

Research Article

Modeling the Spread of COVID-19 Using the Fundamental Principles of Fluid Dynamics

Harris Sajjad Rabbani*¹, Kofi Osei-Bonsu², Jassem Abbasi³, Peter Kwame Osei-Bonsu⁴, Thomas Daniel Seers¹

¹Department of Petroleum Engineering, Texas A&M University at Qatar, Doha, Qatar

²Beekin Inc, London, United Kingdom, NW3 4XL

³Zodan Solutions, London, United Kingdom

⁴Aberdeen Royal Infirmary, NHS Grampian, Scotland

***Corresponding author:** Harris Sajjad Rabbani, Department of Petroleum Engineering, Texas A&M University at Qatar, Doha, Qatar

Received: 15 March 2022; **Accepted:** 22 March 2022; **Published:** 04 April 2022

Citation: Harris Sajjad Rabbani, Kofi Osei-Bonsu, Jassem Abbasi, Peter Kwame Osei-Bonsu, Thomas Daniel Seers. Modeling the Spread of COVID-19 Using the Fundamental Principles of Fluid Dynamics. Fortune Journal of Health Sciences 5 (2022): 205-215.

Abstract

The increasing number of positive cases of SARS-CoV-2 worldwide led to a catastrophic breakdown in the global economy and unprecedented social disruptions. These measures have significantly impacted the world's economy and in many cases has led to the loss of livelihood. Mathematical modeling of pandemics is of critical importance to understand the unfolding of transmission events and to formulate appropriate control measures. In this article, we introduce a physics-based approach for forecasting epidemics such as COVID-19. The proposed physics-based mathematical model stems from the

fundamental principles of fluid dynamics, and can be utilized to make projections of the number of infected people at any scale. Our model takes into account the diffusive transmission of the virus, the growth of the virus inside the human body and the response of the natural immune system of individuals. We demonstrate that the health of individuals plays a critical role in controlling the evolution of the epidemic. In places where the individuals exhibit a strong immune system, the development of pandemic is limited despite the high diffusivity of the virus. Overall, the proposed mathematical model can be beneficial for predicting and designing potential

strategies to mitigate the spread and impact of pandemics.

Keywords: COVID-19, Fluid Dynamics, Infectious Disease Modelling

1. Introduction

In December 2019, a cluster of cases of pneumonia, subsequently associated with a novel coronavirus (Severe Acute Respiratory Syndrome - Coronavirus-2, SARS-CoV-2), named Coronavirus Disease 2019 (COVID-19) by the World Health Organization (WHO), emerged in Wuhan, China. It was rapidly declared a pandemic on March 11, 2020, in view of its exponential spread worldwide [1]. As of 11th June 2021, the WHO had reported 175 million confirmed cases and over 3.79 million deaths globally, with the highest number of cases reported in the United States of America (USA) [2]. The rapid spread of the virus continues to pose a monumental global health challenge.

Different strategies can be administered to mitigate the dire effects of the virus on societies. Although vaccinations are potentially helpful in providing acquired immunity, regrettably, the development of an acceptable vaccine is generally time-consuming and challenging, e.g., it took about 1 year for the development of Pfizer–BioNTech vaccine from December 2019 to December 2020. Consequently, government and public health responses are highly interested in the characterization and applying of the non-pharmacological interventions, especially in the early times of pandemic³. These measures include physical/social distancing to minimize the rate of person-to-person contact, frequent sanitization, the utilization of masks, gloves and other forms of personal protection equipment (PPE), mass testing,

contact tracing and isolation/quarantine of persons with suspected and confirmed cases of COVID-19 infection. Although these interventions have contributed significantly to the gradual decline of the transmission rate and by extension deaths worldwide, there are increasing concerns that the easing of these measures may result in the surge of new cases [3].

