

Convolutional Neural Networks with Particle Swarm Optimization: A Reliable Method for SARS-CoV-2 Detection in X-Ray Images

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Abstract—The coronavirus pandemic, commonly known as COVID-19, set free in Wuhan, China, has travelled globally. This pandemic is quickly spreading all around the world with physical contact and air. The first step to prevent its spread is accurately diagnosing the presence of disease in patients. A much faster and time-saving real-time method of diagnosing this disease is required as traditional methods, including Reverse Transcription Polymerase Reaction, are inefficient and defective. To start, we would gather and organize image data through data synthesis. After the initial step, we would train the proposed 2D-CNN, known as the 2 Dimension Convolutional Neural Network model and test it accordingly. To do this, the image data will be divided into three syndicates, each containing several photos for training, testing, and validation. The features are then classified using the Particle Swarm Optimization (PSO) technique and smoothed using Principle Component Analysis. A data support vector machine (SVM) is employed to classify picture data further. This method delivers the results required to diagnose the illness in several datasets.

Keywords: 2D-Convolutional Neural Network, Swarm Optimization, Coronavirus, Principle Component Analysis, Support Vector Machine.

I. INTRODUCTION

Several persons in China's Guangdong province contracted a severe acute respiratory syndrome virus in February 2013. Eventually, SARS was found in 8000 individuals across 26 countries, and 774 SARS-related deaths were documented by the World Health Organization (WHO). A similar incident involving the Middle East respiratory syndrome virus occurred in September 2012. MERS-CoV was found in 2494 confirmed cases of illness and 858 fatalities. SARS and MERS are less significant than the most recent CoV outbreak regarding human health. Pneumonia-like illnesses with un-

known causes began to appear in Wuhan, China, in November 2019, killing hundreds of people in the first few weeks. The International Committee on the Taxonomy of Viruses designated the SARS-CoV-2 virus as the cause of Coronavirus Disease 2019 (COVID-19) in the early months of 2020. (ICTV). Coronavirus, a serious respiratory illness that spreads when an infected person coughs or sneezes, is beginning to spread in Wuhan, the capital city of China's Hubei province. Common coronavirus symptoms include cough, sore throat, fever, exhaustion, and shortness of breath.

According to a study [1], the basic cause of COVID-19 spread is physical contact and via air through droplets coming out of the mouth during breathing; thus, the primary task in preventing disease spread is to identify people infected with the virus, isolate them, and thus break the virus's spreading chain. A common laboratory test used to identify the coronavirus is the WHO-recommended reverse transcription polymerase chain reaction (RT-PCR) (WHO). However, the RT-PCR test is unreliable, and its results are time-consuming; it takes two days, and during those two days, the patient can be a source of disease propagation. When a person's test results are awaited, he may spread the virus since he is unsure of the outcome, increasing the chance of disease transmission. As a result, a more rapid and dependable method of COVID-19 detection is necessary to replace standard RT-PCR. Until an appropriate medicine is developed, the only option to control the pandemic is to isolate the individual who is ill and provide him with proper medication so that he can recover in isolation.

