INDIAN JOURNAL OF SCIENCE AND TECHNOLOGY

RESEARCH ARTICLE

OPEN ACCESS

Received: 04-02-2023

Accepted: 11-08-2023

Published: 20-11-2023

Citation: Yagan AJC, Jasmine D (2023) Significance of an SEIHR Model with Preventive Class in Declining the Spread of COVID-19. Indian Journal of Science and Technology 16(SP3): 14-21. https://doi.org/10.17485/IJST/v16iSP3.icrtam130

* **Corresponding author**.

joshuajcy@gmail.com

Funding: None

Competing Interests: None

Published By Indian Society for Education and Environment (iSee)

ISSN
Print: 0974-6846
Electronic: 0974-5645

Significance of an SEIHR Model with Preventive Class in Declining the Spread of COVID-19

A Joshua Cyril Yagan[1]*, D Jasmine[1]

1 Department of Mathematics, Bishop Heber College (Autonomous), (Affiliated to Bharathidasan University), Tiruchirappalli, 620 017, Tamil Nadu, India

Abstract

Background/ Objectives: COVID-19 is being a global threat to humankind for past two years. Although the outbreak appears to be restrained at the moment, it is likely to become an epidemic again. Hence, there is an emergence of preventing such situation. This study reveals a model which helps to control this epidemic by sufficient control measures. **Methods:** The proposed model follows a vital dynamic. Two compartments namely hospitalised and preventive class were included along with the SEIR model. Further, the expression for the reproduction number has been derived using the Next-Generation matrix. **Findings:** The proposed model is well-defined. Also, the existence of the equilibrium points of the proposed model is justified. Further, the local stability of the equilibria is exhibited. **Novelty:** This study introduces the Preventive class, which plays a vital role in preventing the spread of outbreak and enhances the necessity of practicing preventive measures. The numerical simulations conclude that the constructed model is explicit and support to control the spread of COVID-19.

Keywords: COVID19; Epidemic; SEIR; NextGeneration Matrix; Preventive Class

1 Introduction

The term COVID-19 is globally popular, from the end of the year 2019. This infection is a contagious disease and it is spawned by the Severe Acute Respiratory Syndrome (SARS). The first victim of this disease was spotted in Wuhan, China. At that instance, the researchers were facing difficulty in understanding the mechanism of the spread of corona virus (CoV). This caused a delay in discovering antidrug for the virus. This scenario has been prevailed earlier at the time of evolvement of Ebola virus. Lot of research is being done to prevent the spreading nature of Ebola virus. For example, Tahir et. al analysed the stability and the spreading nature of the Ebola virus [(1)]. Similarly, Carcione JM et.al, modelled the dynamics of COVID-19 using an SEIR model and made a simulation [(2)]. In 2022, Bhadauria et.al published a research article that justifies the concept of practicing quarantining individual helps in controlling the spread of the disease [(3)]. Likewise, Zeb A. et.al, simulated a mathematical model for corona virus disease with the isolation class to manage the spread of corona virus [(4)].

The evolution of corona virus was challenging the researchers to predict its nature and to control it. Though the origin of COVID-19 has been traced faster, yet the cure is still under research. So researchers preferred alternative suggestions like immunity medicines and vaccinations which had brought a hesitation among people[5]. Researchers Zou et.al modelled the effect of vaccination and quarantine on transmission dynamics of COVID-19[6]. Also, Poonia et.al, suggested an enhanced SEIR model with the effect of vaccination which influenced the importance of getting vaccinated[7]. But people adapted the habit of practicing the advised control measures like wearing face mask, social distancing and sanitizing the surfaces.

Most of the research works are confined to the idea of insisting to get vaccinated and intake medicines. But this paper proposes a model in analysing the spreading nature of COVID-19 with prevention class which focuses on the importance of practicing preventive measures. The article is highlighted through the stability analysis using the corollary of Gershgorin's Circle Theorem[8]. Finally, the article compares the optimality of the proposed model by the numerical simulation[9].

Most of the individuals have been vaccinated yet some still hesitates to get vaccinated. Instead, people prefers to follow the control measures but it is confusing why they hesitate to get vaccinated. In order to dismiss the epidemic, there should be a proper model replicating the foresaid scenario of COVID-19 in controlling the reproduction number of the disease. Hence, this paper emphasise the importance of practicing the preventive measures and shows that the number of infective can be suppressed very quickly by means of proposing this model.

