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Original Article

An SEIQR Model with Vaccination Class Influencing the Significance of Booster Dose for COVID-19

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Abstract *- The necessary step government suggests in existing condition of COVID-19 is to get vaccinated. So, this paper reveals the importance of the booster dose for COVID-19 by using a relevantly framed Susceptible-Exposed-Infected-Quarantined-Recovered compartmental model with vaccination class. Foremost, the paper examines the positivity and boundedness by the system of equations followed by estimating the reproduction number. Later, the local stability of the equilibria and the global stability of the disease-free equilibrium of the model is analyzed. The simulations performed numerically explains the impact of getting vaccinated and also analyses the reproduction number at two equilibriums. The analysis concludes with the fact that the spread of corona virus declines while people get vaccinated and may be eradicate in future.*

Keywords *- Epidemiology, COVID-19, SEIQR, Vaccination, Stability analysis.*

1. Introduction

Since late 2019, COVID-19 has posed a significant risk to humanity. The human coronavirus was first identified in 1965. SARSCoV-2 originated from bats and was transmitted to humans around the same time. Subsequently, it spread from human to human, indicating its contagious nature and leading to a pandemic. The latent period of COVID-19 is estimated to be approximately 14 days. SARS-CoV-2 has undergone genetic changes, resulting in various variants, including Alpha, Beta, Gamma, Delta, and the recently emerged Omicron. In recent times, there has been a noticeable increase in the number of infections, despite a temporary decline in the infection curve on some days. Therefore, it is imperative to focus on controlling the spread of the coronavirus.

As a measure, the government mandated the wearing of face masks. While commendable, not all individuals adhere to this requirement consistently, making it challenging to enforce. Therefore, an alternative approach is necessary. The World Health Organization (WHO) recommends receiving a precautionary dose, commonly referred to as a booster dose. Hence, an effective vaccine could potentially aid in decreasing the number of infections.

Bhadauria, Devi, and Gupta's study titled "Modelling and analysis of a SEIQR model on COVID-19 pandemic with delay" contributes significantly to the ongoing discourse on mathematical modeling of infectious diseases, particularly COVID-19. The SEIQR model proposed in their research offers a nuanced understanding of disease transmission dynamics by incorporating delay factors, which are crucial for capturing real-world complexities. The authors build upon existing epidemiological models to develop a comprehensive framework that accounts for SEIQR (Susceptible-Exposed-Infected-Quarantine-Recovered) individuals, along with a vaccination (V) compartment. Through rigorous mathematical analysis and numerical simulations, they investigate the global stability of the system, employing Lyapunov function and LaSalle's principle. Their findings underscore the pivotal role of vaccination in curbing disease transmission, with the model demonstrating how vaccination efforts contribute to reducing the number of infected individuals and increasing recoveries. Moreover, the study evaluates the effectiveness of the SEIQR model in predicting COVID-19 spread, offering valuable insights into the dynamics of the pandemic and informing public health interventions. Overall, Bhadauria, Devi, and Gupta's research enriches the scientific understanding of COVID-19 dynamics and provides a valuable tool for policymakers and epidemiologists to devise effective strategies for controlling the spread of the disease. [1]

The study by Chengjun Sun and Ying-Hen Hsieh, titled "Global analysis of an SEIR model with varying population size and vaccination," published in the journal Applied Mathematical Modelling, contributes significantly to the field of infectious disease modeling. The research investigates the dynamics of disease transmission within the framework of an SEIR (Susceptible-Exposed-Infectious-Recovered) model, considering variations in population size and the impact of vaccination. The authors extend previous SEIR models by incorporating demographic factors, such as varying population sizes, into their analysis. Through rigorous mathematical analysis and numerical simulations, they explore the global behavior of the model, examining stability conditions and identifying critical parameters that influence disease dynamics.

