SEIR Model for COVID-19 Epidemic Using Delay Differential Equation

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Abstract. SEIR compartmental model for COVID-19 pandemic (SEIR_COVID) with exposed group is proposed and analysed in this paper. The steady state of this model is determined to control the pandemic. Zero Disease equilibrium and pandemic equilibrium are presented in SEIR_COVID model. In each case, the equilibrium prints are locally asymptotically stable under certain conditions. The Routh-Hurwitz criteria are used to study the stability of the equilibrium for COVID-19. This study showed that proposed SEIR_COVID model using Routh-Hurwitz criteria will be more effective for the COVID-19 pandemic prediction.

1. Introduction

The epidemiological reports of COVID-19 indicate that the US and European countries are the epicenters of the epidemic and that nearly 210 countries have registered COVID-19 cases. Government officials and policymakers in the affected countries face the greatest challenge of balancing public health measures and keeping the economy alive.

A compartmental SEIR (Susceptible Exposed, Infectious and Recuperated) model for COVID-19(called as SEIR_COVID in this paper) consists of state variables or control variables to find the optimal solution” (Md. Haider Ali Biswas, 2014). The SEIR_COVID for infectious disease tries to know the responsibility of COVID-19 testing and case-dependent isolation. When the asymptomatic infection occurs the testing results provides the results of developed symptoms of the individuals known as positive cases. “Quarantine policy dependent based on whether a case is i) unknown, ii) known positive, iii) known negative, or recuperated”. (David W. Berger, 2020)

SEIR_COVID epidemic system is calculated by using differential and algebraic equations with their seasonal forcing based on transmission rate. The cases are categorized in three ways based on the number of varying parameters at a time for study. They are i) one parameter ii) two parameters and iii) three parameters for analyze the dynamical nature of the SEIR_COVID epidemic system” (NaYi, 2009).SEIRS model is categorized in different classical epidemic models (e.g., i) SIR and SIS and ii) SEIR and SEIRS) which involve the relationships between the susceptible as S, exposed as E, infected as I, and recuperated as R for every individuals for understanding the infectious diseases (Trawicki, 2016).
The dynamics of SEIR_COVID model propagation measured the poor transmission ability of the incubation period with length. The government takes steps to monitor and isolate infiltration in detail. "Euler integration algorithm" tries to solve the effect of the infectious nature of incubation COVID-19 patients. The authors have presented the SEIR model for COVID-19 to predict the occurrence time for peak numbers cases for China (Shi Pengpeng, 2020) (Dhamodharavadhani & Rathipriya, 2020). A SEIR_COVID epidemic model with minimal evidence of treatment rate is proportional to the number of patients, as long as a certain capacity is low while this number remains stable. Dynamic behaviors studied with the help of mathematical analysis when the number of infections is high (Al-Shaikh, 2012).

The literature study showed that the stability of equilibria is found the reproduction number R0 is not defined as a threshold parameter this model provides the backward bifurcation while there is few number of hospital beds. “The saturated coefficient a is denoted as zero, it is discovered that the model is i) Saddle-Node bifurcation, ii) Hopf bifurcation, and iii) Bogdanov-Takens bifurcation of two dimension” (Gui-Hua Li, 2017).

The simulation model SEIR_COVID is used to identify the number of confirmed cases. Based on the confirmed cases the Municipal Government tries to avoid the infectious in various ways that is to avoid close contact with the other peoples in the society and use of mask is to decrease the infection rate (Zhou Tang, 2020). The CoronaTracker community tier to predict the COVID19 cases, deaths cases, and recovery cases through predictive modelling. This model tries to interpret the patterns of sentiment of the public. The related health information, and assess the political and the various economic influence of the spread of the virus (Fairoza Amira Binti Hamzah, 2020). Based on the literature to study the SEIR for COVID-19 showed that to reduce the contact rate of latent individuals, interventions such as quarantine. Self-isolation is one the best way to decrease the number of COVID-19 cases (Can Hou, 2020) (Dhamodharavadhani & Rathipriya, 2020).

