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Mathematical modeling of basic reproductive strength on COVID 19

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Abstract

Objective: The rapid spread of the COVID-19 has become a global threat affecting almost every country in the world. As countries hit the peak of the epidemic, it is planned to move forward to new norms under different social conditions in order to mitigate the economic impact that the closure of all or part of the operations, businesses, universities, shops, etc. Under such circumstances, the use of mathematical models to assess the spreading risk of COVID-19 in different locations is an essential tool to assist staff in making informed decisions. We examine the epidemiological constants in the model, such as the transmigration rate and the basic reproductive number, using data of released cases. We thus estimate the act of the susceptible, exposed, or latency period in the signs of a COVID-19 infection. By this critical model extensive variety R0, has been utilized to assume the field of persons straight away contaminated by way of the contagious human and classified the depth of susceptible, exposed, and infected populations as soon as the infection is over, it can be at once used to measure the contaminated areas. Based on the strength of R0, susceptible, exposed, and infected people's rate has been calculated via the Runge Kutta Felhberg method, Maple 18. By this investigation, the susceptible people's infectious quotes from COVID 19 are strongly increased whereas the infected people's rate moves up and down and the exposed people's rate decelerates with increases of the basic reproductive number. Several scenarios have been considered to demonstrate the performance of the proposed model. The results showed that the simulations provided useful information in formulating strategies to reduce the risk of the spread of COVID-19 locally.

Keywords

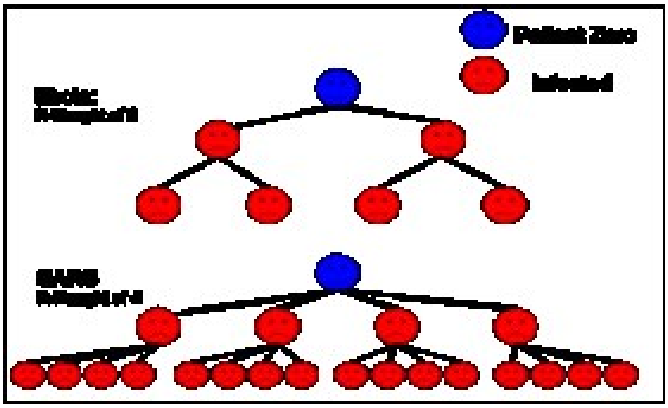
COVID 19; Mathematical modeling; Susceptible, exposed and infected peoples, Reproductive number, Global warming.

Introduction

On January 30, 2020, the World Health Organization informed the 2019 coronavirus (COVID-19) outbreak as an international public health emergency. As of April 10, 2020, 1,684,833 laboratory-confirmed cases were reported and lost 102,136 lives worldwide. COVID-19 is highly contagious, which is transmitted from one host to another through various diffusion patterns such as aerosols that are spread by sneezing or coughing, direct physical contact, and more. In the transfer of agents or sets of agents in a population of weak elements are used. The infection is then transmitted to other drugs via transport and as a result, it can spread to the population. Infectious elements may persist without general symptoms in the early stages of infection. After that, the patient can develop clinical symptoms and be diagnosed with the disease. When the number of cases exceeds the normal mean of events within a short period of time, illness will develop, [1].

Various mathematical tools are used to characterize, predict, or analyze infectious disease transmission processes. Traditional survey methods use experimental data and statistics to obtain information about the spread of disease. However, the guidelines are inappropriate for a number of reasons: i. For infectious diseases in humans, large-scale testing may be impractical or unethical, and ii. The data set applicable to this disease contains only some of the information that is not accurate enough for a reliable statistical study. Mathematical modeling is recognized as an important tool in the computation of the spread of infectious diseases. Mathematical models are widely used to assess the effectiveness of control strategies and to reduce the risks involved. Through mathematical modeling, it is possible to obtain important information about the mechanisms of transmission and distribution. As a result, effective preventive measures or control strategies can be suggested, [2].

