



Alexandria University
Alexandria Engineering Journal

www.elsevier.com/locate/aej
www.sciencedirect.com



An SIER model to estimate optimal transmission rate and initial parameters of COVID-19 dynamic in Sri Lanka

W.P.T.M. Wickramaarachchi^{a,*}, S.S.N. Perera^b

^a *Department of Mathematics, The Open University of Sri Lanka, Nawala, Nugegoda, Sri Lanka*

^b *Research and Development Center for Mathematical Modelling, Department of Mathematics, University of Colombo, Colombo 03, Sri Lanka*

Received 11 July 2020; revised 15 October 2020; accepted 9 November 2020
Available online 19 November 2020

KEYWORDS

COVID-19;
SIER model;
Transmission rate;
Optimal parameters;
Simulation

Abstract COVID-19 global outbreak has been significantly damaging the human well-being, life style of people and the global economy. It is clear that the entire world is moving into a dangerous phase of this epidemic at the moment. With absence of a preventive vaccine, the governments across world implement, monitor and manage various public health and social distancing measures to control the spread of this extremely contagious disease and it is found that most of these responses have been critical results of numerous mathematical and decision support models. In this study, SEIR compartment structure is used to model the COVID-19 transmission in Sri Lanka. Reported cases data during the first 80 days of the outbreak is used to model the time dependent transmission rate of the disease. Optimal transmission rates and initial size of the exposed and infected sizes of the populations are then estimated matching between clinically identified cases to model based simulated outcomes.

© 2020 The Authors. Published by Elsevier B.V. on behalf of Faculty of Engineering, Alexandria University. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

1. Introduction

Corona virus disease 2019 designated as COVID-19 is an infection in the respiratory system of humans caused by a new pathogen named SARS-Cov-2. The initial cases of the disease were identified during late December 2019 from Wuhan city,

Hubei province in China [1]. Since then within six months, this novel virus has spread cross almost all the countries and territories in the world nearly infecting more than 9 million and causing around 450,000 deaths [2]. The world's entire population is at risk of contacting the virus and the global economy is moving into a recession due to worldwide lock down of cities, halting production, restricting travel across countries due to boarder closures, and unemployment. In addition, the change in human life style and getting used to live with more social distancing measures to minimize further transmission of the disease found to have caused various social and psychological issues among vulnerable groups of people [3].

* Corresponding author.

E-mail address: wptharindu86uoc@gmail.com (W.P.T.M. Wickramaarachchi).

Peer review under responsibility of Faculty of Engineering, Alexandria University.

<https://doi.org/10.1016/j.aej.2020.11.010>

1110-0168 © 2020 The Authors. Published by Elsevier B.V. on behalf of Faculty of Engineering, Alexandria University. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Sri Lanka reported its first local COVID-19 case on 10 March 2020 who was a tourist guide. The government of Sri Lanka took serious measures against the virus spread such as closing down schools and universities, limiting non-essential work and travel, closing down country's air port for all international arrivals, imposing nationwide curfew, and introducing mandatory quarantine for all overseas travelers [4]. Due to the timely public health and social distancing measures introduced, the country did not experience dramatic rise in cases during the first 40 days of the outbreak, however sudden rise was taken place as a result of a large cluster in a naval base. The again after 75 days, another jump was reported due to repatriated Sri Lankan immigrant workers mainly from Middle-East countries [5]. The total corona virus infections, active cases, deaths and recoveries in Sri Lanka recorded for the first 82 days of the epidemic are presented in the Fig. 1.

As a result of this extremely dangerous public health problem the whole world has to face, multiple research groups have begun their work to come up with a suitable vaccine candidate or a treatment drug against COVID-19, however most of the developments are in early phases in the cycle [6]. Thus, predicting the transmission through modeling and implementing, monitoring, and managing suitable control measures have been significantly critical to minimize the burden. Mathematical models such as in SIER (Susceptible-Exposed-Infected-Recovered) population compartments are nowadays critical in epidemiological decision making as they reveal significant information on the dynamic, parameters and their sensitivity, and efficacy of control measures [4,7].

This paper mainly has got two objectives; the first study focuses to adopt a compartmental SEIR type mathematical model to predict the infections and to reveal useful qualitative information about the dynamic of COVID-19 transmission in Sri Lanka. Reported cases are used to estimate the doubling time of cases in the community and hence the initial transmission probability is approximated assuming exponential growth behavior of cases. This measure is also applied to model the time-dependent transmission probability during the first

82 days of the epidemic. Secondly, an optimization problem is established to estimate parameter values for the transmission probability β , initial sizes of the exposed E_0 and infected I_0 populations, matching between total reported COVID-19 cases and cumulative infections resulted through numerical simulation of the mathematical model. The number of deaths due to COVID-19 reported in Sri Lanka is significantly low thus, we drop this population from the optimization problem.

