Modelling the transmission dynamics of coronavirus disease 2019 with treatment as a control strategy: the case of India

Sonam Gyeltshen*

Department of Humanities and Management,
Jigme Namgyel Engineering College,
Samdrup Jongkhar, Bhutan
Email: sonamgyeltshen@jnec.edu.bt
*Corresponding author

Thinley Tobgay

Department of Electrical Engineering,
Jigme Namgyel Engineering College,
Samdrup Jongkhar, Bhutan
Email: thinleytobgay555@gmail.com

Abstract: This paper models the transmission dynamics of coronavirus disease 2019 (COVID-19) and its treatment based on the cases in India, by extending the classic SIR model to include exposed, asymptomatic, and treatment classes with a special focus to investigate the effect of ineffective treatment on the transmissibility of the infection with variation in the treatment initiation. The basic reproduction number was computed to understand the relative effect of early treatment initiation from the delayed treatment initiation on the transmissibility of the infection. With the estimated parameters obtained by faithfully fitting the simulation to the observed data, a global sensitivity analysis carried out indicated the treatment initiation to be one of the most influential parameters to infection control. With this concept, a further analysis revealed that an early treatment initiation can be a helpful control strategy on the transmissibility of the infection. However, for it to happen, an intervention such as proactively doing case finding is deemed important.

Keywords: coronavirus; transmission dynamics; treatment initiation; ineffective treatment; SIR; susceptible, infectious and recovery; global sensitivity analysis; basic reproduction number; symptom onset; control strategy; asymptomatic; India.

Reference to this paper should be made as follows: Gyeltshen, S. and Tobgay, T. (2022) 'Modelling the transmission dynamics of coronavirus disease 2019 with treatment as a control strategy: the case of India', *Int. J. Mathematical Modelling and Numerical Optimisation*, Vol. 12, No. 1, pp.29–42.

Biographical notes: Sonam Gyeltshen is a Lecturer in the Department of Humanities and Management at Jigme Namgyel Engineering College, Royal University of Bhutan, Bhutan. He holds a BSc in Physical Science from the Sherubtse College, Bhutan, then under Delhi University, Delhi, India, and MSc in Applied Mathematics from the South Asian University, New Delhi, India. His current research interest includes the mathematical modelling of infectious diseases.

Thinley Tobgay received his Bachelor in Electrical Engineering from the College of Science and Technology under Royal University of Bhutan, Bhutan. He works as an Assistant Lecturer in the Department of Electrical Engineering, Jigme Namgyel Engineering College under Royal University of Bhutan, Bhutan.

1 Introduction

The ongoing pandemic commonly known as coronavirus disease 2019 (COVID-19) is a contagious disease caused by the virus called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Mandal et al., 2020). The disease was first detected in the Chinese city of Wuhan, the capital of Hubei Province, China, towards the end of 2019 (Ndairou et al., 2020). Since then the coronavirus has spread like a wildfire declaring as a global pandemic by the World Health Organization (WHO). As of 8th August 2020, the WHO reports that the total cases stand at 19,187,943, and total death at 716,075 worldwide (Organization, 2020). Based on the current research report the virus is rapidly transmitted from person to person through droplets when a person is in close contact with someone who has respiratory symptoms, fomite when a person is in the infected environment (Ong et al., 2020), and through faeces (Zhang et al., 2020). The recent development was that airborne transmission may also be possible but under certain circumstances (Ndairou et al., 2020).

Presently there is no cure or vaccine for COVID-19. It is still under development. Currently, the treatment for the infected people receive is not a pharmaceutical treatment but a symptomatic treatment that manages the disease by reducing the symptoms when the virus runs its course (Ginot et al., 2006). So, this means that the treatments provided are not fully effective. Amid this shortcoming, different countries have put up non-pharmaceutical interventions such as handwashing with soap, face mask in public places, social distancing, and imposing of lockdown (Gomero, 2012).

Many mathematical models have been developed to understand the behaviour of this infectious disease as it is one of the powerful tools to better understand the epidemiological processes (Omame et al., 2020; Kizito and Tumwiine, 2018). Modelling can help in understanding:

1 the transmissibility of the disease

2 predict the peak time of the disease

3 the effectiveness of the interventions (Kizito and Tumwiine, 2018).

Thus, WHO has recognised the importance of the mathematical model especially a timely developed model where it can play a crucial role in informing policymakers by giving evidence-based information (Tang et al., 2020a). Ndairou et al. (2020) has modelled a transmission dynamics of the COVID-19 by extending the classic SIR model to the SEAIRF model to include a super-spreader and hospitalised classes, where the later is similar to the treatment class which is of interest to this paper. A hospitalised class is a class where symptomatic people and super-spreaders get transitioned to at a certain rate. It reports that the number of hospitalised people is relevant to give an estimate of the intensive care unit needed (Ndairou et al., 2020).

In this study, the researcher will study the transmission dynamics of the COVID-19 with treatment as the control strategy when the treatment is ineffective, which is a status of currently available treatment for the disease. This paper is organised as follows. In Section 2, the model is formulated with the special introduction of the treatment class. Under the qualitative analysis of the model, the subsections include the estimation of basic reproduction number, a sensitivity analysis using the partial rank correlational coefficient method and local stability analysis at disease-free equilibrium is done under Section 3. In Section 4, the numerical simulation includes the fitting of the model to the observed data and the effect of treatment on disease transmission with graphical illustration. The discussion is presented in Section 5.