In (New England Journal of Me, 2020), it was reported that the transmission of the COVID-19 epidemic can occur in people with an infectious disease who have not yet responded as a symptom in (O-China J report). , 2019), it found that people affected by COVID-19 tend to spread the syndrome and experience choking and fever, usually 5 to 6 days after the epidemic (5 to 6 days on average over 1 Up to 14 days). In (Yanget al., 2020), it was recorded that the meantime before the start of the index was 3 days, a minimum of 1 day, and a maximum of 24 days. It is noteworthy that these periods play a key role in the proliferation of COVID-. 19 Please refer to Tables 1-3, [3]. The basic reproduction numbers are a big difference in the results of infected virus design. We can assume that the infected virus has spread along a wave of infection starting with the first confirmed cases. Suppose we have the base reproduction number of 1, in that case the spread would look like this, [4]:



1: Serial changes in Hb levels of each group during the first 48 postoperative hours.

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The reproductive count has become the most commonly cited term in the current COVID-19 epidemic. This number, shown as R0, represents the number of new infections that a single infected person could cause in a vulnerable population. It is used to prove and explain why social distances and other relief strategies must be shut down to keep the number of cases and deaths in this outbreak low.If R0 is greater than 1, each infection will hatch more and more and more outbreaks will continue.If lower than 1, the outbreak will continue. But at lower mortality due to fewer than 1 infected, according to corrections to previous cases by death or recovery, [5,6].

Due to changes in the country, culture, type of calculations, and the R0 epidemic stage, they were reported to vary greatly in magnitude. Although it is important But it seems to be complicated in obtaining precisely calculated values due to the limitations of the data and the inaccuracies of reporting. The first reported R0 came from Wuhan at 2.2 due to direct contact detection. It was questionable given the size of the case, which led to the breakdown of the healthcare system and inadequate testing facilities at that stage, as well as the development of case definitions. Even today, model selection, initial conditions, and other assumptions generate final calculations leading to a wide range of R0 from 2.2-3.6 to 4.1-6.5, [7].

The current study uses the SEIR model as a common channel model in epidemiological studies. Demonstrates how the disease progresses through four channels of interaction: Weak, Sensitive, Contact, and Repairable. It depends on three parameters: the rate at which the vulnerable was exposed (β), exposure to infectious disease (α), and contagious recovery (γ). The last two were inversely related to the latent phase and Duration of infection, respectively. Latency is the amount of time that an infected person has not been able to be contacted and the duration of the contract is the length of time that an infected person can infect others. It can vary from 2-6 days and 3-18 days. This model has the most important characteristic of the epidemiological model, that is, the transition from an exposed-sensitive state. This will change with the size of vulnerable and infected populations and the percentage of exposure between them as well as inversely proportional to the duration of contact,[8-10]. Within 45 days of the first COVID-19 reported in Europe on January 24, 2020, the outbreak affected all 27 EU countries, leading to the closure of all external borders in the EU. Within the next two weeks, local travel restrictions and closures will be followed by a 95% drop in international air travel in the EU. This has caused considerable disagreement, largely due to the lack. The current study aims to find the relationship between closure and changes in outbreak conditions. A dynamic SEIR model was used to reflect the percentage change in contact under the shutdown parameter. The model allows the exact R0 to be calculated in different conditions and the delay time between any social health measure and the impact on the epidemic. The latter is the key factor in deciding how to release the lock in a step-by-step manner, as well as to report the risks of each action,[11-14].

