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Scenario analysis of COVID-19 transmission dynamics in Malaysia with the possibility of reinfection and limited medical resources scenarios

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ABSTRACT

COVID-19 is a major health threat across the globe, which causes severe acute respiratory syndrome (SARS), and it is highly contagious with significant mortality. In this study, we conduct a scenario analysis for COVID-19 in Malaysia using a simple universality class of the SIR system and extensions thereof (i.e., the inclusion of temporary immunity through the reinfection problems and limited medical resources scenarios leads to the SIRS-type model). This system has been employed in order to provide further insights on the long-term outcomes of COVID-19 pandemic. As a case study, the COVID-19 transmission dynamics are investigated using daily confirmed cases in Malaysia, where some of the epidemiological parameters of this system are estimated based on the fitting of the model to real COVID-19 data released by the Ministry of Health Malaysia (MOH). We observe that this model is able to mimic the trend of infection trajectories of COVID-19 pandemic in Malaysia and it is possible for transmission dynamics to be influenced by the reinfection force and limited medical resources problems. A rebound effect in transmission could occur after several years and this situation depends on the intensity of reinfection force. Our analysis also depicts the existence of a critical value in reinfection threshold beyond which the infection dynamics persist and the COVID-19 outbreaks are rather hard to eradicate. Therefore, understanding the interplay between distinct epidemiological factors using mathematical modelling approaches could help to support authorities in making informed decisions so as to control the spread of this pandemic effectively.

1. Introduction

In December 2019, a new coronavirus called SARS-CoV-2 (or previously referred to as 2019-nCoV) and the disease associated with this virus, COVID-19 (or also known as Coronavirus Disease 2019) have emerged [1]. The COVID-19 pandemic is now a major health threat across the globe and as of January 31, 2021, there have been 102,691, 967 confirmed cases and 2,222,403 deaths [2]. For Malaysia only, 214, 959 confirmed cases have been recorded with 760 deaths occurred (as of January 31, 2021) [3]. In general, distinct variants of coronaviruses have spread rapidly throughout different continents, with around 219 countries and territories now having reported the presence of COVID-19 infected cases [4].

To curb the severity of COVID-19 pandemic, the Malaysian government has implemented different non-pharmaceutical intervention measures, which include social distancing, wearing face masks in public, movement control restrictions and quarantine [5–7]. However, after Malaysia has succeeded to flatten the COVID-19 infection curve in the first two waves of infections till September 2020 [8], it can be seen that the number of daily active cases have increased dramatically starting from October 2020 [9,10]. During this third wave, a rebound effect in transmission dynamics of COVID-19 can be observed with the infection is spreading rapidly in the community and the number of active cases spike sporadically [11].

While some reckon that the aforementioned problem happens due to the preventive measures that have been implemented before are being eased up [12–14], other epidemiological factors such as limited medical resources and reinfection problems could also influence the outbreaks of COVID-19 pandemic [16–19]. This investigation is inspired by several reported cases of reinfection that occur across the globe such as in Hong Kong [20], Brazil [21], the United States [22] and the United Kingdom [23–26]. Some public health experts also raise concern that the immunity to SARS-CoV-2 is unlikely to be permanent and may only last for a few months [23]; this issue can cause people who have already

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recovered from COVID-19 to have certain likelihood to get infected again [24–26]. Given SARS-CoV-2 is a newly emerging viral infection, much remains unknown about these disease outbreaks in the context of Malaysia as a developing country with limited medical resources and also the probable reinfection problems; this is in fact the main focus of this research work.

The article is organized as follows. After describing the modeling framework and some techniques employed in the analysis of the system, we compare the predictions of our system with the number of active cases in Malaysia and demonstrate the agreement between the two observations. Then, we assess the combined impacts of reinfection force and limited medical resources problems on the long-term behavior of COVID-19 outbreaks in Malaysia using numerical simulation approaches. We also highlight further empirical evidence and some epidemiological implications of our simulation findings. Finally, we summaries the progress of studies to date and provide some recommendations on effective preventive measures to curb the spread of this pandemic.

2. The model and analysis

2.1. Computation of steady states and stability analysis

To investigate the combined influences of distinct epidemiological factors such as the shortage of medical resources and the possibility of reinfection on COVID-19 outbreaks, we consider a simple universality class of the SIR model and extensions thereof. In particular, the modelling framework is in the form of an ordinary differential equations (ODE) system of SIRS-type [16–19,27,28]:

$$\begin{cases} \frac{dS}{dt} = \eta N - \frac{\delta SI}{N} + \varepsilon R - \nu S \\ \frac{dI}{dt} = \frac{\delta SI}{N} - (\psi + \nu) I - \frac{\rho I}{\Phi + I} \\ \frac{dR}{dt} = \psi I + \frac{\rho I}{\Phi + I} - (\varepsilon + \nu) R \\ N = S + I + R \end{cases} \quad (1)$$

where N represents the total number of populations, which consists of three compartments: (i) the susceptible population represented by the variable $S(t)$; (ii) the infected population denoted by the variable $I(t)$; and (iii) the removal class denoted by $R(t)$ and this variable is made up of recovered and death cases. In the modelling framework (1), the term η is the birth rate, ν is the death rate, δ is the transmission rate and ψ is the recovery rate of population. To examine the possibility of reinfection on COVID-19 transmission dynamics, it is assumed that some proportion of recovered cases from the removal class can re-enter the susceptible compartment with the rate of ε; thus, ε corresponds to the reinfection force [16]. To investigate the impacts of the limited medical resources on the spread of COVID-19 outbreak, the term $\frac{\rho I}{\Phi + I}$ is employed, which is motivated by Zhou and Fan [18]: the parameter ρ represents the medical resources supplied per unit time and Φ corresponds to half-saturation constant. This half-saturation coefficient measures the efficiency of the medical resource supply; in fact, these quantities also represent the efficiency of the supply of available medical resources, and this situation would depend on other factors such as the control strategies (e.g., quarantine, movement control order) and the production of drugs, vaccines, etc [16]. In the absence of the reinfection force and shortage of medical resources assumptions (i.e., $\varepsilon = \rho = 0$), then the system is represented by a simple SIR model, which we will also discuss in detail later on. All of the parameters are assumed to be non-negative to depict the biologically meaningful phenomena of COVID-19 transmission dynamics.