2. Methods

2.1. Mathematical model

Mathematical models in infectious disease have a century long history. Compartment models governed by system of differential equations such as SIR (Susceptible-Infected-Recovered) and SEIR (Susceptible-Exposed-Infected-Recovered) have been widely used in literature, and these models have provided not only critical qualitative aspects of the disease transmission but also have predicted the transmission dynamic for certain extend. One significant advantage of these type of models has been that they accommodate to test the level of various control measures and evaluate the efficacy of numerous treatment procedures to communicable diseases. Thank to computers, the simple to very complex mathematical models with large parameter spaces can be numerically simulated, and the outcomes are extremely useful in decision making related to public health [7,4,15].

In this study, we adopt SEIR (Susceptible-Exposed-Infected-Recovered) compartmental approach to model the transmission of COVID-19 in Sri Lanka. It is assumed that all the clinically identified positive patients for COVID-19 virus are homogeneous with no impact of demographic factors such as age, gender and history of chronic diseases on the disease progression. Natural birth and death process was considered to be negligible and those who recovered to have developed complete immunity against the virus. In this simple model, the susceptible individual may become exposed to the novel

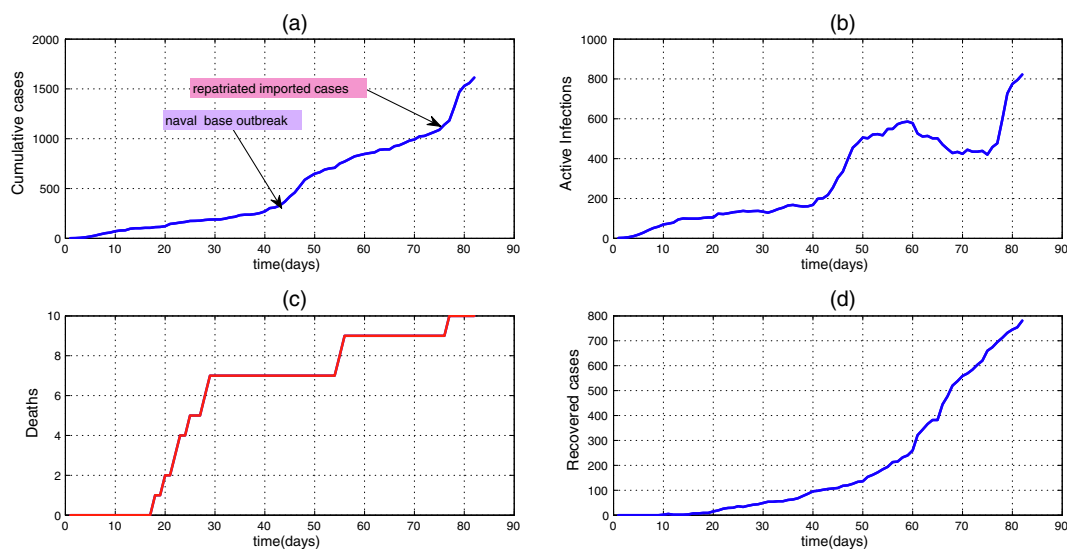


Fig. 1 Cumulative cases (a), active cases (b), deaths (c) and recovered cases (d) of COVID-19 in Sri Lanka during the first 82 days in the epidemic.

corona virus at a probability of β , and this is also defined as the transmission rate of the virus. Let σ denotes the rate an exposed individuals become infectious. As a result of treatments or due to the immunity, the patient can be recovered at a rate of γ . It is noted that some patients whose condition get worse could end up with deaths with a rate of μ . It should be noted that the effective contact rates between the susceptible and infected populations depend on the number of individuals in the entire population (N). The transmission rate between S and I is assumed to be $\frac{d(S/N)}{dt} = -\beta \frac{SI}{N^2}$, and here $\frac{SI}{N^2}$ is the fraction of those contacts between an infectious and susceptible individual which result in the susceptible person becoming infected. Based on these assumptions and dynamics, the transmission of COVID-19 can be represented as follows in a schematic diagram (Fig. 2).

The SIER model of COVID-19 transmission can now be established as a system of non-linear differential equations given by

$$\frac{dS}{dt} = -\frac{\beta}{N}SI \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta}{N}SI - \sigma E \quad (2)$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I \quad (3)$$

$$\frac{dR}{dt} = \gamma I \quad (4)$$

where N is the total size of the population.

