Automatic COVID-19 Diagnosis System Based on Deep Convolutional Neural Networks

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ABSTRACT

A public health emergency threat is happening due to novel coronavirus 2019 (nCoV-2019) throughout the world. nCoV-2019 is also named Severe Acute Respiratory Syndrome-CoronaVirus-2 (SARS-CoV-2). COVID-19 is the disease caused by this virus. The virus originates in bats and is transmitted to humans by some unidentified intermediate animals. This virus started around December 2019 at Wuhan of China. After that, it turned into a pandemic. Even though there is no efficient vaccination, the entire world fights against the COVID-19. This article presents an overview of the scenario of the world as well as India. Some of the leading countries in the world are also affected by this virus badly. Even India is the 2nd highest population, is taking necessary precautions to protect it. With the Government of India's decisions, along with effective social distancing and hygienic measures, India is in a better position. But, in the future, COVID19 cases in India, still unpredictable. We designed an algorithm based on Convolutional Neural Network (CNN), which helps to classify COVID19+ and COVID19- persons using people's chest X-ray images automatically generated within the shortest time. The proposed method discovered that employing CT scan medical images produced more accurate results than X-ray images.

1. INTRODUCTION

In 2019, the novel Corona Virus (nCoV-2019) or Severe Acute Respiratory Syndrome-CoronaVirus-2 (SARS-CoV-2) spread exponentially from Wuhan City, the capital of China Hubei Province, to the rest of the countries [1]. The root cause of this virus came from bats to humans, and unknown intermediate animals transmitted it. From there onwards, it spreads human to human [2]. Coronavirus first started in December 2019 in China. Firstly, it considers an epidemic when it is in China, but rapidly it spreads to the other countries, become into a pandemic. On 30 January 2020 COVID-19 was declared an international emergency for public health by the World Health Organization (WHO), and also, it has announced the novel COVID-19 outbreak a global pandemic on 11th March 2020 by WHO Director-General, Dr. Tedros Adhanom Ghebreyesus [3]. From December 2019 to March 2022, around 472 816 657 confirmed cases and 6 099 380 confirmed deaths have been reported from 213 out of 233 countries or territories globally [4], and its graphical representation shown in Figure 1.

To diagnose COVID-19 disease, present a few diagnostic test methods [5] are available, they are Reverse Transcription Polymerase Chain Reaction (RT-PCR), this is present test system for COVID-19. Still, it is too costly. Another diagnostic system is Loop-Mediated Isothermal Amplification (LAMP): It is a less developed testing system. Lateral flow is another testing system that is hand-held but single-use for an individual patient. An enzyme-linked immunosorbent assay (ELISA) fast and simple usage system ELISA test is not yet well for COVID-19 testing. All these diagnostic systems had

their limitations, due to that the current situation demands a fast, cost-efficient, and accurate method.

In India, a total of 43,018,032 COVID19+ cases and 520,885 deaths have been reported up to March 2022, included with 111 foreign nationals, belonging to 32 states/union territories [6]. The COVID19+ cases report of each state in India is shown in Figure 2, a graphical representation; of the data provided by the Indian government [7]. The disease is mainly caused by the transmission of droplets, contact with infected persons. The fecal-oral transmission was also observed in the fecal samples of the USA and China affected persons [8, 9]. The incubation period of this virus in the human body is approximately 2 to 14 days. During this period, may observe the symptoms like dry cough, fever, throat pain, breathing problem, uneasiness.

Krishna and Kalluri [10] gave a brief review of the CNN and pre-trained networks about detecting and recognizing objects. Sajja et al. [11] proposed a novel network, which detects lung cancer very effectively. The researchers proposed net classifying the malignant and benign CT scan images with 99% accuracy in lung cancer. Hussain et al. [12] used a transfer learning technique to classify the images from large datasets and got 96.5% accuracy. Sethy and Behera [13] compared with the existing networks such as AlexNet, VGG16, VGG19, Resnet50, and GooleNet and decided that ResNet50 gave 95.38% accuracy, which detects the COVID19 disease based on features. Sajja and Kalluri [14] have classified Gender through SVM and SCGBPNN. In this method, the features are extracted manually using the LBPH method. Later, the feature vector is fed to polynomial SVM and SCG Back Propagation Neural Network to achieve 100% accuracy. Still,

this method is applied for small datasets, and also, this is not automatic. Pandit et al. [15] the authors explored the results by using the VGG-16 model for classification, they reported 96% accuracy only.

Al-Waisy et al. [16] The suggested COVID-CheXNet system improved image quality and reduced noise by using the CLAHE technique and the Butterworth bandpass filter, respectively. The suggested COVID-CheXNet system has achieved comparable results to expert radiologists, with a DAR of 99.99%.

