Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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1 Introduction

Artificial intelligence (AI) is presented as a technology that automates computers to integrate the intelligence like human to execute tasks, along with machine learning (ML), natural language processing, virtual reality, knowledge graphs, biometrics, computer vision, and augmented reality (Szegedy et al., 2017). ML is considered as a subset of AI for making the decision and prediction (Yue et al., 2020; Yan et al., 2020a, b) and deep learning (DL) is presented as a subset of ML. There are different ML methods such as logistic regression, decision tree, Adaboost, K-nearest neighbor (KNN), support vector machine, K-means clustering, Naive Bayes, Hidden Markov Models, density clustering, etc. (Breiman, 2001; Ong et al., 2020; van der Maaten and Hinton, 2008) and also several DL methods such as recurrent neural networks, convolutional neural networks, deep belief networks, restricted Boltzmann machines (Greff et al., 2016; Skalic et al., 2019).

AI is significant to automate the task (Li et al., 2007; Martin, 2007; Singh et al., 2014, 2017) by diagnosing the gestures of the diseased person from the collected information by visual sensors such as time-of-flight pressure imaging (Casas et al., 2019), RGB, or thermal cameras. AI-based methods have been successfully applied in different situations and automated treatment and diagnoses in clinical trials. Deep neural networks are applied for COVID-19 treatment using medical images to provide
challenging results (Dogan et al., 2021; Huang et al., 2020a; Ng et al., 2020; Ozturk et al., 2020; Tabik et al., 2020; Wang et al., 2020). These techniques are based on DL (Oh et al., 2020; Toğar et al., 2020; Ucar and Korkmaz, 2020), while the applications of DL model are a challenging topic in the AI field in medical image processing and analysis (Kermany et al., 2018; Lakhani and Sundaram, 2017). In this COVID-19 crisis (Tiwari et al., 2020), the medical fraternity is seeking for technologies to track and monitor the infection status of COVID-19 disease. Due to the rapid spread of this pandemic, many researchers are working to get the solution to help mankind (Jin et al., 2020; Kaye et al., 2020; Lawand and Al Tabbah, 2020; Velavan and Meyer, 2020). AI has been identified as decisive technology to tackle the pandemic. This pandemic poses several challenges to the AI community. AI works as an evidence-based tool and can be used to fight against the Corona virus. AI will help the physicians to identify the symptoms of a patient. The significant use of AI to cope up with COVID-19 is

1. monitoring and prediction of disease;
2. early detection of the disease and prognosis;
3. drug and vaccine;
4. social control or contact tracing of the individuals who affected with the disease;
5. helping health-care workers to fight against COVID-19; and
6. projection of cases and mortality.

AI has the potential and can improve decision making to fight against COVID-19 by developing valuable and advanced algorithms such as DL. In this study, AI applications in a pandemic are considered in three groups: molecular, clinical, and social scales (Bullock et al., 2020). The molecular scale includes molecular modeling to diagnose the proteins found in SARS-CoV-2 infection and identify potential treatment. AI applications of molecular scale comprise predicting protein structure, repurposing the drug, discovering the drug, discovering the vaccine, improving viral nucleic acid testing, and better understanding infection. Most AI tools in the clinical scale are applied to diagnose and treat using medical imaging, such as X-ray scans and computational tomography (CT). AI supports predicting the evolution of the disease and monitoring and measurement processes. AI applications of clinical scale cover diagnosis with medical imaging, disease tracking with noninvasive measurement, and prediction of patient outcome. The social scale is further categorized into two: infodemiology and epidemiology.
This study aims to present different aspects of AI technology to fight against pandemics with various measures for facing the pandemic. Therefore, it is organized as follows. Section 2 gives a comprehensive background of the study. It involves two main parts: related works about pandemic and COVID-19, and applications of AI/ML in emerging diseases. Section 3 presents the AI/ML applications related to COVID-19. Detection, diagnosis monitoring, prediction of disease and mortality, drugs and vaccines preparation, drug repurposing, social awareness, and control by the Internet are discussed in this section. Section 4 gives both challenges and future directions. Section 5 represents the conclusion of the study.