In general, there are different variations of COVID-19 epidemiological models that have been used by researchers across the globe and one of the famous modelling frameworks is to employ an Susceptible-Exposed-Infected-Recovered (SEIR) system [29–31]. This kind of framework adds another state (i.e., Exposed) to the simple SIR-type system to model the influence of incubation period; this period can be defined as the length of time at which exposed people become infectious and show clinical symptoms, which include fever and coughing [29,30]. While the SEIR system has the strength of being epidemiologically more realistic (compared to the SIR-type model), this modelling framework has some drawbacks of having additional unknown components in the system: the incubation (or latent) period and the initial latent population [30]. Moreover, from the perspective of this work, which focusses on Malaysia as a case study, it would be rather hard to obtain the actual data on the Exposed compartment since there is too little information being released and shared by the government with regards to this matter. This problem may also be contributed by the issue of low COVID-19 testing rates in Malaysia compared to its neighbours e.g., Singapore [14,32]. Due to these reasons, we have made a deliberate choice to employ a family of SIR-type system as in the model (1), and we acknowledge that adding a latency or incubation period into this system could delay the initial spread of the disease; this is because the length of this period in human viral diseases significantly correlates with the disease severity [33]. However, it has been demonstrated in some modelling studies that an SIR-type system performs much better than an SEIR model in representing the information contained in the daily confirmed COVID-19 data; this also indicates that predictions of COVID-19 transmission dynamics using more complex models may not be more reliable compared to using a simpler model [30]. Several researchers have also demonstrated that the dynamics of the COVID-19 outbreak belongs to a simple class of the SIR-type model [34]. Consistent with this finding, a modelling work, which uses Germany as a case study illustrates that a modified SIR model can be used to infer change points in the epidemic spread and to gauge the effectiveness of specific confinement measures [35]. Similar approach has also been considered to make predictions of the outbreak in Italy that proved fundamentally right when compared with the observations from the actual COVID-19 cases [36]. All these points illustrate the capability of a simple SIR-type system and lend support to our proposition that this simple framework can be used meaningfully to draw qualitative conclusions on the evolution of COVID-19 pandemic.

In this work, we employ a simple SIR model with the addition of temporary immunity (through the reinfection problems) and limited medical resources scenarios; with the incorporation of these distinct epidemiological components, the model (1) becomes an SIRS-type system with a rate of transfer from R to S (i.e., ε) is added to this SIR model. As we will demonstrate in our findings in the later section, the reinfection force, ε, can play an influential role in determining the transmission dynamics of COVID-19. To better understand the long-term behaviour of the model and the spread of diseases, this goal can be achieved by examining the steady state solutions of the epidemiological system (1). The steady states can be calculated by setting the time derivatives in the model (1) equal to zero and solving the resulting system simultaneously. Two steady states are obtained: (i) $\left(\frac{\eta N}{\nu}, 0, 0\right)$ - this is known as the disease-free equilibrium and it is the desired state that would be aimed in planning any control measures; from epidemiological viewpoints, this disease-free steady state depicts the eradication of the disease and prevent the spread of infection; (ii) (S^*, I^*, R^*) - this is known as the pandemic equilibrium and this steady state demonstrates the persistence of the disease and the COVID-19 infection can spread in the community with more cases generated daily. The stability of these steady states can be evaluated using the Jacobian matrix, J, and it is given as follows:

$$J = \begin{pmatrix} -v - \frac{\delta I}{N} & -\frac{S\delta}{N} & \varepsilon \\ \frac{\delta I}{N} & -v + \frac{S\delta}{N} - \psi + \frac{\rho I}{(I+\Phi)^2} - \frac{\rho}{I+\Phi} & 0 \\ 0 & \psi - \frac{\rho I}{(I+\Phi)^2} + \frac{\rho}{I+\Phi} & -v - \varepsilon \end{pmatrix} \quad (2)$$

Using the Jacobian matrix (2) and local stability analysis, the dynamical behaviour of the model (1) and the nature of steady states can be assessed to understand the qualitative outcomes of this epidemiological system. The stability of a particular steady state can be deduced from the eigenvalues, λ_i; this crucial information is obtained by solving for the characteristic equation of the matrix (2). As an example, for the disease-free equilibrium, $\left(\frac{\eta N}{v}, 0, 0\right)$, there are three eigenvalues: $\lambda_1 = -v$, $\lambda_2 = -v - \varepsilon$ and $\lambda_3 = \frac{-v\rho - v^2\Phi - v\psi\Phi + \delta\Phi\eta}{v\Phi}$. Since all the epidemiological parameters are positive, $\left(\frac{\eta N}{v}, 0, 0\right)$ is unstable if $\lambda_3 > 0$ indicating that $\rho < \frac{\Phi(\delta\eta - v^2 - v\psi)}{v}$; consequently, the pandemic steady state can be stable. This analysis also motivates the choice of our parameter values (apart from fitting the Malaysia daily COVID-19 data to the model) in Section 2.3 later.

2.2. Analysis of basic reproduction number

Another way to comprehend the epidemiological outcomes of the model (1) and explore the severity of transmission dynamics of COVID-19 is by using basic reproduction number R_0 [37–39]. This quantity is an epidemiological metric used to describe the contagiousness of diseases [40]. It is defined as the number of secondary cases one case would produce in a completely susceptible population [38]. For instance, considering the assumption of limited medical resources is relaxed ($\rho = 0$) and performing an eigenvalues analysis to the SIRS model (i.e., by setting some $\lambda_i = 0$), we can get the following equation: $-v^2 - v\psi + \delta\eta = 0$. Rearranging this equation, we obtain the following basic reproduction number, $R_0 = \frac{\delta\eta}{v(\psi+v)}$. Similarly, other threshold quantities for R_0 can be calculated using similar techniques and interested readers are referred to the previous analysis by Mohd and Sulayman (2020) [16] for further discussion on this matter.

2.3. Parameter estimation and numerical simulation

In order to calculate each compartmental group dynamics and estimate the parameters of the system, we employed a Neural Network (NN) technique: this parameter estimation approach is inspired by the previous work of Magri and Doan (2020) [41] whereby they have developed a NN algorithm that solves the optimisation problem for the SIR-type models. This formulation is based on the combination of solving the ODE system (through time integration) and feed forwarding neural network techniques to assimilate the data into the modelling framework to learn the estimated values of parameter and state (or epidemiological) variables. To do this, the model (1) is transformed into vector forms and this vectorised system is then treated as a constrained optimisation problem with the objective to minimise the pre-defined error function, which measures the error between the computed solutions of the model (1) and the data of actual cases (consisting of infected and removed cases). For further information on this NN algorithm, we refer interested readers to the work of Magri and Doan (2020) [41] since detailed discussions on this matter are beyond the scope of the current paper.