In pandemic situations where data could be sparse, mathematical modelling can be a powerful tool to understand and predict the course of the outbreak in order to inform the development of potential control strategies [4]. For. Example, the model developed by Kermack et al [5]. Considers the number of susceptibles, infectious individuals, and recovered individuals (Kermack-McKendrick model) in predicating the epidemic [6]. The most frequently used framework in the case of human transmissions is the so-called SIR model [7]. According to this model, the individuals are categorized into three groups: susceptible S , infected I and recovered R . Mathematically, the transition of individuals among these three groups is computed using the Ordinary Differential Equation (ODE) to predict the overall behavior of the number of infected persons. Several, more complex variants of the SIR model have been developed in an attempt to capture the transmission dynamics of pandemics more accurately.

This is a major advantage of the SIR based models [8]. To improve the predictions, several modifications have been made to the SIR framework to consider the number of deceased (SIRD model) [9] and the effect of public health containment policies [10], including the fraction of undocumented infections and their contagiousness [11]. For considering the incubation period, the exposed term is considered in SEIR model [12]. Particularly in the

case of COVID-19, Wu et al. ¹³ utilized available data to model the case fatality risks of symptomatic persons in Wuhan, China. Giordano et al [14] further extended the model to distinguish between detected and undetected cases and the level of severity of the manifested symptoms during the course of the outbreak.

However, Moein et al. [15] showed that the SIR based models are inefficient in forecasting the COVID-19 epidemic and suggested applying more sophisticated approaches by including more precise epidemiological and biomedical data. In addition, some efforts have been made in derivation of deterministic models for the prediction of pandemics. Ivorra et al [16] suggested a non-SIR deterministic model for the prediction of the COVID-19 pandemic. The model is solved numerically and considered the control measures, case fatality rate, contact rates and transition rates of COVID-19 over societies. Aferni et al [17] provided a mathematical model based on Boltzmann's sigmoidal equation to predict the COVID-19 spreading waves. However, even these deterministic based models use the correlations that relate different parameters of spreading of disease in society. There are several drawbacks with the current modeling methods. One of them is the stability of the model under harsh conditions. Despite the complexities in the current models, the modeling of epidemic within a spatial heterogeneous society with time-dependent infection properties is also a big challenge in available modeling approaches. Developing models that are based on analytical and physical concepts may lead to more accurate prediction of unknown or less-known phenomena without requiring any databases for fitting the parameters. This is especially critical in early times of pandemics.

In this article, we introduce an infectious modeling technique to forecast disease outbreaks, specifically COVID-19, using the fundamental principles of fluid dynamics. Simplistically, we consider a carrier of the virus as a fluid containing a dissolved ionic species. With this intuition, we attempt to derive a simplified theoretical model using the well-known Fluid Transport Equation [18] to predict the transmission and propagation of COVID-19. The proposed physics-based mathematical model takes into account the diffusive transmission of the virus, the growth of virus inside the human body and the response of the natural immune system of individuals. It also demonstrates the impacts of variations in the effective parameters on the extent of pandemic. Also, due to the analytical nature of this model, it works well in a wide range of conditions and can be used as a physics-based alternative for current statistical models. Our analysis demonstrates that a strong immune system could be critical for mitigating the impact of the pandemic. To our knowledge, a physics-based model of this kind has not been discussed in the literature.

2. Results and Discussion

Using the fluid transport equation, we derived the following mathematical model to predict the infected cases of COVID-19. The details concerning the derivation of mathematical model are provided in the methods section.

$$\phi_i^{n+1} = \alpha \phi_i^n + \gamma e^{-\phi_i^n} - \phi_i^{\frac{1}{\beta}} + \phi_i^n \quad (1)$$

The number of infected cases is given by Equation 1 where ϕ is the ratio of total infected cases I , over the initial number of susceptible people S^o (assumed as the entire population of the area). There are three

dimensionless fitting parameters in Equation 1 α , γ and β . α is a diffusion factor that takes into account the diffusive transmission of infection due to person-to-person contact; γ describes the growth of the virus within an individual and β relates to the immune system of the individuals. The subscripts $n + 1$ and n

refer to the new and old cases respectively. The detailed description of the fitting parameters used to solve the model (Equation 1) is given in Table 1. The visual representation of the fitting parameters is shown in Figure 1.

Table 1: Definition of fitting parameters that are used to solve the presented physics-based model and their fitted ranges on the datasets of different regions.