2 Background

2.1 Pandemic and COVID-19

Any disease infection is pretended to occur as a susceptible person creating contact with an infectious person in a community or workplace area. If infection appeared, it spread to the other person and continues to the community in an asymptomatic state. Various infectious diseases caused several lives and led to severe conditions that took enough time to control the disease. The pandemic and epidemic have been applied to explain the nature of disease that appears with a period. If the disease cases are overgrowing than usual and cause the lives in a particular area, then it is declared as an epidemic (Orbann et al., 2017). In other term, pandemic is an infectious disease outbreak that indefinitely raises the morbidity and mortality over a huge geographical area. Epidemic has been increased over the past century due to several factors such as increasing worldwide travel, exploitation of land, and harming the natural resources (Morse, 2001). According to the previous studies, smallpox infection caused 500 million lives in the whole world in the past 100 years (Henderson, 2009). In 1918, the Spanish influenza outbreak caused 17–100 million lives, as an estimation (Spreeuwenberg et al., 2018). Different kinds of pandemics have been reported for the last 20 years such as H1N1 influenza in 2009, Middle East respiratory syndrome coronavirus (MERS-CoV) in 2012, and acute respiratory syndrome coronavirus (SARS-CoV) in 2002–03. We have discussed several pandemics with their period and the death toll in Table 1 (Swapnarekha, 2020; Swapnarekha et al., 2020).

COVID-19 outbreak was reported in Wuhan, China as a pandemic, in December 2019 as a cluster of deadly respiratory infections and grows rapidly as an epidemic all over the world. Coronaviruses are found zoonotic and
easily transmitted among people and animals. It is still under investigation to explore how it is transmitted into animal reservoirs and others. As there was no vaccine and fixed treatment for COVID-19 pandemic, hence social distancing has been declared the most accepted strategy for its control and prevention. It is necessary to isolate the person who has a travel history and contact with the infected patient. Social distancing, quarantine, and isolation play an important role in controlling and prevent the infection of COVID-19 deadly disease.

### 2.2 Applications of AI and ML in emerging diseases

Science and technology considering AI and ML toward several pandemics as well as COVID-19. The health-care sector needs urgent support of new technologies such as IoT, AI, Big Data, and ML to tackle with the new diseases. AI and ML models are significant for practical analysis in the biomedical fields. These tools are significantly effective to combat with various diseases (dengue, flu, zika, ebola, cholera, H1N1, influenza, and swine fever) with other methods such as classification, preprocessing of data, forecasting, prediction, pattern recognition, and monitoring. These methods are significant to identify, treat, and predict pandemic infections. Since the outbreak of COVID-19, AI and ML tools are playing a significant role to combat with the deadly disease (Hollister, 2020). ML is considered as a subset of AI and helps machines to understand “training samples” or patterns in data preprocessing to make or predict intelligent decisions. There are four primary areas of AI (tracking and prediction, treatment and cure, early warning, data dashboard, and alert) to contribute against COVID-19.
Tracking and predicting COVID-19 transmission are prominent data inputs for tackling the pandemic by planning, preparation, and management with the health authorities (Naudé, 2020). It also identifies the epidemiological curve and attending pandemic situation and predicts future projections for taking possible control measures to reduce transmission. Recently, a tracking app “Aarogya Setu” (Aarogya Setu App, 2020) is launched in India to track newly infected cases by using smartphones and Bluetooth to determine any person nearby infected person.

Early warning and alerts help control the disease outbreak, such as COVID-19. AI-based alert models help diagnose the patterns by mining online content, news, and other sources to predict early warnings for preparedness measures such as “Bluedot” (BlueDot, 2020), a Canadian mode, and WHO Early Warning System. These models help take preventive actions such as quarantine, isolation, hotspot mapping, intelligent contact tracing, cluster prediction, and containment.

Treatment and cures. AI advances to find new drug discoveries and repurpose existing drugs for COVID-19 patients. In COVID-19, several data centers and research labs use AI technologies for treatment and vaccine diagnosis. ML techniques are significant to control, check, trail, and approve new drugs.

Data dashboard. Several institutions such as the Johns Hopkins University and the OECD (oecd.ai) have presented attractive dashboards to trace the virus transmission and showing the current status of confirmed, recovered, and diseased cases. COVID-19 tracker is a notable dashboard for several countries to present the country wise data analysis.