Based on the studied, a SEIR_COVID model is proposed as a solution to keep track COVID-19 infection from undiagnosed people and for those who are at isolation, to assess effects of spread in the epidemic dynamics. In this paper, we propose a SEIR_COVID compartmental model using delay differential equations for evaluating the COVID-19 spread during the latent period.

2. Model Description

The SIR model, a basic epidemic model provides a relatively theoretical number of disease infectious cases in closed population overtime. Let us consider that the population for the SIR model is fixed and the development period of the communicable agent is rapid. Generally, the compartment model is consists of three boxes which split the entire population into number of distinct clusters.

S - People that are susceptible to the epidemic. 
I – Already infected people who can spread the disease to the S. 
R - People that are recuperated or deceased.

The incubation period for most of the infectious diseases varied according to their nature. Applying the incubation or development period (immunity period delay, infection period delay and incubation period delay) into the basic model can change the behaviours of the system.

SIR models using time delay is the one of the popular and widely used technique to capture the epidemiological backgrounds. In order to move the basic model to a more realistic level, we create another group called the Revealed Group (C).

E(t) – Number. of infected individuals that are not infectious at time t.
τ - The incubation period represents time period before the infected individuals can become infectious.
N - The fraction of infectious people and the people survived at time t.

βS(t-τ).I(t-τ) e^{-μτ} - The infection rate at ‘τ’ periods above

In this proposed SEIR_COVID model, the infected group I(t) is split into two distinct group namely.

• H(t) - number of COVID infected people and hospitalised.
• HN(t) - number of COVID infected people but not hospitalised (undetected)

In this model, we use
R(t) - number of infected people recuperated from the disease.
D(t) - number of infected people deceased due to the disease.
β - Rate of contact of infected people with the population.
μ - Recruitment and natural death rate.
α - Rate of infected people hospitalised.
γ - Recovery rate of infected people those who are hospitalised.
ω - Death rate due to the disease.

The proposed SEIR_COVID model is

\[
\frac{dS(t)}{dt} = \mu N(t) - \frac{\beta S(t)I(t)}{N(t)} - \mu S(t)
\]

\[
\frac{dE(t)}{dt} = \frac{\beta S(t)I(t)}{N(t)} - \frac{\beta S(t-\tau)I(t-\tau)}{N(t)} e^{-\mu t} - \mu E(t)
\]

\[
\frac{dI(t)}{dt} = \frac{\beta S(t-\tau)I(t-\tau)}{N(t)} e^{-\mu t} - \gamma H(t) - \mu I(t) - (1-\omega)H_N(t)
\]

\[
\frac{dH(t)}{dt} = \alpha I(t) - \gamma H(t) - \mu H(t)
\]

\[
\frac{dH_N(t)}{dt} = (1-\alpha)I(t) - (1-\omega)H_N(t) - \mu H_N(t)
\]

\[
\frac{dR(t)}{dt} = \gamma H(t) + (1-\omega)H_N(t) - \mu R(t)
\]

\[
\frac{dD(t)}{dt} = \omega H_N(t) + (1-\gamma)H(t)
\]

Outputs of the model: Here we present the outputs of the mathematical model used to analyze the results of the simulations.

The number of cases hospitalized at day t is
The number of cases not hospitalized is
\[ H(t) = h_o + \int_0^t [(1 - \alpha)I(t) - (1 - \omega - \mu)H_N(t)] \, dt \]

The number of recuperated cases on day \( t \)
\[ R(t) = r_o + \int_0^t [\gamma H(t) + (1 - \omega)H_N(t) - \mu R(t)] \, dt \]

The number of death due to disease is
\[ D(t) = d_o + \int_0^t [\omega H_N(t) + (1 - \gamma)H(t)] \, dt \]

Where \( h_o, h_no, r_o, d_o \) are the initial values in their respective states.

2.1. Stability analysis

In order to analyse stability of delay differential equations, we will need the steady states and characteristic equations from the set of delay differential equations.

