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# Mathematical Modeling to Perform an Analysis of Social Isolation Periods in the Dissemination of COVID-19

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**ABSTRACT.** The outbreak of COVID-19 has made scientists from all over the world do not measure efforts to understand the dynamics of the disease caused by this coronavirus. Several mathematical models have been proposed to describe the dynamics and make predictions. This work proposes a mathematical model that includes social isolation of susceptible individuals as a strategy of suppression and mitigation of the disease. The Susceptible-Infectious-Isolated-Recovered-Dead (SIQRD) model is proposed to analyze three important issues about the dynamics of the disease taking into account social isolation: when the isolation should begin? How long to keep the isolation? How to get out of this isolation? To get answers, computer simulations are provided and their results discussed. The results obtained show that beginning social isolation on the 10th or 15th days, after confirmation of the 50th case, and with 70% of the population in isolation, seems to be promising, since the infected curve does not grow much until it enters the isolation and remains at a stable level during the isolation. On the other hand an abrupt release of the social isolation will imply a second peak of infected individuals above the first one, which is not desired. Therefore, the release from social isolation should be gradual.

Keywords: mathematical model, COVID-19, social isolation, simulations.

### **1 INTRODUCTION**

Coronavirus is a type of virus that has a zoonotic origin. At the end of 2019, the first COVID-19 victim was diagnosed with the coronavirus in Wuhan, the capital of Hubei Province, China. In

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the following weeks, the disease spread widely in China mainland and other countries. Evidences pointing to human-to-human transmission were found in studies [2, 13, 18]. On 30 January 2020, the coronavirus outbreak was declared a Public Health Emergency of International Concern [17].

Mathematical modeling is an important tool to study infectious diseases. Dynamical models of COVID-19 transmission had been studied by many scientists in different countries [1, 3, 8, 10, 11, 12, 13, 14, 16]. To model epidemics generally are used compartmental models [15]. In our work we introduced in the traditional 3-compartment SIR (Susceptible-Infected-Recovered) model two more compartments, the isolated ones and the dead ones. For each compartment there is a variable that characterizes the size of its population.

The introduction of social isolation as variables in the mathematical models of the COVID-19 dynamics is one of the suggested ways to analyze control strategies in simulations of system dynamics, which can be applied in different compartmental models, such as SIR and SEIR (Susceptible-Exposed-Infected-Recovered). In the works [10, 11, 12, 16], the transmission rate is considered time-dependent and sometimes used as an estimation of social isolation. The mathematical model considering the pandemic mitigation strategy presented in this work is a new proposal.

In the absence of a vaccine, social distancing has emerged as the most widely adopted strategy for its mitigation and control [2]. In this paper, we present an expanded SIR model of the spread of the novel coronavirus that considers social distancing. Two new equations were included to the traditional SIR model [5, 6, 7]: an equation that describes the social isolation of susceptible individuals and the other that indicates dead cases. In this simplified model, the compartment of the tested population was not considered, therefore in the social isolation compartment enter the susceptible, exposed and asymptomatic infected individuals. On the other hand, models with more compartments can be created, but to use them we still need cheaper, more reliable and accessible tests for the entire population. Regarding the compartment of dead individuals, as there is a strict COVID-19 death statistics, it is important to keep the recovered and dead classes separately. Based on this model, several aspects were considered in relation to the social isolation of the susceptible individuals, including answers to the following questions: When this strategy should begin? How long to keep the isolation?

To conduct a meaningful analysis of the proposed model we take into account an application to real data and a comparison of the model simulation results with the real information of infected individuals in Rio Grande do Sul, a state of Southern Brazil. The data used were divulged by the Brazilian Ministry of Health [4].

Several social isolation scenarios of the susceptible population will be investigated in this work considering different periods of confinement. Computer simulations will be carried out to show the best answers to the questions formulated above.

