Project Report

on

Covid-19 Prediction using X-ray Images

Submitted in partial fulfillment of the

requirement for the award of the degree of

B. tech In Computer Science

Under The Supervision of
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Submitted By

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INDIA
MONTH, YEAR

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CANDIDATE'S DECLARATION

I/We hereby certify that the work which is being presented in the project, entitled **"COVID-19 PREDICTION USING XRAY IMAGES"** in partial fulfillment of the requirements for the award of the Bachelor of technology in computer science and engineering specialization in Computer Networks and Cyber Security submitted in the School of Computing Science and Engineering of Galgotias University, Greater Noida, is an original work carried out during the period of July,2021 to July,2022 under the supervision of Hradesh Kumar Assistant Professor, Department of Computer Science and Engineering of School of Computing Science and Engineering , Galgotias University, Greater Noida

The matter presented in the project has not been submitted by us for the award of any other degree of this or any other places.

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This is to certify that the above statement made by the candidates is correct to the best of my knowledge.

Hradesh Kumar
Assistant Professor

CERTIFICATE

The Final Project Viva-Voce examination of Suyash Sharma 18SCSE1140053, Malaika Rastogi 18SCSE1140045, has been held on _____ and his/her work is recommended for the award of Bachelor of technology in computer science and engineering specialization in Computer Networks and Cyber Security

Signature of Examiner(s) **Signature of Supervisor(s)**

Signature of Project Coordinator **Signature of Dean**

Date: December, 2021
Place: Greater Noida

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I am also grateful to the Reviewer: DR. NITIN MISHRA

Thanks for all your encouragement!

Abstract

This is a Web Application build using '***flask',*** a python framework. This project **mainly focuses to integrate a Convolutional Neural Network Model (CNN) in a web application**. Project includes training and evaluating a Convolutional type Neural Network to identify Covid-19 positive patients using X-Ray images. For the implementation Python programming language used with TensorFlow Keras and OpenCV modules.

Our goal is to use the X-ray images to develop AI based approaches to predict and understand the infection. The tasks are as follows using chest X-ray or CT (preference for X-ray) as input to predict these tasks:

- Healthy vs Pneumonia
- Prognostic/severity predictions (survival, need for intubation, need for supplemental oxygen)

The exponential increase in COVID-19 patients is overwhelming healthcare systems across the world. With limited testing kits, it is impossible for every patient with respiratory illness to be tested using conventional techniques (RT-PCR). The tests also have long turn-around time, and limited sensitivity. Detecting possible COVID-19 infections on Chest X-Ray may help quarantine high risk patients while test results are awaited. X-Ray machines are already available in most healthcare systems, and with most modern X-Ray systems already digitized, there is no transportation time involved for the samples either. In this work we propose the use of chest X-Ray to prioritize the selection of patients for further RT-PCR testing. This may be useful in an inpatient setting where the present systems are struggling to decide whether to keep the patient in the ward along with other patients or isolate them in COVID-19 areas. It would also help in identifying patients with high likelihood of COVID with a false negative RT-PCR who would need repeat testing. Further, we propose the use of modern AI techniques to detect the COVID-19 patients using X-Ray images in an automated manner, particularly in settings where radiologists are not available, and help make the proposed testing technology scalable.

Contents

List of Table

Acronyms

B.Tech.	Bachelor of Technology
M.Tech.	Master of Technology
BCA	Bachelor of Computer Applications
MCA	Master of Computer Applications
B.Sc. (CS)	Bachelor of Science in Computer Science
M.Sc. (CS)	Master of Science in Computer Science
SCSE	School of Computing Science and Engineering

CHAPTER-1 Introduction

The sudden spike in the number of patients with COVID-19 , a new respiratory virus, has put unprecedented load over healthcare systems across the world. In many countries, the healthcare systems have already been overwhelmed. There are limited kits for diagnosis, limited hospital beds for admission of such patients, limited personal protective equipment (PPE) for healthcare personnel and limited ventilators. It is thus important to differentiate which patients with severe acute respiratory illness (SARI) could have COVID-19 infection in order to efficiently utilize the limited resources. In this work we propose the use of chest X-Ray to detect COVID-19 infection in the patients exhibiting symptoms of SARI. Using our tool one can classify a given X-Ray in one of the four classes: normal, bacterial pneumonia, viral pneumonia, and covid pneumonia. The use of X-Ray has several advantages over conventional diagnostic tests:

1. X-Ray imaging is much more widespread and cost effective than the conventional diagnostic tests.
2. Transfer of digital X-Ray images does not require any transportation from point of acquisition to the point of analysis, thus making the diagnostic process extremely quick.
3. Unlike CT Scans, portable X-Ray machines also enable testing within an isolation ward itself, hence reducing the requirement of additional Personal Protective Equipment (PPE), an extremely scarce and valuable resource in this scenario. It also reduces the risk of hospital acquired infection for the patients.

The main contribution of this work is in proposing a novel deep neural network based model for highly accurate detection of COVID-19 infection from the chest X-Ray images of the patients. Radiographs in the current setting are in most cases interpreted by non-radiologists. Further, given the novelty of the virus, many of the radiologists themselves may not be familiar with all the nuances of the infection, and may be lacking in the adequate expertise to make highly accurate diagnosis. Therefore this automated tool can serve as a guide for those in the forefront of this analysis. We would like to re-emphasize that we are not proposing the use of the proposed model as alternative to the conventional diagnostic tests for COVID19 infection, but as a triage tool to determine the suitability of a patient with SARI to undergo the test for COVID-19 infection. To help accelerate the research in this area, we are releasing our training code and trained models publicly for open access at https://github.com/ arpanmangal/CovidAID. However, we note that both the model and this report merely captures our current understanding of this rapidly evolving problem, that too on very limited data currently available. We will keep updating the model and this report as we get newer understanding and better results**.**

Corona Virus Statistics

SARS-CoV-2 is a new family of viruses that has never been encountered before. The virus was first discovered in pangolins before its spread to humans [55]. The typical symptoms of COVID-19 include fever, dry cough, fatigue, sputum production, shortness of breath, sore throat, headache, chills, nausea or vomiting, nasal congestion, diarrhoea, haemoptysis, and conjunctival discomfort, although some patients also suffer from general tiredness, runny nose, and loss of taste and/or scent. Figure below shows a bar graph of the common COVID-19 symptoms sorted by their percentage of occurrences.