The remaining manuscript is explained as follows: The history, symptoms, and preventive measures of the coronavirus are briefed in Section 2. Section 3 discussed the methodology of the proposed system. Section 4 gives the experimental setup and results of the network. The conclusions are made in Section 5.
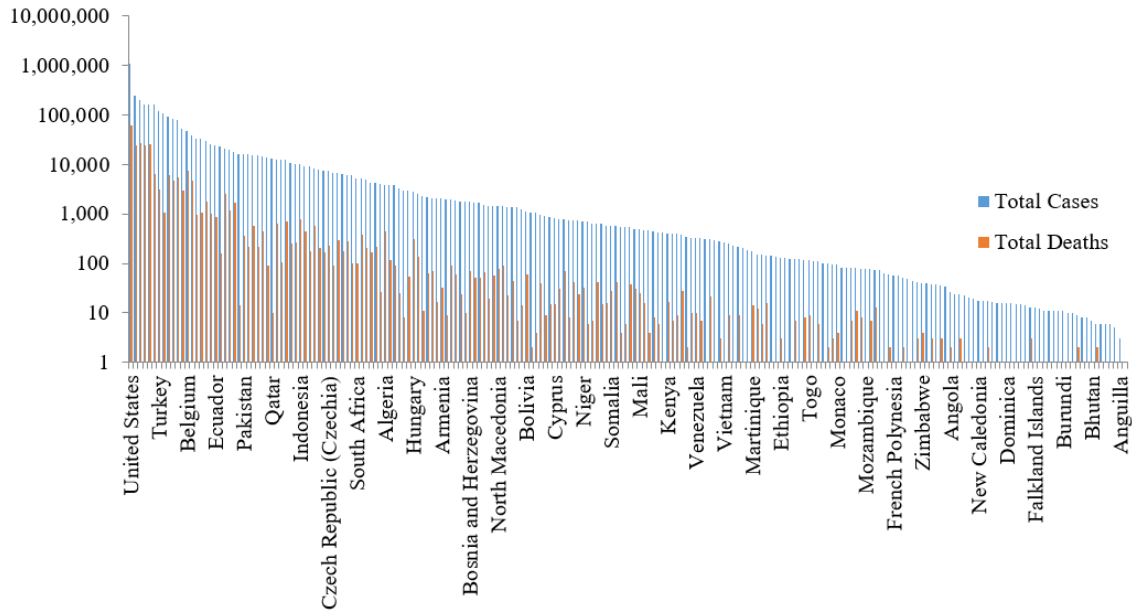

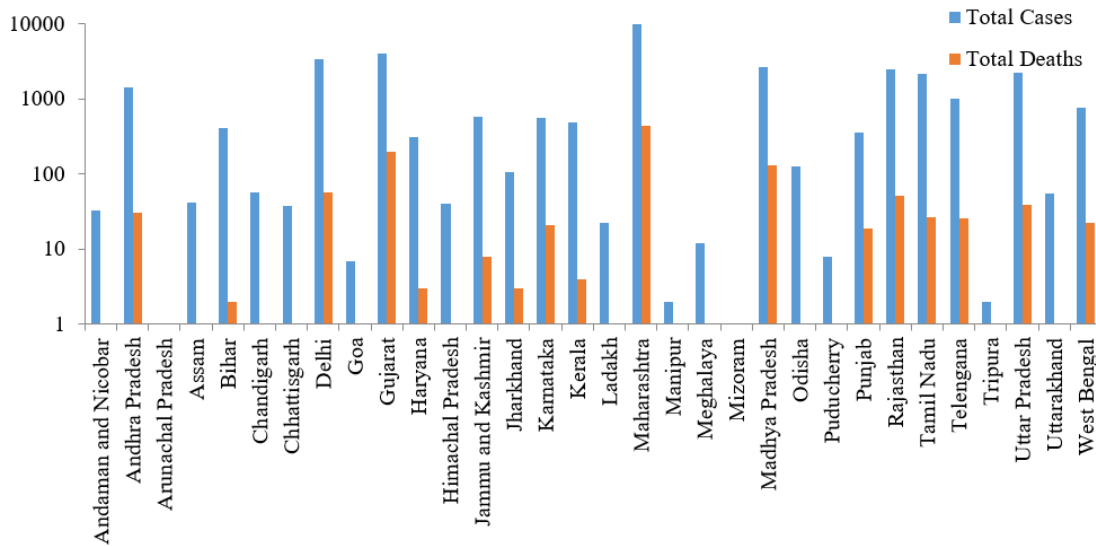**Figure 1.** Country/Territories COVID-19 report in Globe

Figure 2. State-wise COVID-19 report in India

2. HISTORY

Since December 2019, in Wuhan of China, patients have been continuously suffering from fever, dry cough, reduced number of white blood cells diagnosed as pneumonia. SARS - CoV-2 has been identified as the agent causing this unexplained infected pneumonia. After that, bat coronaviruses were given special attention. Because two coronaviruses have already emerged that cause unexpected illnesses in humans.

