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A novel SEIAHR compartment model for accessing the impact of vaccination, intervention policies, and quarantine on the COVID-19 pandemic: a case study of most affected countries Brazil, India, Italy, and USA

Sunil Singh Negi[1] · **Pankaj Singh Rana**[1] · **Nitin Sharma**[1] · **Manvendra Singh Khatri**[1]

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Abstract
In this study, an attempt has been made to formulate a novel SEIAHR deterministic compartmental model for the COVID-19 pandemic by incorporating additionally vaccinated and quarantined compartments. We obtained the basic reproduction number using the next-generation matrix approach. Thereafter, the stability of equilibrium points has been investigated using the basic reproduction number. Furthermore, we have studied the pandemic behaviour in four countries: Brazil, India, Italy, and the USA. We have fitted the proposed model to daily new cases and cumulative cases of the aforementioned countries using the nonlinear least square technique in MATLAB. Moreover, we have also estimated the best-fitted model parameters based on the available data. In addition, a numerical simulation of the model has been added to examine the influence of intervention policies, vaccination rates, vaccine efficacy, and quarantine. It was found that all the control policies had a positive impact on reducing the COVID-19 incidence.

Keywords Coronavirus · Intervention policies · Vaccine efficacy · Vaccination · Quarantine

Mathematics Subject Classification 92B05 · 62P10

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✉ Nitin Sharma
nitinsharma@nituk.ac.in; drnitinsharma@hotmail.com

Sunil Singh Negi
negisunil94@gmail.com

Pankaj Singh Rana
pankajsinghrana032@gmail.com

Manvendra Singh Khatri
mskhatri@gmail.com

[1] National Institute of Technology, Uttarakhand, Srinagar (Garhwal), Uttarakhand 246174, India

1 Introduction

The newest and most effective virus in recent years is COVID-19, a new form of coronavirus that first surfaced in early 2020 and is still uncontrollable. The disease's biological origin is yet to be fully determined, although the first instances were discovered on December 31, 2019, in Wuhan, China. Because untreated lung disorders can result in the quick spread of viruses, SARS-CoV-2, which has a high death rate and may be visible all around the world, the World Health Organisation (WHO) reported it a pandemic (World Health Organization Weakly Report 2022). On March 14, 2022, COVID-19 infected cases confirmed by the WHO touched 456,797,217. There were 6,043,094 deaths worldwide related to the coronavirus disease, and by this date, 10,712,423,741 vaccine doses have been administered. COVID-19 may have been transmitted from animal to human (zoonotic) according to numerous studies (World Health Organization 2022). Furthermore, the high number of new COVID-19 cases highlights the important fact that secondary transmission can occur from individual to individual (Verschaffel et al. 2002) by direct contact or via virus particles dispersed by sneezing or coughing from an infectious individual (Chen et al. 2020).

The concept of mathematical modeling has grown in importance in recent years. Mathematics is now directly associated with everyday life in today's digital culture, and it appears that the emphasis is on the incorporation of this abstract discipline by founding its association with actual life. Modeling is one of the most essential strategies for encapsulating mathematics in structure, which is an immaterial discipline to apply in real life. Mathematical modeling, in its broadest definition, is the procedure of identifying mathematical sequences within these events and occurrences, which is an attempt to mathematically stimulate a non-mathematical event, phenomena, or links between events (Verschaffel et al. 2002). Mathematics is an efficient way of analysing, that uses modeling to come up with resolutions to real-world events and situations.

Lau et al. (2020) have investigated the extent of COVID-19 under-testing and under-reporting in multiple global epicenters using estimated and reported mortality cases. Lin et al. (2020) employed a mathematical model to assess the outbreak in Wuhan by the effects of individual reactions and the government's actions. They also estimated the magnitude of these effects. Mandal et al. (2020) have investigated the role of quarantine and government intervention policies in the eradication and prevention of COVID-19 cases. Ndaïrou et al. (2020) have developed a mathematical model for the spread of COVID-19 disease in Wuhan, China, taking into account the effect of super-spreaders. Ngonghala et al. (2020) have emphasized in their study that maintaining social distance is critical in reducing the burden of COVID-19. Pang et al. (2020) have developed a SEIHR model and investigated the transmission dynamics and control strategies for COVID-19 using confirmed coronavirus cases from Wuhan city. Wang et al. (2022) have developed a novel mathematical model and investigated its behaviour using various dynamical analyses. Gopal et al. (2022) used the SEIR model to estimate the incidence of infected persons during the second phase of the COVID-19 outbreak in India. DarAssi et al. (2022) have used the concept of variable fractional order modeling to examine the infection dynamics of COVID-19 in the presence of hospitalization. Ahmed et al. (2020) examined and presented various COVID-19 models that cover key concerns such as global health services and suggest critical points. They analysed a logistic model for the dynamics of COVID-19 using numerical techniques. Using numerical simulations, Okuonghae and Omame (2020) investigated the effect of control policies on the dynamics of COVID-19, specifically using face masks, social distancing, and case detection

(via successive testing and contact tracing). Foy et al. (2021) evaluated age-specific vaccination distribution strategies with social communication matrices in India using an expanded SEIR model. Further, Farooq and Bazaz (2020) proposed a real-time learning approach based on artificial neural networks (ANN) and data streams to forecast the parameters of the COVID-19 disease's non-competitive, intelligent, adaptive, and online logical model.

Hoang et al. (2020) proposed a fractional-order SIS deterministic model with a saturated contact rate. The dynamics and numerical approximations of the model have been examined. Yang et al. (2021) proposed a mathematical model and assessed the effects of mutation and relaxation in the SARS-CoV-2 on the COVID-19 pandemic in Sao Paulo State, Brazil. Srivastav et al. (2021) proposed a mathematical model to perceive the effect of face mask use, hospitalisation, and quarantine in controlling the COVID-19 pandemic in India. Ngonghala et al. (2020) discussed the impacts of non-pharmaceutical interventions. They examined that the non-pharmaceutical interventions are useful to reduce COVID-19 transmission in the public. Rana and Sharma (2022) lightened the effect of non-pharmaceutical and pharmaceutical interventions on the COVID-19 pandemic for the regions Delhi, Maharashtra, Sikkim, Uttarakhand, and Russia. Gowrisankar et al. (2022) investigated and compared the effects of the omicron variant of COVID-19 for the seven most affected countries. Furthermore, they predicted that the curve of daily infected cases will follow the same order even though omicron is added in existing variants. Additionally, Khajanchi et al. (2022) proposed a model having nine infection stages and determined that a combination of pharmaceutical and non-pharmaceutical control is more effective than individual control. Easwaramoorthy et al. (2021) introduced a model that has predicted the COVID-19 first and second waves in the five utmost affected countries: the United States, Russia, India, Brazil, and the United Kingdom.

In this study, we developed a deterministic mathematical model by incorporating the quarantined, vaccinated, and hospitalised classes. The main purpose of this study is to investigate the impact of intervention strategies, vaccination, and quarantine on the elimination and control of COVID-19. Furthermore, we studied the pandemic behaviour in four countries: Brazil, India, Italy, and the USA. Finally, we show that to control COVID-19 in any community, vaccination and treatment should be implemented. Moreover, our results specify that the use of a combination of or concurrent use of personal protection/preventive measures such as face masks, hand washing, quarantine, and social distancing should be encouraged to reduce the disease incidence.

Since the transmission and eradication of coronavirus depend on various parameters such as immunity, precautions, vaccine efficacy and maintaining the required hygiene, etc. Until proper treatment is available, following the intervention policies, quarantining the infected individuals and the vaccination process is thought to be the best way to protect humans from the coronavirus. Therefore, it is helpful to use mathematical models to determine the potential impact of a hypothetical anti-COVID-19 vaccine. Whereas, it is expected that coronavirus will be eradicated from the population once herd immunity has been achieved. Thus, an endemic model must be developed to assess the impact of the government intervention policies, vaccination process, and quarantine effect on COVID-19 dynamics.