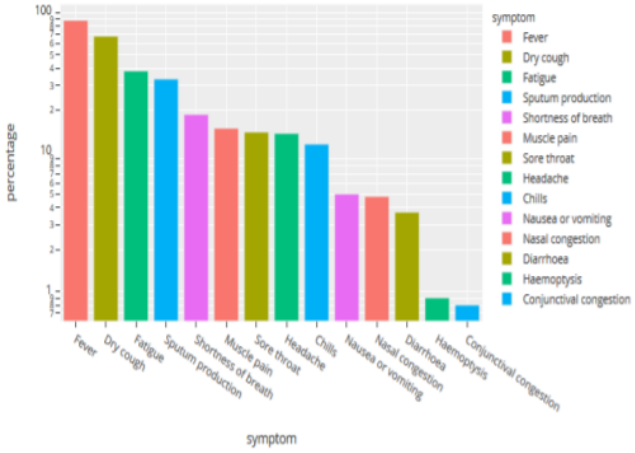


Fig: Common COVID-19 symptoms

In this section, the connection between coastal and noncoastal areas is further explored as a large proportion of infected cases were recorded in coastal areas. On the basis of the collected statistics, COVID-19 has a rapid spread in coastal areas. The following examples support this conclusion: *f*
In Australia, there were more than 7000 confirmed cases. The highest number of confirmed cases were in New South Wales, Victoria, Queensland, Western Australia, South Australia, Tasmania, and Australian Capital Territory and Northern Territory [57]. Figure 3 reveals the most affected areas in Australia

Fig: Areas with the highest number of confirmed cases in Australia

In South Korea, the disease peaked on 20 January 2020, and the number of confirmed cases exceeded 11,000. Figure below shows that the regions that were most severely affected by COVID-19 were coastal or near-coastal areas.

Fig: Areas with the highest number of confirmed cases in South Korea

In India, the number of reported confirmed cases was more than 158,000, and the most-affected places were Maharashtra, Tamil Nadu, Delhi, Gujarat, Rajasthan, Madhya Pradesh, Uttar Pradesh.

Fig: Areas with the highest number of confirmed cases in India

CHAPTER-1.1 Formulation Problem

We aim to classify a given frontal-view chest X-Ray image into the following classes: Normal, Bacterial Pneumonia, Viral Pneumonia and COVID-19. We have trained our model in two configurations, the one which classifies into the above four classes, and the other configuration with three classes (clubbing viral and bacterial pneumonia into one). The motivation behind the four class configuration is to better understand if any confusion between regular pneumonia and COVID-19 is due to the similarity of pathology between COVID-19 and viral pneumonia. Similar to CheXNet [7], we treat each class as a binary classification problem, with input as a frontal-view chest X-Ray image X and output being a binary

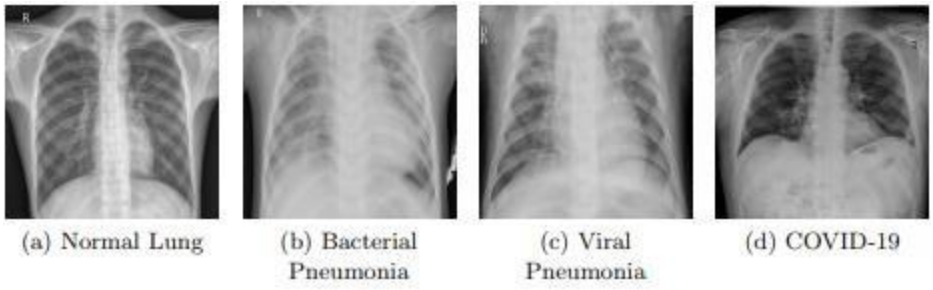


Fig. 1: Class-wise examples of frontal-view chest X-Ray images. The patient with bacterial pneumonia shows consolidation of the right lower lobe. Radiograph of a patient with viral pneumonia shows patchy consolidation in the right middle and lower zone. The last image from a patient with COVID pneumonia shows patchy ground glass opacity in the Left Lower Zone labels yc ∈ {0, 1}, indicating absence or presence of class c symptoms in the image respectively. We use the weighted binary cross-entropy loss as suggested by CheXNet [7]:

labels $y_c \in \{0, 1\}$, indicating absence or presence of class c symptoms in the image respectively. We use the weighted binary cross-entropy loss as suggested by CheXNet [7]:

$$\mathcal{L}(X, y; \theta) = \sum_{c=1}^{C} \left(-w_c^+ \mathbb{1}\{y = c\} \log p_c(\hat{y} = 1 \mid X; \theta) \right.$$
$$\left. - w_c^- \mathbb{1}\{y \neq c\} \log p_c(\hat{y} = 0 \mid X; \theta) \right). \quad (1)$$

Here, C is the number of classes and y is the ground truth for X. pc(ˆy = 1 | X; θ) and pc(ˆy = 0 | X; θ) are the probability scores for X being and not being in class c, respectively, as assigned by the network based on network weights θ. The two terms are weighted by w + c = Nc/(Nc+Pc)and w − c = Pc/(Nc+Pc), where Pc and Nc are the number of positive and negative samples of class c, respectively in the training set.

CHAPTER-1.2 Tools Required

- PYTHON
- Flask
- KERAS : PYTHON DEEP LEARNING API
- TENSOR FLOW:BACKEND

CHAPTER 2 Literature Review

- **Pneumonia detection in Chest X-Rays** Various deep learning based approaches have been developed to identify different thoracic diseases, including pneumonia [7, 8, 11, 13]. We choose CheXNet [7] to build upon, which could detect pneumonia from chest X-Rays at a level exceeding practicing radiologists. CheXNet is trained on ChestX-ray14 [11] (the largest publicly available chest X-ray dataset), gives better performance than previous approaches [11, 13], and has a simpler architecture than later approaches [8]. CheXNet [7] is a 121-layer Dense Net [3] based model trained on the ChestXray14 [11] dataset comprising of 112,120 frontal-view chest X-Ray images. The model is trained to classify X-Ray images into 14 different thoracic disease classes, including pneumonia. Given the visual similarity of the input samples, we found this to be the closest pre-trained backbone to develop a model for identifying COVID-19 pneumonia.

- **COVID-19 detection in Chest X-Rays** Since the recent sudden surge of COVID-19 infections across the world, many alternative screening approaches have been developed to identify suspected cases of COVID-19. However there are only limited such open-source applications available for use [1,5,10] which use chest X-Ray images. Publicly available data on chest X-Rays for COVID-19 are also limited. COVID-Net [10] is the only approach having an open source and actively maintained tool which has ability to identify COVID-19 as well as other pneumonia while showing considerable sensitivity for COVID-19 detection. COVID-Net uses a machine-driven design exploration to learn the architecture design starting from initial design prototype and requirements. It takes as input a chest X-Ray image and outputs a prediction among three classes: Normal, Pneumonia and COVID-19. We treat this model as our baseline, comparing our results with it.

