

Epidemiology of Coronavirus Disease (COVID-19) and Exactitude of Predictions through Models

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Abstract

The outbreak of respiratory illness, coronavirus disease (COVID-19) has occurred in Wuhan, Hubei Province, China in December 2019 and spread to many countries. Globally, there have been 194,608,040 confirmed cases of COVID-19, including 4,170,155 deaths, and in India, 31,440,951 confirmed cases of COVID-19 with 421,382 deaths, as reported to WHO on 27th July 2021. Mathematical models for infectious diseases and their statistical tools have become an integral part of the inputs for planning control and mitigation measures. These models allow us to test different strategies in simulations before applying them to groups of people or individuals. One specific goal of our future modeling is going to be to check the efficiency of testing and make contact with tracing. One must be very cautious regarding model predictions, because different models that lead to similar outcomes in one context may fail to do so in another. In such instances, it is best to conduct further epidemiological and experimental studies in order to discriminate among the different possible mechanisms. Thus, an important role of modelling enterprises is that they can alert us to the deficiencies in our current understanding of the epidemiology of various infectious diseases and suggest crucial questions for investigation and data that need to be collected. Therefore, when models fail to predict, this failure can provide us with important clues for further research.

Keywords: Coronavirus; Covid-19; Mathematical Models

Abbreviations

COVID: Coronavirus Disease; WHO: World Health Organization; SARS-cov2: Severe Acute Respiratory Syndrome Coronavirus 2; ICTV: International Committee on Taxonomy of Viruses; CEST: Central European Summer Time Zone; ODEs: Ordinary Differential Equations; PDEs: Partially Differential Equations; SEIR: Susceptible-Exposed-Infectious-Removed; AI: Artificial Intelligence; GLM: Generalized Linear Model; LSTM: Long Short-Term Memory; SEIR: Susceptible-Exposed-Infectious-Removed-Deceased; IIS: Indian Institute of Science; DFE: Disease Free Equilibrium; EE: Endemic Equilibrium

Introduction

"COVID-19 pandemic-Humanity needs leadership and solidarity to defeat the coronavirus".

United Nations Development Programme (UNDP).

A virus that has changed the world and it seems that it will change the world order. In December 2019, an outbreak of Coronavirus Disease (COVID19) occurred in Wuhan, Hubei Province, China [1], and within two months, COVID-19 had spread rapidly from Wuhan to all parts of the country [2,3]. The pathogen is called Severe Acute Respiratory Syndrome Coronavirus 2 (SARScov2) by the International Committee on Taxonomy of Viruses (ICTV) on February 11, 2020 [4]. This virus is spreading exponentially. Therefore, on March 11, 2020, the World Health Organization (WHO) declared COVID19 a “global pandemic” [5]. The first COVID-19 case in India, a female aged 18 years, was presented in Kerala on January 27, 2020, the identical day that WHO declared it a public health emergency of international concern [6].

Globally, as of 5:54 pm CEST, 27 July 2021, there have been 194,608,040 confirmed cases of COVID-19, including 4,170,155 deaths, and in India, from 3 January 2020 to 5:54pm CEST, 27 July 2021, there have been 31,440,951 confirmed cases of COVID-19 with 421,382 deaths, reported to World Health Organization [7]. Country wise summary of 14-day COVID-19 case notification rate per 100000 is given below (Figure 1) [8]. In India, the picture is gloomy and cases were rising explosively every day in India few months back (Figure 2) [9,10].

