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Analysis and visualization of the pandemics using Artificial Intelligence

Shagun Srivastava¹, P P R Prithivi¹, K Srija¹, P. Vaishnavi², H S S Savitha³, Alka Grover¹, Mohit Saxena⁴ and Shivani Chandra¹ and Ankur Saxena^{1*}

¹Amity Institute of Biotechnology, Amity University Uttar Pradesh, Noida 201313, India

²Dr. B. R. Ambedkar Centre for Biomedical Research, University of Delhi, Delhi, 110007, India

³Mallareddy Institute of Medicine Sciences, Hyderabad, 500055, India

⁴Sup'Biotech, Paris 94800, France

Email: shagun1844@gmail.com

Abstract. Human race has faced many epidemics and pandemics in past. The trajectory reveals that there is a pandemic almost every century. Our generation has witnessed the outbreak of coronavirus disease (COVID-19) pandemic, which turned out to be largest pandemic ever. Viruses have affected global population in the past century can answer the questions of the post Corona trauma. It has been noticed that most of the epidemics and pandemics are inflicted by the influenza viruses. Scientists have elucidated the structures of the viruses that have infected earlier. The homology between them and COVID-19 can be studied in order to fight the virus. In this paper, journey of novel corona virus has been discussed from a simple flu to become a pandemic within a short span of time. All the factors including the major countries responsible for spreading the pandemic owing to their volume, speed of human travel and socio-economic reasons seems to be the reason according to the review. We also compared the structures of the epidemic and pandemic causing viruses. Some of the COVID-19 studies mentioned which used machine learning models, and then by the use of machine learning we analyzed characteristics of three diseases (H1N1, COVID-19, and SARS) to obtain the plots of the autocorrelation against the lag of the number of confirmed cases, recovered cases, and deaths of /caused by COVID-19.

1. Introduction

The 21st century has registered 5 epidemics out of which 3 were caused by Coronaviruses. Coronavirus is a family of viruses which generally cause respiratory diseases or infect the upper respiratory tract [1]. Severe Acute Respiratory syndrome coronavirus (SARS-CoV) in 2003, Middle East Respiratory



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syndrome coronavirus (MERS- CoV) since 2012 and the largest pandemic outbreak SARS CoV2 which causes COVID-19 pandemic are all caused by viruses from Coronavirus family. Coronavirus diseases are caused by infection of virus in the respiratory tract. Like SARS CoV-2, SARS-CoV was epic-entered in China and infected approximately 8000 people worldwide causing about 744 deaths [2][28]. On the other hand, MERS is suspected to have originated from Saudi Arabia, where its first case was reported in 2012. Since then it has infected about 2494 people in 27 different countries causing 858 deaths globally. The rate of infection for SARS CoV and MERS was relatively very low as compared to COVID-19. COVID-19 has so as on June 8, 2020 far infected 218 countries, with approximately 6.42 million people already infected, causing 3,83,000 deaths depicting how dangerous this new coronavirus is [3][19]. It has a very high reproductive rate and in extreme cases, it is reported to pass on from patient to healthy individual without any symptoms after infection, hence becoming more virulent and fatal.

Combating pandemics and epidemics has been an endless journey for the mankind. Genetic selection made viruses vulnerable to evolution. Humankind had witnessed epidemics like Bubonic plague, Ebola, Cholera, Encephalitis and many more (Organization; Patterson & Pyle, 1991; Who, 2011; Ying [4][20]. However, they have been successfully eliminated after development of vaccines, and necessary preventive measures. Since Black Death and Spanish flu, health care has advanced to achieve greater levels and in contrary, viruses and bacteria have evolved too. Hence, when all the pandemics and epidemics from last century were compared by taking into account the preventive measures, treatments, socio-economic factors etc., a key line can be drawn on efficient handling of coronavirus pandemic. Not only the research principles but also statistics and socio-economic factors of all the former tracks were considered to unfold the fate of the novel viruses causing an epidemic or pandemic.