The term \( E(t) \) appears only in the differential equation, derivative of itself, so we can find \( E(t) \) once we know \( S(t) \) and \( I(t) \)

Now let,
\[ \lim S(t) = \lim S(t-\tau) = S^* \]
\[ \lim I(t) = \lim I(t-\tau) = I^* \]

Then, the steady states can be calculated by setting the above differential equations to zero ie,
\[ \frac{dS}{dt} = \frac{dI}{dt} = \frac{dH}{dt} = \frac{dR}{dt} = 0 \]

It is easy to show that, the system has two positive equilibriums, namely
(i) Zero Disease equilibrium \( E_0 = (S_0, I_0, H_0, H_N, R_0) \)
(ii) Pandemic Equilibrium \( E^* = (S^*, I^*, H^*, H_N^*, R^*) \)

Consider the equations
\[ \mu N - \frac{BS^*}{N} I^* - \mu S^* = 0 \quad (1) \]
\[ \frac{BS^*}{N} e^{-\mu \tau} - \gamma I^* - \mu I^* - (1 - \omega)H^* = 0 \]

Since \( H^* \), \( H^*_N \) are subgroups of \( I^* \), we can rewrite the above one as
\[ \frac{BS^*}{N} e^{-\mu \tau} - \gamma I^* - \mu I^* - (1 - \omega)I^* = 0 \]

\[ I^* \left( \frac{BS^*}{N} e^{-\mu \tau} - \mu - \gamma - (1 - \omega) \right) = 0 \]

implies
implies

\[ S^* = \frac{(\gamma + \mu + 1 - \omega)}{\beta e^{-\mu t}} N \]

As the reproduction number \( R_0 = \frac{\beta e^{-\mu t}}{(1 + \gamma + \mu - \omega)} \)

implies \( S^* = \frac{N}{R_0} \)

Substituting \( I^* = 0 \) in equation (1)

\[ \mu N - \mu S^* = 0 \]

implies \( \mu (N - S^*) = 0 \)

implies \( N - S^* = 0 \)

implies \( S^* = N \)

As \( I^* = 0 \) i.e number of infected people is 0

implies \( H = HN = R = 0 \)

Therefore, the first steady state equilibrium,

\( E_0 = (N, 0, 0, 0, 0) \)

Substitute \( S^* = \frac{N}{R_0} \) in equation (1)

\[ \mu N - \frac{\beta N}{R_0} I^* = \mu \frac{N}{R_0} = 0 \]

\[ \mu N \left( 1 - \frac{1}{R_0} \right) = \frac{\beta}{R_0} I^* \]

\[ N \mu (R_0 - 1) = \beta I^* \]

\[ I^* = \frac{\mu N}{\beta} (R_0 - 1) \]

Substitute the value of \( I^* \) in \( \frac{dH(t)}{dt} \), \( \frac{dH_N(t)}{dt} \) and \( \frac{dR(t)}{dt} \), then

\[ \alpha \frac{\mu N}{\beta} (R_0 - 1) - (\gamma + \mu) H(t) = 0 \]

\[ H(t) = \frac{\alpha \mu N (R_0 - 1)}{\beta (\gamma + \mu)} \]

\[ (1 - \alpha) \frac{\mu N (R_0 - 1)}{\beta} = (1 - \omega) H_N(t) - \mu H_N(t) = 0 \]

\[ (1 - \alpha)(R_0 - 1) \frac{\mu N}{\beta} = (1 - \omega + \mu) H_N(t) \]
Therefore,
\[ R(t) = \left[ \frac{\mu N(R_0 - 1)}{\beta (\gamma + \mu)} + \frac{(1 - \omega) \mu N(1 - \omega)(R_0 - 1)}{\beta(1 - \omega + \mu)} \right] \frac{1}{\mu} \]

The second state pandemic equilibrium is
\[ E^* = \left( \frac{N}{R_0}, \frac{\mu N}{\beta} (R_0 - 1), \frac{\alpha N(R_0 - 1)}{R_0}, \frac{\mu N(1 - \omega)(1 - \omega)(R_0 - 1)}{\beta(1 - \omega + \mu)} \right) \]

