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**RESEARCH ARTICLE**

# COVID-19 OUTBREAK ANALYSIS USING CONVOLUTIONAL NEURAL NETWORKS ON X-RAY IMAGES

**Abhishek Sharma[1] and Shubham Sharma[2]**

[1,2] Department of Information Technolopgy *Maharaja Agrasen Institute of Technology, Rohini, Delhi-110086,* abhishek.sharma9484@gmail.com , shubhamsharma7231@gmail.com

**Abstract**

Covid-19 expanding to coronavirus disease 19 is a serious threat to humanity and millions have perished because of it. Earlier vaccine development was a very tough task, so people relied on herd immunity and plasma therapy to battle this disease. But now, Covid-19 vaccine is complete and there are many vaccines around different countries. It is still not enough to control the spread of the disease, since vaccination of the whole inhabitants will take a significant amount of time. In this tough Covid-19 times, we decided to build something related to it. Any technological tool enabling rapid screening of the COVID-19 infection with high accuracy can be crucially helpful to the healthcare professionals. The main clinical tool currently in use for the diagnosis of COVID-19 is the Reverse transcription polymerase chain reaction (RT-PCR), which is expensive, less-sensitive and requires specialized medical personnel. X-ray imaging is an easily accessible tool that can be an excellent alternative in the COVID-19 diagnosis. In this project, we decided to use a deep learning algorithm (to perform the rapid and accurate detection of COVID-19 from chest X-ray images. We used transfer learning with these models to get pretrained models on several images. This is done to save time in model training and improve model accuracy. The models used here are VGG16, MobileNetV2, DenseNet, InceptionResNetV2 with accuracy as 95% ,94% , 94% and 92% respectively.

**Keywords:** X-Ray, VGG16, MobileNetV2, DenseNet, InceptionResNetV2

## Introduction

COVID-19 is a severe acute respiratory syndrome coronavirus 2 (SARS-COV-2) (Huang 2020). In December 2019, the first case was reported in Wuhan, China. World Health Organization declared this as a public health emergency of international concern on 30th Jan 2020 and as a pandemic on 11th Mar 2020.

(WHO 2019; Wang *et al.,* 2020). In order to combat the spreading of COVID-19, effective screening and immediate medical response for the infected patients is a crying need. Reverse Transcription Polymerase chain reaction (RT-PCR) is the most used clinical screening method for COVID-19 patients, which uses respiratory specimens for testing. RT-PCR is used as a reference method for the detection of COVID-19 patients, however, the technique is manual, complicated, laborious, and time-consuming with a positivity rate of only 63%. Moreover, there is a significant shortage of its supply, which leads to delay in the disease prevention efforts (Wang *et al.,* 2020). Many countries are facing difficulties with the incorrect number of COVID-19 positive cases because of not only due to the lack of test kits but also due to the delay in the test results. These delays can lead to infected patients interacting with healthy patients and infecting them in the process.

One of the key measures to check the Covid-19 and lessen new Covid-19 cases is to stop it at the detection stage. This is the aspiration for this study to reduce the covid detection time and make it more effective and optimized. By using deep learning algorithms, the detection time should become very less and with high accuracy can be crucially helpful to the healthcare professionals. Our method uses X-ray images for covid detection and it is very efficient than doing a PT-PCR test.

In this study, we describe a strategy for predicting the COVID-19 cases upsurge. To do so, Deep Learning models are applied to data using Transfer Learning. This includes using five different regression models. These are: VGG16, DenseNet, MobileNetV2, InseptionResNetV2.

## CNN

In deep learning, a convolutional neural network (CNN, or ConvNet) is a class of artificial neural network (ANN), most commonly applied to analyse visual imagery. CNN's are also known as Shift Invariant or Space Invariant Artificial Neural Networks (SIANN), based on the shared-weight architecture of the convolution kernels or filters that slide along input features and provide translation-equivariant responses known as feature maps. Counter-intuitively, most convolutional neural networks are only equivalent, as opposed to invariant, to translation. They have applications in image and video recognition, recommender systems, image classification, image segmentation, medical image analysis, and natural language processing.