Parameter	Physical Description	Mean	Min	Max
α	The diffusive transmission of the virus from person to person	1.093	0.931	1.424
γ	The growth of the virus within an individual	0.763	0.121	1.478
β	Describes the effectiveness of the immune system of the human body	-0.002	-0.016	-3e-4

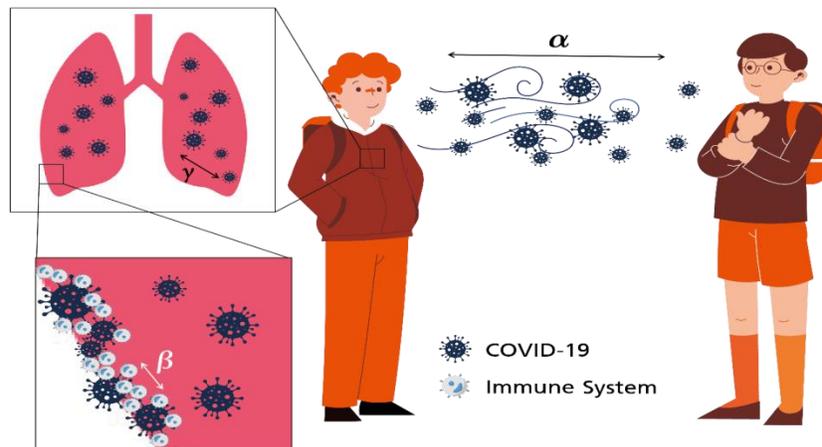


Figure 1: Cartoon depicting the physical meaning of the fitting parameters represented in the model. α Relates to the diffusive transmission of the virus, γ is the activity of virus within the individual and β is related to the strength of the individual's immune system. Both the environmental conditions as well as human interventions such as social distancing and wearing of protective gears (e.g. masks) can have influence α . Whereas the medical condition of individuals affects the γ (the growth of virus) and the β (natural immunity) values.

The value of \emptyset for each country as of 11th June 2021 provided by the EU Open Data Portal [19] is shown on the world map (Figure 2). It can be seen from Figure 2 that the northern and the western part of the world is heavily affected by COVID-19, whereas, in

Oceania, Asia and Africa, the pandemic is relatively less severe. Figure 2 suggests that the environmental changes across the continents can play a significant role in the spread of COVID-19 [20]. Figure 3 shows the comparison of the trend of infected cases as

computed by the model with recorded data for 16 countries provided by EU Open Data Portal [19] as of 11th June 2021. To take account of multiple peaks one can initialize the data according to the cumulative number of cases in the previous cycle. Overall, the model (Equation 1) is able to capture the

trend of the cases and also forecast future cases. The sensitivity analysis of fitting parameters is illustrated in Figure 4. An increase in β reduces the number of infected cases (it should be noted that β is in the range of 0 to 1), whereas an increase in α and γ increases the number of infected cases.

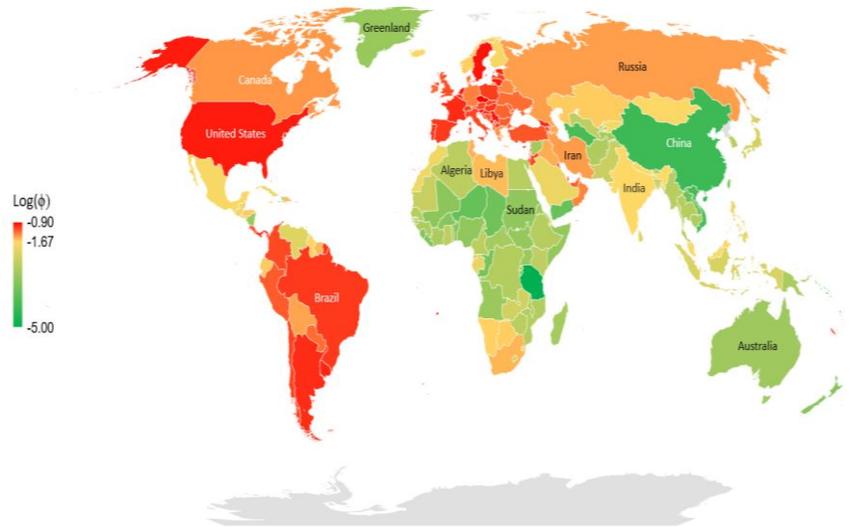


Figure 2: Worldwide distribution of COVID-19 as of 11th June 2021 provided by the EU Open Data Portal (20). In Asian and African countries, the epidemic is less severe than American and European countries. This localized severity of COVID-19 in the northern and western part of the globe may reflect the role of the environment on the impact of the pandemic.