The remaining portion of this paper has been organised as follows: in Sect. 2, we have described the developed mathematical model, including the description of parameters, assumptions for the proposed model, and the feasibility of the system. Section 3, deals with the calculation and global stability analysis of the disease-free equilibrium point, and described the basic reproduction number R_0. In Sect. 4, the global stability analysis of the endemic equilibrium point has been examined. Further, in Sect. 5, model parameters based on the fitting of real incidence data for the four countries, namely Brazil, India, Italy, and the

USA, have been obtained. Finally, in the Sect. 6, numerical analysis for the proposed model for the effect of intervention policies, vaccine efficacy, and quarantine rates on infected and hospitalized individuals has been studied. In the end, a detailed conclusion of our findings has been reported.

2 Description of the model

A non-linear fractional order susceptible-exposed-infected-asymptomatic-recovered-reservoir model has been developed by Veeresha et al. (2021) and susceptible–exposed–infected–recovered model (Kumar et al. 2022) was investigated by researchers for the dynamics and future behaviour of coronavirus. Whereas, in our work we have developed a novel mathematical model by incorporating the quarantined, vaccinated, and hospitalized compartments. We demonstrated the impacts of non-pharmaceutical intervention actions such as lockdown, mask-wearing, hand sanitising, social distancing, and quarantine on disease transmission, as well as pharmaceutical intervention measures such as vaccination rate and vaccine efficacy. A system of eight nonlinear ordinary differential equations (ode) has been obtained for the dynamics of coronavirus in the various human population compartments.

The total human population $N(t)$ has been divided into eight distinct compartments or classes, namely: susceptible $S(t)$, exposed $E(t)$, quarantined $Q(t)$, symptomatic infected $I(t)$, asymptomatic infected $A(t)$, hospitalized $H(t)$, vaccinated $V(t)$ and recovered $R(t)$, as shown in Fig. 1. Susceptible individuals get infected at the rate λ, where λ be the force of infection, n_1 $(0 < n_1 \leq 1)$ is considered the effect of intervention policies for the prevention of additional infection from infected individuals. Here, β is the disease transmission constant due to symptomatic and asymptomatic individuals. Furthermore, vaccinated individuals get infected at the rate of λ_1. The modification parameters θ and θ_1 $(0 < \theta, \theta_1 \leq 1)$ define that the rate of infection is slower in asymptomatic individuals as compared to symptomatic. Susceptible individuals get vaccinated at τ_1 rate and $(n_2\ 0 < n_2 \leq 1)$ measured the vaccine efficacy to protect the further infection from infected individuals. In addition, γ measured the rate of immunity loss after recovery. Exposed individuals join the symptomatic compartment and the asymptomatic compartment with σk_1 and $\sigma\ (1 - k_1)$ rates, respectively. The hospitalisation rates for quarantined, symptomatic, and asymptomatic individuals are implied by ρ_1, γ_1, and γ_2, respectively. While, the recovery rate of quarantined, hospitalised, and asymptomatic individuals is signified by ρ_2, δ, and δ_1 (Table 1)

2.1 Assumptions

- People who will be vaccinated are taken from people who have not been exposed to or vaccinated against the virus.
- The vaccine may not be completely protecting, hence the individuals in the vaccine compartment, i.e., vaccinated people, become infected when they are exposed to the virus.
- Due to immunity loss, the recovered individuals may be susceptible to coronavirus again.
- The COVID-19-induced mortality rate for asymptomatic patients is considered to be zero because they have a lower probability of dying from the coronavirus.
- Some fraction of exposed or symptomatic infected individuals are quarantined.
- Asymptomatic and quarantined individuals have a natural recovery.
- In all the classes, some people adhere to the intervention policies.

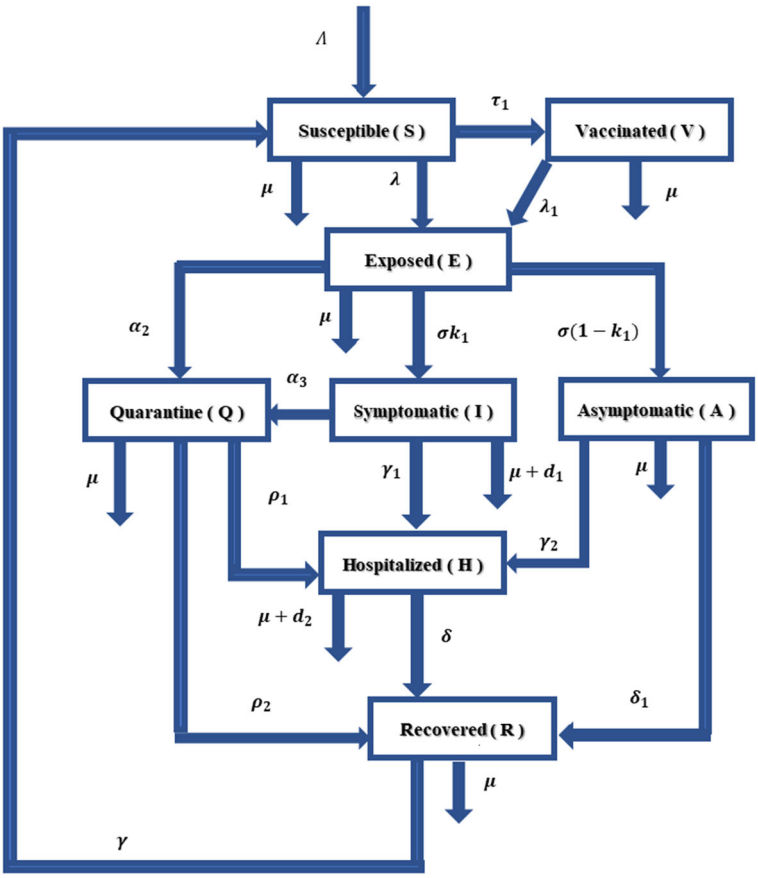


Fig. 1 Flow diagram for the dynamics of COVID-19

Based on the above flow diagram in Fig. 1, we obtain a mathematical model having a system of eight nonlinear ode:

$$\frac{dS}{dt} = \Lambda - \lambda S - \tau_1 S - \mu S + \gamma R$$
$$\frac{dV}{dt} = \tau_1 S - \lambda_1 V - \mu V$$
$$\frac{dE}{dt} = \lambda S + \lambda_1 V - \sigma k_1 E - \sigma(1-k_1)E - \alpha_2 E - \mu E$$
$$\frac{dI}{dt} = \sigma k_1 E - \alpha_3 I - (\mu + d_1)I - \gamma_1 I$$
$$\frac{dA}{dt} = \sigma(1-k_1)E - \gamma_2 A - \delta_1 A - \mu A$$
$$\frac{dQ}{dt} = \alpha_2 E + \alpha_3 I - \rho_1 Q - \rho_2 Q - \mu Q$$
$$\frac{dH}{dt} = \gamma_1 I + \gamma_2 A + \rho_1 Q - \delta H - d_2 H - \mu H$$

Table 1 Parameters used in the model with the description

Parameter	Description
Λ	Recruitment rate of individuals in susceptible class
β	Transmission coefficient per unit time for susceptible class
β_1	Transmission coefficient per unit time for vaccinated class
n_1	Measure of compliance of population with interventions
n_2	Measure of compliance of vaccine efficacy
γ	Rate of joining a susceptible class after immunity loss
μ	Natural death rate of individuals
σ	Incubation period
k_1	Proportion of progression from exposed to symptomatic class
γ_1	Hospitalised rate of symptomatic infectious
γ_2	Hospitalised rate of asymptomatic infectious
δ	Recovery rate of hospitalised individuals
δ_1	Natural recovery rate of asymptomatic individuals
d_1	COVID-19 related death rate for symptomatic
d_2	COVID-19 related death rate for hospitalised
θ	Modification parameter
θ_1	Modification parameter
τ_1	Vaccination rate of susceptible
α_2	Quarantine rate for exposed individuals
α_3	Quarantine rate for symptomatic infected individuals
ρ_1	Rate at quarantine being hospitalised
ρ_2	Natural recovery rate of quarantined individuals

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \delta H + \delta_1 A + \rho_2 Q - \gamma R - \mu R. \tag{1}$$

