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Original Article

Early Detection of COVID-19 in Patients with Comorbidities using a Novel Deep Learning Model

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Abstract *- COVID-19 has become among the most severe and enduring illnesses of recent times because of its widespread distribution. When the sickness has been more broadly dispersed, it is difficult to tell who was actually impacted. Over sixty percent of impacted people claim to have a dry cough. Sneezing and other respiratory noises have been used to create diagnostic models in numerous recent research. Applications for deep learning (DL) in healthcare seem revolutionary. DL makes use of neural networks to boost processing power and produce reliable results. With this cutting-edge medical technology, doctors can accurately analyze any ailment, allowing them to treat it more effectively and, as a result, make better medical judgements. This research proposed a novel DL algorithm, i.e., Bifold Long Short-Term Memory, for detecting COVID-19 infection (BFLLCOV-19) in individuals who may have the possibility of infection with or without comorbidities. This research work acquires datasets received through custom-designed online Google forms and data received from individuals. The COVID-19 pandemic outbreak is, without a doubt, the worst disaster of the twenty-first century and likely the most important worldwide crisis that hit great nations economically. The virus's propensity to spread quickly has forced the global populace to maintain tight protection measures to prevent self and slow down the disease's spread.*

Keywords *- Covid 19, Coronavirus, Deep learning, Prediction models.*

1. Introduction

The Coronavirus Disease (COVID-19) has caused more than 71 million corona tests positive globally as of December 2020 [1]. Governments are putting protective and isolating measures in place all across the world to lessen the spread of viruses. The aforementioned precautions include physical division, hand washing, social meeting restrictions, the wearing of face masks, and stay-at-home rules [2]. As a result, the general public has experienced high levels of COVID-19-related dread, notable changes to daily living, and a wide range of psychological effects, such as sadness, difficulty sleeping, and financial difficulties [3]. Additionally, the infection has been rapidly identified as a unique Coronaviridae-related influenza and designated the name severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). A fatal new coronavirus infection (2019-nCoV) caused by pathogenic bacteria was identified in Wuhan, China, in December 2019. Several new countries have been affected by the SARSCoV-2 coronavirus outbreak. The SARS-CoV-2 virus brought on infectious disease (COVID-19). The majority of those who contract the virus experience moderate to serious respiratory sickness and recover on their own. Nevertheless, certain individuals have severe illness and require medical attention. UNICEF Emergencies According to increasing event reporting rates in Chinese and foreign locations, it was discovered that the particular was a global medical catastrophe on January 30, 2020 [4]. The novel virus SARS-CoV-2's origins were heavily contested by researchers since it was first discovered. It was proposed that behavioural intervention caused SARS-CoV-2 to emerge. However, genomic evidence defies that hypothesis, showing that SARS-CoV-2 was not created from the previously identified virus backbone [5]. SARS-CoV-2 is mainly disseminated via droplets, as per the results. Any time affected individuals talk, cough, or sneeze, droplets containing virus particles are released into the air. These droplets land, usually at a distance of 6 feet (1.8 metres), but occasionally farther, on another person's nasal passage or conjunctiva. It has been obvious that social distance practises were important for healthcare since they prevented diseases from spreading too quickly and overtaxing health services. They might, nevertheless, worsen the pandemic and the preventative actions [23]. As per research, cell activation and cytokine storms in COVID-19 patients were connected to acute lung injury and acute respiratory distress syndrome (ARDS) [7].

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ARDS has been frequently seen in coronavirus episodes that progress to influenza. Red blood cell transmission was connected to pulmonary problems like pulmonary hypertension and transfusion-related serious lung injury. Such detrimental effects may worsen ARDS signs for those with the disorder [8]. Monocytes from people with symptomatic COVID-19 require immediate medical attention because they exhibit an inflammatory response and increased pyroptosis associated with caspase-1 activation [21]. Less thought was given to the method of retrieving cases since the appeal of COVID-19 people will endure in the final stages. Elderly people and those with existing medical disorders, like cancer, heart-related disease, diabetes or any respiratory illness, have been more likely to experience critical diseases. At any age, COVID-19 has the potential to harm or kill anyone badly. Therefore, it becomes the government's and policymakers' duty to implement effective steps to stop the spread of the illness. The COVID-19 disease impacts individuals inversely. Maximum infected individuals will only knowledge severe to medium illness and recuperate without demanding to be hospitalised.

Moreover, the common signs are fever, cough, fatigue, and absence of taste or smell. Fewer communal symptoms comprise a headache, a sore throat, diarrhoea, a skin rash, discoloured toes or fingers, and irritated or red eyes. Chest pain, tininess of breath, difficulties with speech or movement, dizziness, or any of the aforementioned symptoms are serious warning signals. Anyone who exhibits even one of these dangerous symptoms should seek immediate medical assistance. Those who have been normally well but lone have minor signs ought to yield proper upkeep of oneself at home.

1.1. Virus Variant

Viruses undergo continual mutation, which results in the emergence of new infections. Many times, mutations occur and vanish while others persist. The structure of a virus that has the capacity to alter each time it replicates (creates copies of itself) is called a variant. "Mutations" are each of these modifications. Many times, mutations occur and vanish while others persist. A virus, which went through single or multiple mutations, is often called the initial virus's "variant". Certain mutations might impact the virus's fundamental characteristics, like how easy it transmits or how probable it tends to culminate in greater severe illness and even mortality. Covid-19 is brought on by the one-strand RNA virus known as SARS-Cov-2. The SARS-CoV-2 illness has evolved and has been found in several countries all over the globe. Variants are problematic because they could have harmful effects on the nations already overburdened by the healthcare system, such as worsening of symptoms, less resistance to infection, decreased effectiveness of immunizations, etc.