Convolutional networks were inspired by biological processes in that the connectivity pattern between neurons resembles the organization of the animal visual cortex. Individual cortical neurons respond to stimuli only in a restricted region of the visual field known as the receptive field. The receptive fields of different neurons partially overlap, such that they cover the entire visual field.

CNN's use relatively little pre-processing compared to other image classification algorithms. This means that the network learns to optimize the filters (or kernels) through automated learning, whereas in traditional algorithms these filters are hand-engineered. This independence from prior knowledge and human intervention in feature extraction is a major advantage.

A convolutional neural network consists of an input layer, hidden layers and an output layer. In any feed-forward neural network, any middle layers are called hidden because their inputs and outputs are masked by the activation function and final convolution. In a convolutional neural network, the hidden layers include layers that perform convolutions. Typically, this includes a layer that performs a dot product of the convolution kernel with the layer's input matrix. This product is usually the Frobenius inner product, and its activation function is commonly ReLU. As the convolution kernel slides along the input matrix for the layer, the convolution operation generates a feature map, which in turn contributes to the input of the next layer. This is followed by other layers such as pooling layers, fully connected layers, and normalization layers.

**Convolution Layers**

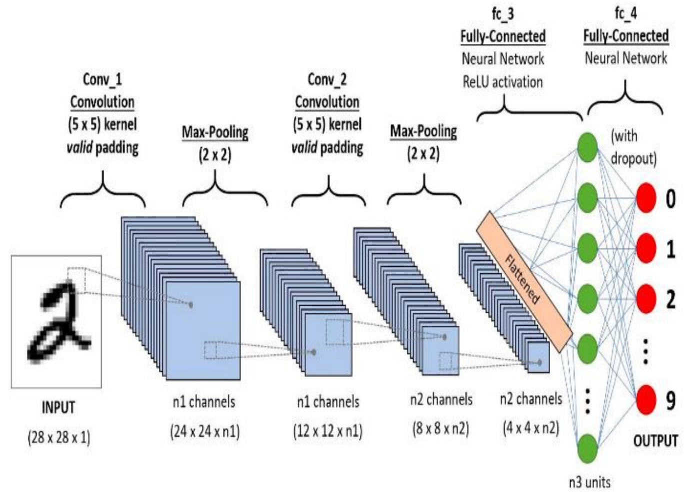
Convolutional layers are the layers where filters are applied to the original image, or to other feature maps in a deep CNN. This is where most of the user-specified parameters are in the network. The most important parameters are the number of kernels and the size of the kernels.

**Pooling layers**

Convolutional networks may include local and/or global pooling layers along with traditional convolutional layers. Pooling layers reduce the dimensions of data by combining the outputs of neuron clusters at one layer into a single neuron in the next layer. Local pooling combines small clusters, and tiling sizes such as 2 x 2 are commonly used. Global pooling acts on all the neurons of the feature map. There are two common types of pooling in popular use: max and average. Max pooling uses the maximum value of each local cluster of neurons in the feature map, while average pooling takes the average value.

**Fully connected layers**

Fully connected layers connect every neuron in one layer to every neuron in another layer. It is the same as a traditional multilayer perceptron neural network (MLP). The flattened matrix goes through a fully connected layer to classify the image (Albawi *et al.*, 2017).




**Transfer Learning**

Transfer learning (TL) is a research problem in machine learning (ML) that focuses on storing knowledge gained while solving one problem and applying it to a different but related problem. For example, knowledge gained while learning to recognize cars could apply when trying to recognize trucks. This area of research bears some relation to the long history of psychological literature on the transfer of learning, although practical ties between the two fields are limited. From a practical standpoint, reusing or transferring information from previously learned tasks for the learning of new tasks has the potential to significantly improve the sample efficiency of a reinforcement learning agent (Zhuang *et al.*, 2020).

**Model Selection**

- **VGG16**

VGG16 is a convolution neural net (CNN) architecture that was used to win ILSVR(Imagenet) competition in 2014. It is considered to be one of the excellent vision model architectures to date. The unique thing about VGG16 is that instead of having a large number of hyperparameters they focused on having convolution layers of a 3x3 filter with a stride 1 and always used the same padding and maxpool layer of a 2x2 filter of stride 2. It follows this arrangement of convolution and max pool layers consistently throughout the whole architecture. In the end, it has 2 FC (fully connected layers) followed by a softmax for output. The 16 in VGG16 refers to it has 16 layers that have weights. This network is a pretty large network, and it has about 138 million (approx) parameters. (Tammina and Srikanth 2019).

