

Epidemiological Challenges in Pandemic Coronavirus Disease (COVID-19): Role of Artificial Intelligence

Abhijit Dasgupta^{1*}, Abhisek Bakshi^{2§}, Srijani Mukherjee¹, Kuntal Das¹, Soumyajeet Talukdar¹, Pratyayee Chatterjee¹, Sagnik Mondal¹, Puspita Das¹, Subhrojit Ghosh¹, Archisman Som¹, Pritha Roy¹, Rima Kundu¹, Akash Sarkar¹, Arnab Biswas¹, Karnelia Paul³, Sujit Basak⁴, Krishnendu Manna⁵, Chinmay Saha⁶, Satinath Mukhopadhyay⁷, Nitai P. Bhattacharyya⁷, and Rajat K. De^{8*}.

¹ Department of Data Science, School of Interdisciplinary Studies, University of Kalyani, Kalyani, Nadia 741235, West Bengal, India; ² Department of Information Technology, Bengal Institute of Technology, Basanti Highway, Kolkata 700150, West Bengal, India; ³ Department of Biotechnology, University of Calcutta, Kolkata 700019, West Bengal, India; ⁴ Department of Physiology and Biophysics, Stony Brook University, Stony Brook, New York 11794, USA; ⁵ Department of Food & Nutrition, University of Kalyani, Kalyani, Nadia 741235, West Bengal, India; ⁶ Department of Genome Science, School of Interdisciplinary Studies, University of Kalyani, Kalyani, Nadia 741235, West Bengal, India; ⁷ Department of Endocrinology and Metabolism, Institute of Post Graduate Medical Education & Research and Seth Sukhlal Karnani Memorial Hospital, Kolkata 700020, West Bengal, India; ⁸ Machine Intelligence Unit, Indian Statistical Institute, 203 B.T. Road, Kolkata 700108, India.

Abstract

World is now experiencing a major health calamity due to the coronavirus disease (COVID-19) pandemic, caused by the severe acute respiratory syndrome coronavirus clade 2 (SARS-CoV-2). The foremost challenge facing the scientific community is to explore the growth and transmission capability of the virus. Use of artificial intelligence (AI), such as, deep learning, in (i) rapid disease detection from x-ray/computerized tomography (CT)/ high-resolution computed tomography (HRCT) images, (ii) accurate prediction of the epidemic patterns and their saturation throughout the globe, (iii) identification of the epicenter in each country/state and forecasting the disease from social networking data, (iv) prediction of drug-protein interactions for repurposing the drugs, and (v) socio-economic impact and prediction of future relapses, has attracted much attention. In the present manuscript, we describe the role of various AI-based technologies for rapid and efficient detection from CT images complementing quantitative real time polymerase chain reaction (qRT-PCR) and immunodiagnostic assays. AI-based technologies to anticipate the current pandemic pattern, possibility of future relapses and socio-economic impact are also discussed. We inspect how the virus transmits depending on different factors, such as, population density and mobility among others. We depict how AI-based mobile app for contact tracing and surveys can prevent the transmission. A modified deep learning technique can assess affinity of the most probable drugs to treat COVID-19.

§ To be considered as 'First Authors'.

* Correspondence should be addressed either to Abhijit Dasgupta, M.Tech., Department of Data Science, School of Interdisciplinary Studies, University of Kalyani, Kalyani, Nadia 741235, West Bengal, India, Email: abhijitju06@gmail.com., or to Rajat K. De, Ph.D., Machine Intelligence Unit, Indian Statistical Institute, 203 B.T. Road, Kolkata 700108, India, Email: rajat@isical.ac.in.

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Here a few effective antiviral drugs, such as, Geneticin, Avermectin B1, and Ancriviroc among others, have been reported with their appropriate validation from previous investigations.

Keywords:

SIRD, Twitter, GHSI, Pre-symptomatic, EHR, Contact tracing, On-line survey, qRT-PCR, X-ray, CT/HRCT, CNN, Autoencoder, Drug affinity, CPI, and Inflation.

1. Introduction

Infection with severe acute respiratory syndrome coronavirus clade 2 (SARS-CoV-2) causes devastating pneumonia COVID-19. Symptoms of the disease are similar to SARS-CoV and Middle East respiratory syndrome coronavirus (MERS-CoV) infections. The worldwide public health is badly affected by the recent pneumonia outbreak caused by SARS-CoV-2. The common symptoms (Figure 1) of coronavirus disease (COVID-19) are fever and dry cough at the onset of illness, but the most distinctive symptom of the patient is suffering from respiratory problems. The health of many patients in the intensive care has been worsened in a short phase of time, leading to death because of respiratory failure¹. Thus speedy and accurate detection of SARS-CoV-2 is essential for appropriate management and preventing the spread. Presently there is no specific treatment for the disease. Thus it is very necessary to establish a quick standard diagnostic test for the detection of COVID-19 to avert consequent secondary spread among individuals.

Reverse transcriptase mediated quantitative real time polymerase chain reaction (qRT-PCR) is a gold standard test for the diagnosis of COVID-19 infection². Real time PCR is expensive and cannot be used for diagnosis of large number of people as screening cum detection test. A number of external factors can also affect qRT-PCR test results. These include sampling operations (sample collection and handling), sample stability (decrease in viral counts due to sample handling time), sampling time (different period of the disease development), availability and performance of detection kits. Thus qRT-PCR technique is difficult to use at population level, and is unable to control epidemic COVID-19 at very initial phase.

Preliminary screening can be done through the presence of six symptoms (fever, cough, respiratory distress, loss of taste, loss of smell and conjunctivitis) associated with COVID-19, followed by normal oxygen saturation level measurement using simple pulse oximeter. Normal oxygen saturation for most individuals is 94-100%, whereas COVID 19 pneumonia patients may have oxygen saturation as low as 50%. Direct confirmatory qRT-PCR test should be performed for symptomatic cases. It will help in differentiating between COVID-19 and other flu cases. Remaining individuals in the community, *i.e.*, presymptomatic and asymptomatic, may further have to undergo a rapid antibody testing. Those who are positive for rapid antibody test, confirmatory qRT-PCR test should be performed for them. Negative cases should be repeated once again for rapid antibody

test after 7days and so. Thus, in order to detect high-risk COVID-19 pneumonia patients, AI-based image processing technology on chest x-ray images can take immense role in identifying those patients in early treatment with oxygen. In addition, improved AI-based image processing of chest computed tomography (CT)/high-resolution computed tomography (HRCT) images can take immense role in identifying COVID-19 patients for early quarantine/isolation/treatment leading to prevention of transmission in near future. Figure 1 depicts the screening and detection steps of COVID-19.

Artificial intelligence (AI) can play an important role in predicting the pattern of worldwide outbreak of COVID-19 and its saturation time^{3,4}. It has been observed in various databases about COVID-19^{1,2,3} that different countries have inconsistent infection and death rate patterns. Thus, it Immediately arises some striking questions:

1. What are the variation of important factors (yet to be explored) responsible for various outbreak patterns in different countries?
2. How are viruses transmitted so fast?
3. What are the possible technology or measures or principles to prevent the spread?
4. Is there any role of social networking data in predicting the epicenters?
5. What will be the possible impact on society and economy due to this pandemic?
6. How can COVID-19 patients be detected rapidly to take quick quarantine/isolation/treatment step managing huge number of affected people worldwide?
7. What are the immediate most probable drugs available in market to treat COVID-19 before the invention of the most appropriate ones?

We are going to find, in this article, suitable answers to aforementioned questions. We will see how AI can help experimental biologist, doctors and pharmacologists for addressing the above questions.

In order to achieve an efficient antiviral treatment, AI-based predictive model may help in exploring possible effective drugs for COVID-19 using available drug databases⁴. In this article, we have predicted some probable drugs, such as, Geneticin, Avermectin B1, and Ancriviroc among others, which have higher binding affinity with proteins coded by SARS-CoV-2 (particularly, spike protein) based on previous works⁵⁻⁷ and modified autoencoder based deep learning methodology⁵. We are going to illustrate more on this topic in the upcoming sections.

Before addressing the aforementioned questions related to current epidemic challenges, we are going to discuss different databases (Section 2) which are

¹<https://www.who.int/emergencies/diseases/novel-coronavirus-2019>

²<https://www.worldometers.info/coronavirus/>

³<https://coronavirus.jhu.edu/map.html>

⁴<https://www.drugbank.ca/>

⁵<https://github.com/zhanglu-cst/Drug-Target-Interaction>

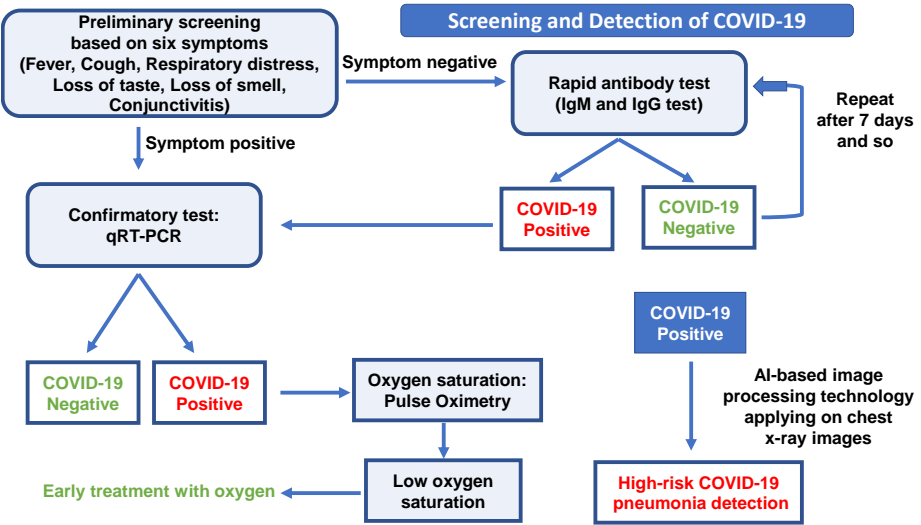


Figure 1. The symptoms of COVID-19 and screening steps for its rapid detection using rapid antibody tests, qRT-PCR, pulse oximetry, and AI based image processing on chest x-ray images. Improved AI-based image processing of chest CT/HRCT images can be used in upcoming days as shown in Figure 3B.