2 Methodology

2.1 Model formulation and its mathematical analysis

The proposed model incorporates the Preventive class and the Hospitalised class with SEIR model. This model stands out from other models and probably reflects the present reality. As people stop practicing wearing mask, maintaining social distance and sanitizing the surrounding, the proposed model would be more needed as it emphasizes the importance of preventive measures. Thus, it is clear that the proposed model differs from the usual SEIR model and is more efficient in controlling the disease.

1. **Assumptions**

The following are the assumptions made for the construction of the proposed model,

- The model is assumed to be of vital dynamics with birth rate Λ and mortality rate μ.
- The infection rate of the susceptible to infected class and the exposed class is denoted by β_1 and β_2 respectively.
- The infection rate of the exposed is given by γ.
- The recovery rates from exposed and the infected is noted as λ and δ_1 respectively.
- The Hospitalized class contains individuals who are at risk.
- The rate at which infected individual move to hospitalized class is given by η.
- Individuals who practice the control measures are considered in Prevention class.
- δ_2 and δ_3 are the recovery rates from hospitalized and prevention class respectively.
- k_1 and k_2 are the rates of disease caused mortalities.
- θ_1 and θ_2 are the rate at which the individuals move from susceptible and hospitalized classes to prevention class respectively.
- ε is the rate of individual who again fall in the susceptible class.

2.2 Mathematical model

System 1:

$$\frac{dS}{dt} = \Lambda - \beta_1 SI - \beta_2 SE - \theta_1 S - \mu S + \varepsilon R$$
$$\frac{dE}{dt} = \beta_2 SE - (\gamma + \lambda + \mu)E$$
$$\frac{dI}{dt} = \beta_1 SI + \gamma E - (\eta + \delta_1 + k_1 + \mu)I$$
$$\frac{dH}{dt} = \eta I - (\delta_2 + k_2 + \mu + \theta_2)H$$
$$\frac{dP}{dt} = \theta_1 S + \theta_2 H - (\mu + \delta_3)P$$
$$\frac{dR}{dt} = \lambda E + \delta_1 I + \delta_2 H + \delta_3 P - (\mu + \varepsilon)R$$

The system (1) consists of the following compartments namely Susceptible $S(t)$, Exposed $E(t)$, Infected $I(t)$, Hospitalized $H(t)$, Preventive $P(t)$ and Recovered $R(t)$satisfying the initial conditions $S(0) = S_0$, $E(0) = E_0$, $I(0) = I_0$, $H(0) = H_0$, $P(0) = P_0$ and $R(0) = R_0$ where, $S(t) + E(t) + I(t) + H(t) + P(t) + R(t) = N(t)$.

2.3 Preliminary properties

Lemma. The system (1) is considered to be well-defined if it defines a positive dynamical system within the domain, $\Phi = \left\{S(t), E(t), I(t), H(t), P(t), R(t) \in R_+^6 : N(t) \le \frac{\Lambda}{\mu}\right\}$.

Proof.

From (1),

$\frac{dS}{dt} = \Lambda - \beta_1 SI - \beta_2 SE - \theta_1 S - \mu S + \varepsilon R$

Integrating and solving, we get

$S(t) \ge S(0)\, e^{-(\mu+\beta_1 I+\beta_2 E)t}$

$S(t) \ge 0$

Similarly, we can say

$E(t) \ge 0, I(t) \ge 0, H(t) \ge 0, P(t) \ge 0$ and $R(t) \ge 0$.

Also,

$\frac{dN(t)}{dt} = S'(t) + E'(t) + I'(t) + H'(t) + P'(t) + R'(t)$

$= \Lambda - \mu N - k_1 I - k_2 H$

$\le \Lambda - \mu N$

$\lim_{t\to\infty} sup N(t) \le \frac{\Lambda}{\mu}$

Thus, the system is well-defined under the initial conditions.

2.4 Existence of equilibrium points

Two types of equilibrium points are required in the case of epidemic. They are Disease-free Equilibrium $\left(E^0\right)$ and Endemic Equilibrium(E^*).