A variant was deemed to have VOI if it has a broad distribution and has changes that have been either recognised as causing or anticipated to generate major changes (for example, documented to cause numerous groupings of infected individuals or detected in numerous nations). The WHO continues to keep an eye on a number of VOI in the instance they develop into VOC. Suppose a variant has been shown to propagate faster, induce serious illness, evade the immune system, change its clinical appearance, or reduce the efficacy of tried-and-true methods such as wellness efforts, diagnostics, medications, and immunizations. In that case, it is referred to as VOC. A VOI turns into a VOC if it has been shown to propagate more quickly, resulting in a more serious illness, evade the immune system's response, modify its clinical appearance, or reduce the efficacy of established tools, like preventative measures, examinations, therapies, and immunizations.

1.1.1. Omicron Variant

The 'Omicron version', a novel variety that is now known, was initially observed in South Africa in November 2021. Omicron, which the WHO identified as a "VOC," was spreading quickly throughout the world, especially in India. It must be highlighted that SARS-COV-2, the infectious agent that produces COVID-19 will keep evolving as long as it continues to propagate, like every virus. Therefore, halting the virus's propagation is the greatest approach to inhibit the emergence of new varieties. Maintain social distancing, wear protective masks, follow discipline while coughing or sneezing, getting vaccinated.

1.2. Limitations

- Early detection of COVID-19 in patients with comorbidities and obtaining large and well-balanced datasets can be challenging.
- Deep learning models, particularly complex ones like convolutional neural networks, often lack interpretability.
- Comorbidities often have complex interactions with COVID-19, and their manifestations can vary across different patient populations. Therefore, models trained on a specific dataset may not perform as well when applied to different populations or when dealing with different comorbid conditions.
- A scarcity of such studies limits the understanding of the true effectiveness and limitations of DL models for early COVID-19 detection in patients with comorbidities.
- Ensuring appropriate data anonymization and compliance with privacy regulations becomes crucial.

1.3. Problem Statements

- Comorbidities are pre-existing health conditions that can increase the severity of COVID-19 and lead to worse outcomes. Detecting COVID-19 early in individuals with comorbidities is crucial for timely medical intervention and appropriate management of their health in earlier studies.

- The proposed work aims to develop a novel deep-learning model specifically tailored for this task, which can accurately identify COVID-19 infection in patients with comorbidities, enabling healthcare professionals to make informed decisions and provide timely treatment.

The rest of the section is given as follows, Section 2 describes the literatures of existing papers related to COVID-19, Section 3 explains the presented workflow and method, Section 4 provides the model's outcome, and Section 5 is the paper's conclusion.

2. Related works

Jun Wang et al. [10] presented a solution using the DL model for earlier retrieval –COVID-19 patients time forecasting employing a 5-fold CPH technique and RSF methods have been learned employing Coxnet Survival Analysis and Random Survival Forest. The Scikit-survival Python module was used to analyze the dataset of CT scan pictures. The results show that iCOVID can still perform admirably, particularly when simply taking into account the highest 20 and 15 attributes, correspondingly that could typically be acquired within 48hrs afterwards admission.

An ensemble multiscale DL predictor (EMDLP) was introduced by Honglei Wang et al. [11] to detect RNA methylation hotspots using DL and NLP. In order to more effectively utilize the worldwide and local data for site forecasting, it naturally blends Bidirectional LSTM (BiLSTM) and dilated convolution. This approach compared the CNN, BiLSTM, and DCNN algorithms to the DCB framework to predict methylation alteration locations predicated on the sequence's characteristic representations. These results show how important the retrieved features were to the ultimate projection.

In order to forecast prospective stock values utilizing both ensemble EMD and LSTM, Yang Yujun et al. [12] devised the LSTM-EMD hybrid technique. The LSTM method has been used to train and forecast every subsequence. Lastly, the anticipated outcomes for the beginning price of stocks time stream have been generated by combining the anticipated results of distinct subsequences. Comparative outcomes show that the predicted values outperform the other 4 forecasting techniques in terms of accuracy. The proposed method, however, has some unexpected effects on the empirical findings of time sequences with impressively ordered transitions.

Luyu Zhou et al. [13] presented an enhanced LSTM-predicated DL method for Covid forecasting employing an optimized approach for a time-series dataset for different countries. With this strategy, age-specific mortality rates across the lifespan are jointly modelled, and multivariate time series are forecasted employing RNN with LSTM architecture. The LSTM design produces predictable projections of death rates across all age groups and years. To confirm the long-term viability of deep learning techniques in modelling human survival, additional research is required to consider alternative RNN architectures, calibration techniques, and sample datasets.

Farah Shahid et al. [14] presented a time-series forecast model using ARIMA, SVR, LSTM, and Bi-LSTM for cases of COVID-19 in various countries. The test results proved that Bi-LSTM is superior to all models. In order to predict confirmed infections, casualties, and recovery rates as time passes in 10 main countries impacted by COVID-19, this methodology recommended predictive models that include autoregressive-based integrated moving average (ARIMA), LSTM, support vector regression (SVR), and Bi-LSTM. Root Mean square error, Mean absolute error, and score indices have been employed to evaluate the model's effectiveness. However, this technique demands a sizable dataset and a powerful computer.

Jayanthi Devaraj et al. [22] presents a comparison study employing LSTM, PROPHET, SLSTM, and ARIMA approaches to predict the prospective forecasting of confirmed mortality and healthier instances. Additionally, Stacked LSTM (SLSTM) and LSTM algorithms fared better than other approaches with greater precision, demonstrating their dependability in forecasting COVID-19 instances. Active training is necessary to build a forecasting framework that considers the data's irregular nature because modelling fails to consider the massive relationships in the time phases.

Aktar et al. [16] proposed using a combined COVID-19 global data set, a machine learning forecasting evaluation, and a systematic review of published worldwide literature. According to our metanalysis, the conditions that have the strongest correlation to COVID-19 severity within the currently available literature include chronic obstructive pulmonary disease (COPD), cerebrovascular disease (CEVD), cardiovascular disease (CVD), type 2 diabetes, malignancy, and hypertensive. COPD, CVD, CKD, type 2 diabetes, malignancy, and hypertension, as well as asthma, were revealed to be the most important factors for categorizing the individuals who were killed vs those that survived COVID-19 utilizing machine learning classification utilizing unique pooled cohort data. The strongest links for COVID-19 mortality were identified for the symptom-comorbidity combinations of pneumonia-hypertension, pneumonia-diabetes, with acute breathing distress syndrome (ARDS)-hypertension. The most important predictors of death were age and gender.

