A Review of Various Machine Learning Techniques for COVID-19 Prediction

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ABSTRACT
Believed to have been originated Chinese province Wuhan in December 2019, the coronavirus has said to cause 95 million cases with overall death rate of 2% of overall cases (as per Jan 2022). This fast-spreading pandemic virus poses a challenge at world level and proposes serious danger to people's health as well as the economy. With time and regions this virus has undergone several mutations resulting in rise of various other viruses, OMICRON being the latest. The most common and widely faced threat in this disease was in the case of asymptomatic patients, the ones who showed no symptoms and yet were carriers of this deadly virus. In recent times, many researchers have started exploring various methods to predict the disease on the basis of medical parameters. Few of the commonly used tools for the same are Machine Learning and Artificial Intelligence. The present paper aims to compile the various models used by researchers in last few years in predicting COVID.
Keywords: - covid19, prediction techniques, coronavirus, artificial intelligence, machine learning, deep learning, hybrid techniques.

I.   INTRODUCTION

The COVID-19 pandemic has affected more than 200 nations and poses a serious threat to world health. Many acute COVID-19 infections and the therapies that follow place a heavy burden on the healthcare system, the economy, and even the patient [1]. An infection with COVID-19 may have long-term health consequences. There are various definitions of long-term conditions nowadays. As of December 2022, the World Health Organization received reports of over 6.6 million deaths worldwide and over 650 million confirmed cases of Corona Virus Disease 2019 (COVID-19), which is brought on by the SARS-CoV-2 coronavirus.Virus transmission and, thus, evolution remain a challenge to date despite attempts to vaccinate and other health precautions, with the number of confirmed cases continuing to climb. The clinical picture of COVID-19 infection is heterogeneous and can range from an asymptomatic or pre-asymptomatic phase to mild to moderate respiratory symptoms to severe viral pneumonia and acute respiratory distress syndrome, septic shock, and/or multiple organ dysfunction requiring admission to the intensive care unit (ICU) [2]. It is essential to identify COVID-19 individuals at risk for critical disease early in order to determine which patients need immediate medical care or who would benefit from treatment the most.A prognostic model would make it possible to pinpoint the patients who are most likely to experience common long COVID symptoms.

Prognostic models are a component of stratified or personalised medicine, which tries to customise treatments for patients by taking into account their unique genetic, psychological, or biological traits.

Due to the great heterogeneity in illness severity, which might essentially be useful for effective triage and optimal allocation of scarce resources (i.e., beds, ventilators), it is more difficult to predict the precise prognosis of COVID-19 clinical outcome. For prognostication and determining severity [3], a more precise subclassification of COVID-19 is necessary. Due to the great degree of complexity in these traits, it has been demonstrated that the pathological, physiological, and immunological responses are insufficient to distinguish between individuals with non-severe and severe forms. Such varied multimodal data could potentially be used for the classification of individuals with COVID-19 using data mining and machine learning (ML) techniques.Thus, AI has been applied to the diagnosis of COVID19 pneumonia, patient stratification, and the creation of a prediction model for the progress of the disease [4]. A technique based on AI and ML can be employed as a prognostic model to forecast outcomes or as a diagnostic tool. Data mining technology's key machine learning tool is the COVID-19 prediction framework. The schematic diagram for the COVID-19 prediction model is shown in Figure 1.
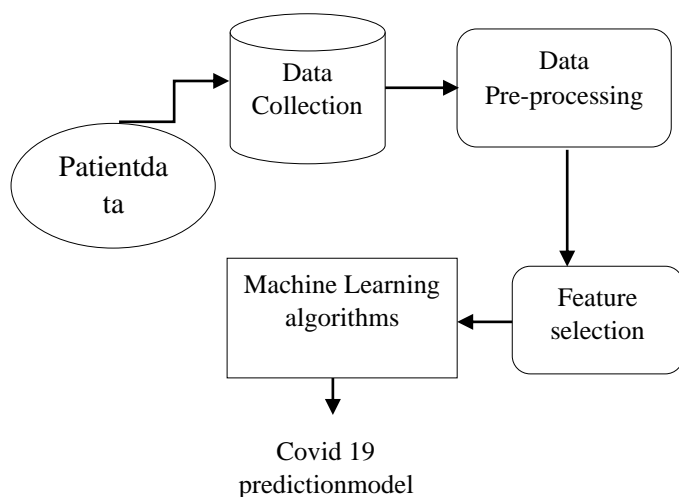
Figure 1: COVID-19 prediction model