A key focus of the study is the role of vaccination in controlling disease spread. By integrating vaccination into the SEIR model, Sun and Hsieh evaluate its effectiveness in reducing the prevalence of infectious individuals and mitigating the impact of epidemics. Their findings provide valuable insights into the optimal allocation of vaccination resources and the potential outcomes of different vaccination strategies. Overall, the research by Sun and Hsieh advances our understanding of infectious disease dynamics, particularly in the context of varying population sizes and vaccination interventions. The study's comprehensive analysis offers valuable guidance for policymakers and public health officials in designing effective strategies for disease control and prevention. [3]

Yavuz, Coşar, Günay, and Özdemir's study titled "A New Mathematical Modeling of the COVID-19 Pandemic Including the Vaccination Campaign," published in the Open Journal of Modelling and Simulation, presents a novel approach to modeling the COVID-19 pandemic, specifically incorporating the dynamics of vaccination campaigns. The research introduces a mathematical model that not only captures the spread of the virus but also accounts for the impact of vaccination efforts. By integrating vaccination parameters into the model, the authors assess the effectiveness of vaccination campaigns in controlling disease transmission and reducing the burden on healthcare systems. Through mathematical analysis and numerical simulations, Yavuz et al. investigate various scenarios to evaluate the potential outcomes of different vaccination strategies.

Their findings provide insights into the optimal allocation of vaccine doses, vaccination coverage rates, and the timing of vaccination campaigns to achieve maximum impact in mitigating the spread of COVID-19. Overall, the study contributes to the growing body of literature on mathematical modeling of infectious diseases, offering valuable insights into the dynamics of COVID-19 transmission and the role of vaccination in disease control. The research findings have important implications for policymakers and public health authorities in formulating effective strategies for combating the pandemic. [9]

Mathematical models play a crucial role in validating and simulating disease spread patterns, offering insights into pandemic management, treatment, and prevention strategies. These models typically comprise of six classes i.e., SEIQRV. In this study, the vaccination class serves as a key strategy for disease control, highlighting the significance of vaccination and its impact on reducing the infectious curve of the COVID-19 pandemic.

2. Formulation and Analysis of Mathematical Model

The model is constructed with the assumptions taken below

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Lambda+\lambda E - \beta SI - (\alpha + \eta_1 + \mu)S \\
\frac{dE}{dt} &= \beta SI - (\gamma + \lambda + \eta_2 + \mu)E \\
\frac{dI}{dt} &= \gamma E - (\delta_1 + \eta_3 + k_1 + \mu)I \\
\frac{dQ}{dt} &= \eta_1 S + \eta_2 E + \eta_3 I - (\delta_2 + k_2 + \mu)Q \\
\frac{dR}{dt} &= \delta_1 I + \delta_2 Q - (\alpha + \mu)R \\
\frac{dV}{dt} &= \alpha S + \alpha R - \mu V
\end{aligned}\right\} \quad (1)$$

Provided with the preliminary conditions, $S(0) = S_0$, $E(0 = E_0$, $I(0) = I_0$, $Q(0) = Q_0$, $R(0) = R_0$ and $V(0) = V_0$. Also, $S(t) + E(t) + I(t) + Q(t) + R(t) + V(t) = N(t)$ where Ndenote the population.

The parameters used in Equation 1 are described in the given Table 1.

Table 1. Description of parameters of the model

Parameters	Description
S	Susceptible individuals
E	Exposed individuals
I	Infected individuals
Q	Quarantined individuals
R	Recovered individuals
V	Vaccination Class
Λ	Birth rate
β	Rate at which individual move from S to I
λ	Rate at which individual move from E to S
γ	Rate at which individual move from E to I
η_1	Rate at which individual move from S to Q
η_2	Rate at which individual move from E to Q
η_3	Rate at which individual move from I to Q
δ_1	Rate at which individual recover from I
δ_2	Rate at which individual recover from Q
k_1	Disease caused death rate in I
k_2	Disease caused death rate in Q
α	Rate of vaccination efficacy
μ	Death rate

2.1. Positivity Analysis of the Model

Theorem 1

Let $\Gamma(t) = [S(t), E(t), I(t), Q(t), R(t), V(t)]^T \in \mathbb{R}^6$ be the solution set of system given in Equation 1.. Then $\Gamma(t)$ is non-negative for all $t > 0$.

Proof.

From the system of equations given in Equation 1., it is obtained as below

$$\frac{dS}{dt} = \Lambda + \lambda E - (\beta I + \alpha + \eta_1 + \mu)S$$

$$\frac{dS}{S} \geq -(\beta I + \alpha + \eta_1 + \mu)dt$$

Integrating and solving,

$$S(t) \geq S(0)e^{-(\beta I+\alpha+\eta_1+\mu)t}$$

Thus,

$$S(t) \geq 0$$

Similarly, for $E(t) \geq 0$, $I(t) \geq 0$, $Q(t) \geq 0$, $R(t) \geq 0$ and $V(t) \geq 0$ it can be proved.