Zhu et al. [17] proposed a Retro investigation that included 181 hospitalized COVID-19-infected patients from a large hospital in Wuhan, China, between January 29, 2020, and March 21, 2020. Death was the main result. 78 clinical data, including information on demographics, comorbidities, vital signs, symptoms, and laboratory testing, were obtained at the point of the first visit. A risk stratification score system and a deep-learning algorithm were created to forecast mortality. Data were divided into 15% for testing and 85% for training. Comparisons were made between prediction accuracy and COVID-19 severity score, CURB-65 score, and PSI.

3. Methodology

The workflow of the presented procedure is shown in Fig.1. Initially, the dataset was collected based on a questionnaire survey, which is attained through online google forms. Hereafter, the collected data is pre-processed, in which the duplicate data are removed, and imputation is performed. Following that, the LSTM model is implemented wherein the 4th and 5th layers are combined together and form layer 6, named Bifold-LSTM, for predicting COVID-19, i.e., BFFLCOV-19. Finally, the output was gathered as normal, advanced, and moderate; the model performance was also evaluated.

3.1. Data Collection

This paperwork involves a dataset that online Google Forms receive. Based on a questionnaire survey, the records were collected. The covid affected, recovered, and unaffected individuals participated in this survey. According to the participant's report, the database is created. The dataset has balanced data with age, gender, comorbidities, symptoms, travel chances etc. The dataset contains 12000 records. The medical personnel received 140 surveys, totalling several hundred. Ten respondents declined to finish the surveys, and 15 were insufficient and useless. 82% of respondents responded in total. Among the 115 healthcare professionals that completed our surveys properly, 48 in the non-COVID-19 sector (41.8%), 67 in the COVID-19 sector (58.2%) sector (physicians, junior doctors, nurses, hospital caregivers/caretakers), there were 67 (58.2%) who were COVID-19 employees. In the pulmonology ward, it was 31 (46.2%), and in the acute care unit, it was 36 (54.8%). The smallest individual was 25 years old, while the most senior member was 65 years old, making the median age of the group 42 years. 102 of them (88.7%) were women. Half of the 115 people, 70 (69.3%), were married and residing with their families. 50 out of the 105 individuals had additional stressful experiences over the time frame, such as the death of a parent. It consists of 26 words that characterize unpleasant feelings in 6 subscales:

- The "sadness/depression" category has six items that denote functionally adverse feelings.
- There are 8 items in the "sadness/depression" category that indicate unhealthily unpleasant emotions.
- There are six components in the "fear" category that represent functionally unfavorable feelings.
- Six categories under the "fear" heading depict dysfunctional unpleasant emotions.
- The operationally negative emotions "fear" and "sadness/depression" are each represented by 12 components.
- The "sadness/depression" and "fear" categories each have 14 items that depict unpleasant feelings.

Symptoms of COVID-19 can range from moderate to severe and may manifest 2–14 days after viral infection. Common complaints include fever, a persistent or productive cough, exhaustion, muscular or body pains, headache, sore throat, loss of taste or smell, congestion or runny nose, nausea or vomiting, and diarrhoea. It is crucial to remember that certain people, especially those with complications, might show milder or unusual symptoms.

Travel and Transmission: When an infected individual coughs, sneezes, speaks, or breathes, Covid-19 is mostly spread by lung droplets. Because infected people can distribute the virus to others while travelling or after arriving at their destination, travel can help the infection spread. International and domestic travel can increase the likelihood of contact with Covid-19, particularly in busy areas like airports, aircraft, or public transit. To lessen the risk of transmission while travelling, it is crucial to heed travel warnings and put preventive measures into practise, including wearing masks, keeping a physical distance, and routinely washing hands.

3.2. Pre-processing

3.2.1. Duplicate Data Removal

When compared items have not been included in a single set, duplicate data might obliterate the distinction between the training, identification, and testing sets. This could result in inaccurate performance predictions that let down the structure with regard to genuine results. The unnecessary information has therefore been eliminated.

3.2.2. Missing Data Imputation

Imputation looks to be a way to maintain the majority of the data held in a repository by substituting an additional number for the data not present in the records. Multiple strategies have been used since it is impractical to delete data from an index after every session completely. This will result in a significantly smaller record, raising questions about prejudice and producing inaccurate analyses. The variable's mean or median is used to replace every instance of missing data inside a statistic.

Following discarding outlier value pairs because they might provide a wrong forecast for any classifier, the procedure to fill in the blanks or null values is carried out. In the suggested design, mean values for attributes are imputed with missing or null data rather than omissions—the mean gains from imputation when the continuous data is assumed without adding outliers.

$$I(x) = \begin{cases} mean(x), if x = null/missed \\ x, otherwise \end{cases} \quad (1)$$

This feature vector $x$consists of instances in $n$space of dimensional $x \in J^n$.

3.3. Data Augmentation

Use label shuffling on the original training dataset throughout the training phase to train the recommended AVAE. Typically, analysing a labelled dataset will reveal the classification of classes. Compared to samples from medical databases, the proportion of samples with uncommon disorders used to be smaller. As a result, machine learning approaches only learn from the more populated classes and ignore the smaller classes. The two primary avenues of study to address this issue are undersampling and oversampling. The most representative class is lowered to an equal number of items in all classes by undersampling. To boost their representation, however, classes containing few constituents are oversampled. Because VAE has been proven to be more efficient than other approaches, they are employed in this research to deal with imbalanced datasets.

To train a deep representation using VAE, a component of deep ensemble learning, feature compression is laborious. This may be accomplished by designing a structure where the amount of source neurons and output neurons is identical, but some hidden layers are bottlenecked. The network of nodes at the bottleneck layer can learn a deep and condensed model of the input data to get the input itself out of the network. Encoders are the layers that come before the bottleneck, while decoders are the layers that come after it. VAE encapsulates the information by acquiring a normal distribution, as opposed to encoding each sample separately. In the latent layer (bottleneck layer), a new feature with a freshly discovered distribution is sampled. When a new data characteristic is added, VAE trains the network by creating a new element that fits into the normal data distributions; artificial data that is similar to actual data may be created.