Below is an explanation of every phase of this prediction framework:

a. Data collection: The Covid-19 dataset can be gathered from a number of locations, including Kaggle [5]. An epidemic dataset typically consists of many instances with different characteristics, such as patient ID, global number (the number provided by the government of a particular country), sex, born date, age, nationality, region, city, illness (TRUE: underlying disease/FALSE: no disease), infection case, infection order, contact details (the number of contacts with people), onset date of symptoms, confirmed date, the date of being confirmed, released date, and state, among others.

b. Pre-processing: The dataset is organized and handled according to the kind and mode of data after it has been acquired. Outliers—records with missing values or differences from other data—are eliminated [6]. The data is then ready for analysis, and the data sets created for pre-processing are carefully reanalysed with managed missing values and validated data. The data set is unbalanced, meaning that the number of records in one class differs from another, because the sample size contains both dead patients and living patients. By specifying two ways of under-sampling or over-sampling, this issue can be resolved.When a class is under-sampled, the larger class's size is equal to that of the smaller class, and when a class is oversampled, the smaller class's size is equal to that of the bigger class [7].

d. Feature Selection: A subset of the initial features is created by feature selection. Filters, wrappers, and embedded methods are the three main categories of feature selection techniques. Filters concentrate on the data's recurring patterns. As a result, they are computationally cheap, independent of the learning method, and capable of making strong generalisations. An induction approach assesses a portion of candidate characteristics for wraps. They require more processing power than filters yet perform better. Since the selection represents a step in the training procedure for the induction technique, embedded methods are located between the filter and the wrapper [8].An induction approach in wrapping assesses a portion of candidate features. They require more computer resources than filters but perform better. Between the filter and the wrapper, there are embedded methods because the selection is a part of the induction method's training procedure. The ideal subset of characteristics is identified during classifier training. As a result, computationally speaking, embedded techniques are less expensive than wrapper methods.

e. Machine learning:The development of epidemiological models of epidemics has created a high degree of complexity, which has led to the emergence of ML (Machine Learning) as a promising technique. Results from machine learning for COVID-19 prediction models are effective. The performance, robustness, and generalizability of ML algorithms are excellent. Machine learning as a computational technique has a lot of potential for corona virus disease prediction.

1.1 Covid 19 Prediction Models

Prediction models' major objective is to aid patients' specific medical decision-making. Therefore, it is crucial to identify a target setting where predictions serve a clinical need (such as an emergency room, intensive care unit, general practice, or symptom monitoring app in the general population) [9], as well as a representative dataset from that setting on which the prediction model can be developed and validated. Preferably, this dataset should consist of consecutive patients. In order to prioritize patients when allocating scarce healthcare resources, medical staff may benefit from prediction models that combine a number of

variables or features to estimate the likelihood that individuals will contract the infection or suffer a negative outcome as a result of the infection.The list of various popular models for predicting the Covid-19 epidemic is provided below.

i. Support Vector Machine**:** The Support Vector Machine (SVM) is used to explore the hyperplane. With this approach, the decision boundary and hyperplane are found, and a lower error rate is obtained [10]. In an SVM, the hyperplane is written as:

$$y = w^t \cdot x + b$$

Thus, x stands for the vector of features, w for the vector of normalised direction to the hyperplane, and b for a threshold type.SVM is an efficient approach that uses kernel-based projection of the dataset into higher dimensions. The expression for a common kernel function K, which can be linear like a dot product or non-linear like an RBF (radial basis function) kernel, is:

$$K(x_1, x_2) = e^{-\gamma \|x_1 - x_2\|^2}$$

In this, a parameter forRbf kernel is defined with γ and $\|x_1 - x_2\|^2$ represents the Euclidean distance.