Hence, for all $t > 0$ the solution set $\Gamma(t)$ is non-negative.

2.2. The Invariant Region of the System

Theorem 2

The solution of the system given in Equation 1. along with the preliminary conditions, are bounded in the region $\Phi \subset \mathbb{R}^6_+$, where. $\Phi = \left\{\left(S(t), E(t), I(t), Q(t), R(t), V(t)\right) \in \mathbb{R}^6_+; N(t) \leq \frac{\Lambda}{\mu}\right\}$

Proof.

By the system of equations as given in Equation 1,

$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dQ(t)}{dt} + \frac{dR(t)}{dt} + \frac{dV(t)}{dt}$$
$$= \Lambda - \mu(S + E + I + Q + R + V) - k_1 I - k_2 Q$$

$$\frac{dN(t)}{dt} \leq \Lambda - \mu N$$

Thus,

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

Therefore, the feasible solution of the system is bounded in Φ.

2.3. Reproduction Number R_0

Every constant in the system, have impact in the characteristic of the disease whereas the most notable constant is the Reproduction number. It is generally denoted by R_0. It has two cases as below,

a. For $R_0 < 1$, the epidemic will reduce and might come to an end.
b. For $R_0 < 1$, the epidemic will prolong.

Thus, the ratio R_0 helps in predicting the sustainability of the disease. The $R_0$of the system given Equation 1 can be determined by the Jacobian matrix of the infectious classes namely Exposed, Infected and Quarantined.

$$J(E,I,Q) = \begin{pmatrix} -(\gamma+\lambda+\eta_2+\mu) & \beta S & 0 \\ \gamma & -(\delta_1+\eta_3+k_1+\mu) & 0 \\ \eta_2 & \eta_3 & -(\delta_2+k_2+\mu) \end{pmatrix}$$

The above matrix is reduced into two matrix namely transmission matrix$F$and transition matrix V.

$$F = \begin{pmatrix} 0 & \beta S & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}; V = \begin{pmatrix} -(\gamma+\lambda+\eta_2+\mu) & 0 & 0 \\ \gamma & -(\delta_1+\eta_3+k_1+\mu) & 0 \\ \eta_2 & \eta_3 & -(\delta_2+k_2+\mu) \end{pmatrix}$$

The inverse of the transition matrix is given by

$$V^{-1} = \begin{pmatrix} \frac{-1}{(\gamma+\lambda+\eta_2+\mu)} & 0 & 0 \\ \frac{\gamma}{(\gamma+\lambda+\eta_2+\mu)(\delta_1+\eta_3+k_1+\mu)} & \frac{-1}{(\delta_1+\eta_3+k_1+\mu)} & 0 \\ \frac{\gamma\eta_3+\eta_2(\delta_1+\eta_3+k_1+\mu)}{(\gamma+\lambda+\eta_2+\mu)(\delta_1+\eta_3+k_1+\mu)(\delta_2+k_2+\mu)} & \frac{-\eta_3}{(\delta_1+\eta_3+k_1+\mu)(\delta_2+k_2+\mu)} & \frac{-1}{(\delta_2+k_2+\mu)} \end{pmatrix}$$

The spectral radius of matrix FV^{-1} denoted by $\rho(FV^{-1})$ gives the reproduction numberR_0as follows

$$R_0 = \frac{\beta S\gamma}{(\gamma+\lambda+\eta_2+\mu)(\delta_1+\eta_3+k_1+\mu)} \tag{2}$$

2.4. Determination of Equilibrium Points

Every system has equilibria namely DFE (Disease-free equilibrium) and EE (Endemic equilibrium). The DFE is a point where a disease doesn't exist and EE is a point where a disease is frequently balanced at minimum level. Thus, the DFE of the system given in Equation 1 at $S_0 = 1$and $E_0 = I_0 = Q_0 = R_0 = 0$is obtained as

$$(S_0,\ E_0,\ I_0,\ Q_0,\ R_0,\ V_0) = \left(\frac{\Lambda}{(\alpha+\eta_1+\mu)},\ 0,0,0,0,\frac{\alpha\Lambda}{\mu(\alpha+\eta_1+\mu)}\right) \tag{3}$$