Like automatic encoders, surrogate autoencoders (SAEs) feature more neurons than inputs and outputs in their hidden layer. Adding a P_1 network must always employ a limited number of neurons due to the regularisation term applied to the latent space layer.

$$\|C\|_1 = |c_1| + |c_2| + \ldots + |c_N| \quad (2)$$

Here $c_x$denotes the connection weight and in layer $x$and $N$is the connection number. Adding $C$to the loss function, P_1 the regularization function forces the network to have small weights.

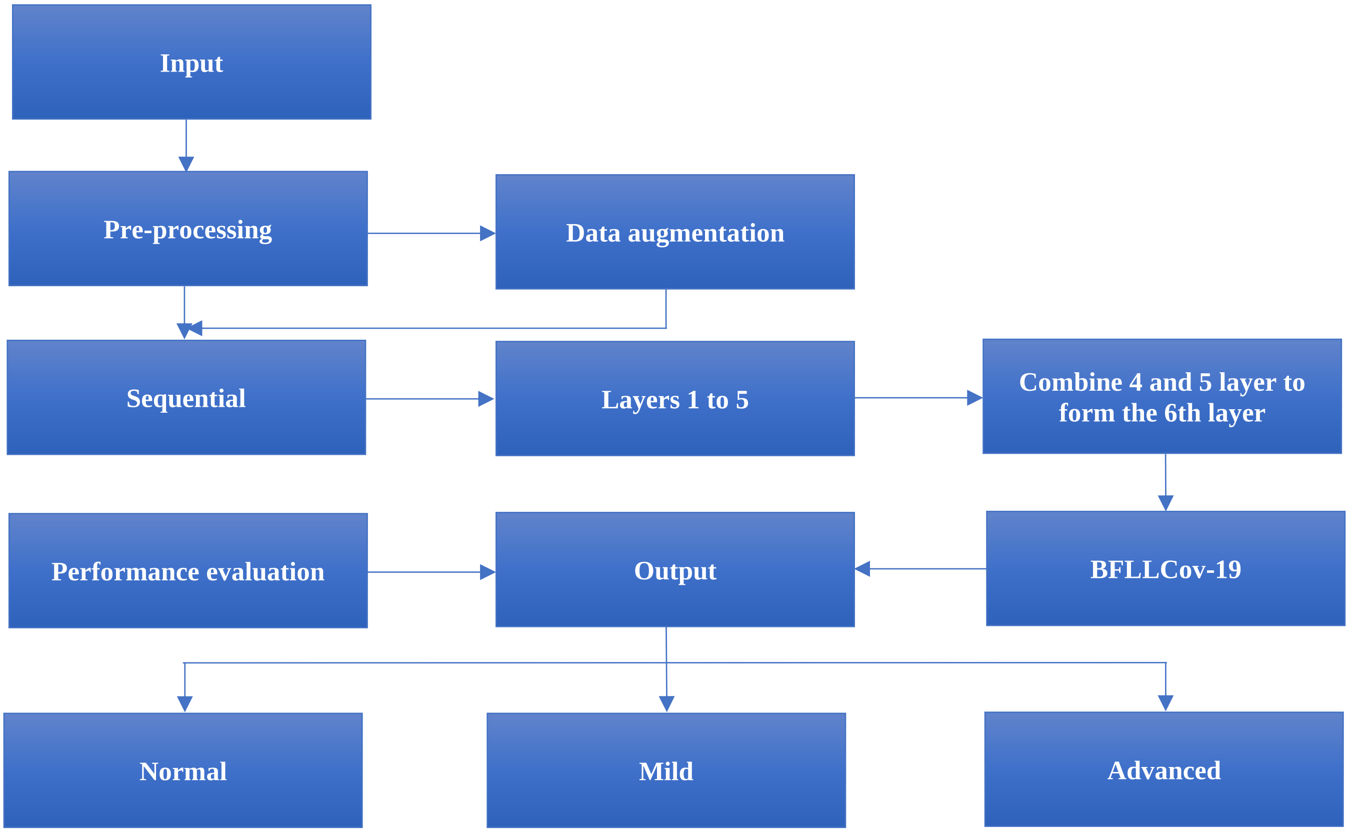


Fig. 1 Proposed workflow

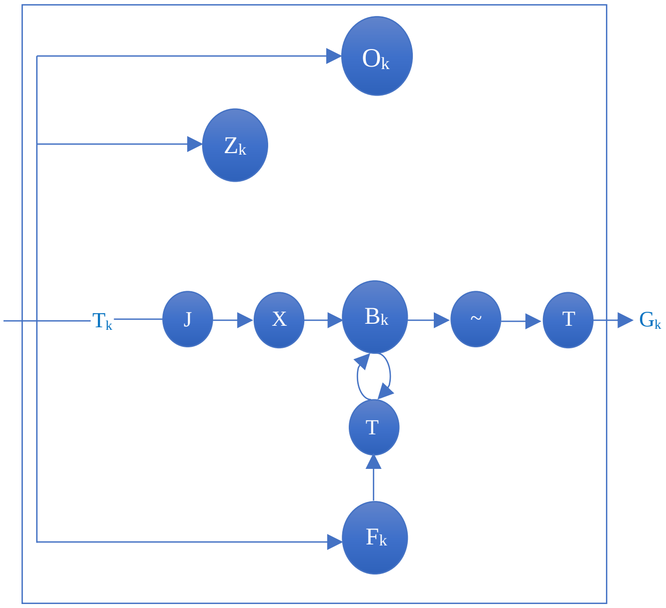
$$Loss = Error(a, \hat{a}) + \lambda \sum_{i=1}^{N} |c_i| \qquad (3)$$

There is a regularization term that λ multiplies the $\hat{a}$ predicted value by the a label of the sample. The regularization's impact on the overall loss computation is greater due to a larger lambda. The network learns to represent our original data with various attributes, enabling us to examine the data from many angles. Data usually qualifies using neural networks and Multi-Layer Perceptions (MLPs). This network has three layers: three layers: an output layer, a concealed layer, and an input layer. Deep learning often uses numerous layers to extract complicated information from incoming data. Using a single output neuron to represent the likelihood that an input belongs to the positive group with a sigmoid activation function is one of the most popular methods for categorizing inputs into positive and negative groups.