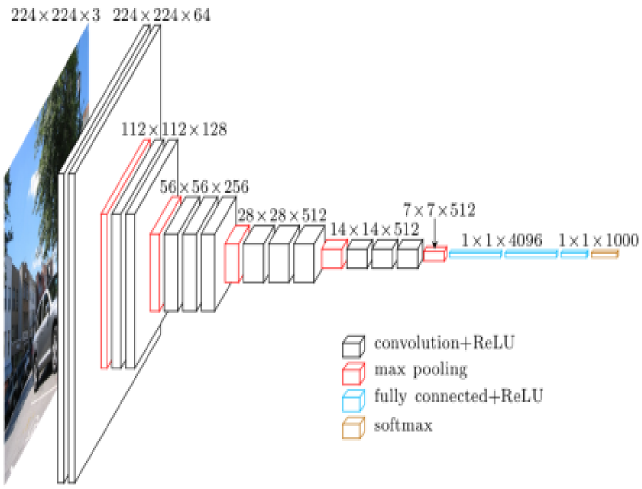



**Fig. 2**: Vgg Model

- **DenseNet**

In DenseNet, each layer obtains additional inputs from all preceding layers and passes on its own feature-maps to all subsequent layers. Concatenation is used. Each layer is receiving a "collective knowledge" from all preceding layers.

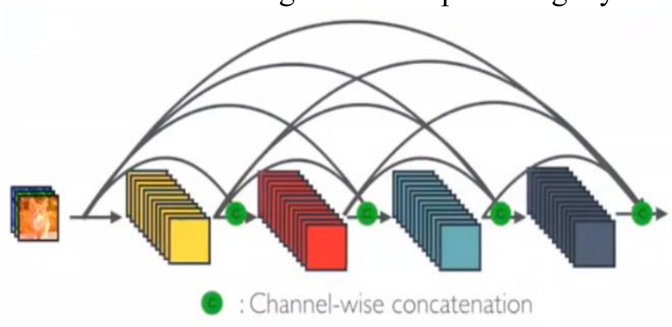



**Fig.3:** Single Layer Concatenation DenseNet

Since each layer receives feature maps from all preceding layers, the network can be thinner and more compact, i.e. number of channels can be fewer. The growth rate k is the additional number of channels for each layer. So, it has higher computational efficiency and memory efficiency. The following figure shows the concept of concatenation during forward propagation. (Huang *et al.*, 2017).

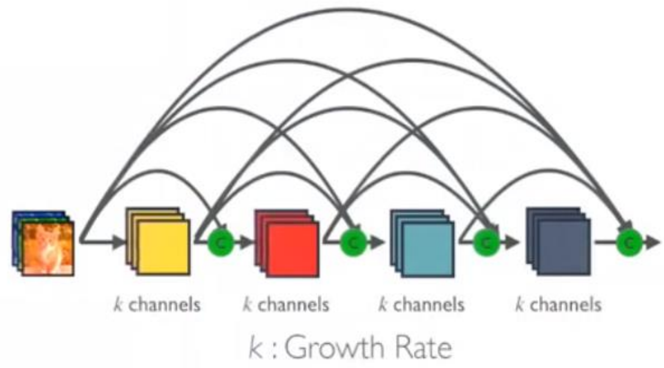



**Fig. 4:** Collective Concatenation DenseNet

- **MobileNetV2**

In MobileNetV2, there are two types of blocks. One is a residual block with a stride of 1, Another one is a block with a stride of 2 for downsizing. There are 3 layers for both types of blocks. This time, the first layer is 1×1 convolution with ReLU6. The second layer is the depth-wise convolution. The third layer is another 1×1 convolution, but without any non-linearity. It is claimed that if ReLU is used again, the deep networks only have the power of a linear classifier on the non-zero volume part of the output domain. And there is an expansion factor t. And t=6 for all main experiments. If the input got 64 channels, the internal output would get 64×t=64×6=384 channels. (Szegedy *et al.*, 2016).