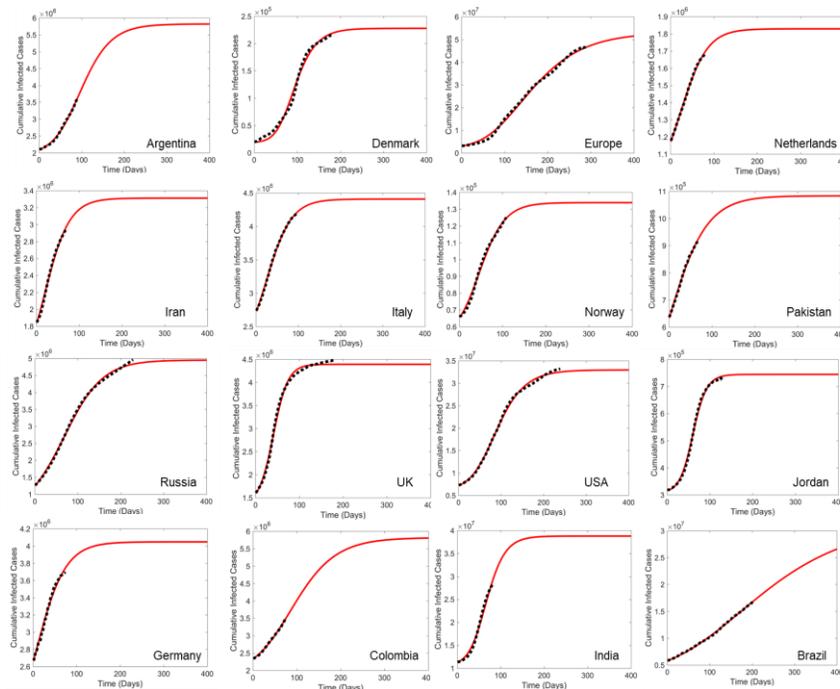


Figure 3: Comparison of real data and model predictions for selected countries. The model is able to capture the trend and forecast the future cases. Only the last Covid-19 peak in each country is utilized as the real data-set and previous data are ignored.

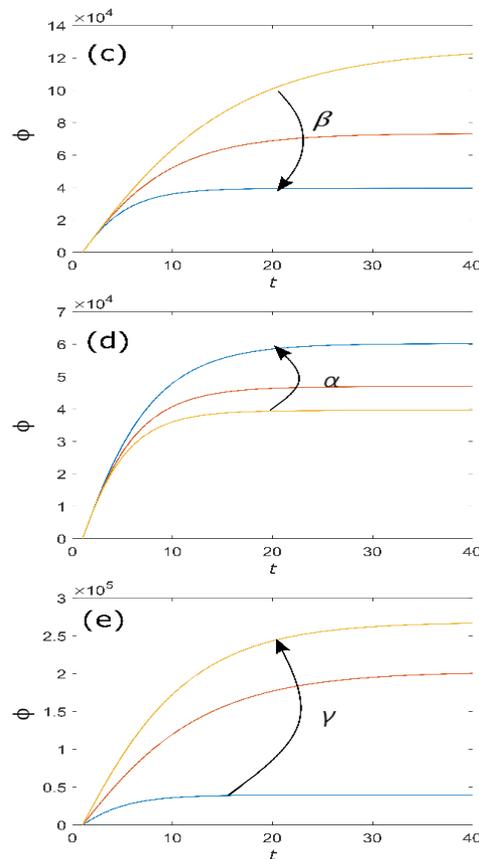


Figure 4: Sensitivity analysis of model fitting parameters on the output. Increasing β decreases the number of cases whereas an increase in α and γ result in an increase in the number of infected cases