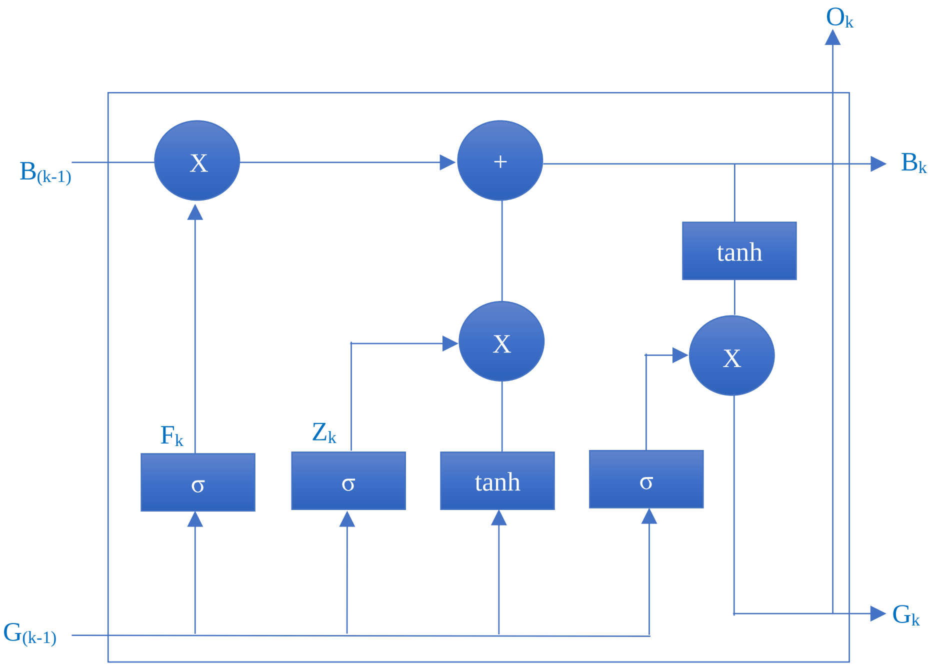
$$f(x) = \frac{1}{1+e^{-x}} \qquad (4)$$

3.4. Long Short-Term Memory (LSTM)

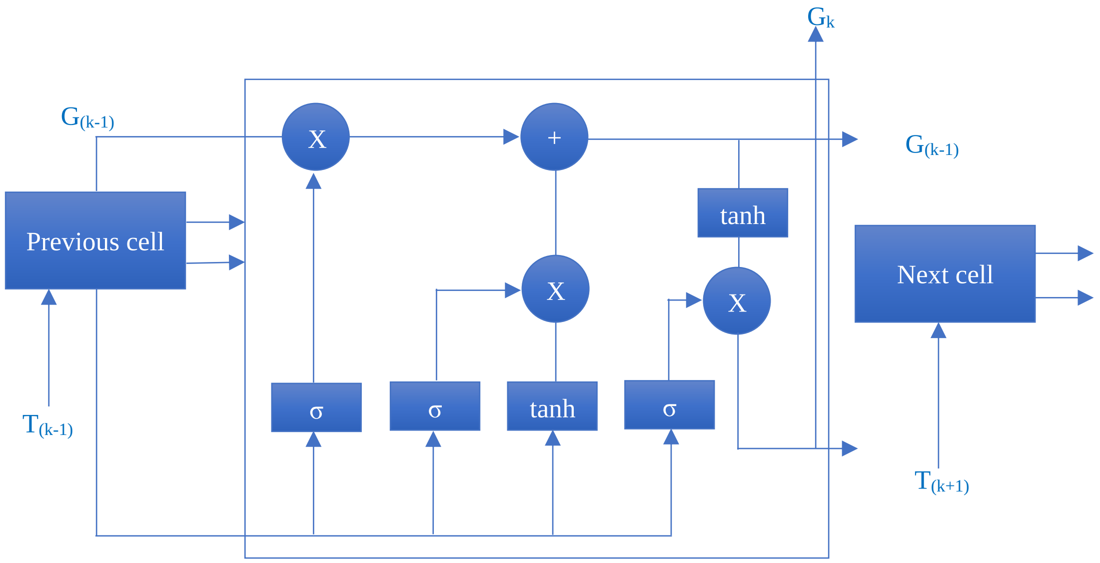
The potential for DL to revolutionize the healthcare sector has been demonstrated. In general, DL offers the possibility to revolutionize healthcare by enhancing diagnosis, speeding up the drug manufacturing process, and offering individualized treatment alternatives. Nevertheless, there have still been issues that must be resolved, including the requirement for more substantial and diverse databases to train DL methods and worries about the security and confidentiality of data. Long short-term memories improve RNN performance. As per LSTM, the problem of disappearing and extending gradients may be overcome by employing memory blocks rather than typical RNN units. It offers a key benefit over RNNs because it records long-term situations using a cell state. Employing an LSTM network, information from the past can be recalled and linked to data received at the current time. Input, output, and forget gates are used in conjunction with an LSTM. The architecture of the presented LSTM model is shown in Fig.2. $T_{(k)}$ denotes the current input, $b_{(k-1)}$ and $b_{(k)}$ denote the previous and current cell states, correspondingly; $G_{(k-1)}$ and $G_{(k)}$ denote the previous and present outcomes, correspondingly.