The initial conditions for the model is as $S(0) = S_0 = N - E_0 - I_0$, $E(0) = E_0$, $I(0) = I_0$, and $R(0) = R_0$. We let the set of solutions denoted by Ω to the system of nonlinear differential equations as

$$\Omega = \{(S, E, I, R) \in \mathbb{R}_+^4 : S + E + I + R \leq N, S, E, I, R \geq 0\}. \quad (5)$$

Initially, the entire population is susceptible to COVID-19, thus, we let

$N \approx S$ and this gives $\frac{\beta}{N}SI \approx \beta I$. Now the model with infection groups can be written as

$$\frac{dE}{dt} = \beta I - \sigma E \quad (6)$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I \quad (7)$$

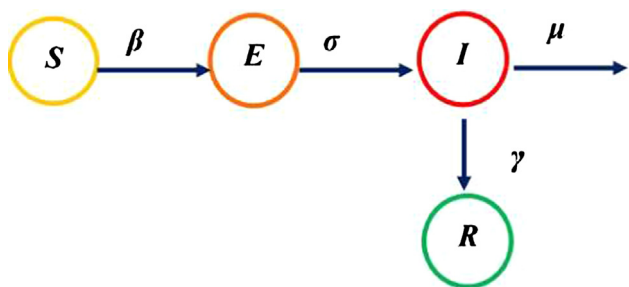


Fig. 2 Schematic diagram.

or in matrix form as

$$\begin{pmatrix} E \\ I \end{pmatrix}' = \begin{pmatrix} -\sigma & \beta \\ \sigma & -(\gamma + \mu) \end{pmatrix} \begin{pmatrix} E \\ I \end{pmatrix}$$

At the early stage of the epidemic, there is a non-linear relationship between the total numbers of cases, $I(t)$ and the force of infection λ which is given as follows [8,9]

$$I(t) \propto I(0)\exp(\lambda t) \quad (8)$$

where $I(0)$ denotes the initial size of the epidemic. Then the doubling time (D) of the number of infections can be obtained as

$$D = \frac{\ln 2}{\lambda}. \quad (9)$$

The doubling time is a useful measure in public health point of view that explains the number of days which takes to double the number of infections. This also reveals critical information such as the level of risk the population is exposed to and the rate of transmission. The initial growth rate of the epidemic is determined by the largest eigenvalue λ of the linear system, and this is given by

$$\lambda = \frac{1}{2} \left[-(\gamma + \sigma + \mu) + \sqrt{(\gamma + \mu - \sigma)^2 + 4\beta\sigma} \right]. \quad (10)$$

Combining Eqs. 9 and 10 yields the following relationship for the transmission probability of the virus β .

$$\beta = \frac{\left[\frac{\ln 4}{D} + (\gamma + \mu + \sigma) \right]^2 - (\gamma + \mu - \sigma)^2}{4\sigma} \quad (11)$$

2.2. Analysis of the model

Basic reproduction number $\mathcal{R}_0$ stands for the number of secondary infections those can be produced by a single infected patients on average [10,11]. It is very critical to distinguish new infections in the dynamic of the population to compute $\mathcal{R}_0$.

Now we present the computation of the basic reproductive number $\mathcal{R}_0$ for the COVID-19 transmission model. For this purpose we now define the new vector of only infected variables $\underline{X} = (E, I)$ containing the classes which are responsible to transmit the virus in the population. Now we establish the following two dimensional system of differential equations involving E and I .

$$\frac{dE}{dt} = \frac{\beta}{N}SI - \sigma E \quad (12)$$

$$\frac{dI}{dt} = \sigma E - (\gamma + \mu)I \quad (13)$$

The next generation matrix method is applied for the computation of $\mathcal{R}_0$ [12,13]. Accordingly, necessary matrices F and V are obtained as follows:

$$F = \begin{pmatrix} 0 & \frac{\beta}{N}S \\ 0 & 0 \end{pmatrix}, \quad (14)$$

and

$$V = \begin{pmatrix} \sigma & 0 \\ -\sigma & (\gamma + \mu) \end{pmatrix}. \quad (15)$$

The basic reproduction number is defined as the spectral radius ρ of the matrix FV^{-1} [12]. Thus, we obtain the following formula for $\mathcal{R}_0$ together with the assumption $S \approx N$ initially

$$\mathcal{R}_0 \approx \frac{\beta}{\gamma + \mu}. \quad (16)$$

Substituting the expression for β in Eq. 11 we get

$$\mathcal{R}_0 \approx \frac{\left[\frac{\ln 4}{D} + (\gamma + \mu + \sigma)\right]^2 - (\gamma + \mu - \sigma)^2}{4\sigma(\gamma + \mu)} \quad (17)$$

The change in $\mathcal{R}_0$ with respect to varying doubling time D is given in Fig. 3 and it clearly indicates that $\mathcal{R}_0$ reduces as the doubling time increases implying reduced level of exposed risk to the disease.