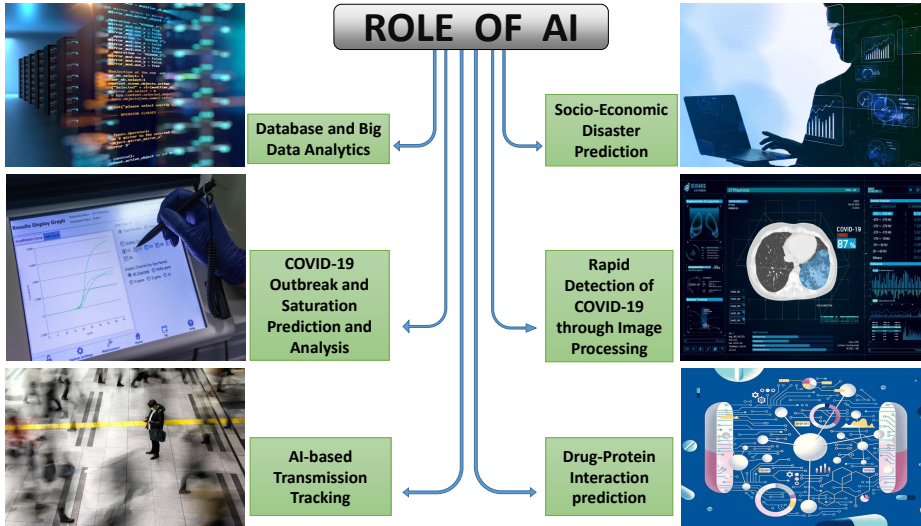


Figure 2. The role of artificial intelligence (AI) in addressing epidemiological challenges in pandemic COVID-19.

essential these challenges in various perspectives. In the following section (Section 3), different rapid detection techniques will be explained elaborately. Next section (Section 4) will deal with different models predicting the outbreak pattern and saturation of the epidemic worldwide. In addition, we have modified SIRD model

in this article, and initial results are provided here (Section 4.1.2). Subsequently, role of social networking in early prediction of epicenters/hotspots as well as pandemic pattern (Section 4.2) with case studies on twitter data (Sections 4.2.2 and 4.2.3) will be elaborated. This section will also include different types of transmission with some influencing factors (Section 4.3). In order to understand the impact of these factors on transmission, here, we will present some statistical analysis on currently available public databases related to COVID-19 (Sections 4.3.2 and 4.3.5). Besides, some AI-based preventive measures, such as, on-line surveys (Section 4.4.1) including our proposal and contact tracing mobile app (Section 4.4.2), will be explored in this section. The succeeding section (Section 5) will present an intricate socio-economic impact and possibilities of future relapses (Section 5.2). A regression based forecast on consumer price index (CPI) and inflation in upcoming days will also be added here (Section 5.1). Next (Section 6), we will deal with current health care management containing treatment as well as preventive measures (Section 6.1), and AI-based models for future drug discovery (Section 6.2). Some of the most probable drugs extracted from a modified autoencoder and feed-forward neural network based model will also be mentioned here with proper validation using previous investigations (Section 6.2.2). Finally, the article will conclude with a discussion and elaboration of future direction (Section 7). In this regard, Figure 2 depicts the role of AI in response to epidemiological challenges in pandemic COVID-19.

2. Databases for epidemiological studies

Recently, Governments of several countries have decided to take immediate action to obtain a solution against such growing pandemic caused by the coronavirus. They have started involving the data science community and shared information related to the disease worldwide. On the other hand, World Health Organization (WHO) and other well known data science communities too have shared various data sets related to COVID-19. Thus, data science community should concentrate on how to explore these publicly available databases to predict some important features of the disease. We have summarized some key characteristics of the publicly available data sets in Supplementary Material to restrict the size of the article. Here we are going to discuss the kinds of predictive analysis possible using these databases.

All such data sets have motivated us to visualize the pattern of the disease with respect to various types of parameters worldwide. Here we can apply the machine learning technique to contemplate how the rate of infection is related to global health security index (GHSI) score which determines how different nations have the risk of pandemic/epidemic attack. In addition, the score tells us the appropriate precautions before the pandemic activities become out of control in a large geographical region. Consequently, we can make cluster of various countries according to their GHSI score as high vulnerability, low vulnerability, and medium vulnerability zones. Such clustering may be highly significant for the Government to reserve sufficient medical equipment to fight against the novel coronavirus.

3. Rapid Detection

Rapid diagnosis is a main part of health care, because it provides details about the health problem of a patient and informs about successive health care decisions. The diagnostic process is a mutual and complex activity that involves clinical analysis and gives information to determine health problem of a patient. In recent decades, modern methods have been developed for the rapid diagnostics of different infections. The main advantages of rapid detection techniques are the possibility of earlier intervention and faster focused action to potential problems, but also improved throughput of analysis. Here we are going to discuss confirmatory detection by qRT-PCR, preliminary screening through rapid antibody test, and finally AI-based image processing techniques using chest x-ray/CT/HRCT images.

3.1. *qRT-PCR*

The most emerging method for the qualitative and quantitative detection of nucleic acid from SARS-CoV-2 in upper and lower respiratory specimens is quantitative real time polymerase chain reaction (qRT-PCR) and is usually measurable during the acute phase of infection. qRT-PCR can sense as little as one virus particle in swabs taken from the mouth or nose.

Sample collected from body parts such as patient's nose or throat, is treated with several chemical solutions that remove proteins and fats, leaving only extracts of RNA in the sample. The RNA extracted is a mixture of a patient's own genetic material and, also coronavirus RNA, if the viral infection is present. The RNA is reverse transcribed to DNA using a specific enzyme. In this reaction mixture small fragments of DNA are added, which are complementary to specific parts of the newly reverse transcribed viral DNA. The mixture is then loaded in a qRT-PCR machine that undergoes temperatures to heat and cool the mixture which helps trigger specific reactions. As new copies of the viral DNA are produced, the marker labels attach to the DNA strands releasing a fluorescent dye that is measured by the software specific to the qRT-PCR machine. The software tracks the amount of fluorescence in the sample, and after reaching a certain level of fluorescence, the presence of virus is confirmed. Although positive results do not completely rule out co-infection with other viruses and bacteria, and therefore, similarly negative results also do not rule out the possibility of SARS-CoV-2 infection. Thus other factors should be considered before taking patient managing decisions. qRT-PCR is followed by Sanger sequencing to further confirm the infection.

Besides, qRT-PCR whole genome sequencing also plays a very important role in detection of COVID-19. The genome analysis will facilitate in understanding the rate of mutation and probable routes of spread of the infection. The development of enzyme-linked immunosorbent assay (ELISA) has also been reported for detection of SARS-CoV but the sensitivity of qRT-PCR is much higher than that of ELISA⁸. In order to tackle huge number of COVID-19 suspected patients worldwide, screening techniques, such as, rapid antibody test, are needed as

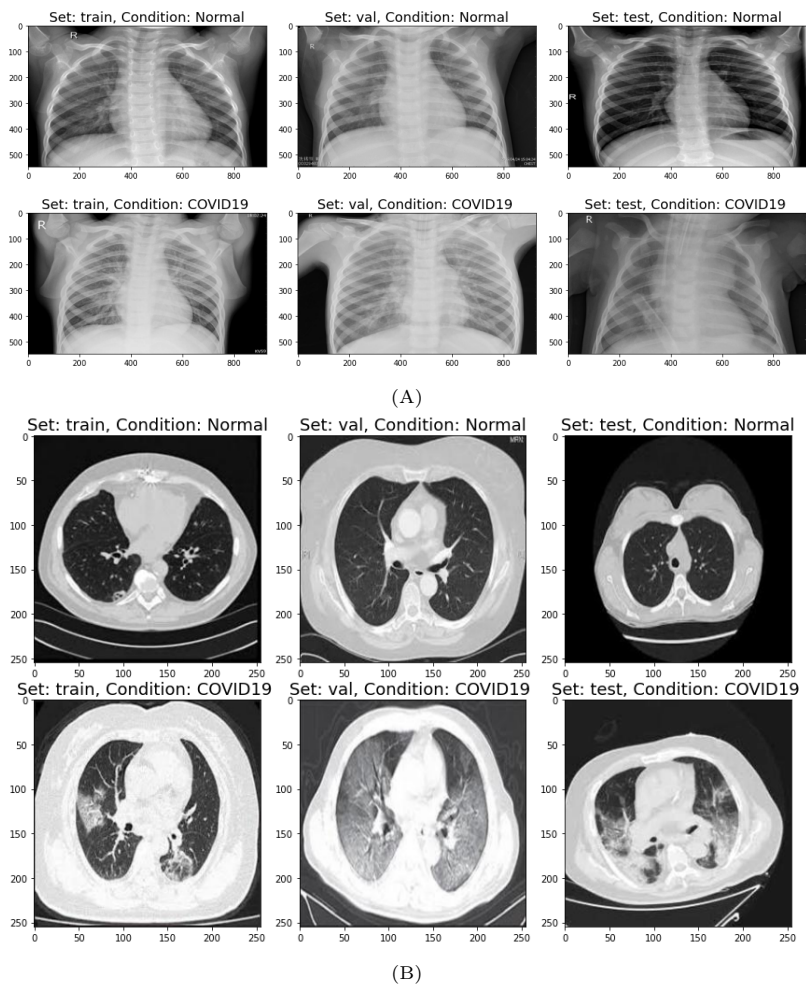


Figure 3. (A) Samples of x-ray images of both normal individuals and COVID-19 patients, used for training, validation and test. The modified image processing method shows test accuracy of 78.57% with precision of 75%, sensitivity of 85.71%, specificity 71.43%, and F1-score of 80 during rapid detection of COVID-19 pneumonia patients with high risk at very early phase. (B) Here the prediction based on CT/HRCT images is depicted. However, due to less number of such images for training, we have not found significant test accuracy. Thus, improved AI-based image processing techniques with sufficient number of chest CT/HRCT images for training need to be developed to get better accuracy for identifying COVID-19 patients more accurately and rapidly.

mentioned earlier to decide immediate quarantine/isolation/treatment measures according to severity.

3.2. Immunodiagnostic test (rapid antibody test)

The immunodiagnostic tests play a crucial role for rapid detection of COVID-19 as mentioned earlier. This antigen detection method detects the presence of viral proteins (antigens) expressed by the COVID-19 virus in a sample collected from the respiratory tract of a person. If the target antigen is present in adequate concentrations within the sample, it will bind to specific antibodies fixed to a paper strip enclosed in a plastic casing and generate a visually detectable signal, approximately within 30 minutes. The detected antigen(s) is expressed only when the virus is actively replicating; thus, such tests can be used to identify acute or early infection. The host antibody detection method detects the presence of antibodies in the blood of people who have been infected with coronavirus. Antibodies are produced over days to weeks after infection with the virus. The strength of antibody response depends on several factors, like severity of disease, age, nutritional status, and certain medications or infections that suppress the immune system.