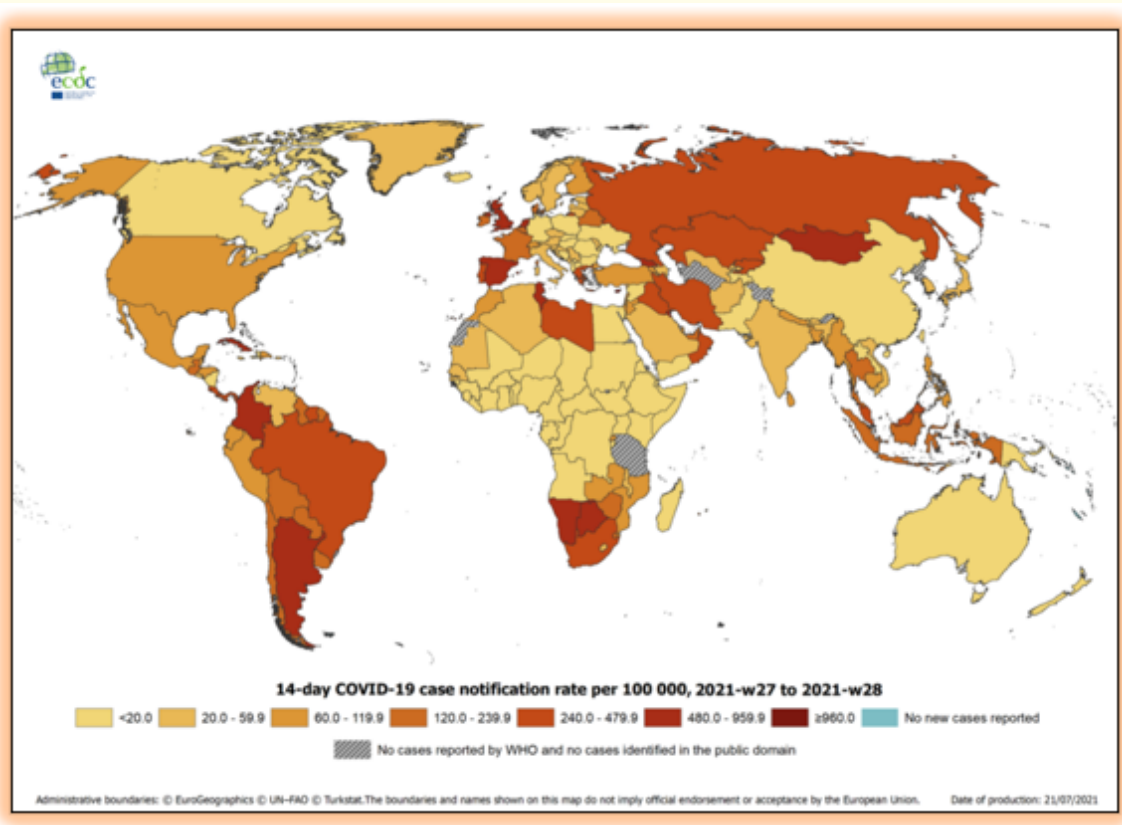


Figure 1: Covid-19 case notification worldwide, in week 27-28, 2021 (14-day COVID-19 case notification rate per 100000).

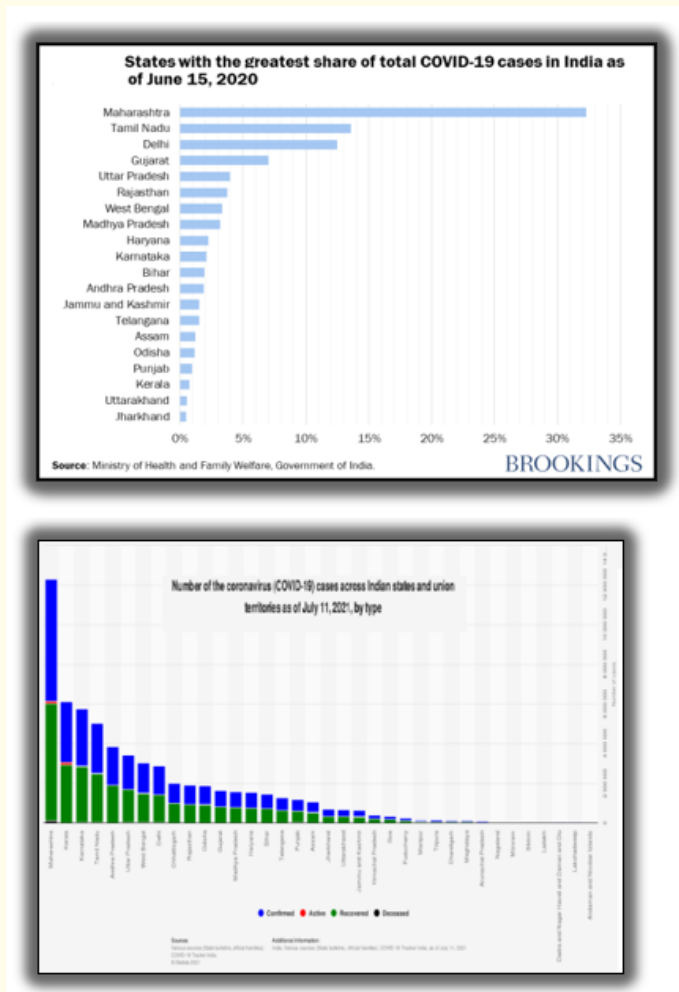


Figure 2: Cases of Covid-19 in June 2020 and May 2021 in Indian States and Union Territories.