The NN algorithm is based on the short-term prediction approach and this technique is often employed in order to estimate the parameter values of the model. We have also validated this NN algorithm for different time frame of the actual COVID-19 data sets in Malaysia. The main lesson that we learnt is that the NN framework has produced good results and the predictions of the algorithm are in agreement with the number of the daily COVID-19 cases in Malaysia. For instance, Fig. 1A–B shows the predicted active (I) and removed (R) cases (respectively), which are obtained using a NN framework (orange curve); in comparison, we also plotted the corresponding actual daily cases in Malaysia (blue curve) in the interval between February, 1 2020 till November, 30 2020. Overall, we can see that the SIR-type model analysis agrees with the number of active cases in Malaysia and this system is able estimate the epidemiological parameters of the model (e.g., δ and ψ) practically. Once the NN framework has learnt the estimated values of important parameters for specific range of daily COVID-19 cases data sets, we then performed numerical simulation of the model (1) and the results are discussed in the next sections so as to demonstrate the long-term behaviour of this epidemiological system. For illustration purpose, in this work, we parametrised this system using daily COVID-19 cases released by the MOH in the interval between December 1, 2020 and January 31, 2021 [3,42]. Unless otherwise stated, parameter values used in the simulation are given in Table 1. In all cases, we employed numerical simulation using MATLAB ode15s solver.

3. Results and discussion

We analyse a compartmental epidemic model (1) and forecast the active cases trajectories for different scenarios in Fig. 2A (dotted curves); in comparison, we also plot the corresponding actual active cases in Malaysia (purple star). Overall, we can see that the modelling framework analysis agrees with the number of active cases in Malaysia. This system is able to mimic the trend of infection trajectories of the COVID-19 in this country. To demonstrate distinct possibilities of COVID-19 transmission dynamics, we consider several hypothetical scenarios (dotted green, black, blue and red curves), which vary according to the complexity of the modelling frameworks and also some epidemiological issues under consideration. First, we examine an elementary case shown by the SIR model [28,40] (green curve) in Fig. 2A where the assumption of limited medical resources is relaxed ($\rho = 0$) and the reinfection force is absent ($\varepsilon = 0$) in this system. It can be seen that the infection trajectory increases on daily basis and it would take around several months for the active cases to peak. Then, the infection frequency starts to decline under this simple scenario analysis (i.e., the SIR system assumes that the medical resources to fight this pandemic are being allocated enough, apart from the optimal screening and isolation strategies have been employed [16]). Consequently, the SIR model predicts that it would take roughly more than a year to flatten the infection curve and reduce the number of infected people to a low level of active cases.

To further examine the transmission dynamics and other possible outcomes of the model (1), we extend this scenario analysis to investigate the severity of COVID-19 outbreaks in Malaysia and its joint effects with several epidemiological forces. This analysis depicts some of the probable epidemiological predictions, which are mediated by the interplay between reinfection force and limited medical resources situations. To do this, we examine the predictions of the model (1) in the presence of reinfection force (ε) and followed by the incorporation of limited medical resources scenarios (ρ). The roles of susceptibility to reinfection on the dynamics of COVID-19 can be examined when $\varepsilon > 0$. Increasing ε yields a larger force of infection, which in turn can affect the COVID-19 epidemiology. To date, it is still uncertain whether the first infection of COVID-19 confers immunity to subsequent reinfections and experts reckon that this problem can happen in a long run [24,26]. Before SARS-CoV-2 emerges, there are four distinct strains of coronaviruses (i.e., 229E, NL63, OC43, and HKU1) that regularly circulate through humans and can be found globally [23]. Once being infected with any of them, this infection can result in immunity of differing lengths, typically lasting for at least one to two years [23].

Motivated by these prior observations, one of the important questions that remain to be answered is that: if reinfections are going to

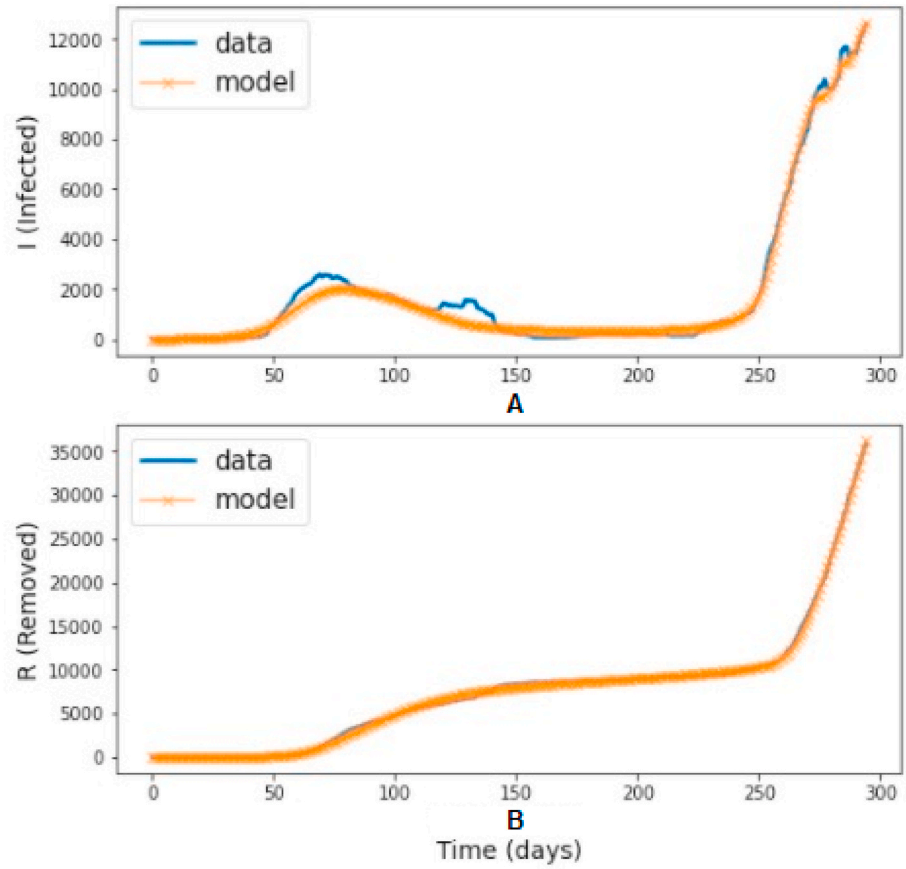

Fig. 1. Actual infected (I) and removed (R) cases in Malaysia (blue curves) and the predictions of a Neural Network (NN) framework (orange curves) used in the parameter estimation for the COVID-19 data in the interval between February 1, 2020 till November 30, 2020.

Table 1
Parameter values.

