Advances and Applications in Mathematical Sciences
Volume 23, Issue 6, April 2024, Pages 505-531

UNRAVELING THE DYNAMICS OF SARS-COV-2: A MATHEMATICAL MODEL INVESTIGATING VACCINATION IMPACT AND INTERVENTION STRATEGIES

JAMAL HUSSAIN* and JOAN LALDINPUII

Department of Mathematics and Computer Science
Mizoram University, Tanhril
Aizawl, 796004, Mizoram, India
E-mail: jamal.mzu@gmail.com
jodi.slem@gmail.com

Abstract

This research presents a comprehensive exploration of mathematical modelling for COVID-19, with a focus on vaccination and intervention strategies. Various preventive measures, such as lockdowns, media campaigns, and social distancing, are analyzed for their impact on disease progression. The stability of Disease-Free and Endemic Equilibrium points is assessed based on the basic reproduction number (R_0). Sensitivity analysis identifies key parameters affecting R_0, with vaccination coverage and contact rate standing out as critical factors. The study underscores the need for persistent and intensive interventions to combat the outbreak effectively. Ultimately, a combination of strict interventions and increased vaccination is recommended to curtail the spread of COVID-19.

1. Introduction

The COVID-19 pandemic has presented an unprecedented global health crisis, requiring rapid and effective strategies to mitigate its impact. Mathematical modelling has become a potent tool for comprehending and forecasting the dynamics of infectious diseases, providing insightful data on the modes of transmission, effects of vaccination, and efficacy of intervention

2020 Mathematics Subject Classification: 92-XX.
Keywords: Mathematical Modelling, COVID-19, Stability Analysis, Vaccination, Sensitivity Analysis, Intervention measure.
*Corresponding author.
Received October 9, 2023; Accepted January 4, 2024

strategies. The use of mathematical modelling is essential for guiding evidence-based decision-making in India, a nation with a sizable population and distinctive demographic traits, to address COVID-19 effectively.

The first Mathematical model in Epidemiology was the work of Daniel Bernoulli on the effect of variolation against smallpox in increasing life expectancy [1], Since Kermack and McKendrick's pioneering work, mathematical models have been applied to provide a framework for comprehending the dynamics of infectious diseases [2]. A number of mathematical models have also been put forth to comprehend the COVID-19 transmission dynamics in India. Several studies have expanded the SI [3], SIS [4], SIR [5], SEIR [6] by including a number of new compartments such as asymptomatic, isolated, quarantined, protected, death, lock-down, hospitalized, etc. [7-13].

This research aims to investigate the mathematical modelling of COVID-19 in India, with a specific focus on studying the impact of vaccination and intervention measures. In this study, we also consider the period from March 2020 to December 2020 of the COVID-19 outbreak where several preventive measures have been implemented in India to measure the strength of intervention measures. The government of India declares a nationwide lockdown from 24 March 2020 for 21 days [14]. In India vaccine was introduced on 16 January 2021, and India began the administration of COVID-19 vaccines. As of 25 March 2022, India has administered over 1.8 billion doses overall. In India, 90% of the eligible population has received at least one shot, and 76% of the eligible population is fully vaccinated [15]. We shall introduce the Vaccine compartment in our model.

The findings will help policymakers, public health professionals, and researchers develop focused strategies to manage the epidemic and ensure the health and wellbeing of the Indian population. This will support evidence-based decision-making.

2. Model Formulation

We create a deterministic compartmental model $SELL_AQR$ to describe the disease transmission mechanism. Let N be the total population of humans. The total population N is divided into six compartments: Susceptible

(S), Vaccinated (V), Exposed (E), Symptomatic Infection (I), Asymptomatic Infection (I_A), and individuals that are either recovered or die from COVID-19 (R). We also include Vital Dynamics: The natural human natality or recruitment rate denoted by Λ and mortality (death) rate denoted by μ.

Susceptible individuals move to the Exposed compartment when they come into contact with Symptomatic Individuals (I) as well as Asymptomatic Individuals (I_A) at a rate β (rate of transmission). It is reported that I_A has a lower chance of transmission than I (MoHFW). So we assume that transmission of the disease from Asymptomatic individuals (I_A) to Susceptible individuals is less than that of Symptomatic Individuals to Susceptible.

We denote the reduction in the rate of transmission from Asymptomatic Individuals to Symptomatic as η where $\eta < 1$. The new infection is given by $\beta S(I + \eta I_A)$

Susceptible Individuals who are Vaccinated move to the Vaccinated compartment at the rate δ. Since Vaccines are not 100% effective (www.cdc.gov), we assume that those in the Vaccination class are not at a complete protective level, and the Vaccinated individuals become infected and move into the Exposed class. We assume that this occurs at a lower transmission rate ω, where $\omega \in [0, 1]$ is the decreasing coefficient.

We adapt the model to include several intervention techniques. The use of preventive measures such as lock-downs, media campaigns to raise awareness, effective handwashing techniques, social seclusion, mask use, etc., as part of intervention strategies, slows the spread of disease.

The application of the intervention suggests that there would be a decrease in the rate of disease transmission in terms of model parameters. The strength of the intervention, h where $h \in [0, 1]$, is deemed to have decreased at this rate of transmission.

During implementation, the parameter β is transformed to $(1 - h)\beta$ when there is intervention. The Exposed individuals move to the Infected class i.e., I, I_A at a rate γ. A fraction of the population moves from Expose to the

Symptomatic class at a rate r, and the remaining fraction moves to the Asymptomatic class at the rate $(1 - r)$.

Individuals from Symptomatic and Asymptomatic recover at a rate α, η respectively. Each of these classes may decrease as a result of mortality μ, while an individual who shows COVID-19 Symptoms may have a lower chance of survival, therefore Symptomatic class decreases as a result of death from COVID-19 at a rate θ.