ii. Decision tree: An algorithm that produces a graphical tree-like structure is called a decision tree. This algorithm uses a root node with a test condition (such as if the subject has a sore throat) and branches that provide replies, labels, or the alleged class to categorise situations. According to J.R. Quinlan's study "Learning Decision Tree Classifiers," a tree can be either a test node or a leaf node. If the instances belong to different classes, it is called a test node, in which a condition is appended to the value of the attribute, and a test node can further be represented in two or more subtrees [11]. The leaf node denotes the class to which all instances belong.If the cases are members of different classes, it is declared a test node, in which a condition is appended to the value of the feature, and a test node can further be characterized in two or many subtrees. The leaf node is the representation of the class to which all cases belong. J48 DT is a well-liked decision tree method that is frequently employed for classification tasks. It employs the divide-and-conquer principle, which separates the instances into subcategories based on the values of the characteristics [12].

iii. Random Forest:A forest of distinct DTs (decision trees) is built using the RF (Random Forest) technique, which results in the composition of an ensemble. The data is predicted using each tree using the majority votes. As a result, the class receiving the most votes is taken into account for the final projection. As a result, the data are effectively predicted using the combination of individual uncorrelated systems. The correlation between trees can be kept as low as feasible using RF. Bagging is used for this objective. Because DTs are sensitive to training data, RF focuses on creating trees using data that is randomly collected with replacement. As a result, different trees are created that have little in common with one another [13].Additionally, because each tree has the option to base its decisions on a random selection of features rather than selecting each characteristic from the dataset, the Random Forest technique is effective at maintaining Feature Randomness. This produces a wide range in the variables at which each tree is built up. As a result, this technique was helped by bagging and feature randomness during training with random dataset samples as well as with various feature subsets to achieve prediction. A sufficiently big parameter set can also benefit from hyperparameter adjustment to avoid overfitting the data.

II. LITERATURE REVIEW

R. M. Ansari, et.al (2021) constructed and implemented aframework to predict the coronavirus disease-2019 infection severity in the patients and understand their condition [14]. This study emphasized on recognizing thepredictors of Covid-19 outcomes whose evaluation was done in 2 diverse ways such astotal T-cell levels in the blood having T-cell subsets and amount of cells in the blood having virus. Two techniques called MR (multiple regression) and LR (logistic regression) were implemented based onlongitudinal data for building the predictive models. The results indicated that the multivariate LR algorithm had generated more optimal outcomes to predict Covid-19 Infection severity.

S. Ahuja, et.al (2022) introduced a DL (deep learning)-based PNSN (P-shot N-ways Siamese network) with PNN (prototypical nearest

neighbor)algorithm for predicting coronavirus disease-2019infection from lung CT (Computed tomography) scans [15]. SN (Siamese network) was adopted with anidentical sub-network to classify the image on restricteddataset for every class. Thepre-trained sub-networks consisted of weight sharing considered to generate thefeature vectors. This algorithm assisted in classifying the infection in lungs as: zero for 0% (i.e. CT-0), Low for < 25% (CT-1), and Intermediate for 25%–50% infection (CT-2).MosMed dataset of COVID-19 infections was executed to quantify the introduced algorithm. The introduced algorithm yielded 98.07% accuracy, 95.66%sensitivity,98.83%specificity and95.10%F1-score as compared to the existing techniques.

J. Zhou, et.al (2022) suggested a MFLF (multi-modality feature learning and fusion) techniqueto forecast the severity of coronavirus disease-2019based on the blood test supported EMR (electronic medical record) and chest CT (computerized tomography) scans [16]. Theco-occurrence of salient clinical attributes was utilized for computing the severity, for which HoFN (High-order Factorization Network) algorithm was presented for learning the impact of a set of clinical attributes. Additionally, an ADCNN (attention-based deep convolutional neural network) was implemented based on pre-trained metrics for processing the lung CT images. Finally, cohesion of cross-modality representation was attained using a loss function for shifting deep attributes. This technique was proved robust. Experimental results exhibited the effectiveness of the suggested technique in reliable scenario.

R. Y. Wang, et.al (2020) presented ML (machine learning)to analyze GVs (genetic variants)available in the observed comorbidity patterns for predicting COVID-19 [17]. Additionally, GVs were integrated with phenotypes of patients to construct a NN (Neural Network) and RF (Random Forest) modelsso that probability of coronavirus disease-2019infection was predicted. This approach focused on recognizing thesymptoms such as feeling cold or shortness of breath as a predictor. Moreover, the comorbid disease impact ranking had consistency with phenotypic comorbidity patterns. The presented approach attained an accuracy of 91% using initial model and 92% from latter one for predicting the probability of COVID-19 infection in a person. Moreover, the supremacy and consistency of RF was proved.