Chapter 3 Functionality/Working of Project

Model Architecture

Our model contains pre-trained CheXNet [7], with a 121-layer Dense Convolutional Network (DenseNet) [3] backbone, followed by a fully connected layer. We
replace CheXNet's [7] final classifier of 14 classes with our classification layer of 4 classes (3 classes for the clubbed pneumonia configuration), each with a sigmoid activation to produce the final output.

Training

For training we initialize our model with pre-trained weights from CheXNet implementation by Weng et al. [12], and then following the two-stage training process described below:

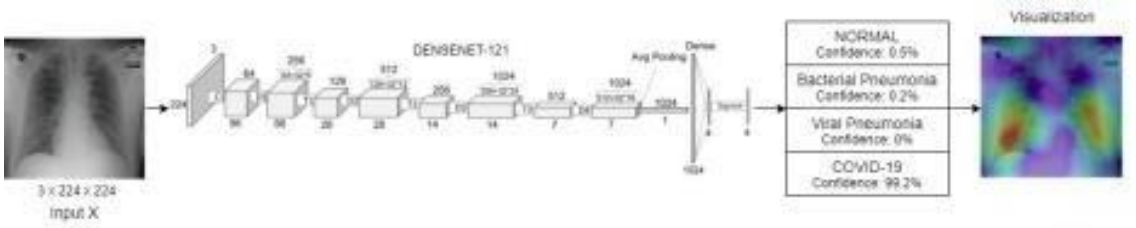


Fig. 2: CovidAID model (DenseNet image from [9])

1. In the first step, DenseNet's backbone weights are frozen and only the final fully connected layer is trained. Training is performed using Adam optimizer with following parameters: $\beta 1 = 0.9$, $\beta 2 = 0.999$, and learning rate 10^{-4} . We use mini-batches of size 16, and train for about 30 epochs. The model with the lowest validation loss is selected for next stage.
2. In the second stage, the network weights are initialized from above, but the whole network is trained end-to-end (all layers), using the same hyperparameters. We use mini-batch size of 8 in this stage due to memory constraints, and train for 10 epochs. Again, the model with lowest validation loss is selected for testing.

Dataset and Evaluation

We use the covid-chestxray-dataset [2] for COVID-19 frontal-view chest X-Ray images and chest-xray-pneumonia dataset [4] for frontal-view chest X-Ray images with bacterial/viral pneumonia as well as of normal lungs. We use the pre-trained CheXNet model, thus implicitly using robust features obtained after training on ChestX-ray14 [11] dataset. The covid-chestxray-dataset [2] does not contain proper data split for training purposes, so we perform our own split, as shown in Tables 1 and 2. Since multiple images for the same patient could be found in the dataset, we split the data by patient-IDs to prevent any information leakage. We choose 20% of the images as test set, and 10 images are kept as validation set.

	Normal	Pneumonia		COVID-19	Total
		Bacterial	Viral		
Train	1341	2530	1337	115	5323
Val	8	8	8	10	37
Test	234	242	148	30	654

Table 1: Sample-wise Data Split

	Normal	Pneumonia		COVID-19	Total
		Bacterial	Viral		
Train	1000	1353	1083	80	3516
Val	8	7	7	7	29
Test	202	77	126	19	424

Table 2: Patient-wise Data Split

Sampling

The combined dataset (covid-chestxray-dataset and chest-xray-pneumonia) has a high data imbalance due to scarce COVID-19 data. Note that this imbalance is different from the positive-negative class imbalance (for which $w+$ and $w-$ were introduced in the loss function). To ensure that training loss due to COVID-19 does not get masked by training loss due to other classes, we consider only a random subset of pneumonia data in each batch. The size of this subset should neither be too small, which will lead to overfitting on the COVID-19 data, nor too large to mask the COVID-19 loss, and is fixed empirically. In each batch we take data from classes Normal, Bacterial Pneumonia, Viral Pneumonia and COVID-19 in the ratio $5 : 5 : 5 : 1$. In case of the three class classification network, this ratio is $7 : 7 : 1$.

CHAPTER 4 Result and discussions

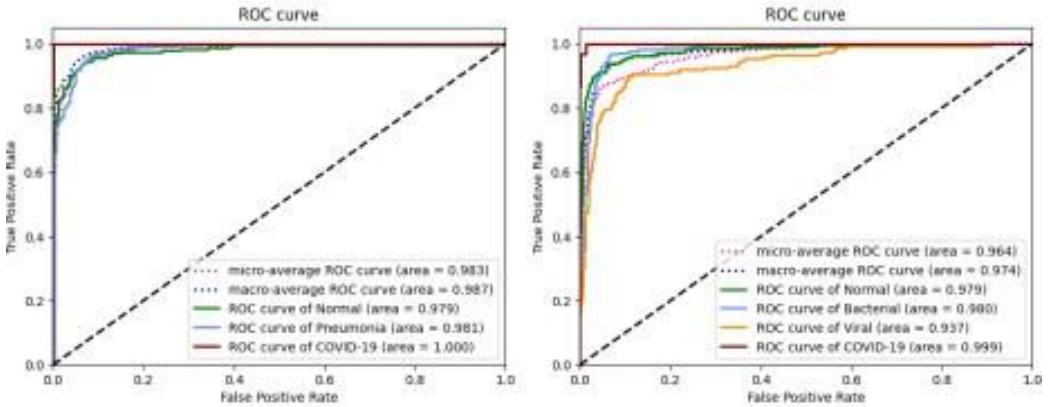
Our results indicate that this approach can lead to COVID-19 detection from X Ray images with an AUROC (Area under ROC curve) of 0.9994 for the COVID19 positive class, with a mean AUROC of 0.9738 (for 4-class classification configuration). Since we have modeled the problem as a binary classification problem for each class, given an input image X, we treat the class with maximum confidence score as the final prediction for calculating Accuracy, Sensitivity (Recall), PPV and confusion matrix.

