2022 IEEE 7th International conference for Convergence in Technology (I2CT)
Pune, India. Apr 07-09, 2022

Detection of COVID-19 using Chest X-rays

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2022 IEEE 7th International conference for Convergence in Technology (I2CT) | 978-1-6654-2168-3/22/$31.00 ©2022 IEEE | DOI: 10.1109/I2CT54291.2022.9824121

***Abstract*—We train a deep learning algorithm to flag potential covid-19 infected in chest x-rays. The deep learning algorithm used is a Convolutional Neural Network that is 121 layers deep. Due to the lack of a large open-source of covid-19 infected x-ray images, we combine data from five different sources. Combined, the dataset has 17,194 images that are used for training procedure. The model classifies a given chest X-ray image as either a "Normal", "Covid-19", or a 'Pneumonia" infection. The trained model has a 0.93 F1 Score and 93.496% accuracy.**

Keywords—covid-19 detection, deep learning, convolutional neural network, chest x-ray, computer aided diagnosis, coronavirus.

I. Introduction

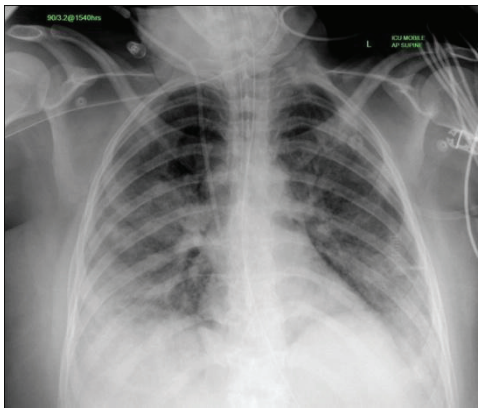
aIn 2019, a few strange cases of pneumonia were registered in the Wuhan city of China [13]. They were caused by the novel coronavirus which we know today as the Covid-19. The disease was declared a pandemic as it disseminated throughout the globe. A crucial part of controlling the spread of the disease was to test the population and quarantine the infected individuals. The current gold standard for testing the coronavirus is the RT-PCR test [8]. While the accuracy of the test is very high, it can take up to 2 days to get the final results. Since time is of the essence in controlling the spread of the virus, it is important to flag the potential individuals who may be at a high risk of getting infected with the virus swiftly and with a high degree of confidence. What this paper proposes is a solution to the above-mentioned problems by leveraging the recent developments in machine vision and the image classification abilities of the Convolutional Neural Networks. Covid-19 causes opacity in the lungs as a result, white patches can be seen in the infected person's chest X-ray which is absent in a normal chest X-ray. This paper proposes to train a deep learning model to learn the features of a covid infected chest X-ray and differentiate between a "Normal", "Covid-19", and "Pneumonia" chest X-rays.

II. Literature Survey

A. Conventional Methods

Novel coronavirus has multiple methods of detecting strains of COVID -19. One such method is nucleic acid analysis [5]. It is a simple method where the lateral flow method is used for rapid analysis. The results are given in 30 minutes after the combination of the lateral flow method and Isothermal amplification technology. These steps can be integrated into small microchips for portability and rapid detection purpose. Another such method is the molecular method including RT-PCR and reverses transcription loop-mediated isothermal amplification (RT-LAMP) [8]. The RT-PCR is a nuclear-derived method used for detecting strains of COVID-19 in a pathogen. A radioactive isotope or fluorescent dyes are used to detect targeted genetic material.

The results are shown almost immediately and it is currently the most widely used method in the world. The LAMP method is faster more accurate for amplification of the target region. The DNA produced in LAMP is higher than that produced in RT-PCR and hence is a more reliable method without any assistance of another method.



Input Image:
Frontal chest x-ray

Covid Detection Model

Output:
"Covid-19" (99.84% probability)

B. Deep Learning Based Approach

Using chest X-rays and ct-scans for computer-aided diagnosis has received increasing attention with methods [11] for lung nodule detection and [12] for hemorrhage detection proving to be quite effective. Mangal, A et al. in [1], used transfer learning with the base model as CheXNet, as there was limited availability of open-sourced data of images of Chest X-Rays on Covid-19. Model training was on a small dataset with about 1341 Normal, 3867 Pneumonia and 115 Covid images. Due to its small training set, it lacks in its applicability to real-world use. Similarly, Ravneet Punia et al. in [2], used transfer learning with ResNet as the backbone. It was trained with a very small dataset (374 images in each category) - Normal, Pneumonia, Covid - 19. This has a very high error rate of 27.62% which could be improved upon.