Bullock et al. (2020) have presented a survey with AI applications to show how AI can efficiently reduce the diagnosis and perform cheaper and faster COVID-19 tests. Authors have categorized the applications of AI in several ways: molecular scale, clinical scale, and social scale. A hierarchical representation of AI applications has shown in Fig. 1.

2.2.1 AI applications at molecular scale
Molecular scale covers molecular modeling to diagnose the proteins involved in SARS-CoV-2 and identify potential treatment. There are some structural proteins such as envelope proteins (E), nucleocapsid proteins (N), spike proteins (S), and membrane proteins (M), and nonstructural proteins such as 3-chymotrypsin-like, protease, and the papain-like protease (Liu et al., 2020; Zhavoronkov et al., 2020).
AI application of molecular scale comprises prediction of associated proteins structure, diagnosing drugs that can effectively target these proteins, and new compounds to make the further test as a possible treatment (Naudé, 2020). Several molecular scales have been discussed in this section.

Prediction of protein structure. Experimental approaches such as X-ray crystallography generally describe protein structure, but sometimes they are expensive and time consuming, so computational models are applied to predict the structure of proteins. There are two primary approaches, template modeling to predict structure as a template-free modeling and template sequence for unknown related systems.

Repurposing of drug. Several studies have been focused on detecting known elements that can be useful in lessening infections along with approved drugs. For repurposing the drug, four different approaches can be managed by AI, such as the forecasting of protein–ligand binding affinities, the construction of biomedical knowledge graphs, molecular docking simulations, and gene expression signatures analysis.

Discovery of drug. Some studies offer to explore utterly new aggregate to target SARS-CoV-2. Tang et al. (2020) have applied a reinforcement learning approach to explore the aggregates constrain the 3C-like protease. They have designed a novel “deep Q-learning network along with the fragment-based drug design” (ADQN-FBDD) to generate the lead elements that targets SARS-CoV-2 3CLpro. This work resulted the derivatives series from
extracted lead elements by the structure-based optimization policy. Finally, they have extracted 47 lead compounds from their AI model and derivatives. Nguyen et al. (2020) have used a generative network complex for finding the drug. They have designed a structural-based drug repositioning model that is based on mathematics and learning to explore 1465 drugs in the DrugBank that is approved by the Food and Drug Administration and it is found that these drugs are deeply effective to 2019-nCoV. Bung et al. (2021) designed a generative model for SMILES input strings. This model is proposed as a classifier to predict the next character of strings.

**Discovery of vaccine.** Vaccine discovery is a different area as drug discovery. Antibodies are developed for virus neutralizing with the help of B-cells and the body needs T-cells to kill the virus precisely. Generally, vaccine design aims two significant objectives: (a) diagnosing proper epitopes for achieving and (b) assuring that these epitopes can be described by major histocompatibility protein that are generated by human leukocyte antigen allele.

**Improving viral nucleic acid testing.** ML techniques are applying to enhance the virus nucleic acid diagnosing test. Metsky et al. (2020) associated ML with CRISPR tool to design assay samples for diagnosing 67 respiratory viruses along with SARS-CoV-2. ML models have been constructed to create assays that are predicted specifically, quickly, and sensitively. They have experimentally explored four SARS-CoV-2 develops with a CRISPR-Cas13 identification system and then tested the performance of SARS-CoV-2. They also describe the speed and sensitivity of this assay by applying synthetic targets along with fluorescent as well as lateral flow detection. Lopez-Rincon et al. (2020) follow convolutional neural network model for nucleic acid sequences to categorize where it is linked to SARS-CoV-2. This work has proposed a deep convolutional neural network that can design features automatically by the virus’s genome sequence. This work has proposed a state-of-the-art deep convolutional neural network that is able to create features automatically by the virus’s genome sequence. Results has shown that proposed method is suitable to categorize SARS-CoV-2 and differentiating by other strains of coronavirus such as HCoV-OC43, MERS-CoV, HCoV-229E, HCoV-HKU1, etc.