1. \[ \frac{\gamma \mu N(R_0 - 1)}{\beta (\gamma + \mu)} + \frac{\mu N(1 - \omega)(1 - \omega)(R_0 - 1)}{\beta(1 - \omega + \mu)} \]

2.1.1. Theorem 1
The Zero Disease equilibrium of the SEIR\_COVID system is asymptotically stable locally if \( R_0 < 1 \) and unstable if \( R_0 > 1 \)

**proof:**
Consider the following equations for Jacobian Matrix
\[
\frac{dS(t)}{dt} = \mu N - \frac{\beta S I}{N} - \mu S \\
\frac{dI}{dt} = \frac{\beta S I e^{-\mu t}}{N} - \gamma I - \mu I - (1 - \omega) I \\
\frac{dR}{dt} = \gamma I + (1 - \omega) I - \mu R
\]

Jacobian Matrix for the above equation
\[
J = \begin{bmatrix} -\frac{\beta I}{N} & -\frac{\beta S}{N} & 0 \\ \frac{\beta S I e^{-\mu t}}{N} - \gamma - \mu + \omega - 1 & 0 \\ 0 & N & -\mu \end{bmatrix}
\]

The Jacobian matrix at the deceased equilibrium point is given as
\[
J_{E0} = \begin{bmatrix} -\frac{\mu}{\gamma + 1 - \omega} & -\frac{\beta}{\gamma + 1 - \omega} & 0 \\ 0 & \beta e^{-\mu t} - \gamma - \mu + \omega - 1 & 0 \\ 0 & 0 & -\mu - \lambda \end{bmatrix}
\]

The characteristic equation for the Jacobian matrix \( J_{E0} \) is \( \det(J_{E0} - \lambda I) = 0 \) where \( I \) is the 3x3 unit matrix. Therefore,
\[
\begin{vmatrix} -\mu - \lambda & -\frac{\beta}{\gamma + 1 - \omega} & 0 \\ 0 & \beta e^{-\mu t} - \gamma - \mu + \omega - 1 - \lambda & 0 \\ 0 & 0 & -\mu - \lambda \end{vmatrix} = 0
\]
Therefore, all the Eigen values of the characteristic equation are negative if $R_0 < 1$. Hence the equilibrium point $E_0$ is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

2.1.2. Theorem 2
Therefore, all the Eigen values of the characteristic equation are negative if $R_0 > 1$, the pandemic equilibrium point $E^*$ is locally asymptotically stable.

**Proof:**
The Jacobian matrix is

$$J = \begin{bmatrix}
-\frac{\beta I}{N} - \mu & -\frac{\beta S}{N} & 0 \\
\frac{\beta I e^{-\mu t}}{N} & \frac{\beta S e^{-\mu t}}{N} e^{-\mu t} - \gamma - \mu + \omega - 1 & 0 \\
0 & \gamma + 1 - \omega & -\mu
\end{bmatrix}$$

Pandemic equilibrium point $E^*$, then Jacobian matrix is

$$J_{E^*} = \begin{bmatrix}
-\frac{\beta N}{N} \cdot \frac{\mu N}{\beta} (R_0 - 1) & -\frac{\beta N}{N} \cdot \frac{N}{R_0} & 0 \\
\frac{\beta N e^{-\mu t}}{R_0} e^{-\mu t} - \gamma - \mu + \omega - 1 & 0 \\
0 & \gamma + 1 - \omega & -\mu
\end{bmatrix}$$