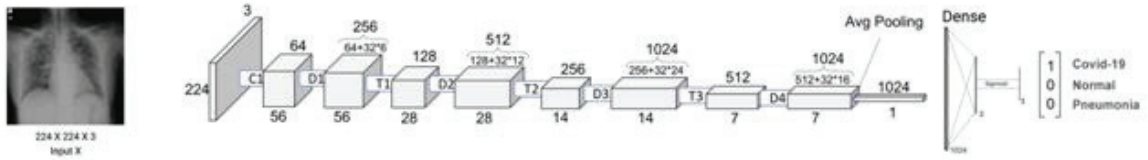


Fig. 2. The architecture of DenseNet 121 model which is initialised with CheXNet weights.

C. *Ensemble Learning Based Methods*

Chandra Tej Bahadur et al. in [3] proposed a majority voting system where they used an ensemble of 5 supervised classification algorithms to find out the presence of Covid-19 infection. The method used a two-stage classification approach. In phase-1 the model classified whether the given input chest X-ray was Normal or Abnormal and in the second phase, it classified whether it was Covid-19 infection or Pneumonia. They reported an accuracy of 91.329% and an AUC of 0.831 for the second phase. Pedro Silva et al. in [4] proposed a voting based schema using an ensemble of different deep learning architectures based on the EfficientNet family.

III. Problem Formulation

As seen in the Literature Survey section, due to the scarcity of available data, the above solution lacked in terms of applicability to real-world use. The datasets that these models were trained on were small, for eg. [1] contains only 115 Covid-19 infected chest x-ray images in the training set. The models could not be generalised as the dataset wasn't comprehensive and indicative of the universal set. As a result, improvements had to be made to the dataset and the training procedure as an extension.

The Covid-19 detection is structured such that it accepts frontal chest x-ray image as the input and predicts a binary class label y {0, 1} which shows the presence or absence of that particular class. Due to the class imbalance in the dataset, the model sees training examples of Normal and Pneumonia chest X-rays more often than the Covid infected chest X-ray as a result, the model biases towards predicting those classes and decrease the training loss. In order to deal with this bias in the prediction, we use a weighted binary cross-entropy loss function as in (1). The class weights are assigned based on the number of training examples in the respective class.

$$J(\boldsymbol{w}) = -\frac{1}{N}\sum_{n=1}^{N}[C * y_n log a(z)_n + (1-y_n) log(1-(a(z))_n)] \quad (1)$$

Equation (1) represents the modified cost function of the binary crossentropy loss which uses class weights to address the imbalance in the training samples between the 3 classes (Covid-19, Normal, Pneumonia). In (1), (N) is the number of training samples, (C) represents the Class weights, (a(z)) is the hypothesis, the prediction and (y_n) is the true label. The negative sign is to represent the minimization objective of the training procedure.

IV. Model Architecture

Given the recent success of the CheXNet model [10] in predicting the presence of various lung diseases in chest X-rays, we decided to use the CheXNet weights as an initial point to train our Covid-19 detection model. The CheXNet model trained on 112,120 frontal chest X-ray images has learnt a robust set of features that are fine-tuned to detect Covid-19 infection.

We used a 121 layer Dense Convolution Network (DenseNets) as the model backbone [9]. In DenseNets, every layer of the network is connected to every subsequent layer in a feed-forward fashion. DenseNets are efficient in dealing with the vanishing gradient problem and they also strengthen feature propagation through the same network. DenseNets achieves significant performance gains over the other models on image recognition datasets such as CIFAR-10, CIFAR-100, SVHN, and ImageNet, whilst reducing the computational requirements. The DenseNets consists of "Dense Blocks" which contains a stack of 1x1 and 3x3 convolutions that are applied on the input. Each of these layers is connected to every subsequent layer. Down-sampling is an essential part of a convolutional neural network as it reduces the input size while preserving the information. The DenseNet achieves downsampling by applying "Transition Layers" between the Dense Blocks. The Transition Layers have 1x1 convolutional layers and a 2x2 average pooling layer with stride = 2 that carries out the downsampling operation.

We apply the Global Average Pooling function to the output of the convolutional base to get a 1-D representation of the extracted features. Finally, the prediction layer of the network is replaced with a classification layer with 3 output neurons and a sigmoid activation function is applied. Table 1 shows the model architecture with the output size and kernel size in detail.

$$a(z) = \frac{1}{1+e^{-z}} \quad (2)$$

Equation (2) represents the activation function applied to the prediction layer. It is the sigmoidal activation function that computes the probability score for each class (Covid-19, Normal and Pneumonia) as a value in the range [0, 1].