The story of the human coronavirus began in 1965, when Tyrrell and Baino discovered that they could spread an epidemic called B814 [11]. Since that point only 31 additional strains are recovered. Ten of those were originally recovered in human embryonic tracheal organ cultures only, and therefore the remainder in monolayer cell cultures [12].

Most of the people get infected with one or others at some point of your time in their lives, causing mild infection just like the respiratory disorder. Based on recent findings, it’s been established that the present epidemic incorporates a specific signature. First, it exhibits a singular communicability timeline. The SARS-COV-2 virus incorporates a relatively long period (defined because the length of time between the individual’s exposure to the virus, and also the presence of symptoms). The average period has been estimated to be approximately 6 days, with observed variations between 2 and 27 days [13].

However, researchers in their studies have shown that people infect others before their own symptoms appear [14-17].

In addition, the degree of infectiousness varies for an individual along this presymptomatic stage, with a maximum around 2 - 3 days before symptom's onset, following an initial latent period, with lower communicability. Newer epidemiological research of COVID 19 has also revealed a significant carrier state (broadly estimated between 6 and 41%) [18].

Since the carriers never show symptoms, they do not know that they have the virus. Their infectiousness is significantly lower than that of individuals who are in different stages of development of symptoms, but can still make a significant contribution to the dynamics of the epidemic. Distinction between pre-symptomatic and asymptomatic people is therefore very important when formulating public health strategies to control its transmission, but it is also very difficult to make guidelines and requires careful follow-up strategies.

Pre-symptomatic and asymptomatic transmission plus limited testing and follow-up care resources are the main constraints that hamper detection and contribute to the pandemic spread. Another aspect of COVID 19 is that it exhibits significant age differences in the development of symptoms and prognosis. Children and young population, exposed to the virus can be contaminated as much as the more advanced age groups. However, their milder symptoms can pass unnoticed, and they can more easily act as carriers of the virus. On the other hand, the elderly population is more likely to exhibit serious to critical clinical features following exposure. The mortality rates differ in age groups. Third, it has been established that COVID 19 may not develop long-term immunity, allowing people to get reinfection and this also questions viability of social measures like herd immunity [19].

Common Covid models and exactitude of predictions

In order to understand the spread of various infectious diseases including COVID19 among plants, humans or other animals, mathematicians applied this concept of differentiation and integration to model the dynamics of that disease in the form of ordinary differential equations (ODEs) or partially differential equations (PDEs) that could be used to predict the transmission of that disease within a specific population. This prediction is particularly necessary for a country like India with very high population density in several states.

Scholars from various countries have attempted to study and analyze the epidemic situation of COVID-19 by using different models to predict the COVID-19 epidemic trends.

Scholars from various countries have attempted to study and analyze the epidemic situation of COVID-19 by using different models to predict the COVID-19 epidemic trends.

S. No.	Researcher	Model	Country
	Read., <i>et al.</i> [20]	SEIR and AI	China
	Tang., <i>et al.</i> [21]	SEIR	China
	Huang., <i>et al.</i> [22]	Data-driven model based on natural growth	China
	Wang., <i>et al.</i> [23]	SEIR	China
	Wu., <i>et al.</i> [24]	SEIR	China
	Kraemer., <i>et al.</i> [25]	GLM	China
	Koshy [26]	SUTRA	India
	Mwalili., <i>et al.</i> [27]	SEIR	Kenya
	Radulescu., <i>et al.</i> [19]	SEIR	USA
	Ahmad., <i>et al.</i> [28]	SEIR	Pakistan
	Bedi., <i>et al.</i> [29]	SEIRD	India

On January 24, 2020, British scholars Read, *et al.* used the SEIR model to predict the trend of the Prediction of the COVID-19 epidemic trends based on SEIR and AI models. They predicted that the number of infections in Wuhan would reach 190,000 by February 4, 2021. This estimate obviously overestimates the breakthrough trend [20].