Equating the first equation in system (1) to zero and solving for S^0, we obtain

$0 = \Lambda - \beta_1 S^0 I^0 - \beta_2 S^0 E^0 - \theta_1 S^0 - \mu S^0 + \varepsilon R^0$

$0 = \Lambda - (\theta_1 + \mu) S^0$

$S^0 = \frac{\Lambda}{(\theta_1+\mu)}$

Substituting the value of S^0 we obtained the expression for P^0 as follows

$P^0 = \frac{\Lambda\theta_1}{(\delta_3+\mu)(\theta_1+\mu)}$

Thus, the DFE is obtained as $\left(S^0,\ E^0, I^0, H^0, P^0, R^0\right) = \left(\frac{\Lambda}{(\theta_1+\mu)},\ 0,0,0, \frac{\Lambda\theta_1}{(\delta_3+\mu)(\theta_1+\mu)}, 0\right)$.

Similarly, the EE is derived as follows,

$S^* = \frac{(\gamma+\lambda+\mu)}{\beta_2}$

$E^* = \frac{\beta_2(\eta+\delta_1+k_1+\mu)-\beta_1(\gamma+\lambda+\mu)}{\gamma\beta_2} I^*$

$I^* = \frac{\Lambda(1-\varepsilon)+B_1\varepsilon-B_3}{(A_1M_2-B_2\varepsilon)}$

$H^* = \frac{\eta[\Lambda+\varepsilon R-M_2(\theta_1+\mu)]}{(\delta_2+k_2+\theta_2+\mu)(\beta_1+\beta_2 M_1)M_2}$

$P^* = \frac{1}{(\delta_3+\mu)}\left[\frac{\theta_1(\gamma+\lambda+\mu)}{\beta_2} + \frac{\theta_2\eta[\Lambda+\varepsilon R-M_2(\theta_1+\mu)]}{(\delta_2+k_2+\theta_2+\mu)(\beta_1+\beta_2 M_1)M_2}\right]$

$R^* = \frac{(\theta_1+\mu)(\gamma+\lambda+\mu)}{\varepsilon\beta_2} + \left[\frac{\beta_1(\gamma+\lambda+\mu)}{\beta_2} + M_1(\gamma+\lambda+\mu)\right] I^* - \Lambda$

where,

$A_1 = \beta_1 + \beta_2 M_1$

$M_1 = \frac{\beta_2(\eta+\delta_1+k_1+\mu)-\beta_1(\gamma+\lambda+\mu)}{\gamma\beta_2}$

$M_2 = \frac{(\gamma+\lambda+\mu)}{\beta_2}$

$B_1 = M_2\frac{(\theta_1+\mu)}{\varepsilon}$

$B_2 = M_2\beta_1 + M_1(\gamma+\lambda+\mu)$

$B_3 = M_2(\theta_1+\mu)$

2.5 Determination of reproduction number

Reproduction number is a constant value denoted as R_0 which defines the existence of the outbreak. The characteristic of the epidemic can be defined by the R_0 value as follows

(1) If $R_0 < 1$, then the outbreak will decline and might come to an end.
(2) If $R_0 > 1$, then the outbreak continues to be a pandemic.
The reproduction number of the system (1) can be obtained by the next generation matrix.
The Jacobian of the infective classes namely Exposed, Infected and Hospitalized classes is as follows:

$$J(E,I,H) = \begin{pmatrix} \beta_2 S - (\gamma + \lambda + \mu) & 0 & 0 \\ \gamma & \beta_1 S - (\eta + \delta_1 + k_1 + \mu) & 0 \\ 0 & \eta & -(\delta_2 + k_2 + \theta_2 + \mu) \end{pmatrix}$$

The transmission and the transition matrix is obtained as follows:

$$F = \begin{pmatrix} \beta_2 S & 0 & 0 \\ 0 & \beta_1 S & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and}$$

$$V^{-1} = \begin{pmatrix} \frac{-1}{(\gamma+\lambda+\mu)} & 0 & 0 \\ \frac{\gamma}{(\gamma+\lambda+\mu)(\eta+\delta_1+k_1+\mu)} & \frac{-1}{(\eta+\delta_1+k_1+\mu)} & 0 \\ \frac{-\gamma\eta}{(\gamma+\lambda+\mu)(\eta+\delta_1+k_1+\mu)(\delta_2+k_2+\theta_2+\mu)} & \frac{\eta}{(\eta+\delta_1+k_1+\mu)(\delta_2+k_2+\theta_2+\mu)} & \frac{-1}{(\delta_2+k_2+\theta_2+\mu)} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} \frac{-S\beta_2}{(\gamma+\lambda+\mu)} & 0 & 0 \\ \frac{\gamma\beta_1 S}{(\gamma+\lambda+\mu)(\eta+\delta_1+k_1+\mu)} & \frac{-S\beta_1}{(\eta+\delta_1+k_1+\mu)} & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

Thus, the eigenvalues of the above matrix are $0, \frac{-S\beta_2}{(\gamma+\lambda+\mu)}$ and $\frac{-S\beta_1}{(\eta+\delta_1+k_1+\mu)}$.