## 2 MATHEMATICAL MODELING OF THE EPIDEMIOLOGICAL PROBLEM WITH SOCIAL ISOLATION STRATEGY

The mathematical modeling of the epidemiological problem is based on the widely known SIR model. The model includes two equations that will return with information on the number of susceptible individuals who are isolated and the number of infected individuals who will die, respectively. In the first equation, additional variables are placed to activate and to disable the isolation, that is, it will be a process of turning on and off the isolation entry and exit, respectively. Furthermore, there will be the same variables in the third equation for entering and leaving isolation, however, with opposite signs. In the system, the individuals are classified into five types: susceptible (S), infectious (I), isolated (Q), removed (R), and death (D). The mathematical model SIQRD, with first order differential equations, is given by:

$$\frac{dS}{dt} = -\frac{\beta}{N}SI - \alpha S + \delta Q,$$

$$\frac{dI}{dt} = \frac{\beta}{N}SI - \gamma I - \mu I,$$

$$\frac{dQ}{dt} = \alpha S - \delta Q,$$

$$\frac{dR}{dt} = \gamma I,$$

$$\frac{dD}{dt} = \mu I,$$
(2.1)

where  $\beta$  is the transmission rate,  $\gamma$  is the recovery rate,  $\alpha$  is the rate at which susceptible people are sent to social isolation (activated when the isolation starts and disabled when the isolation ends),  $\delta$  is the rate at which individuals in social isolation return to the susceptible class (only activated when it ends),  $\mu$  is the mortality rate of infected individuals and *N* is the total population size. As in the classic SIR model, here the population (*N*) is given as constant, that is N =S+I+Q+R+D.

As a hypothesis for the formulation of the epidemiological problem, only susceptible individuals will be isolated, since infected individuals should be treated, and the others have already recovered from the disease or have died. The traditional SIR model is based on the hypothesis that the susceptible and infected individuals are mixed homogeneously, and that the rate of contamination is constant. In real life the process is much more complex, since there are individuals infected with mild form and others who are asymptomatic, and the contamination happens in several places, with different rates. Isolating patients in hospitals and homes does not eliminate the contamination of susceptible individuals. Therefore, this work only involves investigating how strict isolation influences the process of spreading the disease using the traditional SIR model. The decision on the best social isolation scenario will be based on the number of infected individuals. The structure of health units and hospitals capacity is not taken into account, although they are influenced by the number of infected individuals. The idea is to analyze a simple mathematical modeling, in which it is possible to take out some fundamental aspects of suppression of disease spread and growth, such as the beginning of social isolation, isolation time, the number of isolated individuals or how quickly isolated individuals can be released.

### 2.1 Considerations about the model coefficient values

The coefficients of the SIR model are widely discussed in the literature of COVID-19, with a significant variation depending on each work to be considered. Therefore, based on [9, 10, 14], the values used in this work are:  $\beta = 0.5$ ,  $\gamma = 0.19$ ,  $\mu = 0.01$ , and  $N = 1 \times 10^5$ . That means a transmissibility of the virus  $\beta = 0.5$  and the mean infection duration  $1/\gamma = 5.3$  days. Note that it is common for mathematical modeling works on COVID-19 to use a sample of N = 100,000 individuals. However, obtaining the values of  $\alpha$  and  $\delta$  deserves further clarification. In the period before the social isolation, the values of  $\alpha$  and  $\delta$  are zero. For the initial condition is considered that 50 individuals are infected.

• Determination of  $\alpha$ 

The value of  $\alpha$  can be determined through simulations. Let us assume that 50% of the population goes to social isolation on the 5th day after confirmation of the 50th case. Thus, when we simulate the model, we are testing values of  $\alpha$  and t > 5 that make Q rise to 50% of the population. When Q reaches this value,  $\alpha$  returns to zero.

For example, for a social isolation of 50% of the population from the 5th day onwards after confirmation of the 50th case, Q reaches the value of 50% when t reaches 10 days, with  $\alpha = 0.11$ , and when t > 10,  $\alpha = 0$ .