Pathology	AUROC	Sensitivity	PPV
Normal Lung	0.9795	0.744	0.989
Pneumonia	0.9814	0.995	0.868
COVID-19	0.9997	1.000	0.968

Table 3: Class-wise results for 3-class classification

Pathology	AUROC	Sensitivity	PPV
Normal Lung	0.9788	0.761	0.989
Bact. Pneumonia	0.9798	0.961	0.881
Viral Pneumonia	0.9370	0.872	0.721
COVID-19	0.9994	1.000	0.938

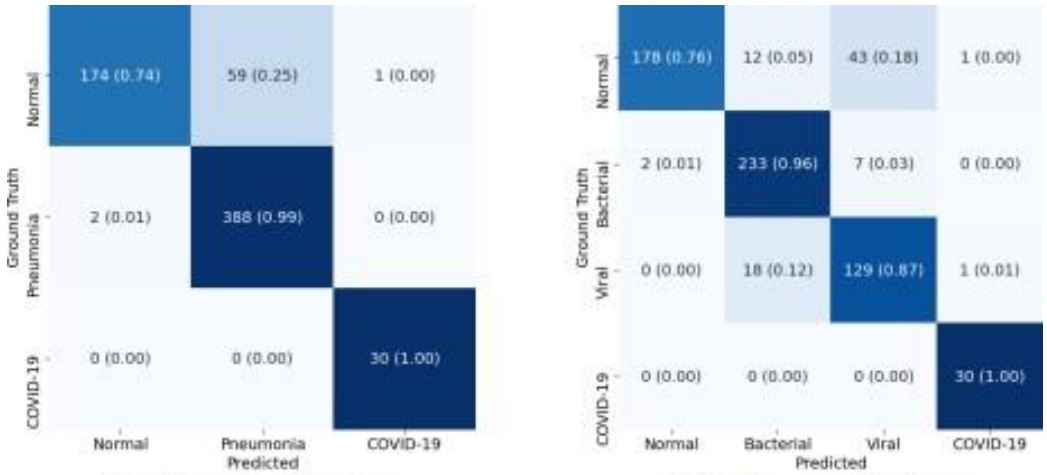
Table 4: Class-wise results for 4-class classification



(a) 3-class classification (b) 4-class classification

Fig. 3: ROC curves for our two configurations

We obtained an accuracy of 87.2% for 4-class classification configuration and 90.5% for the 3-class classification. The class-wise results for AUROC, Sensitivity (Recall) and PPV (Positive Predictive Value or Precision) are given in Tables 3 and 4. The corresponding ROC curves are shown in Fig. 3



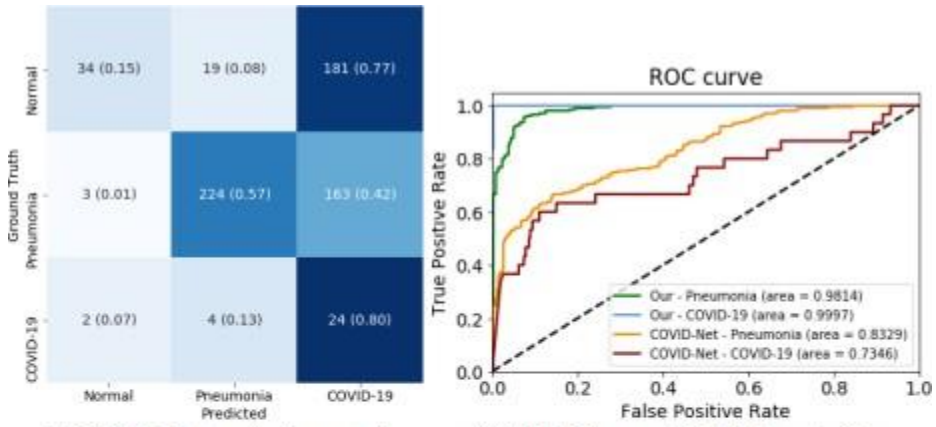
(a) 3-class classification (b) 4-class classification

Fig. 4: Confusion matrices for our two configurations

The confusion matrices on the test data for the two configurations of our model are shown in Fig. 4. It can be seen that viral pneumonia, having a sensitivity (recall) value of 0.87 is often confused with bacterial pneumonia. This is likely due to the overlapping imaging characteristics. Our sensitivity (recall) for COVID-19 positive class is 1.0, which is at par with the sensitivity (recall) for bacterial pneumonia.

Comparison with COVID-Net

To compare our approach with COVID-Net [10] we evaluate their published pre-trained models on the same test data split as ours. Fig. 5 compares their ROC curves with our model along with the confusion matrix. The COVIDNet inference shown here is made using their 'Small' variant which seemed to perform better among their two variants. It can be seen that our model outperforms COVID-Net by >0.14 AUROC in detecting regular Pneumonia as well as COVID-19. It should be noted that we used a different Pneumonia dataset from that used by COVID-Net, however, the COVID-19 data used is the same.



(a) COVID-Net confusion matrix (b) ROC Curves: COVID-Net v/s Ours

Fig. 5: Comparison with COVID-Net

Model	F1 Score	95% Confidence Interval
COVID-Net	0.3591	0.3508 - 0.3674
CovidAID	0.9230	0.9178 - 0.9282

Table 5: F1 Score (95% CI) comparison

We compute F1 scores for CovidAID and Covid-Net [10] over 10,000 bootstrapped samples from our test set of 654 images. 100 instances are taken (with replacement) of size 100 each for the bootstrap. The F1 scores along with their 95% confidence intervals are shown in Table 5. The high margin of difference of the F1 scores of the two models clearly establish the superior performance of our model over COVID-Net.

Visualizations

To demonstrate the results qualitatively, we generate saliency maps for our model's predictions using RISE [6]. In this approach 1000 randomly masked versions of a given X-ray image are queried and their classification scores are used to create a weighted mask corresponding to each output class. The core idea behind the RISE [6] approach is that masks which preserve semantically important parts of the image will lead to a higher classification score and hence a higher weight in the final mask for the respective class.