The reproduction number can be obtained by the spectral radius of matrix FV^{-1}. Spectral radius of a matrix is defined to be the maximum of the absolute values of its eigenvalues.

Hence, the reproduction number is obtained as given below

$$R_0 = \rho\left(FV^{-1}\right) = max\left\{\frac{S\beta_2}{(\gamma+\lambda+\mu)}, \frac{S\beta_1}{(\eta+\delta_1+k_1+\mu)}\right\}$$

2.6 Stability analysis of the equilibrium point

Theorem 1. If $R_0 < 1$ then the system (1) is stable at the DFE.

Proof. The Jacobian matrix of the system (1) at the DFE is as follows.

$$J(E_0) = \begin{pmatrix} -(\theta_1+\mu) & -\beta_2 S_0 & -\beta_1 S_0 & 0 & 0 & \varepsilon \\ 0 & \beta_2 S_0 - (\gamma+\lambda+\mu) & 0 & 0 & 0 & 0 \\ 0 & \gamma & \beta_1 S_0 - (\eta+\delta_1+k_1+\mu) & 0 & 0 & 0 \\ 0 & 0 & \eta & -(\delta_2+k_2+\theta_2+\mu) & 0 & 0 \\ \theta_1 & 0 & 0 & \theta_2 & -(\delta_3+\mu) & 0 \\ 0 & 0 & \delta_1 & \delta_2 & \delta_3 & -(\mu+\varepsilon) \end{pmatrix}$$

Clearly, the eigenvalues $\lambda_1 = -(\mu+\varepsilon)$, $\lambda_2 = -(\delta_3+\mu)$, $\lambda_3 = -(\delta_2+k_2+\theta_2+\mu)$ and $\lambda_4 = -(\theta_1+\mu)$ are all negative.
Whereas, the other two eigenvalues must satisfy the following conditions for the system to be stable.
(a) $\beta_2 S_0 > (\gamma+\lambda+\mu)$ and
(b) $\beta_1 S_0 - (\eta+\delta_1+k_1+\mu > \gamma)$
Obviously, (a) and (b) are satisfied if $R_0 < 1$.
Thus, the system (1) is stable at DFE for $R_0 < 1$.

Theorem 2. If $R_0 > 1$, then the system (1) is stable at EE.

Proof. The Jacobian matrix of the system at the EE is given by

$$J(E^*) = \begin{pmatrix} -\beta_1 I^* - \beta_2 E^* - \theta_1 - \mu & -\beta_2 S^* & -\beta_1 S^* & 0 & 0 & \varepsilon \\ \beta_2 E^* & \beta_2 S^* - (\gamma+\lambda+\mu) & 0 & 0 & 0 & 0 \\ \beta_1 I^* & \gamma & \beta_1 S^* - (\eta+\delta_1+k_1+\mu) & 0 & 0 & 0 \\ 0 & 0 & \eta & -(\delta_2+k_2+\theta_2+\mu) & 0 & 0 \\ \theta_1 & 0 & 0 & \theta_2 & -(\delta_3+\mu) & 0 \\ 0 & \lambda & \delta_1 & \delta_2 & \delta_3 & -(\mu+\varepsilon) \end{pmatrix}$$

For the system to be stable, all the eigenvalues must be negative. So, the diagonal elements must satisfy the following conditions

(i)$(\beta_1 I^* + \beta_2 E^* + \theta_1 + \mu) > (\beta_2 S^* + \beta_1 S^* - \varepsilon)$,
(ii)$\beta_2 S^* - (\gamma+\lambda+\mu) > \beta_2 E^*$

(iii)$\beta_1 S^* - (\eta + \delta_1 + k_1 + \mu) > (\beta_1 I^* + \gamma)$,
(iv)$(\delta_2 + k_2 + \theta_2 + \mu) > \eta$,
(v) $(\delta_3 + \mu) > (\theta_1 + \theta_2)$ and
(vi)$(\mu + \varepsilon) > (\lambda + \delta_1 + \delta_2 + \delta_3)$
Thus, for $R_0 > 1$ the system will be stable at the EE if the above conditions are satisfied.