Based on the assumption we propose the following model; a system of non-linear differential equations. The Schematic diagram is shown in Figure 1.

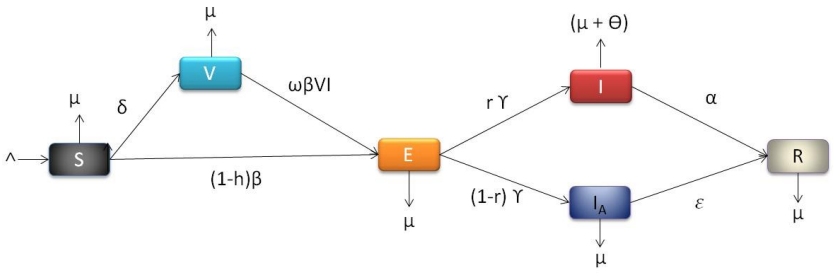

Figure 1. Schematic Diagram of $SVELL_AR$.

$$\frac{dS}{dt} = \Lambda - (1 - h)\beta S(I + \eta I_A) - \delta S - \mu S,$$

$$\frac{dV}{dt} = \beta\delta S - \omega\beta VI - \mu V,$$

$$\frac{dE}{dt} = (1 - h)\beta S(I + \eta I_A) + \omega\beta VI - \gamma E - \mu E, \tag{1}$$

Table 1. Parameter Description.

Parameter	Description	Value
Λ	Birth rate	$\frac{10000}{59x365}$ [6]
μ	Death rate	$\frac{1}{59x365}$ [16]
β	Rate of transmission	1.7399 [7]
γ	Rate of transition from Exposed to infected class i.e., I, I_A	0.1923 [17]
r	Fraction of population moves from Exposed to symptomatic class	0.4579 [7]
$(1-r)$	Fraction of population moves from Exposed to asymptomatic class	0.5422
α	Recovery rate of symptomatic infected class	0.004165 (assume)
η	Reduction in the transmission from asymptomatic, $\eta < 1$	0.1002 [7]
ϵ	Recovery rate of asymptomatic infection	0.13978 [18]
θ	Rate of disease induced death	0.0175 (COVID-19 India 2020)
δ	Rate at which susceptible individual are vaccinated	0.4 (assume)
ω	Rate of reduction in risk of infection due to vaccination	0.2(assume)
h	Strength of intervention	0;0.5042; 0.6544; 0.7282 [7]

$$\frac{dI}{dt} = r\gamma E - (\mu + \theta)I - \alpha I,$$

$$\frac{dI_A}{dt} = (1 - r)\gamma E - \epsilon I_A - \mu I_A,$$

$$\frac{dR}{dt} = \alpha I + \epsilon I_A - \mu R,$$

with nonnegative initial conditions given by

$$S(0) > 0,\ V(0) > 0,\ E(0) > 0,\ I(0) > 0,\ I_A > 0,\ R(0) > 0. \tag{2}$$

All the parameters of the system (1) are assumed to be positive for all time $t > 0$.

3. Mathematical Model Analysis

3.1 Positivity of Solutions

For the COVID-19 model system 1 to be epidemiologically realistic, it is necessary to prove that all the state variables remain positive for all time.

Theorem 1. *Let the initial data be* $\{(S, V, E, I, I_A, R) \le 0\} \in \phi$. *Then the solution set* $\{S(t), V(t), E(t), I(t), I_A(t), R(t)\}$ *of the model system is non negative for all time t.*

Proof. Considering the non-linear system of the model (1), we take the first equation

$$\frac{dS}{dt} = \Lambda - (1 - h)\beta S(I + I_A) - \delta S - \mu S,$$

$$\frac{dS}{dt} \ge -[(1 - h)\beta S(I + I_A) + \delta + \mu]S,$$

$$\int \frac{dS}{S} \ge -\int [(1 - h)\beta S(I + I_A) + \delta + \mu]dt,$$

$$\ln S \ge -[(1 - h)\beta S(I + I_A) + \delta + \mu]t + c,$$

$$S \ge e^{-[(1-h)\beta S(I+I_A)+\delta+\mu]t} + e^c,$$

$$S(t) \ge S(0)e^{-[(1-h)\beta S(I+I_A)+\delta+\mu]t}.$$

Similarly, it can also been shown that $V(t) > 0$, $E(t) > 0$, $I(t), > 0$, $I_A(t) > 0$, $R(t) > 0$ for all $t > 0$. Therefore, the disease is uniformly persistent for every positive solution.

3.2 Invariant Region

Theorem 2. *For the initial conditions* (2), *the solutions of system* (1) *are contained in the region* $\phi \subset R_+^6$ *defined by*

$$\phi = \left[\{S(t), V(t), E(t), I(t), I_A(t), R(t)\} \in R_+^6 : N(t) \leq \frac{\Lambda}{\mu}\right].$$

Proof. Let $N = S + V + E + I + I_A + R$

$$\frac{dN}{dt} = \Lambda - (S + V + E + I + I_A + R)\mu - \theta I \tag{3}$$

$$\frac{dN}{dt} = \Lambda - \mu N - \theta I \tag{4}$$

$$\frac{dN}{dt} \leq \Lambda - \mu N \tag{5}$$

$$\frac{dN}{dt} + \mu N \leq \Lambda \tag{6}$$

$$Ne^{\mu t} \leq \int e^{\mu t}\Lambda + C \tag{7}$$

$$Ne^{\mu t} \leq \frac{\Lambda e^{\mu t}}{\mu} + C \tag{8}$$

$$N \leq \frac{\Lambda}{\mu} + Ce^{-\mu t}. \tag{9}$$

At $t \to \infty$, $N \to \frac{\Lambda}{\mu}$. Clearly

$$\phi = \left[\{S(t), V(t), E(t), I(t), I_A(t), R(t)\} \in R_+^6 : N(t) \leq \frac{\Lambda}{\mu}\right].$$

3.3 Analysis of Disease-Free Equilibrium (DFE) E_0

The model gets DFE when the disease has zero induction

Taking the first equation of system (1) with $E = I = I_A = Q = R = 0$ into consideration.