2 Mathematical formulation of the model

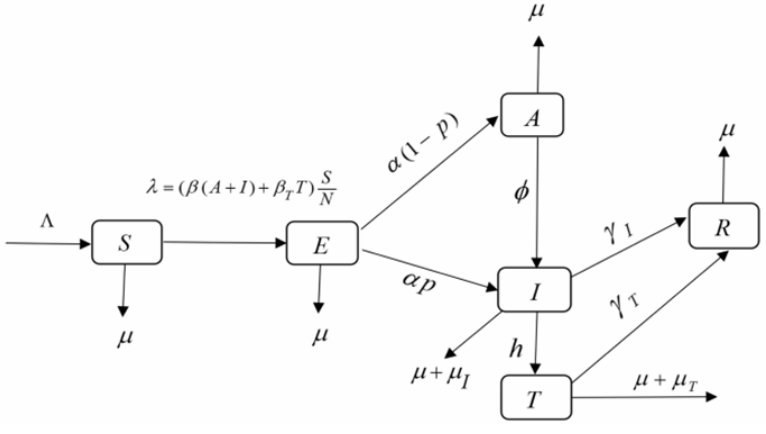
In this section, a *SEAITR* model is being modelled. To formulate the model mathematically the total population at the time t is given by $N(t)$ which is divided into seven exclusive classes based on the disease status of the individuals. Those are susceptible $S(t)$, exposed $E(t)$, infectious but asymptomatic $A(t)$, infectious and symptomatic $I(t)$, treatment $T(t)$ and recovered $R(t)$, mathematically expressed as $N(t) = S(t) + E(t) + A(t) + \mathrm{I}(t) + T(t) + R(t)$: individuals are recruited into the susceptible class through birth or immigration. But in the context of India recruitment rate Λ, through only birth is considered as the country was under lockdown with no immigration during the pandemic spread. When the susceptible individuals have effective contact with infectious individuals the force of infection from symptomatic, asymptomatic, and treatment classes act on the susceptible class and work to turn them into infective at a rate:

$$\lambda = \left(\beta(A+I) + \beta_T T\right)\frac{S}{N} \tag{1}$$

The asymptomatic class is infected individuals who are infectious but without symptoms, while symptomatic are infectious with symptoms. Both of these classes are untreated. A separate class is built for people who are hospitalised and are on treatment. People on treatment in the hospital remain ill but with reduced symptoms as treatment is a symptomatic treatment that is not fully effective. That is why even people on treatment are infectious but less infectious than asymptomatic and symptomatic individuals. Figure 1 is a schematic representation of the model SEAITR with different compartments interacting with each other in a human population. It shows the disease status of individuals in the population. Each of the class is governed by the parameters attached to each class. Their interactions are indicated by the arrows between them. The model assumes a homogeneous mixing of the individuals in the population where every individual is equally likely to get exposed or infected with the disease. As of now, it is not yet clear if the recovered individuals would gain a lifelong immunity or wane its immunity over the period (Zeb et al., 2020), so this model assumes that the recovered individual does not fall back again to the susceptible class. It also assumes that individuals on treatment receive treatment that is not fully effective to cure the disease. However, as most of the infected individuals on treatment would remain hospitalised

their effective contact rate with susceptible would be very minimal contributing less to the disease transmission.

Figure 1 Schematic representation of the model SEAITR with different compartments interacting with each other in a human population



The rate of change of population in each class at any instant of time t is described by the following nonlinear autonomous system of ordinary differential equations:

$$\begin{cases} \dfrac{dS}{dt} = \Lambda - \left(\beta(A+I) + \beta_T T\right)\dfrac{S}{N} - \mu S \\ \dfrac{dE}{dt} = \left(\beta(A+I) + \beta_T T\right)\dfrac{S}{N} - (\alpha + \mu)E \\ \dfrac{dA}{dt} = \alpha(1-p)E - (\mu + \phi)A \\ \dfrac{dI}{dt} = \alpha pE + \phi A - \left(\gamma_I + \mu_I + \mu + h\right)I \\ \dfrac{dT}{dt} = hI - \left(\gamma_T + \mu_T + \mu\right)T \\ \dfrac{dR}{dt} = \gamma_I I + \gamma_T T - \mu R \end{cases} \tag{2}$$

With the initial conditions:

$$\begin{cases} S(t_0) = S_0,\ E(t_0) = E_0,\ A(t_0) = A_0 \\ I(t_0) = I_0,\ T(t_0) = T_0,\ R(t_0) = R_0 \end{cases} \tag{3}$$

In the model (2), β represent the transmission coefficient per unit day per person due to asymptomatic and symptomatic individuals and β_T the transmission coefficient per unit day per person due to individuals on treatment. Here, α is the rate at which exposed individuals become infectious by becoming asymptomatic or symptomatic; ϕ is the rate at which the asymptomatic individual becomes symptomatic; h is the rate at which the treatment is initiated which is the reciprocal of the average day the treatment starts from the onset of the symptom. The constant $p (0 < p < 1)$ is the proportion of progression from

the exposed class to the symptomatic class while the other constant $1 - p$ is the proportion of progression from the exposed class to the asymptomatic class. The demographic effect is considered in the model by including Λ the rate of recruitment through birth only to the susceptible population and μ as the natural mortality rate leaving from each of the six classes. Symbols γ_I and γ_T symbolises recovery rate from symptomatic and treatment compartment respectively while disease induced mortality rate from symptomatic and treatment compartment is symbolised by μ_I and μ_T respectively.