3 Result and Discussion

The reproduction number R_0 is very much helpful in predicting the nature of the outbreak. By considering, the data used by Nwokoye et.al, in the article entitled 'The SEIQR–V Model: On a More Accurate Analytical Characterization of Malicious Threat Defence', we have $S_0 = 100,\ E_0 = 3,\ I_0 = 1,\ H_0 = 0, P_0 = 0,\ R_0 = 0,\ \Lambda = 0.1,\ \beta_1 = 0.1,\ \beta_2 = 0.1,\ \theta_1 = \theta_2 = 0.25,\ \varepsilon = 0.08,\ \gamma = 0.8,\ \lambda = 0.3,\ \eta = 0.1,\ \delta_1 = \delta_2 = \delta_3 = 0.4,\ k_1 = k_2 = 0.25$ and $\mu = 0.003$.

Substituting the above values and simplifying, we get all the possible values of Reproduction number at both the equilibrium points as follows:

Case (a): For $R_0 = \frac{S\beta_2}{(\gamma+\lambda+\mu)}$

(i) At disease-free equilibrium:

$R_0 = \frac{S_0\beta_2}{(\gamma+\lambda+\mu)} = \frac{0.3953\times 0.1}{1.103} = 0.0358$

Thus, $R_0 = 0.0358 < 1$

(ii) Similarly, at endemic equilibrium:

$R_0 = \frac{S^*\beta_2}{(\gamma+\lambda+\mu)} = \frac{11.03\times 0.1}{1.103} = 1$

Thus, $R_0 = 1$

Case (b): For $R_0 = \frac{S\beta_1}{(\eta+\delta_1+k_1+\mu)}$

(i) At disease-free equilibrium:

$R_0 = \frac{S_0\beta_1}{(\eta+\delta_1+k_1+\mu)} = \frac{0.3953\times 0.1}{0.753} = 0.0525$

$\therefore R_0 = 0.0525 < 1$

(ii) Similarly, at endemic equilibrium:

$R_0 = \frac{S^*\beta_1}{(\eta+\delta_1+k_1+\mu)} = \frac{11.03\times 0.1}{0.753} = 1.4648$

Hence, $R_0 = 1.4648 > 1$

Further, using MATLAB each compartment of the proposed model is compared with the corresponding compartment of a general SEIR model with quarantine class. Each curve plot exhibits the optimality of the proposed model comparing the considered SEIQR model. The following are the comparison curves of each class where $S*$, $E*$, $I*$, $Q*$ and $R*$ denotes the compartments of the considered model:

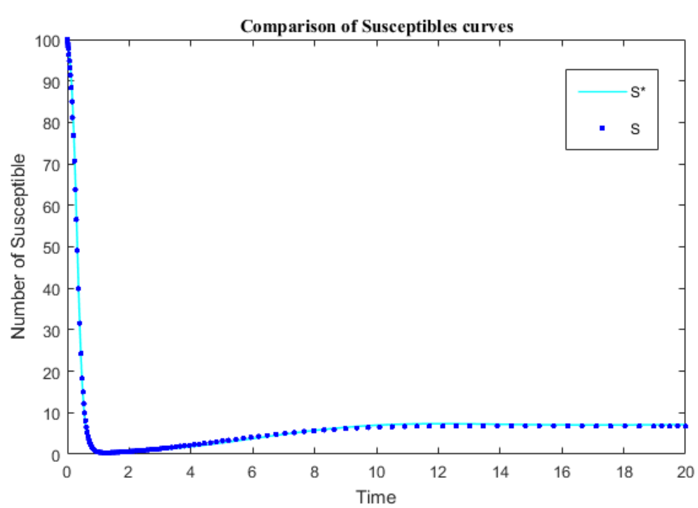

Fig 1. Comparison of susceptible curves

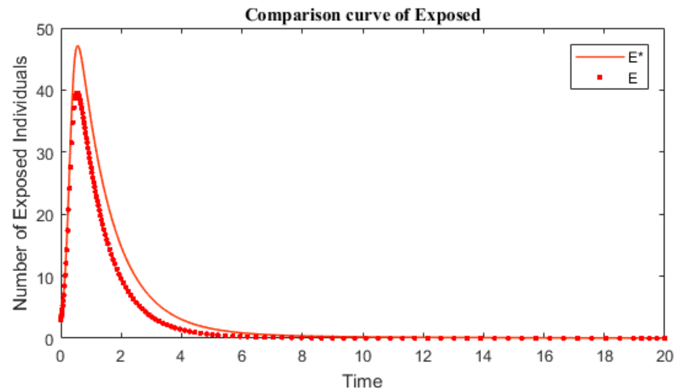

Fig 2. Comparison curve of exposed

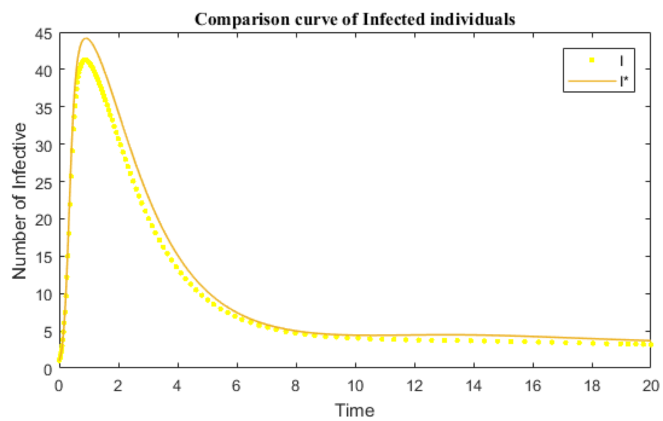

Fig 3. Comparison curve of infected individuals

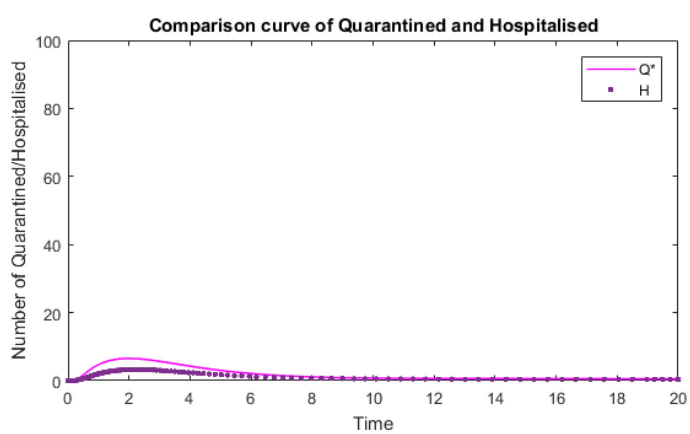

Fig 4. Comparison curve of quarantined and hospitalised

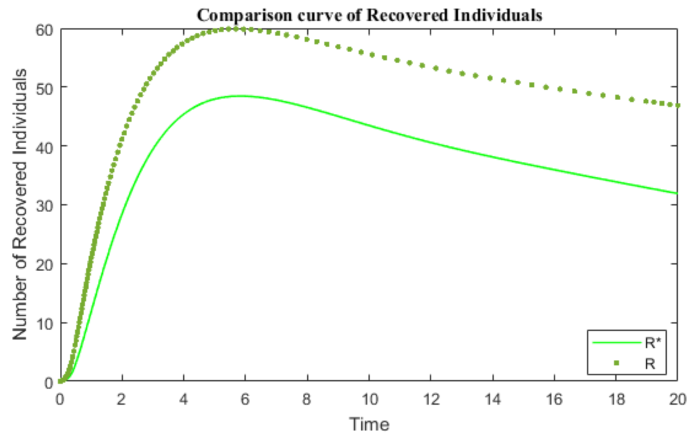

Fig 5. Comparison curve of recovered individuals

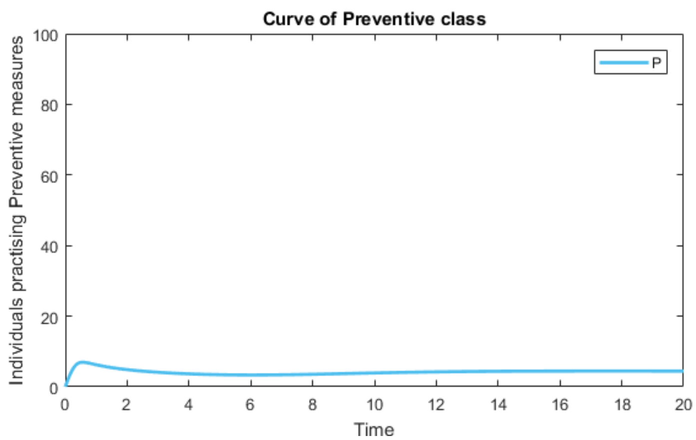

Fig 6. Curve of preventive class

The numerical simulation clearly states that the reproduction number for Case (a) at the disease-free equilibrium justifies Theorem 1 with the value of 0.0358 which is much lesser value implying that the outbreak is least or doesn't prevail. Also, at the endemic equilibrium the value of reproduction number is 1 which proves system (1) is stable. Further, from Figures 1, 2, 3, 4, 5 and 6, it is observed that the chance of susceptible individual getting infected is less, comparatively. Also, the exposed and the infected curve increases initially and it gradually drops down later. Figure 4 treats the hospitalised individuals of the proposed model and the quarantined individuals of the SEIQR model as relatively same category and hence compared. The recovered curve inclines and is more appreciable comparing the other model showing the prevention class helps in controlling the disease spread.

4 Conclusion

Eventually, it is expressed with clarified proofs that the prevention class plays a vital role in reducing the spread of COVID-19. The simulation performed reveals that maximum 7 among 100 individuals practicing the preventive measures can show a great variation in reducing the spread of COVID-19. The proposed model can be applied in the real data like case study and the zonal statistics can be obtained which helps in understanding the spreading nature of the disease. So, many awareness camps must be conducted regarding this issue. Hence, this article recommends practicing preventive measures helps to control the spread of COVID-19.

5 Declaration

Presented in "International Conference on Recent Trends in Applied Mathematics (ICRTAM 2023)" during 24th-25th February 2023, organized by Department of Mathematics, Loyola College, Chennai, Tamil Nadu, India. The Organizers claim the peer review responsibility.