With the initial conditions $S(0) = S_0,\ E(0) = E_0,\ I(0) = I_0,\ A(0) = A_0,\ Q(0) = Q_0,$

$$H(0) = H_0,\ V(0) = V_0,\ R(0) = R_0$$

$$\text{where } \lambda = \frac{\beta(I + \theta A)(1 - n_1)}{N} \text{ and } \lambda_1 = \frac{\beta_1(I + \theta_1 A)(1 - n_2)}{N}$$

and the total human population is given by $N(t)$

$$N(t) = S(t) + V(t) + E(t) + I(t) + A(t) + H(t) + Q(t) + R(t).$$

2.2 Invariant region

The positively invariant region can be obtained by adding the total human host population such that

$$\frac{\mathrm{d}N}{\mathrm{d}t} = \frac{\mathrm{d}S}{\mathrm{d}t} + \frac{\mathrm{d}E}{\mathrm{d}t} + \frac{\mathrm{d}I}{\mathrm{d}t} + \frac{\mathrm{d}A}{\mathrm{d}t} + \frac{\mathrm{d}H}{\mathrm{d}t} + \frac{\mathrm{d}Q}{\mathrm{d}t} + \frac{\mathrm{d}V}{\mathrm{d}t} + \frac{\mathrm{d}R}{\mathrm{d}t}.$$

From model system (1) adding the equations yields;

$$\frac{dN}{dt} = \Lambda - \mu N$$

$$N(t) \leq \frac{\Lambda}{\mu} + \left(N_0 - \frac{\Lambda}{\mu}\right)e^{-\mu t}$$

$$\text{as t} \to \infty,\ N(t) \to \frac{\Lambda}{\mu} \text{implies that } 0 \leq N(t) \leq \frac{\Lambda}{\mu}.$$

Thus, the feasible solution set of model system (1) remains in the region,

$$\Omega = \left\{(S,\ E,\ I,\ A,\ H,\ Q,\ V,\ R) \in \mathbb{R}_+^8 : N \leq \frac{\Lambda}{\mu}\right\}.$$

Hence, our model system (1) has biological sense and is mathematically well posed.

3 Disease-free equilibrium (DFE)

The DFE state $X^0 = \left(S^0,\ E^0,\ I^0,\ A^0,\ Q^0,\ H^0,\ V^0,\ R^0\right)$ can be obtained by placing the right hand of the system (1) to zero. Solving the system of nonlinear equations with the conditions for infection-free human host population dynamics $I^0 = A^0 = 0$, implies;

$$E^0 = Q^0 = H^0 = R^0 = 0,\ S^0 = \frac{\Lambda}{\tau_1 + \mu} \text{and } V^0 = \frac{\tau_1 \Lambda}{\mu(\tau_1 + \mu)}.$$

3.1 Basic reproduction number (R_0)

The basic reproduction number is the average number of secondary infections induced by a single infected individual into an otherwise susceptible population during his infectious period (Kumar 2019). The epidemic will spread quickly or not, depends on the value of R_0, either it is greater than or less than unity, i.e. if $R_0 > 1$ would imply a disease outbreak, while $R_0 < 1$ its disappearance. It is related to the peak and final size of an epidemic and characterizes the local asymptotic stability of epidemic models (Diekmann et al. 1990). We have used the next-generation matrix approach to obtain R_0 as follows in Diekmann et al. (1990). The basic reproduction number R_0 can be obtain as $R_0 = \rho\left(FV^{-1}\right)$, where ρ denotes the spectral radius of any square matrix. Where, F denotes the new infection terms in the compartments and V denotes the other transition terms such as death rate, recovery rate, vaccination rate, hospitalized rate, and quarantine rate.

$$f = \begin{bmatrix} \lambda S \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{and } v = \begin{bmatrix} -\sigma k_1 E + \sigma(1-k_1)E + \alpha_2 E + \mu E \\ -\sigma k_1 E + \alpha_3 I + (\mu + d_1)I + \gamma_1 I \\ -\sigma(1-k_1)E + \gamma_2 A + \delta_1 A + \mu A \\ -\alpha_2 E - \alpha_3 I + \rho_1 Q + \rho_2 Q + \mu Q \\ -\gamma_1 I - \gamma_2 A - \rho_1 Q + \delta H + d_2 H + \mu H \end{bmatrix}$$

$$F = \begin{bmatrix} 0 & \frac{\beta S^0(1-n_1)}{N} + \frac{\beta_1 V^0(1-n_2)}{N} & \frac{\beta\theta S^0(1-n_1)}{N} + \frac{\beta_1\theta_1 V^0(1-n_2)}{N} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \sigma+\alpha_2+\mu & 0 & 0 & 0 & 0 \\ -\sigma k_1 & \alpha_3 + +\mu + d_1 + \gamma_1 & 0 & 0 & 0 \\ -\sigma(1-k_1) & 0 & \gamma_2+\delta_1+\mu & 0 & 0 \\ -\alpha_2 & \alpha_3 & 0 & \rho_1+\rho_2+\mu & 0 \\ 0 & -\gamma_1 & -\gamma_2 & -\rho_1 & \delta+d_2+\mu \end{bmatrix}.$$

The basic reproduction number R_0 can be obtained as $R_0 = \rho\left(FV^{-1}\right)$

$$R_{0s} = \frac{\sigma}{N(\sigma+\alpha_2+\mu)}\left\{\frac{k_1 S^0\beta(1-n_1)}{(\alpha_3+\mu+d_1+\gamma_1)} + \frac{(1-k_1)S^0\theta\beta(1-n_1)}{(\gamma_2+\delta_1+\mu)}\right\}$$

$$R_{0v} = \frac{\sigma}{N(\sigma+\alpha_2+\mu)}\left\{\frac{k_1\beta_1 V^0(1-n_2)}{(\alpha_3+\mu+d_1+\gamma_1)} + \frac{(1-k_1)\theta_1\beta_1 V^0(1-n_2)}{(\gamma_2+\delta_1+\mu)}\right\}$$

$$R_0 = R_{0s} + R_{0v}$$

Here R_{0s} is the basic reproduction number in the absence of vaccination, R_{0v} are the infected indviduals after vaccination, and R_0 be the basic reproduction number in presence of vaccination.

3.2 Global stability of DFE

For the global stability analysis of DFE, we follow the methods used in Silva and Torres (2015) and Bhunu et al. (2009). By following the methods, the DFE will be globally asymptotically stable, whenever $R_0 < 1$ and satisfies the following conditions:

$$(\mathbf{H}1): \frac{\mathrm{d}X}{\mathrm{d}t} = F(X, Z)$$

$$(\mathbf{H}2): \frac{\mathrm{d}Z}{\mathrm{d}t} = G(X, Z) = DZ - \widehat{G}(X, Z),\ \widehat{G}(X, Z) \geq 0 \text{ for } (X, Z) \in \Omega,$$

where Ω is the region in which the model system (1) has a biological sense.

For the global stability of DFE, we reword the model system (1) as follows:

$$\frac{\mathrm{d}X}{\mathrm{d}t} = F(X, Z) = \begin{bmatrix} \Lambda - \lambda S - \tau_1 S - \mu S + \gamma R \\ \delta H + \delta_1 A + \rho_2 Q - \gamma R - \mu R \\ \tau_1 S - \lambda_1 V - \mu V \end{bmatrix}$$

$$\frac{\mathrm{d}Z}{\mathrm{d}t} = G(X, Z) = \begin{bmatrix} \lambda S + \lambda_1 V - \sigma k_1 E - \sigma(1-k_1)E - \alpha_2 E - \mu E \\ \sigma k_1 E - \alpha_3 I - (\mu + d_1)I - \gamma_1 I \\ \sigma(1-k_1)E - \gamma_2 A - \delta_1 A - \mu A \\ \alpha_2 E + \alpha_3 I - \rho_1 Q - \rho_2 Q - \mu Q \\ \gamma_1 I + \gamma_2 A + \rho_1 Q - \delta H - d_2 H - \mu H \end{bmatrix} \tag{2}$$

$$\widehat{G}(X, Z) = \begin{bmatrix} \widehat{G}_1(X, Z) \\ \widehat{G}_2(X, Z) \\ \widehat{G}_3(X, Z) \\ \widehat{G}_4(X, Z) \\ \widehat{G}_5(X, Z) \end{bmatrix} = \begin{bmatrix} \lambda\left(S^0 - S\right) + \lambda_1(V^0 - V) \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}.$$

Here, $\widehat{G}_1(X, Z) \geq 0$ as $S^0 \leq S$, $V^0 \leq V$, $0 \leq n_1 \leq 1$ and $0 \leq n_2 \leq 1$, that implies $\widehat{G}(X, Z) \geq 0$.