3 Qualitative analysis of the model

3.1 Basic reproduction number

A basic reproduction number is the average number of secondary infections a single infection can cause during its infectious period in a completely susceptible population (Wang et al., 2020; Van den Driessche and Watmough, 2000). Sarkar et al. (2020) asserts that it is a crucial parameter that determines if the disease would persist or die out in a population. Further, Tang et al. (2020b) stress that the basic reproduction number can help in determining the potential and severity of the outbreak and provide important information for identifying the type of diseases intervention and intensity. Only if the basic reproduction number is above the threshold value will the disease spread in susceptible population (Krämer et al., 2010). As outlined in Diekmann et al. (1990), Van den Driessche and Watmough (2002), the basic reproduction number can be computed using a next-generation matrix approach to model (2). It considers below mentioned the non-negative matrix $\mathcal{F}$ and the non-singular M-matrix $\mathcal{V}$ (Sarkar et al., 2020) which are associated with the appearance of new infections and the corresponding transition part respectively for the system (2) is described by:

$$\mathcal{F} = \begin{vmatrix} \beta(A+I)\dfrac{S}{N} + \beta_T T \dfrac{S}{N} \\ 0 \\ 0 \\ 0 \end{vmatrix} \quad \mathcal{V} = \begin{vmatrix} (\alpha+\mu)E \\ (\mu+\phi)A - \alpha(1-p)E \\ (h+\gamma_I+\mu_I+\mu)I - \alpha pE - \phi A \\ (\gamma_T+\mu_T+\mu)T - hI \end{vmatrix}$$

At disease-free equilibrium, $E = A = I = T = R = 0$, the generation matrices that are Jacobian matrices associated with $\mathcal{F}$ and $\mathcal{V}$ are given by:

$$F = \begin{vmatrix} 0 & \beta & \beta & \beta_T \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{vmatrix} \quad V = \begin{vmatrix} \omega_1 & 0 & 0 & 0 \\ -\omega_2 & \omega_3 & 0 & 0 \\ -\omega_4 & -\phi & \omega_5 & 0 \\ 0 & 0 & -h & \omega_6 \end{vmatrix}$$

where

$$\begin{cases} \omega_1 = \alpha\mu, \omega_2 = \alpha(1-p), \omega_3 = \mu + \phi \\ \omega_4 = \alpha p, \omega_5 = \gamma_I + \mu_I + \mu + h \\ \omega_6 = \gamma_T + \mu_T + \mu \end{cases} \tag{4}$$

The inverse of the above matrix V exists, then the next generation matrix FV^{-1} is:

$$\begin{vmatrix} \frac{\beta\omega_1}{\omega_1\omega_3} + A & \frac{\beta}{\omega_3} + B & \frac{\beta}{\omega_5} + \frac{\beta_T h}{\omega_5\omega_6} & \frac{\beta_T}{\omega_6} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{vmatrix}$$

where

$$\begin{cases} A = \dfrac{\beta(\phi\omega_2 + \omega_3\omega_4)}{\omega_1\omega_3\omega_5} + \dfrac{\beta_T h(\phi\omega_2 + \omega_3\omega_4)}{\omega_1\omega_3\omega_5\omega_6} \\ B = \dfrac{\beta\phi}{\omega_3\omega_5} + \dfrac{\beta_T h\phi}{\omega_3\omega_5\omega_6} \end{cases} \tag{5}$$

The basic reproduction number R_0 is obtained as the spectral radius of the next generation matrix (Roser et al., 2020). Thus, the basic reproduction number for the model (2) is:

$$R_0 = \rho(FV^{-1}) = \frac{\beta(\phi\omega_2 + \omega_2\omega_5 + \omega_3\omega_4)}{\omega_1\omega_3\omega_5} + \frac{\beta_T h(\phi\omega_2 + \omega_3\omega_4)}{\omega_1\omega_3\omega_5\omega_6} \tag{6}$$

In interpreting the basic reproduction number, the first term represents the average number of secondary infections generated by the asymptomatic and symptomatic individuals, and the second term the average number of secondary infections generated by the individuals on treatment. Using the parameters estimated from the simulation (see Table 1), the basic reproduction number is computed to be R_0 = 1.3667. This indicates that the outbreak of the epidemic in India is not under control and is going to persist in the population.