We arrive at

$$S_0 = \frac{\Lambda}{(\delta + \mu)}, V_0 = \frac{\delta\Lambda}{\mu(\delta + \mu)}$$

Then, the disease-free equilibrium (DFE) state E_0 is given by

$$E_0 = \left[\frac{\Lambda}{(\delta + \mu)}, \frac{\delta\Lambda}{\mu(\delta + \mu)}, 0, 0, 0, 0\right].$$

4. Basic Reproductive Number R_0

R_0 refers to the average number of secondarily infected persons infected by one primary infected patient during the infectious period. To obtain the basic reproduction number, we used the next-generation matrix method by Diekmann et al. [19] and Dietz [20], where $\mathcal{F}$ is the matrix of the new infection terms and $\mathcal{V}$ is the matrix of the transition terms.

At disease-free equilibrium

$$E_0 = \left[\frac{\Lambda}{(\delta + \mu)}, \frac{\delta\Lambda}{\mu(\delta + \mu)}, 0, 0, 0, 0\right]$$

$$\mathcal{F} = \begin{bmatrix} 0 & \frac{(1-h)\beta\Lambda}{(\delta+\mu)} + \frac{\omega\beta\delta\Lambda}{\mu(\delta+\mu)} & \frac{(1-h)\beta\eta\Lambda}{(\delta+\mu)} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} \gamma + \mu & 0 & 0 & 0 \\ -r\gamma & (\mu + \theta + \alpha) & 0 & 0 \\ -(1-r)\gamma & 0 & \epsilon + \mu & 0 \\ 0 & -\alpha & -\epsilon & \mu \end{bmatrix}.$$

Now, $\mathcal{F}\mathcal{V}^{-1}$

$$= \begin{bmatrix} \dfrac{\gamma r\left[\dfrac{(1-h)\beta\Lambda}{(\mu+\delta)} + \dfrac{\beta\delta\Lambda\omega}{\mu(\mu+\delta)}\right]}{(\mu+\gamma)(\alpha+\theta+\mu)} - \dfrac{\beta\gamma\eta\Lambda(r-1)}{(\mu+\eta)(\mu+\gamma)(\mu+\delta)} & \dfrac{(1-h)\beta\Lambda}{\mu+\delta} + \dfrac{\beta\delta\Lambda\omega}{\mu(\mu+\delta)} & \dfrac{\beta\eta\Lambda}{(\mu+\epsilon)(\mu+\delta)} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

The basic Reproduction number is given by

$$R_0 = \frac{\gamma r\left[\dfrac{(1-h)\beta\Lambda}{(\mu+\delta)} + \dfrac{\beta\delta\Lambda\omega}{\mu(\mu+\delta)}\right]}{(\mu+\gamma)(\alpha+\theta+\mu)} - \frac{\beta\gamma\eta\Lambda(r-1)}{(\mu+\eta)(\mu+\gamma)(\mu+\delta)}.$$

5. Stability Analysis of DFE

5.1 Local stability of disease-free equilibrium

Theorem 3. *The Disease Free Equilibrium DEF is locally asymptotically stable if* $R_0 < 1$.

Proof. The Jacobian matrix w.r.t. system 1 is given by which implies

$$J_{DFE} = \begin{bmatrix} -p & 0 & 0 & -(1-h)\beta S_0 & -(1-h)\beta\eta S_0 & 0 \\ \delta & -\mu & 0 & -\omega\beta V_0 & 0 & 0 \\ 0 & 0 & -q & (1-h)\beta S_0 & (1-h)\beta\eta S_0 & 0 \\ 0 & 0 & r\gamma & -z & 0 & 0 \\ 0 & 0 & (1-r)\gamma & 0 & -t & 0 \\ 0 & 0 & 0 & \alpha & \epsilon & -\mu \end{bmatrix}$$

where

$$p = (\delta+\mu),\ q = (\gamma+\mu),\ z = (\mu+\theta+\alpha),\ t = (\epsilon+\mu).$$

Clearly, two eigenvalues of the matrix JDFE are negative such as -μ and -μ. The remaining eigenvalues are the roots of the following Polynomial equation

$$\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0$$

where

$$a_3 = -(-p-q-z-t) = (p+q+z+t)$$

$$a_2 = [(p+q+z+t)^2 - (p^2+q^2+z^2+t^2)]/2 - (1-h)\beta\gamma r S_0 - (1-h)\beta\gamma\eta S_0(1-r)$$

$$a_1 = [z(z^2 + (1-h)\beta\gamma r S_0)]/3 - ((p+q+t+z)(p^2+q^2+t^2+z^2 + 2(1-h)\beta\gamma r S_0 - 2(1-h)\beta\gamma\eta S_0(r-1)))/2 + [(p+q+t+z)^3]/6 + p^3/3 + (t(t^2 - (1-h)\beta\gamma\eta S_0(r-1)))/3 + (q(q^2 - (1-h)\beta\gamma r S_0 - (1-h)\beta\eta S_0 t)(r-1))/3 - (\gamma((1-h)\beta\eta q S_0 + (1-h)\beta\eta S_0 t)(r-1))/3 + (\gamma r(1-h)\beta\eta q S_0 + (1-h)\beta\eta S_0 z))/3 + (\beta S_0(\gamma q r + \gamma r z))/3 - ((1-h)\beta\eta S_0(\gamma q(r-1) + \gamma t(r-1)))/3$$

$$a_0 = p(1-R_0)(qtz - (1-h)\beta\gamma r S_0 t - (1-h)\beta\gamma\eta S_0 z + (1-h)\beta\gamma\eta r S_0 z).$$