• Determination of  $\delta$ 

From the third equation of system (2.1), taking into account the end of the social isolation period, i.e.,  $\alpha = 0$ , this equation will be given only by

$$\frac{dQ}{dt} = -\delta Q, \qquad (2.2)$$

whose analytical solution have the form

$$Q(t) = Ce^{-\delta t}, \qquad (2.3)$$

where *C* is an integration constant. Considering that the process of social isolation started at  $t_0$ , we calculate the value of *C* as

$$Q(t_0) = Ce^{-\delta t_0},\tag{2.4}$$

what yields

$$C = Q(t_0)e^{\delta t_0}.$$
 (2.5)

Replacing equation (2.5) in equation (2.3), we obtain:

$$Q(t) = Q(t_0)e^{\delta(t_0 - t)}.$$
(2.6)

At the moment  $t_1$  we will have the population  $Q(t_1)$ , so

$$Q(t_1) = Q(t_0)e^{\delta(t_0 - t_1)}.$$
(2.7)

By assigning  $\tau = t_0 - t_1$ , and isolating  $\delta$ , we obtain:

$$\delta = \frac{1}{\tau} \ln \frac{Q(t_1)}{Q(t_0)},\tag{2.8}$$

in with  $\tau$  is the period (in days) it takes to reduce the number of isolated individuals  $Q(t_1)$ , at the end of social isolation to the number of individuals  $Q(t_0)$  that will remain in it.

For example, if  $Q(t_1) = 8x10^4$  and it is desired that in 10 days ( $\tau = 10$ ) the number of individuals still isolated to be  $Q(t_0) = 1x10^4$ , then  $\delta = 0.21$ .

### 2.2 Model application to real data

Regarding the application of model (2.1) to real data, a comparison will be shown of the model simulation results with the real information of infected individuals in Rio Grande do Sul, a state of Southern Brazil. This state has approximately  $N = 1.14 \times 10^7$  inhabitants. Figure 1 shows a comparison of the data obtained by simulating system (2.1) and the real data of infected individuals, considering 50% of social isolation and without isolation. In fact, in this state there was applied social isolation, which was around 50% of the population. Thus, the growth of infected individuals without isolation is obtained only by simulating the proposed model.

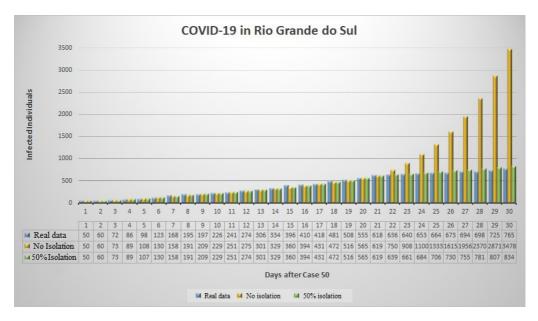


Figure 1: COVID-19 in Rio Grande do Sul, a comparison between real and simulated data.

The period considered was from March 16, 2020, and the simulations begin after confirmation of the 50th case. Social isolation started on March 22, with an estimated 50% of the isolated population. The isolation effect can be observed around 14 days after its beginning, which occurs when a greater differentiation between the values in figure 1 appears.

We considered this period for analysis, as it coincided with the closure of schools, universities and non-essential services. On the other hand, the impact with the use of personal protective equipment, such as masks, alcohol gel and physical distance between individuals was not considered. On April 20, 2020, a gradual resumption of the reopening of commerce across the state began.

One can observe in figure 1 a good correspondence between the real data and simulated data. However, it is worth mentioning that there are many variations of real data from one place to another. Thus, for each place, the model input data should be updated. The data used are divulged by the Brazilian Ministry of Health [4].

# **3 RESULTS AND DISCUSSIONS**

The first case of COVID-19 in the state of Rio Grande do Sul was notified on March 10, and universities closed on March 16 (6 days after notification of the first case). Subsequently, schools closed, and the rest of non-essential services closed on March 23 (13 days after notification of the first case).

For the model simulations, three important issues are considered. The first is about entering the social isolation and the differences between entries after 5, 10, 15 and 20 days from the start, considering 50%, 70% and 80% of the population in isolation. The second is about the duration of the isolation and the third is about the exit from the isolation, what is the impact of the exit being sudden or gradual.

The social isolation-structured system (2.1) was solved numerically using Runge-Kutta fourth order method and implemented using *Scilab* Software. The model coefficients used are those presented above. The initial conditions considered in all simulations are: (N - 50, 50, 0, 0, 0).