References

1) Tahir M, Anwar N, Shah SIA, Khan T. Modeling and stability analysis of epidemic expansion disease Ebola virus with implications prevention in population. *Cogent Biology*. 2019;5(1):1–11. Available from: https://doi.org/10.1080/23312025.2019.1619219.
2) Carcione JM, Santos JE, Bagaini C, Ba J. A Simulation of a COVID-19 Epidemic Based on a Deterministic SEIR Model. *Frontiers in Public Health*. 2020;8:1–13. Available from: https://doi.org/10.3389/fpubh.2020.00230.
3) Bhadauria AS, Devi S, Gupta N. Modelling and analysis of a SEIQR model on COVID-19 pandemic with delay. *Modeling Earth Systems and Environment*. 2022;8:3201–3214. Available from: https://doi.org/10.1007/s40808-021-01279-1.
4) Zeb A, Alzahrani E, Erturk VS, Zaman G. Mathematical Model for Coronavirus Disease 2019 (COVID-19) Containing Isolation Class. *BioMed Research International*. 2020;2020:1–7. Available from: https://doi.org/10.1155/2020/3452402.
5) Ghosh SK, Ghosh SK. A mathematical model for COVID-19 considering waning immunity, vaccination and control measures. *Scientific Reports*. 2023;13(1):1–25. Available from: https://doi.org/10.1038/s41598-023-30800-y.
6) Zou Y, Yang W, Lai J, Hou J, Lin W. Vaccination and Quarantine Effect on COVID-19 Transmission Dynamics Incorporating Chinese-Spring-Festival Travel Rush: Modeling and Simulations. *Bulletin of Mathematical Biology*. 2022;84(2):1–19. Available from: https://doi.org/10.1007/s11538-021-00958-5.
7) Poonia RC, Saudagar AKJ, Altameem A, Alkhathami M, Khan MB, Hasanat MHA. An Enhanced SEIR Model for Prediction of COVID-19 with Vaccination Effect. *Life*. 2022;12(5):1–14. Available from: https://doi.org/10.3390/life12050647.
8) Adom-Konadu A, Sackitey AL, Anokye M. Local Stability Analysis of epidemic models using a Corollary of Gershgorin's Circle Theorem. *Applied Mathematics E-Notes*. 2023;23:159–174. Available from: https://www.emis.de/journals/AMEN/2023/AMEN-220223.pdf.
9) A M, G C, Qm AM. Mathematical modeling and simulation of SEIR model for COVID-19 outbreak: A case study of Trivandrum. *Frontiers in Applied Mathematics and Statistics*. 2023;9:1–9. Available from: https://doi.org/10.3389/fams.2023.1124897.