The 21st century is due for bats as a consequence of Severe Acute Coronavirus Syndrome (SARS-CoV) and the Middle-

Eastern Coronavirus Respiratory Syndrome (MERS-CoV). So, Bats are identified as the potential repositories of a wide variety of viruses [2]. Various known coronaviruses are circulating in animals, but humans do not yet infect them. Earlier, two coronaviruses are observed as epidemics [17]. SARS source country is Hong Kong in China; SARS-CoV was transmitted due to Asian civet cats to humans in China in 2002. MERS source country is Saudi Arabia. MERS-CoV was transmitted due to camels to humans in Saudi Arabia in 2012. In 2019, the pandemic novel Corona Virus source country was China's Wuhan city. nCoV-2019 transmitted through

unknown animals to humans. Flowchart for the transition of the virus and the sources of coronavirus seen in Figure 3. Based on currently available information, coronaviruses may be transmitted from person to person through droplets or contact, etc. The reported cases and death cases of total and origin country, the relationship of SARS, MERS, and COVID19 are shown in Figure 4 for comparative purposes.

For conversational sake, some buzzwords are used to know the importance of those and help understand the health news. Regularly some words we frequently hear such as Pandemic, Epidemic, and Outbreak [18].

• AN EPIDEMIC is a buzzword that describes a disease that affects a wide geographical region of more people than usual, for example, Ebola.

• A PANDEMIC is an epidemic; it spreads in a geographical region and affects Whole County or multiple countries.

AN OUTBREAK is an increasingly unknown disease rapidly than expected. If it is not controlled, then it can become an epidemic.

Present, the entire world is rigorously fighting with an invisible enemy, which is popular nowadays as the coronavirus. The disease caused by this virus is termed COVID-19 [19]. The persons affected by this virus are called COVID-19+ patients. Under the microscope, the virus appears as a point structure that is covered like a crown. The schematic diagram of the coronavirus is shown in Figure 5.

Coronavirus structure has four main structural proteins, such Spike protein (S), Membrane protein(M), an Envelope protein (E), and Nucleoprotein (N) [20].

Spike Protein (S)

Coronavirus, Spike, S is an important viral transcriptional protein multifunctional. The S protein is between 1160 and 1400 amino acids. The Spike is preferably one of the vital immune-dominant coronaviral proteins which can induce immune action in the host.

Membrane Protein (M)

The M protein is the viral protein most critically found in a virion particle and gives the viral envelope a definite form. It contains N protein and acts as a key organizer for the assembly of coronaviruses.

Envelope Protein (E)

The coronaviruses, E, are the smallest and most enigmatic of the main structural proteins. In pathogenesis, assemblage, and release of the virus, it has a multifunctional role.

Nucleoprotein (N)

Coronavirus N protein is multifunctional. The M protein interaction, which is necessary during the virus assembly, facilitates and improves the virus transcription efficiency, plays a part among several functionalities in complex formation.

Symptoms

In humans, novel coronavirus (nCoV-2019) causes a mild infection in the upper respiratory portion, like the common old, but more severe in lower respiratory region infections. These infections have been declared as pneumonia or a severe respiratory illness called a nCoV SARS-2 or coronavirus disease 19 (COVID-19). If persons are affected with COVID-19, they might be suffering from some symptoms like dry cough, fever, runny nose, muscle aches, sore throat, and taste loss. Some rare cases may lead to severe breathing problems, kidney failure, and causes death.

Preventive measures

Still, there is no vaccination for nCoV-2019 but follows social distancing and maintains effective hygienic practices [21]. The two most successful preventive measures to control the outbreak are currently in place.

The only efficient method is Lockdown to maintain social distancing. Chloroquine derivative hydroxyl chloroquine (HCQ) sulfate is effective against novel coronavirus [22]. Fortunately, this drug is produced in India, despite the shortage of medicines. All countries urged for medicines [23].

As COVID-19+ growth rates grew up on 21 March 2020, Indian Prime Minister Shri Narendra Modi, on 22 March 2020, declared "Janata Curfew" a one-day lockdown, which reduced positive growth from 3 to 1 [24]. This led to a 21-day further Lockdown declaration in the country until 14 April 2020. During this period, the cases were increased rapidly. The government focused on the rapid growth, then the viral news coming out as most of the positive persons participate, a religious meeting named "TablighiJamaat" at Nizamuddin in Delhi held in March. Day by day, the cases are grown; this leads to the lockdown period further extended up to 3rd May 2020 again it was extended to 17th May 2020. Due to this Lockdown and self-hygienic, the positive cases are significantly less compared to other countries in India.
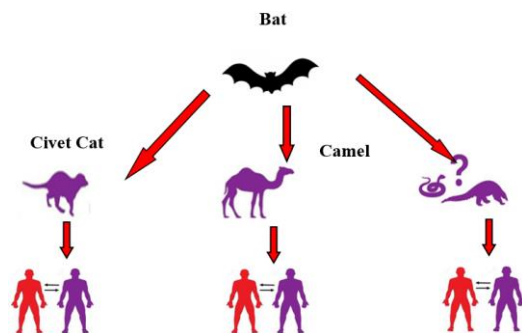