1.1 Epidemics and Pandemics in past After summarizing epidemics and pandemics, authors depict that influenza viruses are the one which resulted in major wipeouts of population in compared to other viruses and bacteria. The seasonal flu had also been a pandemic taking nearly one million lives. Since the outbreak of Spanish flu, which caused the largest epidemic in the last century, to the COVID-19, all of them have been the influenza viruses that were responsible for annihilation across the world. Before the Coronavirus Pandemic, there have been viruses related to respiratory afflictions taking part in epidemics and pandemics such as Spanish flu, Asian flu, Hong Kong flu, London flu, Severe Acute Respiratory Syndrome (SARS), Swine flu, Middle East Respiratory Syndrome (MERS) (Vonk & Shackelford, 2012). Post Spanish flu trauma all the other viruses have been controlled after the onset (Friedson, McNichols, Sabia, & Dave, 2020). The genome sequences of SARS, MERS-CoV, and COVID-19 have been found out to be homologous (Patterson & Pyle, 1991).

Pandemic/Epidemic	Virus	Envelope	Capsid Structure	NUCLEIC ACID
r andenne/Epidenne	v ii us	Envelope	Capsia Structure	No ellere nelle
Spanish flu (1918-20)	H1N1	Present	Helical nucleocapsid	Single-stranded negative sense RNA strand
Asian flu (1957)	H2N2	Present	Helical nucleocapsid	Single-stranded negative sense RNA strand
Hong Kong (1968)	H3N2	Present	Helical nucleocapsid	Single-stranded negative sense RNA strand
Small pox	Variola virus	Present	Brick shaped with complex internal structure	Double stranded linear DNA
Polio	Enterovirus	Absent	Icosahedral shape	Positive sense RNA virus
HIV	Lentivirus (retrovirus)	Present	Conical	Positive sense RNA virus
Ebola	Zaire Ebola Virus	Present	Helical nucleocapsid	Single stranded negative sense RNA
Corona virus	SARS-CoV	Present	Helical nucleocapsid	Positive sense RNA virus

Table 1. Major pandemics and Pandemics witnessed in 21st century.

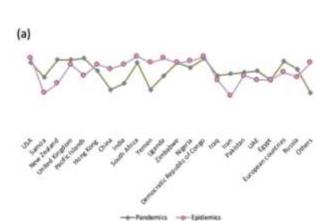
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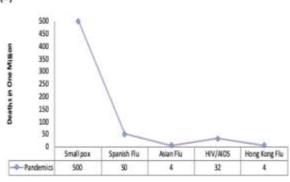
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(a) Novel corona virus COVID-19 Present Spherical or pleomo(phic Positive sense RNA virus Zaire Ebdia Wrus PANDEMICS EPIDEMICS SUBSCOV Small Pox, 1877-1977 SWIS Coll-2 Spanish Flu, 1920 Small pop Virus 1946-1952, Polymyelitis (USA) Asian flu, 1957-1958 HIVWINE HIV/AIDS, 1960-Present Polic Virus Hong Kong flu, 1968-1969 1972-1973, London flu HIN1 Vins 2001, Cholera (Nigeria, South Africa) SARS, 2002-2004 2008-2009, Cholera (Zimbabwe) 2009-2010, Meningitis (West Africa) Swine flu, 2009-2010 Figure 1. (a) Time line of pandemic and epidemics 2010-2017, Cholera (Hispaniola) and the infecting viruses. This gives us hope that 2010-2014, Measles (Congo) COVID-19 can be taken care of as other deadly MERS, 2012- Present viruses had been and (b) a Phylogenetic tree to Ebola Virus, 2013-2016 show the origin and similarity of virus from 2015, Swine flu (India) different times as listed in Table (1). 2016-2019, Cholera (Yemen) 2017-2018; Influenza (USA) 2018-Present, Ebola Virus (Congo and Uganda) 2019-Present, Measles (Congo) COVID-19, 2019-Present

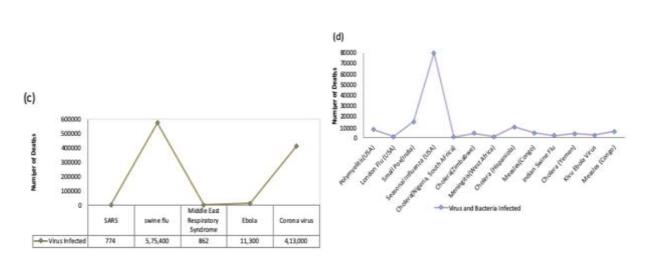
Spanish flu trauma all the other viruses have been controlled after the onset. [5] The genome sequences of SARS, MERS-CoV, and COVID-19 have been found out to be homologous. [6]

