the proposed CP_DeepNet on Covid, normal and pneumonia

The classification performance of the model can vary on the basis of the count of classes utilized in the dataset. In multiclass classification, the classification models are used to categorize the data into three or more classes. In this work, we have also performed multiclass classification to check the efficiency of the developed CP_DeepNet on multiclass datasets. We added another class of pneumonia patients to the Radiography [20] dataset. We employed the CP_DeepNet framework to classify 3 classes of dataset including COVID-19, pneumonia, and normal persons. In the multiclass dataset, the CP_DeepNet

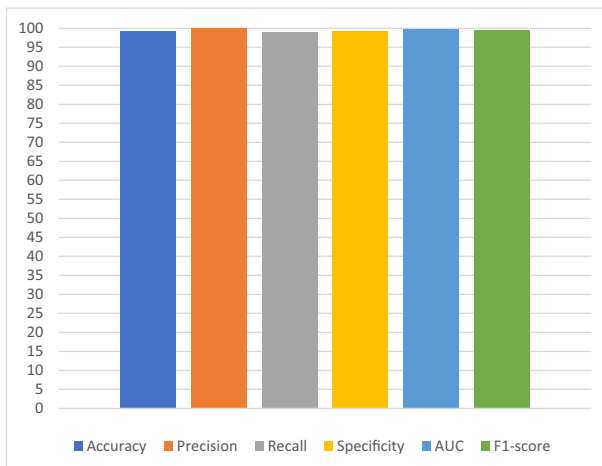


Fig. 5 Performance evaluation of CP_DeepNet on Covid and Normal

achieved the accuracy, precision, recall, specificity, area under the curve, and F1-score of 99.62%, 99.79%, 99.52%, 99.69%, 99.62%, and 99.72%, respectively. Details outcomes are shown in Fig. 6. These significant results indicate that CP_DeepNet model has the ability to identify both pneumonia and COVID-19 with higher accuracy and precision. Normally, CNN models perform better on binary classification problems, but their performance decreases on the multiclass dataset [22]. In contrast of that, the proposed CP_DeepNet model performed better on the multiclass dataset and achieved higher results as compared to the binary image data. Therefore, the proposed model has provide the advantage to identify multiple diseases including pneumonia and COVID-19, by utilizing a single framework with high accuracy an precision rates.

4.4 Error matrix analysis

An error matrix is created for evaluating the classification effectiveness of the proposed framework over the testing set of data. It gives a comprehensive overview of the classification outcomes predicted by the proposed framework. The number count of all accurate and erroneous forecasts is given by the error matrix. It provides the advantage of direct comparison of different prediction values such as True Positive, True Negative, False positive, and False Negative. Therefore, it is essential to calculate the error matrix, which provides a clear idea about the classification performance of the developed model.

In the proposed research, we also created an error matrix to evaluate the classification performance of the customized SqueezeNet model for the detection of COVID-19 individuals. As per the SqueezeNet confusion matrix, it becomes evident that the proposed framework misidentified 1 normal person as a COVID-19 patient, but it didn't misclassify any COVID-19 patients as normal. To be more precise, the proposed framework obtained a precision of 100% and a 99% recall rate as given in Table 4. Based on these results, the proposed framework has only a 1% false-positive rate without any false-negative rate, and the CP_DeepNet framework is very efficient and dependable for the identification of COVID-19 disease.

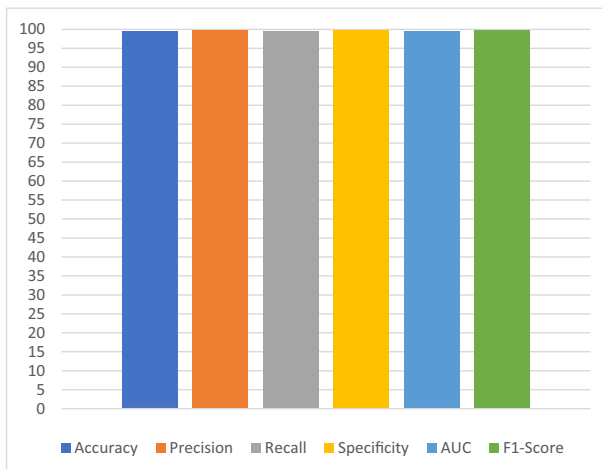


Fig. 6 Performance of CP_DeepNet on COVID-19, Normal, and Pneumonia

Table 4 Error Matrix of CP_DeepNet for 2 Classes

Predicted Class	Actual Class	
	Normal	Covid
Normal	99	0
Covid	1	100

Table 5 Confusion Matrix of CP_DeepNet for 3 Classes

Predicted Class	Actual Class		
	Normal	Covid	Pneumonia
Normal	99	0	0
Covid	1	100	0
Pneumonia	0	0	100

We have also created a error matrix for three classes of dataset named as Normal, Covid, and Pneumonia. The confusion matrix shows that the CP_DeepNet model has accurately classified both covid and pneumonia patients, but it misclassified only 1 normal person as covid patient as given in Table 5. The developed CP_DeepNet model obtained a precision of 99.79% and a recall of 99.52%. These outcomes show that the proposed CP_DeepNet model can be utilized for the accurate classification of multi-class dataset. Therefore, we can employ the proposed model to identify both Pneumonia and COVID-19 diseases.