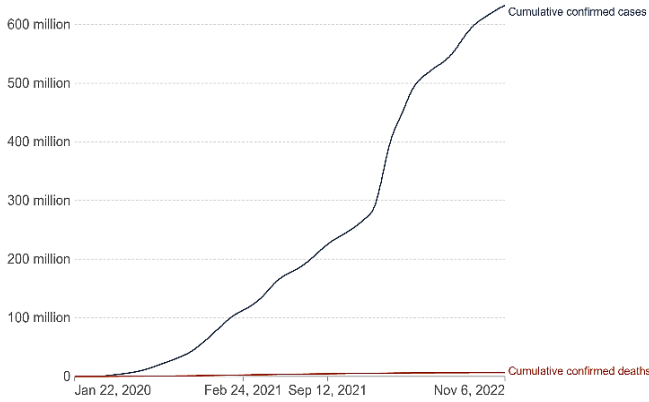


Fig. 1. Corona Virus Cases vs Death Rate

The Pandemic affected millions of people across the world. The COVID-19 pandemic has affected the entire world, with over 113.13 Million people and 2.50 Million fatalities so far (as per reports of 25th February 2021). According to the death rate in western countries and Europe, countries are more than compared to other countries. The mortality rate of coronavirus across the world is approx. 2%. The death rate in western countries is comparatively high, especially in America, Brazil and European countries. Out of 2.5 million casualties, 0.5 million people died in America, which is very alarming, especially for developed countries like America and Brazil. Isolation / Quarantine and taking care of patients are key to being safe from this pandemic disease. China has overcome and stopped the spreading of coronavirus by lockdown and social distancing, especially by isolating suspicious patients. This disease is dangerous because it is easily transmissible by contacting the affected people. COVID-19 is a dangerous disease for mostly those with diabetes, heart disease, lung disease and kidney/liver disease and also people who do not have a good immune system to fight against this pandemic disease. Many countries have imposed border restrictions, flight restrictions, social distancing and awareness programs for social distancing and forced lockdowns to prevent the spreading of coronavirus and decrease the rate of positive patients.

Main Contributions

A brief summary of our research is as follows: we would propose a method which can replace the inefficient RT-PCR test worldwide.

This paper proposes using the 2-D CNN method for feature extraction and using data pre-processing to arrange the data by grouping/clustering data that will help further diagnose the disease in several clusters of data. Then features are chosen by using Particle Swarm Optimization and other analysis approaches. To detect a disease from a large set of data, Support Vector Machine (SVM) is further used for classification. In compari-

son to the RT-PCR test, this method enforces effective and accurate results to detect the disease quickly.

To determine the relative effectiveness of this approach, the accuracy rates of genetic research and particle swarm optimization are compared to those of the earlier experiments. Our study would also concentrate on the proper model evaluation through dataset organization, using various techniques to arrange and correlate data to assess the accuracy of both the test and hybrid models.

II. LITERATURE REVIEW

To deal with epidemic disease, the researchers [3] have designed many techniques to detect for COVID-19 to get a better system. We have reviewed some of the systems to detect COVID-19 through X-Ray images. Early detection of COVID-19 through CT scan images using Harmony Search and Otsu threshold method. The region of interest is extracted from binary images to check the level of infection or disease. The CNN technique with VGG19 for image modalities and classification uses X-Ray, Ultrasound and CT-scan images. To deal with the challenge, the datasets [4] available for COVID-19 are used for pre-processing to test and develop deep learning techniques. Deep learning technology is used in healthcare applications, i.e., lung classification and thyroid diagnosis. Deep learning can also be used to diagnose the COVID-19 pandemic to reduce the spreading of COVID-19 worldwide. Deep architecture, also called COVID-Net model [5], is designed to detect COVID-19 with utmost taxonomy. In this method, the two datasets, which include positive COVID-19/pneumonia confirmed and normal X-Ray images, are used to identify the COVID-19 detected patients using deep learning techniques, i.e. CNN model for classification. This tested model gives results with an accuracy of up to 96.78%. In binary classification, this process has an accuracy of 98.08%, and in multi-class classification, it has an accuracy of 87.02%. In this method, feature extraction is done using a combined neural network, and disease detection from X-ray pictures is done using a long short-term memory (LSTM). The method uses deep neural networks [6] to detect coronavirus from X-Ray images. CNN is used to extract features, and SVM is an approach which classifies the virus-affected x-ray image. This method first uses pre-trained models for feature extraction. Then it uses SVM to classify and detect the virus from extracted features' x-ray images and give results with an accuracy of 95.38%. This tested model gives results by using ResNet50 with an SVM classifier. Using radiological images, i.e. X-Ray images, the coronavirus is detected using CNN and LSTM models and the Residual attention network approach; the accuracy for testing of COVID-19 is 98%. The model is designed using Residual Attention Network with feature extraction by using various models, i.e. VGG, mobilNET, and DenseNET.