3.3. AI-based image processing technique

Chest x-ray/CT/HRCT imaging technique can be an useful option to detect suspected COVID-19 pneumonia patients with high risk at early stage. In this regard, efficient image processing techniques based on the concept of machine learning may accurately detect COVID-19 pneumonia confirmed cases.

3.3.1. Some previous studies

A recent study⁹ has uncovered the shape of COVID-19 as bilateral distribution of patchy shadows and ground glass opacity. In addition, in order to extract the significant features from chest CT scan images, deep learning approach¹⁰, such as convolution neural network (CNN), may be employed. CNN has already shown improved performance to recognize the nature of pulmonary nodules¹¹. Subsequently, it has also accurately uncovered the position of polyps from colonoscopies and many more¹²⁻¹⁴. In this pandemic, AI-based image processing techniques^{15,16} has already shown good efficiency to detect COVID-19 using chest CT scan of affected individuals at very early phase of the disease. In comparison with qRT-PCR it has been found¹⁵ that approximately 98% of COVID-19 cases have initially been detected accurately by non contrast chest CT scan, while qRT-PCR has become successful in detecting 71% of the such initial cases. Additionally, it has been shown that 3% of 167 patients had negative qRT-PCR data for the virus despite chest CT findings of viral pneumonia¹⁶. It shows that the use of chest CT can be significant to decrease false negative data¹⁶ during the early phase of COVID-19.

3.3.2. A short study

In order to verify the previous findings, we have reimplemented a CNN-based existing method⁶ (testing accuracy of 71%) to detect mostly chest x-ray images

⁶<https://github.com/JordanMicahBennett/>

(with a very few chest CT/HRCT images) of COVID-19 affected patients. Here the number of training dataset has been enhanced to include chest HRCT, CT, and x-ray images from different view points. In addition, the number of hidden layers has been increased and the weights are updated accordingly. We have trained the CNN-based model⁷ using publicly available databases^{8,9,10}. Here 5412 chest images (mostly x-ray with very few CT/HRCT) for training (75 of normal individuals and 5337 of COVID-19 affected patients) and 42 such images for test (21 normal images and 21 COVID-19 positive images) have been considered. Figure 3A depicts a few samples of training and test chest x-ray images. Due to enhanced training images and hidden layers, it improves the testing accuracy by 7.57% compared to the existing one¹¹. Thus the method shows test accuracy of 78.57% with precision of 75%, sensitivity of 85.71%, specificity 71.43%, and F1-score of 80. Figure 3B depicts a few successful classification of chest CT/HRCT images of normal individuals and COVID-19 patients. However, test accuracy is not significant due to lack of chest CT/HRCT images of COVID-19 patients for training the model. Future improvement in algorithm with more number of chest CT/HRCT images for training leads to more rapid and accurate detection of COVID-19 pneumonia patients with high risk at very early stage.

Similar investigations can be found in other published¹⁷ and unpublished¹⁸ works with better test accuracy. It is clear from our study that on availability of more training samples of CT/HRCT images of all possible respiratory syndromes, more efficient and accurate deep learning based algorithms can be developed for rapid detection of not only high risk COVID-19 pneumonia patients but also other respiratory diseases in upcoming days. In addition, pre-symptomatic CT/HRCT/x-ray images can be used for early detection of COVID-19 patients based on deep learning based techniques leading us a step ahead to fight against the current as well as upcoming pandemic.

4. Outbreak, Saturation, Transmission and Prevention

Past few decades have experienced a lot of technological innovation in various scientific fields, particularly in medical science. The application of natural language processing¹⁹⁻²¹, medical image processing^{22,23}, and deep learning techniques^{24,25} are some examples of such advancement. The influence of artificial intelligence (AI) has added a lot of potential in health care sector to anticipate the diagnosis in a faster way. Thus it must have a potential role to fight against the current global health calamity due to pandemic COVID-19²⁶.

Previous investigations^{27,28} have claimed a close association of novel coronavirus with severe acute respiratory syndrome (SARS)²⁹. However, a recent

⁷<https://github.com/abhisekbakshi/Image-Classification-COVID-19>

⁸<https://www.kaggle.com/praveengovi/coronahack-chest-xraydataset>

⁹<https://www.kaggle.com/parthachakraborty/pneumonia-chest-x-ray>

¹⁰<https://www.kaggle.com/paultimothymooney/chest-xray-pneumonia>

¹¹<https://github.com/JordanMicahBennett/>

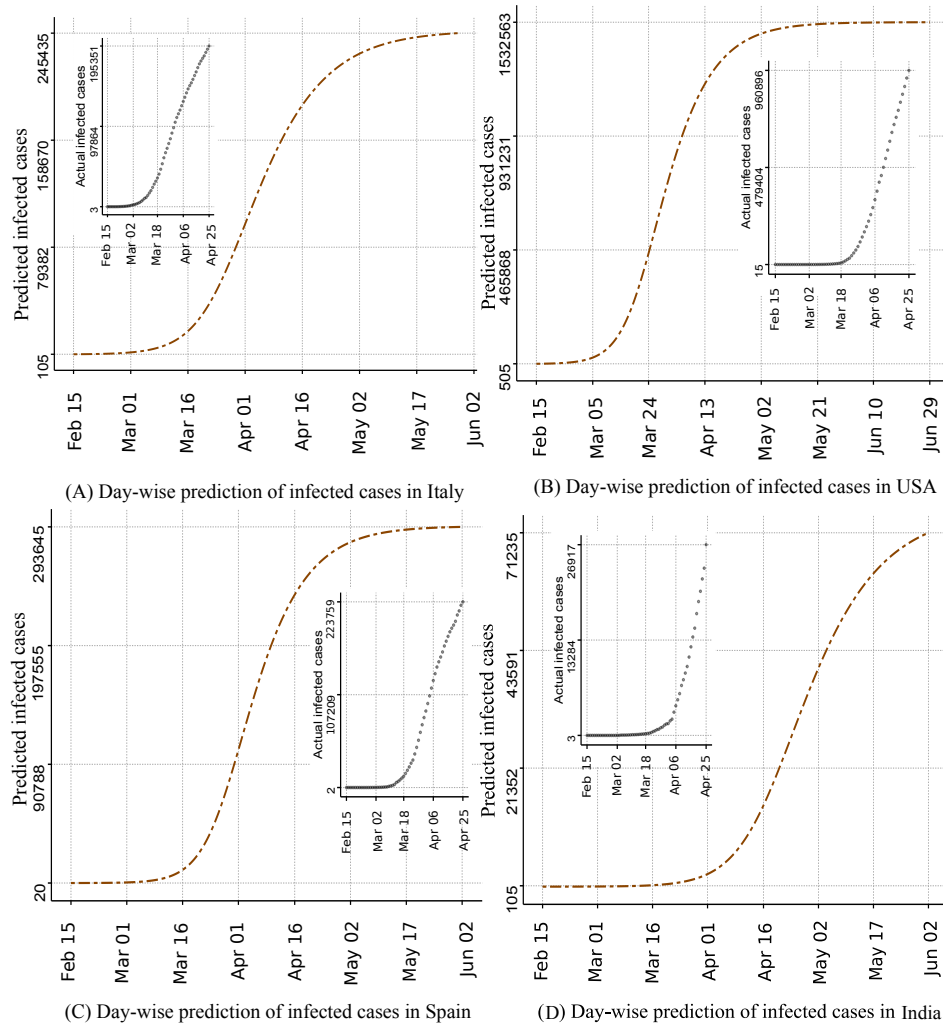


Figure 4. Our modified Susceptible-Infectious-Recovered-Death (SIRD) model predicts (initial result) the total number of COVID-19 infected cases and saturation time for (A) Italy, (B) United States of America (USA), (C) Spain, and (D) India.

study³⁰ has argued that the ultimate spread of COVID-19 may become more influencing over SARS in 2003. Thus, in order to prevent the outbreak of such a disease, it requires a set of appropriate guidelines. However, these strictly imposing such guidelines on the common people through out a large geographical area is a very hard task to accomplish. Here AI can guide us by predicting different aspects of this pandemic based on noise free publicly available databases (as discussed earlier) about COVID-19. Even social networking data have played a crucial role in forecasting a number of important facts in health care sectors^{31–33}.

In the following subsections, we are going to discuss how AI-based prediction on COVID-19 outbreak, saturation, transmission and prevention can help us to take necessary steps against the epidemic.

4.1. Outbreak and saturation

According to the WHO, COVID-19 has become pandemic from the second week of March, 2020. It is clear from worldwide research and reports of WHO that the exponential spread of this disease may continue up to the upcoming winter of this year. In this context, statistics and machine learning based efficient models may be effective to estimate the growth of future affected people as well as its saturation time.

4.1.1. Previous models predicting outbreak pattern of Ebola virus diseases

Here we can look back some previously developed models, *viz.*, a transmission model³⁴ based on human movement data to predict the spatial outbreak of Ebola virus diseases (EVD) in West Africa during 2014-2016. This model has used weekly probable and confirmed case data obtained from WHO. In addition, it has predicted human movements based on three definite mathematical formulations such as gravity model, radiation model and adjacency network considering each district as a vertex. Based on poisson regression, the first two models have tried to predict the total number of individuals moving from one district to another depending on some parameters, such as, population size at origin & destination, and distance between two districts among others. The predicted human movement data have helped in estimating spatial spread of EVD with a certain speed as well as its saturation period. Similar kind of studies^{3,35-37} have been found on predicting spread and saturation of EVD and SARS in the past. All these studies have estimated the best-fit model solution to the reported data using nonlinear least squares fitting. However, it has been claimed that the uncertainty of the models can be reduced with the availability of more data. In short, we can summarize that all such aforesaid models can be highly beneficial for designing a real-time decision making system.