Conditions H1 and H2 are satisfied by the system (2), so we can conclude that a DFE state is globally asymptotically stable whenever $R_0 < 1$.

4 Endemic equilibrium point

Let $X^* = (S^*, E^*, I^*, A^*, Q^*, H^*, V^*, R^*)$ be the endemic equilibrium point of model system (1), which can be obtained by keeping the right-hand side of the system (1) to zero. So, the endemic equilibrium point is as follows:

$$
\begin{aligned}
I^* &= \frac{\sigma k_1}{\alpha_3 + \mu + d_1 + \gamma_1} E^* \\
A^* &= \frac{\sigma(1-k_1)}{\delta_1 + \mu + \gamma_2} E^* \\
Q^* &= \frac{1}{\rho_1 + \rho_2 + \mu}\left[\alpha_2 E^* + \alpha_3 I^*\right] \\
H^* &= \frac{1}{\delta + d_2 + \mu}[\gamma_1 \mathrm{I}^* + \gamma_2 A^* + \rho_1 Q^*] \\
R^* &= \frac{1}{\gamma + \mu}[\delta \mathrm{H}^* + \delta_1 A^* + \rho_2 Q^*] \\
S^* &= \frac{1}{\lambda + \tau_1 + \mu}[\wedge + \gamma R^*] \\
V^* &= \frac{1}{\lambda_1}[\lambda S^* + (\sigma + \alpha_2 + \mu) E^*.
\end{aligned}
$$

4.1 Global stability analysis of endemic equilibrium point (EE)

Theorem 1 follows the Theorem 3.3 of Fall et al. (2007).

Theorem 1 *If $R_0 > 1$, then the endemic equilibrium state $X^* = (S^*, E^*, I^*, A^*, Q^*, H^*, V^*, R^*)$ is globally asymptotically stable in Ω^*.*

Proof We created the Lyapunov function 'L' using the following method (Rana and Sharma 2020), which is commonly used to assess the stability of epidemic models; $L : \{(S^*, E^*, I^*, A^*, Q^*, H^*, V^*, R^*) \in \Omega^*\} \to R$, where

$$\Omega^* = \{(S^*, E^*, I^*, A^*, Q^*, H^*, V^*, R^*) \in R_+^8 : S(t), E(t), I(t), A(t), Q(t), H(t), V(t), R(t) > 0\}.$$

$$
\begin{aligned}
L =& U_1\left\{S - S^* ln\left(\frac{S}{S^*}\right)\right\} + U_2\left\{E - E^* ln\left(\frac{E}{E^*}\right)\right\} \\
&+ U_3\left\{I - I^* ln\left(\frac{I}{I^*}\right)\right\} + U_4\left\{A - A^* ln\left(\frac{A}{A^*}\right)\right\} \\
&+ U_5\left\{Q - Q^* ln\left(\frac{Q}{Q^*}\right)\right\} + U_6\left\{H - H^* ln\left(\frac{H}{H^*}\right)\right\} \\
&+ U_7\left\{V - V^* ln\left(\frac{V}{V^*}\right)\right\} + U_8\left\{R - R^* ln\left(\frac{R}{R^*}\right)\right\},
\end{aligned}
$$

where U_1, U_2, U_3, U_4, U_5, U_6, U_7 and U_8 remain non-negative in variable in Ω^*.

The time derivative $\frac{dL}{dt}$ will be:

$$\begin{aligned}\frac{dL}{dt} &= U_1\frac{(S-S^*)}{S}\frac{dS}{dt} + U_2\frac{(E-E^*)}{E}\frac{dE}{dt}\\ &+ U_3\frac{(I-I^*)}{I}\frac{dI}{dt} + U_4\frac{(A-A^*)}{A}\frac{dA}{dt}\\ &+ U_5\frac{(Q-Q^*)}{Q}\frac{dQ}{dt} + U_6\frac{(H-H^*)}{H}\frac{dH}{dt}\\ &+ U_7\frac{V-V^*)}{V}\frac{dV}{dt} + U_8\frac{(R-R^*)}{R}\frac{dR}{dt}\\ \frac{dL}{dt} &= -\frac{\mu(S-S^*)^2}{S} + f(S,\ E,\ I,\ A,\ Q,\ H,\ V,\ R).\end{aligned}$$

By following the approach used in Bhunu et al. (2009) and Rana and Sharma (2020), we can conclude that the quantity $f(S,\ E,\ I,\ A,\ Q,\ H,\ V,\ R)$ is non-positive, that is $f \leq 0$ for every $S,\ E,\ I,\ A,\ Q,\ H,\ V,\ R > 0$. Thus, $\frac{dL}{dt} \leq 0$ and $\frac{dL}{dt} = 0$, when $S = S^*$, $E = E^*$, $I = I^*$, $A = A^*$, $Q = Q^*$, $H = H^*$, $V = V^*$, $R = R^*$. Hence $\{X^*\}$, the endemic equilibrium point is the largest compacted invariant singleton set in the domain for which $\frac{dL}{dt} = 0$. Thus, using the LaSalle invariance principle, $\{X^*\}$ is globally asymptotically stable in Ω^*, for $R_0 > 1$.

5 Parameters estimation

We obtained model parameters based on the fitting of real incidence data for the four countries, namely Brazil (Daily and Cumulative Cases Brazil 2022), India (Daily and Cumulative Cases India 2022), Italy (Daily and Cumulative Cases Italy 2022), and the USA (Daily and Cumulative Cases USA 2022). We used some parameters from the literature, such as recruitment rate to the susceptible compartment and natural death rate, while the rest of the parameters were obtained from the fitted data of the mentioned countries from December 1, 2021, to February 8, 2022. MATLAB's fitting function *lsqnonlin* used to fit the reported daily incidence data and cumulative data to our suggested model. Figure 2 depicts daily cases versus model fitting, whereas Fig. 3 depicts cumulative cases versus model fitting.

6 Numerical analysis

In this section, we have studied the numerical study of the model (1) by using the parameters from Table2 and the initial conditions from Table3. The unit of time is being considered as a day. The numerical simulation has shown the effect of intervention policies, vaccine efficacy, vaccination rate, and quarantine effect.

6.1 Stability of DFE and EE

In Yousuf et al. (2022), researchers have determined the various equilibrium points of the *Jupiter-Europa* system and examined the linear stability of the system under the significance of oblateness. In this section, we have analysed the stability of our system based on the characteristic roots of the Jacobian matrix of the system (1). To calculate the eigenvalues,

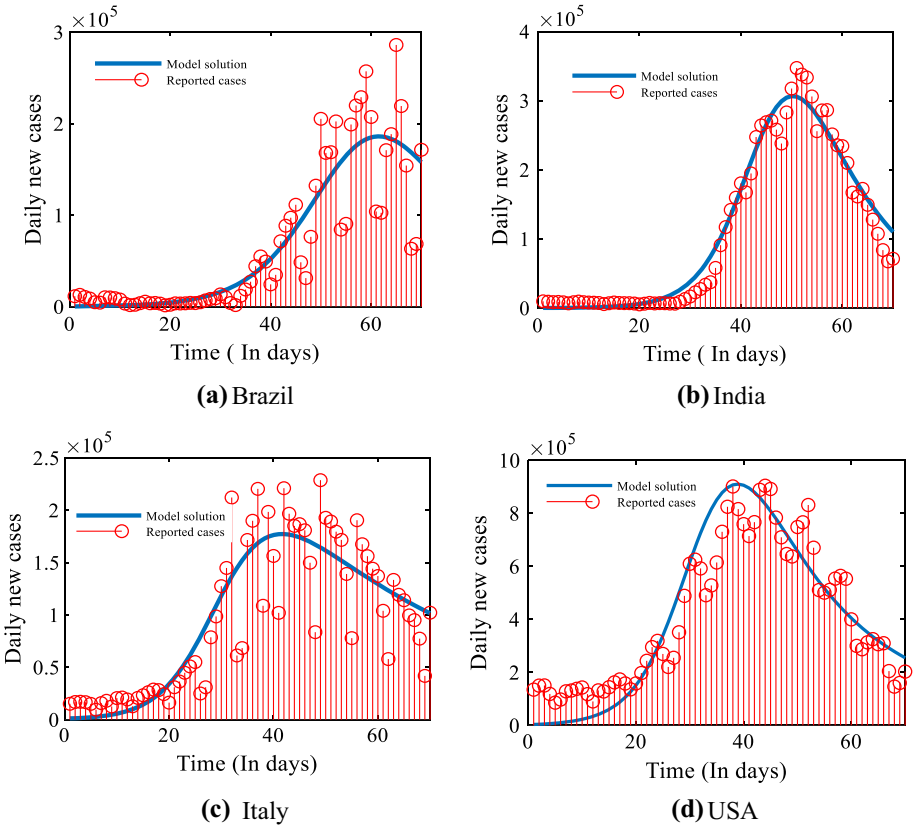


Fig. 2 Model fitting based on daily reported new cases

basic reproduction number, and plotting phase diagram we have used the parameter values from Table 2.