According to the Routh-Hurwitz criterion, the above equation will give negative roots or roots with negative real parts if the following condition is satisfied:

$$a_3 > 0, \begin{vmatrix} a_3 & a_1 \\ 1 & a_2 \end{vmatrix} > 0, \begin{vmatrix} a_3 & a_1 & 0 \\ 1 & a_2 & a_0 \\ 0 & a_3 & a_1 \end{vmatrix} > 0.$$

Hence, the disease-free equilibrium point E_0 of the system is locally asymptotically stable, when $R_0 < 1$.

5.2 Global stability of disease-free equilibrium

We now study the global stability of disease-free equilibrium, using the theorem by Castillo-Chavez et al. [21]

Theorem 4. *If the given mathematical model can be written in the form*:

$$\frac{dX}{dt} = F(X, Y)$$

$$\frac{dY}{dt} = G(X, Y),\ G(X, Y) = 0 \tag{10}$$

where $X = (S, V)^T$, $Y = (E, I, I_A, R)^T$, *denoting the number of uninfected*

individuals and denoting the number of COVID-19-*infected people respectively. Let the disease-free equilibrium of this system be*

$$U_0 = (X^*, 0) = \left(\frac{\Lambda}{\delta + \mu}, \frac{\delta\Lambda}{\mu(\delta + \mu)}, 0\right)$$

where 0 *is a zero vector.*

For the global asymptotically stable, the following condition (H1) *and* (H2) *must be satisfied.*

(H1): For $\frac{dX}{dt} = F(X, 0)$, 0 *is global asymptotically stable.*

(H2): $G(X, Y) = AY - \hat{G}(X, Y)$, $\hat{G}(X, Y) \geq 0$ for $(X, Y) \in \Omega$

where $A = D_Y G(X^*, 0)$ *is an M-matrix* (*the off-diagonal elements of A are nonnegative*) *and* Ω *is the region where the model makes biological sense. If the given system of differential equations of our model satisfies the given condition in* (2) *then the fixed point* $U_0 = (X^*, 0)$ *is a global asymptotically stable* (*g.a.s*) *equilibrium of* (2) *provided* $R_0 < 1$, *and the assumption* (H1) *and* (H2) *are satisfied.*

Theorem 5. *The DFE* E_0 *of model* (1) *is global asymptotically stable if* $R_0 < 1$.

Proof. First, we rewrite the system of differential equation of our model (1) as $X = (S, V)^T$ and $Y = (E, I, I_A, R)^T$.

Then, the DFE is given by

$$U_0 = (X^*, 0) = \left(\frac{\Lambda}{\delta + \mu}, \frac{\delta\Lambda}{\mu(\delta + \mu)}, 0\right)$$

and the system $\frac{dX}{dt} = F(X, 0)$ becomes

$$\dot{S} = \Lambda - (\delta + \mu)S$$

$$\dot{V} = \delta S - \mu V \tag{11}$$

This equation has a unique equilibrium point

$$X^* = \left(\frac{\Lambda}{\delta + \mu}, \frac{\delta\Lambda}{\mu(\delta + \mu)} \right) \tag{12}$$

which is globally asymptotically stable. Therefore, condition (H1) is satisfied. We now verify the second condition (H2). For model (1), we have

$$G(X, Y) = \begin{bmatrix} (1-h)\beta S(I + \eta I_A) + \omega\beta VI - \gamma E - \mu E \\ r\gamma E - (\mu + \theta)I - \alpha I \\ (1-r)\gamma E - \epsilon I_A - \mu I_A \\ \alpha I + \epsilon I_A - \mu R \end{bmatrix}$$

$$D_Y G(X^*, 0) = A = F - V$$

$$= \begin{bmatrix} -(\gamma + \mu) & (1-h)\beta S_0 + \omega\beta V_0 & (1-h)\beta S_0 & 0 \\ p_1\gamma & -(\mu + \theta + \alpha) & 0 & 0 \\ p_2\gamma & 0 & -(\epsilon + \mu) & 0 \\ p_3\gamma & 0 & \epsilon & -\mu \end{bmatrix}$$

Clearly, we see that A is an M-matrix, i.e. all the off-diagonal elements of A are non-negative.

$$\hat{G}(X, Y) = AY - G(X, Y) = \begin{bmatrix} [(1-h)\beta(I + I_A)](S - S_0) + \omega\beta I(V - V_0) \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

which implies that $\hat{G}(X, Y) \geq 0$ for all $(X, Y) \in \Omega$. Therefore, conditions (H1) and (H2) are satisfied. Hence, disease-free equilibrium is globally asymptotically stable.