Several countries have been affected due to these pandemics and epidemics. Authors found that the most devastated ones by the fatality of the epidemics are USA, New Zealand, United Kingdom, European region, South Africa, Hong Kong, Nigeria, the Democratic Republic of Congo as in Figure 2 [7]. Besides, the soaring mortality rate can be seen in the 20th century when compared to 21st century as in Figure 3 and 4. Due to the pandemic outbreaks such as Bubonic Plague, Spanish flu and Encephalitis in the early 20th century, the fatality rates have been greater whereas in the late 20th century because of the Small Pox taking 500 Million lives and more 50 million lives by Spanish flu as in Figure 3 [8].





3



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Figure 2. (a) Since the Black Death that has affected all the countries from large to small, as shown in here it has been USA, New Zealand, United Kingdom, African Countries and the European Countries along with trade leading Asian Countries that have been recorded more mortality from all the past epidemics and pandemics (b) Mortality rate due to the Pandemics across the world. The 1918 Spanish flu to the Hong Kong flu, most of the viruses that inflicted higher mortality rate across the globe are respiratory ailment related as shown in the above graph. (Until 14/04/20) (c)Mortality rate due to the Epidemics across the world. As shown in the Graph 3 COVID 19 has surpassed the number of deaths SARS, Ebola and MERS viruses have inflicted across the globe. (Until 08/06/20) (d) Mortality rate due to the Epidemics. The deadliest Epidemic since the last century showing the greatest mortality rate surprisingly was due to a seasonal flu outbreak in USA. (Until 14/04/20).

In 21st century, outbreak of Swine flu has caused 575,400 deaths across the world and more significantly in the USA, Northern Ireland, India, Nepal, Pakistan and middle Asian Countries as in Figure 4. Seasonal Influenza in the late 20th century witnessed about 80,000 cases of mortality to become the more severe pandemic of the century as in Figure 5[9][18]. Thus, an easy conclusion can be drawn that USA, USSR, South Africa and East Asian countries are more vulnerable to pandemics and epidemics[10][24]. The mortality rate (Figure 4) does not depend only on the disease inflicted by the virus but also on the socio-economic reasons that do not allow one to take enough measures from being exposed to the virus [11][35].

1.2 Viruses and Pandemics Viruses have inherent advantage in preserving and transmission of the information because of their relatively simple structure compared to other prokaryotic and eukaryotic organisms [12][36]. When dealing with a virus, one needs to keep in mind the structure of the virus as understanding them can tell us how to prepare drugs that can be used to fight them [13][37].

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Table 2: Bibliographic	summary of similar	work already published

References	Objective	Methodology Used	Conclusion
[27]	To help doctors identify COVID-19 patients based on early symptoms and to separate out severe cases.	A prognostic prediction model based on XGBoost machine learning algorithm.	The 3 indices-based prognostic prediction model predicted the mortality risk, and present a clinical route to the recognition of critical cases from severe cases.
[19]	This analysis was aimed at tracing a trend related to death counts expected at the 5th and 6th week of the COVID-19 in India.	Multiple regression and linear regression analyses.	According to the analysis, projected death rate (n) is 211 and 467 at the end of the 5th and 6th week from now, respectively.
[30]	To develop a fully automatic framework to detect COVID-19 using chest CT and evaluate its performances.	A deep learning model and neural network (COVNet) for COVID-19 detection,	Identify COVID-19 on chest CT exams & community acquired pneumonia on chest CT exams.
[31]	To estimate the number of COVID- 19 infected patients by April-2020 and the required healthcare system to cope with it.	Data collected from reliable sources for prediction of possible number of cases in coming days.	If the exponential trend continues, more than 2500 hospital beds in intensive care units will be required within a week in Italy.
[32]	To review the basic reproduction number (R_0) of the COVID-19 virus.	PubMed, bioRxiv and Google Scholar were used to search for eligible data.	Estimated mean R_0 for COVID-19 is around 3.28, with a median of 2.79 and IQR of 1.16, which is considerably higher than the WHO's estimate at 1.95.