Symbol	Description	Value
η	The birth rate	0.000006 [16]
υ	The death rate	0.00002 [16]
δ	The transmission rate	0.11 (Estimated - Section 2.3)
ψ	The recovery rate	0.026 (Estimated - Section 2.3)
ϵ	The reinfection force	Vary (Hypothetical Values)
ρ	The medical resources supplied per unit time	0.0584 [18]
Φ	Half-saturation constant	3.0173 [18]
$S(0)$	Initial susceptible population	Vary [3,42]
$I(0)$	Initial infected population	Vary [3,42]
$R(0)$	Initial removal class population	Vary [3,42]

happen for COVID-19, how frequently are they happening? To explore these possibilities, we allow for some degree of reinfection ($\varepsilon > 0$) in the epidemiological model (1). It can be observed that a rebound effect in transmission (Fig. 2A: black curve) occurs after several years and this situation depends on the intensity of ε. In this case, the basic reproduction number, R_0, calculated from this model is 1.27 (as discussed in Section 2) and this estimate agrees with the forecasted R_0 of Malaysia published by Ministry of Health (MOH) in January–February 2020 whereby MOH found that the infectivity rate lies in the range of 1.2 [43]. Theoretically, $R_0 > 1$ means that the infection is spreading in the community, with more cases generated daily [37]. It is observed that when the reinfection force is rather low (as in Fig. 2B), the number of active cases (black curves) can spike again in approximately two years time after the flattening of initial waves of infection. Other small outbreaks are also possible in one to two years time after that. This finding is consistent with previous evidence on endemic coronaviruses: some experts suggest that these new waves of infection can occur eventually and this problem may be induced by the waning of immunity [23,44]. In fact, emerging variant of the novel coronavirus called B.1.1.7 has been discovered in England at the end of last year and this SARS-CoV-2 variant is more transmissible than previously circulating coronaviruses [23]. This new virus strain could also evade the human immune response causing 'immune escapes' phenomenon, where mutated coronavirus strains could get more aggressive and escape a weak immune response [45]. Consequently, even people who have already recovered from the disease could get infected again [45].

As can be observed in Fig. 2B, we forecast that the peaks for the subsequent waves of infection might be lower indicating that this reinfection problem appears to be less severe and possibly less lethal. This insight is also in parallel with some clinical studies, which reported that most of the SARS-CoV-2 reinfections have been milder than the first encounters with the coronavirus (although some have been more harmful) [23]. Using PCR and antibody testing, an early evidence by Public Health England also suggests that some of those recovered from COVID-19 may still be able to pass the virus on to other people [23]. Out of several thousands patients who tested positive for antibodies, it is found that a small portion of patients had potential of COVID-19 reinfections [23]. Recent research also discovers that among several thousands of healthcare workers who had been infected with COVID-19 during the first wave of the pandemic in the United Kingdom, none of them had symptomatic reinfection in the second wave of pandemic [26,46]. Due to this reason, some researchers suggested that immunity to reinfection lasted at least six months in the case of SARS-CoV-2 virus

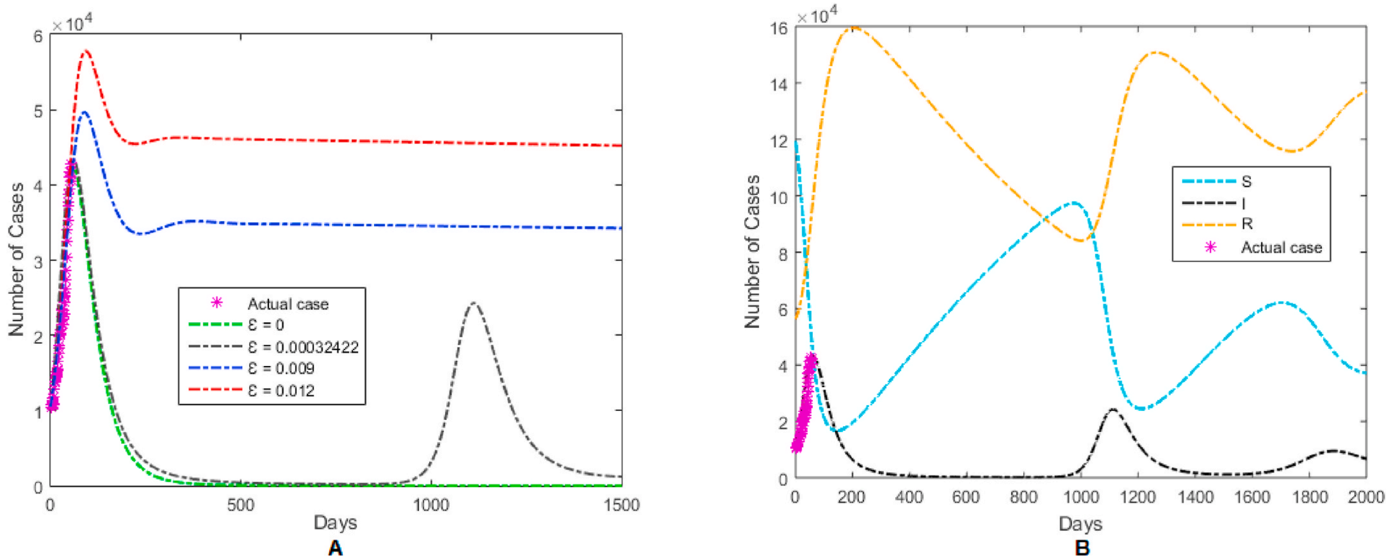

Fig. 2. The prediction of COVID-19 transmission dynamics using an SIRS-type model (1) with the assumption of limited medical resources is relaxed ($\rho = 0$) under varying magnitude of reinfection force (ε). (A) Time series results of SIR ($\varepsilon = 0$: dotted green curve) and SIRS ($\varepsilon > 0$: dotted black, blue and red curves) models and comparison with the number of active cases in Malaysia (purple stars). (B) Time series result of SIRS when reinfection force is low (corresponding to dotted black curve in Fig. 2A) and comparison with the number of active cases in Malaysia (purple stars). Other parameter values as in Table 1. Initial conditions: $S(0) = 119169$, $I(0) = 10495$, $R(0) = 56311$ and $N = S + I + R$.

[26,46]. Additionally, another important point that can be seen from our finding in Fig. 2B is that the number of COVID-19 active cases rises less steeply in the future waves of infection. This possibility demonstrates that the prevalence of COVID-19 infections maybe lower compared to the previous outbreaks. This would give us some hope that our health-care systems may not be overwhelmed in times to come though the re-infections of COVID-19 can occur in the future.