(a)



(b)



(c)

Fig. 2 (a), (b), (c) shows how the proposed LSTM is formed

The basic functioning of the LSTM input gate has been shown by the following Eqns. (5), (6), and (7).

$$I_{(k)} = [(G_{(k-1)}, T_{(k)}) \times W_{(k)} + A_{(I)}] \times \sigma \qquad (5)$$

$$b'_{(k)} = tanh\times ([G_{(k-1)}, T_{(k)}] \times W_{(k)} + A_{(I)}) \qquad (6)$$

$$b_{(k)} = b_{(k-1)} \times F_{(k)} + I_{(k)} \times b'_{(k)} \qquad (7)$$

$G_{(k-1)}$ and $T_{(k)}$ are fed via a sigmoid layer using Eqn. (1) to figure out which portion of the information must be included. Fresh data has been then acquired using Eqn. (2) after transiting via tanh layer employing $G_{(k-1)}$ and $T_{(k)}$. The current-moment data, $b'_{(k)}$, and the long-term reminiscence data, $b_{(k-1)}$ $b_{(K)}$, have been connected in Eqn. (5) wherein $W_{(I)}$ signifies a result and $b'_{(k)}$ indicates a tan*h* result. In this instance, weight matrices have been designated by $W_{(k)}$, while the LSTM's input gate bias is expressed by $B_{(I)}$. The LSTM's forget gate then makes it possible for selective data transmission through the utilisation of a sigmoid layer and a dot product. Equation (8) determines whether to remember important information from earlier cells with a particular likelihood. In this equation, the weighted matrix $W_{(F)}$, the offset $A_{(F)}$, and the sigmoid function are all represented by letters. Moreover, the layers in the presented BFFLCOV-19 model are shown in Fig.3.

$$F_{(k)} = \sigma \times ([G_{(k-1)}, T_{(k)}] \times W_{(F)} + A_{(F)}) \qquad (8)$$

The state required for the LSTM's output unit to continue provided by the $G_{(k-1)}$ and $T_{(k)}$ inputs in equations (5) and (9). The state judgement vectors from the tanh layer that carry new data, b(k), are obtained and multiplied to obtain the result.

$$O_{(k)} = \sigma([G_{(k-1)}, T_{(k)}] \times W_{(O)} + A_{(O)}) \qquad (9)$$

$$G(k) = tanh[b_{(k)}]O_{(k)} \qquad (10)$$

Where in the output gate's weighted matrix W(O), as well as LSTM output B(O), have been used correspondingly.

Table 1. System configuration, tools and packages used for evaluation

Tool	**Version**
Python	3.9
Jupyter Notebook	6.4.8
Packages	**Version**
pandas	1.4.1
numpy	1.20.3
seaborn	0.11.2
matplotlib	3.5.0
sklearn	1.0.2
keras	2.6.0
System Configuration	
OS	Windows 10
RAM	16GB
Core	Core i5
Hard Disk	1TB

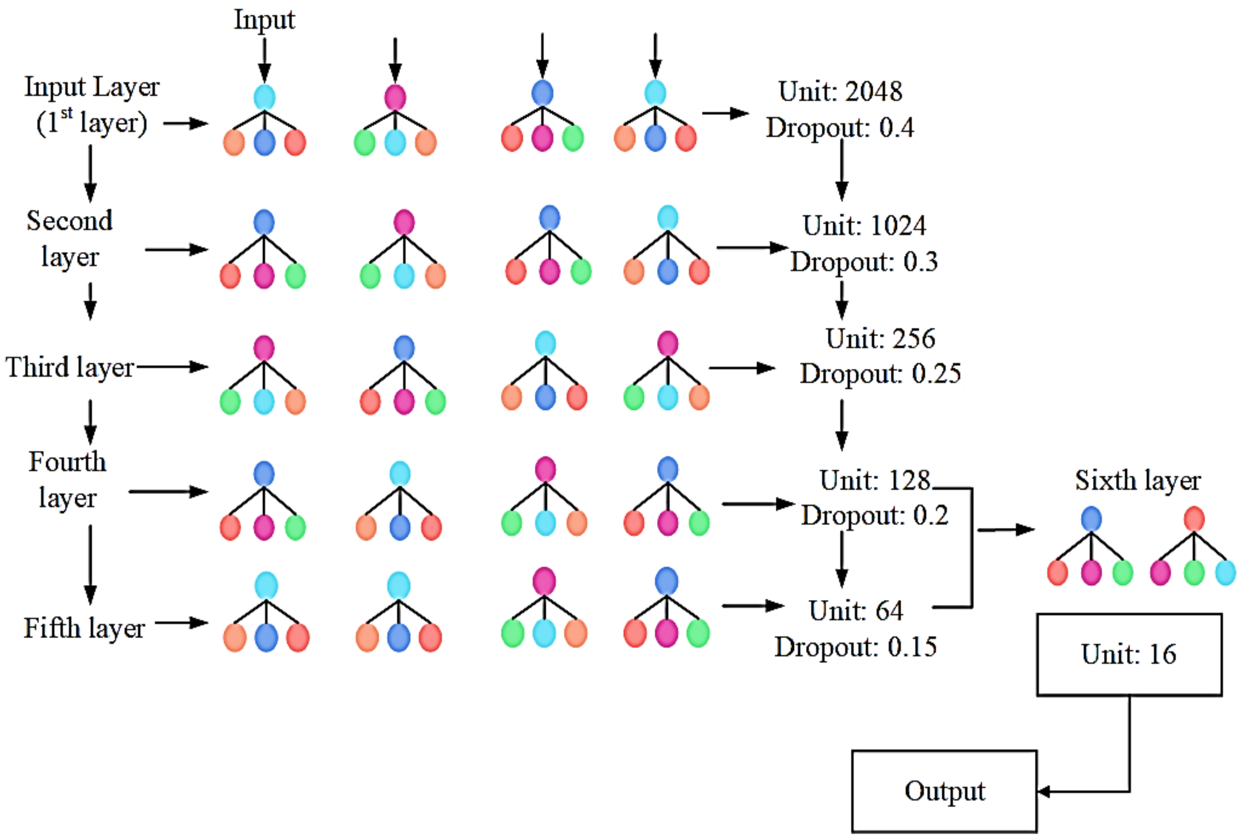


Fig. 3 Layers in proposed BFFLCOV-19

4. Experimental Setup

This section assesses and contrasts the performance of the proposed DL-based prediction method. The simulation results have been obtained for various models using various performance indicators to evaluate the recommended DL model-based prediction effectiveness. Python 3.9 was used to implement the stipulated method, and the expected experimental results have been attained.