R (t), the effective diffusion number, is an important parameter in this model as it reflects the change in R0 (fundamental diffusion number) with time and mitigation strategy. The European R0 is at 4.5, the highest in Spain, France, and Germany, with almost 6.0, and the lowest in Estonia, Slovenia, and Malta, with around 1.4. The current effective reproduction number Rt is much lower with the EU average of 0.72, the highest in Slovakia, Sweden, and Bulgaria at around 1.1, and the lowest in Austria, Cyprus, and France at around 0. The relative decline in reproduction numbers was highest in Sweden, Hungary, and Denmark, between 0.58 and 0.44. The delay time for air travel restrictions to reduce the effective reproduction rate ranges from 1 day in France and Luxembourg to 30 days in Malta, with an EU average of 13 days,[15-16]. The reproduction number is defined using the transfer and recovery numbers. If the rate of transmission tells us how many patients will transmit the disease and the recovery rate tells us how long the person will remain contagious, we can calculate the basic reproduction number as follows:

The SEIR model showed that herd immunity can infect approximately 78% if the reproductive count is 4.5.The dynamics models used here allow the exposure percentage change and help predict transient states far beyond the final herd's immune balance. It can show big and swift changes as travel restrictions and social measures ease. But can be studied from this model. Effective changes in the number of reproduction can also measure the strength of public health measures to formulate policies to control outbreaks. It also shed light on the impact of public health interventions, especially travel restrictions, which France responded the fastest and Sweden the least. The duration of any observed impact on the transmission curve was the smallest in France in one day and the slowest in Sweden at 21 days, [17-19].

Researchers are also using machine learning to assess massive amounts of data from the pandemic and to examine trends and relationships. For example, the most efficient reproductive numbers are produced in the EU. This is higher than the World Health Organization (WHO) figures cited from the early exposure detection study in Wuhan at 2.2 but is comparable to the current figure 5.7 for the Wuhan epidemic. The researchers set up three sets of conditions. One in which the current diffusion number Rt is constant at the effective spread number R (t); and two more reflect the impact of the transition from Rt to the base R0 reproductive number for that country, whether more than a month or more than 3 months. Sweden does not enforce logins and the number of reproduction numbers is still higher than 1 among the few European countries in the same situation. However, Sweden's situation is unlikely to change if the current moderate guidance is removed, unlike the steep rises expected in other countries such as Austria following the cancellation of the closure. The difference lies in the willingness to take responsibility for the health of each person,[20-23].

The transmission of COVID-19 in a facility is a complex pattern in which discriminatory behavior and risk depend on interpersonal interactions rather than on individual characteristics within the system. Due to this study, we are searching about the impact of fundamental reproductive variety on coronavirus susceptible, exposed, and infected peoples are retrieved out with the aid of exploiting R. K. Fehlberg device with the backing of MAPLE 18. We will examine the role of the basic reproductive number on the COVID-19 infected virus, that is, the duration of time in which freshly affected persons are asymptomatic and non-infectious. We illustrate the role of the basic reproductive number on COVID 19 in Fig. 1. In the current article, we establish mathematical designs to analyze the effect of the basic reproductive number on the COVID 19 virus.

This work is organized as follows: Part 2 introduces the basic concepts of mathematical modeling. In Part 3, the model is presented numerically, MAPLE 18 coding. In Part 4, the results and nature of the proposed method are discussed. Finally, in Section 6, a conclusion is drawn.

This is the time t≥(to) in days (to) is the start date of the epidemic, S(t) is the number of people at risk of infection at that time t, E(t) is the number of individuals who were not infected. Asymptomatic over time t, I(t) is the number of persons asymptomatic. But infected at time t, R(t) is the number of infected persons with symptoms reported at time t, U(t) is the number of infected persons with unreported symptoms at time t, this system is supplemented by data

$$S(to)=So>0,E(to)=Eo>0,I(to)=Io>0,U(to)=Uo>0,S(to)=Ro=0 \quad (6)$$

Here t≥(to) is time in days, (to) is the beginning date of the epidemic, S(t) is the number of individuals susceptible to infection at time t, E(t) is the number of asymptomatic non-infectious individuals at time t, I(t) is the number of asymptomatic but infectious individuals at time t, R(t) is the number of reported symptomatic infectious individuals at time t, U(t) is the number of unreported symptomatic infectious individuals at time t, This system is supplemented by initial data

Exposed class E output currents are described by the term-αE(t), which means that the exposure time follows the exponential law, and the average exposure time is 1/α, which is 6 hours, 12 hours, 1 day. 2 days, 3 days etc., is possible. The model consisted of an asymptomatic infection class corresponding to the I(t) equation. The dynamics of the infected person with the symptoms are degraded into the R(t) equation, consistent with those infected with the reported symptoms. (Which is a highly contagious disease) and the equation U(t) individualst individuals corresponding to an infected person with unreported symptoms (symptoms). The flow of the person who left the class I is γI(t). We assume that fractions f are reported and fractions 1-f are unreported. Thus γ1=γf and γ2=γ(1-f).