Without taking into account the social isolation, the system (2.1) is equivalent to the traditional SIR model, whose temporal trajectories are shown in figure 2.

# 3.1 Scenarios of entry and stay in social isolation

The scenarios in this section consider 50%, 70%, and 80% of the population in isolation, respectively, and starting on the 5th, 10th, 15th, and 20th day, after confirmation of the 50th case, respectively. Figures 3 to 7 show the temporal trajectories of the system (2.1) for these scenarios.

In figure 3 it is not possible to visualize the peak in the infected individuals that occurs right at the beginning of the social isolation, therefore in figure 4 a simulation is presented only until the 35th day, allowing the visualization of the situation of the beginning of the isolation.

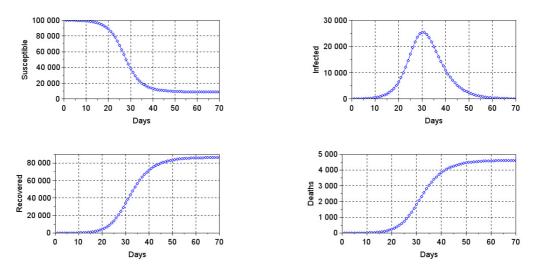


Figure 2: Temporal trajectories of system (2.1) without social isolation, i. e.  $\alpha = 0$  and  $\delta = 0$ .

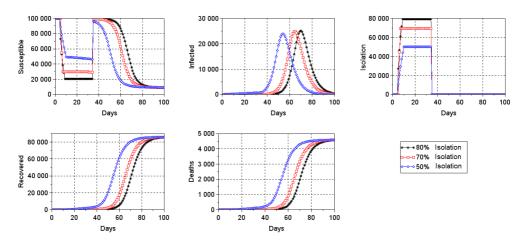


Figure 3: 50%, 70% and 80% of the population isolated for 30 days, starting isolation on the 5th day after confirmation of the 50th case.

In figures 3 and 4, it can be observed that starting social isolation on the 5th day after confirmation of the 50th case may not be the best option, since there are still few infected individuals, unless it is possible to identify and isolate infected individuals after the isolation. Thus, figures 5 and 6 show the beginning of the social isolation on the 10th and 15th day after confirmation of the 50th case, respectively.

One can observe in figures 5 and 6 that although it seems more appropriate to start social isolation on the 10th or 15th day after confirmation of the 50th case, the number of infected individuals continues to reach high levels. This is because isolation has only delays the peak of infected

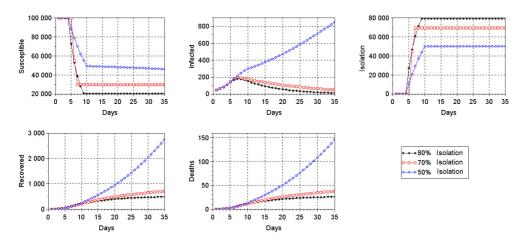


Figure 4: 50%, 70% and 80% of the population isolated for 30 days, starting isolation on the 5th day after confirmation of the 50th case, with 35 days of simulation.

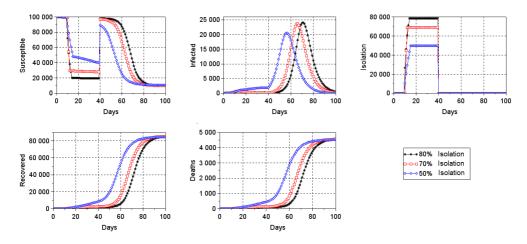


Figure 5: 50%, 70% and 80% of the population isolated for 30 days, starting isolation on the 10th day after confirmation of the 50th case.

individuals. In this sense, it will be necessary to analyze the isolation output, which will be done in the next subsection.

As a last simulation for analyzing the social isolation of the population (entry and stay), figure 7 shows a 30-day isolation, starting on the 20th.

From figure 7, one can note that starting social isolation only on the 20th day after confirmation of the 50th case is also not a good option as the number of infected individuals in the first peak is higher than in the other scenarios.