In Table 4, the eigenvalues of the Jacobian for system (1) have the negative real part. This implies that whenever $R_0 \leq 1$, the DFE point (for India) is locally asymptotically stable, whereas for $R_0 > 1$ endemic equilibrium point is locally asymptotically stable (for Brazil, Italy, and the USA). These results can also be seen in Fig. 4.

In Fig. 4b, the phase trajectory in the *S–V–I* plane has been plotted, whenever $R_0 < 1$ the trajectory converges to the DFE, whereas in Fig. 4 (a, c-d), for $R_0 > 1$ the phase trajectory in the *S–E–I* plane has been plotted. From the solution of endemic points in Sect. 4, we can conclude that the values of *A, H, Q, V,* and *R* can be calculated by the values of *S, E*, and *I*. Therefore, we can conclude that for $R_0 > 1$ every solution converges to an endemic equilibrium point. Hence, the model system (1) is locally asymptotically stable.

6.2 Effect of intervention policies

The consequence of interventions such as social distancing, wearing masks, isolation, etc. is evaluated by using the parameter $n_1 (0 \leq n_1 \leq 1)$, $n_1 = 0$ implies no control intervention policies have been functional either by government or individuals, whereas $n_1 = 1$ implies the

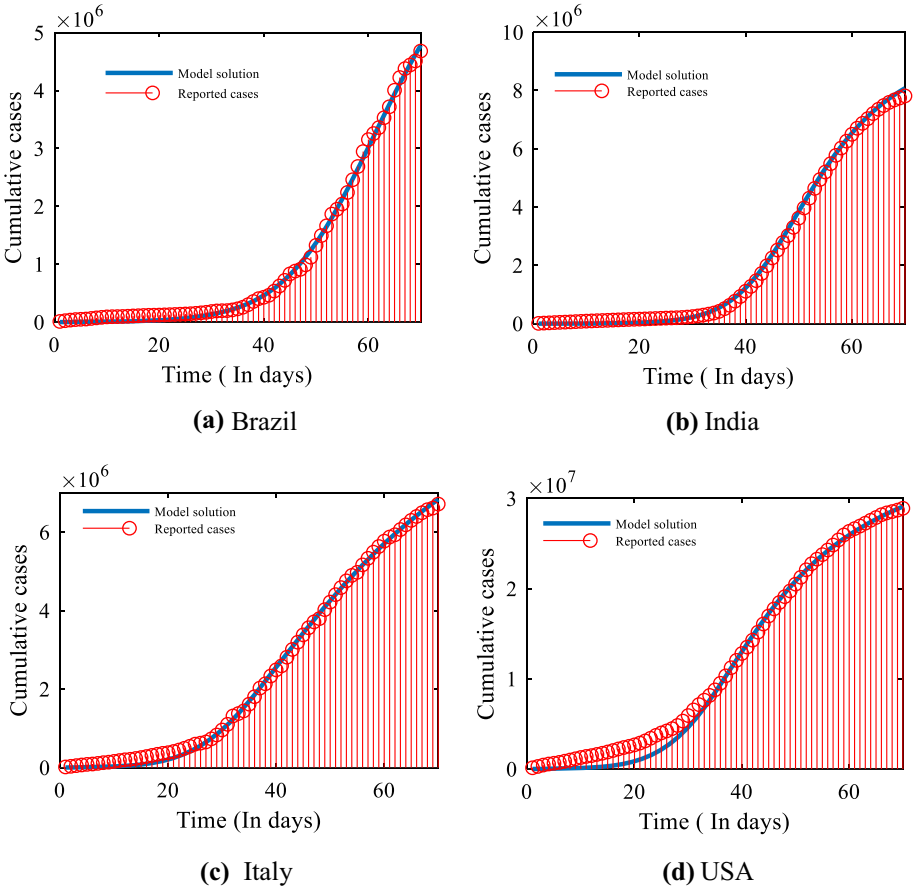


Fig. 3 Model fitting based on the real data of cumulative cases

whole population following intervention policies, meaning that the disease will be no longer exist in the population. The simulation results show a decrease in infected and hospitalised individuals with an increase in a parameter value n_1, as shown in Fig. 5.

6.3 Effect of vaccine efficacy

The Covid-19 vaccine protects individuals from being hospitalised with coronavirus. Vaccine effectiveness is a metric that tests how the vaccine effectively protects people from diseases, symptomatic infections, hospitalisation, and death. The effectiveness of the vaccine is often tested with observational studies aimed at measuring individual protection against vaccination under "real-world" conditions. In our study, we have used the parameter n_2 for the effectiveness of the vaccine. n_2 is taken as $(0 \leq n_2 \leq 1)$, $n_2 = 0$ implies a vaccine is not effective for individuals, whereas $n_2 = 1$ implies the vaccine is 100% effective for individuals. The simulation results demonstrate a decrease in infected and hospitalized individuals, with an increase in the parameter value n_2, as shown in Fig. 6.

Table 2 Model parameters values and source

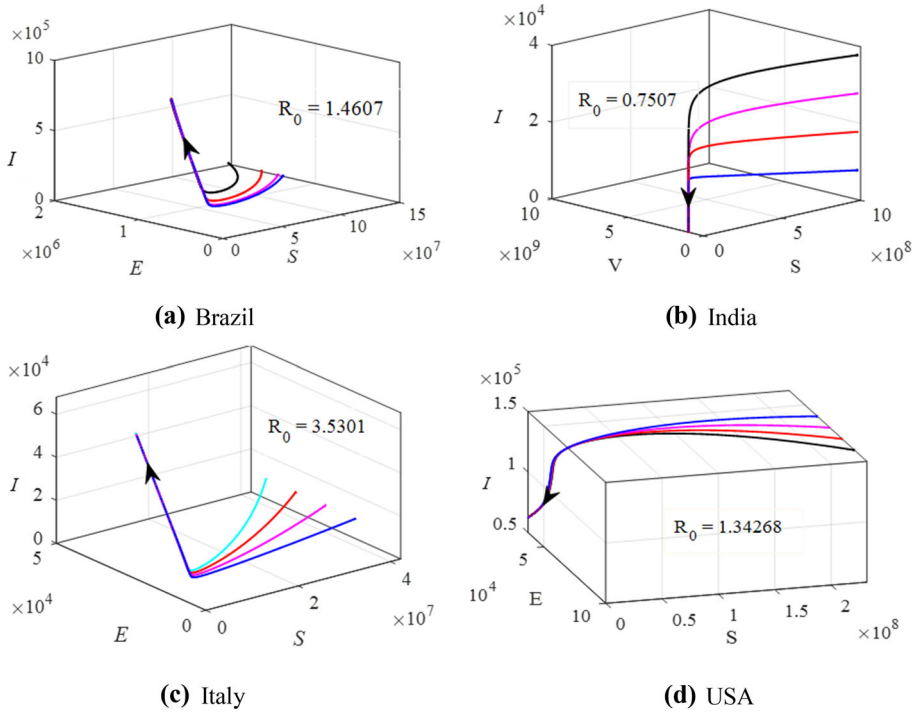
Parameter	Brazil	India	Italy	USA	Source
β	0.8081	0.8728	0.7895	0.7309	Fitted
γ_1	0.0255	0.0285	0.0000271	0.0100	Fitted
γ_2	0.0223	0.1303	0.0345	0.0565	Fitted
δ	0.0481	0.0010	0.0164	0.0077	Fitted
δ_1	0.0912	0.0054	0.0017	0.0127	Fitted
d_1	0.0270	0.0283	0.0061	0.0122	Fitted
d_2	0.3071	6.2×10^{-6}	0.1382	0.1506	Fitted
τ_1	0.8020	0.9812	0.7823	0.7329	Fitted
ρ_1	0.9318	0.9037	0.8911	0.8886	Fitted
ρ_2	0.0259	0.0486	0.0313	0.0242	Fitted
α_2	0.7602	0.7214	0.9131	0.8995	Fitted
α_3	0.0256	0.0285	0.0038	0.0127	Fitted
k_1	0.466	0.508	0.4050	0.463	Fitted
γ	0.9398	0.8010	0.9684	0.8143	Fitted
β_1	0.9586	0.8990	0.9597	0.9521	Fitted
σ	0.1428	0.1428	0.1428	0.1428	Silva and Torres (2015)
n_1	0.2	0.4	0.2	0.4	Fitted
n_2	0.4	0.6	0.4	0.4	Fitted
$\wedge$	6636	59,617	1991	11,505	$\mu \times N(0)$
θ	0.7	0.5	0.7	0.7	Fitted
θ_1	0.65	0.65	0.65	0.65	Fitted
μ	3.158×10^{-5}	3.9×10^{-5}	3.33×10^{-5}	5.21×10^{-7}	Efimov and Ushirobira (2021), Rajput et al. (2021), Mahajan et al. (2021)
N	2.1×10^7	1.38×10^9	6×10^7	3.31×10^8	Efimov and Ushirobira (2021), Rajput et al. (2021) and Mahajan et al. (2021)