The parameter is time dependent, τ(t) is the transmission rate. In the early stages of the epidemic, when the cumulative number of reported cases becomes the approximate exponent, is a constant value τo. After Jan. 23, strong government measures across China, such as quarantine, quarantine and public shutdown, have had a profound impact on new business transfers. The real effects of these measures are complex, and we use τ(t) a time-lowered transmission rate to absorb these effects after an early exponential increase in phase. The formula for τ(t) during the exponential reduction phases is derived from the appropriate steps for the data:

The people were classified into five divisions: exposed peoples (EP), symptomatic infected peoples (IP), susceptible peoples (SP), asymptomatic infected peoples (AP), symptomatic infected peoples (IP), asymptomatic infected peoples (AP), and removed peoples (RP) adding recovered and death peoples. The death rate and birth rate of peoples were defined as mP and nP. In this model, we assumed ΛP = nP × NP, where NP indicates the total number of people. The incubation and latent period of infection peoples were noted as 1/ωP and 1/ω'P. The infectious time of IP and AP was coded as 1/γP and 1/γ'P. The proportion of asymptomatic infection was coded as δP. The SP will be infected via sufficient contact with W and IP, and the spreading rates were coded as βW and βP. We also assumed that the transmissibility of AP was κ times that of IP, where 0≤ κ ≤ 1. We are utilized the susceptible, exposed, infected and recovered peoples design, SEIR, [13].

The current study uses SEIR [21] as a common channel model in epidemiological studies. Demonstrates how the disease progresses through four channels of interaction: susceptible, exposed, infectious, and recovered. It depends on three parameters: the rate at which vulnerable people are exposed, exposure, becoming contagious, and contagious recovery. The last two were inversely related to latency and infection duration, respectively. The contamination that exists in infectious zones is aimed at renting a definable classification framework [21,22]. We think individuals in the region are aware that they are aware of many of these aspects, $S_p,E_p,I_p,L_1,L_2,L_3,L_4,D_1,D_2$ and R_0.

Control Panel: Definition of 2019 New Corona Virus (2019-nCoV)

The definition of the 2019-nCoV effect differs depending on the context in which it is used.

Case definition of the Chinese Centers for Disease Control and Prevention (CDC)

A suspected or probable case is defined as a case that meets: (1) three clinical criteria or (2) two clinical and one epidemiological criteria. Clinical criteria are fever, radiation evidence of pneumonia or acute respiratory distress syndrome. Low or normal white blood cell count or low white blood cell count Epidemiological criteria: Living in Wuhan or traveling to Wuhan within 14 days before the onset; Contact a patient with fever and symptoms of a respiratory infection within 14 days of onset.

The first confirmed case definitions in the province are suspected or possible, with viral nucleic acid testing at the urban CDC and the provincial CDC for the second case and case. This definition is a suspected or possible case with viral nucleic acid detection at the urban CDC.

Case definitions used in the case execution model in this study

We define cases as individuals with symptoms that can be detected by temperature controls at international borders, or people with serious illness requiring hospitalization or both, including travel history to Wuhan.