On January 27, 2020, Tang, *et al.* using the epidemic data from January 10 to 22, the epidemic recovery rate is predicted to be 6.47 (95% confidence interval 5.71 - 7.23) by the SEIR model and statistical calculation method. Their model estimated that the number of infections would peak on approximately March 10, 2020. It is worth mentioning that our model made a very good prediction of the confirmed cases from 23 to 29 January 2020, particularly, the predicted confirmed cases were 7723 as of 29 January 2020, which was very close to the real number of cases of 7711 [21].

Huang, *et al.* proposed a simple data-driven model based on natural growth, predicting that the number of infections would peak on approximately February 5, 2020 with a cumulative number of confirmed cases between 37,000 and 44,000 [22].

On February 24, 2020, Wang, *et al.* used SEIR model and proposed that the infection coefficient R_0 decreased from 2.5 to 0.5 The virus and changes in government policies have affected forecasts [23]. On 19 March 2020, Wu, *et al.* used SEIR model and they study the influence of infection rate, recovery rate and migration data of different age groups in the projection model [24].

On March 25, 2020, Kraemer, *et al.* used GLM (generalized linear models) model to consider the impact of population migration and age on the number of infected people [25].

As predicted by the team of Indian Institute of Science (IISc), Bengaluru, by May 2021, 1.36 million people in India will be infected. By September 1, 153 million people will be infected. The second wave will peak in mid-April with 730,000 active transactions [30] but actual cases reported on 31st May, 2021 were 28 million [31] and the peak was observed on 6th May 2021 (4,14,188 new cases in a day) [32].

In April 2021, India is completely unprepared for the increase in the number of patients with the new coronavirus disease (COVID19). The Union Ministry of Science and Technology's mathematical model, SUTRA (Susceptible, Undetected, Tested (positive), and Removed), failed to predict the second wave and grossly underestimated the caseload that the government should have been prepared to deal with [33].

The SUTRA group put out a statement, carried by the Press Information Bureau, that the government had solicited its inputs He said that the "second wave" will reach its peak in the third week of April, leaving about 1 million cases. It is clear that in this case, the model's prediction is wrong [26].

The model shows that control measures such as social distancing, wearing of masks in Wash your hands frequently in public places and limit non-essential travel necessary to prevent the COVID19 pandemic. There is a growing concern that this disease could continue to ravage the human population globally since many aspects of COVID19 has not yet been discovered, which also poses a challenge to the long-term mathematical modelling of the disease. The model was developed to monitor the dynamics of transmission, so it does not describe the severity of illness or death. Since we assumed parameters at the beginning of the pandemic, the model may overestimate the pandemic at a later point in time [27].

To investigate the spread of coronavirus in Pakistan, researchers developed the SEIR time fractional model with newly, developed fractional operator of Atangana-Baleanu. They presented briefly the analysis of the given model and discuss its applications using World Health Organization (WHO) reported data for Pakistan. They considered the available infection cases from 19th March 2020, till 31st March 2020 and accordingly, various parameters are fitted or estimated. It is worth noting that they calculated the basic reproduction number which shows that virus is spreading rapidly. Stability analysis of the model at disease free equilibrium (DFE) and endemic equilibriums (EE) was performed to observe the dynamics and transmission of the model. Finally, numerically solve the fractional AB model. Several

graphs were drawn to show the influence of various built-in parameters (such as the fracture parameter α) in the model. It is worth noting that the base of their investigation, they have predicted the spread of disease for next 200 days [28].

It was observed by the researchers that both knowledge of the epidemic parameters, and a few of the characteristics of the SARS-COV2 virus are constantly changing. This changing scenario makes it additionally difficult to capture updated magnitude of the problem, and produce reliable predictions. They aimed to make their model specifically designed to use the clinical and social data pertinent to the present epidemic, while keeping it sufficiently vigorous exercise to come up with general predictions that may be easily adapted to the rapid fluctuations in data trends. For future repetition of the exercise, they were engaged on including the time-depending aspect within the epidemic parameters, and on incorporating a number of the known feedback loops that contribute to the complexity of this technique [20].