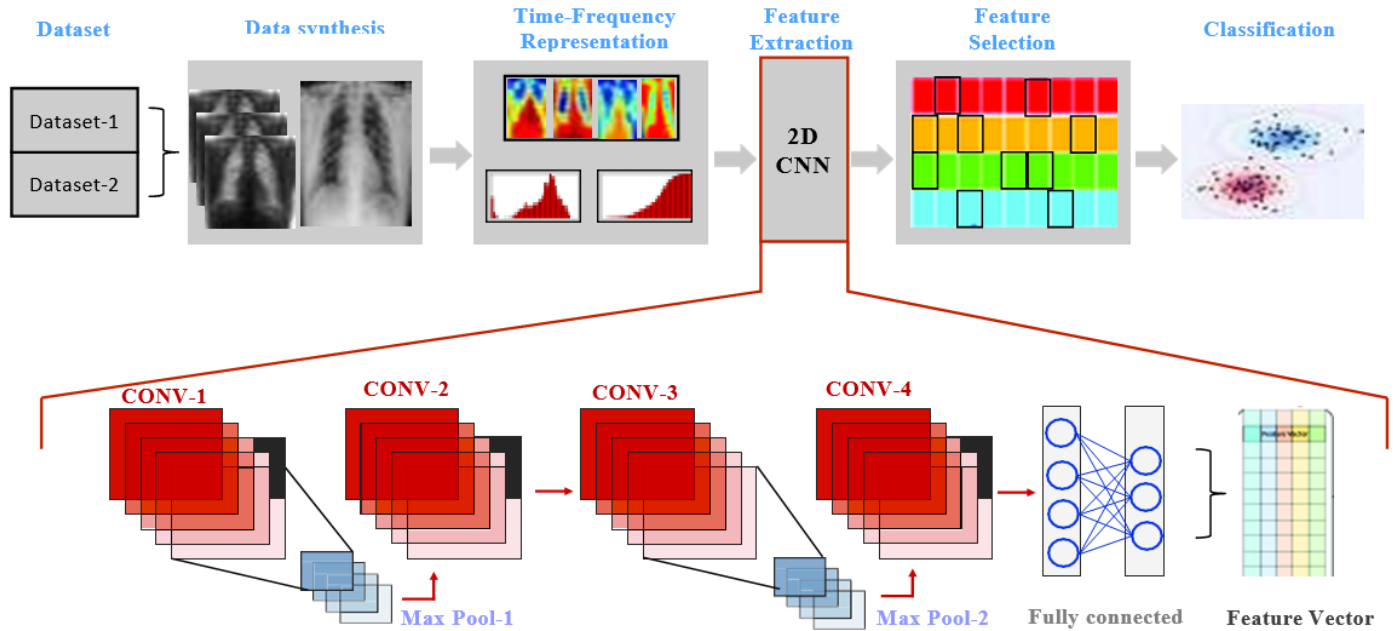


Figure 2. Framework that is suggested and 2D-CNN architecture

Using the convolutional CapsNet approach [1] to diagnose COVID-19 utilizing X-Ray pictures and capsule networks is suggested. The suggested method is used to identify coronavirus using binary classification (COVID-19 vs Not detected) and multiclass classification, with an accuracy of 97.24% for binary classification and 84.22% for multiclass classification (COVID-19 vs No disease found vs Pneumonia).

III. MATERIALS AND METHODS

A. Data Synthesis

Our work includes a critical process known as data synthesis. This task acts as a continual flow of information from the neural network. To begin, the dataset is partitioned and pre-processed to fit the model. This involves scaling, cropping, increasing quality, reducing noise, segmentation, and presenting the photos. The significance of this procedure is that raw photos can have a significant impact on biomedical image processing. One potential concern is that producers may "fabricate" the material to trick the discriminator into thinking their data belongs to the desired distribution. Any incorrect measurements are removed before image processing begins to avoid inaccuracies that could lead to misclassification.

B. Time-Frequency Representation that is Not Separatable

The Non-separable Wavelet Transform (nSWT) [10] converts an image into a two-dimensional time-frequency spectrogram. This technique is frequently used in medical imaging to detect minor differences in pictures, identify changes in an X-ray image, and transform it into a spectral image. The X-ray image, initially in raw form,

is first divided into a series of features created from the primary (prototype) wavelet utilizing dilation and translation properties. The image is then analyzed using the Separable Wavelet Transform (SWT) with a manifold resolution scale factor, resulting in greater dimensions [10]. We use a non-focused filter and a non-separable wavelet transform (nSWT) with an unseparated sample (low resolution) to reduce the image to a single resolution. This transformation creates an picture with low resolution and a non-directional wavelet sub-image. The image is transformed for binary channel output using the equation below. Figure 3 depicts the spectrogram of the non-separable transform.