**Better infection understanding.** ML is used to pay more attention for better understanding of SARS-CoV-2 infectivity and infection severity such as support vector machines (Cortes and Vapnik, 1995) and KNNs, along with decision trees, to predict the hierarchical viruses classifications (Randhawa et al., 2020) based on their genomic sequence.
2.2.2 AI applications at clinical scale

Most AI and ML techniques are used to diagnose and treat medical imaging, such as X-ray scans and CT. AI supports to predict the evolution of the disease and for monitoring and measurement process.

*Diagnosing with medical imaging.* AI techniques are widely applied in diagnostic methodologies such as screening, medical imaging, and diagnosing of COVID-19 patients (Ai et al., 2020). Medical imaging (Fang et al., 2020; Kanne et al., 2020) can observe image patterns and radiological signatures for COVID-19 cases. ML approaches can help promote the analysis of scanning by using different architecture such as Inception (Szegedy et al., 2015), ResNet (He et al., 2016; Zhou et al., 2018) that can train directly.

*Disease tracking with noninvasive measurement.* Several approaches not required medical imaging equipment for tracking and diagnosing COVID-19 disease. Various efforts have been done to use mobile apps for identifying COVID-19 with the help of embedded sensors to diagnose COVID-19 symptoms (Maghdid et al., 2020) and identify high-risk patients through phone-based surveys.

*Prediction of patient outcome.* It is difficult to predict outcomes of patient about planning, preparation, and optimization in health systems for COVID-19 epidemic. It is important to diagnose the aspects that cause patients at risk, developing respiratory syndrome, and fatalities due to respiratory failure. Some approaches such as support vector machines (Cortes and Vapnik, 1995) and XGBoost algorithm (Chen and Guestrin, 2016) are used to detect important measurable factors to predict death risk. Medical imaging is also applied in several areas for predicting patient outcome.

2.2.3 Social scale: Infodemiology and epidemiology

The social scale is further categorized into two: infodemiology and epidemiology. This section will further discuss it.

*Infodemiology.* Online web sources and social media are the key channels for disseminating the virus information and explaining its dynamics. Although AI and ML carried enough research but still need a better understanding of social dynamics in pandemics. Several factors are discussed to disseminate information related to the pandemic, such as spread and infection, hate speech, and positive action. Singh et al. (2020) use Twitter for the dissemination of spread and infection. They have analyzed a huge volume of tweets related to coronavirus queries. They have explored that an important spatiotemporal relationship available among new cases and information flow of COVID-19. It is also noticed that this research has taken first step to
understand the conversation of social media about COVID-19. Gallotti et al. (2020) also examined twitter social media posts across 64 languages. They have designed an Infodemic Risk Index to measure the magnitude of risk to irrelevant news across the globe. This study explored that measurable waves of unreliable news anticipated the growth of COVID-19 contagion and these fake news can cause a critical threat to public health. Mejova and Kalimeri (2020) have analyzed the Facebook advertisements to explore the spread and infection information. An incremental growth has been observed in hate speech and verbal abuses that can cause physical violence in any country during the pandemic. Several efforts are going on for curating the particular news data about the virus and conduct fact checking to analyze the relevancy. Pandey et al. (2022) have presented a method for analyzing the similarity among the World Health Organization (WHO) recommendations and regular headlines of news. They have explored that a multipronged device learning application conveying vernacular bite-sized audios and also revealed that conversational AI is an impressive approach to lessen the unreliable information.

Epidemiology. SARS-CoV-2 virus transmission received much attention to forecast models and new information. The epidemiological research area is vast and resulted in several modeling efforts. Most of the models build on well-designed classical models such as SIR and SEIR models with ML techniques for modeling tasks such as forecasting and modeling statistics, clustering, Bayesian analysis, and risk assessment. Several AI applications have been designed for forecasting local and national data, such as total confirmed cases, recovery rates, and fatality cases. Several models have been offered to examine the model structure and optimal approaches for forecasting data daily. They have applied different modeling techniques such as LSTM-GRU architecture (Cho et al., 2014; Hochreiter and Schmidhuber, 1997) for time-series prediction and analysis (Dutta and Bandyopadhyay, 2020) and CNN-based approaches (LeCun et al., 2015), where integer facts have been merged and reframed into “images” (Huang et al., 2020b). Clustering is another ML technique that aims to create groups considering similarities among clusters. Carrillo-Larco and Castillo-Cara (2020) have implemented the ML techniques for detecting general public health-care aptitude and interest associated with COVID-19. Hu et al. (2020) proposed AI-based methods for the forecasting of real-time COVID-19 data to measure the length, size, and controlling duration of pandemic in China. Bayesian analysis techniques also presented significant insights to handle the uncertainty and small datasets.
Table 2 discusses how ML techniques are applied in different emerging diseases and played an important role in tackling the diseases.