In another study conducted in India, a modified SEIRD model was proposed and presented to perform COVID-19 predictions for India and its four states having the high load of total cases. This model also considered asymptomatic infectious population for making the predictions and also identifying peak for the infection. Further, LSTM model was utilized to compute short-term predictions. Both models used the reported data. The results showed that the predictions of the proposed modified SEIRD model closely corresponded with the predictions obtained from the LSTM model. Because LSTM is only suitable for short-term prediction; therefore the proposed model is used to calculate the long-term forecast of COVID19 in India and its states. Increased number of cases was attributed to different Hindu festivals like Ganesh Chaturthi, and Onam where large gathering of people was seen. The data as of September 6, 2020 was been used to predict pandemic trends for experimental purposes. The results obtained by the proposed modified SEIRD model and LSTM model were compared for the following 30 days. The results were also statistically analyzed employing 't' test for short-term predictions. They obtained good results using the models presented for predictions, but there is a further scope of improved results by considering and analyzing the age and co-morbidity of the population [29].

Conclusion

Because the strength of models, both to adjust and to predict future dynamics, depends on the accuracy in case reporting, it is very important to analyze the uncertainties in the adjustment and evaluate the degree of change in parameter estimates [34].

Mathematical models for infectious diseases and their statistical tools have become an integral part of the inputs for planning control and mitigation measures. These models allow us to test different strategies in simulations before applying them to groups of people or individuals [35].

Mathematical modeling for infectious diseases uses many sources of data and various assumptions. Robust predictions can never be expected from vague/incomplete/wrong assumptions. The attempts of simplification, approximation, idealization and abstraction have resulted in all models being described as part of the actual operating mechanism. Therefore, the reliability of each model should be judged based on whether its assumptions are roughly realistic [36].

One specific goal of our future modeling is going to be to check the efficiency of testing and make contact with tracing (which permits early detection and adequate reduction within the travel vector of infected and even exposed individuals). Another important aspect is that the feedback introduced by reaching the health care capacity at very high infection counts (which is probably going to impact the recovery versus fatality rates). Finally, a major feedback contribution comes from the psychological effects. One obvious example is "tolerance:" people could also be inclined to loosen isolation measures in absence of a right away epidemic threat, thus contributing to increasing this very threat.

An important advantage of using models is that the mathematical representation of biological processes is transparent and accurate. Epidemiological hypotheses allow us to verify our understanding of disease epidemiology by comparing model results with observed patterns [37].

A model can also assist in decision-making by making projections regarding important issues such as intervention-induced changes in the spread of disease. It should be emphasized that the mode of transmission is based on the current understanding of the natural origin of infection and immunity. In cases where such knowledge is lacking, assumptions can be made regarding these processes. However, in such cases there can be several possible mechanisms, and therefore several different models, which can lead to similar observed patterns, so that it is not always possible to learn about underlying mechanisms by comparing model outcomes. One must then be very cautious regarding model predictions, because different models that lead to similar outcomes in one context may fail to do so in another. In such instances, it is best to conduct further epidemiological and experimental studies in order to discriminate among the different possible mechanisms.

Thus, an important role of modelling enterprises is that they can alert us to the deficiencies in our current understanding of the epidemiology of various infectious diseases, and suggest crucial questions for investigation and data that need to be collected. Therefore, when models fail to predict, this failure can provide us with important clues for further research [35].

Bibliography

1. Adhikari S., *et al.* "Epidemiology, causes, clinical manifestation and diagnosis, prevention and control of coronavirus disease (COVID-19) during the early outbreak period: a scoping review". *Infectious Diseases of Poverty* 9.29 (2020): 1-12.
2. Li L., *et al.* "Propagation analysis and prediction of the COVID-19". *Infectious Disease Modelling* 5.7 (2020): 282-292.
3. Li Y., *et al.* "Mathematical modeling and epidemic prediction of COVID-19 and its significance to epidemic prevention and control measures". *Annals of Infectious Disease and Epidemiology* 5.1 (2020): 1-9.
4. Naming the coronavirus disease (COVID-19) and the virus that causes it (2021).
5. WHO. Coronavirus disease 2019 (COVID-19): situation report, 51 (2020).
6. Andrews MA., *et al.* "First confirmed case of COVID-19 infection in India: A case report". *Indian Journal of Medical Research* 151.5 (2020): 490-492.
7. World Health Organization. Coronavirus Disease (COVID-19) Dashboard (2021).
8. COVID-19 situation update worldwide, as of week 27, updated 15 July 2021". *European Centre for Disease Prevention and Control* (2021).
9. Bharali I., *et al.* "How well is India responding to COVID-19?" Brookings (2020).
10. Number of the coronavirus (COVID-19) cases across Indian states and union territories as of July 11, 2021, by type. Various sources (State bulletins, official handles); COVID-19 Tracker India; as of July 11, (2021).
11. Tyrrell DA and Bynoe ML. "Cultivation of viruses from a high proportion of patients with colds". *Lancet* 1 (1966): 76-77.
12. Kapikian AZ. "The coronaviruses". *Developments in Biological Standardization* 28 (1975): 42-64.
13. Lauer SA., *et al.* "The incubation period of coronavirus disease 2019 (covid-19) from publicly reported confirmed cases: estimation and application". *Annals of Internal Medicine* 172.9 (2020): 577-582.