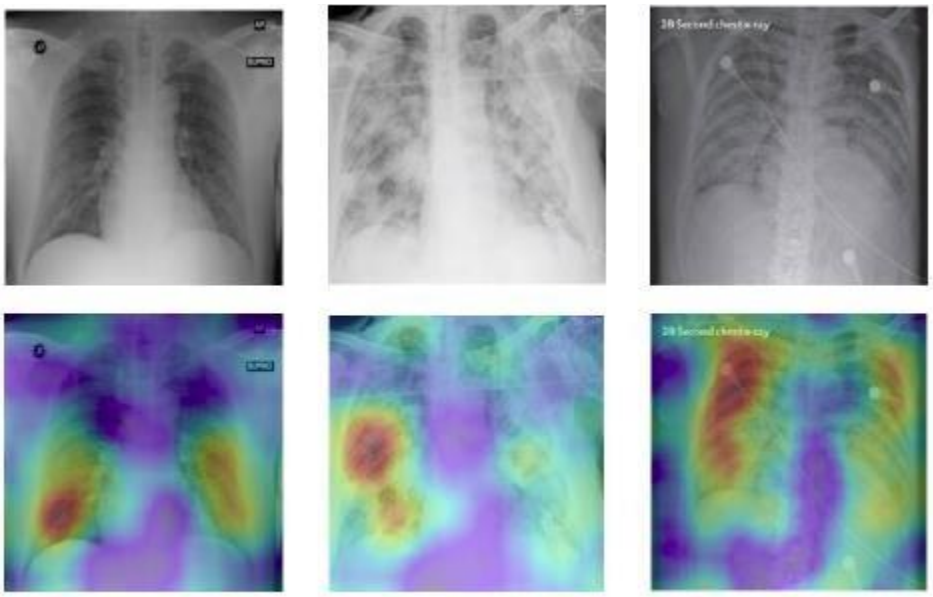


Fig. 6: Saliency map visaulization over COVID-19 positive X-Rays.
Red denotes region of greater importance.

The purpose of these visualizations was to have an additional check to rule out model over-fitting as well as to validate whether the regions of attention correspond to the right features from a radiologist's perspective. Fig. 6 shows some of the saliency maps on COVID-19 positive X-rays.

Deep Learning techniques have been on a rise since the last few years and have completely changed the scenario of many re- search fields. Especially, in medical field, image data set such as retina image, chest X-ray, and brain MRI provides promising re- sults with an extended accuracy% by using the deep learning tech- niques [15–17] . As we know, X-ray machines provides inexpen- sive and faster results for scanning of various human organs in the hospitals. The interpretation of various X-rays images is usu- ally performed manually by an expert radiologists. As a data sci- entist, if we train those captured images with the significance of deep learning that will be a great aid to medical experts for de- tecting the COVID-19 patients. This will help the developing coun- tries where the X-ray facility is available but the availability of an expert is still a dream. To this advantage, we also aim to develop a deep neural network named 'nCOVnet' that can analyze the X-ray images of lungs and detect whether the person tests positive for the virus or not. Among various deep learning classifiers, in par- ticular, the Convolutional Neural Networks (CNN) have been im- mensely effective in computer vision and medical image analysis tasks. The results of CNN have proven its cogency in mapping of image data to a precise and expected output. Since the lungs are the primary target of the virus, analysing their changes can give an explicit result of presence of the virus. The main contribution of this research work is to propose a CNN based model, which is able to train the images of corona virus infected lungs and those of healthy lungs. Proposed model is able to detect the COVID-19 cases at a faster speed by detecting the features of infected patients as hazy or shadowy patches in the X-ray images of lungs. The ma- jor research contributions of this paper can be summarized as follows:

• We have proposed an algorithm nCOVnet to detect the COVID- 19 patients using X-ray images.

• We have focused on the observational analysis of lockdown is not only the solution and some artificial intelligence methods are extremely required to overcome from this solution.

• We have presented the fast detection method using X-ray im- age analysis that would be a contribution to the society.

• We have carefully analyzed the X-ray images of lungs for per- son in order to detect the COVID-19.

• The obtained results have been evaluated by using three dif- ferent parameters known as- confusion matrix, AUC of ROC, and Training Accuracy.

• Proposed model correctly detect the COVID-19 positive patients with an accuracy of 97% whereas the overall accuracy of the proposed model is 88%.

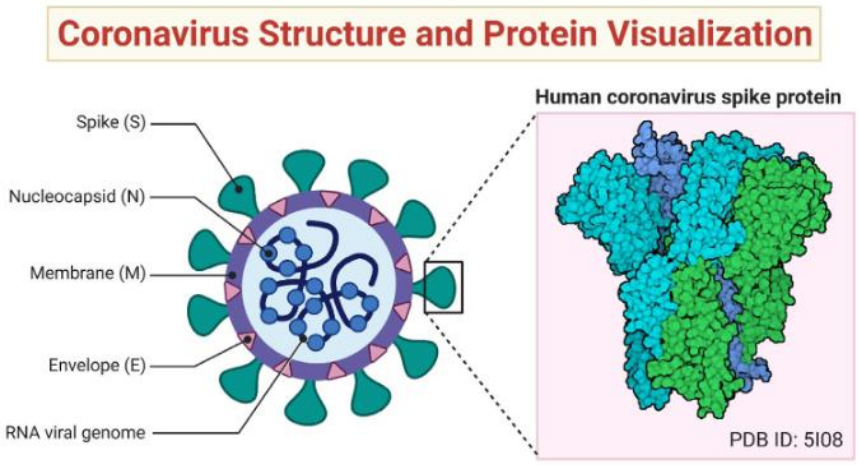


Fig: The 2019-nCoV structure. Corona viruses belong in the family Coronaviridae and can cause disease in mammals and birds. The corona virus spike (S) protein mediates membrane fusion by binding to cellular receptors. (reprinted from [5] with permission under the terms of Creative Commons Attribution 4.0 International License.

Methodology

Data set collection

The data set used in this work is an open source compiled by Cohen et al. which currently consists of around 192 X- Ray images of COVID-19 positive patients and total 337 images. The repository of images is open for contributions and new images are added frequently. All the images are verified and annotated in- cluding the findings of the X-ray. Websites such as Radiopedia.org and Figure1.com were used to collect the images. In the data set we have Posterior Anterior (PA), Anterior Posterior (AP) and An- terior Posterior Supine (AP Supine) views of the lungs. Here, we have selected only the PA views in the training and testing for the chest X-Rays. After selecting PA view, we have 142 X-ray im- ages of COVID-19 positive patients. For normal healthy patients, we have used the Kaggle's Chest X-Ray Images (Pneumonia) consist- ing of 5863 images. These images are divided into four different class values– 'Normal' 'Bacterial Pneumonia' and 'Viral Pneumonia'. From this data set, we have selected around 142 images of normal X-rays. This data set is further converted into training and testing with the split of 70% data for training of proposed deep learning model and 30% data for testing purpose.

Data pre-processing

Since the data set is not uniform and the X-ray images are of different sizes therefore, we have converted all the images into the same size of 224 x 224 pixels. For this, RGB reordering has been applied and the final input to the proposed model is provided as 224 ×224 ×3 image. It has been noted that the data set is limited therefore, we have performed the data augmentation with a rotation range of 20. The X-ray images were flipped horizontally and vertically so as to increase the diversity of data set significantly. Now, this data set is able to train on more images with the same data set.