V. Model Training

The network is initialised with CheXNet [10] weights and the convolution base is frozen. The prediction layer of the network is then trained with a Stochastic Gradient Descent optimizer with standard parameters (momentum = 0.9). The model is trained with mini-batches of size 16. The learning rate is initially set to 0.01 and is decayed with a factor of 10 after a set number of epochs. The selection criteria for the model is to have the least validation loss.

The prediction layer of the model is activated with the sigmoidal activation function and the aim of the training is to minimise the Binary Cross-Entropy loss.

TABLE I

MODEL SUMMARY

Layer	Output Shape	Kernel
input_1 (InputLayer)	(224, 224, 3)	-
zero_padding2d (ZeroPadding2D)	(230, 230, 3)	-
conv1/conv (Conv2D)	(112, 112, 64)	7 X 7
conv1/bn (BatchNormalization)	(112, 112, 64)	-
conv1/relu (Activation)	(112, 112, 64)	-
zero_padding2d_1 (ZeroPadding2D)	(114, 114, 64)	-
pool1 (MaxPooling2D)	(56, 56, 64)	3 X 3
Dense Block (1)	(56, 56, 256)	$\left[\frac{1x1conv}{3x3conv}\right] x6$
Transition Layer (1)	(56, 56, 128)	1 x 1 (conv)
	(28, 28, 128)	2 x 2 (Average Pooling, stride = 2)
Dense Block (2)	(28, 28, 512)	$\left[\frac{1x1conv}{3x3conv}\right] x12$
Transition Layer (1)	(28, 28, 256)	1 x 1 (conv)
	(14, 14, 256)	2 x 2 (Average Pooling, stride = 2)
Dense Block (3)	(14, 14, 1024)	$\left[\frac{1x1conv}{3x3conv}\right] x24$
Transition Layer (3)	(14, 14, 512)	1 x 1 (conv)
	(7, 7, 512)	2 x 2 (Average Pooling, stride = 2)
DenseBlock (4)	(7, 7, 1024)	$\left[\frac{1x1conv}{3x3conv}\right] x16$
global_average_pooling2d	(None, 1024)	7x7
prediction (Dense)	(None, 3)	-

$$w_{new} = w_{old} - \alpha \nabla J_i(w) \quad (3)$$

Equation (3) represents the weights updation according to the stochastic gradient descent rule. Alpha is the learning rate.

VI. DATASET

Due to the lack of open-sourced datasets for Covid-19 chest x-ray images, we combined the x-ray images from five different datasets. The five datasets used were the covid-chest x-ray-dataset released by Joseph Paul Cohen et al. [6], Figure 1 COVID-19 Chest X-ray Dataset released by Audrey Chung et al., Actualmed COVID-19 Chest X-ray Dataset released by Audrey Chung et al., COVID-19 Radiography Database released by M.E.H. Chowdhury et al. [7] and RSNA pneumonia dataset. Combined, the dataset contains 17,194 sample images in the training set and 1553 sample images in the test set. Class-wise categorisation of images is shown in table 1

For the covid detection problem, we randomly split the dataset into training (15,475 images), validation (1,719 images), test (1,553 images) sets. A resizing operation is carried out on the input images and they are normalised according to the DenseNet preprocessing function. The input images from all three sources were resized to 224 X 224 as it was the standard input size for DenseNet architecture.

A. Dataset Statistics

TABLE II

Number of images

	Covid-19	*Normal*	*Pnuemonia*
Training Set	3753	7966	5475
Test Set	74	885	594

VII. Result and Analysis

We implemented the proposed model in TensorFlow and used Kaggle notebooks as it provides free GPU options for training. We discuss the model performance in this section. For the comprehensive analysis of the network, we use metrics such as F1-score, accuracy, precision and recall. Precision is defined as the fraction of the classes predicted as positive that are actually correct.

$$\text{Precision} = \left[\frac{T.P}{T.P+F.P}\right] \quad (4)$$

Whereas Recall is the fraction of true positives that are labelled correctly. In a given scenario, optimising for either one of precision or recall is not ideal as improving one of the metrics reduces the other. Thus to gain a better understanding of a model's performance, we generally compute the F1-score.

$$\text{Recall} = \left[\frac{T.P}{T.P+F.N}\right] \quad (5)$$

$$\text{F1-score} = 2\left[\frac{P*R}{P+R}\right] \quad (6)$$

Equation (4), (5), (6) represent the precision, ,recall, and F1-score respectively. T.P is the number of "True Positives", F.P is the number of "False Positives" and F.N is the number of "False Negatives".