2. Methodology. In the present scenario, drugs in the form of monoclonal antibodies have shown progress against previous viral outbreaks like SARS-CoV and MERS-CoV but they haven't been much effective against the new Novel coronavirus COVID-19.[14][18] This suggests that there are a variability of epitopes involved in the monoclonal antibodies[15]21]. Studies have shown that they have a great tendency for gene recombination, and adaptive mutation. Thus, focusing on its capability to attach to host receptors for vaccine production directly won't solve the problem as virus evolves and enhances its affinity for various other receptors present on host cells.[16][20]

Since the plague, people were aware of quarantine and isolation as the disease spread via rats and fleas, where the infection could not be prevented. Thus, limited movement and transport patterns prevented the spread of infection [17] [23].

The extent of the pandemic successively reflected the increasing expansion of global transport and movements. The speed of spread left the world population susceptible to infection. The availability of regular air and seaway traffic is one of the major cause for the spread of novel coronavirus. The fatality rate for the pandemic is less as compared to other pandemics but the speed and volume of spread are many folds higher than the others, indicating its high risk of increased global transport and further spread of other pandemics.

In this paper, we have studied the journey of spread of COVID-19 and how it became a pandemic. China is the epicenter for spread of the novel coronavirus and the outbreak reached all through USA, South Korea, Iran, middle-east region, European countries, Turkey significantly. The novel coronavirus has high mortality rates in countries known for people travelling around the world as given the Table 1 and Table 2 obtained from WHO situation reports. As of June 8, 2020, out of 197 countries in the world that

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have been affected by COVID-19, except Kiribati, Marshall Islands, Micronesia, Nauru, North Korea, Palau, Samoa, Solomon Islands, Tonga, Turkmenistan, Tuvalu, and Vanuatu.

Country	Total Infections	Mortality Cases	Cured Cases
Australia	7171	103	6582
Brazil	468338	27944	189476
Canada	89418	6979	47518
China	83000	4634	78302
Egypt	22082	879	5511
France	149668	28714	67803
Germany	183019	8594	163941
India	173763	4971	82370
Italy	232248	33229	152844
Japan	16759	882	14147
Netherlands	46126	5931	-
Poland	23155	1051	10692
Portugal	31946	1383	18691
Russia	387623	4374	159257
Saudi Arabia	81766	458	57013
South Africa	27403	577	14370
South Korea	11441	269	10398
Spain	238564	27121	150376
United Kingdom	271222	38161	-
United States	1783132	104166	384821

Table 3. Approximate number of people infected dead and recovered due to COVID-19. (Until 30/05/2020)

Table 4. Approximate number of people infected dead and recovereddue to SARS, H1N1 and COVID-19. (Until 30/05/2020)

Country	Disease	Confirmed Cases	Mortality	Cured Cases
China	SARS	5327	349	4949
Canada	SARS	251	41	200
Singapore	SARS	238	33	205
Viet Nam	SARS	63	5	58

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United States	SARS	33	0	26
China	H1N1	62871	714	62157
United States	H1N1	57602	2653	54949
Thailand	H1N1	30588	218	30370
United Kingdom	H1N1	28823	447	28376
India	H1N1	28465	1404	27061
United States	COVID-19	1484579	88523	327751
Spain	COVID-19	274367	27459	188967
Russian Federation	COVID-19	272043	2537	63166
United Kingdom	COVID-19	236711	33998	
Italy	COVID-19	223885	31610	120205

Table 5. Approximate number of infections, deaths caused by COVID-19 and number of recovered cases. (Until 30/05/2020)

Continent	Total Cases	Mortality	Cured Cases
Asia	1085667	29756	653460
Africa	137677	3945	58225
Europe	1996536	172742	973249
North America	2015861	122348	649802
Oceania	8793	125	8187
South America	800398	38185	327866

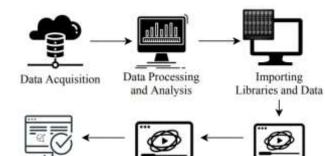


Figure 3. Overview of methodology.

Data Visualisation

Machine Learning

Data Visualisation

Analysis of

Results

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For this study, global pandemic data was collected from WHO and worldometer for consecutive date in the .xlsx format which was converted to .csv format for formatting, training, validation and testing. The CSV data file was then uploaded on Jupyter notebook for analysis with python 3.7 (64- bit Graphical Installer). The Input Values included corresponding column names from the dataset.