Figure 3. Flowchart for coronavirus transition from the origin (Bat) to human
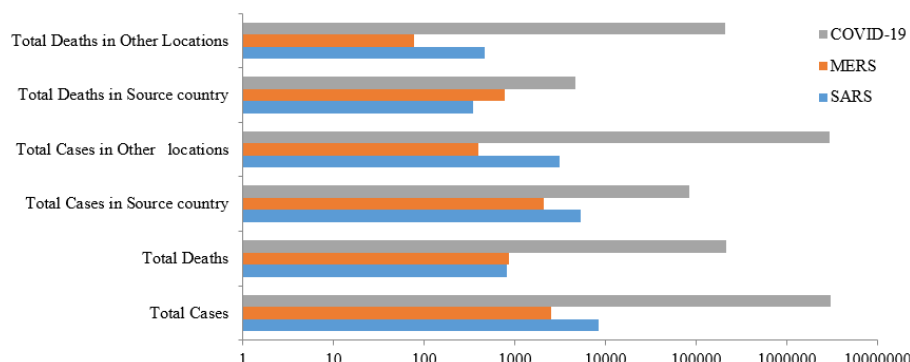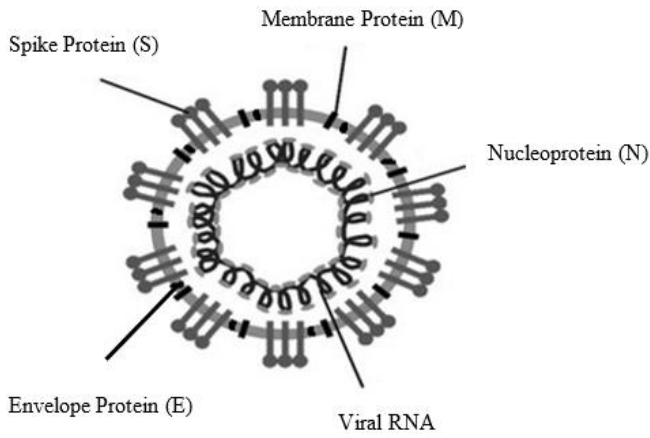

Figure 4. Comparative relation between SARS, MERS, and COVID-19 cases the origin (Bat) to human

Coronavirus

Figure 5. Schematic representation of the nCov-2019 structure the origin (Bat) to human

3. METHODS

Currently, due to a lack of diagnosis systems everywhere, this causes a panic situation. From the above section, we concluded the COVID19 attacks on the respiratory system, so we can use X-ray images to analyze the patient belongs to COVID19+ or COVID19-. The X-ray images are easily available with the diagnostics, and nearly all hospitals have X-ray machines. It is possible to use X-ray images to test this disease without particular test kits. Based on the X-ray images, we can't say directly whether a person is negative or positive. We need a radiology expert who belongs to analyze the X-ray images properly, which is also time taking and precious in this situation. Therefore, an automated system is necessary to make decisions that save experts' time.

This paper proposed a model to classify the positive and negative persons based on the automated system. This system constitutes convolutional neural networks. For classifications some existing architectures developed such as AlexNet [25], GoogleNet [26], VGG16 [27, 28], VGG19 [28] and ResNet50 [28, 29]. The problem is analyzed using these existing architectures and the proposed model. To sum up, the performance of the proposed model is better than modern models. The proposed architecture and a detailed module view are shown in Figure 6.