### 3 Applications of AI and ML in COVID-19

Practitioners encounter critical issues in the diagnosis of nCov–2019 because SAR-CoV-2 viruses spread quickly. As the approved system employed for diagnosing COVID-19, the RT-PCR approach is not useful due to few barriers (Singh et al., 2018). The limitations of RT-PCR can be anticipated analyzing medical images because growing digital methods help to control pandemic by employing statistics, ML/AI methods (Swapnarekha, 2020). The capability of these models has been presented in a different form of usage, from disease detection and forecasting to social control. Various applications include real-time data study for detecting disease, treatment monitoring, drug/vaccines development, and forecasting of infection and death (Patel et al., 2019).

#### 3.1 Detection and diagnosis

COVID-19 outbreak is not only appeared as a medical contagious but also it is an economic contagious (Baldwin, 2020). Early detection of the infection is critical for personalized patient care, satisfactory patient quarantine, and diagnosis. Since the first, the false-negative test may delay treatment and boost the danger of viral transmission to healthy people; fast detection of infected people with COVID-19 is essential. AI techniques are equipped to expand the early detection of disease infection. Mei et al. (2020) aimed to create an AI-based early detection model that can recognize coronavirus
infection by considering chest CT scans. They have integrated AI algorithms to assimilate chest CT results with clinical systems, laboratory testing, and exposure history to speedily identify infected patients.

### 3.2 Treatment monitoring

Epidemiological research at the population and individual level should be procured at a specified period, with infection-oriented data gathered longitudinally. Diagnosis and treatment ways are minimal because of the limited knowledge of novel viruses at the beginning of an epidemic. Moreover, infectious diseases can be spread rapidly from one person to the other. Therefore, unknown aspects of the virus, symptoms’ severity, and critical fatality rates cause the prediction problem’s seriousness, especially the pandemic size and location (Agrebi and Larbi, 2020). Various forecasting models based on ML methods can be applied to forecast the infection by using different variables such as age, sex, underlying diseases, and preexisting immunity. Postnikov (2020) asserts a simple ML model can represent the epidemic parameters qualitatively. He has proposed an appropriate model to reproduce the pandemic dynamics qualitatively as well as quantitatively along with high degree of correlation that helps to estimate predictions. This model is a three-compartmental SIR (susceptible-infectious-recovered-removed) model to the logistic regression with the primary characteristics of the epidemic process. Wu et al. (2020) measured COVID-19 pandemic size and predicted the scope of public health risks locally and globally using the SEIR (susceptible-exposed infectious-recovered) model. Shao and Shan (2020) explained using some critical estimation to smoother the infection of the pandemic. They have designed a SEIRD model to simulate the control measures and pandemic prevention.

### 3.3 Prediction of disease and mortality

Creating pandemic prediction models with high accuracy is required to reveal insights about the spread and outcomes of the outbreak. These models are critical for governments and lawmakers to recommend effective strategies and evaluate the implemented strategies’ results (Remuzzi and Remuzzi, 2020). SEIR models consider the considerable incubation time when people are infected and increase the accuracy of the prediction model for the Varicella and Zika outbreaks (Pan et al., 2012; Zha et al., 2020). The incubation time is a random variable in SEIR and SIR models, and there is a balance without thinking about the disease (Dantas et al., 2018). However,
traditional SIR and SEIR models do not consider variables such as social distance and quarantines (Imran et al., 2017). Another common technique mainly applied to a contagious disease is that the R0 calculates the number of individuals who can infect another infected person. In the R0 model, additional weight is used for individuals who were not infected with the disease or were not protected by a vaccine (Chimmula and Zhang, 2020). It can also be applied to detect a novel virus’s infection rate (Zhang et al., 2020). In such techniques, however, it is hard to determine the initial point of the contagious disease and the interaction with others during the incubation time.