- **InceptionResNetV2**

Inception-ResNet-v2 is a convolutional neural network that is trained on more than a million images from the ImageNet database. The network is 164 layers deep and can classify images into 1000 object categories, such as keyboard, mouse, pencil, and many animals.

Inception-ResNet-v2 is a variation of the Inception V3 model, and it is considerably deeper than the previous Inception V3. Below is the figure is an easier-to-read version of the same network where the repeated residual blocks have been compressed. Here, notice that the inception blocks have been simplified, containing fewer parallel towers than the previous Inception V3. The Inception-ResNet-v2 architecture is more accurate than the previous state-of-the-art models. (Szegedy., 2020).

### Implementation

The models we used are pre trained using the transfer learning method and imagenet nweights, an image data generator to generate images, AveragePooling2D, flatten, dense layers, and dropout layers. We also pre-processed the data and performed data augmentation, before detecting pneumonia. A classification matrix was also generated to evaluate *F*1-score, precision, and recall and then to calculate accuracy, sensitivity, and specificity.

We trained the models using the pre-processed data and the parameters used in the model are.

- The Epoch we used is 20, Batch Size-is 32 and the Learning rate is 10^-4.
- Average Pooling of pool size 2,2 then flatten the fully connected layer.
- We extracted 126 neurons with activation function as Relu and dropout of 0.5.
- We extracted 64 neurons with activation function as Relu and used dropout 0.5.
- We extracted 3 classification features Normal, Covid and Pneumonia. The activation function used was as Soft max.
- We used Adam optimizer and CategoricalCrossentropy for classification.

### Validation Parameters

### True Positive (TP)

The following table shows 3 examples of a True Positive (TP). The first row is a generic example, where 1 represents the Positive prediction. The following two rows are examples with labels. Internally, the algorithms would use the 1/0 representation, but I used labels here for a more intuitive understanding.

### False Positive (FP)

These False Positives (FP) examples illustrate making wrong predictions, predicting Positive samples for a actual Negative samples. Such failed prediction is called False Positive.

### True Negative (TN)

For the True Negative (TN) example, the cat classifier correctly identifies a photo as not having a cat in it, and the medical image as the patient having no cancer. So the prediction is Negative and correct (True).

### False Negative (FN)

In the False Negative (FN) case, the classifier has predicted a Negative result, while the actual result was positive. Like no cat when there is a cat. So, the prediction was Negative and wrong (False). Thus, it is a False Negative.

### Confusion Matrix

A confusion matrix is sometimes used to illustrate classifier performance based on the above four values (TP, FP, TN, FN). These are plotted against each other to show a confusion matrix.

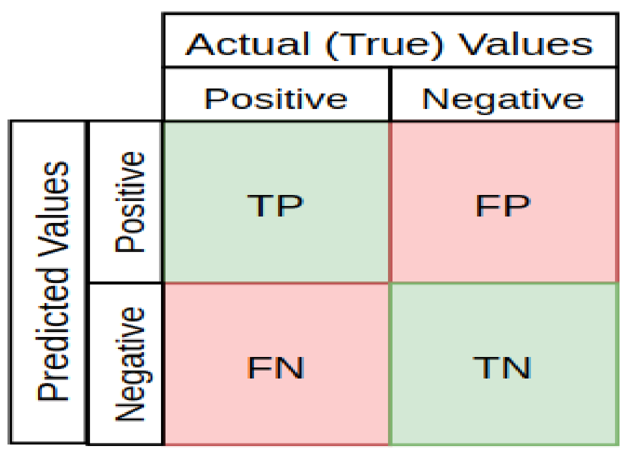



**Fig. 5:** Confusion Matrix Visualisation

The parameters we are using for validation are Precision, Recall / Sensitivity, f1-score, support

$$Accuracy\ (for\ each\ class) = \frac{TP+TN}{TP+FP+TN+FN}$$

$$Specificity = \frac{TN}{TN+FP}$$

$$Sensitivity = \frac{TP}{TP+FN}$$

$$Precision = \frac{TP}{TP+FP}$$

$$F1 = 2 \times \frac{Precision * Recall}{Precision + Recall}$$

**Dataset**

We have used two open-source datasets in our work. The covid chest X-ray dataset is taken from Kaggle (COVID-19 Radiography Database | Kaggle).This dataset consists of 3616 COVID-19 positive cases along with 10,192 Normal, 6012 Lung Opacity (Non-COVID lung infection), and 1345 Viral Pneumonia images and corresponding lung masks from different patients.