The test set contains 1553 images. The performance of the model on the test set is described in detail below. To find the best performing model, we trained our classification model with different train-validation split ratios and batch sizes with the F1 score being the benchmark for selection. The model with the maximum F1 score was selected as the final model. We choose the model with a train-validation split of 0.1 and training batch size of 16 as our final model as it has the best overall testing performance. On the test set, the model has a precision of 93.437% and a recall of 92.594% which gives an overall F1 score of 0.93. The accuracy of the model on the test set is 93.496%.

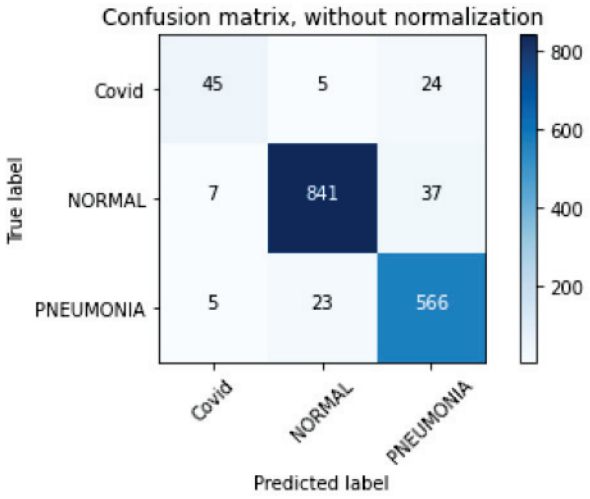


Fig. 3. Confusion matrix

The performance comparison of the model with different train-validation splits and different training batch size is shown in the table below.

TABLE III. Performance Analysis

(Batch Size, Splits)	F1 Score		
	0.1	***0.2***	***0.3***
16	0.9301	0.9214	0.9199
32	0.9213	0.9278	0.9235

VIII. Conclusion and Future Scope

The study we performed discusses the detection of COVID-19 strains in the lungs using Chest X-Ray images. Our model proposes an accuracy of 93.496% and an F1 score of 0.93 which reinforces a positive result and gives us a useful secondary method to detect the virus. This method reduces the stress of having false-positive reports and showing negative cases to ease the burden on the system. The biggest problem that we could overcome using this model was the false positives that we get using the current testing method. There are a lot of cases where people get a positive result of COVID-19 even when they have pneumonia, and this happens because the pneumonia strain is very much like that of the COVID-19 strain. Further advances can also be used to test the severity of the infection. We can improve the accuracy of this model by great amounts by processing more images and by using systems that are faster at image processing. This method does not only solve the accuracy problems but also solves all the other problems related to regular testing methods. Firstly, it makes it much cheaper because most of the countries have several CT scan machines in their hospitals hence it cuts the cost of setting up the medical infrastructure and hence makes it very much affordable. Secondly, our models can predict whether a patient has COVID-19 or not in a few seconds with good accuracy as compared to the regular testing in which we take hours for the results to come. The current testing process has a very big downside to it because not every patient is quarantined for those 6-8 hours and hence they end up spreading the disease, which makes it difficult for the

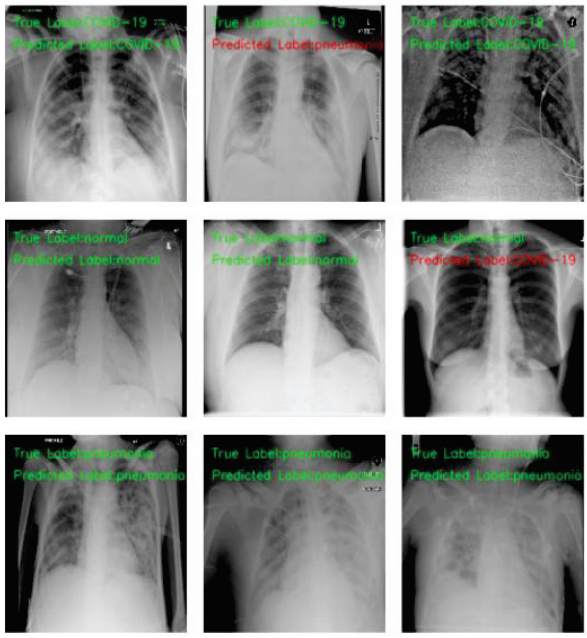


Fig. 4. Shows the true labels and predicted labels on some of the input test images.

officials to track the movement of the patient, eventually making it harder for us to reduce the spreading of the disease. From this entire experience, we learn how interlinked are the worlds of technology and medical healthcare. If we use our knowledge wisely we can use existing resources to solve a lot of problems in a much more efficient way rather than using other resources. We can use this Model for detecting a lot of other diseases using X-rays and save on time, money, and several other resources.

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