Similarly, by necessary simplifications the EE can be obtained as below,

$$S^* = \frac{\Lambda(\gamma+\lambda+\eta_2+\mu)}{\beta I^*(\gamma+\eta_2+\mu)+(\alpha+\eta_1+\mu)(\gamma+\lambda+\eta_2+\mu)}$$

$$E^* = \frac{\Lambda\beta I^*}{\beta I^*(\gamma+\eta_2+\mu)+(\alpha+\eta_1+\mu)(\gamma+\lambda+\eta_2+\mu)}$$

$$Q^* = \frac{\Lambda[\eta_1(\delta_1+\eta_3+k_1+\mu)(\gamma+\lambda+\eta_2+\mu)+\eta_2\beta I^*(\delta_1+\eta_3+k_1+\mu)+\eta_3\gamma\beta I^*]}{(\delta_2+k_2+\mu)(\delta_1+\eta_3+k_1+\mu)[\beta I^*(\gamma+\eta_2+\mu)+(\alpha+\eta_1+\mu)(\gamma+\lambda+\eta_2+\mu)]}$$

$$R^* = \frac{\delta_1 \Lambda \gamma \beta I^*}{(\alpha+\mu)(\delta_1+\eta_3+k_1+\mu)\left[\beta I^*(\gamma+\eta_2+\mu)+(\alpha+\eta_1+\mu)(\gamma+\lambda+\eta_2+\mu)\right]}$$
$$+\frac{\Lambda\delta_2\left[\eta_1(\delta_1+\eta_3+k_1+\mu)(\gamma+\lambda+\eta_2+\mu)+\eta_2\beta I^*(\delta_1+\eta_3+k_1+\mu)+\eta_3\gamma\beta I^*\right]}{(\alpha+\mu)(\delta_2+k_2+\mu)(\delta_1+\eta_3+k_1+\mu)\left[\beta I^*(\gamma+\eta_2+\mu)+(\alpha+\eta_1+\mu)(\gamma+\lambda+\eta_2+\mu)\right]}$$
$$V^* = \frac{\alpha\Lambda(\gamma+\lambda+\eta_2+\mu)}{\mu[\beta I^*(\gamma+\eta_2+\mu)+(\alpha+\eta_1+\mu)(\gamma+\lambda+\eta_2+\mu)]}+\frac{\alpha}{\mu}R^*$$

Where,

$$I^* = \frac{\Lambda\beta\gamma-(\alpha+\eta_1+\mu)(\gamma+\lambda+\eta_2+\mu)(\delta_1+\eta_3+k_1+\mu)}{\beta(\gamma+\eta_2+\mu)(\delta_1+\eta_3+k_1+\mu)} \quad (4)$$

2.5. Local Stability Analysis of the Equilibrium Points

Here, the local stability of the system is determined at disease-free equilibrium and at endemic equilibrium given in Equation 3 and Equation 4. The equilibrium point will be locally asymptotically stable if it is stable and locally attractive. The local stability of the equilibria is determined by the following two theorems.

Theorem 3

If $R_0 < 1$, then the system given in Equation 1. at D. F. E is locally asymptotically stable.

Proof.

Let the system given in Equation 1. at D. F. E be $M_1 = (S, E, I, Q, R, V)$. The Jacobian matrix at D. F. E is given by

$$J(M_1) = \begin{pmatrix} -(\alpha+\eta_1+\mu) & \lambda & \frac{-\Lambda\beta}{(\alpha+\eta_1+\mu)} & 0 & 0 & 0 \\ 0 & -(\gamma+\lambda+\eta_2+\mu) & \frac{\Lambda\beta}{(\alpha+\eta_1+\mu)} & 0 & 0 & 0 \\ 0 & \gamma & -(\delta_1+\eta_3+k_1+\mu) & 0 & 0 & 0 \\ \eta_1 & \eta_2 & \eta_3 & -(\delta_2+k_2+\mu) & 0 & 0 \\ 0 & 0 & \delta_1 & \delta_2 & -(\alpha+\mu) & 0 \\ \alpha & 0 & 0 & 0 & \alpha & -\mu \end{pmatrix} \quad (5)$$

Thus, the eigenvalues of the above Jacobian matrix are as follows

$\lambda_1 = -(\alpha+\eta_1+\mu), \lambda_2 = -(\gamma+\lambda+\eta_2+\mu), \lambda_3 = -(\delta_1+\eta_3+k_1+\mu),\ \lambda_4 = -(\delta_1+k_2+\mu),\ \lambda_5 = -(\alpha+\mu),\ \lambda_6 = -\mu.$

Clearly, all are negative only if $R_0 < 1$.