- **Preprocessing**

Chest X-ray images were only resized before applying as input to the networks. Input requirements for different CNNs are different. For mobilenetv2, ResNet18, ResNet101, VGG19 and DenseNet101, the images were resized to 224×224 pixels; and for InceptionResNetV2 the images were resized to 299×299 pixels. All images were normalized according to the pre-trained model standards. In the study1, the image augmentation technique was not applied to the training data. Since COVID-19 positive chest X-ray images were 3616, the number of X-ray images for normal (10,192) and viral pneumonia (1345) images. To balance the dataset we only use 1345 samples of normal and covid images and then shuffle them to obtain a more robust data set to work with.

Testing was done using a ratio of 80% for training and 20%. Moreover, the overall image number in any class was not several thousand. Therefore, Image augmentation techniques were applied to viral pneumonia, normal, and COVID-19 X-ray images for training to create a balanced training set.

**Image Augmentation**

We applied augmentation to include a greater number of images for our training. In this step of *data augmentation*, we will *rotate* and *flip* each of the images in our dataset. The rotation operation used for image augmentation was done by rotating the images in the clockwise and counter clockwise directions with an angle of 15 degrees.

**Results**

We used various models with imagenet weights to train our model for classification purposes. The Dataset consists of 1345 samples of covid, normal and viral pneumonia X-ray images.

- **VGG16**

As per table 1 the Accuracy achieved by using the vgg16 model is 94.8% with a 17.4% loss. The precision of COVID-19 prediction is 96%, recall is 92%, and the F1-score is 94%, whereas the precision for normal case detection is 92%, recall is 94%, F1-score is 93%, and the precision for pneumonia prediction is 97%, recall is 99%, and F1-score is 98%.

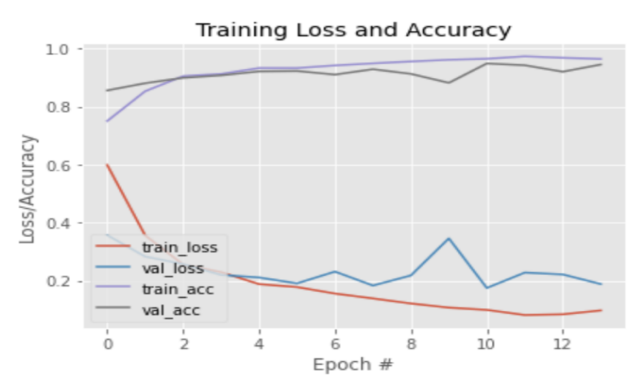



**Fig. 6:** Training Loss and accuracy VGG 16

**Table 1**: Test results of VGG16 Model

| | Precision | Recall/Sensitivity | F1 - Score | Support |
|---|---|---|---|---|
| **Covid** | .96 | .92 | .94 | 269 |
| **Normal** | .92 | .94 | .93 | 269 |
| **Viral Pneumonia** | .97 | .99 | .98 | 269 |
| **Accuracy** | | | .95 | 807 |
| **Macro accuracy** | .95 | .95 | .95 | 807 |
| **Weighted accuracy** | .95 | .95 | .95 | 807 |

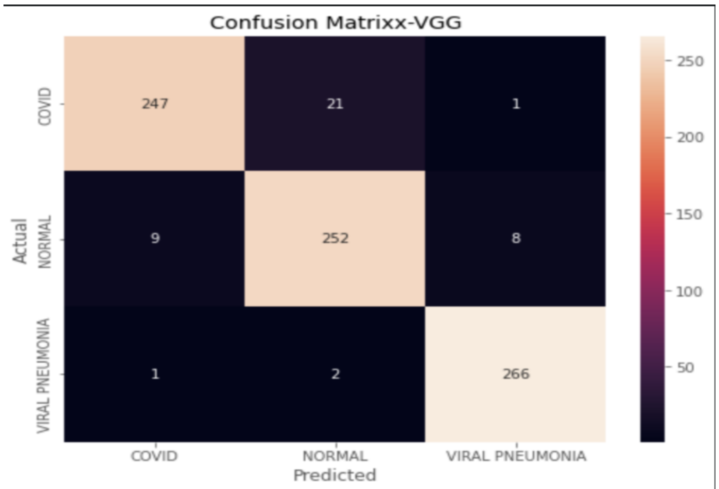



**Fig.7:** Confusion MATRIX COVID-19, Normal and Viral Pneumonia VGG 16

As per figure 7 above TP and TN covid prediction cases and FP and FN covid prediction cases to make this result clearer:

A total of 269 people were found to be affected with covid, and 247 people truly did not have pneumonia. Simultaneously, the model also gives false assumptions: a total of 21 people were falsely diagnosed as having covid while were normal.

- **DenseNet**

As per table 2 The Accuracy achieved by using the DenseNet model is 93.8% with a 19.4% loss. The precision of COVID-19 prediction is 93%, recall is 92%, and F1-score is 92%, whereas the precision for normal case detection is 91%, recall is 92%, F1-score is 91%, and the precision for pneumonia prediction is 98%, recall is 97%, and F1-score is 98%.

**Table 2:** Test results of DenseNet Model

| | Precision | Recall/Sensitivity | F1 - Score | Support |
|---|---|---|---|---|
| **Covid** | .93 | .92 | .92 | 269 |
| **Normal** | .91 | .92 | .91 | 269 |
| **Viral Pneumonia** | .98 | .97 | .98 | 269 |
| **Accuracy** | | | .94 | 807 |
| **Macro accuracy** | .94 | .94 | .94 | 807 |
| **Weighted accuracy** | .94 | .94 | .94 | 807 |

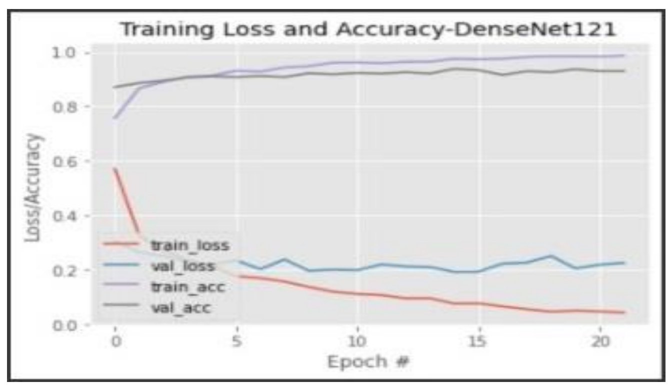



**Fig. 8**: Training Loss and accuracy DenseNet

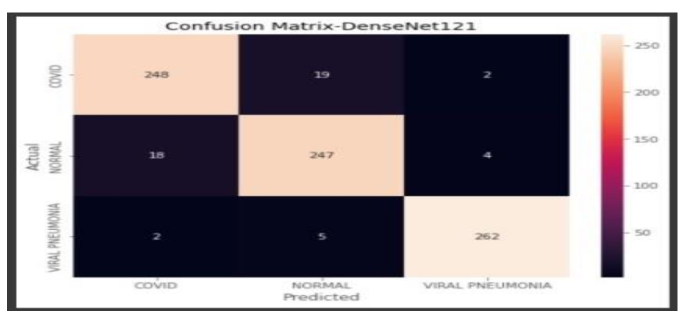



**Fig. 9:** Confusion MATRIX COVID-19, Normal AND Viral Pneumonia DenseNet

As per figure 9 TP and TN covid prediction cases and FP and FN covid prediction cases to make this result clearer:

A total of 269 people were found to be affected with covid, and 248 people truly did not have pneumonia. Simultaneously, the model also gives false assumptions: a total of 19 people were falsely diagnosed as having covid while were normal.

- ***MobileNetV2***

As per table 3 The Accuracy achieved by using MobileNetV2 model is 93.5% with 18.5% loss. The precision of COVID-19 prediction is 92%, recall is 94%, and F1-score is 93%, whereas the precision for normal case detection is 93%, recall is 89%, F1-score is 91%, and the precision for pneumonia prediction is 96%, recall is 98%, and F1-score is 97%.