Using the proposed mathematical model (Equation 1) we modelled the progression of COVID-19 with the data of 136 countries provided by the EU Open Data Portal [19]. By fitting the model to the data set, we deduced the projected final number of COVID-19 cases ϕ^f and the values of fitting parameters α , β and γ for each country. A statistical overview of the fitted parameters (i.e. mean, minimum, and maximum) is provided in Table 1. The variations in β as a function of ϕ^f is presented in Figure 5 (a). It can be identified from Figure 5 (a) that there is a strong inverse relationship between the natural reaction of the human body represented by β and the projected number of final cases ϕ^f . This indicates that in regions where on average people have a strong immune system, the impact of the COVID-19 outbreak may be relatively less influential. Another noteworthy observation from our model is that α , related to the diffusive

transmission of the virus, is proportional to the ϕ^f , as shown in Figure 5 (b). Thus, in countries where there are frequent interactions between infected individuals and the population without protective measures (e.g., social distancing and masks), the number of projected cases ϕ^f was mainly high. This is also true for the relation of ϕ^f with γ in Figure 5 (c) where there is a positive correlation between the growth capacity of virus within the body of individuals (affected by parameters such as age, vaccination and background diseases) and the severity of pandemic. Figure 5 (d) indicates that in regions where the diffusive transmission of virus i.e. α is high, there are a lower growth of virus in body of individuals or natural immunity rate (γ). However, the low R^2 error of the fittings (high spreading of the points) in Figure 5 shows that there are mixture of factors that affect the spreading of COVID-19 in societies.