The proposed network consists of an input layer that accepts a 224x224 size image, followed by three convolutional layers before modules, a fully connected layer, a softmax layer, and an output classification layer. In the proposed network, we used six modules containing a stack of convolutional layers. Each module is constructed with different sizes of kernels. Instead of applying the kernels directly in the module, we used 1x1 convolution before kernels (3x3, 5x5), then all the convolution results are concatenated at the end of the module. Because of these 1x1 convolutions, the number of dimensions was reduced drastically, which leads to less learnable parameters. The proposed net was trained with 2,618,722 lakhs, learnable parameters, detailed layers, and learnable parameters in Table 1. The proposed net achieved good performance with lakhs of parameters only, but pre-trained networks trained with millions of parameters [10]. The parameter comparison with pre-trained networks is placed in Table 2. It achieves better performance results than the existing nets.
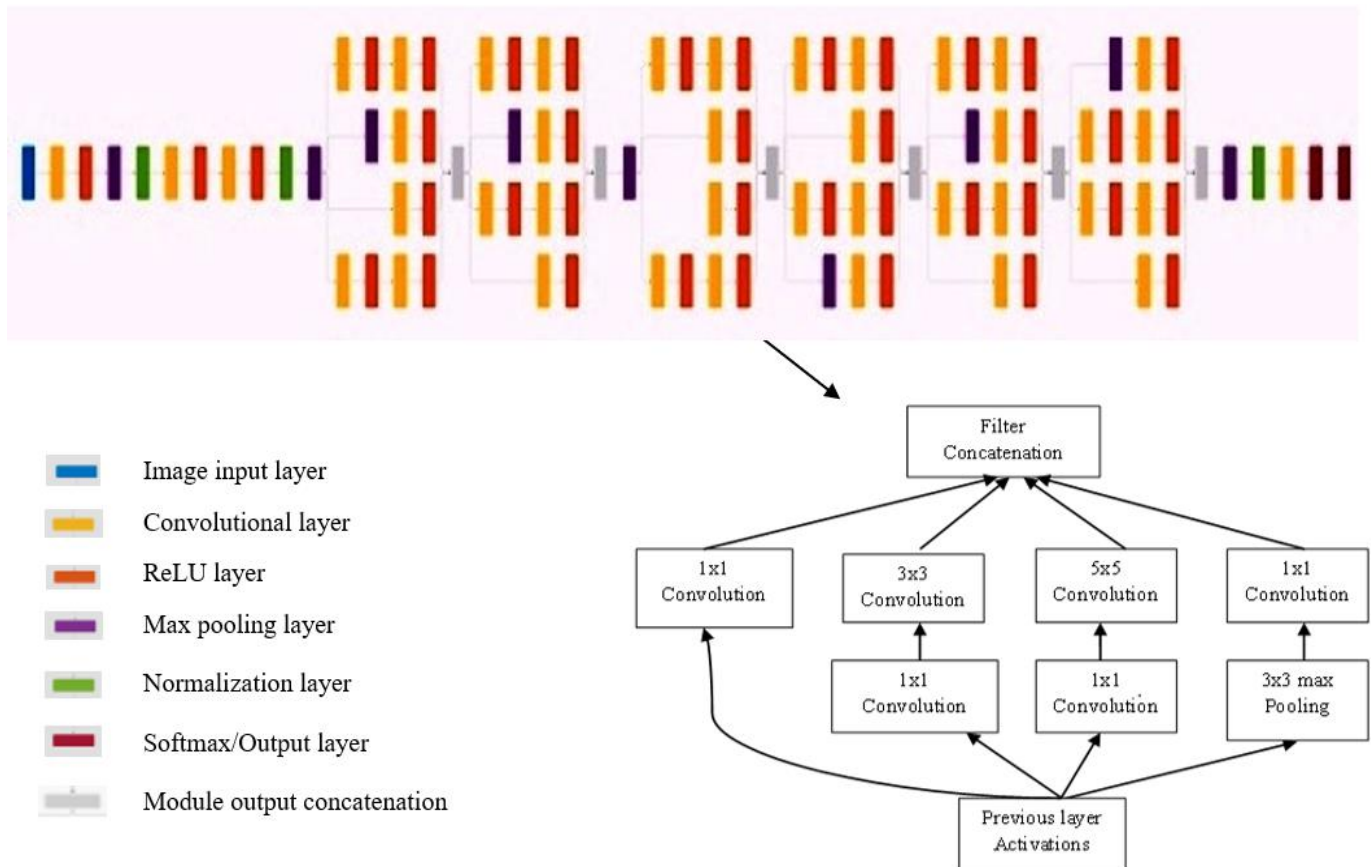
Figure 6. Proposed architecture (from left to right)

Table 1. Proposed net parameter calculations for convolutional layers and their modules