Based on our stability analysis, the finding in Fig. 2B is caused by the endemic outcome having the nature of steady state of stable focus-node type. In this three-dimensional system, it is observed that one real eigenvalue and a pair of complex-conjugate eigenvalues appear with all of them have negative real parts. This stable focus-node equilibrium indicates that the possible outcomes from the model can be reasonably damped, and transient oscillations of the infection (black), susceptible (cyan) and recovered (orange) compartments are expected in a long run, as shown by Fig. 2B. We have also conducted further analysis using this modelling framework and the main lesson that we realised is: stable limit cycles (i.e., oscillatory behaviour) are not evident for different parametrisations of the model that have been considered. While there exists some theoretical studies that propose the emergence of super-critical Hopf bifurcation and stable limit cycles in certain COVID-19 epidemiological systems [47,48], this insight should be interpreted with care so that it would not cause mass fear and panic phenomena. The in-phase oscillatory solutions would lead to recurrent pattern of epi-demics and it has been observed in the incidence of distinct infectious diseases (e.g., influenza and measles) before. This situation has resulted in some dramatic annual outbreaks throughout the years [49,50]. Based on the findings of our modelling framework (1), we suggest that one of the plausible scenarios for COVID-19 future outbreaks in Malaysia is in the form of (damped) transient oscillations, where the infection trajec-tories would level off as a result of large time behavior of solutions. However, we caution that this prediction depends on the levels of reinfection force. Increasing the intensity of ε (Fig. 2A: dotted blue and red curves) would lead to the COVID-19 infections to engender a plateau phenomenon, whereby the number of people infected by the disease stay at certain levels during an extended period of time. Note that this plateau phenomenon has been observed in the real world COVID-19 data from different countries such as in the United States and Qatar [2,42,51].

Other dynamical behaviour is also possible when the limited medical resources factor is incorporated in the model (1), as shown in Fig. 3. We observe that the reinfection force (ε) can interact with limited medical resources factor (ρ) to determine the transmission dynamics of COVID-19 via the occurrence of alternative stable states. In this case, the bist-ability occurs with both pandemic (Fig. 3A) and disease-free (Fig. 3B) equilibria are stable; convergence to either one of these steady states depends on initial abundances of individuals in susceptible, infected and removal classes. Bifurcation analysis results [16] demonstrate that local bifurcations such as transcritical bifurcation are the best known mech-anism that can mediate (dis-)appearance of distinct steady states in this epidemiological system. In general, the outbreaks may establish, or not, depending on whether the initial conditions belong to the basin of attraction of pandemic or of disease-free equilibria. The alternative stable states phenomenon can be demonstrated in Fig. 3, in which we show the steady state solutions of the model (1) for the same parameter values with two different initial conditions: when the initial fraction of infected group is high, the outbreak is established (Fig. 3A); meanwhile, for a rather low initial fraction of infected people, the outbreak is eliminated in a long run (Fig. 3B). Thus, under essentially the same conditions - that is the same epidemiological parameters and only different densities on initial populations, this COVID-19 epidemiological system may achieve significantly distinct outcomes. It has also been highlighted in a pathological study related to SARS-CoV-2 variants that the alternative stable states could occur as a result of immune function disruption. This possibility may lead to failure in controlling the virus and can cause chronic inflammation, particularly when placed in the context of regulatory feedback that raise the likelihood of alternative stable states [52].

We also investigate the long-term predictions of the model (1) with limited medical resources scenarios ($\rho > 0$) under varying reinfection forces (ε) as shown by Fig. 4. This diagram is computed using the same parametrisation of Malaysia COVID-19 active cases data [3,42] as in Table 1. Overall, this figure shows temporal evolution for COVID-19 infections as ε changes. Taking $\varepsilon = 0$, we observe similar dynamical behaviour of SIR model as illustrated by the predictions in Fig. 2A (dotted green curve) where the infection curve can be flatten. The number of infected people can also be reduced to a low level after approximately more than a year. Increasing the intensity of ε would lead

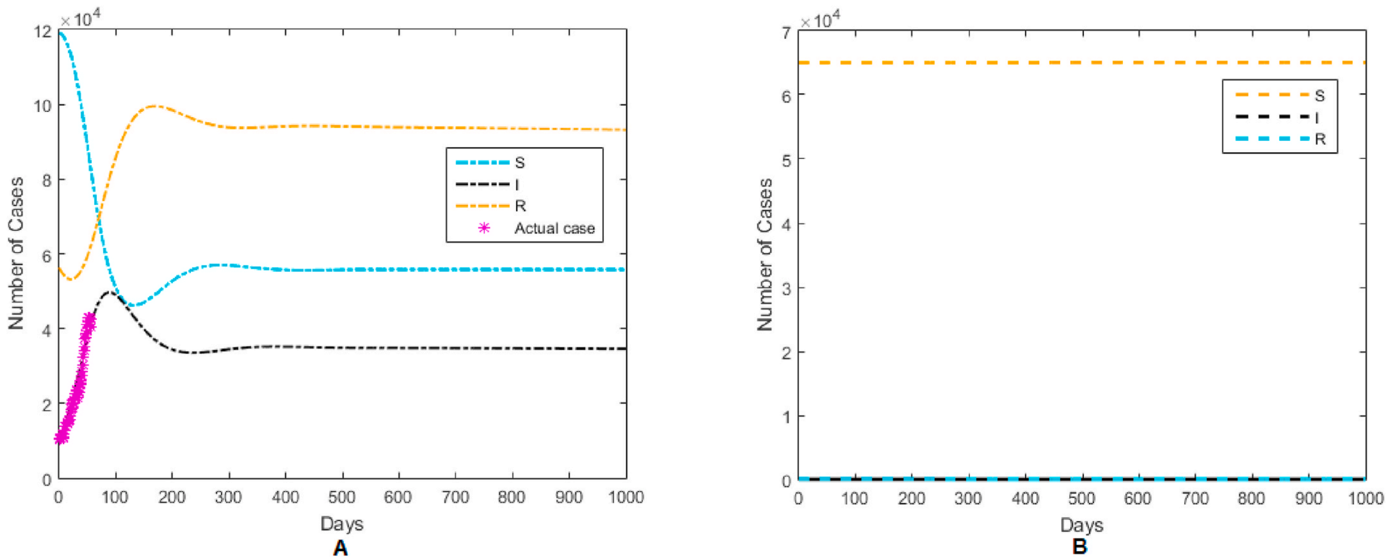

Fig. 3. The alternative stable states phenomenon in the SIRS-type model (1) with limited medical resources ($\rho > 0$) and reinfection problems ($\varepsilon > 0$). (A) Time series result when the initial fraction of infected group is high: $S(0) = 119169$, $I(0) = 10495$ and $R(0) = 56311$; (B) Time series result when the initial fraction of infected group is low: $S(0) = 65000$, $I(0) = 10$ and $R(0) = 100$. Other parameter values as in Table 1 and $N = S + I + R$.