Many well-known and undiscovered variables included in the outbreak, the confusion of community response in different areas, and differentiation in avoiding tactics had strikingly extended model difficulty (Chimmula and Zhang, 2020; Darwish et al., 2020). Eventually, conventional pandemic prediction models encounter unusual difficulties in delivering more stronger effects. Therefore, various new models have developed, including some assumptions such as social distancing and quarantines (Rypdal and Sugihara, 2019; Scarpino and Petri, 2019; Zhan et al., 2019).

Some ML-based methods have been proposed to predict the spread and results of the outbreak to master the limitations of these kinds of statistical methods (Chimmula and Zhang, 2020; Ucar and Korkmaz, 2020). Long short-term memory (LSTM) networks based on DL were applied in some studies to forecast coronavirus infections (Dutta and Bandyopadhyay, 2020; Huang et al., 2020b; Tomar and Gupta, 2020). The LSTM models employed in the networks cannot describe the spatiotemporal elements together in these studies. Chimmula and Zhang (2020) presented an LSTM model by adjusting alternative internal connections between the input and output cells. Ardabili et al. (2020) applied multilayered perceptron and adaptive network-based fuzzy inference system methods to the extremely complicated nature of COVID-19 and behavioral differences in several countries (Italy, China, Iran, Germany, and the United States).

Table 3 gives the various ML techniques that used to predict COVID-19 outbreak.

### 3.4 Drugs and vaccines preparation

Drug and vaccine improvement is a critical responsibility in fighting a pandemic. AI can reduce drug discovery duration and improve performance, although it is highly costly and time consuming (Mamoshina et al., 2016). A scientific team at the MIT built a model to prevent the coronavirus...
that conduces toward COVID-19 by creating a “decoy” receptor that might be considered as a vaccination. Coronaviruses bind ACE2 receptors in the body and induce sickness. The MIT professionals have applied an AI method to affect the link between the bats and the virus (Busse et al., 2020). Some studies concentrate on discovering novel composites for practice in centering on SARS-Cov2 by using a particular method to identify inhibitors for the 3Clike protease (Zhavoronkov et al., 2020). Such techniques employ three kinds of information: the protein structure, the cocrystalized ligands, and the homology form of the protein. Several approaches, such as Generative Auto-encoders and Generative Adversarial Networks, are applied for each type of information (Makhzani et al., 2015). The experts examine possible candidates applying a reinforcement learning method with a prize capacity that combines determinants, such as medication measurements, similarity, newness, and variety. AI balances to not dramatically change the whole pharmaceutical life cycle, from regulative procedures to pharmacovigilance. In summary, AI and ML speed up drug testing in real time and recognize beneficial drugs for the treatment of patients with COVID-19.

| References                | ML approach                   | Explanation                                                                                     |
|---------------------------|-------------------------------|------------------------------------------------------------------------------------------------|
| Tuli et al. (2020)        | Robust Weibull fitting model  | Levenberg–Marquardt algorithm                                                                 |
| Pourghasemi et al. (2020) | Random forest                 | Provides risk maps to manage and control the pandemic in Iran                                   |
| Chimmula and Zhang (2020) | Long short–term memory networks | Considers the fundamental characteristics of COVID-19 to predict the trends and possible stopping time in Canada and around the world |
| Alzahrani et al. (2020)   | ARIMA                         | Predicts the anticipated everyday count of COVID-19 infected cases in Saudi Arabia               |
| Ribeiro et al. (2020)     | More than one                 | Compares short–term prediction methods in Brazilian                                             |
| Ahamad et al. (2020)      | More than one                 | Analyzes patient symptoms to predict the pandemic diagnoses                                     |
| Zhu et al. (2020)         | Deep learning                 | Predicts the possible hosts of coronaviruses                                                   |
| Fong et al. (2020)        | Polynomial neural network     | Proposes three ML techniques that can work with scarse data                                       |
Moreover, AI can support screening prepared drugs and speeding up antiviral progress to treat COVID-19. CORD-19 dataset can be used to train AI and ML algorithms. The resulting prototype can be practiced to monitor for current drugs that probably show effectiveness in the treatment of patients with COVID-19 (Ahuja et al., 2020).