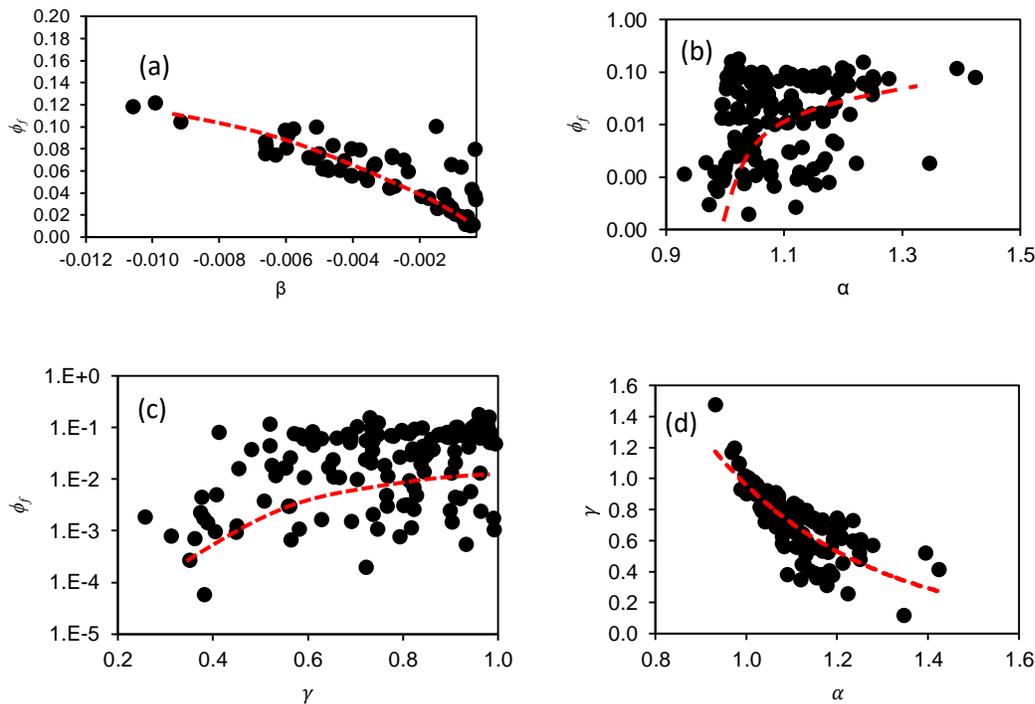


Figure 5: Relationship between model parameters. (a) The negative correlation between natural immunity β and the total predicated cases ϕ^f , indicating in countries where on average individuals have a strong immune system, the size of the epidemic is less extensive. (b) Increase in ϕ^f as α increases, highlighting an increase in the social interaction of asymptomatic individuals. (c) Increase ϕ^f in as γ increases, (d) Reflects the inverse relationship between γ and α . In regions where there is high diffusion transmission of virus individuals, the natural growth rate of virus in bodies are low. This is interpreted as the natural immunity phenomena.

According to Davies et al [21], susceptibility to the virus increases with age. Our mathematical model supports the investigation of Davies et al. [23] suggesting that it is the natural ability of young individual's body to resist the growth of virus that makes them less susceptible in comparison to old aged individuals. In countries with high diffusive transmission and low number projected cases ϕ^f (such as those located in Asia and Africa), social interaction may primarily be within age groups that are less susceptible to the virus [21]. This may affect the total number of symptomatic cases recorded since such individuals may be asymptomatic and yet maintain social interactions. However, it is important to note that in these regions the susceptible group of individuals might be at high risk of being infected, as the majority of the population may not modify their behavior. Alternatively, if the outbreak is localized, the number of cases within that zone in relation to the entire population could still be low in spite of the social interactions.

We have presented an infectious modeling approach for forecasting the course of COVID-19 using fundamental principles of fluid transport. In this physics-based model, the infected individual is considered analogous to a fluid containing special species such as ions which spread in the direction of fluid flow, such that the transmission from person to person is dependent on the activity of the virus in the host and their immune response. The proposed model

demonstrates the relationship between the diffusive transmission of the virus, the growth of the virus inside the human body and the natural immune system of the individual that are the primary factors in controlling the size of the pandemic. Our model suggests that the health/immune response of individuals might be one of the keys to limiting the effects of the pandemic. Despite the simplicity of our approach and the limited data used, the results are promising. Also, this model is capable to consider the variable properties of epidemy in highly heterogeneous systems. In future, other external information such as age demographics, socioeconomics and environmental data will be incorporated to boost the efficacy of the model.

3. Materials and Methods

The mass transport phenomenon is a critical concept in the physics, chemistry, biology and engineering fields [22]. This phenomenon is defined is the tendency of transferring mass to minimize the concentration difference within the system. Fick's First Law governs the mass transport in a system that is defined as the molar flux due to diffusion is proportional to the concentration gradient of the substance and the diffusivity of the substance in the medium. This mass diffusion-reaction-advection phenomena also has several applications in modeling different biological processes like bacteria and virus transport in living species [23, 24]. The general form

of this equation by considering the reactive, diffusive, and advective terms is [18].

$$\frac{\partial c}{\partial t} = D(\nabla^2 \cdot c) - \nabla \cdot (vc) + R \quad (2)$$

$\frac{\partial c}{\partial t}$ relates to the rate of change in the concentration of species c ($mole/m^3$) in fluid, D (m^2/s) is the diffusive flux of species, ∇^2 is the Laplace indicating spatial coordinates and R ($mole/m^3/s$) is the net growth of species (sink/source term). Also, v is the velocity of moving medium. Ignoring the advective flux term ($\nabla \cdot (vc)$), the Equation 2 is written as;

$$\frac{\partial c}{\partial t} = D(\nabla^2 \cdot c) + R \quad (3)$$

Following our intuition that a fluid is a carrier of species such as salts, an infected individual could also be conceptualized as the carrier of virus. Utilizing this approach, we substitute c with ϕ (dimensionless) which represents the ratio of total infected cases I , over the initial number of susceptible people S^o (assumed as the total population of the specific country). It is assumed that the number of deaths is a tiny fraction of total population, so the

$$\frac{\phi_i^{n+1} - \phi_i^n}{\Delta t} = d \left[\frac{\phi_{i+1}^n - 2\phi_i^n + \phi_{i-1}^n}{\Delta x^2} + \frac{\phi_{i+1}^n - 2\phi_i^n + \phi_{i-1}^n}{\Delta y^2} + \frac{\phi_{i+1}^n - 2\phi_i^n + \phi_{i-1}^n}{\Delta z^2} \right] + me^{-\phi} + \phi_i^{n+1} \beta - \phi_i^n \beta \Delta t \quad (6)$$