4.1. Implications for Practice and Policy

To stop the spread of COVID-19, governments and health organizations must establish and enforce public health measures such as extensive vaccination drives, mask requirements, social distancing rules, and routine testing. These precautions lessen the strain on healthcare systems while helping to safeguard individuals and communities from illness. To quickly identify and contain COVID-19 outbreaks, effective monitoring systems and early detection procedures are essential. For the purpose of identifying and following the spread of novel variations and implementing effective countermeasures, governments and health organizations should invest in surveillance infrastructure, including successful testing methods, contact tracking, and genomic sequencing. It is crucial to guarantee that everyone has access to COVID-19 vaccinations. Governments and global health organisations must collaborate to overcome obstacles related to vaccine manufacturing and distribution issues, vaccination hesitancy, and resolving vaccine disparities among various populations and areas. Globally, the epidemic has had a major influence on mental health. To address the psychological effects of COVID-19, enough resources and assistance should be made available, including improved access to mental health services, psychotherapy, and community support initiatives. Communication concerning COVID-19 must be accurate, precise, and consistent. Governments and health organizations should make frequent updates, evidence-based information, and guidance available to the public through various channels to counteract disinformation and encourage adherence to advised preventative actions. Global crisis COVID-19 call for worldwide engagement and cooperation. To jointly confront the problems presented by the pandemic, governments, health organizations, and researchers should exchange data, research findings, and best practices. Collaboration is essential for creating virus-fighting medications, vaccines, and tactics.

5. Results and Discussions

DL uses data to create algorithms applied to other data to generate predictions. In the DL toolset (Neural Network), recognition, classification, and other methods are frequently applied. In order to overcome this problem, the provided BFLLCOV-19 model will be examined and put on display using various techniques, including KNN and LSTM, in this study. DL was utilised a lot while creating forecasts and estimations. In the field of DL, LSTMs have been employed. Numerous RNNs are prone to developing long-term connections, especially regarding sequence prediction problems.

Along with isolated data streams like pictures, LSTM also features feedback linkages that enable stream-wide analysis. Among other things, this is helpful for speech detection and machine translation. The LSTM has been a unique RNN that benefits from resolving numerous issues. In the case of the k-nearest neighbours (KNN) technique, a non-parametric, supervised training classifier uses immediacy to categorise and predict how a certain data point might be categorised. In everyday circumstances, it is commonly disregarded because of its non-parametric environment, which implies that it offers no fundamental statements about data distribution.

5.1. Model's Performance Evaluation

Every mathematical activity includes a critical step called model evaluation. It becomes considerably more important in combined modelling prediction where variability and varied degrees of effectiveness should be thoroughly measured, i.e., Accuracy, Recall, Precision, and F1-Score. The obtained rates for models are shown in table.2 and Fig.4.

Table 2. Obtained rates for the selected models

	KNN	LSTM	BFLLCOV-19
TP	89	92	96
FP	8	6	5
FN	11	8	4
TN	5	3	2

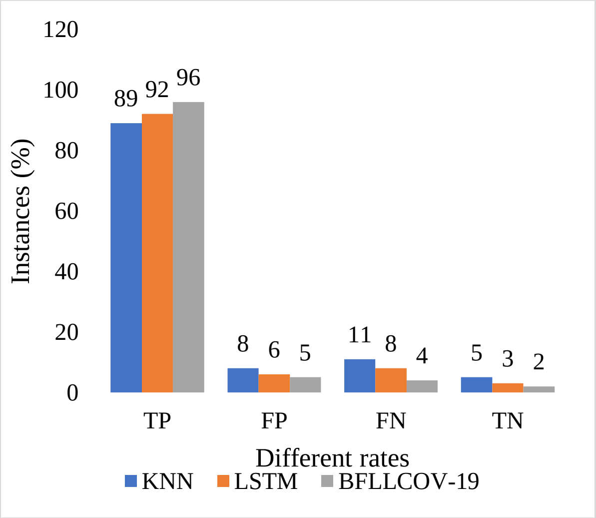


Fig. 4 Model's obtained rates

True positive (TP) defines correctly forecasted abnormal examples, while true negative (TN) defines correctly forecasted normal instances. False positive (FP) defines incorrect forecasting of normal as abnormal instances, and false negative (FN) defines abnormal cases as normal cases.

The confusion matrix has frequently been used to assess accuracy in order to determine how effective an algorithm is. Eqn. (11) was used to compute the precision of the approach.

$$Accuracy = \frac{T_P + T_N}{T_P + T_N + F_P + F_N} \tag{11}$$

Precision has been the proportion of real positives to all expected positives. In simple terms, precision represents the count of the instances the classifier determined to be true. Eqn. (12) was employed to evaluate the model's precision.

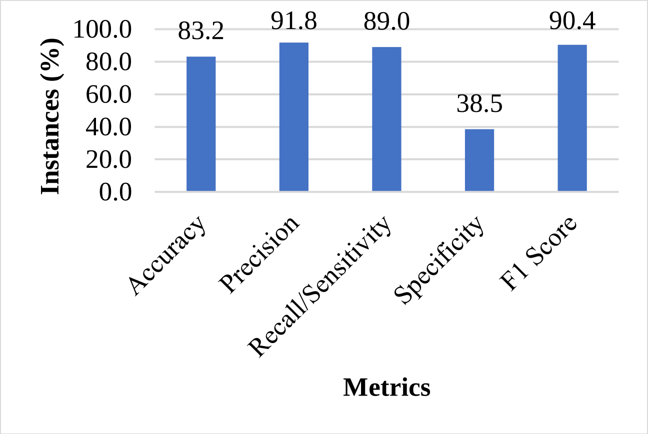
$$Precision = \frac{T_P}{T_P + F_P} \tag{12}$$

The F-measure represents the geometric average of recall and precision. Overall, the low recall has been connected with increasing accuracy; hence precision (P) and recall (R) are incompatible. Eqn. (10) was used to obtain the F-measure for the given model.