6. Stability Analysis of EE

6.1 Existence of Endemic Equilibrium point

Let us denote the Endemic Equilibrium by $E_1 = (S^*, V^*, E^*, I^*, I_A^*, R^*)$ The Endemic Equilibrium is given by

$$S^* = \frac{\Lambda}{(1-h)\beta(I^* + \gamma B) + \delta + \mu} = C$$

$$V^* = \frac{\delta C}{\omega\beta I^* + \mu} = D$$

$$E^* = \frac{(\mu + \theta + \alpha)I^*}{(\epsilon + \mu)} = A$$

$$I_A^* = \frac{(1-r)\gamma A}{(\epsilon + \mu)} = B$$

$$I^* = \frac{(\mu+\gamma)(\mu+\delta)(\alpha+\theta+\mu) + (1-h)\beta\gamma\Lambda r\left[\frac{\eta(r-1)(\alpha+\theta+\mu)}{r(\mu+\epsilon)} - 1\right]}{\beta(1-h)(\mu+\gamma)\left[\frac{\eta(r-1)(\alpha+\theta+\mu)}{r(\mu+\epsilon)} - 1\right](\alpha+\theta+\mu)}(R_0 - 1)$$

$$R^* = \frac{\alpha I^* + \epsilon B}{\mu}$$

6.2 Local stability of endemic equilibrium

Theorem 6. *The endemic equilibrium E_1 is locally asymptotically stable if $R_0 > 1$, otherwise it is unstable.*

Proof. The Jacobian matrix of the system (1) at endemic equilibrium point E_1 is obtained as follows:

$$J_{E1} = \begin{bmatrix} -a & 0 & 0 & -(1-h)\beta S^* & -(1-h)\beta\eta S^* & 0 \\ \alpha & -d & 0 & -\omega\beta V^* & 0 & 0 \\ a_{31} & \omega\beta I^* & -f & a_{34} & (1-h)\beta\eta S^* & 0 \\ 0 & 0 & r\gamma & -j & 0 & 0 \\ 0 & 0 & (1-r)\gamma & 0 & -l & 0 \\ 0 & 0 & 0 & \alpha & \epsilon & -\mu \end{bmatrix}$$

where

$$a = [(1-h)\beta(I^* + \eta I_A^*) + \delta + \mu]$$

$$d = [\omega\beta I^* + \mu]$$

$$f = (\gamma + \mu)$$

$$j = (\mu + \theta + \alpha)$$

$$l = (\epsilon + \mu)$$

$$a_{31} = (1 - h)\beta(I^* + \eta I_A^*)$$

$$a_{34} = (1 - h)\beta S^* + \omega\beta V^*.$$

Clearly, one eigenvalue of the matrix J_{E1} is negative -μ and the remaining eigenvalues are the roots of the following Polynomial equation:

$$\lambda^5 + c_4\lambda^4 + c_3\lambda^3 + c_2\lambda^2 + c_1\lambda^2 + c_1\lambda + c_0 = 0$$

where

$$c_4 = a + d + f + j + l$$

$$c_3 = [(a + d + f + j - l)^2]/2 - a_{34}r\gamma - \alpha^2/2 - f^2/2 - j^2/2 - l^2/2$$

$$- (1 - h)\beta\eta S^*(1 - r)\gamma$$

$$c_2 = adf + adj - aa_{34}r\gamma - adl + afj - afl - da_{34}r\gamma + dfj - dfl - ajl - djl$$

$$+ a_3r\gamma l - fjl + (1 - h)\beta a_{31}r\gamma S^* + \beta^2 r\gamma I^* v^* \omega^2 - a(1 - h)\beta(1 - r)\gamma\eta S^*$$

$$- (1 - h)\beta d(1 - r)\gamma\eta S^* + (1 - h)\beta a_{31}(1 - r)\gamma\eta S^* - (1 - h)\beta j(1 - r)\gamma\eta S^*$$

$$c_1 = adfj - ada_{34}r\gamma - adfl - adjl + aa_{34}r\gamma l - afjl + da_{34}r\gamma l$$

$$- dfjl + (1 - h)\beta da_{31}r\gamma S^* - (1 - h)\beta a_{31}r\gamma lS^* + \beta^2\delta r\gamma I^* S^*\omega + a\beta^2 r\gamma I^* V^*\omega^2$$

$$- \beta^2 r\gamma I^* lV^*\omega^2 a(1 - h)\beta d(1 - r)\gamma\eta S^*$$

$$+ (1 - h)\beta da_{31}(1 - r)\gamma\eta S^* - a(1 - h)\beta j(1 - r)\gamma\eta S^*$$

$$- (1 - h)\beta dj(1 - r)\gamma\eta S^* + (1 - h)\beta a_{31}j(1 - r)\gamma\eta S^*$$

$$+ \beta^2\delta I^*(1 - r)\gamma\eta S^*\omega$$

$$c_0 = adfjl - ada_{34}r\gamma l + (1 - h)\beta da_{31}r\gamma lS^*$$

$$+ a\beta^2 r\gamma I^* l V^* \omega^2 + a(1-h)\beta dj(1-r)\gamma\eta S^*$$

$$- (1-h)\beta d a_{31} j(1-r)\gamma\eta S^* + \beta^2\delta r\gamma I^* S^* l\omega$$

$$- \beta^2\delta I^* j(1-r)\gamma\eta S^*\omega.$$

According to the Routh-Hurwitz criterion, the above equation will give negative roots or negative real parts if the following condition is satisfied:

$$c_4 > 0, \begin{vmatrix} c_4 & c_2 \\ 1 & c_3 \end{vmatrix} > 0, \begin{vmatrix} c_4 & c_2 & c_0 \\ 1 & c_3 & c_1 \\ 0 & a_4 & a_2 \end{vmatrix} > 0, \begin{vmatrix} c_4 & c_2 & c_0 & 0 \\ 1 & c_3 & c_1 & 0 \\ 0 & c_4 & c_2 & c_0 \\ 0 & 1 & c_3 & c_1 \end{vmatrix} > 0$$

Hence, the endemic equilibrium point E_1 of the system is locally asymptotically stable when $R_0 > 1$.