Here, the spatial and temporal discretization of parameters are shown by i and n , respectively. Δx , Δy and Δz are the individual distance in cartesian space, and Δt is the time difference. To further simplify Equation 6, below boundary conditions are applied:

$$\begin{aligned} \phi_{i+1}^n &= 0 \\ \phi_{i-1}^n &= 0 \end{aligned} \quad (7)$$

In this simplification, it is assumed that there is no pandemic situation in surrounding regions of the investigating unit. Also, it is assumed that $\phi_i^{n+1} \beta = 0$.

S^o remains constant through the time. Also, D is redefined as d (m^2/s) to represent the flux of infected individuals. The reactive term in Equation 3 is also redefined as the net growth of virus in the body of individuals that is defined as below:

$$R = me^{-\phi} + \frac{\partial \phi^\beta}{\partial t} \quad (4)$$

where $me^{-\phi}$ is the growth of virus within infected individuals controlled by m ($1/s$) coefficient, and $\frac{\partial \phi^\beta}{\partial t}$ suggests temporal changes in the virus activity due to the response of the natural immune system of individuals. So, equation 3 is rewritten as:

$$\frac{\partial \phi}{\partial t} = d(\nabla^2 \cdot \phi) + me^{-\phi} + \frac{\partial \phi^\beta}{\partial t} \quad (5)$$

In the above equation, d represents the flux of infected individuals in the system (society). Discretizing Equation 5 using the FTCS (Forward Time Centered Space) method results in;

In order to non-dimensionalize Equation 5, we substitute $2d\Delta t \left[\frac{1}{\Delta x^2} + \frac{1}{\Delta y^2} + \frac{1}{\Delta z^2} \right]$ and $m\Delta t$ with α and γ respectively. Although this substitution is not generally necessary, it will help us to improve the generality of the equation and makes it simpler to use in societal applications. However, in the case of having special aims, other parameterization strategies are also possible.

This results in the derivation of the final equational form, which relates the increase in the infected cases $\phi_i^{n+1} - \phi_i^n$ with the transmission of the virus due to diffusion, $\alpha\phi_i^n$, the growth of the virus within an infected individual, $\gamma e^{-\phi_i^n}$, and the suppression of

virus growth inside the infected individual due to the natural immune system, $\phi_i^{\frac{1}{\beta}}$

$$\phi_i^{n+1} = \alpha \phi_i^n + \gamma e^{-\phi_i^n} - \phi_i^{\frac{1}{\beta}} + \phi_i^n \quad (8)$$

In this equation, the ratio of total infected individuals is calculated by having the current value of the infected individuals and α , β , and γ values. The values of α , β , and γ are possibly changed during the pandemic due to changes in the government policy changes and also changes in the immunity of individuals.

The mathematical model was implemented in Matlab programming environment. The used code and algorithms are provided in the supplementary materials. A derivative-free algorithm that finds minimum of unconstrained multivariable functions (Nelder-Mead simplex algorithm)²⁵ was used as the optimization algorithm for fitting the developed model on the cumulative COVID-19 cases in each region and finding the α , β , and γ values.

Acknowledgements

The financial assistance of Qatar Foundation, the Qatar National Research Fund (NPRP10-0104-170104) and Texas Engineering Experimental Station are gratefully acknowledged by the authors. Dr. Harris Sajjad Rabbani would like to acknowledge Dr. Nida Jaleel for the insightful discussion on the topic.

Data Availability

The developed code and the dataset is provided on the GitHub online repository.

Competing Interest

The authors declare no conflict of interest.

Author Contributions

H.S Rabbani designed the research and derived the mathematical model. All authors participated in performing the analysis and writing the manuscript.