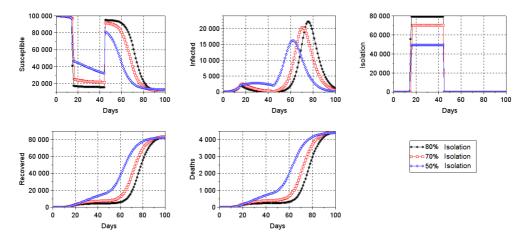


Figure 6: 50%, 70% and 80% of the population isolated for 30 days, starting isolation on the 15th day after confirmation of the 50th case.

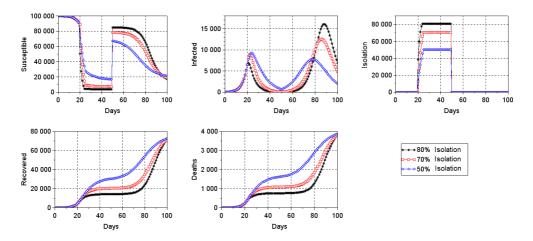


Figure 7: 50%, 70% and 80% of the population isolated for 30 days, starting isolation on the 20th day after confirmation of the 50th case.

On the other hand, there was no need to carry out simulations with longer social isolation periods, since this will only delays the second peak of infected individuals, especially when dealing with 70% and 80% of the population in isolation. In addition, economic factors become extremely relevant for longer social isolation periods and will not be analyzed in this work.

Therefore, in sequence social isolation release scenarios will be performed and analyzed.

### 3.2 Social isolation release scenarios

Three scenarios were carried out for the individuals to leave each of the three situations of social isolation: 50%, 70% and 80%, respectively, with all scenarios starting isolation on the 15th day after confirmation of the 50th case (which was chosen to be the best option of the previous simulations).

Leaving the social isolation containing 50% of the population was considered abruptly, with  $\delta =$  1, and gradual, with the maintenance of 10%, 20%, and 30% of the population still in isolation after 30 days after a 30-day isolation, as shown in figure 8. The amount 10%, 20%, and 30% was taken here as arbitrary, but in case of real application, this amount must be adapted for each situation. Therefore, the  $\delta$  value is calculated from the equation (2.8) and is given by 0.0536479, 0.030543, and 0.0170275, respectively.

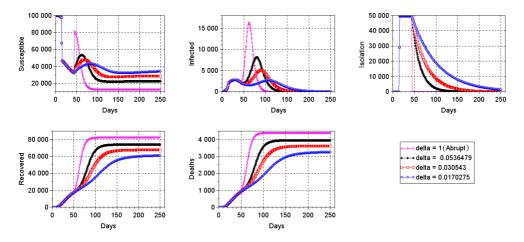


Figure 8: Abrupt and gradual release of the 30-day isolation of 50% of the population.

Analyzing the gradual release of 50% of the isolated population, it can be noted that longer periods than 30 days of isolation are not necessary if the release is sufficiently gradual. Thus, in the next figures, figure 9 and figure 10, for 70% and 80% of the isolated population, respectively, only the gradual release of a 30-day isolation will be presented.

With abrupt release, it was considered  $\delta = 1$  and gradual, with the maintenance of 20%, 30% and 50% of the population still in isolation after 30 days after a 30-day isolation. Moreover, the amount 20%, 30%, and 50% was taken here as arbitrary and  $\delta$  values obtained from the equation (2.8).

In the three scenarios, the slower exit from social isolation implies a smaller number of infected individuals, which was to be expected from these simulations. Considering the three scenarios for releasing the isolation, the one with 70% of the population in isolation proved to be the best, as it resulted in less deaths. On the other hand, there are several particularities to be considered,

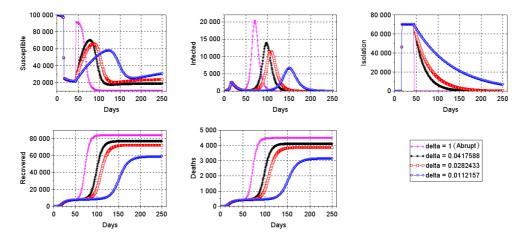


Figure 9: Abrupt and gradual release of the 30-day isolation of 70% of the population.