6.3 Global stability of disease-free equilibrium

Theorem 7. *The endemic equilibrium* $E_1 = (S^*, V^*, E^*, I^*, I_A^*, R^*)$ *of our mathematical model is globally asymptotically stable.*

Proof. For the global stability result, we will use the method discussed in Korobeinikov [21] and Wake, Li and Muldowney [22]. From (1), a person was infected with coronavirus and then fully recovered. After that, we assume that a person has permanent immunity. The first five equations are independent of R in (1) and we will study the following sub-system.

$$\frac{dS}{dt} = \Lambda - (1-h)\beta S(I + \eta I_A) - \delta S - \mu S$$

$$\frac{dV}{dt} = \delta S - \omega V I - \mu V$$

$$\frac{dE}{dt} = (1-h)\beta S(I + \eta I_A) + \omega\beta V I = \gamma E - \mu E$$

$$\frac{dI}{dt} = r\gamma E - (\mu + \theta)I - \alpha I$$

$$\frac{dI_A}{dt} = (1-r)\gamma E - \epsilon I_A - \mu I_A \tag{13}$$

Let

$$x_1 = \frac{S}{S^*},\ y_1 = \frac{V}{V^*},\ z_1 = \frac{E}{E^*},\ u_1 = \frac{I}{I^*},\ v_1 = \frac{I_A}{I_A^*}.$$

The model of the system of equation (13) is transformed into the following form

$$\frac{dx_1}{dt} = x_1\left[\frac{\Lambda}{S^*}\left(\frac{1}{x_1}\right) - (1-h)\beta I^*(u_1 - 1) - (1-h)\beta\eta I_A^*(v_1 - 1)\right]$$

$$\frac{dy_1}{dt} = y_1\left[\frac{\delta S^*}{V^*}\left(\frac{x_1}{y_1} - 1\right) - \omega\beta I^*(u_1 - 1)\right]$$

$$\frac{dz_1}{dt} = z_1$$

$$\left[\frac{(1-h)\beta S^* I^*}{E^*}\left(\frac{x_1 u_1}{z_1} - 1\right) + \frac{(1-h)\beta\eta S^* I_A^*}{E^*}\left(\frac{x_1 v_1}{z_1} - 1\right) + \frac{\omega\beta V^* I^*}{E^*}\left(\frac{y_1 u_1}{z_1} - 1\right)\right]$$

$$\frac{du_1}{dt} = u_1\frac{r\gamma E^*}{I^*}\left(\frac{z_1}{u_1} - 1\right)$$

$$\frac{du_1}{dt} = u_1\frac{r\gamma E^*}{I^*}\left(\frac{z_1}{u_1} - 1\right).$$

Here it is easy to find that the system of equation (14) has unique endemic equilibrium $E_1(1, 1, 1, 1, 1)$ and the global stability of $E_1(1, 1, 1, 1, 1)$ is same as that of E_1. Thus we investigate the global stability of $E_1(1, 1, 1, 1, 1)$ instead of E_1.

Defining the Volterra type Lyapunov function

$$L(x_1, y_1, z_1, u_1, v_1) = S^*(x_1 - 1 - \ln x_1) + V^*(y_1 - 1 - \ln y_1)$$

$$+ E^*(z_1 - 1 - \ln z_1)$$

$$+ \frac{(1-h)\beta I^*(S^* + \omega V^*)}{r\gamma E^*}(u_1 - 1 - \ln u_1)$$

$$+ \frac{(1-h)\beta\eta I_A^*(S^* + \omega V^*)}{\gamma(1-r)E^*}(v_1 - 1 - \ln v_1)$$

From equilibrium state E_1 we have the following equations

$$\Lambda = (1-h)\beta S^*(I^* + \eta I_A^*) + (\delta + \mu)S^*$$

$$\delta S^* = \omega\beta V^* I^* + \mu V^*$$

$$(\gamma + \mu)E^* = (1-h)\beta S^*(I^* + \eta I_A^*) + \omega\beta V^* I^*$$

$$r\gamma E^* - (\alpha + \mu)I^*$$

$$\gamma(1-r)E^* = (\epsilon + \mu)I_A^*$$

Then, differentiating L w.r.t. 't' along the solution curve of the system of the equation of model (14) and considering the above equation gives

$$\frac{dL}{dt} = S^*(x_1 - 1)\frac{\dot{x}_1}{x_1} + V^*(y_1 - 1)\frac{\dot{y}_1}{y_1} + E^*(z_1 - 1)\frac{\dot{z}_1}{z_1}$$

$$+ \frac{(1-h)\beta I^*(S^* + \omega V^*)}{r\gamma E^*}(u_1 - 1)\frac{\dot{u}_1}{u_1} + \frac{(1-h)\beta\eta I_A^*(S^* + \omega V^*)}{\gamma(1-r)E^*}(v_1 - 1)\frac{\dot{v}_1}{v_1}$$

$$= (x_1 - 1)\left[\Lambda\left(\frac{1}{x_1} - 1\right) - (1-h)\beta S^* I^*(u_1 - 1) - (1-h)\beta\eta S^* I_A^*(v_1 - 1)\right]$$

$$+ (y_1 - 1)\left[\delta S^*\left(\frac{x_1}{y_1} - 1\right) - \omega\beta V^* I^*(u_1 - 1)\right]$$

$$+ (z_1 - 1)\left[(1-h)\beta S^* I^*\left(\frac{x - 1u_1}{z_1} - 1\right) + (1-h)\beta\eta S^* I_A^*\left(\frac{x - 1v_1}{z_1} - 1\right)\right.$$

$$\left. + \omega\beta V^* I^*\left(\frac{y - 1u_1}{z_1} - 1\right)\right] + (1-h)\beta I^*(S^* + \omega V^*)(u_1 - 1)\left(\frac{z_1}{u_1} - 1\right)$$

$$+ (1-h)\beta\eta I_A^*(S^* + \omega V^*)(v_1 - 1)\left(\frac{z_1}{v_1} - 1\right).$$