References

1. Maier BF & Brockmann D. Effective containment explains subexponential growth in recent confirmed COVID-19 cases in China. *Science* (80-.) 368 (2020): 742–746.
2. WHO. *Novel coronavirus situation report -2* (2020).
3. Ferguson N, Cummings D, Fraser C, Nature JC. undefined. Strategies for mitigating an influenza pandemic. *nature.com* (2006).
4. Vespignani A, Tian H, Dye C, Physics JL-S-... R. & 2020 undefined. Modelling covid-19. *nature.com*
5. Kermack, W. O. & McKendrick, A. G. A contribution to the mathematical theory of epidemics. *Proc. R. Soc. london. Ser. A, Contain. Pap. a Math. Phys. character* 115 (1927): 700–721.
6. Brauer F. Mathematical epidemiology: Past, present, and future. *Infect. Dis. Model* 2 (2017): 113–127.
7. Ehrhardt M. *et al. A M C M SIR-based Mathematical Modeling of Infectious Diseases with Vaccination and Waning Immunity SIR-BASED MATHEMATICAL MODELING OF INFECTIOUS DISEASES WITH VACCINATION AND WANING IMMUNITY. Elsevier* (2019).
8. Tang L *et al.* A Review of Multi-Compartment Infectious Disease Models. *Int. Stat. Rev* 88 (2020): 462–513.
9. Anastassopoulou C, Russo L, Tsakris A & Siettos C. Data-based analysis, modelling and forecasting of the COVID-19 outbreak.

- PLoS One* 15 (2020).
10. Tuite A, Fisman D, Cmaj AG- & 2020 undefined. Mathematical modelling of COVID-19 transmission and mitigation strategies in the population of Ontario, Canada. *Can Med Assoc* (2020).
 11. Li R. *et al.* Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV-2). *science.sciencemag.org*
 12. Biswas MHA, Paiva LT & De Pinho MDRA SEIR model for control of infectious diseases with constraints. *Math. Biosci. Eng* 11 (2014): 761.
 13. Wu J. *et al.* Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China. *nature.com*
 14. Giordano G, Blanchini F, Bruno R, medicine PC-N & 2020 undefined. Modelling the COVID-19 epidemic and implementation of population-wide interventions in Italy. *nature.com*
 15. Moein S. *et al.* Inefficiency of SIR models in forecasting COVID-19 epidemic: a case study of Isfahan. *Sci. Rep* 11 (2021): 1–9.
 16. Ivorra B, Ferrández MR, Vela-Pérez M & Ramos AM. Mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19) taking into account the undetected infections. The case of China. *Commun. Nonlinear Sci. Numer. Simul* 88 (2020): 105303.
 17. El Aferni A, Guettari M & Tajouri T. Mathematical model of Boltzmann's sigmoidal equation applicable to the spreading of the coronavirus (Covid-19) waves. *Environ. Sci. Pollut. Res* (2020).
 18. Versteeg HK & Malalasekera W. *An introduction to computational fluid dynamics: the finite volume method* (2007).
 19. European-Data-Portal. Europeandataportal.eu (2020).
 20. Prata D, Rodrigues W, Environment PB-S of the T & 2020 undefined. Temperature significantly changes COVID-19 transmission in (sub) tropical cities of Brazil. *Elsevier*
 21. Davies N. *et al.* Age-dependent effects in the transmission and control of COVID-19 epidemics. *nature.com*
 22. Koryta J. *Diffusion. Mass Transfer in Fluid Systems. Journal of Electroanalytical Chemistry and Interfacial Electrochemistry* 194 (1985).
 23. Anekal SG, Zhu Y, Graham MD & Yin J. Dynamics of virus spread in the presence of fluid flow. *Integr. Biol* 1 (2009): 664–671.
 24. Grave M & Coutinho ALGA. Adaptive mesh refinement and coarsening for diffusion–reaction epidemiological models. *Comput. Mech* (2021): 1–23.
 25. Lopez C. *MATLAB optimization techniques* (2014).



This article is an open access article distributed under the terms and conditions of the

[Creative Commons Attribution \(CC-BY\) license 4.0](https://creativecommons.org/licenses/by/4.0/)