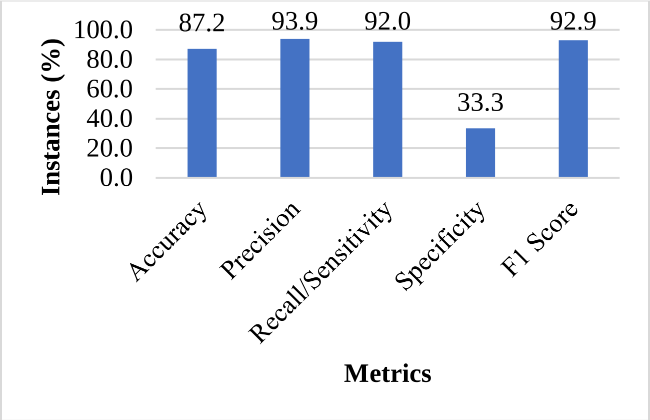
The accuracy, specificity, precision, F-measure and recall for the KNN, LSTM, and BFFLCOV-19 models are shown in Fig.5 (a), (b), and (c), respectively. Moreover, the overall effectiveness of different models is shown in Table.3.

Table 3. Overall performance of the models

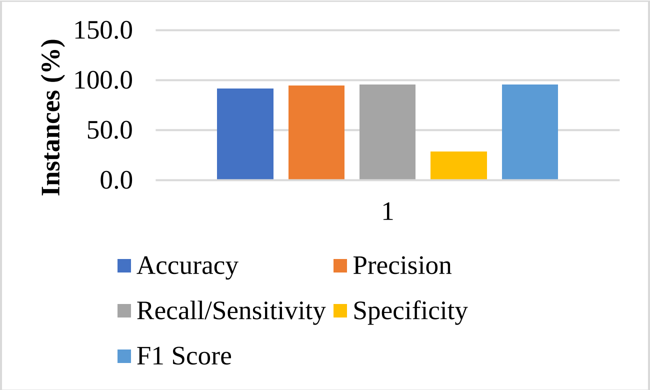
	KNN	LSTM	BFLLCOV-19
Accuracy (%)	83.2	87.2	91.6
Precision (%)	91.8	93.9	95.0
Recall/Sensitivity (%)	89.0	92.0	96.0
Specificity (%)	38.5	33.3	28.6
F1 Score (%)	90.4	92.9	95.5



(a)



(b)



(c)

Fig. 5 Performances (a) KNN (b) LSTM (c) BFLLCOV-19

The proposed BFLLCOV-19 technique was contrasted with other methods like Support Vector Machine (SVM), the developed KNN, and LSTM, which is denoted by Table 4 and Fig. 6. The study outcomes indicated that the suggested model had attained higher reliability than other approaches.

Table 4. Sensitivity and accuracy comparison

Reference	Approach	Accuracy (%)	Sensitivity (%)
[18]	SVM	90.0%	91.67%
	KNN	83.2	89
	LSTM	87.2	92
	Presented BFLLCOV-19	91.6	96
[19]	GBDT	91.5%	60.7%
	LR	87.1%	36.8%
	NN	88.8%	47.4%

The suggested BFLLCOV-19 algorithm would have undergone thorough assessment and validation procedures to claim improved outcomes. The algorithm's performance would be compared to established standards, its sensitivity, specificity, accuracy, and other pertinent metrics would be evaluated, and it may even undergo external validation on different datasets to guarantee its dependability and generalizability. The field of COVID-19 detection and deep learning is rapidly evolving. Future work should focus on continuous improvement and iteration of the BFLLCOV-19 algorithm. This involves incorporating feedback from clinical use, refining the algorithm based on new data and research findings, and staying updated with advancements in deep learning techniques and COVID-19 knowledge.

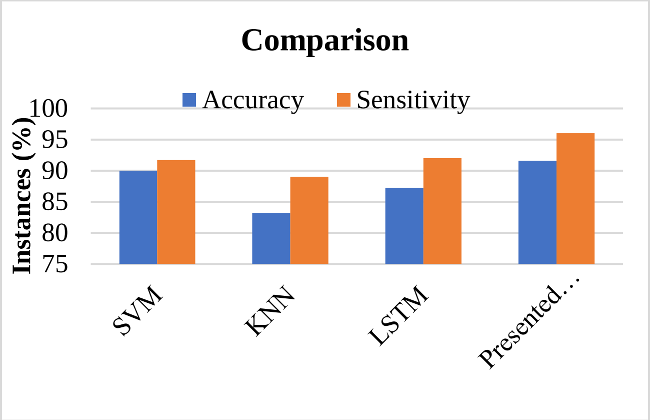


Fig. 6 Accuracy and sensitivity comparison

6. Conclusion

Covid 19 has been a nightmare for human beings since 2019. There was no strict rule to say who would be the infection victim. Experiments reveal that persons in age groups 50 and above are likely to get infected with the Covid 19 virus. Also, without any doubt, the risk was on the group of people who were with comorbidities such as long-term medication for Diabetes, Heart disease, or Cancer. A model is designed and developed for early diagnosis of Covid 19 that will help them save their life. Improved accuracy is seen in the efficient analysis of infection of Covid-19 in individuals. This model has effectively reduced False positive results. The suggested strategy was influenced by a review of pertinent studies emphasizing the value of LSTM in healthcare. The source for the suggested DL-based COVID-19 forecasting method uses online Google Forms.

Additionally, imputation for missing data and pre-processing to eliminate duplicate data was carried out. After that, a brand-new COVID-19 prediction model called BFLLCOV-19 has finally been put into practice. The outcome showed that the provided model had achieved higher accuracy compared to other current and cutting-edge methodologies. As a result, the given BFLLCOV-19 model has a greater level of prediction accuracy. Moreover, the proposed BFLLCOV-19 prediction method is highly effective and accurate in diagnosing Covid 19 as Normal, Mild and Advanced.

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