Table 3 Initial conditions (Taken from subject to data fitting)

Variable	Brazil	India	Italy	USA
S_0	$0.7 \times N$	$0.7 \times N$	$0.7 \times N$	$0.7 \times N$
E_0	54,000	55,050	45,000	90,050
I_0	20,000	38,000	9394	15,000
A_0	30,000	30,000	11,000	20,000
Q_0	15,000	20,000	12,000	15,000
H_0	16,000	30,000	7408	30,000
V_0	3000	5000	12,000	30,000
R_0	5000	6000	10,000	10,000

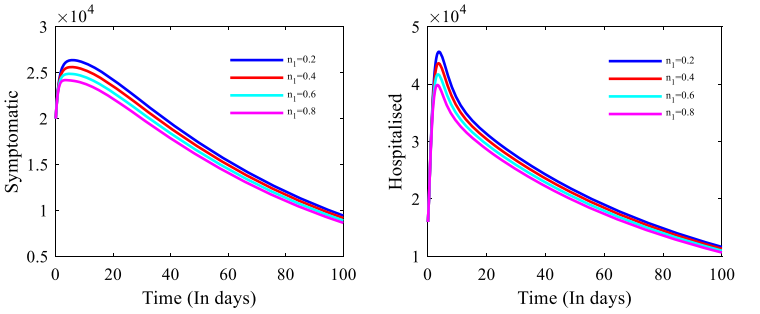
Table 4 Characteristic roots of the Jacobian system (1) with values of R_0

Characteristic roots			
Brazil	India	Italy	USA
− 0.8024	− 0.000042	− 0.7869	− 0.7331
− 0.9494 + 0.0082i	− 0.9812	− 0.9717	− 0.9128
− 0.9494 − 0.0082i	− 0.8010	− 0.9181	− 0.2837
− 0.3814	− 0.0010	− 0.2135	− 0.1584
− 0.3628	− 0.9523	− 0.1583	− 0.8144
− 0.0004 + 0.0029i	− 0.1357	− 0.0004 + 0.0025i	− 0.0674
− 0.0004 − 0.0029i	− 0.2421	− 0.0004 − 0.0025i	− 0.0001 + 0.0032i
− 0.1007	− 0.0853	− 0.0304	− 0.0001 − 0.0032i
Basic reproduction number (R_0)			
1.4607	0.7507	3.5301	1.3427

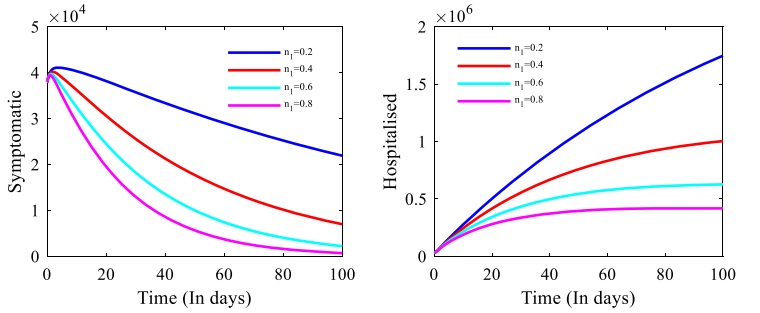


(a) Brazil **(b)** India **(c)** Italy **(d)** USA

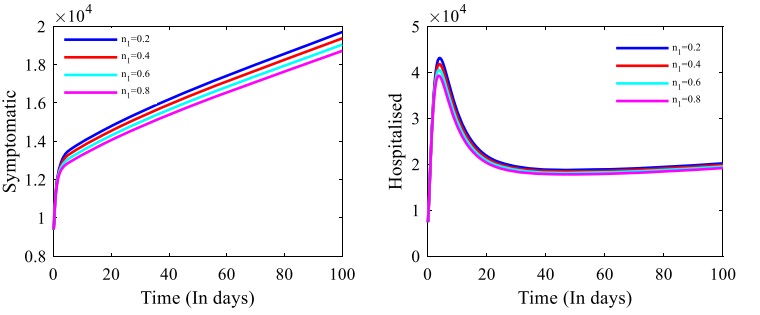
Fig. 4 Phase trajectory for **a** Brazil, **b** India, **c** Italy, **d** the USA