**Table 3:** Test results of MobileNetV2 Model

| | Precision | Recall/Sensitivity | F1 - Score | Support |
|---|---|---|---|---|
| **Covid** | .92 | .94 | .93 | 269 |
| **Normal** | .93 | .89 | .91 | 269 |
| **Viral Pneumonia** | .96 | .98 | .97 | 269 |
| **Accuracy** | - | - | .94 | 807 |
| **Macro accuracy** | .94 | .94 | .94 | 807 |
| **Weighted accuracy** | .94 | .94 | .94 | 807 |

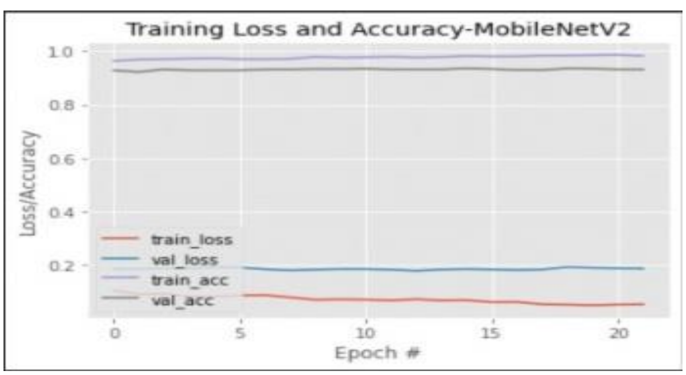



**Fig. 10:** Training Loss and accuracy MobileNetV2

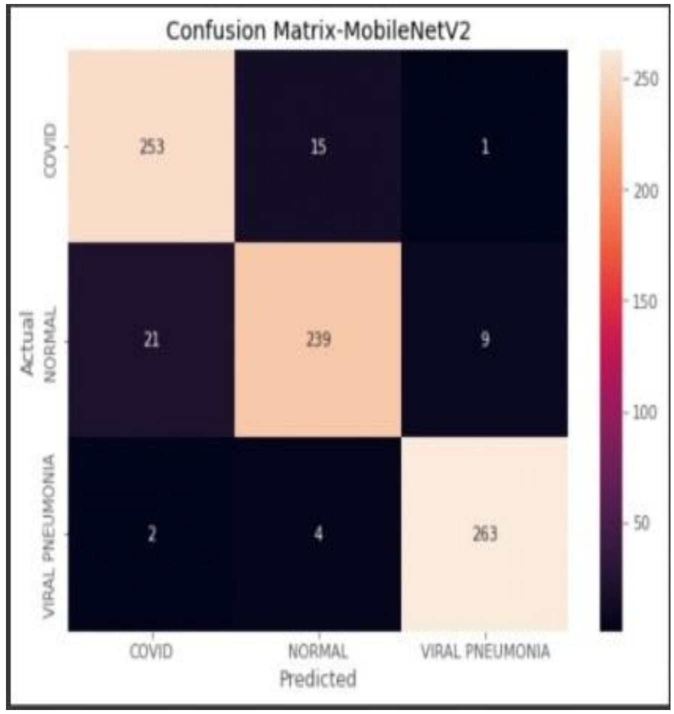



**Fig.11:** Confusion MATRIX COVID-19 , Normal AND Viral Pneumonia Mobil2NetV2

As per figure 11 TP and TN covid prediction cases and FP and FN covid prediction cases to make this result clearer:

A total of 269 people were found to be affected with covid, and 253 people truly did not have pneumonia. Simultaneously, the model also gives false assumptions: a total of 15 people were falsely diagnosed as having covid while were normal.

- **InceptionResNetV2**

As per table 4 The Accuracy achieved by using InceptionResNetV2 model is 91.5% with 27.8% loss. The precision of COVID-19 prediction is 89%, recall is 90%, and F1-score is 90%, whereas the precision for normal case detection is 89%, recall is 86%, F1-score is 88%, and the precision for pneumonia prediction is 96%, recall is 99%, and F1-score is 97%.