4.1.2. A modified SIRD model predicting the outbreak pattern of current pandemic

Inspired from the previous investigations as well as Susceptible-Infectious-Recovered-Death (SIRD) model³⁸ and recently developed SIRD-X model⁴ considering containment rate and quarantine measures, we have developed a modified SIRD model. Here we are incorporating different factors, such as containment, isolation, quarantine, treatment, vaccination and mobility, and stochasticity to make the model more robust and accurate to predict different outbreak patterns and corresponding saturation throughout various countries. In this article, we present some initial results predicting the outbreak patterns and its saturation of United States of America, Italy, Spain and India. Figure 4 depicts that Italy and Spain may reach at saturation with respect to total infected cases at the beginning of June, 2020. United States may reach at infection saturation point little late, probably in second week of June, 2020. However, the prediction does

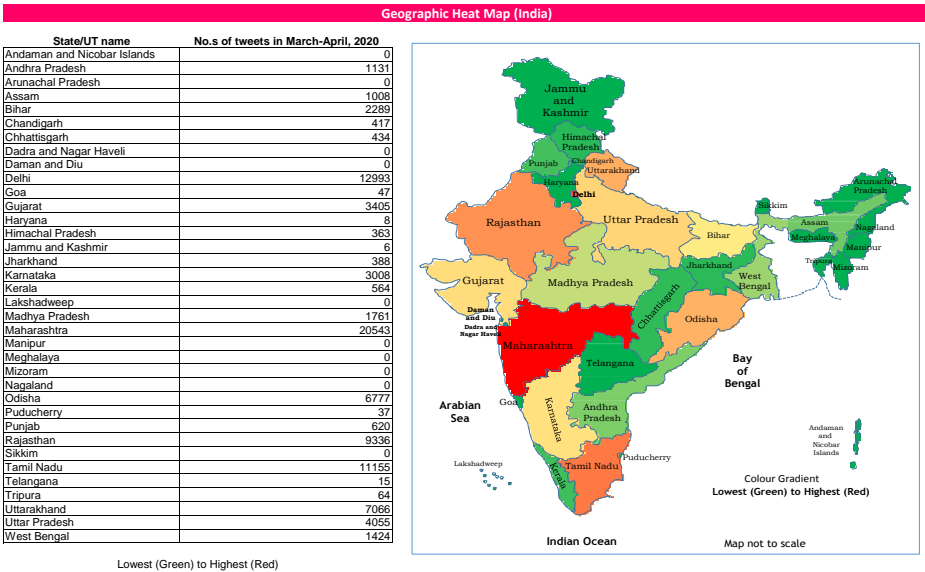


Figure 5. Real time surveillance system to detect COVID-19 epicenters/hotspots in India based on total number of tweets with keywords "coronavirus" and "covid" during March 09-April 15, 2020

not guarantee the infection saturation of India in the first week of June, 2020. In addition, Figure S5 shows that these four countries may experience more death cases at least up to first week of June, 2020. According to our results, although United States, Italy and Spain may reach at saturation in the first week of June 2020 with respect to death cases, it may happen that India may still suffer with more death cases at that time.

4.2. Prediction through social networking data

In the course of pandemic activities during COVID-19, the early prediction of growth of the disease is the major task. A group of scientists have employed a statistical approach³⁹ based on general global optimization algorithm⁴⁰ to estimate the dynamics. Additionally, it has been observed that internet based query through social networking websites has played a crucial role in prediction of various prevalent incidents throughout the world.

4.2.1. Early Prediction of new cases in China based on social networking data

Recently, Cuilian et. al.⁴¹ have observed that the most searched words in various social networks and search engines, such as, Google Trends, Baidu Index and many more, are “coronavirus” and “pneumonia”. Such a high correlation between the searched words and future circumstances has been noticed almost 2 weeks earlier than the newly confirmed cases as well as newly suspected cases in China have been reported. Analyzing the previous investigations, we can realize that the future effect of COVID-19 can be predicted with the help of

an intelligent social networking data mining tool with respect to some specific keywords. It can anticipate the dynamics of the epidemic in the early stage helping the Government in preparing the medical facilities to resist such pandemic activity.

4.2.2. A case study predicting COVID-19 hotspots in India based on twitter data

Here we demonstrate how social networking data can be used to detect the epicenters/hotspots of COVID-19 efficiently and in a faster way without consuming large amount of resources including manpower. Here we have collected twitter data (Kaggle database¹² and our downloaded data) with hashtag of “covid” and “coronavirus” from different Indian regions during March 09-April 15, 2020. Subsequently, we have found out total number of such tweets from different Indian states and Union Territories. Based on that we have generated the geographical heat map of India using an excel template¹³ to generate Figure 5. The figure depicts the current state-wise COVID-19 hotspots/epicenters of India. Our prediction has detected Delhi and Maharashtra as the most critical hotspots followed by Tamil Nadu, Rajasthan and Uttarakhand as epicentres. This result is quite compatible with the report published by Indian Government¹⁴. However, our result for Kerala is not satisfactory. It may be due to the efficient, strict and prompt strategies adopted by Kerala Government, leading to an early flattening of the epidemic curve¹⁵.

4.2.3. A short study to explore the correlation between twitter data and ongoing pandemic pattern

We have collected twitter data (same data source as mentioned above) of the United States (mostly affected and official language is English), United Kingdom (moderately affected and official language is English), and New-Zealand (less affected and official language is English) with the same hashtag as mentioned before during the same period (March 09-April 15, 2020). Figure 6 reflects a clear correlation (correlation coefficient of 0.995) between the total number confirmed COVID-19 cases (up to April 15, 2020) and total number such tweets for each country. It may happen that people have become more anxious and post tweets when the pandemic knocks their door.

Thus our study may establish a fact that using social networking data, such as Facebook and Twitter, we can easily detect the probable hotspots/epicenters of COVID-19 very fast without much help of manpower and consuming resources.

¹²<https://www.kaggle.com/smid80/coronavirus-covid19-tweets>

¹³<https://www.coursehero.com/file/50494168/indzara-Geographic-Heat-Map-India-v4xlsx/>

¹⁴<https://www.jagranjosh.com/current-affairs/coronavirus-hotspot-areas-in-india-what-are-hotspots-know-all-covid-hotspots-1586411869-1>

¹⁵<https://www.indiatoday.in/magazine/cover-story/story/20200427-how-kerala-flattened-the-curve-1668033-2020-04-18>

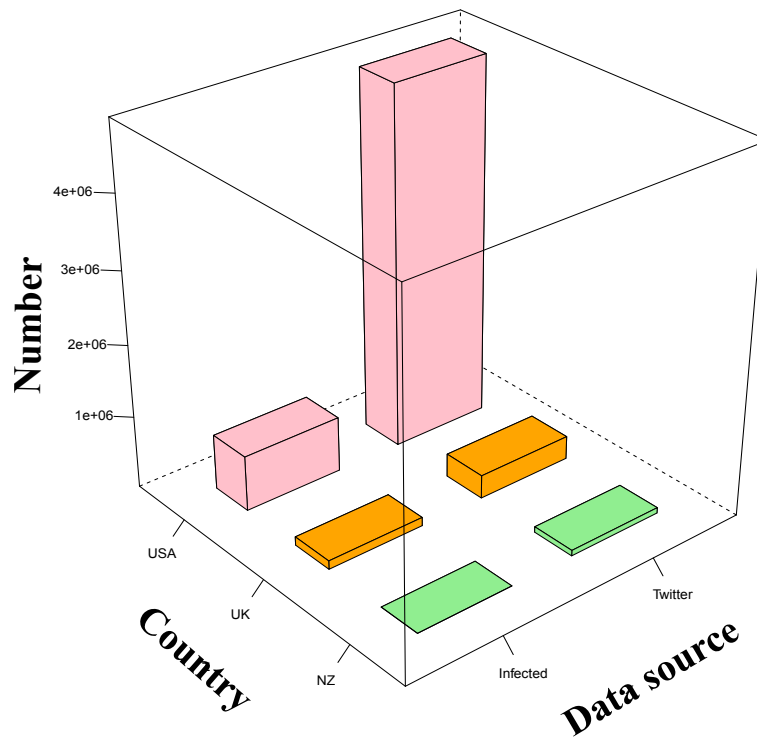


Figure 6. Illustrating a clear correlation (correlation coefficient of 0.995) between total number tweets (of United States of America (USA), United Kingdom (UK) and New-Zealand (NZ)) during March 09- April 15, 2020 and total number of confirmed COVID-19 cases up to April 15, 2020 in three countries under consideration.

4.3. Transmission

One of the major reasons behind such pandemic by the novel coronavirus is that it can spread in various ways. In addition, different factors can influence its transmission. Here AI can help in preventing the transmission using on-line surveys and contact tracing mobile app.

4.3.1. Transmission through droplets

One of the most important ways is respiratory droplets. Here angiotensin converting enzyme 2 (ACE2) and SARS-CoV receptor have been found in lungs and gastrointestinal tract of human body. Therefore, it spreads through respiratory droplets over a relatively close distances. The statistical analysis⁴² on the experimental data shows that SARS-CoV remains infectious in suspension as well as in the temperature below 60°C.

4.3.2. Regression based analysis determining relation between average temperature and transmission

According to our regression based study, Figure 7A depicts the rate of infection of COVID-19 with respect to average temperature during January-March, 2020 throughout eleven countries of the world. Here, we can see that the rate of infection is higher within the range of temperature -10°C - 30°C . This observation may explain one of the probable reasons of high infection rate in Spain, Italy, USA and Germany, and low infection rate in Russia (temperature range in $(-20^{\circ}\text{C} - 0^{\circ}\text{C})$ approximately). This preliminary result requires further studies.

4.3.3. Transmission through different surfaces

The stability of the virus in various surface is also a great enhancer for sustainability of the disease in a large geographical region. Although airborne transmission of the virus has not been proven till date, but in accordance with a report of WHO, the transmission may occur by aerosol-generating medical procedure (AGMP)⁴³. A recent evidence⁴⁴ has shown that SARS-CoV-2 remains infectious in aerosols ($< 5 \mu\text{m}$) and its intensity reduces with respect to time in exponential manner as in the case of SARS-CoV. In order to estimate the decay rate, they have employed a Bayesian regression model elucidating that SARS-CoV-2 is more stable on plastic and stainless steel surfaces than on copper and card-board surfaces. Moreover, it exists up to 4 hours on the copper surface, whereas in the case of plastic and stainless steel surfaces, it survives more than 72 hours. Thus, with the capability to resist different environmental factors, the virus becomes more threatening in terms of transferring between contaminated hosts via the hands and surfaces.

4.3.4. Transmission and health condition

Researchers have observed that infants, elderly people and immunosuppressed patients are under high risk of getting affected by COVID-19⁴². In addition, the study has revealed that COVID-19 can promote many other diseases such as digestive dysfunctions, necrotizing enterocolitis in newborns, diarrhea, and other gastrointestinal symptoms associated with heart problems among others⁴². According to an unpublished work⁴⁵, people with blood group of 'A' are more prone to COVID-19, whereas persons with blood group of 'O' are less susceptible than the others. However, this finding is still to be experimentally verified.

4.3.5. A study on transmission, population density and global health security index (GHSI)

In order to explore the effect of population density on transmission, we have used regression based method to find the relation between population density and rate of infection. Interestingly, we have found that the rate of infection is higher for the countries with less population density (Figure 7B). Our observation clearly contradicts with previous study⁴⁶ which has concluded that contact rates tend to increase with population density.