After some algebraic manipulation, we have

$$\frac{dL}{dt} = \mu S^*\left(2 - x_1 - \frac{1}{x_1}\right) + \mu V^*\left(3 - \frac{a}{x_1} - y_1 - \frac{x_1}{y_1}\right)$$

$$+ (1-h)\beta S^* I^*\left(3 - \frac{1}{x_1} - \frac{x_1 u_1}{z_1} - \frac{z_1}{u_1}\right) + (1-h)\beta\eta S^* I_A^*\left(3 - \frac{1}{x_1} - \frac{x_1 v_1}{z_1} - \frac{z_1}{v_1}\right)$$

$$+ \omega\beta V^* I^*\left(4 - \frac{1}{x_1} - \frac{x_1}{y_1} - \frac{y_1 u_1}{z_1} - \frac{z_1}{u_1}\right).$$

Since the arithmetic mean is greater than or equal to the geometric mean, we have

$$\left(2 - x_1 - \frac{1}{x_1}\right) \leq 0$$

$$\left(3 - \frac{1}{x_1} - y_1 - \frac{x_1}{y_1}\right) \leq 0$$

$$\left(3 - \frac{1}{x_1} - \frac{x_1 u_1}{z_1} - \frac{z_1}{u_1}\right) \leq 0$$

$$\left(3 - \frac{1}{x_1} - \frac{x_1 v_1}{z_1} - \frac{z_1}{v_1}\right) \leq 0$$

$$\left(4 - \frac{1}{x_1} - \frac{x_1}{y_1} - \frac{y_1 u_1}{z_1} - \frac{z_1}{u_1}\right) \leq 0.$$

Thus it is easy to observe that $\frac{dL}{dt} \leq 0$ and the equality $\frac{dL}{dt} = 0$ hold for

$$x_1 = y_1 = 1, z_1 = u_1 = v_1$$

which corresponds to the set $[(S, V, E, I, I_A : S = S^*, V - V^*, E = E^*, I = I^*, I_A = I_A^*)]$. Hence from LaSalle's invariance principle [23], the equilibrium E_1 of the given system is globally asymptotically stable for $R_0 > 1$.

7. Sensitivity Analysis

In this section, we examine the impact of the parameters used to express the basic reproduction number, R_0, through sensitivity analysis. This demonstrates that an alteration in these parameters results in an alteration in R_0. It is used to identify the variables with a significant impact on R_0 and determine which ones should be the focus of intervention measures. Sensitivity indices make it possible to quantify the proportional change in a variable when a parameter is altered.

The forward sensitivity index of a variable, with regard to a specific parameter, is used for that

$$\alpha_{\phi}^{R_0} = \frac{\partial R_0}{\partial \phi} \frac{\phi}{R_0}$$

where $\phi = [\gamma, \mu, r, \theta, \alpha, \epsilon, \beta, \delta, \Lambda, \omega, \eta, h]$. The analytical equation for the sensitivity of R_0 to each parameter it comprises can be calculated using the formula mentioned above. As a result, Figure 2 shows the sensitivity index of parameters i.e. $\gamma, \mu, r, \theta, \alpha, \epsilon, \beta, \delta, \Lambda, \omega, \eta, h$ respectively on R0. The positive indices indicate a direct relationship between the parameters and R_0, that is if the parameter increases/decrease then the value of R_0 will increase/decrease. Therefore in order to control COVID-19 from the population, we need to reduce the Basic Reproduction number, we can achieve this by reducing the parameters which give positive indices i.e. $\gamma, r, \beta, \omega, \eta, \Lambda$, here birth rate Λ and rate of transmission β are the most sensitive parameters of R_0, since it is not possible to control the birth rate we are left with the rate of transmission, we can reduce this by limiting our contact rate, which is why there was a suggestion like quarantine, social distancing, etc. If the rate of reduction in risk of infection due to vaccine ω decreases then R_0 also decreases, the higher the number of vaccinated people the lower the Vaccine-induced decrease in infection risk, therefore the Basic Reproduction number can be reduced.

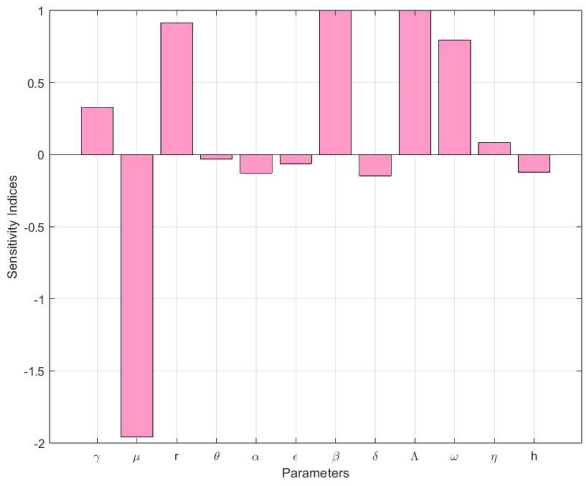

Figure 2. Forward sensitivity of R_0.

The negative indices indicate that there is an inverse relationship between the parameters and R_0, that is if the parameter decrease/increases then the value of R_0 will increase/decrease. μ, θ, α, ϵ, δ, η, h have negative indices, among the μ is the highest sensitive if the death rate increase than R_0 decrease. The strength of intervention h has negative indices which imply that if we implement strict intervention measures then R_0 will decrease which will lead to a decrease in the Infected population.