The Jacobian matrix at the DFE J_0 is then obtained as

$$J_0 = \begin{pmatrix} -\sigma & \beta \\ \sigma & -(\gamma + \mu) \end{pmatrix}. \quad (18)$$

By diagonalizing J_0 , we get the characteristic polynomial of the form $a_0x^2 + a_1x + a_2 = 0$ where

$$\begin{aligned} a_0 &= 1 \\ a_1 &= \gamma + \mu + \sigma \text{ and} \\ a_2 &= \sigma(\gamma - \beta + \mu). \end{aligned}$$

Routh-Hurwitz stability criterion for second order polynomials is used to determine the stability of the DFE. According to the criteria, the coefficients should satisfy $a_0 > 0$, $a_1 > 0$ and $a_2 > 0$. Clearly $a_0 > 0$ and $a_1 > 0$. Thus, DFE is asymptotically locally stable if $\gamma - \beta + \mu > 0$ if and only if $\frac{\beta}{\gamma + \mu} < 1$ if and only if $\mathcal{R}_0 < 1$ [14,15].

3. Estimation of initial parameters

In the model for COVID-19 in Eqs. (1)–(4), the transmission probability β is assumed to be fixed. However, in the realistic case this transmission probability depends on time as the governments introduces various control measures to minimize the transmission of virus with respect to time. This results a SEIR model with a time depended transmission rate as follows:

$$\frac{dS}{dt} = -\frac{\beta(t)}{N} SI \quad (19)$$

$$\frac{dE}{dt} = \frac{\beta(t)}{N} SI - \sigma E \quad (20)$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I \quad (21)$$

$$\frac{dR}{dt} = \gamma I \quad (22)$$

where

$$\beta(t) = \begin{cases} \beta_1, & \text{if } t < 14; \\ \beta_2, & \text{if } 14 \leq t < 28; \\ \beta_3, & \text{if } 28 \leq t < 42; \\ \beta_4, & \text{if } 42 \leq t < 56; \\ \beta_5, & \text{if } t \geq 56; \end{cases} \quad (23)$$

It should be noted that if $\beta_i = \beta$ for $i = 1, 2, 3, 4, 5$ then the model reduces to the system in Eqs. (1)–(4).

Next, we attempt to estimate the parameter β , and the initial exposed and infected populations E_0 and I_0 using reported COVID-19 cases data in Sri Lanka. We define the following least-squares functional for the matching between simulated output from system Eqs. (1)–(4) and the reported data for the period of eighty days since the first local COVID-19 case was identified during the second week of March 2020 [16,17].

$$J(\underline{u}) = \int_0^T [(I(t) + R(t)) - Y(t)]^2 + \frac{1}{2} C_1 \beta^2 + \frac{1}{2} C_2 E_0^2 + \frac{1}{2} C_3 I_0^2 dt, \quad (24)$$

where $Y(t)$ for $t \in [0, T]$ is the time series of clinically identified COVID-19 commutative cases in Sri Lanka and that should be matched with the sum of simulated results for infected $I(t)$ and recovered $R(t)$ for $t \in [0, T]$. Here $\underline{u} = (\beta, E_0, I_0)$ the unknown parameters should be estimated. The regularization term $\frac{1}{2} C_1 \beta^2 + \frac{1}{2} C_2 E_0^2 + \frac{1}{2} C_3 I_0^2$ is included to the cost functional to ensure the convexity where C_k for $k = 1, 2, 3$ are constants and they are responsible to relatively balance the contribution

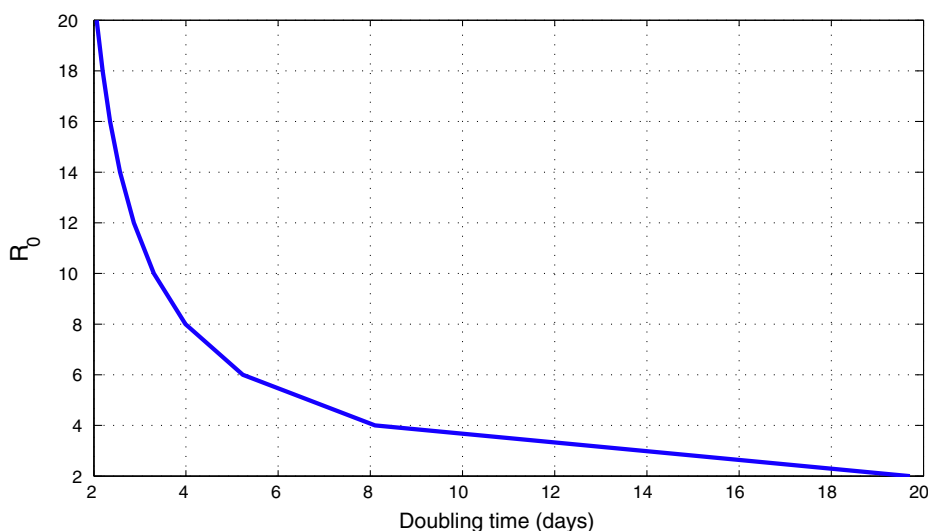


Fig. 3 The change in R_0 with respect to doubling time D .