14. Jang S., *et al.* "Cluster of coronavirus disease associated with fitness dance classes, South Korea". *Emerging Infectious Diseases* 26.8 (2020): 1917.
15. Luo L., *et al.* "Modes of contact and risk of transmission in covid-19: a prospective cohort study 4950 close contact persons in Guangzhou of China". *The Lancet* (2020).
16. Tong ZD., *et al.* "Potential presymptomatic transmission of sars-cov-2, Zhejiang Province, China, 2020". *Emerging Infectious Diseases* 26.5 (2020): 1052.
17. Ping Y., *et al.* "A familial cluster of infection associated with the 2019 novel coronavirus indicating possible person-to-person transmission during the incubation period". *The Journal of Infectious Diseases* 221.11 (2020): 1757-1761.
18. Byambasuren O., *et al.* "Estimating the extent of true asymptomatic covid19 and its potential for community transmission: systematic review and meta-analysis". *Journal of Association of Medical Microbiology and Infectious Disease* 5.4 (2020): 223-234.
19. Radulescu A., *et al.* "Management strategies in a SEIR type model of COVID 19 community spread". *Scientific Reports* 10 (2020): 21256.
20. Read JM., *et al.* "Novel coronavirus 2019-nCoV: early estimation of epidemiological parameters and epidemic predictions". *Philosophical Transactions Royal Society B* 376 (2021): 20200265.
21. Tang B., *et al.* "Estimation of the transmission risk of 2019-nCov and its implication for public health interventions". *Journal of Clinical Medicine* 9 (2020): 462.
22. Huang N and Qiao F. "A data driven time- dependent transmission rate for tracking an epidemic: A case study of 2019-nCoV". *Science Bulletin* 65.6 (2020): 425-427.
23. Wang H., *et al.* "Phase-adjusted estimation of the number of Coronavirus Disease 2019 cases in Wuhan, China". *Cell Discovery* 6 (2020): 10.
24. Wu JT., *et al.* "Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China". *Nature Medicine* 26 (2020): 506-510.
25. Kraemer M., *et al.* "The effect of human mobility and control measures on the COVID-19 epidemic in China". *Science* 368 (2020): 493-497.
26. Koshy J. "Scientists see flaws in govt-backed model's approach to forecast pandemic". *The Hindu New Delhi* (2021).
27. Mwalili S., *et al.* "SEIR model for COVID-19 dynamics incorporating the environment and social distancing". *BMC Res Notes* 13 (2020): 352.
28. Ahmad Z., *et al.* "A report on COVID 19 epidemic in Pakistan using SEIR fractional model". *Scientific Reports* 10 (2020): 22268.
29. Bedi P., *et al.* "Prediction of COVID-19 Trend in India and its four worst-affected states using modified SEIRD and LSTM models". *SN Computer Science* 2 (2021): number:224.
30. COVID-19, The News Minute 19 (2021): 12.
31. DH Web Desk, MAY 31 2021, 05:43 ISTUPDATED 12 (2021): 03 IST.
32. Singh VB. "The human costs of COVID-19 policy failures in India". *Nature Human Behaviour* 5 (2021): 810-811.
33. Varshney V. "SUTRA modellers' claim of India reaching herd immunity last September was wrong". *Down to Earth* (2021).

34. Lopez L and Rodo X. "A modified SEIR model to predict the COVID-19 outbreak in Spain and Italy: Simulating control scenarios and multi-scale epidemics". *Results in Physics* 21 (2021): 103746.
35. Huppert A and Katriel G. "Mathematical modelling and prediction in infectious disease epidemiology". *Clinical Microbiology and Infection* 19.11 (2013): 999-1005.
36. Kotwal A., *et al.* "Predictive models of COVID-19 in India: A rapid review". *Medical Journal Armed Forces India* 76.4 (2020): 377-386.
37. May RM. "Uses and abuses of mathematics in biology". *Science* 303 (2004): 790-793.

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