C. Feature Extraction

A 2D convolutional neural network is used to extract features in our suggested method (CNN). CNN is a widely utilised biomedical and machine learning method, allowing scientists and researchers to perform rapid recognition and categorization. CNN is an artificial intelligence technology for automatically identifying objects. In this study, we create a 2D CNN model with X-ray training data and testing data. The CNN receives the TFR images from the nSWT. The CNN model is then tested on a new dataset. We have validated our suggested model with GoogleNet and EfficientNet. The multi-layered neural network with 12 layers for feature extraction comprises four convolutional layers, two max-pooling layers, two dropouts, and two fully connected layers. Table I shows all the parameters, including the output image size for each layer. This network's input layer is equipped with a 224x224 input map. Fig 2 depicts the general tiered organization of a 2D Convolutional Neural Network. To prevent overfitting, the output vector (features data) contains 1000 attributes with a 50% exclusion layer for each layer. As a result, the final feature vector is 930x1000.

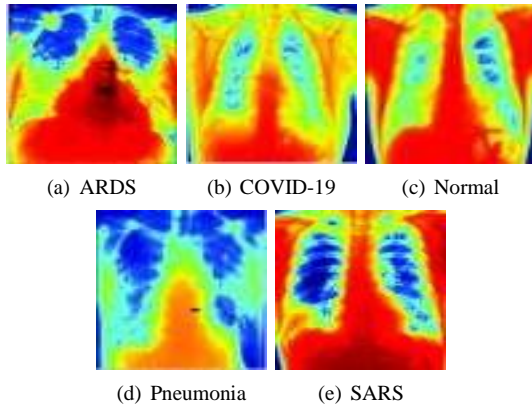


Fig. 3. Different X-ray Images Represented by Time-Frequency [1]

TABLE I
PROPOSED 2D-CNN MODEL LAYER PARAMETERS

Layer	Name	Size	Kernel	Parameter	Stride
Layer1	Input	224×224	-	-	1
Layer2	Conv-1	32×128	3	576	2
Layer3	MaxPool-1	-	-	-	1
Layer4	Conv-2	32×128	128	73,728	2
Layer5	Conv-3	64×64	128	294,192	1
Layer6	MaxPool-2	-	-	-	2
Layer7	Conv-4	16×16	512	1,179,648	1
Layer8	FC-1	1000	1000	2,097,152	-
Layer9	Dropout-1	-	50%	-	-
Layer10	FC-2	1000	1000	1,362,712	-
Layer11	Dropout-2	-	50%	-	-
Layer12	Output	1×1000	-	42,000	-

D. Selection and Reduction of Features

1) *Particle Swarm Optimization (PSO)*: This technique performs intelligent function grouping [12]. Jams Kennedy developed PSO in 1995, and [13] offered an upgraded binary PSO (iB-PSO) used for cancer staging. In our paper, we apply PSO in a similar mode to classify COVID-19. PSO is used to lower the size/dimensions of the output by selecting higher-quality and less computationally intensive functions. PSO is an algorithm for collective intelligent search. This search is carried out using a set of randomly generated probable solutions. A swarm is a collection of potential solutions; each potential solution is referred to as a particle. The function's quality is dictated by the particles' social and cognitive learning rates. These velocities are used to assess the function's quality. As a result, the rest of the feature values are ignored, yielding a low-size dimensional feature vector.

2) *Principle Component Analysis (PCA)*: While the Particle Swarm Optimization (PSO) method intelligently clusters functions, the Principal Component Analysis (PCA) [14] technique is used to smooth and minimize characteristics. A sequence of data collected for a correlation variable, such as one with fluctuating numerical values, is transformed into a collection of mono values, which are non-correlated variables, through the analytical process known as PCA. The term "main components" refers to these values. The goal of this

conversion is to increase the likelihood that the limit will change with each succeeding component. Therefore, the key component that was found first would have the most probability of altering. A resulting vector, or set of non-correlated or orthogonal criteria, is what this method produces. Furthermore, the PCA method is sensitive to the initial input variable's magnitude.