3.5 Drugs repurposing

With no vaccine or potential treatment recently available, the coronavirus has outbreak speedily across the globe and affected the world’s economy and an ever-increasing amount of fatalities. It is an initial task to search for any existing drug repurposed to save the human population.

Drug discovery is a complex process, needing several validation layers before the drug may come into use. Considering the present scenario of the pandemic, a dual approach is required to protect the human from this deadly disease (Zhou et al., 2020):

- Repurposed drugs—diagnose the opportunities in the available set of known drugs; and
- Drug screening—work on new optimized molecules.

Drug repurposing, identifying effective drugs from available drugs, will lessen the time and cost compared to the new drug discovery. Though drug repurposing is sometimes based on chance observations, target-based repurposing depends on a prior understanding of the specific molecular or cellular element that the proposed drug recognizes (Pizzorno et al., 2019). The focus could be on already approved marketed drugs or those under clinical trials against the CoVs in general, and the SARS-CoV-2 in particular.

For repurposed drugs, it is essential to compare the genome of several coronaviruses, which infects humans. The target does not need to have the exact mechanism of action in both the diseased states. So, the drug could be an antivirals agent that will target the viral proteins essential tool of the viral life cycle, such as virus-host cell interactions, replication, assembly, etc., would belong to this class. Several drugs have been repurposed as anti-HCoV, using network proximity analysis (Cheng et al., 2018) and “complementary exposure” pattern (Cheng et al., 2019) of drugs and HCoV-host interactions in the human genome.

Besides drug repurposing, a virtual screening based on molecular docking appears as an essential tool for gaining new antiviral molecules. Researchers and physicians can apply this tool as a complementary method
to synthesize new compounds or assign the repositioning of drugs (Marinho et al., 2020; Milite et al., 2019).

One aspect of proposing a new drug is to find the drug pockets in the structure of the viral proteins. Since the quaternary structure of COVID-19 spike (S) glycoprotein is resolved (Wrapp et al., 2020), and can be downloaded from the Protein Data Bank opens to Structural Biology new aspects to find new drugs specific to spike protein. The S glycoprotein plays the main role in COVID-19 infection by mediating attachment of viral particles to the host cell receptor, it is also involved in cell-to-cell fusion and activates neutralizing antibodies, addressing also virulence determinants (Spaan et al., 1988). The quaternary structure is important for the virus’s virulent property. By using databases such as PockDrug-Server (Hussein et al., 2015), it is believed that analysis of protomer-protomer COVID-19 interfaces S glycoprotein could be a proper initial or beginning point for the prediction of new ligands and that by intervening with quaternary structure assembly of COVID-19 S glycoprotein may present therapeutic process against viral life cycle (Bongini et al., 2020).

3.6 Social awareness and control by the Internet

Social media platforms present many opportunities at both individual and enterprise levels, such as targeting marketing, personalized campaigns, valuable insights about the business, and fast communication. However, they cause a crisis over people. Populaces are exposed to misinformation that may lead to propagation. The WHO’s response to challenging this problem based on wrong information in social media is practicing its Information Network for Epidemics (EPIWIN) platform for presenting the correct data to principal partners (Zarocostas, 2020). Besides, the Facebook Ad Library (Facebook, 2020) investigated all advertisements using the keywords “COVID-19” and “coronavirus” from 34 countries. Maddah and Beigzadeh (2020) have introduced a scheme for COVID-19 detection by using the data collected from individuals' smartphones and sensors. In another study, a smartphone’s sound taken from a microphone was processed to identify the cough type (Nemati et al., 2019). AI and ML algorithms can learn and predict the threat contamination that can signify early detection of a jeopardous case for quarantine purposes. Therefore, an AI-based application can decrease the spread of the virus to weak populations (Allam and Jones, 2020).
4 Challenges and future directions

AI, as an effective method, has been generally used in health care. Among the existing analytical techniques, AI has been explored as the most promising tool for humankind. AI is used in various medical sectors such as medical data analysis, disease identification and diagnosis, drug manufacturing and discovery, vaccine development, robotic surgery, monitoring the patient’s condition, tracking, and forecasting the nature of the virus.