Data leakage

Preventing data leakage is one of the crucial tasks of the methodology since in the applied data set a single patient with a unique patient id may have more than one X-ray images. The X-ray images of the same patient are present from different days they have visited in the hospital. Thus, while splitting we cannot use the train_test_split command anymore and instead have to come up with a new logic which will split the data at individual patient level. We have performed this by manually assigning 70% of the patients for training purpose and remaining 30% (31 patients) for testing purpose. We had altogether 127 COVID-19 pos- itive patients' X-ray images for training, on contrary, 31 COVID-19 positive patients' X-ray images for testing. By doing this, we could be sure that there is no data leakage among training and testing data sets.

Convolutional Neural Network (CNN)

Deep learning techniques are used to reveal those features of the data set such as image and video which are hidden in the original data set. For this, Convolutional Neural Network (CNN) has been significantly applied to extract the features, and this unique characteristic has been immensely applied in medical image anal- ysis that provides a great support in the advancement of health community research. CNN is a type of artificial neural net- work which has multiple layers, and is expert to process the high volume of data with higher accuracy and less computational cost. The basic structure of CNN comprises convolution, pooling, flatten- ing, and fully connected layers. A basic architecture of CNN is presented in Fig. 3 showing the input X-ray image, networks, pool- ing and output.

Proposed Model

The proposed model depends on the working of deep learn- ing based CNN known as nCOVnet. The applied parameters in this model are tabulated in Table 1 which consists of 24 layers. The first layer indicates the input layer and is fixed with the size of 224 x 224 x 3 pixels which makes it a RGB image. The next 18 layers are the combination of Convolution+ReLU and Max Pooling layers. These layers are part of the pre-trained VGG16 Model proposed in [35] and trained on the ImageNet dataset. ImageNet contains around 15 million annotated images from 22,0 0 0 different cate- gories and VGG16 was able to achieve 92.7% accuracy on ImageNet. Therefore, we used the VGG16 model as depicted in Fig. 5 for fea- ture extraction as a base model. Then we have applied a transfer learning model using the proposed 5 different layers and trained the proposed model on the COVID-19 dataset. These 5 layers are an integral part of the head model where the first layer acts as an Average Pooling 2D layer with pool size of (4,4). In average pooling, the average value of all the pixels in the batch is selected unlike max pooling where the maximum value is selected. Next, we use a flatten layer whose role is to ap- ply a flattening transformation on the tensor converting the two- dimensional matrix of features into a vector that can be fed into a fully connected neural network classifier. Once, we have the trans- formed vector we then input it into a fully dense connected layer with a size of 64 units and a ReLU activation function. Then, we apply dropout with a threshold of 0.5. The dropout layer simply ignores some units (neurons) taking in consideration the threshold value which we provided. Finally, we have an output layer having just two units. Now, the model is optimized using the Adam opti- mizer. Adaptive moment estimation or Adam is an optimiza- tion algorithm which is used in place of vanilla stochastic gradient descent.

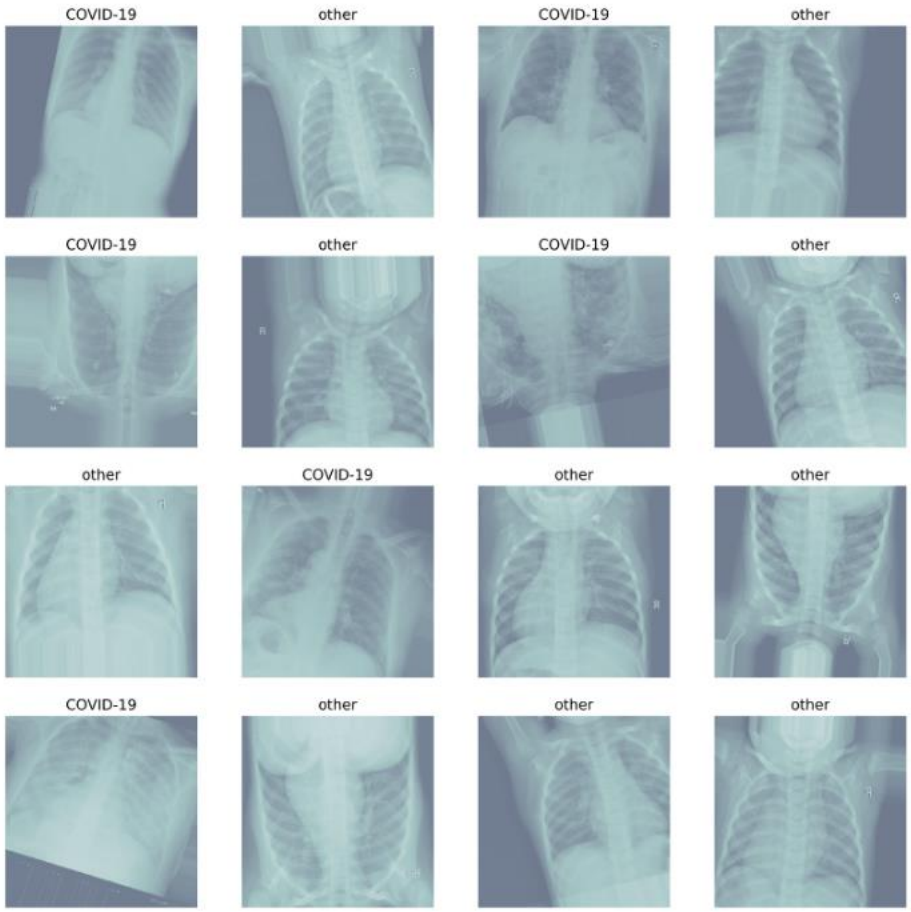


Fig: Sample of the labelled X-rays after data augmentation taken from the combined data set of COVID-19 patients and normal patients.

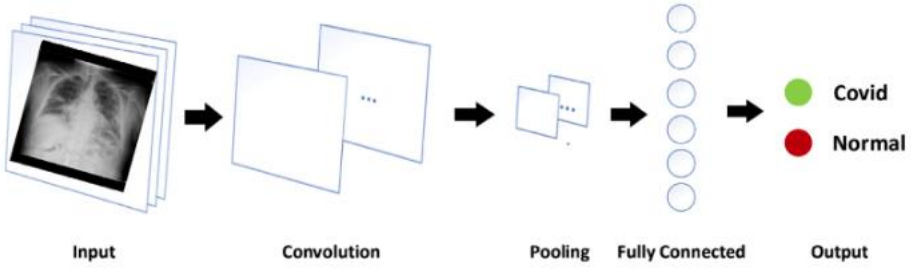


Fig: Basic CNN architecture for classification and detection of COVID-19.