3.2 Sensitivity analysis using partial rank correlation coefficient (PRCC) method

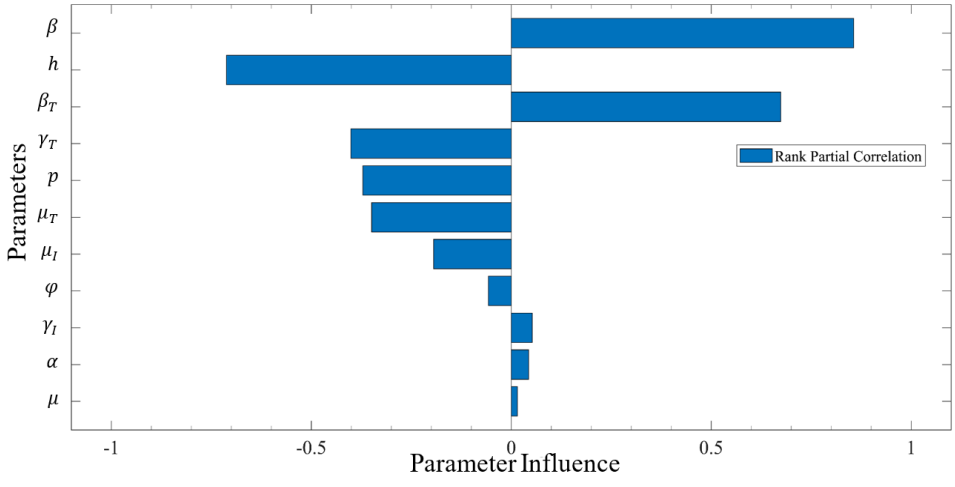
The goal of the sensitivity analysis is to identify the most influential parameters to the model variables (Saltelli et al., 2010; Ziyadi and Yakubu, 2016) in this case to the infection variables ($I + A + T$). It allows measuring the relative importance of the parameters (Blower and Dowlatabadi, 1994; Cacuci et al., 2005; Ginot et al., 2006). Knowledge of the relative importance of the parameters can help guide in developing efficient intervention strategies during COVID-19 transmission (Chitnis et al., 2008). Here the primary model variable of interest for sensitivity analysis is the infected states ($I + A + T$) against all the parameter values. A global sensitivity analysis is considered for this purpose. Global sensitive analysis (GSA) examines the change in the model variables which results from the change in all model parameter values that are within the ranges (Wu et al., 2013; Marino et al., 2008).

Table 1 Parameters estimate of SEAITR model (2) for which $R_0 = 1.3667$

Parameter	*Parameter meaning*	*Values*	*Units*
Λ	Rate of recruitment through birth	77575	day^{-1}
β	Transmission coefficient due to asymptomatic and symptomatic individuals	0.23156	day^{-1}
β_T	Transmission coefficient due to people on treatment	0.0017268	day^{-1}
α	Rate at which expose become infectious	1.9545	day^{-1}
p	Proportion of progression from exposed to symptomatic I	0.79443	Dimensionless
ϕ	Rate at which asymptomatic become symptomatic	2.5999	day^{-1}
h	Rate of initiation of treatment from the day of symptom	0.077772	day^{-1}
γ_I	Recovery rate of symptomatic individuals	0.0003047	day^{-1}
γ_T	Recovery rate of treated individuals	0.11837	day^{-1}
μ_I	Disease induced mortality rate from symptomatic individual	0.094245	day^{-1}
μ_T	Disease induced mortality rate from individuals on treatment	0.038901	day^{-1}
μ	Natural mortality rate	0.000039638	day^{-1}

Here, for sensitivity analysis, Latin hypercube sampling (LHS) with PRCC technique was adopted (Gomero, 2012; Helton and Davis, 2002; Legrand et al., 2008). PRCC is an efficient and reliable sampling-based sensitivity analysis method that provides a nonlinear but monotonic relationship between the parameters and model variables by removing the linear effects of all parameters except the parameters of interest (Wu et al., 2013; Gomero, 2012). Using LHS, 150 samples from a uniform distribution of the parameter ranges for the output model was taken. For simulation, the PRCC values vary between +1.0 to –1.0 with absolute values closer to 1 indicating the parameter has a strong influence on the model variables (Wu et al., 2013). The sign indicates a qualitative relationship between the parameters and model variables. Negative and positive signs indicate the parameters being inversely and directly proportional to the output measures, respectively (Gomero, 2012). The result of the PRCC as shown in Figure 2 using parameters value estimates represents that the highly positively correlated parameters are the transmission coefficient due to infected individual β and the transmission due to people on treatment β_T whereas the highly negatively correlated parameters are the rate of treatment initiation from the day of symptom h, the recovery rate of treated individuals γ_T, the proportion of progression of individuals from exposed to symptomatic p and disease-induced mortality rate of the individuals on treatment μ_T. Therefore, the most influential parameters to the model variable are β, h, β_T, γ_T, p and μ_T from out of 11 parameters. Therefore, the interventions should target more in dealing with all of these influential parameters.

Figure 2 Parameter sensitivity (see online version for colours)



Note: PRCC illustrating the sensitivity indices of the estimated parameters (see Table 1) of SEAITR model against the model output ($I + A + T$).