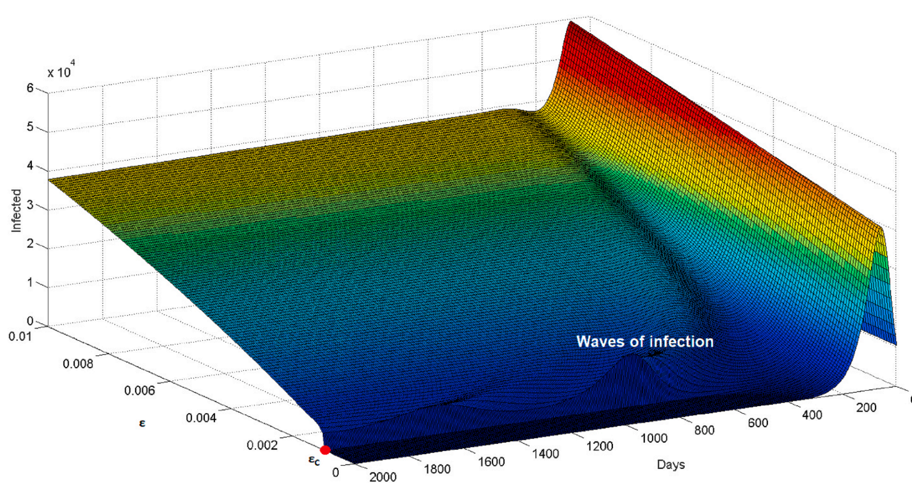

Fig. 4. The temporal evolution for COVID-19 infections as ε changes. Other parameter values as in Table 1. There occurs a transcritical bifurcation (red point), which corresponds to the minimum threshold level of reinfection force below which the infection dynamics can be eradicated efficiently and effectively. The emergence of multiple waves of infection is also possible under a low intensity of ε.

to some catastrophic changes in dynamics due to the alternative stable states phenomenon. There occurs a threshold value in reinfection force i.e., ε_C corresponding to a transcritical bifurcation (red point). From an epidemiological viewpoint, ε_C is a minimum threshold level of reinfection force below which the infection dynamics can be reduced efficiently and effectively. When $\varepsilon < \varepsilon_C$, we observe that the disease-free equilibrium is stable and the COVID-19 pandemic can be eliminated in a long run. However, when $\varepsilon > \varepsilon_C$, this situation leads to rapidly evolving pandemic outbreaks via alternative stable states. The long-term outcomes are similar to our findings in Fig. 3A–B whereby the convergence to either one of the pandemic and disease-free steady states depends on initial abundances of individuals. The occurrence of multiple waves of infection is also possible under a low intensity of ε. This case causes a rebound effect in the outbreaks of pandemic to emerge after several years (as depicted in Fig. 2A–B: black curves) following the transient oscillatory behaviour. Eventually, the infection trajectories would level off and this situation leads to the persistence of COVID-19 infection in communities.

4. Implications and conclusion

Before we highlight further implications of our findings and conclude this paper, we summarise the key points as follows:

1 It is discovered that the dynamics of the COVID-19 outbreak belongs to a simple universality class of the SIR system and extensions thereof (i.e., the inclusion of temporary immunity through the reinfection problems and limited medical resources scenarios leads to the SIRS-type model);
2 A rebound effect in transmission dynamics could emerge even when the reinfection force is rather low and this situation can occur due to the waning of immunity;
3 There occurs a critical value in reinfection threshold beyond (respectively, below) which the severity of infection persists (respectively, reduces) and the COVID-19 outbreaks may not (respectively, may) be eradicated.
4. A plateauing phenomenon is also realised in the presence of high levels of reinfection force and limited medical resources scenarios.

As the COVID-19 pandemic progresses, many countries including Malaysia have tried their best to implement a variety of responses and control measures [11]. Our scenario analysis using a family of SIR-type frameworks demonstrates that it would be necessary to consider the problems of reinfection and also the effects of limited medical resources in combating the outbreaks of pandemic effectively. This is because it is evident from some preliminary studies that more people who have had COVID-19 remain susceptible to reinfection, and that proven vaccines may, at some point, need an update [45]. Additionally, combination of non-pharmaceutical intervention measures should also be employed strictly. For instance, the policy of wearing face masks in public could help communities to slow the spread of COVID-19 when these masks are used along with other preventive measures [53,54], such as social distancing, movement control restrictions and quarantine [55]. These preventive measures may have the potential to suppress the transmission of COVID-19 and to push R_0 to be below than one [8]. Furthermore, these combined strategies are crucial in order to rapidly reduce the case incidence [56]. We have also discovered that the spread of the COVID-19 pandemic falls into the universality class of SIR-type models and extensions thereof. Owing to this reason, we caution the policy makers about the importance to conduct (early and) more testing so that we will be able to detect the possibility of community transmission and asymptomatic cases [14,32]. If we increase our testing capacity, then more possible cases will be picked up. The number of cases is likely to increase, however the quality of data will be much better than what we have now, thus, allowing us to come up with a better prediction. The outbreak investigation and management of COVID-19 data also need to be improved and better coordinated so as to fight this pandemic in an objective way. It is also vital to rapidly share detailed data and information on COVID-19 testing conducted by the government agencies since this will certainly improve the predictions of the models and could help in controlling the overall severity of the outbreak. In other words, the real-time sharing of data, research publications, equipment and etc. to fight COVID-19 through open science initiatives [57,58] is needed and transparency is now more critical than ever before.

Additionally, our findings demonstrate that a rebound effect in transmission dynamics could occur even in the presence of a low level of reinfection force. This situation can get worse if the control measures such as social distancing strategies are eased up too soon (and too quickly), which can give the novel coronavirus more opportunities to spread back in our communities. We also observe a plateau phenomenon in our scenario analysis and this observation is in parallel with the real world COVID-19 data from different countries such as in the United States and Qatar [2,42,51]. Interestingly, this finding is consistent with the predictions of equation-free modeling framework in the analysis of COVID-19 data sets for Malaysia [59]. This consistency highlights the generality of our predictions and we establish that some of the epidemiological phenomena realised in this work are robust. In particular, these observations are less restricted to specific details and assumptions of the modelling frameworks. It should also be noted that for a developing country like Malaysia, which faces the issues of limited medical resources, a resurgence into high community transmission cases should be avoided at all cost. This is because it could cause serious spike in number of active cases and deaths, and waste all the progress that has been made so far. To avoid this worst-case scenario, strict preventive measures will need to be maintained until large stocks of vaccine are available to immunise the populations. Finally, this work should also motivate modellers as a call to arms and decision makers as a guide for forecasting outbreaks, planning of resource allocation and examining the feasibility of certain intervention strategies before (and after) these measures are being implemented.