To be clear, we believe that populations in that zone are always allocated the same. (can be developed by separating some regions into a set of shorter regions with the same characteristics). We agree that reincarnation is an ineffective entity. We do not monitor international individual movements. We used the following mathematical design for the succeeding Susceptible-Exposed-Infectious-Recovered (SEIR) to calculate the Wuhan-infected virus as expected in December 2019 [21-23]:

calculate the Wuhan-infected virus as expected in December 2019 [21-23]:

$$\frac{dS(t)}{dt}=-\frac{S(t)}{N}\left(\frac{R_0}{D_1}I(t)+z_0\right)+L_1+L_2-\left(\frac{L_3}{N}+\frac{L_4}{N}\right)S(t) \quad (1)$$

$$\frac{dE(t)}{dt}=\frac{S(t)}{N}\left(\frac{R_0}{D_1}I(t)+z_0\right)-\frac{E(t)}{D_2}-\left(\frac{L_3}{N}+\frac{L_4}{N}\right)E(t) \quad (2)$$

$$\frac{dI(t)}{dt}=\frac{E(t)}{D_2}-\frac{I(t)}{D_1}-\left(\frac{L_3}{N}+\frac{L_4}{N}\right)I(t) \quad (3)$$

with boundary conditions

$$S(0)=S_0,\ u(0)=-\frac{S_0}{N}\left(\frac{R_0}{D_1}I(0)+z_0\right)+L_1+L_2-\left(\frac{L_3}{N}+\frac{L_4}{N}\right)S_0, E(0)=0,\ I(0)=0 \text{ when } t=0;$$

$$u(l)=1,\ E(l)=1,\ I(l)=1 \text{ as } t\to l; \quad (4)$$

Assume that $E=E_0,I=I_0$ when $t = 0$; $E=E_l,I=I_l$ as $t\to l$; with

E(t) Λ(EΛ_0-E_l)=(E-E_l), I(t) Λ(IΛ_0-I_l)=(I-I_l), where S_0 - Newly birth people, E_0- Exposed people before coronavirus infection, I_0- Infected people before coronavirus infection, E_l- Exposed people from coronavirus infection, I_l- Infected people from coronavirus infection. L_1-International inbound air passengers, L_2-Domestic inbound passengers, L_3- Outbound International passengers, L_4- Domestic outbound passengers, D_1-Infectious period, D_2-Mean latent, R_0 -Essential generative quantity, Z_0 - The zoonotic strength of infectivity, N- Total number peoples. S(t)- Number of susceptible peoples, E(t)-Number of exposed peoples, I(t) – Number of infected peoples, R(t)- Number of detached entities at time t.

Numerical analysis

Agree with the analysis project to illustrate the natural problems of people infected with vulnerable coronavirus during the current dispute. It is appreciated to confirm this mathematical mechanism and scientific computing procedure, especially in solving physical or geometric multiplicity problems. We know that computational algorithms normally manipulate numerical software to solve a number of complex problems. But we need to know that each encryption software has verified the performance of the previous analysis. Coding systems for scientific research have been managed to predict problems. However, numerical mechanisms have been enabled to predict vulnerable, unprotected, and sick citizens for practical efforts.

Let α, τ, and ς recognize that this is related to fragile, unprotected and infectious coronavirus rates. Complementing this product, the Runge Kutta Felhberg technique, which is underestimated to control the limit problems Dsolve has numbers, contains MAPLE 18. Efforts to approve u ‘(0), E’ (0) and I ‘(0) to α, τ and ς are predicted as v (0) = α, p (0) = τ and h (0.) = ς with a link of trial and error. The numerical papers have proven that the number of vulnerable, unprotected and ill communities is caused by COVID 19 infection.

Results and discussions

The researchers used computational and mathematical methods to simulate the spread of disease. An open and vulnerable set of infectious agents due to the numerical investigation of the COVID 19 and specific conditions. The scheme for equations (6) - (8) are not logically unraveling, and the situation-responsive mathematical explanation (9) is expected to be successful in passing the very important MAPLE 18. The software is based on the Runge Kutta Felhberg technique with a verified procedure to verify the math limit problem.