Name	Kernel Size	Activations	Learnable	Total Learnables Parameters
conv1	7x7	112×112×64	Weights, Bias, 7×7×3×64, 1×1×64	9472
conv2	1x1	56×56×64	Weights, Bias, 1×1×64×64, 1×1×64	4160
conv3	3x3	56×56×192	Weights, Bias, 3×3×64×192, 1×1×192	110784
module 1	3x3_reduce	28×28×96	Weights, Bias, 1×1×192×96, 1×1×96	18528
	1x1	28×28×64	Weights, Bias, 1×1×192×64, 1×1×64	12352
	5x5_reduce	28×28×16	Weights, Bias, 1×1×192×16, 1×1×16	3088
	pool_proj	28×28×32	Weights, Bias, 1×1×192×32, 1×1×32	6176
	5x5	28×28×32	Weights, Bias, 5×5×16×32, 1×1×32	12832
	3x3	28×28×128	Weights, Bias, 3×3×96×128, 1×1×128	110720
module 2	3x3_reduce	28×28×128	Weights, Bias, 1×1×256×128, 1×1×128	32896
	pool_proj	28×28×64	Weights, Bias, 1×1×256×64, 1×1×64	16448
	3x3	28×28×192	Weights, Bias, 3×3×128×192, 1×1×192	221376
	1x1	28×28×128	Weights, Bias, 1×1×256×128, 1×1×128	32896
	5x5_reduce	28×28×32	Weights, Bias, 1×1×256×32, 1×1×32	8224
	5x5	28×28×96	Weights, Bias, 5×5×32×96, 1×1×96	76896
module 3	5x5_reduce	14×14×16	Weights, Bias, 1×1×480×16, 1×1×16	7696
	1x1	14×14×192	Weights, Bias, 1×1×480×192, 1×1×192	92352
	5x5	14×14×48	Weights, Bias, 5×5×16×48, 1×1×48	19248
	3x3_reduce	14×14×96	Weights, Bias, 1×1×480×96, 1×1×96	46176
	3x3	14×14×208	Weights, Bias, 3×3×96×208, 1×1×208	179920
	pool_proj	14×14×64	Weights, Bias, 1×1×480×64, 1×1×64	30784
module 4	5x5_reduce	14×14×24	Weights, Bias, 1×1×512×24, 1×1×24	12312
	5x5	14×14×64	Weights, Bias, 5×5×24×64, 1×1×64	38464
	3x3_reduce	14×14×112	Weights, Bias, 1×1×512×112, 1×1×112	57456
	3x3	14×14×224	Weights, Bias, 3×3×112×224, 1×1×224	226016
	pool_proj	14×14×64	Weights, Bias, 1×1×512×64, 1×1×64	32832
	1x1	14×14×160	Weights, Bias, 1×1×512×160, 1×1×160	82080
module 5	3x3_reduce	14×14×128	Weights, Bias, 1×1×512×128, 1×1×128	65664
	1x1	14×14×128	Weights, Bias, 1×1×512×128, 1×1×128	65664
	5x5_reduce	14×14×24	Weights, Bias, 1×1×512×24, 1×1×24	12312
	pool_proj	14×14×64	Weights, Bias, 1×1×512×64, 1×1×64	32832
	5x5	14×14×64	Weights, Bias, 5×5×24×64, 1×1×64	38464
	3x3	14×14×256	Weights, Bias, 3×3×128×256, 1×1×256	295168
module 6	3x3_reduce	14×14×144	Weights, Bias, 1×1×512×144, 1×1×144	73872
	5x5_reduce	14×14×32	Weights, Bias, 1×1×512×32, 1×1×32	16416
	1x1	14×14×112	Weights, Bias, 1×1×512×112, 1×1×112	57456
	3x3	14×14×288	Weights, Bias, 3×3×144×288, 1×1×288	373536
	5x5	14×14×64	Weights, Bias, 5×5×32×64, 1×1×64	51264
	pool_proj	14×14×64	Weights, Bias, 1×1×512×64, 1×1×64	32832
	Dropout	1×1×528	-	0
	Fully Connected	1×1×2	Weights, Bias, 2×528, 2×1	1058
		Total parameters		2618722

Table 2. Parameter comparison with proposed net and pre-trained model

Model	Learnable Parameters
Alexnet	62.3 million
VGG16	138 million
VGG19	143 million
GoogleNet	4 million
Resnet50	25 million
Proposed Net	**2.6 million**

The proposed net uses different layers; the explanation regarding each layer is discussed in the following.

3.1 Input layer

It holds the raw pixels of the image; the network accepts the WidthxHeightxDepth (WxHxD) image. This is the first layer of the network.

3.2 Convolutional layer

The stacks of kernels are convolved on top of the image, which gives a convolved stack of images. This layer accepts the input from the input layer as WinxHinxDin and need hyperparameters like filter size f, Stride s, padding p, number of kernels k, and produce output size as WoutxHoutxDout.

Here Wout, Hout, and Doutcalculated from Eq. (1).

$$\left. \begin{array}{l} Wout = (Win - f + 2p)/(s + 1) \\ Hout = (Hin - f + 2p)/(s + 1) \\ Dout = k \end{array} \right\} \quad (1)$$

3.3 Activation function

This is one type of activation function. In neural networks, the most popular activation function is ReLU. Mathematically it is defined from Eq. (2). For all negative input values, it is zero.

$$b = \max(0, a) \qquad (2)$$

$$f(a) = \begin{cases} 0, & a < 0 \\ a, & a \geq 0 \end{cases} \qquad (3)$$

Here f(a) is zero when a is less than zero, and f(a) is equal to a when a is greater than or equal to zero.

3.4 Max-pooling layer

Pooling layers have three types, max pooling, min pooling, and average pooling. In our proposed net, max pooling is used because it gives a high value from the specified block, has significant features. This layer accepts the input from the input layer as WprevxHprevxDprev and need hyperparameters like filter size f, Stride s, and produce output size as WnxtxHnxtxDnxt.

Here Wnxt, Hnxt, and Dnxt. Calculated from Eq. (3).

$$\left. \begin{array}{l} Wnxt = (Wprev - f)/(s + 1) \\ Hnxt = (Hprev - f)/(s + 1) \\ Dnxt = Dprev \end{array} \right\} \qquad (4)$$

3.5 Normalization layer

After fetching the features, the range of all features is not in the same range; this causes the learning delay. To speed up the learning process, we have to normalize all the features from 0 to 1. This normalization done batch-wise is called Batch Normalization.

$$y = \frac{x_i - \mu_b}{\sqrt{\sigma_b^2 + \epsilon}} \qquad (5)$$

where,

$$\sigma_b = \frac{1}{m} \sum_{i=1}^{m} (x_i - \mu_b)^2 \qquad (6)$$

$$\mu_b = \frac{1}{m} x_i \qquad (7)$$

m=Number of inputs; xi= 1 to m.
σ_b=standard deviation; μ_b=Mean of input data; y=normalized values.