4.5 Performance comparison with other methods

It has been reported that the CNN performance varies on binary classification and multi-class classification. The research community has developed frameworks for both binary classification of COVID-19 and normal persons, and also multiclass classification of COVID-19, pneumonia, and normal persons. To examine the significance of our developed system, we have compared it with other modern techniques developed for the identification of COVID-19. Table 6 provides comparison of the outcomes of CP_DeepNet model with the results of other modern methods [23–25] developed to detect COVID-19. From Table 6, It is evident from Zha. et al. [24] used the DenseNet121-FPN method and achieved the lowest results with 85% accuracy, 79.35% recall, 71.43% specificity, and 86%AUC. In [23], the author employed a pre-trained VGG-19 model for the multiclass categorization of COVID-19, pneumonia, and normal person. This model achieved 87.8% accuracy, which is 11.42% less than the three-class accuracy of the proposed model. The author trained the model on 202 videos and 59 images, and obtained accuracy, recall, and specificity of 87.8%, 88%, and 94% respectively. In [25], the author suggested a technique that accounts for the size of the infection for the binary classification of COVID-19 and normal persons and achieved an accuracy of 87.90%, which is 11.52% less than the accuracy of the proposed model. Shi F, et al. [25] employed Infection size-aware method on 2,685 images, and obtained 87.90% accuracy, 90.70% recall, 83.30% specificity, and 94.20% AUC. We also trained the baseline SqueezeNet model [19] on the same dataset provided utilized in this study, and it obtained accuracy of 96.24% and sensitivity of 96.8%. Whereas, our proposed CP_DeepNet performed best as compared to the other methods, and achieved. an accuracy of 99.32%, the precision of 100%, 99% recall, 99.2% specificity, 99.78% area under the

Table 6 Comparative Analysis of Performance with Other Approaches

Authors	Methods	Dataset Values	Accuracy	Recall	Specificity	AUC
Born, J., et al. [23]	VGG-19	202 videos and 59 images	87.8	88	94	–
Wang S, et al. [24]	DenseNet121-FPN	1,266 images	85	79.35	71.43	86
Xia F, et al. [25]	infection size-aware	2,685 images	87.90	90.70	83.30	94.20
Celik et al. [26]	CovidDWNet + GB	15,153 images but unbalanced (COVID-19 = 3616, Normal = 10,192, Pneumonia = 1345)	96.81	97	95.54	97.98
Ghafoor K. et al. [27]	Modified CNN + KNN	122 images	95.7	95.7	–	–
Sanghvi, H. et al. [22]	DenseNet-201	15,153 images but unbalanced (COVID-19 = 3616, Normal = 10,192, Pneumonia = 1345)	99.10	98.5	98.5	–
Londala et al. [19]	Baseline SqueezeNet	10,500 images and balanced dataset	96.24	96.8	–	–
In this study	CP_DeepNet	10,500 images and balanced dataset	99.62	99.52	99.69	99.62

curve, and 99.49% F1-score. From the above analysis, we can conclude that our proposed CP_DeepNet framework has superior performance unlike alternative techniques, and it can be employed for identifying COVID-19 disease.

5 Conclusion

In this paper, we developed a novel deep-learning framework for the identification of COVID-19 using an X-ray image dataset. The developed CP_DeepNet is a trustworthy COVID-19 detection framework, that has the ability to identify COVID-19 patients with better precision and accuracy. We utilized the COVID-19 chest Radiography dataset, which is comprised of 3 classes such as COVID-19 individuals, pneumonia individuals, and normal persons. Moreover, we employed a customized SqueezeNet model and achieved 99.32% accuracy, 100% precision, 99% recall, 99.2% specificity, 99.78% AUC, and 99.49% f1-score. We also used CP_DeepNet for multiclass classification of COVID-19, pneumonia, and normal persons, which obtained accuracy, precision, recall, specificity, area under curve, and F1-score of 99.62%, 99.79%, 99.52%, 99.69, 99.62, and 99.72%, respectively. We also performed a comparison with other modern techniques, which manifested the dominance and efficiency of the suggested framework for the automatic identification of COVID-19 using X-ray images. From the above analysis, we conclude that our proposed framework shows excellent results and is dependable to be used in healthcare and COVID-19 diagnostic labs. In the future, we are determined to collect an extensive COVID-19 patient dataset, the number of fatalities, and recoveries in different territories. We also strive to employ the developed model in a higher number of classes of datasets.

6 Limitations

In this study, we have introduced an innovative deep learning methodology for detecting COVID-19 and pneumonia, integrating advanced pre-processing methods and data augmentation to enhance the capacity of CP_DeepNet model to learn distinctive features from medical images. While these methodologies contribute to the robustness of model and generalization capability, it is imperative to acknowledge the absence of cross-validation as a notable limitation in the experimental design. Cross-validation is a standard practice in machine learning model evaluation, offering a comprehensive assessment of the performance of model across different subsets of the dataset. The exclusion of cross-validation in this study represents a limitation, as it overlooks the systematic evaluation of model generalization to unseen data and the potential impact of data variability on performance. Future research endeavors should consider integrating cross-validation methodologies to support the reliability and robustness of the proposed approach, ensuring consistent evaluation of the effectiveness of model across diverse patient populations and imaging conditions.

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Authors and Affiliations

Muhammad Hamza Mehmood¹ · Farman Hassan²  · Auliya Ur Rahman³ · Wasiat Khan⁴ · Samih M. Mostafa⁵ · Yazeed Yasin Ghadi⁶ · Abdulmohsen Algarni⁷ · Mudasser Ali⁸

✉ Farman Hassan
farman.hassan@studio.unibo.it

¹ School of Computer Science and Technology, University of Science and Technology of China, Hefei, China

² University of Bologna, Bologna, Italy

³ UET Peshawar, KPK, Peshawar, Pakistan

⁴ UST Bannu, KPK, Bannu, Pakistan

⁵ Computer Science Department, Faculty of Computers and Information, South Valley University, Qena 83523, Egypt

⁶ Department of Computer Science, Al Ain University, Al Ain, UAE

⁷ Department of Computer Science, King Khalid University, 61421 Abha, Saudi Arabia

⁸ Arid University, Punjab, Pakistan