Experimental Analysis

For evaluation of proposed model, we have calculated the con- fusion matrix, Area Under Curve (AUC) of Receiver Operating Characteristics (ROC), and plotted the training accuracy.

Confusion Matrix

Confusion matrix is based on four primary parameters known as True Positive (TP), False Positive (FP), False Negative (FN), and True Negative (TN) as shown in Table 2 . Here, rows represent the 'Actual class values', and the attributes are the 'Predicted/Detected class values'. This has been prominently used for evaluating the performance of model. From confusion matrix on the test data set, we have achieved the sensitivity of 97.62% and specificity of 78.57%. Where Sensitiv- ity refers to the measure of True Positives (TP) or COVID-19 posi- tive patients in this case. Therefore, out of the 42 positive patients in used training data set we were able to correctly predict COVID- 19 in 41 of them providing 97.62% probability. This implies that we can detect COVID-19 in infected patients, X-Ray with only 2.38% er- ror. Specificity refers the measure of True Negatives (TN) or COVID- 19 negative patients in this case. So, out of the 42 negative pa- tients in used testing data set, we were able to correctly predict that a person is not infected by COVID-19 in 33 patients providing 78.57% probability. This implies that we can detect the COVID-19 in infected patients' X-ray with an error rate of 21.43%. By calculating the accuracy of proposed model through the confusion matrix we have achieved an overall accuracy of 88.10% considering the limited amount of data used for training.

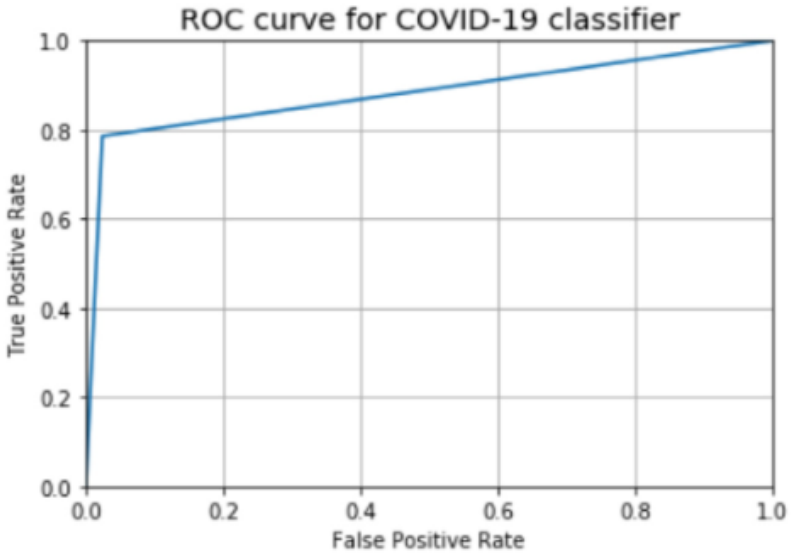


Fig: ROC curve for nCOVnet

Receiver operating characteristics (ROC)

ROC is a 2-dimensional graph, plots between the true positive rate (TPR) and false negative rate (FPR), in other words, it can be defined as the trade-off between sensitivity and specificity [37] . We have plotted the Receiver Operating Characteristic (ROC) curve with True Positive Rate on the y-axis and False Positive Rate on the x-axis. In medical diagnosis higher area under curve (AUCs) are required. As a result, in clinical data analysis research, its computation allows the data scientist to simplify the data analysis with predictive knowledge on medical research [38] . The calculation of

AUC is done by the well known trapezoidal method. This method calculates AUC by dividing the area into a number of sections with equal width. Here, trapezoid (T) refers to the integration of points - (a, b) from a functional form which is divided into n equal pieces. The summation of the area of each section by the area of the trapezium formed when the upper end is replaced by a chord and the sum of these approximations pro- vides the final numerical result of the AUC. The trapezoidal rule is indicated as a definite function integral ∫ b a f(x) dx, and the points of domain subdivision of the integration (a, b) are labeled as { x 0 , x 1 ,x n }; where { x 0 = a, x n = b, x r = x 0 + r(b −a) /n } .

$$T(a,b,n) = \left(\frac{b-a}{n}\right) \times \left(\frac{f(a)-f(b)}{2}\right) \times \left(\frac{f(a)-f(b-a)}{n}\right) \quad (1)$$

Hence, this is an effective way to calculate the accuracy of ROC produced by model. The plotted AUC of ROC as shown in Figure above of proposed model is above the threshold level is calculated as 0.88095 which is a good indication of model and comes under the good rank of classification, and also considered to be ‘excellent’ in the field of medical diagnosis.

Training Accuracy

We have trained the proposed model for 80 epochs and set the learning rate to be 0.0 0 01. The training accuracy as seen in the graph lies around 93 −97% . Whereas, the training loss goes as low as 0.2% as highlighted in Figure below. Although obtained results represents that the training accuracy is up to 97% which could be considered as one of the good measure for assessing classification models especially in the field of medical diagnosis. It is because during calculating training accuracy we have assigned equal cost to both false negatives and false positives. Therefore, we have con- sidered the confusion matrix as a better evaluation parameter as it provides the accuracy separately for each metrics i.e. true positives, true negative, false positives, and false negatives. The problem of treating false positives and false negatives with equal costs is that we cannot afford to diagnose a COVID-19 pos- itive patient as negative, since in such a case the patient may go back to the society thinking She/he is no longer a COVID-19 patient and this may result in community spread of the disease.

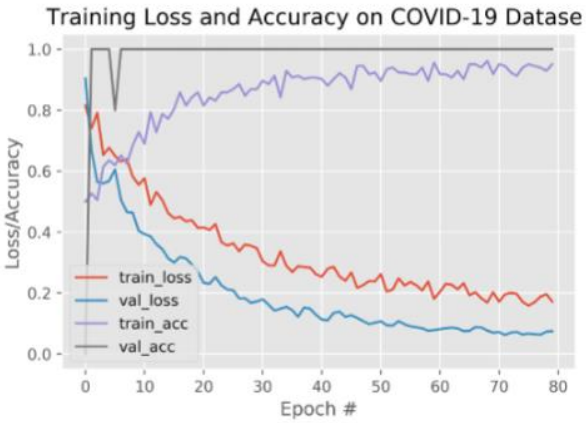


Fig: Training curve of loss and Accuracy for nCOVnet models

System Design

Our proposed deep learning-based COVID-19 detection comprises several phases, as illustrated in Figure 1. The phases are summarized in the following five steps:

Step 1: Collect the chest X-ray images for the dataset from COVID-19 patients and healthy persons.
Step 2: Generate 1000 chest X-ray images using data augmentation.
Step 3: Represent the images in a feature space and apply deep learning.
Step 4: Split the dataset into two sets: a training set and a validation set.
Step 5: Evaluate the performance of the detector on the validation dataset.