3.3 Local stability analysis at diseases free equilibrium (DFE)

For the model (2), the sixth equation being an uncoupled equation from the rest of the coupled system can be separated to find its analytical solution through direct integration as follows:

$$R(t) = \gamma_I \int_0^t I(s)ds + \gamma_T \int_0^t T(s)ds - \mu \int_0^t R(s)ds \tag{7}$$

The local stability of the model (2) at DFE can be studied using the remaining coupled system of equations of five state variables such as S, E, A, I and T. The Jacobian matrix associated with the model (2) at DFE is:

$$J = \begin{vmatrix} -\mu & 0 & -\beta & -\beta & -\beta_T \\ 0 & -\omega_1 & \beta & \beta & \beta_T \\ 0 & \omega_2 & -\omega_3 & 0 & 0 \\ 0 & \omega_4 & \phi & -\omega_5 & 0 \\ 0 & 0 & 0 & h & -\omega_6 \end{vmatrix}$$

where ω_1, ω_2, ω_3, ω_4, ω_5, and ω_6 are defined in (4). Matrix J has eigenvalue $\lambda = -\mu$ while other eigenvalues are obtained from the characteristic equation (8).

$$f(\lambda) = \lambda^4 + a_1\lambda^3 + (a_2 - \beta b_2)\lambda^2 + \left[a_3 - (\beta b_3 + \beta_T b_4)\right]\lambda + a_4 - (\beta b_5 + \beta_T b_6) = 0 \tag{8}$$

where

$$\begin{cases} a_1 = \omega_1 + \omega_3 + \omega_5 + \omega_6 \\ a_2 = \omega_1\omega_3 + \omega_1\omega_5 + \omega_1\omega_6 + \omega_3\omega_5 + \omega_3\omega_6 + \omega_5\omega_6 \\ a_3 = \omega_1\omega_3\omega_5 + \omega_1\omega_3\omega_6 + \omega_1\omega_5\omega_6 + \omega_3\omega_5\omega_6 \\ a_4 = \omega_1\omega_3\omega_5\omega_6, b_2 = \omega_2 + \omega_4 \\ b_3 = \omega_2\omega_5 + \omega_3\omega_4 + \omega_2\omega_6 + \omega_4\omega_6 + \phi\omega_2, b_4 = h\omega_4 \\ b_5 = \omega_3\omega_4\omega_6 + \omega_2\omega_5\omega_6 + \phi\omega_2\omega_6 \\ b_6 = h(\phi\omega_2 + \omega_3\omega_4) \end{cases} \tag{9}$$

Now, if $R_0 < 1$, and if $\beta b_2 < a_2$, $\beta b_3 + \beta_I b_4 < a_3$ and $\beta b_5 + \beta_I b_6 < a_4$, then by Descarte's rule of signs, the characteristic equation (8) will have four real negative (or complex negative real parts) eigenvalues in addition to $\lambda = -\mu$. In conclusion, we just proved the following result:

Theorem: If $R_0 < 1$, and if $\beta b_2 < a_2$, $\beta b_3 + \beta_I b_4 < a_3$, $\beta b_5 + \beta_I b_6 < a_4$, then the disease-free equilibrium is locally asymptotically stable. Otherwise, it is unstable.

4 Numerical simulation

In this section of numerical simulation, the simulated model results are compared with the observed data to validate the simulated model. The starting day for the simulation is 30th January 2020 (day 0) where the first infected case was reported and up to 20th August 2020 (day 202), which is a simulation of 203 days. The observed data were retrieved from the dataset published by our world in data (Roser et al., 2020) and the parameters related information from worldometers (Zhu et al., 2020). As part of the validation of the simulated model, a curve fitting of the simulated model was done to the observed daily new cases as is depicted in Figure 3. The curves correspond to the number of confirmed cases per day. The black curve corresponds to the model simulated for the infection ($I + A + T$) while the red curve corresponds to the observed daily new cases. It is observed in Figure 3 that the simulated model fits quite well to the observed data. Since the disease is still at an early stage of the epidemic, there is not enough data to get a full blown-out data curve fitting to the simulation model. However, the calibration done here is modest. Once the model was calibrated to the observed data the parameters were estimated (see Table 1). These estimated parameters were used for calibration.

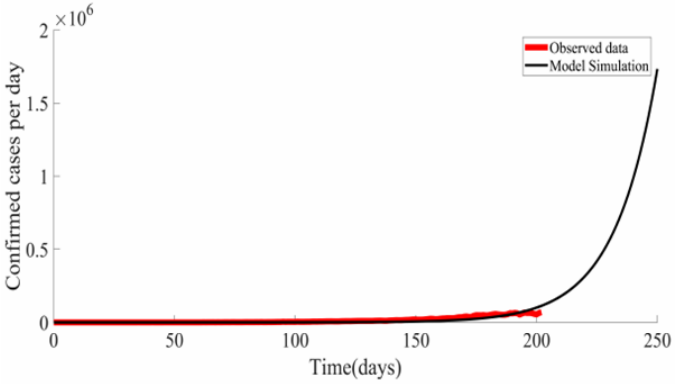
As obvious, India's population is very huge and dense, hence the daily new cases picked up ever since the infection begun in the country. The total population of India is about 1.38 billion. The initial conditions fixed for the simulation are: N = 1,380,004,385, $S_0 = N - 1$, $E_0 = 0$, $A_0 = 0$, $I_0 = 1$, $T_0 = 0$, $R_0 = 0$.