E. Classification

1) *Linear Support Vector Machine (LSVM)*: A support vector machine (SVM) classifier with linear kernel functions is used in this classification approach [15]. LSVM is more effective when the number of classes is limited, like in our class 3 and 5 data. The LSVM classifier works well with the 2D CNN functions. Because fewer calculations are required, the selected feature vector may be detected quickly. The classifier's results outperform the usual COVID-19 detection technique.

2) *k-Nearest Neighbor (k-NN)*: The second classifier employed in our work for COVID-19 classification is the k-Nearest Neighbor (k-NN) method [15]. Similar to how SVM uses a linear kernel to classify data, k-NN does the same. The distance between the feature values of each class is calculated using the selected features, and the feature value establishes the feature class. Figure 5 displays the k-NN classifier's classification performance. At k=2, classification performance is at its best.

3) *Naive Bayes*: A Naive Bayes classification [16] is a strategy that integrates numerous predictive models to build a new one. Many names know Bayes models, e.g. simple Bayes, naïve Bayes and independent Bayes. It is extensively employed in machine learning models for pattern identification. It employs a probability-based ranking to determine the most powerful assumptions of dependency between attribute values. In our work, we validated the proposed strategy using a set and obtained better results than a single model.

IV. EXPERIMENTS AND RESULTS

A. Dataset

Datasets Da-taset-1 and Dataset-2 from Kaggle [17] are the publicly accessible datasets used in this research. Approximately 6,000 radiographs of healthy volunteers, patients with bacterial pneumonia, and patients with viral pneumonia are included in Dataset-1. The photos are divided 80/20 into training, testing, and validation folders, with dataset class subfolders. The three categories of pneumonia in Dataset-1 are typical bacterial pneumonia, viral pneumonia, and mixed pneumonia. 930 5-degree radiographs of patients with Covid19, SARS, typical pneumonia, and ARDS are included in Dataset 2. Unlike the RT-PCR test, both data sets are recognized or labelled initially.

TABLE II
PERFORMANCE METRICS USING VARIOUS MODELS

Model	Feature Dimension	Sensitivity	Parameters	No of Layers	F-1 score	Training time	Recall
AlexNet	930 × 4096	0.89	61M	8	0.90	22.08	0.81
2D-CNN (Proposed)	930 × 1000	0.92	42K	12	0.99	3.41	0.84
2D-CNN-PSO (Proposed)	618 × 1000	0.92	42K	12	0.91	2.82	0.87
GoogleNet	930 × 4096	0.83	7M	22	0.86	12.64	0.79
2D-CNN PSO PCA (Proposed)	250 × 412	0.92	42K	12	0.98	1.30	0.88

B. Network Modeling and Training

The suggested 2D CNN model is trained on a device with an AMD GTX 1080 graphics processing unit using Windows 10. Network formation time is sped up through feature selection and reduction. Thus, the selected feature can perform learning processing using a straightforward corei3 procedure. The suggested network's error rate during validation is shown in Figure 4. It has been shown that the error decreases as the number of epochs increases.

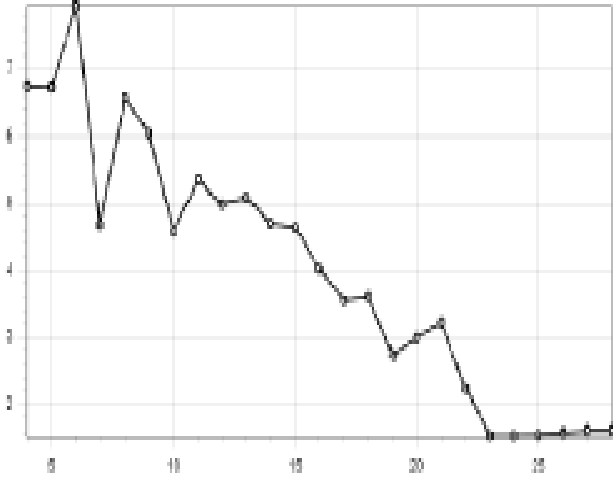


Fig. 4. Testing Error Rate of 2D-CNN

C. Classification Performance

1) *Evaluation Metrics*: To prevent the over-fitting issue, the dataset is partitioned into M randomly chosen portions, each of equal volume. The technique is tested on the remaining part after training on M-1 pieces. The total metric is determined by adding up the measurements from M training cycles. The effectiveness of the training dataset and the training times obtained through cross-validation are shown in Table II.