Hence the system is locally asymptotically stable if $R_0 < 1$.

Theorem 4

The system shown in Equation 1. at the endemic stage, $M_2 = (S^*, E^*, I^*, Q^*, R^*, V^*)$ is locally asymptotically stable only if $R_0 > 1$and the system is unstable if $R_0 < 1$.

Proof.

To determine the stability the Jacobian matrix is obtained as specified.

$$J(M_2) = \begin{pmatrix} -(\alpha\beta I^*+\eta_1+\mu) & \lambda & -\beta S^* & 0 & 0 & 0 \\ \beta I^* & -(\gamma+\lambda+\eta_2+\mu) & \beta S^* & 0 & 0 & 0 \\ 0 & \gamma & -(\delta_1+\eta_3+k_1+\mu) & 0 & 0 & 0 \\ \eta_1 & \eta_2 & \eta_3 & -(\delta_2+k_2+\mu) & 0 & 0 \\ 0 & 0 & \delta_1 & \delta_2 & -(\alpha+\mu) & 0 \\ \alpha & 0 & 0 & 0 & \alpha & -\mu \end{pmatrix} \quad (6)$$

The eigenvalues of the above matrix are

$\lambda_1^* = -\mu, \lambda_2^* = -(\alpha+\mu), \lambda_3^* = -(\delta_2+k_2+\mu), \lambda_4^* = -(\delta_1+\eta_3+k_1+\mu).$

whereas, $\lambda_5^*$and λ_6^* are obtained by solving the below characteristic equation

$$\lambda_*^2 + (\beta I^* + \alpha + \eta_1 + \gamma + \lambda + \eta_2 + 2\mu)\lambda_*^2 + [(\beta I^* + \alpha + \eta_1 + \mu)(\gamma + \lambda + \eta_2 + \mu) - \beta I^* \lambda] = 0$$

Hence, the system is asymptotically stable at the endemic stage if$R_0 > 1$and if $R_0 < 1$, it is unstable.

2.6. Global Stability Analysis of the Equilibrium Point

This section determines, the global stability of the system at disease-free equilibrium shown in Equation 3.

Theorem 5

The system in Equation 1. is globally asymptotically stable at the D. F. E, if $R_0 < 1$ and unstable otherwise.

Proof.

Let us consider the following Lyapunov function,

$$L(t) = C_1 E + C_2 I$$

The derivative of the Lyapunov function is obtained as follows,

$$\frac{dL(t)}{dt} = C_1\left[\beta SI - \omega_1 E\right] + C_2\left[\gamma E - \omega_2 I\right]$$

$$= [C_1\beta SI - C_2\omega_2]I + [C_2\gamma - C_1\omega_1]E$$

$$= \left[C_1\beta SI - C_2\omega_2\right]I + C_1\omega_1\left[\frac{C_2\gamma}{C_1\omega_1} - 1\right]E$$

Where $\omega_1 = (\gamma + \lambda + \eta_2 + \mu)$and $\omega_2 = (\delta_1 + \eta_3 + k_1 + \mu)$.

Choosing $C_1 = \omega_2$, $C_2 = \beta S$, the above equation becomes

$$\frac{dL(t)}{dt} = \omega_1\omega_2[R_0 - 1]E$$

Thus, it is clear that, $\frac{dL(t)}{dt} \leq 0$for $R_0 < 1$.

By LaSalle's invariance principle, the Lyapunov function is stable which completes the proof.

3. Numerical Simulation

Here, certain numerical simulations are performed to expose the optimality of model given in Equation 1 and to show the effect of vaccination in dynamical behavior of corona virus. The simulation is performed with the following initial values considered [6].

For,$S = 100, E = 3, I = 1, Q = 0, R = 0, V = 0, \Lambda = 0.1, \beta = 0.1, \lambda = 0.3, \gamma = 0.3, \eta_1 = 0.1, \eta_2 = 0.1, \eta_3 = 0.1, \delta_1 = 0.4, \delta_2 = 0.4, k_1 = 0.2, k_2 = 0.2, \mu = 0.003$.