T. Mahmud, et.al (2021) developed a hybrid NN (neural network)named CovTANet that was a MO (multiphase optimization)techniqueto incorporate an effective network of segmenting the lesion into a complete optimization model for diagnosing and predicting theseverity of coronavirus disease-2019jointly from CT-volume [18].TA-SegNet (tri-level attention mechanism and parallel optimization of multi-scale encoded–decoded feature maps in the segmentation network) helped in enhancing the process to segment the lesion. This approach was proved effective in diagnosing and predicting the severity of disease. For this,the effects of redundant attributes were de-emphasized from the whole CT-volumes. The results revealed that the developed algorithm was capable of predicting the disease atsevere infection phases as well as detecting it at initial phases when the patients hadmild infections, at higher precision. Hence, the probable harm occurred due to the corona disease was mitigated.

P. Wu, et.al (2021) recommended a ML (machine learning) based model called RF-SMA-SVM to predict severity of coronavirus disease-2019on the basis of ML (machine learning) methods [19]. SMA (slime mould algorithm) was implemented to optimize RF (random forest) andSVM (support vector machine). RF algorithm was useful for recognizing the key factorslike basic patient information and 26 blood routine indicators.The optimal SVM model was trained through SMA approach. A dataset was employed to quantify the recommended model in the experimentation. The recommended model performed effectively to classify corona disease and proved stable on 4 parameters for predicting and differentiating severeCOVID-19 patients from the healthy ones. This model offered efficacy to diagnose the COVID-19 infection.

C. Moremada, et.al (2021) aimed to track the user and predict the infection probability of COVID-19 on the basis of these social interactions [20]. SIT (social interaction tracking) system based on EE (energy-efficient)-BLE (Bluetooth Low Energy) was formulated to predict this disease. Thereafter, the collected data employed for suggesting an algorithm so that the possibility to attain the coronavirus disease-2019. At last,a prototype with a mobile app and a web monitoring tool applied to determine whether the formulated system was practical or not. This system was quantified in the simulation. The formulated system led to save the energy up to 90% foridle users and diminish the

required number of PCR (polymerase chain reaction) tests and provided superior accuracy.

F. Y.Aryatama, et.al (2023) presented a prediction application to predict the coronavirus disease-2019pandemic situation in Indonesia based on public compliance with surveillance policies for which the SPCIRD model was applied [21]. SPCIRD model was adopted withLM (LevenbergMarquardt) on Python at optimal results for predicting COVID-19. The questionnaire and black box executed to test the presented application. The presented approach attainedR2 around -1.248 for predicting active cases, -0.235 for recovered and -3.982 for deaths for 281 number of iterations. The accuracy of this approach was found 93.3% for predicting pattern from coronavirus diseases.

Y. Song, et.al (2023) suggested a framework known as STG-Net to predict coronavirus disease-2019on the basis of MST (multivariate spatio-temporal) information [22]. In this,SIM (Spatial Information Mining module) and TIM (Temporal Information Mining module) put forward for mining the ST information of the data in a deeper level.The fluctuation trend of the data was mined using SF (slope feature) technique. Besides, GAF (Gramian Angular Field) was assisted in transforming 1D (one-dimensional) data into 2D images to improve the capacity to mine the networkin time and feature dimension. For this,ST information was integrated for predicting confirmed cases on daily basis. The experimental outcomes exhibited the supremacy of the suggested framework over the traditional methods andattained decision coefficient R2 around 98.23% on the datasets of five countries, and proved robust for predicting COVID-19.

S. Garg, et.al (2022) projected a novel method on the basis of MSDTL (multi-source deep transfer learning) for efficiently forecasting the future coronavirus disease-2019infections [23]. RNN (recurrent neural network)model calledLSTM (Long-short term memory) was employed to accomplish history-dependent tasks. The comparison of projected technique was done with the traditional methods. Therefore, this technique was implemented for improving the potential to predict the corona disease. A dataset taken from 62 provinces executed to compute the projected technique. Diverse parameters such asMAE (mean absolute error) and the coefficient of determination employed to compute this method. The results demonstrated that the projected method attained superior accuracy around 96% to predict theCOVID-19 infection in comparison with the traditional method.