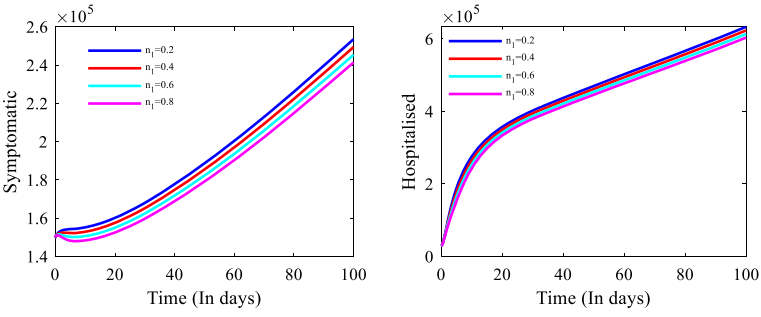
(a) Brazil



(b) India

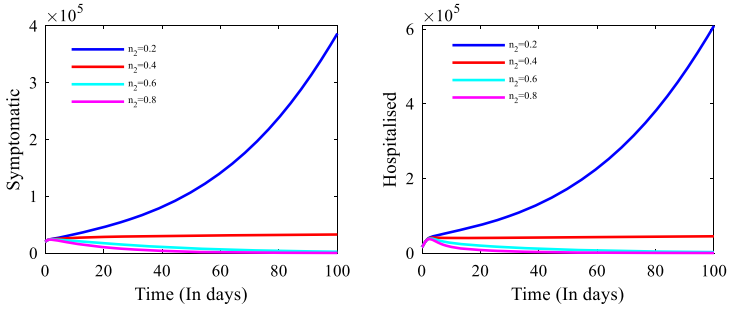


(c) Italy

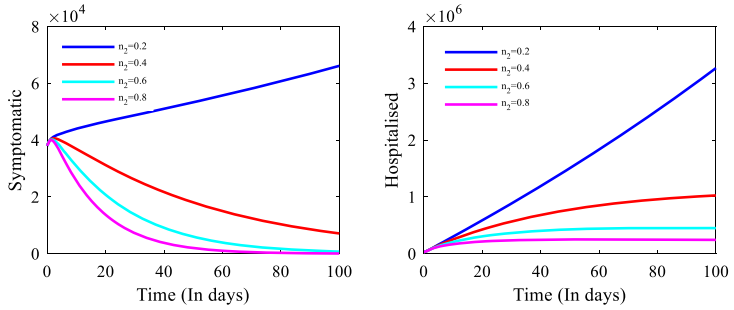


(d) USA

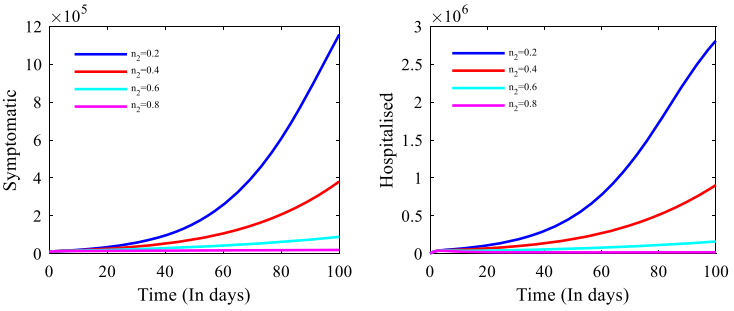
Fig. 5 Effect of intervention policies on symptomatic infected and hospitalised individuals in **a** Brazil, **b** India, **c** Italy, **d** USA



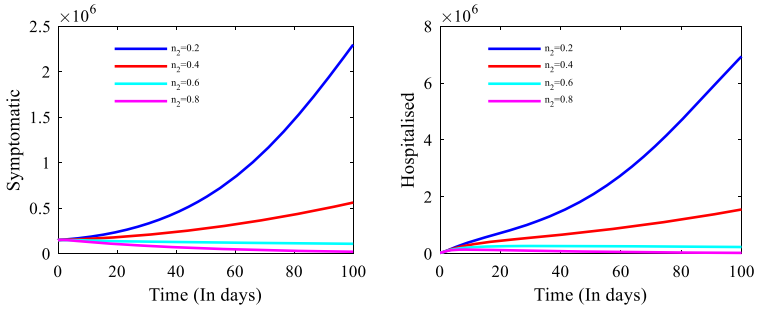
(a) Brazil



(b) India



(c) Italy



(d) USA

Fig. 6 Effect of vaccine efficacy on symptomatic infected and hospitalised individuals in **a** Brazil, **b** India, **c** Italy, **d** USA

6.4 Impact of vaccination rate

Vaccination is significant for reducing the infection rate of COVID-19. In our model, we have used τ_1 for the vaccination rate of susceptible populations. In Fig. 7, the effect of vaccination rate on symptomatic infected and hospitalised individuals in Brazil, India, Italy, and the USA can be shown. It has been found that increasing the vaccination rate reduces the incidence of symptomatic infected as well as the number of people who are hospitalised.

6.5 Effect of quarantine

Quarantine is viewed as a successful cure in the early stages of an epidemic. During the coronavirus outbreak, quarantine was also advised and used as a critical guideline for preventing illness and its further spread. The effect of quarantine on the infected population was observed by simulating the model for different quarantine rates of exposed (α_2) and symptomatic infected (α_3).

6.5.1 Quarantine of exposed individuals

As represented in Fig. 8, symptomatic infected and hospitalized individuals are rapidly increasing, reaching a peak, and then decreasing with lower values of (α_2), 0.2602 for Brazil, 0.2214 for India, 0.2131 for Italy, and 0.2995 for the USA. As compared to lower quarantine rates, when these rates are increased to 0.8602 for Brazil, 0.8214 for India, 0.8131 for Italy, and 0.8995 for the USA, the number of symptomatic infected and hospitalised patients drops. This implies that putting affected people in quarantine can help to slow the spread of coronavirus in the early stages of the epidemic.

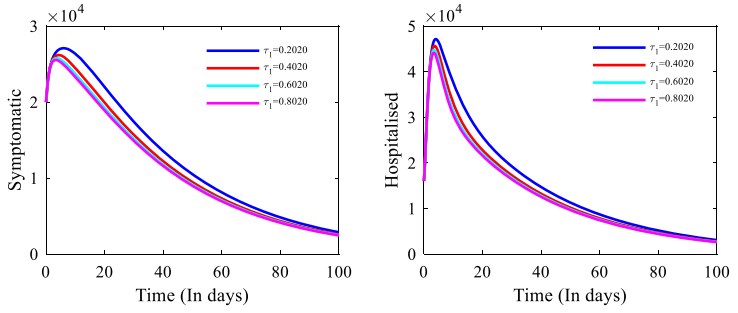
6.5.2 Quarantine of symptomatic infected individuals

Figure 9 shows symptomatic infected and hospitalised individuals are growing rapidly for lower values of (α_3), 0.02656 for Brazil, 0.0285 for India, 0.0028 for Italy, and 0.2227 for the USA, reaching a greater peak value and then dropping. When we increase these quarantine rates to 0.08656 for Brazil, 0.0885 for India, 0.0088 for Italy, and 0.8227 for the USA, the peak value for symptomatic infected and hospitalised patients decreases. This implies that quarantining infected individuals can aid in reducing the spread of COVID-19.

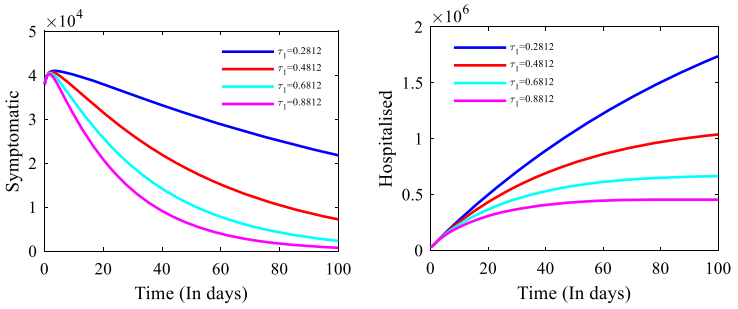
7 Conclusion

In the current study, we developed a deterministic compartmental model for COVID-19 transmission dynamics by adding vaccination and quarantine compartments. The model is theoretically examined by the basic reproduction number (R_0). Further, the equilibrium states of the model system are calculated as disease-free equilibrium point and endemic equilibrium point, both of which are proved to be globally asymptotically stable. In fact, the disease could be eradicated from any population if the basic reproduction number is less than unity.

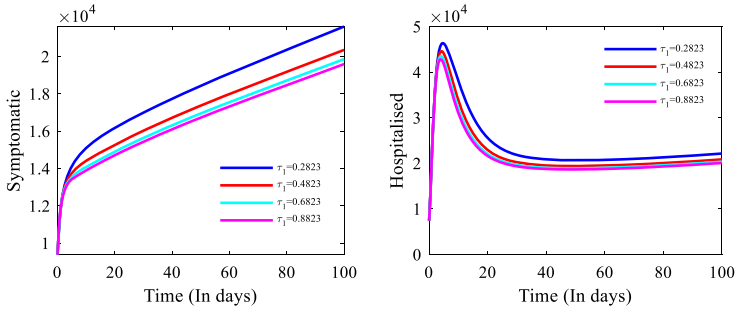
The crucial vaccination threshold is calculated, and it is found that if vaccine efficacy is lower and disease reproduction is high, even if a huge fraction of the population is vaccinated, the disease will still not be eradicated. That is, even if vaccine coverage is high, extra efforts will be required to reduce R_0 below unity or to remove disease from the population.