Here, the proposed model is compared with the general SEIQR model to show that with the help of vaccination class the spread of corona virus can be controlled and reduced. The curve of the SEIQR and SEIQRV model is given in the below figures correspondingly.

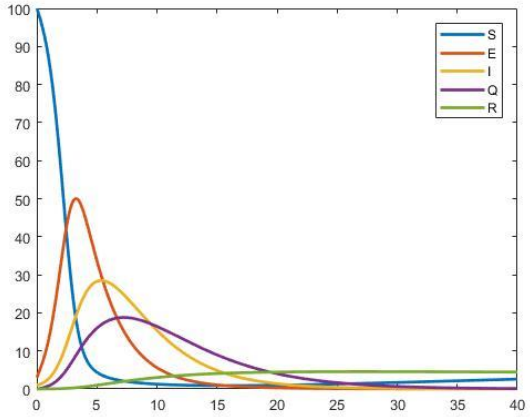

Fig. 1 SEIQR model without vaccination class

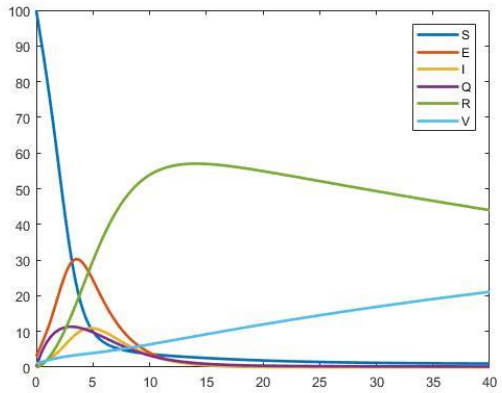

Fig. 2 SEIQR model with vaccination with $\alpha = 0.01$

It is possible to solve using various methods and one among them is by using a software named MATLAB. It is a mathematics oriented software which is more helpful in solving a tedious problem.

The impact of getting vaccinated is understood by comparing the Figure 1 and Figure 2. In Figure 1, though the susceptible individuals begin to decrease, after some days it again starts to increase slightly. So the risk of getting infected is prevailed. The exposed and the infected individuals in SEIQR model is high comparing SEIQR-V model. Also, even for increase in quarantine the recovery curve is not appreciably high in SEIQR model. Whereas in SEIQR-V model, for gradual increase in vaccination with$\alpha = 0.01$, the exposed and the infected individuals decreases more sufficiently. It is also observed that the quarantined individuals is also less. The more essential thing to be observed is the recovered individuals is very high comparing the SEIQR model. Thus, for a least value of α there is an optimal result in the recovery curve.

3.1. Analysis of the Reproduction Number R_0

The initial values considered in [6] is used in equation (2) to derive the value ofR_0at D.F.E. and E.E. as follows:-

(a) At disease-free equilibrium:

$$R_0 = \frac{\beta S \gamma}{(\gamma + \lambda + \eta_2 + \mu)(\delta_1 + \eta_3 + k_1 + \mu)}$$

$$= \frac{0.1 \times 0.885 \times 0.3}{(0.3 + 0.3 + 0.1 + 0.003) \times (0.4 + 0.1 + 0.2 + 0.003)}$$

$$R_0 = 0.0537 < 1$$

Thus, the value of R_0 is less than 1 showing the spread of COVID-19 will decline and may be removed soon.

(b) At endemic equilibrium the value of $R_0 = 1$, which reveals the fact that the disease prevails but it would not be a great threat which is the exact present scenario.

4. Conclusion

The SEIQRV model constructed provides a comprehensive representation of the dynamics of COVID-19. Global stability analysis is conducted using Lyapunov function and concluded through LaSalle's principle. Subsequent numerical simulations demonstrate that vaccination reduces the number of infected individuals, consequently increasing the number of recoveries, affirming the efficacy of the SEIQRV model. Additionally, numerical analysis of the reproduction number provides further evidence of the model's effectiveness, validating its authenticity. The proposed model facilitates the assessment of vaccination requirements for controlling COVID-19 spread, thus offering predictive insights into future cases. Accordingly, the model is tailored to the current pandemic scenario, enhancing its utility in forecasting future trends and informing public health strategies. By providing a reliable framework for analyzing COVID-19 dynamics and vaccination strategies, the SEIQRV model contributes significantly to the ongoing efforts to mitigate the impact of the pandemic and prevent future outbreaks.

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