The collected dataset was unstructured data with several null or unstructured values which cannot undergo pre-processing. This unstructured data was structured by removing all the null values which were not appropriate for the study or may cause bias and errors while execution of the codes. Required Python Libraries were imported into the Jupyter Notebook to provide predetermined and pretested set of helper functions for specific functionality. The format of dataset used in this study is summarized in table 3, 4, and 5.

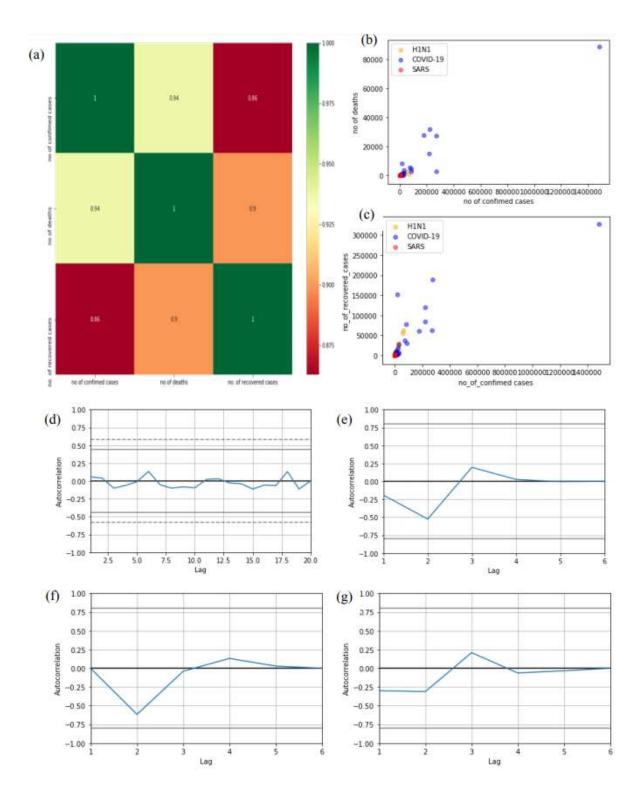
3. Results. Since its appearance in the city of Wuhan (Hebei district) in China, Coronavirus has been a relentless march of new cases and deaths [22][28]. WHO along with governments have already taken strong measures including complete or partial lockdown of both its internal and external borders to restrict the mobility along with social isolation of the suspected and confirmed patients. If the situation continues in the present state; projected death rate (n) is 211 and 467 at the end of the 5th and 6th weeks from now, respectively [29]. R0 estimates for SARS have been reported to range between 2 and 5, which is within the range of the mean R0 for COVID-19 and due to similarities of both pathogen and region of exposure, this is expected but, despite the heightened public awareness and the impressive strong interventional response, the COVID-19 is already more widespread than SARS, indicating it may be more transmissible [23]. Due to high transmission rate COVID-19 has now become a pandemic that has led to shut down to the world's most powerful nations like the USA, France, Italy, etc. It is affecting the world economy, stocks, share markets etc. The poorer nations with less developed medical facilities are worst affected. In India, daily wage workers are suffering from the loss of income which has led them to step out on their foot, with their families in the hope to reach their hometown amid lockdown. The infection is rising under these circumstances. In our study we have collected the data of three pandemics of 21st century: SARS-COVID which spread in 2003, H1N1, or swine flu which spread in 2009-10 and COVID-19. We have used heat maps to compare the data. Heat maps and clustering are used frequently in expression analysis studies for data visualization and quality control [26][33][38]. Heat maps use color gradient for analysis of data which makes it possible visualize the huge volume of data easily and effectively. In this study, we used heat maps for analysis of following characteristics of three diseases (H1N1, COVID-19, and SARS): no. of suspected cases, no. of probable cases, no. of confirmed cases, no. of suspected deaths, no. of probable deaths, no. of suspected deaths. k-Nearest-Neighbors(k-NN) is implemented further as a supervised learning model, as the model here learns from the input data and makes out the predicted value that isn't seen. As the data is split into the input value and the target value, the building and the training of the data and for training the model, fit function was used and once our data was trained the predictions was be made. In our work, the value of the K is determined by the optimal classification or the accuracy classification. The value is determined to be 11 with the maximum depth of 3 and n neighbors to be 5 with a range of (1, 15) and an accuracy of 79.41176470588235 was achieved. Fig 4(h) plots the accuracy (y-label) and the k values (x-label), the values of x were number of confirmed cases', 'number of deaths', 'number. of recovered cases which were the provider values and the values for y were disease which were the target value. The auto co-relation with the lag zero was always equal to 1 because it represents the autocorrelation between each term and itself. It was calculated using the following equation [25] [39].