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References

[1] WHO Coronavirus (2019-nCoV) Report, Novel Coronavirus (2019-nCoV) Situation Report, World Health Organization (WHO), 2020. https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200121-sitrep-1-2019-ncov.pdf.

[2] Worldometers, COVID-19 coronavirus pandemic cases worldwide. https://www.worldometers.info/coronavirus/https://edition.cnn.com/interactive/2020/health/coronavirus-maps-and-cases/, 2020.

[3] N.H. Abdullah, From the Desk of the Director-General of Health Malaysia (DG Press Statement - Current Situation COVID-19 in Malaysia), 2021. https://kpkesihatan.com/.

[4] CNN, Tracking coronavirus global spread. https://edition.cnn.com/interactive/2020/health/coronavirus-maps-and-cases/, 2021.

[5] K.H.D. Tang, Movement control as an effective measure against Covid-19 spread in Malaysia: an overview, J. Publ. Health (2020) 1–4.

[6] A. Elengoe, COVID-19 outbreak in Malaysia, Osong Publ. Health Res. Perspect. 11 (3) (2020) 93.

[7] A. Alsayed, H. Sadir, R. Kamil, H. Sari, Prediction of epidemic peak and infected cases for COVID-19 disease in Malaysia, 2020, Int. J. Environ. Res. Publ. Health 17 (11) (2020) 4076.

[8] K.I. Musa, W.N. Arifin, M.H. Mohd, M.S. Jamiluddin, N.A. Ahmad, X.W. Chen, A. Bulgiba, Measuring time-varying effective reproduction numbers for COVID-19 and their relationship with movement control order in Malaysia, Int. J. Environ. Res. Publ. Health 18 (6) (2021) 3273.

[9] R.S. Bedi, COVID-19 spike: 277 new cases; 270 from Bukit Jalil detention centre, Star (2020). https://www.thestar.com.my/news/nation/2020/06/04/covid-19-spike-277-new-cases-no-deaths-for-13-straight-days.

[10] T. Sukumaran, Coronavirus Malaysia: PM blames Sabah election as among causes of huge infection surge, South China Morning Post. (2020). https://www.scmp.com/week-asia/health-environment/article/3104421/coronavirus-malaysia-pm-blames-sabah-election-among.

[11] L. Rampal, B.S. Liew, M. Choolani, K. Ganasegeran, A. Pramanick, S. A. Vallibhakara, V.C. Hoe, Battling COVID-19 pandemic waves in six South-East Asian countries: a real-time consensus review, Med. J. Malaysia 75 (6) (2020) 613.

[12] WHO Action in Countries Report, Strong preparedness and leadership for a successful COVID-19 response. https://www.who.int/docs/default-source/coronaviruse/country-case-studies/malaysia-c19-case-study-20-august.pdf?sfvrsn=a0f793582download=true, 2020.

[13] M.H. Mohd, N.A. Ahmad, K.I. Musa, M.S. Jamiluddin, Urgent need for more testing now, Star (2020). https://www.thestar.com.my/opinion/letters/2020/10/31/urgent-need-for-more-testing-now.

[14] L. Rampal, B.S. Liew, Malaysia's third COVID-19 wave-a paradigm shift required, Med. J. Malaysia 76 (1) (2021) 1–4.

[16] M.H. Mohd, F. Sulayman, Unravelling the myths of R0 in controlling the dynamics of COVID-19 outbreak: a modelling perspective, Chaos, Solit. Fractals (2020) 109943.

[17] H.W. Hethcote, The mathematics of infectious diseases, SIAM Rev. 42 (4) (2000) 599653.

[18] L. Zhou, M. Fan, Dynamics of an SIR epidemic model with limited medical resources revisited, Nonlinear Anal. R. World Appl. 13 (1) (2012) 31224.

[19] Y. Muroya, H. Li, T. Kuniya, Complete global analysis of an SIRS epidemic model with graded cure and incomplete recovery rates, J. Math. Anal. Appl. 410 (2) (2014) 71932.

[20] J. Parry, Covid-19: Hong Kong scientists report first confirmed case of reinfection, BMJ 370 (2020) m3340, 2020.

[21] N.R. Faria, I.M. Claro, D. Candido, L.A. Moyses Franco, Genomic Characterisation of an Emergent SARS-CoV-2 Lineage in Manaus: Preliminary Findings, Virological.org, 2021. https://virological.org/t/genomiccharacterisation-of-an-emergent-sars-cov-2-lineage-in-manaus-preliminary-findings/586.

[22] A.G. Letizia, Y. Ge, S. Vangeti, C. Goforth, D.L. Weir, N.A. Kuzmina, S.C. Sealfon, SARS-CoV-2 seropositivity and subsequent infection risk in healthy young adults: a prospective cohort study, medRxiv (2021).

[23] C. Stokel-Walker, What we know about Covid-19 reinfection so far, BMJ 372 (2021) n99, 2021.

[24] A.S. Breathnach, P.A. Riley, M.P. Cotter, A.C. Houston, M.S. Habibi, T.D. Planche, Prior COVID-19 significantly reduces the risk of subsequent infection, but reinfections are seen after eight months, J. Infect. (2021).

[25] E. Wilkinson, Covid-19 reinfection rare says NHS study but some may still pass the virus on. Pulse. www.pulsetoday.co.uk/news/coronavirus/covid-19-reinfection-rare-says-nhs-studybut- some-may-still-pass-the-virus-on, 2021.

[26] A.T. Hanrath, B.A. Payne, C.J. Duncan, Prior SARS-CoV-2 infection is associated with protection against symptomatic reinfection, J. Infect. (2020).

[27] Y. Shi, Y. Wang, C. Shao, J. Huang, J. Gan, X. Huang, E. Bucci, M. Piacentini, G. Ippolito, G. Melino, Covid-19 infection: the perspectives on immune responses, Cell Death Differ. 27 (2020) 14511454.

[28] W.O. Kermack, A.G. McKendrick, A contribution to the mathematical theory of epidemics, Proc. Roy. Soc. Lond. Ser. A 115 (772) (1927) 700–721.