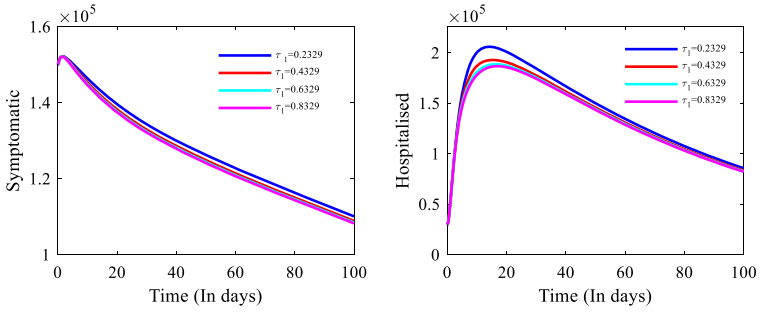
(a) Brazil



(b) India

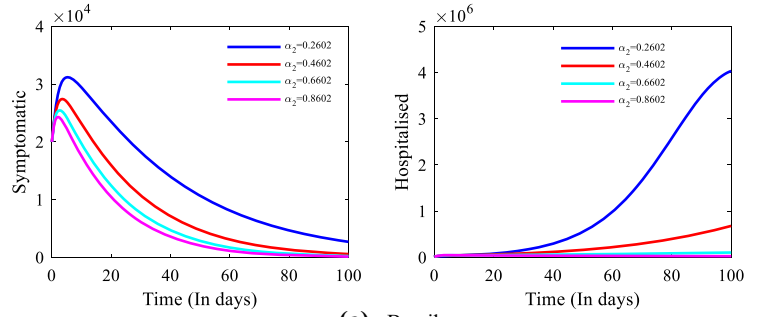


(c) Italy

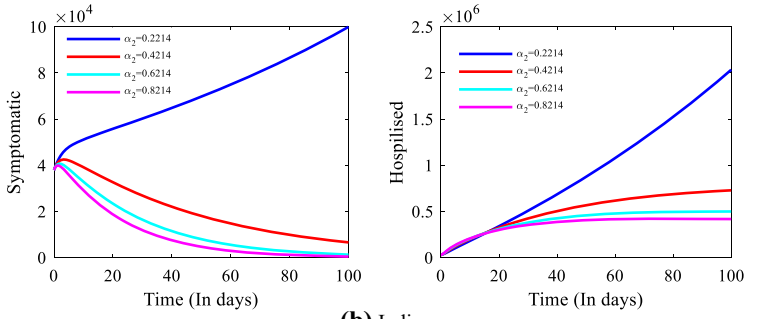


(d) USA

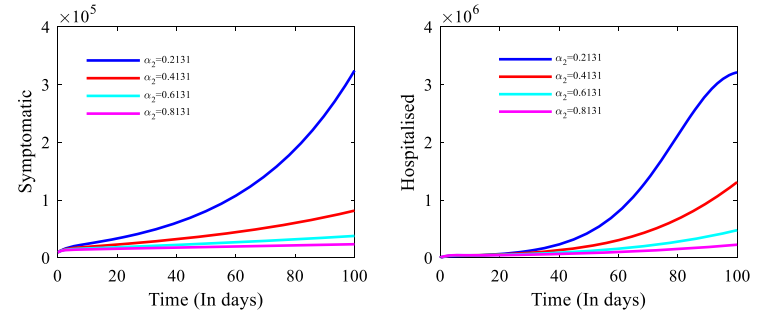
Fig. 7 Effect of vaccination rate on symptomatic infected and hospitalised individuals in **a** Brazil, **b** India, **c** Italy, **d** USA



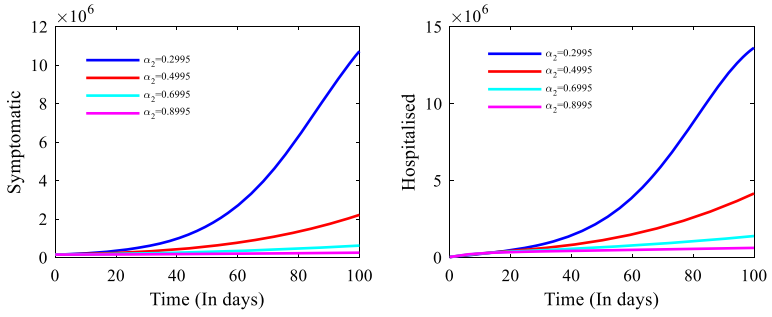
(a) Brazil



(b) India

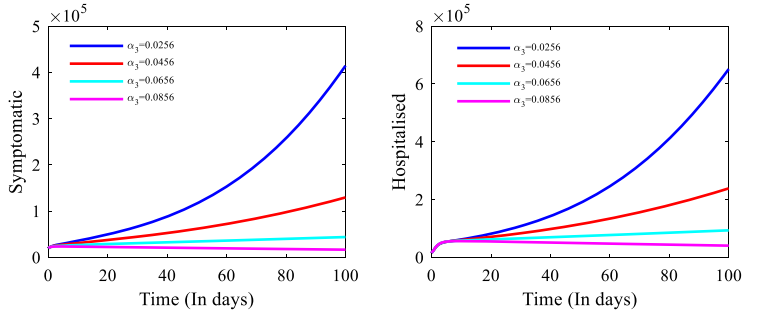


(c) Italy

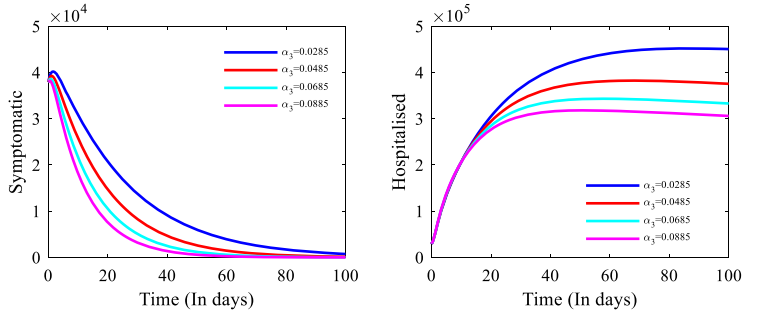


(d) USA

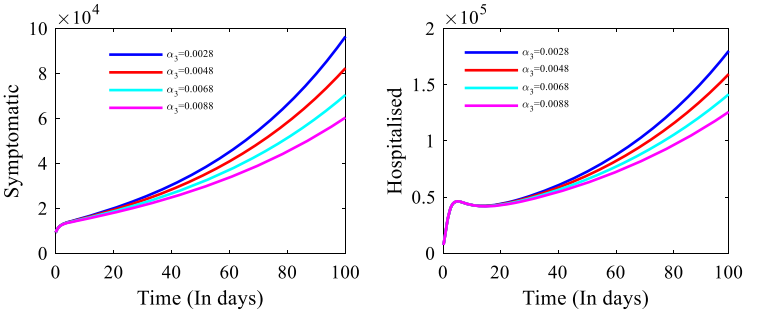
Fig. 8 Effect of quarantine of exposed individuals on symptomatic infected and hospitalised individuals in **a** Brazil, **b** India, **c** Italy, **d** USA



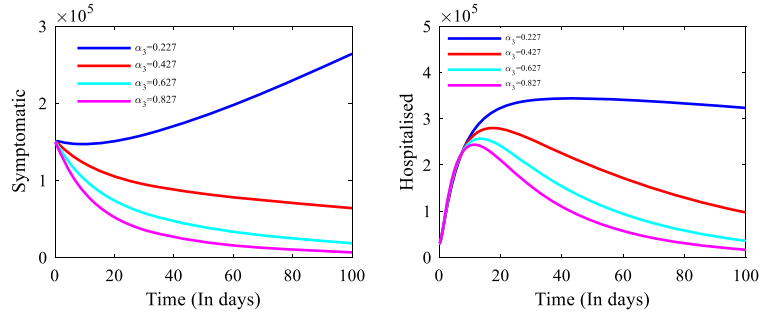
(a) Brazil



(b) India



(c) Italy



(d) USA

Fig. 9 Effect of quarantine of symptomatic infected individuals on symptomatic infected and hospitalised individuals in **a** Brazil, **b** India, **c** Italy, **d** USA

It can be visualized from the model fitting that our model fits pretty well with the reported daily new cases and cumulative case data for the COVID-19 outbreak in Brazil, India, Italy, and the USA. A set of model parameter values for all the above-mentioned regions are estimated using the model fitting technique. The results represent that to control the spread of COVID-19 in any community, vaccination and treatment should be implemented. Our findings suggest that vaccines and therapy are quite efficient in preventing COVID-19 from spreading, so additional work is needed to eradicate the disease. Moreover, our results specify that using a mixture or concurrently using personal protection/preventive measures such as face masks, hand washing and sanitizing, quarantine, and social distancing should be encouraged to reduce the disease incidence.

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Daily and Cumulative Cases Italy, retrieved february 9, 2022, from www.worldometers.info/coronavirus/country/italy/

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