The effects of basic reproduction numbers on coronavirus infection have been effectively described. The spread of vulnerable, touched, and infected individuals is expected to be eliminated from coronavirus infection and used to protect life, Figs. 5-8. The baseline reproductive rate is the biggest factor in reducing coronavirus infection. It expresses what can happen when an infected person reaches a sensitive, open, and fully infected target, so it is a milestone. The number of reproduction depends on the current population’s susceptibility to the coronavirus. Effective Ro moves from time to time and is determined depending on the environmental conditions achieved within the population. The main indication of coronavirus is almost entirely based on the stiffness of the pulmonary respiration. All countries have introduced new travel regulations for arrivals and departures to curb coronavirus infection.

Effects of basic reproduction and inbound travel number on COVID 19 infection

No international and domestic arrivals:

- Number of vulnerable peoples for Ro < 1 firstly decelerates and then accelerates while for Ro > 1 there is no significant change with an increase of reproductive number.
- In the presence of Ro >1 and Ro < 1, the number of exposed and infected people’s rate rise with the increase of reproductive number.
- The density of exposed and infected people’s rate for Ro < 1 is stronger as compared to Ro >1 with rising of reproductive number.

The forceful reproduction quantity depends on the people’s recent susceptibility, exposes, and infectivity, Fig.5.

International and domestic arrivals:

- In the occurrence of Ro >1 and Ro < 1, the number of susceptible peoples rate decelerates whereas exposed and infected people’s rate rise with an increase of reproductive number.
- The intensity of vulnerable, uncovered, and diseased people’s rate for Ro < 1 is stronger as compared to Ro >1 with rising of reproductive number because the reduction of reproductive number hit a powerful role in controlling the coronavirus infection.
- Our research underlines the shorten of Ro is the main task as to restrain the coronavirus infected significantly, Fig.5.

The controlling up of coronavirus infects depends on the changes of Ro. Therefore, Ro is a powerful factor for estimating realistic situations within the population.

Impact of basic reproductive number and outbound travellers on coronavirus infection

without International and domestic outbound air passengers,

- Number of vulnerable revealed and infected peoples rate for Ro < 1 jumps down and up simultaneously whereas for Ro > 1, the number of vulnerable, exposed and infected peoples rate decelerate with rising of reproductive number. The forceful reproduction quantity depends on the people’s recent susceptibility, exposure, and infectivity.
- Multinational and internal outbound air passengers are the major elements for controlling coronavirus remarkably very fast. The reproduction number (R0) is used to manage coronavirus infection.
- The strength of vulnerable, uncovered and diseased people’s rate for Ro < 1 is more energetic as correlated to Ro >1 with grow up of reproductive number because the reduction of reproductive quantity act an efficient role on governing to control the coronavirus infection, Fig.6.

with International and domestic outbound air passengers

- In the experience for Ro >1 and Ro < 1, number of susceptible, exposed and infected peoples rate accelerates with rise of reproductive number.
- The thickness of defenseless, revealed and contaminated people’s rate for Ro < 1 is more stronger as associated with Ro >1 with rise of reproductive number because the reduction of reproductive

number play an important task on regulating the coronavirus infection.

Impact of coronavirus infectivity depends on basic reproductive value

- From Table 1, Figs.7 and 8, the rate of susceptible and exposed peoples decrease and infected peoples rate increase with the increase of international and domestic inbound air passengers when the high basic reproductive number, Ro =2.0.

- When the small basic reproductive value (Ro = -2.0), the susceptible people's rate reduces, exposed people's rate rise and finally the infected people's rate reduces to small with enhancing of International and domestic inbound air passengers, Table 1, Figs.7 and 8.

- When the reproductive value is very small, nearer to zero (Ro = 0.0), it is predicted that the rate of susceptible peoples reduce very fast and the rate of exposed and infected peoples are controlled with an increase of international and domestic inbound air passengers, Table 1, Figs.7 and 8.

- It is interesting to note that the exposed peoples from COVID 19 is high with an increase of basic reproductive number, 3D graph, Fig.7.