3.6 Softmax layer

This is also an activation function like ReLU, etc. This layer gives the probabilities of the input classes for the output within the range of 0 to 1. The probabilities are calculated using Eq. (7).

$$f(x) = \frac{\exp(x_i)}{\sum_{j=0}^{u} \exp(x_j)} \qquad (8)$$

where i=0, 1, …, u.

3.7 Dropout

This is used for regularization purposes. During the training phase, randomly, some specified percentage of neurons are deactivated to prevent overfitting. The name itself indicated the dropout of the neurons. In the proposed network, 50% of the neurons were dropped.

3.8 Fully connected layer

Data taken from the previous layer is converted into a 1-D vector and predict the correct labels. And calculate the probabilities of each label. The usage of the fully connected layer in each model may be different. The equation is for this layer is shown in Eq. (8). The parameter for the fully connected layer is 2 in our proposed model because the classes are 2.

$$s_i = \sum_j w_{ij} y_j \qquad (9)$$

where i,j represents neuron number, w_ij weight in the hidden layer, y_j value of hidden neuron, s_i the output value for this layer.

3.9 Output layer

This layer gives the final classification output from the probabilities of the softmax layer. The output is equal to the number of classes. In this proposed net, the model concludes COVID19+ and COVID19- the patient.

4. EXPERIMENTAL RESULTS

Dataset 1
A research team from various countries created this X-ray image dataset in collaboration with doctors in the medical field [30]. The dataset includes 219 X-ray images and 1,341 pictures of normal people. The X-ray images infected are grouped into COVID-19+ and normal COVID-19- pictures are collected. In the Kaggle repository, the X-ray images are collected. The details of the dataset are shown in Table 3, and some of the images are shown in Figure 7.
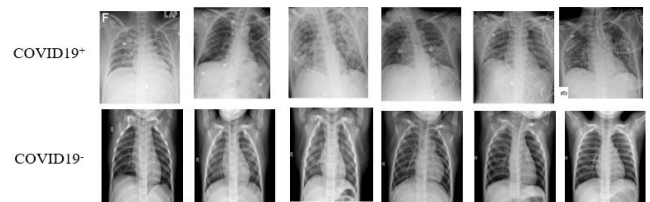

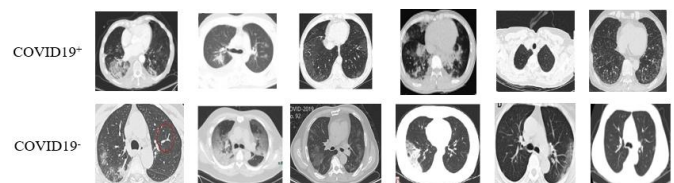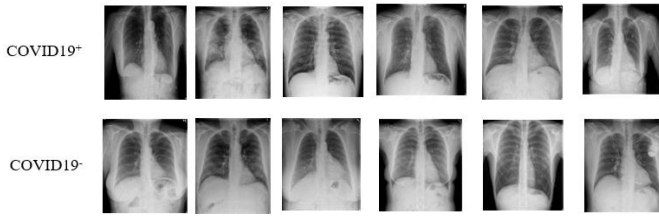**Figure 7.** Sample images of an infected and normal from Dataset 1

Figure 8. Sample images of an infected and normal from Dataset 2

Figure 9. Sample images of an infected and normal from Dataset 3

Dataset 2

COVID-19 CT scan images [31] are very useful during the pandemic. This dataset was available publicly with a total number of 746 images of JPG format. Out of total images 349 positive cases and 397 negative cases. All images were captured from same equipment. The details of the dataset are shown in Table 3, and some of the images are shown in Figure 8.

Dataset 3

COVIDGR dataset [32] contains total of 852 images. They are categorized into COVID-19+ and COVID-19- cases, 426 positive cases and 426 negative cases. These images were captured using RT-PCR within a time span of at most 24 hours between the x-ray scanned image and the test. The details of the dataset are shown in Table 3, and some of the images are shown in Figure 9.

Performance metrics

A confusion matrix is a flexible and possible visual depiction of the performance of architecture in a binary or multi-class class. Basic terminology for model performance measurement [33].

True Positive (TP): A person's chest image is predicted as positive, and its ground truth is also positive.

True Negative (TN): A person's chest image is predicted as Negative, and its ground truth is also Negative.

False Positive (FP): A chest image of a person is predicted as Negative, but actually, it is positive.

False Negative (FN): A person's chest image is predicted as positive, but it is negative.

The performance of the proposed model is measured by using the Eqns. (10)-(14).