This contradiction can be addressed in two ways: (i) the early preventive measures taken by the countries with high population density by imposing lock-down, quarantine of suspected people, isolation of affected people, rapid testing, and total shutdown of epicenters among others; (ii) the countries, with low population density, have higher global health security index (GHSI) (between 60 and 100), resulting them to become more confident of their capability to tackle infectious diseases with their above-average medical infrastructure. Here people of the countries with higher GHSI naturally tend to be more optimistic regarding their health security, which results in an underestimation of the danger of a pandemic like COVID-19. Compared to the developing nations, developed countries are relatively inelastic to their needs and may be initially reluctant to compromise on factors involving community mobility, like easy access to public transport and international and domestic flights, and prompt availability of foods and groceries during emergencies. This expectation driven reluctance makes them prone to infection through community spread.

Figure 7C clearly depicts that 65.23% of total infected people throughout the world belong to the countries with higher GHSI between 60 to 100. It may be considered as an evidence behind our hypothesis. In addition, a recent investigation⁴⁷ has shown that restriction on international travel can help in slowing down the transmission of disease. This finding further strengthens our hypothetical claim.

4.3.6. Types of Transmission

According to recent study⁴⁸, transmission can broadly be classified in four categories, such as, ‘symptomatic’ (a direct transference from symptomatically infected individuals to a non infected one), ‘pre-symptomatic’ (direct transmission from an infected individual before he/she experiences noticeable symptoms), ‘asymptomatic’ (a direct transmission from an infected individual who has never experienced any symptoms) and ‘environmental’ transmission (transference through contamination without a typically attributable path or source). This study shows that pre-symptomatic contact has 45% probability to spread COVID-19 (as depicted in Figure 7E, which differs significantly from the outbreak studies for previous SARS-CoV).

In contrary, WHO has firstly categorized transmission as ‘under investigation’, ‘imported cases only’, ‘local transmission’, ‘community transmission’ and ‘interrupted transmission’. After April 09, 2020, WHO again reclassified transmission as ‘no cases’, ‘sporadic cases’, ‘cluster of cases’, and ‘community transmission’ with proper guidelines. However, WHO now depends only on the report from the countries to determine the transmission types in these countries. According to this self-reporting system, as on April 12, 2020, 81 countries have reported their stages as a cluster of cases that includes China (over 83,000 cases), India (over 10,000 cases) and even Maldives (19 cases). As countries are determining their transmission types, we are facing with confusing data (community transmission should conceptually depict the most number of confirmed cases, whereas it shows only 10% of total confirmed COVID-19 cases throughout the world) as depicted in Figure 7D. Countries with higher infection rates, such as Italy, Spain, France

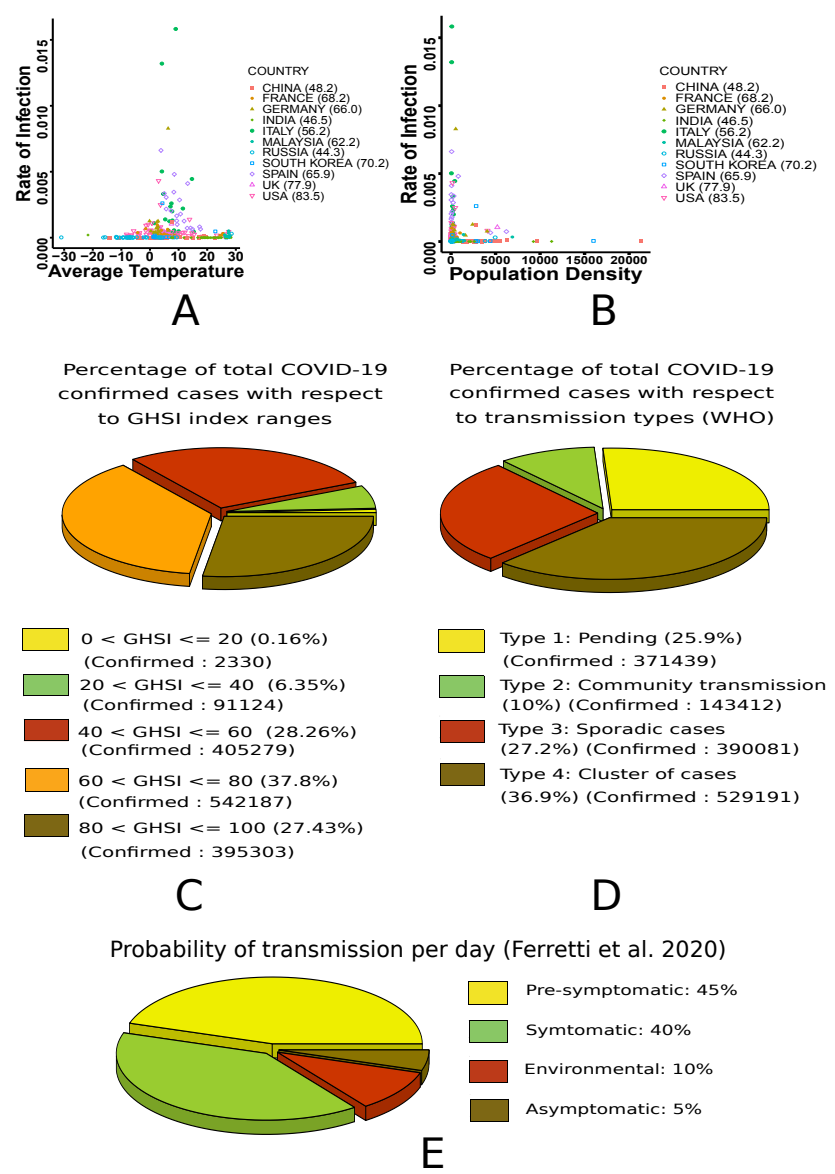


Figure 7. A. Regression based study to find correlation between rate of COVID-19 infection and average temperature, B. Regression based study to find correlation between rate of COVID-19 infection and population density, C. Distribution of total number of infection in the countries with different global health security index (GHSI), D. Different types of transmission along with percentage of total COVID-19 confirmend cases according to WHO after April 09, 2020 E. A recent study⁴⁸ shows probability of transmission per day for different types of transmission.

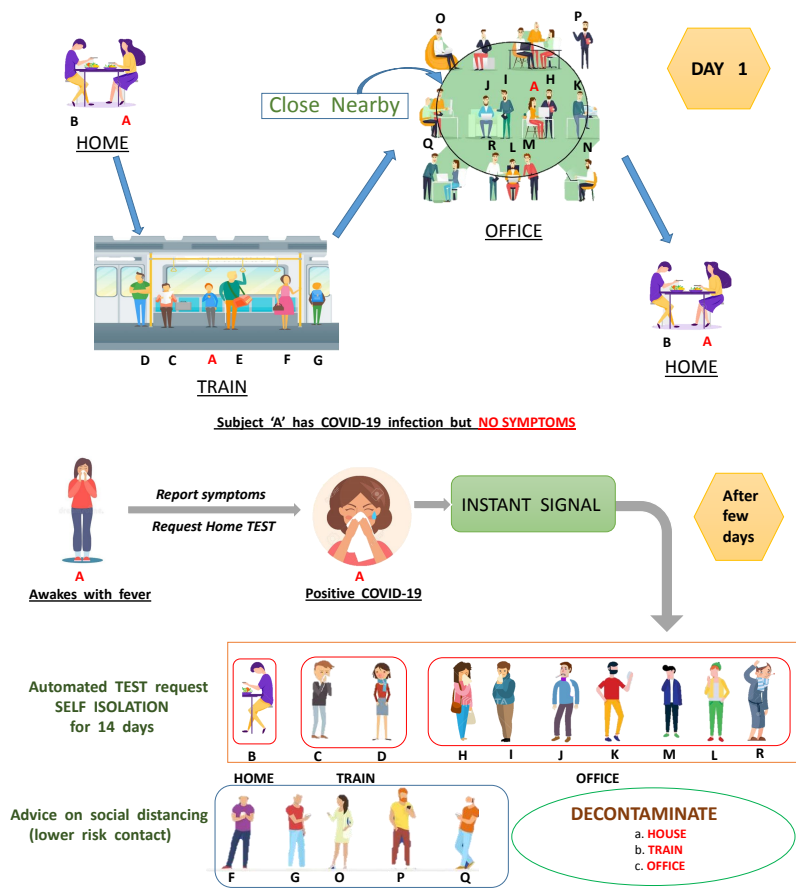


Figure 8. The figure illustrates how the contact tracing mobile app⁴⁸ works to detect COVID-19 suspected people to be isolated/quarantined/hospitalized according to severity. This kind of mobile app continuously tracks the people contacted with a COVID-19 suspected person. Whenever the suspected person will be found as COVID-19 positive patient, the contacted people will receive messages to keep themselves self-quarantine/isolation.

and UK are not among 22 countries with community transmission, whereas Syria with a small number of total infection and death has been reported as community transmission. This inconsistent data is leading to confusion for predicting the future growth of epidemic and transmission category of a country or a region.

4.4. AI based prevention

In order to arrest the pandemic of a viral disease, an in-depth investigation of every individuals in a particular region is highly needed. Unfortunately, due to some unwanted behavior of a set people, the chance of blocking community transmission of the disease may become under threat. In most of the cases it has been revealed that hiding actual information about the health status of the

potential patients may be the foremost cause behind that. In this situation, a set of tactful questionnaires may help any health care professionals to identify the potential patients who may be at a risk of getting infected by the viral disease, like COVID-19.

4.4.1. On-line surveys

In order to get right information about the health condition of an individual, here, we propose a hypothesis to identify such patients. Here we may require a set of questionnaires that does not comprise any question related to specific disease symptom directly. In spite of that, the answers of the indirect questions signify most important information about the health status of the individuals. On the other hand, we assume that the electronic health record (EHR) of various patients is maintained at corresponding local hospitals. In addition, the availability of medicine purchase history of those patients from corresponding local medicine shop as well as from different online delivery companies is taken into account.

Collecting all such information from various sources, we can verify the answers of the questionnaires with the databases to ensure the correctness of the information. If the correctness percentage does not cross the threshold, we can re-evaluate the data by asking similar questionnaires again. In the supplementary material, we have presented a set of sample questionnaires (Table S1) related to a set of symptoms of the disease caused by COVID-19. Subsequently, Figure S6 depicts the order of the questions to be asked to an individual. If an individual is found suspected to be COVID-19 patient based on his/her satisfactory correct health information collected by the proposed approach, the person may undergo with another survey to detect his/her severity in two ways:

- **On-line survey before treatment:** Online survey through particular websites, email and mobile apps may be used to predict possible COVID-19 affected populations more quickly with the help of machine learning techniques. Recently, a group of scientists⁴⁹ has already done a mobile phone based survey to collect address, age, gender, travelling information for the last 14 days, particulars about direct close contact with COVID-19 affected people or not and health condition among other details. Here Figure S7 depicts flowchart of their algorithm to identify possible affected people using aforementioned survey data. This algorithm may help us to identify actual patients suffering from COVID-19 and provide them early treatment/isolation/quarantine preferred to other suspected ones.
- **Electronic health record based survey:** It may be better to design a survey based on EHR using machine learning techniques to detect the severity of patients suffering from COVID-19 as well as risk of being affected by the viral disease. Here EHR helps in finding any kind of association among patients and their disease(s), and treatment trajectory(s). Thus we propose an EHR based survey, which can be designed as follows.