[29] A.L. Lloyd, Sensitivity of model-based epidemiological parameter estimation to model assumptions, in: Mathematical and Statistical Estimation Approaches in Epidemiology, Springer, Dordrecht, 2009, pp. 123–141.
[30] W.C. Roda, M.B. Varughese, D. Han, M.Y. Li, Why is it difficult to accurately predict the COVID-19 epidemic? Infect. Dis. Modell. 5 (2020) 271–281.
[31] Amir Khan, et al., Stability analysis and optimal control of covid-19 with convex incidence rate in Khyber Pakhtunkhawa (Pakistan), Results in Physics 20 (2021), https://doi.org/10.1016/j.rinp.2020.103703.
[32] L. Rampal, B.S. Liew, M. Choolani, K. Ganasegeran, A. Pramanick, S. A. Vallibhakara, V.C. Hoe, Battling COVID-19 pandemic waves in six South-East Asian countries: a real-time consensus review, Med. J. Malaysia 75 (6) (2020) 613.
[33] A.B. Gussow, N. Auslander, Y.I. Wolf, E.V. Koonin, Prediction of the incubation period for COVID-19 and future virus disease outbreaks, BMC Biol. 18 (1) (2020) 1–12.
[34] T. Carletti, D. Fanelli, F. Piazza, COVID-19: the unreasonable effectiveness of simple models, Chaos, Solit. Fractals 5 (2020) 100034.
[35] J. Dehning, J. Zierenberg, F.P. Spitzner, M. Wibral, J.P. Neto, M. Wilczek, V. Priesemann, Inferring change points in the spread of COVID-19 reveals the effectiveness of interventions, Science 369 (6500) (2020).
[36] D. Fanelli, F. Piazza, Analysis and forecast of COVID-19 spreading in China, Italy and France, Chaos, Solit. Fractals 134 (2020) 109761.
[37] K.I. Musa, W.N. Ariffin, M.H. Mohd, M.S. Jamiluddin, N.A. Ahmad, C.X. Wee, A. Bulgiba, Measuring Time-Varying Effective Reproduction (Rt) Numbers for COVID-19 and Their Relationship with Movement Control Order (MCO) in Malaysia, Preprints, 2021, p. 2021010264.
[38] B. Rahman, I.A. Aziz, F.W. Khdhr, D.F. Mahmood, Preliminary estimation of the basic reproduction number of SARS-CoV-2 in the Middle East, 2020, https://doi.org/10.2471/BLT,20.
[39] C.P. Farrington, H.J. Whitaker, Estimation of effective reproduction numbers for infectious diseases using serological survey data, Biostatistics 4 (4) (2003) 621–632.
[40] J. Tolles, T. Luong, Modeling epidemics with compartmental models, J. Am. Med. Assoc. 323 (24) (2020) 2515–2516.
[41] L. Magri, N.A.K. Doan, First-principles Machine Learning Modelling of COVID-19, 2020 arXiv preprint arXiv:2004.09478.
[42] E. Dong, H. Du, L. Gardner, An interactive web-based dashboard to track COVID-19 in real time, Lancet Infect. Dis. 20 (5) (2020) 533–534.
[43] Ministry of Health Malaysia, COVID-19: R0 Malaysia projected on 1 February 2021. http://covid-19.moh.gov.my/kajian-dan-penyelidikan/nilai-r-malaysia/unjuran-r-naught-hari-ini-01022021, 2020.
[44] P.G. Choe, K.H. Kim, C.K. Kang, H.J. Suh, E. Kang, S.Y. Lee, M.D. Oh, Antibody responses 8 Months after asymptomatic or mild SARS-CoV-2 infection, Emerg. Infect. Dis. 27 (3) (2020).
[45] K. Kupferschmidt, New coronavirus variants could cause more reinfections, require updated vaccines, in: Science COVID-19 Report, 2021, https://doi.org/10.1126/science.abg6028.
[46] S.F. Lumley, D. ODonnell, N.E. Stoesser, P.C. Matthews, A. Howarth, S.B. Hatch, D. W. Eyre, Antibody status and incidence of SARS-CoV-2 infection in health care workers, N. Engl. J. Med. (2020).
[47] M. Radha, S. Balamuralitharan, A study on COVID-19 transmission dynamics: stability analysis of SEIR model with Hopf bifurcation for effect of time delay, Adv. Differ. Equ. 2020 (1) (2020) 1–20.
[48] A. Ajbar, R.T. Alqahtani, Bifurcation analysis of a SEIR epidemic system with governmental action and individual reaction, Adv. Differ. Equ. 2020 (1) (2020) 1–14.
[49] H.W. Hethcote, S.A. Levin, Periodicity in epidemiological models, in: Applied Mathematical Ecology, Springer, Berlin, Heidelberg, 1989, pp. 193–211.
[50] M. Erdem, M. Safan, C. Castillo-Chavez, Mathematical analysis of an SIQR influenza model with imperfect quarantine, Bull. Math. Biol. 79 (7) (2017) 1612–1636.
[51] Z. Wu, H. Liao, A. Vidmer, M. Zhou, W. Chen, COVID-19 Plateau: A Phenomenon of Epidemic Development under Adaptive Prevention Strategies, 2020 arXiv preprint arXiv:2011.03376.
[52] C.J.E. Metcalf, B.T. Grenfell, A.L. Graham, Disentangling the dynamical underpinnings of differences in SARS-CoV-2 pathology using within-host ecological models, PLoS Pathog. 16 (12) (2020), e1009105.
[53] J. Howard, A. Huang, Z. Li, Z. Tufekci, V. Zdimal, H.M. van der Westhuizen, A. W. Rimoin, An evidence review of face masks against COVID-19, Proc. Natl. Acad. Sci. Unit. States Am. 118 (4) (2021).
[54] R.O. Stutt, R. Retkute, M. Bradley, C.A. Gilligan, J. Colvin, A modelling framework to assess the likely effectiveness of facemasks in combination with lock-down in managing the COVID-19 pandemic, Proc. Roy. Soc. A 476 (2238) (2020) 20200376.
[55] N. Salim, W.H. Chan, S. Mansor, N.E.N. Bazin, S. Amaran, A.A.M. Faudzi, S. M. Shithil, COVID-19 epidemic in Malaysia: impact of lock-down on infection dynamics, medRxiv (2020).
[56] K.B. Law, K.M. Peariasamy, B.S. Gill, S. Singh, B.M. Sundram, K. Rajendran, N. H. Abdullah, Tracking the early depleting transmission dynamics of COVID-19 with a time-varying SIR model, Sci. Rep. 10 (1) (2020) 1–11.
[57] J. CutcherGershenfeld, K.S. Baker, N. Berente, P.A. Berkman, P. Canavan, F. A. Feltus, P. Veazey, Negotiated sharing of pandemic data, models, and resources, Negot. J. 36 (4) (2020) 497–534.
[58] M. Zastrow, Open science takes on the coronavirus pandemic, Nature (2020).
[59] N. Ahmad, M.H. Mohd, Memory-dependent forecasting of COVID-19: the flexibility of extrapolated kernel least mean square algorithm, TechRxiv (2021), https://doi.org/10.36227/techrxiv.14077361.v1.