$$\hat{\gamma}(h) = \frac{1}{n} \sum_{t=1}^{n-|h|} (x_{t+h} - \bar{x}) (x_t - \bar{x})$$

Value and value with lag zero will always will be the same.

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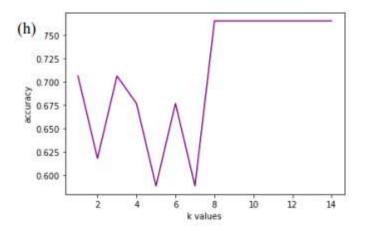


Figure 4: (a) Heat-map of co-relation between combined number of confirmed cases, deaths, recovered cases of H1N1, COVID-19 AND SARS from table 4, (b) Scatter plot of number of deaths versus total confirmed cases from table 4, (c) Scatter plot of number of recovered cases versus total confirmed cases from table 4, (d) Autocorrect plot against the lag versus number of coronavirus disease infection from table 3, (e) Autocorrect plot against the lag versus number of infections for coronavirus disease from table 5, (f) Autocorrect plot against the lag versus number of deaths from coronavirus disease from table 5, (g) Autocorrect plot against the lag versus number of cases recovered from coronavirus disease from table 5, (h) Plot for most appropriate K-value.

4. Conclusion. COVID-19 spread the entire globe within a matter of months. One of the main reasons for the quick spread of the disease is the volume and speed of human travel. The traveler across the globe were unaware of the infection they were carrying and unknowingly spread it to several countries. Secondly, the capacity of the virus to survive in the different weather and spread quickly through cough and cold is another reason for quick spread. Third, the irresponsible behavior of the people in quarantine added to the spread of the virus. Lastly, the unavailability of the vaccine or medicine to combat the virus makes it difficult for the doctors to fight the disease. In this study, the epidemics and pandemics that occurred in the last century, the number of countries they affected, and their mortality rates were discussed so as to compare them. Then the structures of the viruses that caused the pandemics were discussed to understand the pathogenicity. And then the reasons why tackling Covid-19 is harder to deal with when compared to other viruses are discussed along with the number of countries that are affected by Covid-19, the mortality rate. Then some COVID-19 studies that used the artificial intelligence/machine learning models were discussed. Then by the use of one such model, analysis of following characteristics of three diseases (H1N1, COVID-19, and SARS): number of suspected cases, number of probable cases, number of confirmed cases, number of suspected deaths, number of probable deaths, and the number of suspected deaths, was done. It was seen that the amount of confirmed cases of COVID-19, amount of deaths caused by COVID-19 and the number of recovered patients recovering from COVID-19 are more when compared to the same numbers of H1N1 and SARS. Also, a heat map was prepared to show the correlation between the number of confirmed cases, number of deaths, and the number of recovered cases of H1N1, COVID-19, and SARS. Also, three plots representing the autocorrelation against the lag of the number of confirmed cases, the number of recovered cases of COVID-19, and the number of deaths caused by COVID-19 were prepared. The lockdown and social distancing in many countries have helped overcome the fast spread of the virus, however, this has resulted in slowing down of the economy. The only blessing in disguise is that Mother Nature got a chance to heal itself. In conclusion, we can interpret that it is not the first time that a pandemic has hit the globe. Earth has seen epidemics and pandemics other than COVID-19. Scientists, pharmaceuticals, and global leaders have always come up with ways to deal with epidemics and pandemics. The scientists and pharmaceutical companies across the globe have put up some commendable work on a war footing in the field of developing testing kits, developing vaccines and preparing post-symptomatic treatment

protocols to deal with COVID-19. Social distancing and lockdowns in many countries have already reduced the rate of spread and the hope is the vaccine will be available sooner than later.

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