Let us assume, some regular medicines enhance the immunity of human to fight against COVID-19. They have taken the medicine just before the

outbreak or take regularly. We also consider a positive correlation of getting affected by COVID-19 with some specific disease in their medical history. In order to illustrate the scenario, we have considered six categories of sample medicines, such as M1, M2, ..., M6. Subsequently, 10 various types of diseases, represented by D1, D2, ..., D10 are taken into consideration. Thereafter, we have presented a flow chart (Figure S8) that examine previous medicines consumed as well as diseases in medical history. In accordance with several combinations of these two considerations, we have partitioned the population into 14 disjoint groups (represented by G_i , where $i = 1, 2, \dots, 14$). Finally, we have assessed the risk of getting affected by the coronavirus into five different stratus as depicted in Table S2 in Supplementary Material: (i) 'Very High Risk', (ii) 'High Risk', (iii) 'Moderate Risk', (iv) 'Low Risk', and (v) 'No Risk'. However, the data present in the EHR should be error free in order to obtain a satisfactory predictive result using proposed artificial intelligence based algorithm.

4.4.2. Contact tracing mobile app

Contact tracing and case isolation are the two main keys to contain this epidemic. A manual contact tracing is a huge job. However, it can be made easier, faster and more efficient using a contact tracing mobile app. We can contain further transmission by isolating people with risk without mass quarantine.

A recent study shows the ethical requirement for that purpose⁴⁸. According to it, we can employ two kinds of interventions to minimize the impact on larger population: (i) isolation of symptomatic individuals, and (ii) tracing the contacts of symptomatic cases and quarantining them. Successful interventions of the data generated from the app may lead to successful control of the pandemic. Most importantly, this method can replace the manual contact tracing effort along almost a week with instantaneous detection of such tracing by signal transmission. Moreover, it can inform a particular individual about his/her risk of being affected. Depending on that, the person can request for a test through the app immediately without any delay. Efficiency of this method can be calculated as: $(\text{proportion of the population using the app})^2 \times (\text{probability of the app detecting infectious contacts}) \times (\text{fractional reduction in infectiousness resulting from being notified as a contact})$. Figure 8 depicts the conceptual workflow of aforementioned contact tracing mobile app.

Several countries have supported the development of some contact tracing applications, such as Alipay¹⁶ by China, TraceTogether¹⁷ by Singapore, eRouska (eFacemask)¹⁸ of Czech Republic, GH Covid-19 Tracker App¹⁹ of Ghana, and

¹⁶<https://thenextweb.com/china/2020/03/03/chinas-covid-19-app-reportedly-color-codes-people-and-shares-data-with-cops/>

¹⁷<https://en.m.wikipedia.org/wiki/TraceTogether>

¹⁸<https://www.praguemorning.cz/erouska-app-can-trace-your-contacts-without-sacrificing-your-privacy/>

¹⁹<https://ghcovid19.com/>

Aarogya Setu²⁰ by India among others. Thus we may conclude that contact tracing using mobile apps may work as an escape from strict lock-down measures. Keeping the idea of contact tracing, recently, Apple and Google have decided to work together for the development of such artificial intelligence based mobile app²¹.

5. Health care management

Since the outbreak of COVID-19 has been declared as "Global Pandemic", the critical strategies to manage COVID-19 outbreak are divided into multiple parameters of early identification, early diagnosis, and rapid isolation along with the early protection⁵⁰. Unfortunately, there is no targeted therapy exists for SARS-CoV-2 management. Supportive medicines have been prescribed with diffident outcomes.

5.1. Treatment and preventive measures

As mentioned earlier, the significant symptoms found in COVID-19 are fever and non-productive cough. Therefore, the first line of treatment must be to reduce the pyretic symptoms. Different types of antipyretic agents, such as, Paracetamol, Aspirin, and related salicylates, NSAID, are given to the patients along with the antitussive agents like dextromethorphan, guaifenesin⁵¹. Several antiviral medications (*i.e.*, Remdesivir, Ritonavir/Lopinavir) have been used for supportive therapy to manage viral pneumonia without knowing the precise mode of action^{52,53}. Several randomized clinical trials have been initiated to explore the mechanism of action and the benefits of Remdesivir. Till now, no results of randomized controlled trials are available to establish the fact of antiviral therapy. A few antimalarial agents, Hydroxychloroquine and Chloroquine has been used to suppress the disease severity but the proper efficacy of this drug in COVID-19 is controversial⁵⁴.

The administration of supplementary oxygen can manage severe respiratory distress at 5 L/min to patients, and the oxygen saturation is equilibrated to $\geq 92-95\%$ in pregnant patients and $\geq 90\%$ in all other patients⁵¹. Sometimes, patients with septic shock and acute kidney injury have been managed with sepsis protocol and renal replacement therapy (RRT) respectively⁵⁵. Alternatively, the use of convalescent plasma and IgG from fully recovered patients has been started as salvage therapy in critical cases, but there is no strong evidence for this practice⁵⁶.

Despite rapidly accumulating knowledge, public health measures are fundamental for management of the spread of COVID-19 in majority of the cases. Hence, the entire goal has been laid on the rationale of "social distancing", "break the chain", and "flattening of the curve" concept to reduce the rapid increase of new cases⁵⁷.

²⁰<https://www.mygov.in/aarogya-setu-app/>

²¹<https://www.economist.com/science-and-technology/2020/04/16/app-based-contact-tracing-may-help-countries-get-out-of-lockdown>

5.2. AI-based prediction on possible effective drug in market

It is clear from previous subsection that exploring appropriate drug in market for COVID-19 treatment has become inevitable need of mankind nowadays. In this regard, deep neural networks has shown satisfactory level of accuracy for prediction of various bioactivities as well as molecular properties for drug design.

5.2.1. Previous AI-based models on drug discovery

A group of scientists have firstly applied Bayesian machine learning models to uncover the active compounds against Ebola virus (EBOV)⁵⁸. The *in silico* technique is able to detect three *in vitro* active molecules such as tilorone, pyronaridine, and quinacrine. More recently, researchers have developed a novel machine learning technique to predict the possible point mutations that appear on alignments of primary RNA sequence structure⁵⁹. In addition, they are successful in anticipating the genotype of each nucleotide in the RNA sequence. They have employed an algorithm based on rough set to extract the point mutation patterns with satisfactory level of accuracy. Subsequently, Ekins. et. al⁶⁰ have studied the usefulness of machine learning techniques to realize the treatments for rare diseases. The authors illustrated the methodology with three major iterative steps: (i) associating the targets with rare diseases, (ii) designing a model for such targets related to those diseases, and (iii) applying a machine learning technique that may discover other molecules for future test and validation.

During recent pandemic, an unpublished pre-trained deep learning based drug-interaction model, called Molecule-Transformer-Drug-Target-Interaction⁶¹, has checked whether the available drugs may act upon the viral proteins generated during COVID-19. It has been found that Atazanavir, an antiretroviral medication known to manage HIV, is the best chemical compound with inhibitory potency with efficacy K_d of 94.94 nM against COVID-19 3C, like proteinase, followed by application of efavirenz(199.17nM), rotonavir(204.05nM) and dolutegravir(339.91nM). In addition, atazanavir may also bind with the replication complex components of COVID-19. However, there is no real evidence to support this prediction.

There is another unpublished approach⁶² based on machine learning, trying to predict the possible inhibitory synthetic antibodies for COVID-19. Here 1933 virus antibody sequence associated with clinical patient neutralization response has been collected. This model has predicted 8 stable antibodies, helping possibly in inhibiting the novel corona virus. Stability of the antibodies inhibiting COVID-19 has been verified using combination of molecule dynamic simulations, bioinformatics and structural biology tools. However, this prediction is under inspection to verify.

5.2.2. An autoencoder and feed-forward network based modified method

The genome sequence analysis of SARS-CoV-2 has revealed a significant identity homology with β -coronavirus subtype, which is implicated as the causative factor of severe respiratory distress syndrome. The β subtype is originated from

bat, which has been the leading player behind the global outbreak of SARS in 2003. The invention of new antiviral agents against SARS-CoV has been started during the time of the epidemic. Unfortunately, no such antiviral formulation has successfully been reported due to the complex disease pathophysiology and host-pathogen interaction. However, information obtained from the broad area of research findings and the successive endeavours might be useful to identify the potent therapeutics.

Researchers and data analysts everywhere throughout the globe are perpetually working to explore the infection modalities alongside conceivable treatment regimens by finding dynamic remedial agents. Severe complexity in the drug design and development process, as well as the elongated regulatory protocol of clinical trial, sometimes decelerates the new drug discovery to stop the pandemic. Drug repurposing can be beneficial to combat the outbreak when no such exclusively standardized therapeutics available in the market. The objective of repurposing drugs is to find ways to employ the existing approved drug molecules to establish an innovative path in epidemic warfare.

Nowadays, a remarkable advancement in the computational power coupled with artificially intelligent methodology, has been adopted to figure out the putative drug molecules as mentioned in some of the previous investigations. Based on the machine learning based prediction, a known antiviral, broad-spectrum antiparasitic, antibiotic, conventional protease inhibitor can be identified⁶³, which may be useful for the successful therapy of COVID-19. The predictive model of AI and its structured algorithm can accurately envisage the drug-target interactions underlying the complex information regarding the chemical bond formation.

In the study, several known drug targets and the respective inhibitor have been used to trained the machine learning system. On the other hand, the Food and Drug Administration (FDA) approved drugs, as well as conventional drugs, have been taken from the Drug Bank²² and Pubchem database²³ as a test model to predict a new drug. The first approach has been taken to calculate the inhibitory probability of drug molecule on the spike protein of SARS-CoV-2. The interaction of SARS-CoV-2 spike protein with the ACE-2 receptor is the initial point to invade the type-II alveolar cells for the initiation of viral replication followed by infection. Recently, a report has demonstrated an enhanced cell fusion capability by SARS-CoV-2, which is much higher than SARS-CoV. Thus, blocking in either ACE-2 receptor or spike protein may mitigate the disease progression. A series of lipopeptides, EK1C4, may inhibit the cell fusion function of the spike protein HR1 domain, suggesting the possibility of new drug development in preventing the infection.