4.1 Effect of treatment on the disease transmission

As is evident from the sensitivity analysis Section 3.2, the treatment initiation has the maximum negative parameter influence on the model output. In this section, the influence of control strategies such as a treatment that is ineffective on the disease transmission dynamic is investigated by varying the treatment initiation h which in turn depends inversely on the day of onset of symptom. Considering this, people on ineffective

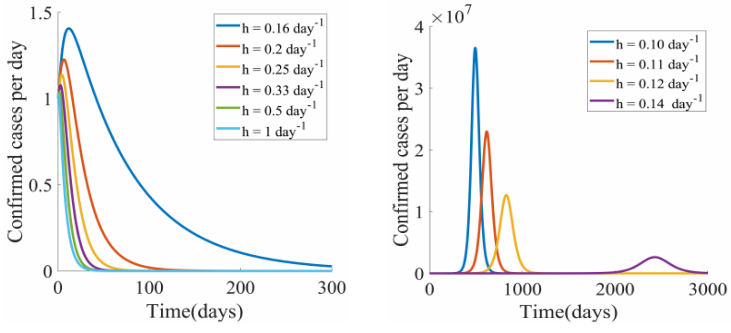
treatment in coming in contact with the susceptible would act with the force of infection $\beta_T T \frac{S}{N}$ in converting them into infected in addition to the force of infection from other two infectious classes. With this intuition, subsequent conclusions are drawn.

Figure 3 Number of confirmed cases per day (see online version for colours)



Note: The red line corresponds to observed data obtained from the dataset (Roser et al., 2020) of 203 days and the black line to the model simulated for infection ($I + A + T$).

Figure 4 Effect of ineffective treatment initiation, (a) ineffective treatment initiated can help in controlling the disease transmission $R_0 < 1$ if initiated latest by or within the seventh day of the appearance of the symptom, (b) ineffective treatment initiated beyond the seventh day would have less effect on the disease transmission $R_0 > 1$ although it may help in delaying the peak of the epidemic (see online version for colours)

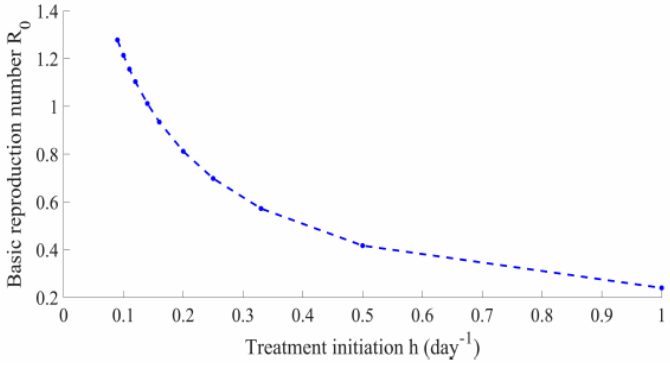


(a) (b)

The contribution of ineffective treatment in controlling disease transmission is studied as shown in Figure 4. Using the estimated parameters (see Table 1) and varying the rate of treatment initiation h, Figure 4 is obtained. Figure 4(a) illustrates that when the ineffective treatment is initiated within the seventh day of the onset of the symptom it can help in controlling the disease transmission, $R_0 < 1$. The peak of prevalence is reached earlier but with a reduction in its peak and the disease dies out from the population earlier. Likewise, Figure 4(b) illustrates that if the ineffective treatment is initiated on the seventh day of onset of symptoms or beyond, the treatment would have less effect on the

control of the disease transmission that is $R_0 > 1$. The peak of prevalence is delayed and the disease slowly dies out from the population as is illustrated in Figure 4(b). Also, the relationship between the basic reproduction number R_0 and the treatment initiation h is inversely proportional as is illustrated in Figure 5.

Figure 5 Relationship between the basic reproduction number R_0 and the treatment initiation h showing an inverse relationship (see online version for colours)



5 Discussion

In this work, a SEAITR model for COVID-19 was developed that specifically include asymptomatic, symptomatic, and treatment classes to capture the real characteristics of the disease dynamics. While people under these three classes are responsible for the disease transmission here the focus was given more on the treatment class which is further investigated by considering the ineffectiveness of the treatment.

The simulated model fits quite well to the early part of the data reported in Roser et al. (2020). This indicates that the finding from this model to a certain extent can be useful in informing the health authorities in estimating the number of people who would be on treatment and accordingly plan for the required number of hospital beds and other related treatment amenities (Ndairou et al., 2020).

Using the estimated parameter values this model predicts the basic reproduction number to be $R_0 = 1.3667$ in India which is below 1.4–2.5 in Wuhan, China as per WHO as of 23rd January 2020 (Croda and Garcia, 2020). R_0 in India is less than the WHO estimation because by then the disease reached India, authorities were more aware of the precautionary measures and gave time to prepare for COVID-19 due to which more restrictions were put in place such as lockdown, social distancing, wearing of face mask in public, and practising of good personal hygiene, during the outbreak.

From the sensitivity analysis, it points to the fact that more attention needs to be given to reducing the transmission coefficient β as it is the most influential factor in the disease dynamics which in turn depends on the contact rate and the probability of infection in each contact of infected with the susceptible population. In this regard, an appropriate control strategy would be in keeping the susceptible without contact with the infected which can be done through social distancing and lockdown.