All countries are ready to take special steps to wear masks at transport centers, seaports, as well as airports, and border crossings to control the spread of COVID-19 infection. International and domestic arrivals and departures are key factors in the spread of the unusually fast coronavirus. The Reproductive Number (Ro) is used to control coronavirus infection and to estimate the value of SEIR people caused by secondary coronavirus infection.

Conclusion

COVID-19 has become a global threat affecting almost every country in the world. The health implications of the acquisition of COVID-19 have forced many governments to issue controls. The inside of the facility has an increased chance of infection. Within these spaces, there is contact between people who interact with each other in the same space. However, there are hardly any specific countermeasures associated with these facilities or studies that analyze a possible coherent strategy. As a result of COVID 19 infection, we have identified a scientific investigation to reduce COVID 19 infection. The infection of international and domestic air passengers was controlled by basic reproduction values and investigated through the Runge Kutta Felhberg strategy by MAPLE 18.

- Exchange of circumstances and decelerate coronavirus transmission depends on the reproductive number. This research depends on the impact of the reproduction strength of infectivity. Infected peoples from coronavirus due to International and Domestic inbound air travelers are also controlled by this output.

- The frequency of coronavirus infection and expected infectious quality is strongly dependent on the modification of Ro.

- Whenever the reproductive value is decelerated into small, the infected populations will be decreased by tiny. Every period the reproductive value can further be diminished to very small, so, the number of coronavirus infectious will slowly thin and eventually disintegrate.

Our research suggests the impact of reducing the coronavirus infection transmissibility between the population at this moment. Future daily occurrences and probable outbreak size are largely dependent on R0 dynamics, our findings highlight the importance of reducing R0 to control outbreak size at this stage.

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Ethical procedure

Research meets all relevant standards on experimental ethics and research integrity and, hereinafter, certified / declared real. As a scientist, expert, and co-author in the respective field, this article has been submitted with full responsibility, in accordance with appropriate ethical procedures, and without any republishing, fraud, plagiarism, or experimental concerns in animal or human.

Declaration of competing interest

The author of this article has no financial or personal relationship with any other person or organization that may improperly influence or benefit the content of the document. This is specifically to say that "There is no competitive interest and no conflict of interest" with other people or organizations that may influence or unduly bias the content of this article.

References

1. Siegel, Ethan., Why 'Exponential Growth' Is So Scary For The COVID-19 Coronavirus. Forbes. Retrieved March 19, 2020.
2. N. Milligan, Gregg, ; D.T. Barrett, Alan, Vaccinology : An essential guide. Chichester, West Sussex: Wiley Blackwell. p. 310. (2015),ISBN 978-1-118-63652-7. OCLC 881386962.
3. Christophe Fraser; Christl A. Donnelly; Simon Cauchemez et al. Pandemic Potential of a Strain of Influenza A (H1N1): Early Findings. Science. 324 (2009) 1557–1561.
4. Becker, Niels G. Glass, Kathryn; Barnes, Belinda; Caley, Peter; Philp, David; McCaw, James; Mc Vernon, Jodie; Wood, James, The reproduction number. Using Mathematical Models to Assess Responses to an Outbreak of an Emerged Viral Respiratory Disease. National Centre for Epidemiology and Population Health. (2020) ISBN 1-74186-357-0.
5. Z. Liu, P. Magal, O. Seydi, G. Webb, A COVID-19 epidemic model with latency period, Infectious Disease Modelling 5 (2020) 323 – 337.
6. P. Delamater, Paul, J. Street Erica, F. Leslie Timothy, Yang, Y. Tony, H. Jacobsen Kathryn, Complexity of the Basic Reproduction Number (R0). Emerging Infectious Diseases. 25 (1) (2019) 1–4. doi:10.3201/eid2501.171901. ISSN 1080-6040. PMC 6302597. PMID 30560777.
7. Fine, Paul, Eames, Ken, Heymann, David L, Herd Immunity: A Rough Guide. Clinical Infectious Diseases 52 (2011) 911–916.
8. Smith, David L, Battle, Katherine E, Hay, Simon I, Barker, Christopher M, Scott, Thomas W, McKenzie, F. Ellis, Ross, Macdonald, and a Theory for the Dynamics and Control of Mosquito-Transmitted Pathogens PLOS Pathogens (2012) 8 (4):E1002588. doi:10.1371/journal.ppat.1002588. ISSN 1553-7366.
9. G. Macdonald, The analysis of equilibrium in malaria. Tropical Diseases Bulletin. 49 (1952) 813–829.
10. S.M. Blower, A.R. Mclean,T.C. Porco, P.M. Small, P.C. Hopewell, M.A. Sanchez, The intrinsic transmission dynamics of tuberculosis epidemics. Nature Medicine. 1 (1995) 815–821.
11. Y. Ma, C.R. Horsburgh, L.F. White, H.E. Jenkins, Quantifying TB transmission: a systematic review of reproduction number and serial interval estimates for tuberculosis. Epidemiol Infect. 146 (2018) 1478–1494.