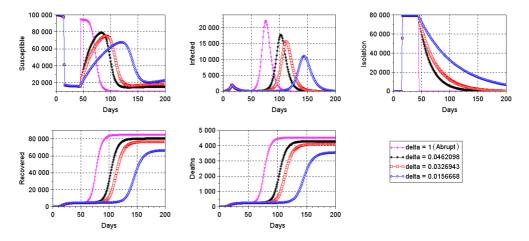


Figure 10: Abrupt and gradual release of the 30-day isolation of 80% of the population.

such as the possibility of having a social isolation with 50%, 70%, or 80% of the population; the feasibility of maintaining a 30-day isolation; how to reintroduce the isolated population in their routine activities and how fast this can be done.

### 4 CONCLUSIONS AND REMARKS

This work aimed to present and analyze a mathematical model that describes the behavior of COVID-19, including isolation of susceptible individuals as a strategy for suppressing the growth of the disease and mitigating its impacts on society.

Several aspects were considered in relation to social isolation. Seeking to analyze the important issues of this form of disease mitigation: when to start isolation; how long to keep the isolation and how to get out of the isolation.

In section 2, model simulations were performed and compared with real data from COVID-19 of the state of Rio Grande do Sul. A good correspondence was noticed between the simulated data and the real ones. However, it should be mentioned that in order to have good correspondence between model simulations results and real data, the model coefficients should be adjusted for each situation under analysis.

To reach the conclusions, scenarios with a population size of  $1 \times 10^5$  were simulated, from which it can be concluded that:

- Entry into the social isolation on the 5th day, as shown in figure 4, could be the ideal way, since it is possible to completely isolate infected individuals after isolation, otherwise there will only delays the growth of the infected individuals curve, as shown in figure 3. We emphasize that in this work we considered infected individuals to be those who are proven (through testing) infected by the disease. All others are considered susceptible, recovered or dead.
- The beginning of the social isolation on the 10th or 15th days after confirmation of the 50th case seems to be promising, since the infected curve does not grow much until it enters the isolation and remains at a stable level during the isolation, as shown in figures 5 and 6. On the other hand, it is more efficient to carry out a gradual release of isolated individuals than to increase the isolation period beyond 30 days.
- Entry into social isolation on the 20th day after confirmation of the 50th case proved to be late, as the population of infected individuals will have reached a level above than that of the other scenarios, as shown in figure 7, which for most health systems may not be appropriate, as they are not prepared for this number of sick individuals.
- Analyzing the social isolation release scenarios, figures 8 to 10, it can be noted that in any situation, an abrupt release will imply a second peak of infected individuals above the first one, which is not desired. Therefore, the option should be a gradual release of the isolated population. Figure 9 shows that a 30-day social isolation and the slowest release is the most efficient way to deal with the scenario under consideration.

The mathematical model used in the present work stands out for the simplicity of the equations, however, these were sufficient for a significant analysis of the COVID-19 dynamics, including a disease control strategy. The modeling can be improved including other hypotheses, such as exposure of individuals to the virus, hospitalizations, release from social isolation from certain layers of society, parametric variations, among others. However, any additional variable or equation will make the model more loaded and with loss of simplicity, also with the insertion of more parametric uncertainties. To investigate the influence of social isolation on the economy, bio-economic models can be created, which may be the topic of further work.