from least-squares error. We find the optimal control measures $\underline{u}^* = (\beta^*, E_0^*, I_0^*)$ such that

$$J(\beta^*, E_0^*, I_0^*) = \min_{\underline{u}} J(\beta, E_0, I_0) \quad (25)$$

with $\beta^* \in (0, 1)$, $E_0^* \geq 0$ and $I_0^* \geq 0$.

4. Optimization

Now we discuss the method of obtaining the solution to the problem (24). For this, it is necessary to define the Lagrangian and Hamiltonian for the optimal control problem (24). Thus, the Lagrangian L is stated as

$$L(I, R, Y, \underline{u}) = [I(t) + R(t) - Y(t)]^2 + \frac{1}{2} C_1 \beta^2 + \frac{1}{2} C_2 E_0^2 + \frac{1}{2} C_3 I_0^2, \quad (26)$$

and for the Hamiltonian we let $\underline{X} = (S, E, I, R)$ and $\lambda = (\lambda_1, \lambda_2, \lambda_3, \lambda_4)$, and we write

$$H(\underline{X}, \underline{u}, \lambda) = L(I, R, Y, \underline{u}) + \lambda_1 \left[-\frac{\beta}{N} SI \right] + \lambda_1 \left[\frac{\beta}{N} SI - \sigma E \right] + \lambda_3 [\sigma E - \gamma I - \mu I] + \lambda_4 [\gamma I] \quad (27)$$

where $\lambda_j, j \in \{1, 2, 3, 4\}$ are the adjoint variables. Next derivation is the necessary conditions as described in detail in [18,19] for the Hamiltonian H for the equation given in (27).

Theorem 1. Given an optimal control $\underline{u}^* = (\beta^*, E_0^*, I_0^*)$ and a solution $\underline{X}^* = (S^*, E^*, I^*, R^*)$ with respect to the system Eqs. (1)–(4), there exist adjoint variables $\lambda_j, j \in \{1, 2, 3, 4\}$ satisfying

$$\frac{d\lambda_1}{dt} = \frac{I\beta(\lambda_1 - \lambda_2)}{N} \quad (28)$$

$$\frac{d\lambda_2}{dt} = \sigma(\lambda_2 - \lambda_3) \quad (29)$$

$$\frac{d\lambda_3}{dt} = 2(Y - R - I) - \lambda_4\gamma + \frac{S\beta}{N}(\lambda_1 - \lambda_2) + \lambda_3(\gamma + \mu) \quad (30)$$

$$\frac{d\lambda_4}{dt} = 2(Y - R - I) \quad (31)$$

with transversality conditions

$$\lambda_j(t_f) = 0, j \in \{1, 2, 3, 4\}. \quad (32)$$

Proof. The system Eqs. (1)–(4) is obtained by taking the derivative

$$\frac{d\underline{X}}{dt} = \frac{\partial H(t, \underline{u}^*, \lambda_1, \lambda_2, \lambda_3, \lambda_4)}{\partial \underline{X}}$$

and the adjoint system is obtained taking

$$\frac{d\lambda}{dt} = -\frac{\partial H(t, \underline{u}^*, \lambda_1, \lambda_2, \lambda_3, \lambda_4)}{\partial \underline{X}^*}. \quad \square$$

5. Numerical results and discussion

In this section, we obtain the numerical solutions for the system given in Eqs. (21)–(24) considering time varying transmis-

sion rate β as established in (23). The differential system is numerically solved using ODE45 solver in MATLAB package that uses a variable step Runge–Kutta Method to solve differential equations numerically. The time dependent form of β is computed considering daily COVID-19 data in Sri Lanka for the first 80 days from the first local case is reported. The following algorithm is applied for the computation.

STEP 1

Select the COVID-19 total daily cases for given period.

STEP 2

Fit the exponential curve considering, $I(t) = a \exp(\lambda t)$, $a \in \mathbb{R}^+$ with 95% confidence interval.

STEP 3

Obtain force of infection λ , and then compute doubling time using Eq. (9).

STEP 4

Repeat the process choosing different time intervals as indicated in (23).

STEP 5

Compute the true value of β and 95% confidence interval for each time period using Eq. (11).

The computed true values of β and the 95% confidence interval for each time period is presented in Table 1.