Once there is the prevalence of infected cases the control strategy such as the treatment even when ineffective may still help in controlling the infection transmission to

a certain extent if the treatment is initiated within a certain day from the onset of the symptoms. The treatment initiation value close to one indicates an early treatment initiation. So, for treatment to help control transmission dynamic the treatment should be initiated early. However, for it to happen the intervention such as proactively doing case finding is deemed important (Li et al., 2020).

The majority of the prior studies done on COVID-19 related control strategies emphasised that social distancing, isolation, quarantine, and lockdown as some of the important control strategies. More so, a similar study was done on COVID-19 by Ullah and Khan (2020) and their findings are that a mild social distancing can reduce the number of cases while a stricter social distancing for an extended period would avoid a significant COVID-19 outbreak. Their study also highlights that the highly effective quarantine would reduce the peak of the pandemic. On the other hand, this study is distinctive because it highlights the effect of treatment of COVID-19 also as the control strategies for the disease. Therefore, the distinctive findings of this study are that the symptomatic treatment even if it is ineffective in curing the disease would certainly help in controlling the number of the cases which in turn may help in slowing the transmission dynamics of the disease as is depicted in Figure 4(a). Also, this study indicates that the transmission coefficient β to be one of the most influential parameters. Such finding would help the policymakers to decide on the kind of interventions or control strategies to be put in place or measure its effectiveness if already in place.

While this study may have its own merits but also has its limitations. The COVID-19 itself being relatively a new disease has many things to be yet known. From whatever has been known to date a mathematical model is done considering the process as an instantaneous process. However, the dynamics of COVID-19 is such that it has a latent period and some delay in the recovery. So in the future, it would be more realistic if instead of the ordinary differential equations a system of delay differential equations is used.

References

Blower, S.M. and Dowlatabadi, H. (1994) 'Sensitivity and uncertainty analysis of complex models of disease transmission: an HIV model, as an example', *International Statistical Review/Revue Internationale de Statistique*, Vol. 62, No. 2, pp.229–243.

Cacuci, D.G., Ionescu-Bujor, M. and Navon, I.M. (2005) *Sensitivity and Uncertainty Analysis, Volume II: Applications to Large-Scale Systems*, Vol. 2, CRC Press, Florida, USA.

Chitnis, N., Hyman, J.M. and Cushing, J.M. (2008) 'Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model', *Bulletin of mathematical biology*, Vol. 70, No. 5, p.1272.

Croda, J.H.R. and Garcia, L.P. (2020) 'Immediate health surveillance response to covid-19 epidemic', *Epidemiology and Health Services*, Vol. 29, No. 1, pp.883–891.

Diekmann, O., Heesterbeek, J.A.P. and Metz, J.A. (1990) 'On the definition and the computation of the basic reproduction ratio r0 in models for infectious diseases in heterogeneous populations', *Journal of Mathematical Biology*, Vol. 28, No. 4, pp.365–382.

Ginot, V., Gaba, S., Beaudouin, R., Aries, F. and Monod, H. (2006) 'Combined use of local and ANOVA-based global sensitivity analyses for the investigation of a stochastic dynamic model: application to the case study of an individual-based model of a fish population', *Ecological Modelling*, Vol. 193, No. 3, pp.479–491.

Gomero, B. (2012) *Latin Hypercube Sampling and Partial Rank Correlation Coefficient Analysis Applied to an Optimal Control Problem*, Master's thesis, University of Tennessee [online] https://trace.tennessee.edu/utk_gradthes/1278.

Helton, J.C. and Davis, F. (2002) 'Illustration of sampling-based methods for uncertainty and sensitivity analysis', *Risk Analysis*, Vol. 22, No. 3, pp.591–622.

Kizito, M. and Tumwiine, J. (2018) 'A mathematical model of treatment and vaccination interventions of pneumococcal pneumonia infection dynamics', *Journal of Applied Mathematics*, Vol. 2018, No. 16, p.16.

Krämer, A., Kretzschmar, M. and Krickeberg, K. (2010) 'Mathematical models in infectious disease epidemiology', *Modern Infectious Disease Epidemiology. Statistics for Biology and Health*. Vol. 12, No. 2, pp.209–221.

Legrand, J., Sanchez, A., Le Pont, F., Camacho, L. and Larouze, B. (2008) 'Modeling the impact of tuberculosis control strategies in highly endemic overcrowded prisons', *PLoS One*, Vol. 3, No. 5, p.e2100.

Li, Z., Chen, Q., Feng, L., Rodewald, L., Xia, Y., Yu, H., Zhang, R., An, Z., Yin, W., Chen, W. et al. (2020) 'Active case finding with case management: the key to tackling the covid-19 pandemic', *The Lancet*, Vol. 396, No. 1, pp.63–70.

Mandal, M., Jana, S., Nandi, S.K., Khatua, A., Adak, S. and Kar, T. (2020) 'A model based study on the dynamics of covid-19: prediction and control', *Chaos, Solitons and Fractals*, Vol. 136, No. 1, p.109889.