**Table 4:** Test results of InceptionResNetV2 Model

| | Precision | Recall/Sensitivity | F1 - Score | Support |
|---|---|---|---|---|
| **Covid** | .89 | .90 | .90 | 269 |
| **Normal** | .89 | .86 | .88 | 269 |
| **Viral Pneumonia** | .96 | .99 | .97 | 269 |
| **Accuracy** | | | .92 | 807 |
| **Macro accuracy** | .92 | .92 | .92 | 807 |
| **Weighted accuracy** | .92 | .92 | .92 | 807 |

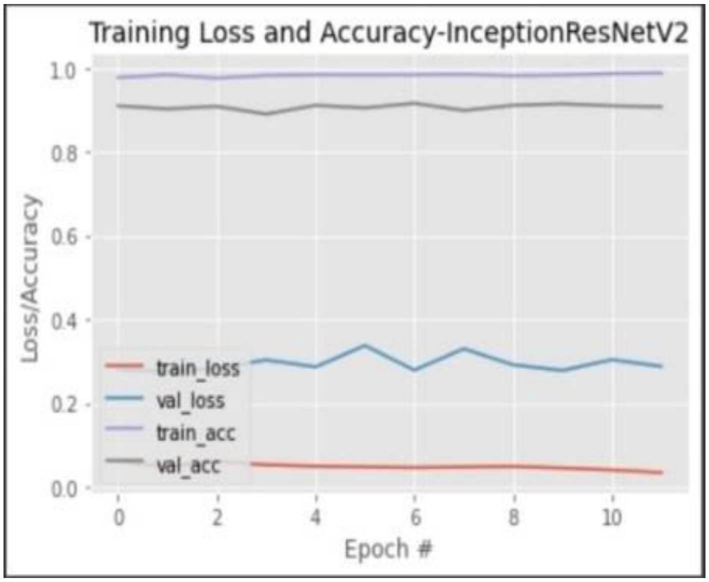



**Fig. 12:** Training Loss and accuracy InseptionResNetv2

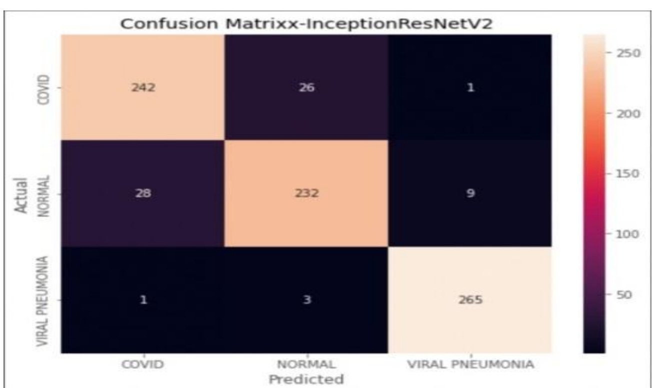



**Fig.13:** Confusion MATRIX COVID-19, Normal and Viral Pneumonia InseptionResNetV2

As per figure 13 TP and TN covid prediction cases and FP and FN covid prediction cases to make this result clearer: a total of 269 people were found to be affected with covid, and 242 people truly did not have pneumonia. Simultaneously, the model also gives false assumptions: a total of 26 people were falsely diagnosed as having covid while we're normal.

## Conclusion

Even after the development of vaccines, Covid-19 disease is a genuine danger because of its quick spreading conduct. In view of inadequate health services and an extremely thick populace in India, the disease should be considered very intimidating.

This research suggests deep learning techniques using lung X-ray images to identify COVID-19- pneumonia patients.

The Dataset we obtained consists of 10192 Normal, 3161 Covid, and 1345 Viral Pneumonia images, so to balance the dataset we only use 1345 samples of normal and covid images and then shuffle them to obtain a more robust data set to be work with.

The research showed the best performance in differentiating COVID-19 patients and pneumonia patients using the VGG16 model.

Although the other models were comparable in accuracy, the VGG16 is the model with the highest precision and F1 score in COVID-19 classification and minimum false positive and false negative COVID-19 values.

It also reduces training loss and increases accuracy. Parallel testing can be used in the current scenario to prevent infection spread to frontline workers and generate primary diagnoses to determine whether a patient is affected by COVID-19.

The F1 score for pneumonia detection was very high, Therefore, the proposed method can be used as an alternative diagnostic tool for detecting pneumonia cases. Future research can improve the

CNN architecture performance by adjusting the hyperparameters and transfer learning combinations. Another feasible way to determine the best model for pneumonia and COVID-19 could be an improved, complex network structure.

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