In the context of local transmission of COVID-19 in Sri Lanka, the spread triggered due to a large number of imported cases to the country mainly from European Union countries and from South Korea. Thus, for the simulation we take $E(0) = 600$ and $I(0) = 50$. We also let $S(0) = N - E(0) - I(0)$ and $R(0) = 0$.

According to Fig. 4, susceptible population is decreasing with respect to time whilst the population of infected people grows exponentially over the first 10–15 days of the outbreak, reaches the maximum size of the active infections in the range between 500–600, and then decays over the time. The outcomes clearly indicate the sensitivity of transmission probability β as there are three distinct curves for its true value, upper and lower boundary of the 95% confidence interval. Fig. 4 plot (d) represents the dynamic of the total cases reported in Sri Lanka for the period, that is the sum of infected and recovered patients, however, deaths are not included as there are only 11

Table 1 The estimated values for true β and its 95% confidence interval. In Eq. (11), the rest of the parameter values are $\gamma = 1/25$, $\mu = 0.00001$ and $\sigma = 1/3$ [4,5,7].

Time Period	True value of β	95% Confidence Interval
$t < 14$	0.0343	[0.0257, 0.0439]
$14 \leq t < 28$	0.0142	[0.0124, 0.0162]
$28 \leq t < 42$	0.0106	[0.0099, 0.0114]
$42 \leq t < 56$	0.0126	[0.0121, 0.0132]
$t \geq 56$	0.0104	[0.0100, 0.0109]

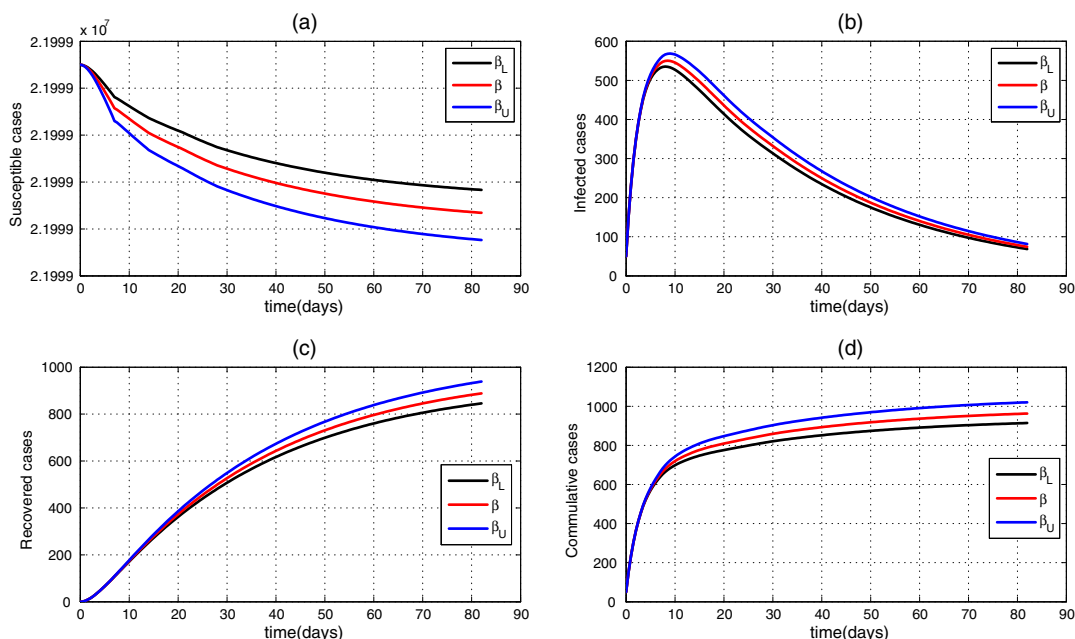


Fig. 4 Numerical outcomes of the system Eqs. (21)–(24), Susceptible (a), Infected (b), Recovered (c) and Cumulative cases (d). The values of β is as given in Table 1 and the rest of the parameter values are $N = 22000000$, $\gamma = 1/25$, $\mu = 0.00001$ and $\sigma = 1/3$ [4,5,7].

fatalities over the time horizon considered for this study which is about 0.56%.

Now the system in Eqs. (1)–(4) is solved to estimate the parameters β , E_0 and I_0 matching with reported COVID-19 cases in Sri Lanka in the first 80 days of its outbreak. Numerical schemes presented in [20–22,16] are coupled with Runge–Kutta method of order four to carry out the simulation of the problem in optimization. The algorithm stops once the termination condition $|J(u_{m+1}) - J(u_m)| < ERR$ is satisfied. The outcome of this simulation is given in Fig. 5. The blue dotted line represents the reported COVID-19 cases whilst the red thick line stands for the simulated curve.