Marino, S., Hogue, I.B., Ray, C.J. and Kirschner, D.E. (2008) 'Amethodology for performing global uncertainty and sensitivity analysis in systems biology', *Journal of Theoretical Biology*, Vol. 254, No. 1, pp.178–196.

Ndairou, F., Area, I., Nieto, J.J. and Torres, D.F. (2020) 'Mathematical modeling of covid-19 transmission dynamics with a case study of Wuhan', *Chaos, Solitons and Fractals*, Vol. 135, No. 1, p.109846.

Omame, A., Sene, N., Nometa, I., Nwakanma, C.I., Nwafor, E.U., Iheonu, N.O. and Okuonghae, D. (2020) 'Analysis of Covid-19 and comorbidity coinfection model with optimal control', *Medrxiv*, Vol. 2020, No. 1, pp.1–28.

Ong, S.W.X., Tan, Y.K., Chia, P.Y., Lee, T.H., Ng, O.T., Wong, M.S.Y. and Marimuthu, K. (2020) 'Air, surface environmental, and personal protective equipment contamination by severe acute respiratory syndrome coronavirus 2 (sars-cov-2) from a symptomatic patient', *Jama*, Vol. 323, No. 16, pp.1610–1612.

Organization, W.H. (2020) *Coronavirus Disease (Covid-19): Situation Report 182* [online] https://www.who.int/docs/default-source/coronaviruse/situationreports/20200720-covid-19-sitrep-182.pdf?sfvrsn=60aabc5c_2.

Roser, M., Ritchie, H., Ortiz-Ospina, E. and Hasell, J. (2020) 'Coronavirus pandemic (covid-19)', *Our World in Data* [online] http://www.ourworldindata.org/coronavirus.

Saltelli, A., Annoni, P., Azzini, I., Campolongo, F., Ratto, M. and Tarantola, S. (2010) 'Variance based sensitivity analysis of model output design and estimator for the total sensitivity index', *Computer Physics Communications*, Vol. 181, No. 2, pp.259–270.

Sarkar, K., Khajanchi, S. and Nieto, J.J. (2020) 'Modeling and forecasting the covid-19 pandemic in India', *Chaos, Solitons and Fractals*, Vol. 139, No. 1, p.110049.

Tang, B., Bragazzi, N.L., Li, Q., Tang, S., Xiao, Y. and Wu, J. (2020a) 'An updated estimation of the risk of transmission of the novel coronavirus (2019-ncov)', *Infectious Disease Modelling* Vol. 5, No. 1, pp.248–255.

Tang, B., Wang, X., Li, Q., Bragazzi, N.L., Tang, S., Xiao, Y. and Wu, J. (2020b) 'Estimation of the transmission risk of the 2019-ncov and its implication for public health interventions', *Journal of Clinical Medicine*, Vol. 9, No. 2, p.462.

Ullah, S. and Khan, M.A. (2020) 'Modeling the impact of non-pharmaceutical interventions on the dynamics of novel coronavirus with optimal control analysis with a case study', *Chaos, Solitons and Fractals*, Vol. 139, No. 1, p.110075.

Van den Driessche, P. and Watmough, J. (2000) 'A simple sis epidemic model with a backward bifurcation', *Journal of Mathematical Biology*, Vol. 40, No. 6, pp.525–540.

Van den Driessche, P. and Watmough, J. (2002) 'Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission', *Mathematical Biosciences*, Vol. 180, No. 2, pp.29–48.

Wang, H., Wang, Z., Dong, Y., Chang, R., Xu, C., Yu, X., Zhang, S., Tsamlag, L., Shang, M., Huang, J. et al. (2020) 'Phase-adjusted estimation of the number of coronavirus disease 2019 cases in Wuhan, China', *Cell Discovery*, Vol. 6, No. 1, pp.1–8.

Wu, J., Dhingra, R., Gambhir, M. and Remais, J.V. (2013) 'Sensitivity analysis of infectious disease models: methods, advances and their application', *Journal of the Royal Society Interface*, Vol. 10, No. 86, p.20121018.

Zeb, A., Alzahrani, E., Erturk, V.S. and Zaman, G. (2020) 'Mathematical model for coronavirus disease 2019 (covid-19) containing isolation class', *BioMed Research International*, Vol. 2020, No. 1, pp.1–7.

Zhang, Y., Chen, C., Zhu, S., Shu, C., Wang, D., Song, J., Song, Y., Zhen, W., Feng, Z., Wu, G. et al. (2020) 'Isolation of 2019-ncov from a stool specimen of a laboratory-confirmed case of the coronavirus disease 2019 (covid-19)', *China CDC Weekly*, Vol. 2, No. 8, pp.123–124.

Zhu, X., Ge, Y., Wu, T., Zhao, K., Chen, Y., Wu, B., Zhu, F., Zhu, B. and Cui, L. (2020) 'Co-infection with respiratory pathogens among covid-2019 cases', *Virus Research*, Vol. 285, No. 1, p.198005.

Ziyadi, N. and Yakubu, A.A. (2016) 'Local and global sensitivity analysis in a discrete-time SEIS epidemic model', *Advances in Dynamical Systems and Applications*, Vol. 11, No. 1, pp.15–33.