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### REFERENCES

- C. Anastassopoulou, L. Russo, A. Tsakris & C. Siettos. Data-based analysis, modelling and forecasting of the COVID-19 outbreak. *Plos One* (2020). doi:10.1371/journal.pone.0230405.
- [2] J. F-W. Chan, S. Yuan, K-H. Kok, K. K-W. To, H. Chu, J. Yang, F. Xing, J. Liu, C. C-Y. Yip, R. W-S. Poon, H-W. Tsoi, S. K-F. Lo, K-H. Chan, V. K-M. Poon, W-M. Chan, J. D. Ip, J-P. Cai, V. C-C. Cheng, H. Chen, C. K-M. Hui & K-Y. Yuen. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. *The Lancet Infectious Diseases*, **395**(10223) (2020), 514–523. doi:10.1016/S0140-6736(20)30154-9.
- [3] D. Fanelli & F. Piazza. Analysis and forecast of COVID-19 spreading in China, Italy and France. *Chaos, Solitons and Fractals*, 134(1-5) (2020). doi:10.1016/j.chaos.2020.109761.
- [4] Panel of cases of coronavirus disease 2019 (COVID-19) in Brazil by the Ministry of Health. (2020). https://covid.saude.gov.br/.
- [5] W. Kermack & A. McKendrick. Contributions to the mathematical theory of epidemics-I. Bulletin of Mathematical Biology, 53(1-2) (1927), 33–55. doi:10.1007/BF02464423.
- [6] W. Kermack & A. McKendrick. Contributions to the mathematical theory of epidemics-II. The problem of endemicity. *Bulletin of Mathematical Biology*, **53**(1-2) (1991), 57–87. doi:10.1007/BF02464424.
- [7] W. Kermack & A. McKendrick. Contributions to the mathematical theory of epidemics-III. Further studies of the problem of endemicity. *Bulletin of Mathematical Biology*, 53(1-2) (1991), 89–118. doi:10. 1007/BF02464425.
- [8] T. Kuniya. Prediction of the epidemic peak of coronavirus disease in Japan. Journal of Clinical Medicine, 9 (2020). doi:10.3390/jcm9030789.
- [9] R. Y. Li, S. Pei, B. Che, Y. Song, T. Zhang, W. Yang & J. Shaman. Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV2). *Science* (2020), 1–9. doi:10. 1126/science.abb3221.
- [10] Q. Lin, S. Zhao, D. Gao, Y. Lou, S. Yang, S. S. Musa, M. H. Wang, Y. C. Weiming Wang, L. Yang & D. He. A conceptual model for the coronavirus disease 2019 (COVID-19) outbreak in Wuhan, China with individual reaction and governmental action. *International Journal of Infectious Diseases*, 93 (2020), 211–216. doi:10.1016/j.ijid.2020.02.058.
- [11] L. R. Lopez & X. Rodo. A modified SEIR model to predict the COVID-19 outbreak in spain: simulating control scenarios and multi-scale epidemics. *MedRxiv* (2020). doi:10.1101/2020.03.27. 20045005.
- [12] W. C. Roda, M. B. Varughese, D. Han & M. Y. Li. Why is it difficult to accurately predict the COVID-19 epidemic? *Infectious Disease Modelling*, 5 (2020), 271–281. doi:10.1016/j.idm.2020.03.001.

- [13] C. Rothe, M. Schunk, P. Sothmann, G. Bretzel, G. Froeschl, C. Wallrauch, T. Zimmer, V. Thiel, C. Janke, W. Guggemos, M. Seilmaier, C. Drosten, P. Vollmar, K. Zwirglmaier, S. Zange, R. Wölfel, M. Hoelscher. Transmission of 2019-nCoV Infection from an Asymptomatic Contact in Germany. *New England Journal of Medicine*, **382**(10) (2020), 970–971. doi:10.1056/NEJMc2001468.
- [14] A. R. Tuite, D. N. Fisman & A. L. Greer. Mathematical modelling of COVID-19 transmission and mitigation strategies in the population of Ontario, Canada. *CMAJ: Health Services* (2020), 1–9. doi:10. 1503/cmaj.200476.
- [15] J. X. Velasco-Hernández & M. C. A. Leite. A model for the A(H1N1) epidemic in Mexico, including social isolation. *Salud Publica Mexico* 53 (2011), 40–47. doi:10.1590/s0036-36342011000100007.
- [16] H. Wang, Z. Wang, Y. Dong, R. Chang, C. Xu, X. Yu, S. Zhang, L. Tsamlag, M. Shang, J. Huang, Y. Wang, G. Xu, T. Shen, X. Zhang & Y. Cai. Phase-adjusted estimation of the number of Coronavirus Disease 2019 cases in Wuhan, China. *Cell Discovery*, 6(10) (2020). doi:10.1038/s41421-020-0148-0.
- [17] World Health Organization. (2020). https://www.who.int/.
- [18] J. Wu, K. Leung & G. Leung. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *The Lancet Infectious Diseases*, **395**(10225) (2020), 689–697. doi:10.1016/S0140-6736(20)30260-9.