A. Dataset

Two types of datasets were used in the evaluation, the original dataset (without augmentation) and the augmented dataset, which are summarised in Tables 1 and 2, respectively. The dataset contained the following: a) a healthy dataset containing chest X-ray images of healthy persons and b) a COVID-19 dataset containing chest X-ray images of COVID19 patients.

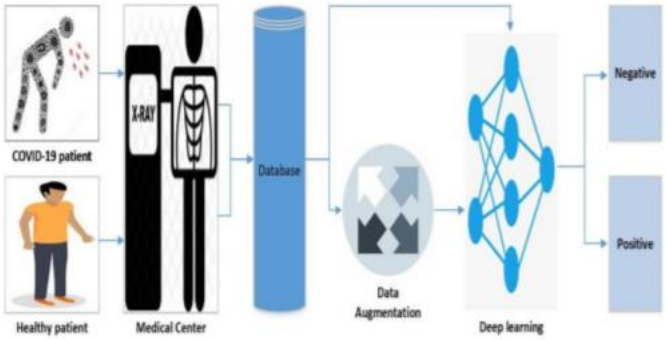


Fig: Architecture of the proposed system

Owing to the limited availability of chest X-ray images, we generated our dataset using data augmentation. Data augmentation is an AI method for increasing the size and the diversity of labelled training sets by generating different iterations of the samples in a dataset. Data augmentation methods are commonly used in ML to address class imbalance problems, reduce overfitting in deep learning, and improve convergence, which ultimately contributes to better results. The total number of images in the dataset became 1000 after applying augmentation, as presented in Table 2

Table 1 Original dataset (without augmentation)

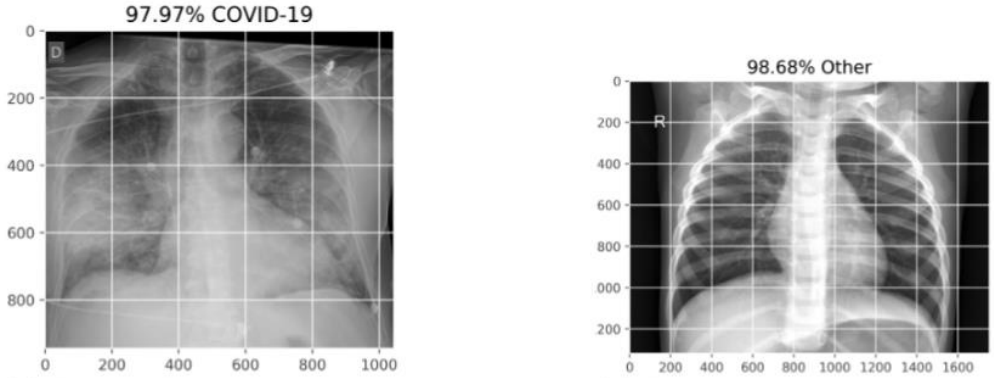
X-ray images	***Number***
Healthy	28
COVID-19	70
Total	**128**

Table 2 Augmented dataset

X-ray images	***Number***
Healthy	500
COVID-19	500
Total	**1000**

Prediction

When we have applied prediction on the proposed model, it is able to classify the COVID-19 patient correctly with 97.97% confi- dence as shown in Fig. 8 . And applying prediction on COVID-19 negative patients the model was able to provide the correct result with 98.68% confidence. The measure of confidence can help us to only select those results which the nCOVnet is confident about. We have predicted a COVID-19 patient correctly with only 2.03% error in under 5 seconds, and we know that in the case of COVID- 19 positive patients we have achieved an accuracy of 97.62%. From the obtained results this can be seen that the proposed nCOVnet model can be used as a substitute to RT-PCR which takes around 4 −10 hours for detecting COVID-19 patient. Since nCOVnet predicts with a confidence measure we can use the RT-PCR testing in the few cases where nCOVnet is not confident about to decrease the chances of errors. 6. Discussion and conclusions This is a proven fact that rigorous testing and social distancing are some of the most important measures to be taken by the governments in different parts of the world to control the COVID- 19 pandemic. There are mainly two types of tests that are being conducted throughout the world to detect COVID-19, the antibody test and the RT-PCR test. The antibody test can find whether or not the immune system has encountered the virus and is an in- direct way of testing. Since anti-bodies can take up to 9–28 days after the infection has set in, it is a very slow process and by that time the infected person can spread the disease if not properly iso- lated. On the other hand, RT-PCR testing is rather fast and can de- tect COVID-19 in around 4–6 hours. Looking at the magnitude of the pandemic this is also not too fast and RT-PCR testing has other limitations as well. One such limitation is the high cost of import- ing the chemicals and other elements used in the kits. One test can cost up to 60$, and the rate may vary in different parts of the world depending on the availability. Which brings us to the next limitation, availability, not every part of the world has the same requirements and resources. Some countries have a greater population and less availability of kits whereas some countries have more kits than required. These limitations can be overcome with the proposed nCOVnet model. Proposed model can detect a COVID-19 positive patient in Figure below. Prediction results of Covid-19.



(a) CXR of COVID-19 positive patient predicted correctly by nCOVnet with 97.97% confidence

(b) CXR of a normal patient predicted correctly by nCOVnet with 98.68% confidence

Fig: Prediction results of Covid-19.

Chapter 5- Conclusion and Future Scope

We have presented some initial results on detecting COVID-19 positive cases from chest X-Rays using a deep-learning model. We have demonstrated significant improvement in performance over COVID-Net [10], the only publicly maintained tool for classification of COVID-19 positive X-rays, on the same chest-xray-pneumonia dataset [4]. The results look promising, though the size of the publicly available dataset is small. We plan to further validate our approach using larger COVID-19 X-ray image datasets and clinical trials.

Future Scope:

- Application deploys the previously trained CNN model in a web application using a Python backend with a Flask web development framework. The frontend of the website is created with HTML and JavaScript.
- We load the x-ray image into the web app.
- JavaScript code used to upload the image and it coverts the image into Base64image and send it to python backend.
- Click on ‘Predict’ and it predicts the Covid-19 +ve or –ve.
- It also Provides the accuracy.

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