A local minimum is obtained for the optimization problem in (24) and the estimated parameter values are

$\beta = 0.3582$, $E_0 = 17$ and $I_0 = 0$ suggesting that there were around significant number of exposed cases while no infections initially. It is clearly observed from Fig. 5 that during about first 25 days, the simulated curve and the actual data fit closely however, there are two major deviations as a result sudden rise in COVID-19 cases, firstly due to the outbreak in Naval Bases (after 45 days) and secondly due to imported infected cases of migrant Sri Lankan workers repatriated from Middle-East countries (after 75 days).

6. Conclusions

The wide spread transmission of COVID-19 has been the major public health, social and global economic concern at

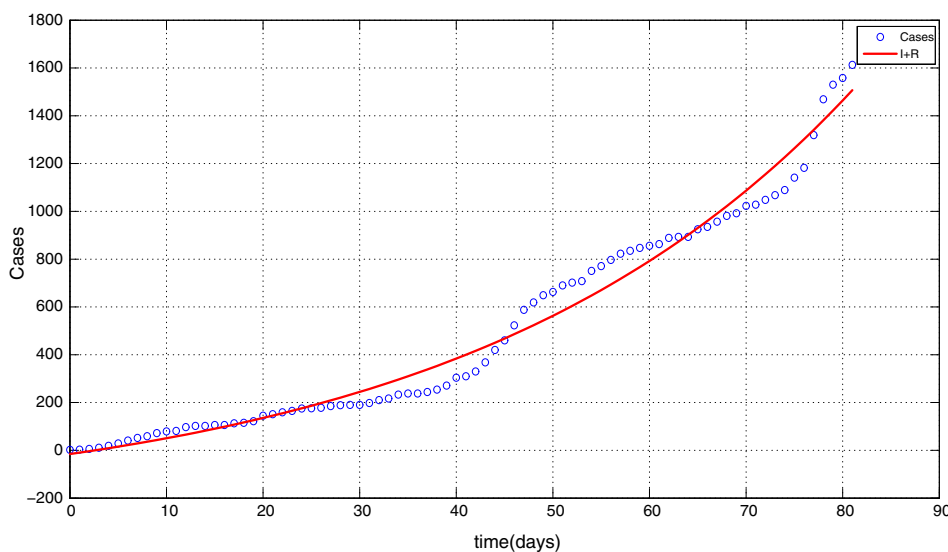


Fig. 5 Numerical outcomes of the system Eqs. (1)–(4) matching with reported COVID-19 cases during the first 80 days of the outbreak. The parameter values are $N = 22000000$, $\gamma = 1/25$, $\mu = 0.00001$ and $\sigma = 1/3$ [4,5,7].

the moment. Entire world is transforming into new norms to live with this novel virus in the absence of an effective vaccine found so far, however, number of clinical trials are in progress to assess a suitable vaccine candidate against corona virus.

Mathematical models are used to predict the dynamic of the disease, evaluate control measures, and obtain optimal policy decision against the disease burden. In this study, we apply SEIR model to predict the dynamic of COVID-19 in Sri Lanka and the transmission rate β is estimated as a step function in time using real data of transmission in the country reported during the first 82 days of the epidemic assuming the exponential growth of cases in the early period of the epidemic. The doubling time parameter is defined and it is estimated using reported data in Sri Lanka during the early stage of the epidemic. This measure provides critical insight about the dynamic in terms of the risk faced by the population, and the level of transmission of the virus over the community. The transmission probability and the basic reproduction number of the disease also modeled using the doubling time in functional form. It is shown that if effective public health and social distancing measures are able to increase the doubling time then the basic reproduction number can be reduced. The numerical simulation of the SEIR model using time dependent transmission probability suggests that the peak of the infected cases may be occurred during the first 10–20 days of the outbreak, and its size is closed to 600 patients. In addition, the simulated model based outcomes are matched between the reported COVID-19 cases introducing a cost functional, and the optimal average transmission rate, initial size of the exposed cases, and size of infected cases are estimated receptively as $\beta = 0.3582$, $E_0 = 17$ and $I_0 = 0$.

The plot representing simulated cases and the reported cases show a clear similarity in terms of the exponential growth behavior during the early phase of the COVID-19 outbreak in Sri Lanka, however, there can also be seen couple of deviations between the two curves mainly due to the large cluster of cases from the Naval Base outbreak and as a result the repatriated migrant citizens with the virus mainly from high risk middle-East countries.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