2.1 Comparison Table

Author	Year	Technique Used	Results	Limitations
R. M. Ansari, et.al	2021	MR (multiple regression) and LR (logistic regression) algorithms	The results indicated that the multivariate LR algorithm had generated more optimal outcomes to predict Covid-19 Infection severity.	The major disadvantage of this work was that the sample size was small and the data was gathered only from one medical site for analyzing thepatients suffered from COVID-19. Moreover, its results were restricted only toa particular group having 340 patients.
S. Ahuja, et.al	2022	DL (deep learning)-based PNSN (P-shot N-ways Siamese network) with PNN (prototypical nearest neighbor)algorithm	The introduced algorithm yielded 98.07% accuracy, 95.66%sensitivity,98.83%specificity and95.10%F1-score as compared to the existing techniques.	This algorithm consumed higher cost as there was a necessity of numerous CT scansfor follow-up patients.

J. Zhou, et.al	2022	MFLF (multi-modality feature learning and fusion) technique	Experimental results exhibited the effectiveness of the suggested technique in reliable scenario.	This technique was incapable of using any temporal attributeof an impatient that was required for predicting the situation of patients.
R. Y. Wang, et.al	2020	NN (Neural Network) model and RF (Random Forest) models	The presented approach attained an accuracy of 91% using initial model and 92% from latter one for predicting the probability of COVID-19 infection in a person. Moreover, the supremacy and consistency of RF was proved.	The constricted amount of data was employed to train the model. When the raw data was filtered and pre-processed, only ninety among 6000 sets were found applicable for training, and loading of only 30 sets was done into model as diverseunexpected conditions were there.
T. Mahmud, et.al	2021	CovTANet	The results revealed that the developed algorithm was capable of predicting the disease atsevere infection phases as well as detecting it at initial phases when the patients hadmild infections, at higher precision.	The data collected in this study was not taken fromdifferent geographic locations for understanding the mutation and evolution of this toxic virus
P. Wu, et.al	2021	RF-SMA-SVM model	The recommended model performed effectively to classify corona disease and proved stable on 4 parameters for predicting and differentiating severeCOVID-19 patients from the healthy ones.	The dataset was single-centered and the sample size was found small due to which the accuracy was alleviated. Moreover, external validation was not possible.
C. Moremada, et.al	2021	SIT (social interaction tracking) system based on EE-BLE	The formulated system led to save the energy up to 90% foridle users and diminish the required number of PCR (polymerase chain reaction) tests, and provided superior accuracy.	This system was not much secure to gather data and it was incapable of predicting any other disease which was similar to corona disease.
F. Y. Aryatama, et.al	2023	SPCIRD model withLM (Levenberg-Marquardt)	The presented approach attainedR2 around -1.248 for predicting active cases, -0.235 for recovered and -3.982 for deaths for 281 number of iterations. The accuracy of this	The dataset was not pre-processed effectively because of which it was mixed foreach

			approach was found 93.3% for predicting pattern from coronavirus diseases.	facies.
Y. Song, et.al	2023	STG-Net	The experimental outcomes exhibited the supremacy of the suggested framework over the traditional methods andattained decision coefficient R2 around 98.23% on the datasets of five countries, and proved robust for predicting COVID-19.	The information related to social relationship of every diseased patient was not utilized in this approach.
S. Garg, et.al	2022	MSDTL (multi-source deep transfer learning)	The results demonstrated that the projected method attained superior accuracy around 96% to predict theCOVID-19 infection in comparison with the traditional method.	Theavailable province-specific dataset was least in amount which caused the issue of lower variance and higher bias was occurred.

CONCLUSION

Undoubtedly, the deadly corona virus has resulted in millions of death and infections (leaving lifelong effects) worldwide. Due to the spread of this disease, emergency departments of hospitals are occupied were patients of COVID-19. Thus, there is necessity to make quick decision related to in-or outpatient care. The virus leads to create characteristic abnormalities in CXR (chest radiographs). However, the sensitivity of CXR is lower because of which it is essential to predict the risk considering the additional variables and criteria. Moreover, the social interaction tracking methods and prediction methods, which can work reliably and practically, are required to predict the probability of this disease. This paper defines that preventing its spread is the main challenge for researchers in present times. Furthermore, the major intend is to track the user and predict the infection probability on the basis of social interactions and other attributes.

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