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN} \tag{10}$$

$$Sensitivity \text{ or recall} = \frac{TP}{TP + FN} \tag{11}$$

$$Specificity = \frac{FP}{FP + TN} \tag{12}$$

$$Precision = \frac{TP}{FP + TP} \tag{13}$$

$$F - score = \frac{2 * precision * recall}{precision + recall} \tag{14}$$

Table 3. Details about datasets

		# of Images	Total Images	Image Format
X-ray Images	COVID-19+	219	1560	PNG
	COVID-19-	1341		
COVID-19 CT Scan Images	COVID-19+	349	746	JPG
	COVID-19-	397		
COVID-19 GR X-ray Images	COVID-19+	426	852	JPG
	COVID-19-	426		

Table 4. Analysis of different existing classification models with proposed CNN model on various datasets

Model	Accuracy	Sensitivity	Specificity	Precision	F-Score
Alexnet	81.20	81.20	81.20	67.64	87.20
VGG16	92.76	97.47	88.05	64.56	90.76
VGG19	92.91	95.11	90.70	92.78	92.91
GoogleNet	95.00	95.83	95.83	73.00	96.69
Resnet50	95.54	87.26	87.26	86.92	82.43
Proposed Net with Dataset 1	**98.98**	**99.01**	**97.74**	**59.47**	**97.98**
Proposed Net with Dataset 2	**99**	**95.55**	**84.27**	**71.05**	**98.2**
Proposed Net with Dataset 3	**96.43**	**95.04**	**88**	**64.5**	**95.15**
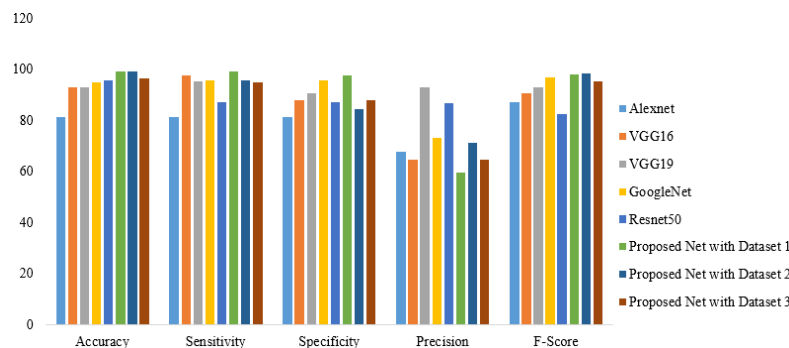
Figure 10. Graphical analysis of existing and proposed model performances
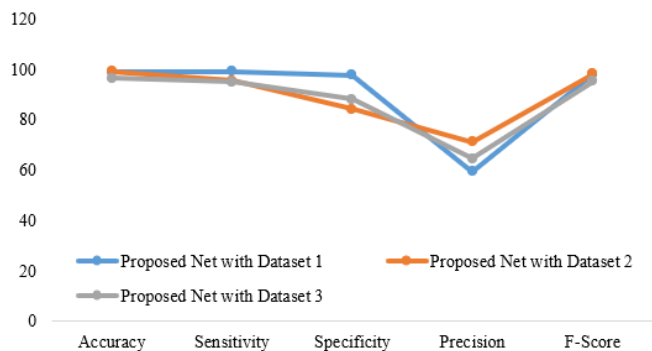
Figure 11. Graphical plot for proposed model performance measures on various datasets

In this paper, the performance was measured in terms of accuracy, sensitivity, specificity, recall, and F- score. The experimental results were observed by using a deep learning toolbox of MATLAB 2019a licensed version. The training and testing ratios are selected randomly by using 10-fold cross-validation. The average values are considered as the final result. Table 4 shows that the accuracy of the proposed net is higher than the other models, which is shown in Figure 10 and Figure 11. The proposed net with dataset 1 results is accuracy, sensitivity, specificity, precision, and F-score is 98.98%, 99.01%, 97.74%, 59.47%, and 97.98%, respectively. The proposed net with dataset 2 results is accuracy, sensitivity, specificity, precision, and F-score is 99%, 95.55%, 84.27%, 71.05%, 98.2%. The proposed net with dataset 3 results is accuracy, sensitivity, specificity, precision, and F-score is 96.43%, 95.04%, 88%, 64.5%, 95.15%.

5. CONCLUSION

This paper gives an overview of the COVID19 and also proposes a diagnosis system based on neural networks. It gives an overview of the origin of the disease and the early viruses, a comparison among them, and India's current scenario. To validate the test results of COVID+, there is no accurate, fast, low-cost equipment in India. So, we proposed a CNN-based network that helps classify COVID19+ and COVID19- persons based on their chest X-ray images. The network consists of layers, along with input, convolutional, pooling, normalization, and six special modules used while designing the network. A module consists of different kernels, but before applying each convolution operation, 1x1 convolution happened, causes dimensionality reduction, and the number of parameters, as well as the number of operations, also reduced. The proposed net was compared with the available pre-trained networks. Our proposed method discovered that employing CT scan medical images produced more accurate results than X-ray images.

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