Using a confusion matrix, we calculated precision, accuracy, recall, specificity and f1-score. The above parameters are computed using the keywords listed below. We calculate the above parameters using the keywords listed below

$K_{positive}$ means disease is predictable and is present.

$P_{positive}$ means disease is predictable and is not present.

$K_{negative}$ means disease is not predictable and is not present.

$P_{negative}$ means disease is not predictable and is present.

The accuracy of the training set is given by

$$Acc = \frac{K_{negative} + K_{positive}}{negative + positive}$$

The precision of the training set is given by

$$Prec = \frac{K_{positive}}{F_{positive} + T_{positive}}$$

Specificity is taken from

$$Spec = \frac{K_{negative}}{K_{positive} + K_{negative}}$$

Recall of the training set is estimated by

$$Recall = \frac{K_{positive}}{P_{negative} + K_{positive}}$$

f1-score is provided by

$$f1\text{-score} = 2 \times \frac{Prec \times Recall}{Prec + Recall}$$

The parameters above can be used to assess the model's performance. LSVM, NB and k-NN perform grouping by cross-examining the extracted features' results with characteristics from already proposed groupings and classification techniques, primarily using cross-validation because it is highly dependable.

D. Comparison with the existing method

To confirm the validity of our proposed network, we compare it to existing COVID-19 detection techniques and a trained neural network for benchmarking and validation. As shown in table II, our proposed feature selection combined with the CNN method for identifying COVID-19 surpasses recent corona detection methods. When comparing the proposed method to a pre-trained neural network, namely the AlexNet image classification algorithm, it is discovered that GoogleNet, which has the ability of training a large - scale dataset and is capable of grouping images into 1000 objects, provides us with the accuracy shown in table II.

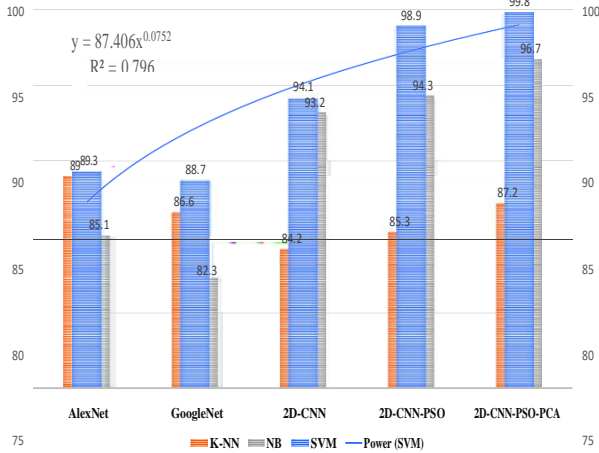


Fig. 5. Classification Performance

TABLE III

COMPARISON WITH RECENT COVID-19 DETECTION METHODS

Technique	Classification	Accuracy %
Binary Classification [3]	DNN	87.02
LSTM [4]	CNN	99.4
Transfer Learning [5]	CNN	96.78
Convolutional CapsNet [6]	NANN	95.38
ResNet50 [8]	DNN	95.33
2D-CNN-PSO-PCA [Proposed]	SVM	99.80

Different techniques are used with different classification methods for detecting the coronavirus in the body using X-rays images. The accuracies of the models are shown in table III

V. CONCLUSION

The WHO RT-PCR test for detection is time-consuming and unreliable, therefore, a faster and more suitable substitute for particle swarm optimization is one technique for collecting and detecting data with the help of genetic research. As the recent Corona Virus (COVID-19) epidemic is causing alarm worldwide owing to its rapid spread, the only way to manage the pandemic until a solution is discovered is to segregate those who have the sickness. This study proposes a more accurate and efficient COVID-19 diagnosis than already in use methods. The data is grouped, extracted, and put into the precise model chosen; the model is evaluated, tested, and confirmed using three separate sets of data before being used for feature selection utilizing PSO methods. This data is analysed by classification, using SVM and ensemble. In contrast to the RT-PCR test, which can take up to two days and raises the risk of disease transmission and infection among health-care workers, this process is extremely trustworthy and has a 99.80% overall accuracy.

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