4.1 Challenges

AI has a significant role on the health-care industry and great potential to solve health-care problems. Even though widespread applications of AI in health care are emerging, but enormous challenges lie hard. Some of the challenges of AI in health-care:

AI tools, that are adopted by health-care industries, are not matured and entirely sophisticated (Panch et al., 2019). Premature use of AI tools will record inefficient output and harm the users.

Regularity body. Even though the exponential growth of AI applications continues, there is no regularity body to deal with emerging algorithms.

Lack of Big Data. Many organizations do not have big data to enable AI in their organizations. AI methods need a huge quantity of data for training of the model.

Adoptability. Many health-care professionals lack the capabilities to use/adopt AI in health-care. Human barriers to the adoption of AI are substantial. The health-care industry is lagging in adopting (Wiljer and Hakim, 2019).

Data ownership, control, and consent are also a challenge for implementing AI in health-care.

Standard policy. Organizations must adopt procedures and policies for data privacy. Organizations that adopt AI must safeguard the data with all stakeholders.

Lack of regulation. Regulations to adopt AI in medical research lack standard. One main regulatory issue in choosing AI in health care is archaic regulatory infrastructure. Traditional regulations for health-care cannot be applied to AI-based health-care systems (Analytics India Magazine, 2020a).

Metrics, used in AI for measuring the performance of the algorithm, often do not reflect the clinical applicability. Parameters such as accuracy and area
under the curve do not necessarily represent clinical efficacy (Keane and Topol, 2018; Saito and Rehmsmeier, 2015).

Data exchanging is another challenge in adopting AI in health-care. The sharing of health-care data is critical in the operationalization of AI. AI systems require data from various clinical studies. All the parties in the health-care ecosystem should exchange data considering privacy (Jiang et al., 2017).

Risk of adversarial attack. AI algorithms are susceptible to the risk of adversarial attack (Finlayson et al., 2019).

Algorithmic bias. Another challenge in adopting AI in health-care systems is algorithm bias. There are three types of bias namely, (i) model bias, (ii) model variance, and (iii) outcome noise (Kelly et al., 2019).

Interoperability. AI systems are having a lack of interoperability with other health-care platforms (Analytics India Magazine, 2020b). One of the significant challenges in adopting AI in health-care is inconsistency in health-care records, which cause inaccurate analysis (MindFields, 2020).

Uncertainty and mixed data. Due to uncertain and mixed health-care data, standard models record lower accuracy for predicting pandemic diseases.

4.2 Future directions

Even though AI has solved some of the health-care sector’s complex challenges, the implementation of AI in health-care is still at the nascent stage, and the extent of AI to the health-care sector should be increased.

AI should be integrated with susceptible-exposed-infectious-recovered (SEIR) model to enhance the prediction of epidemic diseases in terms of accuracy. There should be some benchmark framework to assess the current AI techniques. Transfer learning methods and computational efficiency can be adopted, and inference using pretrained networks can be adopted along with AI for new applications (Panayides et al., 2020).

Novel algorithms must be developed to provide a more accurate diagnosis and prediction of diseases with a reduced response. In the future, AI will become more advanced and can carry a wide range of tasks. AI should be more ethical and should make more ethical decisions, and AI will not substitute the doctors for three reasons: responsibility, credibility, and accuracy. Public-private partnerships will help the progress of AI in health-care. Testing AI/ML algorithms will increase trust in AI/ML.
5 Conclusions

AI and ML are advanced analytical techniques having great potential to deal with uncertainties, incompleteness, and inconsistencies in data. These techniques are promising and, therefore, used by many researchers focused on COVID-19. Researchers and scientists are exploring all possible efforts to fight COVID-19 pandemic. This chapter presents a thorough review of the pandemic and COVID-19, applications of AI/ML in emerging diseases, and applications in AI/ML COVID-19, such as detection and diagnosis, treatment monitoring, prediction of disease, and mortality, drugs and vaccines preparations, and drugs repurposing. Several challenges have been presented to make an impact on the health-care industry and have great potential to solve health-care problems. Finally, the chapter has concluded with the future directions that will help researchers, academicians, practitioners, and physician for finding the details about AI/ML techniques in pandemic.

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