12. O Diekmann; J.A.P. Heesterbeek; J.A.J. Metz, On the definition and the computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous populations. Journal of Mathematical Biology. 28 (1990) 356–382.
13. Lipsitch, Marc, Cohen, Ted, Cooper, Ben, Robins, James M., Ma, Stefan, James, Lyn, Gopalakrishna, Gowri, Chew, Suok Kai, Tan, Chorh Chuan, Samore, Matthew H, Fisman, David, Transmission Dynamics and Control of Severe Acute Respiratory Syndrome. Science. 300 (2003) 1966–1970.
14. J. Li, D. Blakeley, R.J. Smith, The Failure of R0. Computational and Mathematical Methods in Medicine (2011) (527610): 1–17.
15. O. Diekmann, J.A. Heesterbeek, The Basic Reproduction Ratio. Mathematical Epidemiology of Infectious Diseases : Model Building, Analysis and Interpretation. New York: Wiley. (2000) 73–98.
16. G. Chowell, N.W. Hengartnerb, C. Castillo-Chaveza, P.W. Fenimorea, J.M. Hyman, The basic reproductive number of Ebola and the effects of public health measures: the cases of Congo and Uganda. Journal of Theoretical Biology 229 (2004) 119–126.
17. M. Ajelli, M. Iannelli, P. Manfredi, M.L. Ciofi degli Atti, Basic mathematical models for the temporal dynamics of HAV in medium-endemicity Italian areas. Vaccine. 26 (2008): 1697–1707.
18. J.M. Heffernan, R.J. Smith, L.M. Wahl, Perspectives on the Basic Reproductive Ratio. Journal of the Royal Society Interface 2 (2005) 281–293.
19. Byrne, Michael, The Misunderstood Number That Predicts Epidemics, vice.com (2020).
20. Held Leonhard, Hens Niel, D. O'Neill Philip, Wallinga Jacco, Handbook of Infectious Disease Data Analysis. CRC Press. p. 347. ISBN 978-1-351-83932-7 (2019).
21. Tian-Mu Chen, Jia Rui, Qiu-Peng Wang, Ze-Yu Zhao, Jing-An Cui, Ling Yin, A mathematical model for simulating the phase-based transmissibility of a novel coronavirus. Infectious Diseases of Poverty, https://doi.org/10.1186/s40249-020-00640-3 (2020).
22. Joseph T Wu, Kathy Leung, Gabriel M Leung, Nowcasting and forecasting the manageable domestic and international unfold of the 2019-nCoV outbreak originating in Wuhan. China: a modelling study. Lancet, 395(2020) 689–697.
23. Zi-Wei Ye, Shuofeng Yuan, Kit-San Yuen, Sin-Yee Fung, Chi-Ping Chan, Dong-Yan Jin, Zoonotic origins of human coronaviruses. Int J Biol Sci. 16(2020): 1686-1697.

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