The characteristic equation for the Jacobian matrix is $\det(J_{E^*} - \lambda I) = 0$

$$\begin{vmatrix}
-\mu(R_0 - 1) - \lambda & -\frac{\beta}{R_0} & 0 \\
\mu(R_0 - 1)e^{-\mu t} & \frac{\beta e^{-\mu t}}{R_0} - \gamma - \mu + \omega - 1 - \lambda & 0 \\
0 & \gamma + 1 - \omega & -\mu - \lambda
\end{vmatrix} = 0$$

$$[-\mu(R_0 - 1) - \lambda]\left(\frac{\beta e^{-\mu t}}{R_0} - \gamma - \mu + \omega - 1 - \lambda\right)(-\mu - \lambda) + \frac{\beta}{R_0} [(\gamma + 1 - \omega)\mu(R_0 - 1)e^{-\mu t} - 0] = 0$$
\[-\mu(R_0 - 1) - \lambda\left[\left(\frac{R_0(y - \mu + 1 - \omega)}{R_0} - (y + \mu + 1 - \omega) - \lambda(-\mu - \lambda)\right)\right]
\]
\[+ \frac{\beta}{R_0} [(-\mu - \lambda)\mu(R_0 - 1)e^{-\mu\tau} - 0] = 0 \]
\[-\mu(R_0 - 1) - \lambda][\lambda\mu + \lambda^2] + \frac{\beta}{R_0} [(-\mu - \lambda) - \mu e^{-\mu\tau} (R_0 - 1)] = 0 \]
\[-\lambda^3 + \lambda^2[-\mu(R_0 - 1) - \mu] + \lambda\left[-\mu^2(R_0 - 1) - \frac{\beta\mu}{R_0} e^{-\mu\tau} (R_0 - 1)\right] - \frac{-\mu^2\beta e^{-\mu\tau}}{R_0} R_0 - 1 = 0 \]
\[\Lambda^3 + \lambda^2[\mu(R_0 - 1) + \mu] + \lambda\left[\mu^2(R_0 - 1) + \frac{\beta\mu}{R_0} e^{-\mu\tau} (R_0 - 1)\right] + \frac{\mu^2\beta e^{-\mu\tau}}{R_0} (R_0 - 1) = 0 \]
\[\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0 \]
where \((R_0 - 1) > 0\), that is
\[a_1 = [\mu(R_0 - 1) + \mu] > 0 \]
\[a_2 = \left[\mu^2(R_0 - 1) \frac{\beta\mu e^{-\mu\tau}}{R_0} (R_0 - 1)\right] > 0 \]
\[a_3 = \frac{\mu^2\beta e^{-\mu\tau}}{R_0} \]
If \(R_0 > 1\) ie \(a_1,a_2, a_3\) are positive if \(R_0 > 1\).
By Routh-Hurwitz criterion, the system is asymptotically stable if \(a_1,a_3 > 0\) and \(a_1,a_2 > a_3\).

Then \(E^* = \left(\frac{N}{R_0} \frac{\mu N}{\beta} (R_0 - 1) \frac{1}{\mu} \left(\frac{\nu N(R_0-1)}{\beta(y+\mu)} + \frac{\mu N(1-\nu)(1-\omega)(R_0-1)}{\beta(1-\omega+\mu)}\right)\right)\)
is asymptotically stable.

3. Data Analysis, Model fitting and results
COVID-19 epidemic in India with an \(R_0\) value of March to September are represented in table 1. The epidemic is clearly not growing at that rate in India. In figure 1 represents as the day wise COVID-19 cases (confirmed, active, cured and death) in India and day wise COVID-19 death cases of Tamil Nadu and Maharashtra are shown in figure 2.
Table 1. $R_0$ value of India

| Month       | $R_0$ |
|-------------|-------|
| March, 2020 | 1.83  |
| April, 2020 | 1.55  |
| May, 2020   | 1.49  |
| June, 2020  | 1.2   |
| July, 2020  | 1.19  |
| August, 2020| 1.58  |
| September, 2020 | 1.08 |

Figure 1. Day Wise Cases: India
4. Conclusion

The SEIR_COVID compartmental model with an exposed group has been proposed and analysed for COVID-19. The steady-state of this model has been studied using Routh-Hurwitz criteria. Zero Disease equilibrium and pandemic equilibrium variables have been used in this SEIR_COVID model for better prognosis of infections. Our proposed SEIR_COVID model will be effective in predicting the COVID-19 epidemic.

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