In order to anticipate the affinity of 33 COVID-19 protein sequences as the target of 3632 drugs (extracted from Drugbank²⁴), here, we have modified a

²²<https://www.drugbank.ca/>

²³<https://pubchem.ncbi.nlm.nih.gov/>

²⁴<https://www.drugbank.ca/>

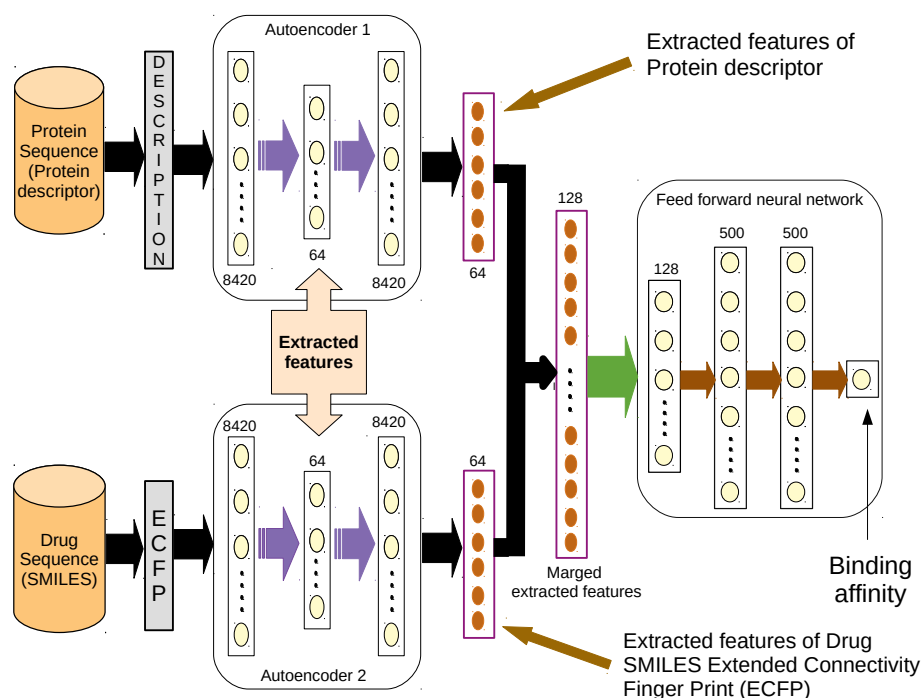


Figure 9. This figure illustrates the conceptual framework of the deep learning technique to predict the binding affinity of various readily available drugs with proteins, associated with corona virus. The framework employs two autoencoders to extract the features from the drugs and proteins. Thereafter, the extracted features have been concatenated and fed through an artificial neural network to assess the binding affinity.

deep learning-based AI model²⁵. Such a model usually requires comprehensive learning on various drug-target interactions. Thus, we have exploited 34,515 protein-drug combinations to train a feed-forward network. Here, we have represented the structural and physicochemical features of the proteins with the help of chemical features protein sequence composition (PSC) descriptor⁶⁴ (8420 features). On the other side, the chemical structure of the drugs has been characterized through extended connectivity fingerprint (ECFP)⁶⁵ based or Morgan algorithm⁶⁶ (2048 features). In order to reduce the complexity of the feed-forward network, we have extracted the high-level features (64 features) of proteins and drugs separately using two autoencoders. In consequence with output of the autoencoder, the high-level features are fed to the feed-forward network. As a result, the model has successfully assessed the probability of the proteins associated with COVID-19 as the target of 3632 unknown candidate drugs. Figure 9 depicts the outline of the algorithm for predicting probable

²⁵<https://github.com/zhangu-cst/Drug-Target-Interaction>

drugs to treat COVID-19.

From the results generated by the aforesaid model, we have selected a few drugs with the highest probability values. All such selected drugs possess significant antiviral properties. Here, the deep learning based program²⁶ has suggested some drugs that may inhibit the spike protein. In a previous report, Geneticin, an aminoglycosidic antibiotic, has been found to inhibit DENV-2 viral replication, and translation. Interestingly, the predictive algorithm reveals that this drug may inhibit the SARS-CoV-2 spike protein fusion with the host cell. Doramectin, an FDA approved veterinary drug for the treatment of parasitic disease of livestock, can be useful for COVID-19 treatment as it may inhibit the spike protein fusion. Doramectin is a derivative of Ivermectin.

A semisynthetic derivative of Avarmectin family, Dehydroavermectin B1, has inhibited NS3 helicase activity of several flaviviruses in an *in vitro* system. Previously, Ivermectin has been proved to be a selective inhibitor of the replication of the Yellow Fever Virus (YFV). In our study, the predictive model has revealed a possible inhibitory role of Ivermectin in spike protein-cell fusion machinery. Here, we have also targeted the other repurposed drugs towards the interaction with the other protein targets of SARS-CoV-2 for useful treatment of COVID-19, which can speed up the clinical trial. The set of selected drugs, along with their target proteins, has been presented in Table 1.

Table 1. List of some important target proteins along with predicted drugs available in market with significant probability of affinity.

Interaction type	Target protein	Name of drug	Affinity probability (in %)
Viral protein-drug interaction	Spike Protein	Geneticin	100
	Spike Protein	Doramectin	100
	Spike Protein	Avermectin B1	99.99
	Spike Protein	Dolutegravir Sodium	99.99
	Spike Protein	Doxycycline Hydrochloride	99.80
	Nucleocapsid Phosphoprotein	Tempostatin	100
	Nucleocapsid Phosphoprotein	Radicicol	100
	ORF10	Artesunate	100
	ORF11	Laninamivir Octanoate	100
Host protein-drug interaction	ACE-2	Brincidofovir	100
	DPP4	Ancriviroc	100
	Toll Like Receptor 4	Chloroquanil	100
	Nuclear Factor κ B	Cinchonine	100

²⁶<https://github.com/abhisekbakshi/Drug-target-prediction-COVID-19>

6. Other Issues: Socio-economic Impact and Plausibility of Future Relapses

COVID-19 has led to different social and economic challenges to the world to be dealt with. Irrespective of racial, religious and ideological differences, the entire world is now fighting unitedly against these challenges. We have discussed different types of socio-economic challenges due to pandemic COVID-19 as well as a small case study of the epidemic impact on Indian service sector in the Supplementary Material to restrict the size of the article. In addition, we are going to forecast inflation of United States of America, China and India up to December, 2020 based on regression analysis. For clarity, we have included some key terminologies in Supplementary Material. Thereafter, we will discuss the probability of future relapses having massive impact on global socio-economic sectors.

6.1. Predictive analysis on socio-economic perspectives

In the wake of COVID-19 outbreak, countries across the globe have imposed nationwide lock-down, leading to standstill economy. As the demand of non-essential goods and services is slumping down, the supply chain has suffered heavily. It has been observed that decrease in inflation and enhancement in unemployment indicate the upcoming major recession. In order to get an idea about the inflation rate, here, we have considered the Consumer Price Index (CPI) for three large economies, such as, India, China and the United States. CPI measures the changes in price level for a basket of goods and services. With the help of monthly CPI, the inflation rate can easily be calculated.

Our regression based analysis (Figure 10) depicts a decline in forecasted CPI values for India. CPI of March 2020 (2.16) sharply decrease to 1.48. It may happen due to the decreased demand from consumers with slower growth in the manufacturing and service sectors. However, there is a silver lining. Economists have expected retail inflation to ease more in the upcoming months from 6.58%. This will help RBI in implementing desperately required rate cut²⁷. Similar to India, China also reveals falling in CPI. However, a rise in CPI in China to about 1.96 during the period of August to October 2020 with a peak in September 2020 may be a sign of health. Here, as a major exporter of manufacturing goods, China may be able to revive some of their losses till as indicated by our prediction. On the other hand, USA shows drop in forecasted CPI to become from 1.645 (March 2020) to 1.628 in December 2020.

Based on the forecasting, it can be summarized that the aforementioned three countries will observe drops in CPI resulting in fall in inflation rates. As mentioned earlier, it may happen due to the less demand during pandemic. In addition, people may tend to save more beyond their necessities and become

²⁷<https://economictimes.indiatimes.com/markets/stocks/news/covid-count-inflation-data-stimulus-hopes-among-key-factors-that-may-drive-market-this-week/articleshow/75103852.cms>

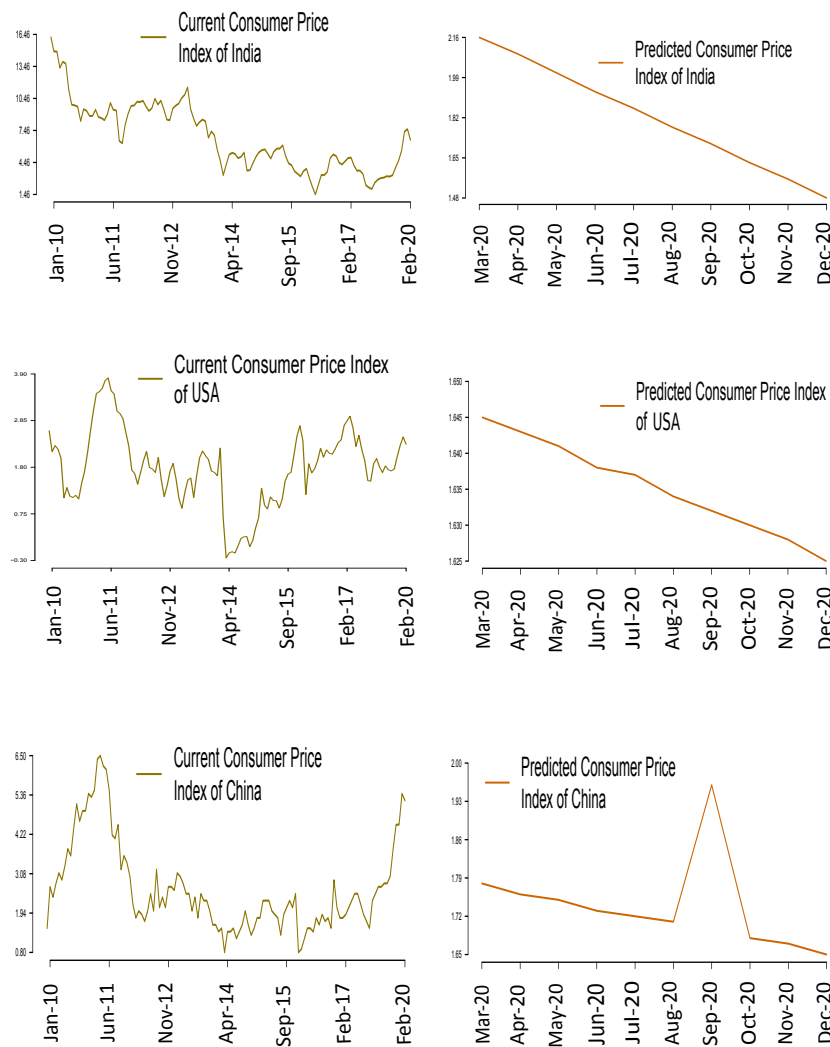


Figure 10. Regression based forecasting the consumer price index (CPI) of India, United States and China up to December 2020 using last ten years monthly CPI data.

reluctant to luxurious goods. The fall of global oil price and Russia-Saudi Arabia oil price war may also have an adverse effect. In evidence of the circumstances, United States has experienced drop in prices of oil by 34%, crude oil by 26%, and Brent oil by 24%. Global institutions, such as, International Monetary Fund (IMF) and World Bank, have also predicted a huge recession hitting the global economy. Even worldwide labour statistics indicates an uncontrolled level of unemployment. It will be a bitter impact on unorganized sector. Moreover,

according to the forecast of Bank of America²⁸, United states will experience a major recession, resulting in more than 15% unemployment in upcoming days.