- [1] D.-G. Chen, X. Chen, Reconstructing and forecasting the covid-19 epidemic in the united states using a 5-parameter logistic growth model, *Glob. Health Res. Policy* 2020 (2020) 1–7, <https://doi.org/10.1186/s41256-020-00152-5>.
- [2] WHO, Coronavirus disease (covid-19) situation report 155, https://www.who.int/docs/default-source/coronavirus/situation-reports/20200623-covid-19-sitrep-155.pdf?sfvrsn=ca01ebe_2.
- [3] A. Haleem, M. Javaid, Effects of covid-19 pandemic in daily life, letter to editor, *Curr. Med. Res. Pract.* 10 (2020) 78–79, <https://doi.org/10.1016/j.cmrp.2020.03.011>.
- [4] W. Wickramaarachchi, S. Perera, Covid-19 epidemic in sri lanka: A mathematical and computational modelling approach to control, *MedRxiv preprint* (2020) 1–13, <https://doi.org/10.1101/2020.04.21.20073734>.
- [5] Covid-19 <https://hpb.health.gov.lk/covid19-dashboard/>.
- [6] P. Boldog, T. Tekeli, Risk assessment of novel coronavirus covid-19 outbreaks outside china, *J. Clin. Med.* 9 (2020) 1–12, <https://doi.org/10.3390/jcm9020571>.
- [7] Q. Lin, S. Zhao, A conceptual model for the coronavirus disease 2019 (covid-19) outbreak in wuhan, china with individual reaction and governmental action, *Int. J. Infect. Dis.* 93 (2020) 211–216, <https://doi.org/10.1016/j.ijid.2020.02.058>.
- [8] C. Kirkeby, T. Halasa, Methods for estimating disease transmission rates: evaluating the precision of poisson regression and two novel methods, *Sci. Rep.* 7 (2017) 1–11, <https://doi.org/10.1038/s41598-017-09209-x>.
- [9] S. Sanche, Y.T. Lin, High contagiousness and rapid spread of severe acute respiratory syndrome coronavirus 2, *Emerg. Infect. Dis.* 26 (7) (2020) 1470–1477, <https://doi.org/10.3201/eid2607.200282>.
- [10] P. Driessche, Reproduction numbers of infectious disease models, *Adv. Res. Evol. Sci.* 2 (2017) 288–303, <https://doi.org/10.1016/j.idm.2017.06.002>.
- [11] B. Ridenhour, J.M. Kowalik, Unraveling r0: considerations for public health applications, *Am. J. Public Health* 104 (2014) 32–41, <https://doi.org/10.2105/AJPH.2013.301704>.
- [12] P. Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, *Math. Biosci. Elsevier Sci. Inc* 180 (2002) 29–48, [https://doi.org/10.1016/S0025-5564\(02\)00108-6](https://doi.org/10.1016/S0025-5564(02)00108-6).
- [13] M. Khan, K. Ali, Mathematical modeling and stability analysis of pine wilt disease with optimal control, *Sci. Rep.* 7. doi:10.1038/s41598-017-03179-w.
- [14] M.A. Safi, S. Garba, Global stability analysis of seir model with holling type incidence function, *Comput. Math. Methods Med.* 2012 (2012) 1–8, <https://doi.org/10.1155/2012/826052>.
- [15] P. Singh, S. Srivastava, Stability of seir model of infectious diseases with human immunity, *Glob. J. Pure Appl. Math.* 13 (2017) 1811–1819, <http://www.ripublication.com/gjpam.htm>.
- [16] M. Raissi, N. Ramezani, On parameter estimation approaches for predicting disease transmission through optimization, deep learning and statistical inference methods, *Lett. Biomathematics* (2019) 1–26, <https://doi.org/10.1080/23737867.2019.1676172>.
- [17] A.A. Ding, H. Wu, Estimation of ordinary differential equation parameters using constrained local polynomial regression, *HHS Public Access* 24 (2014) 1613–1631, <https://doi.org/10.5705/ss.2012.304>.
- [18] D.L. Lukes, *Differential Equations: Classical to Controlled, Mathematics in Science and Engineering*, Academic Press, New York, 1982, ISBN 9780080956688.
- [19] S. Lenhart, J.T. Workman, *Optimal Control Applied to Biological Models: Mathematical and Computational Biology Series*, first ed., CRC Press, London, 2007.
- [20] E. Bonyah, M.A. Khan, Modelling the effects of heavy alcohol consumption on the transmission dynamics of gonorrhea with optimal control, *Math. Biosciences* 309 (2019) 1–11, <https://doi.org/10.1016/j.mbs.2018.12.015>.
- [21] A. Hugo, O.D. Makinde, Optimal control and cost effectiveness analysis for newcastle disease eco-epidemiological model in tanzania, *J. Biol. Dyn.* 11 (2017) 190–209, <https://doi.org/10.1080/17513758.2016.1258093>.
- [22] R.L.M. Neilan, E. Schaefer, Modeling optimal intervention strategies for cholera, *Bull. Math. Biol.* 72 (2010) 2004–2018, <https://doi.org/10.1007/s11538-010-9521-8>.