6.2. Possibility of future relapses

Due to the higher human to human transmission, COVID-19 is now uncontrollable, and in recent times, this disease is a challenge to the healthcare of most developed countries. This situation will become more complex if relapse of this epidemics happens again²⁹. A few recovered patients have also showed COVID-19 positive symptoms. There are two following arguments given by the scientific community.

1. **Short memory of immunity:** Immunity against COVID-19 may be short. After few days or months, body forgets the immunity against the virus.
2. **Disease causing from other strains of the same virus:** If any patient has immunity for a particular strain of virus, he/she would be susceptible to other strain of the same virus.

Within a few months, a lot of information about this SARS-CoV-2 have been gathered and more useful information will be collected in near future.

In addition to aforementioned facts, the biggest question is waiting ahead to the world leaders, “When will a country reopen after lock-down considering the balance between the economy of the nation and public health?” In current situation, with sufficient amount of personal protective equipment (PPE) and ventilation, the initial blow of this virus can be overcome but the consequences of the post-pandemic is unpredictable and would be long lasting and devastating. Viral behavior, environmental transmission and immunity are the major parameters out of the many unknown ones involved in the dynamics of SARS-CoV-2, and are needed to understand the consequences and recurrence of this pandemic again in future.

Kissler et al.⁶⁷ have designed a model from the transmission pattern of human coronavirus (HCoV) OC43 and HKu1 strains from the past data, and then predict the outcomes of COVID-19 post-pandemic period. Still due to the absence of prominent answer to this pandemic, post-pandemic consequences are depending on several ifs and buts. Definitely, the unusual weather transition during season change, short immunity memory from this SARS-CoV-2 and any cross immunity gained from the other SARS and MERS will be determining factors for the relapse of COVID-19. If these parameters will not change in the post-pandemic period, their model has predicted that it will reappear in every winter as a huge wave to human health care up to at least 2025. Nevertheless, the discovery of the vaccine within that time will also be a great impact on the recurrence of this disease.

²⁸<https://www.bbc.com/news/business-52137727>

²⁹<https://www.independent.co.uk/life-style/health-and-families/coronavirus-immunity-reinfection-get-covid-19-twice-sick-spread-relapse-a9400691.html>

In this situation, the only remedy is the prolonged social distancing. It also imports several effects on the economy, and educational and social interactions. Thus only expectation would be like that over the time, more data on this virus with improved model will give more clearer picture of our future socio-economic scenario and will spur more innovative ideas to cope with it.

7. Discussion and Future Direction

In the present study, we have tried to find some fruitful ways to contain current pandemic from many aspects with the help of artificial intelligence. First of all, We have discussed elaborately about different databases, helping us in analyzing current scenario in various perspectives. In demand of rapid testing, a CNN based chest image (mostly x-ray with very few CT/HRCT) processing technique have detected COVID-19 pneumonia with 78.57% accuracy. In addition, improved AI-based image processing techniques for chest CT/HRCT images can be developed in near future to detect high risky COVID-19 pneumonia more accurately and rapidly. Thus, it may be a good support of qRT-PCR and antigen detection method. On the other hand, our primary concern has dealt with how to address different patterns of confirmed infections and deaths in different countries. Our observation has found that United States, Italy, Spain and India may suffer from the disease at least up to first week of June 2020. However, in this regard, more robust and accurate mathematical models are needed to capture the variation in infection and death throughout the world. Our twitter data based short analysis reveals that social networking data can give useful clue about the outbreak pattern, helping in finding the probable hotspots/epicenters of COVID-19 throughout the world without involving too much manpower and other resources. Here efficient machine learning algorithms for sentiment analysis based on social networking data may be developed in near future.

Moreover, we have explored different factors and medium of the infection transmission. Our statistical analysis of infection rate with respect to average temperature shows an interesting result depicting maximum infection rate in interval of temperature $[-10^{\circ}\text{C}$ to $30^{\circ}\text{C}]$. However, this prediction is not sufficient to draw any conclusion but definitely can serve as a clue of further analysis. In addition, we have not found proper validation of a previous finding claiming that people with blood group 'A' is more prone to be affected by COVID-19. Evidence of higher infection rate in the countries with higher GHSI and lower population density concludes that mobility may be a major issue for transmission of COVID-19. This observation needs more validation with appropriate mathematical model in upcoming days. We have discussed higher transmission probability through pre-symptomatic person. However, transmission classification by WHO creates a lot of confusion. Different artificial intelligence based preventive measures, such as, contact tracing mobile app and on-line surveys, have been figured out to stop the transmission of COVID-19 without vigorous lock-down and mass quarantine.

During treatment, medical practitioners have found common symptoms in COVID-19 affected patients including fever and non-productive cough. Due to

unavailability of any deterministic way to arrest the disease, the doctors depend on a set of supportive medicines for treatment. Although some random clinical trials have been performed to uncover the effect of various drugs, its results have not ensured a set of particular drugs against the virus. Moreover, a considerable amount of time needs to be invested for each trial. In this consequence, artificial intelligence may help to anticipate the effect of various drugs in a faster way.

We have investigated a deep learning based framework employing two autoencoders followed by a feed-forward artificial neural network. Here the autoencoders have extracted the highly significant features from the molecular fingerprint of the drugs and proteins, whereas the artificial neural network has predicted the binding affinity between readily available drugs and proteins. Consequently, we have found a set of drugs which may have some inhibitory effects on the spike proteins associated with the coronavirus, such as, Geneticin, Doramectin and Avermectin B1 among others. Several earlier investigations support our claim in this regard. However, further investigations through docking and *in vivo/in vitro* experiments are needed to confirm our findings. Thus, in order to speed up the drug design process, more efficient deep learning based techniques are needed to develop for predicting not only the drug-protein interactions but also the structures of proteins and associated drugs.

Interestingly, if approximately 50-70% of the population become immune against a disease epidemic, the epidemic itself ceases. For example, a COVID 19 patient can infect approximately 4 people, but if the latter becomes immune for the disease then the former will be incapable of infecting them. Thus the virus remains in the body of the COVID 19 patient and dies maximum within 4 weeks. In this way an epidemic can be controlled. The concept of vaccine is to increase the herd immunity⁶⁸. Various epidemics, such as, polio and measles, have been eradicated in this way. It would be interesting to see whether AI can help in predicting the people with low clinical risk and also immune individuals, leading to building up a rapid and high herd immunity in near future.

Any infection may lead to formation of two types of antibody in the body *i.e.*, IgM and IgG⁵⁶. Presence of IgM in the body of the host means that it still contains acute infection.. Presence of both IgM and IgG in the body means that the host has started acquiring immunity against the disease but the infection is still persisting as IgM is still present. Absence of IgM and presence of only IgG means that the host has probably become immune to the disease and therefore further spread of the disease is not possible. As it takes a minimum of one week for the antibodies to be produced, rapid antibody testing is preferably done in the 7th day, then 14th day and so on, until IgM becomes negative and IgG becomes positive. Theoretically an immune person can neither get infected and nor can spread the disease. However, as COVID 19 is a new disease and apparently many individuals are getting infected second time, it cannot be surely declared that one is completely immune after being infected for the first time. Thus it would be very useful if AI can help in detecting the individuals who are completely immune to COVID 19.

During testing, once qRT-PCR test proves a person COVID 19 negative, we should wait for a month to watch whether that person is getting re-infected or

not. If not then it is expected that the plasma of this person contains lots of IgG. This plasma can be collected and injected in critically ill patients to see whether condition of the patient is improving or not. A few case reports say that such condition is improved on applying the above method⁶⁹, whereas many cases show that there is no significant improvement. Therefore, it would be helpful if AI can facilitate identifying the individuals who are immune to COVID 19. It will help in deciding whether their plasma can be collected for the therapy for saving coronavirus patients. In this regard, social networking as well as EHR data related to COVID-19 cases may help in developing such AI-based model in upcoming days.

During current pandemic, the question about extending the lock down and underlying effect of the circumstances from various perspective are still unsettled. In the course of lock down, supply of the essential items is a major challenge. Moreover, the economic status of poor people, particularly in developing and under developed countries, would be foremost challenge in next few months. In this regard, present study has discussed various upcoming economic hazards in terms of consumer price index (CPI) and inflation rate. In addition, we have found that world may feel such epidemic situation in every winter up to at least 2025. Such analysis and predictions are of great interest in terms of future precautions during current and upcoming public health emergencies.

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Author Contributions Statement

AD, NPB, AB¹, RKD, CS, KM, KP, SM³ and SM¹ conceptualized the content of the article. SM¹, ST, PC, RK, KD, and AD performed the prediction based on modified SIRD model under development. PD, SM², AD, AB¹, KD, SM¹, ST, and PC performed the prediction based on Twitter data. PC, ST, SM¹, AD, SG, PR, AS², and AB² performed the prediction on transmission. KD performed the experiment on rapid detection using CT/HRCT/X-ray images. AB¹, AD, CS, KM, KP, and SB performed the drug affinity prediction. AS¹, SG and AD performed the CPI prediction. AD, KM, KP, CS, AB¹, SB, SM¹, ST, PC, AS¹, AS², RK, KD, PD, SM², SG, PR and AB² wrote the first draft of the article. AB¹, PR, PC, ST, KD and AD made the figures. RKD, NPB and SM³ read the article and gave fruitful suggestions to edit the manuscript.

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Conflict of Interest

There is no conflict of interest.

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