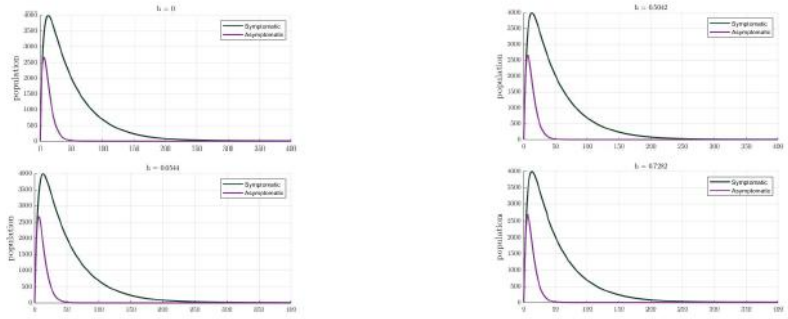

Figure 3. Variation of Infected population with time for different values of h.

8. Numerical Simulation

For the Numerical Simulation of the proposed model, we illustrate the mathematical findings using the MATLAB program, the value of parameters are listed in the table. Figure 3 shows the variation of the infected population with time t for different values of h. First, we take the strength of intervention h to be $h = 0$, which means that there is no intervention measure taken during this period. We consider this period to be from the start of March 2020 till 24 March 2020 when no action has yet been taken by the Government of India.

On 24 March 2020, the Government of India declared a nationwide lockdown for the period of 21 days [14]. After the nationwide lockdown and by the Ministry of Health and Family Welfare, Government of India, many preventive measures for COVID-19 were taken by India. We notice that from COVID-19 case data from the World Health Organization, the infected case curve began to slope down from mid-September 2020 till the first week of

February 2021. In order to investigate the impact of intervention strategies, the strength of intervention is assumed as $h = 0.5042$, during the period of March to July 2020, where the early preventive measure has been implemented, the COVID-19 positive case curve keeps on increasing; $h = 0.6544$, during the period from July to September 2020, where the increasing curve has been slow down and $h = 0.7282$, where strict intervention measures have been taken including social distancing, wearing a mask, awareness through various media, etc, it is noticed that the curve has been miraculously kept on decreasing till 8 February 2021. From Figure 3 We can see that by strengthening the intervention strategy i.e. by increasing the strength of intervention h the curve of Symptomatic infection and Asymptomatic infection can e positively decreased.

Figure 4 shows the Variation of $SVEII_AR$ with time corresponding to the values of $R_0 < 1$ for different values of initial numbers of each compartment with time $t = 0$ to 1000. Figure 5 shows Variation of SV EIIAR with time corresponding to $R_0 > 1$ from $t = 0$ to 40. Figure 6 shows Variation of SV EIIAR with time corresponding to the values of $R_0 > 1$ from $t = 0$ to 1000. Figure 7 shows the Variation of $SVEII_AR$ with time corresponding to the values of $R_0 > 1$ for different values of initial numbers of each compartment with time $t = 0$ to 600. Figure 8 shows the variation of $SVEII_AR$ with time for different values of h. This is to show how no intervention measure, implementation of the intervention, and strict intervention change the cure of Susceptible, Vaccinated, Exposed, Symptomatic, Asymptomatic, and Recovered Population. Figure 9 shows the Variation of the Infected population with time for different values of β, ω, and h. We have 4 cases, we choose $\beta = 1.5$, $\omega = 0.5$, $h = 0.6544$; $\beta = 1$, $\omega = 0.2$, $h = 0.05042$; $\beta = 0.5$, $\omega = 0$, $h = 0$; $\beta = 2$, $\omega = 1$, $h = 0.7282$, and from here we can suggest that a combination of strict intervention measures and increased vaccination can be the most effective solution in reducing the number of people infected with the coronavirus.

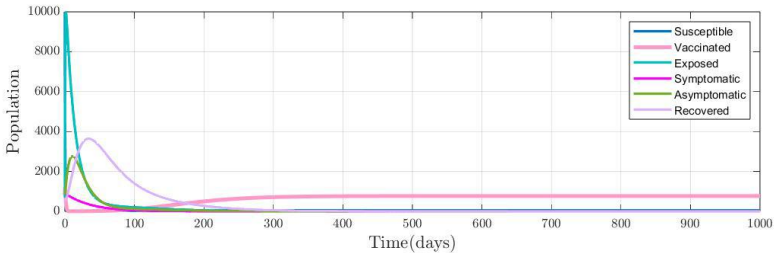

Figure 4. Variation of $SVEII_AR$ with time corresponding to the values of $R_0 > 1$ for different values of initial numbers of each compartment with time $t = 0$ to 1000.

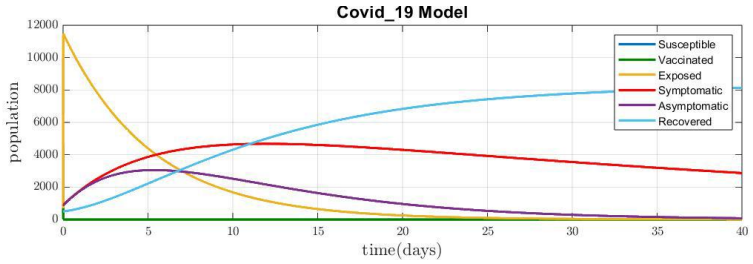

Figure 5. Variation of $SVEII_AR$ with time corresponding to $R_0 > 1$ from $t = 0$ to 40.

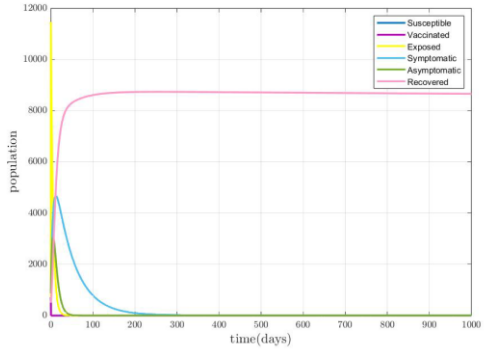

Figure 6. Variation of $SVEII_AR$ with time corresponding to $R_0 > 1$ from $t = 0$ to 1000.

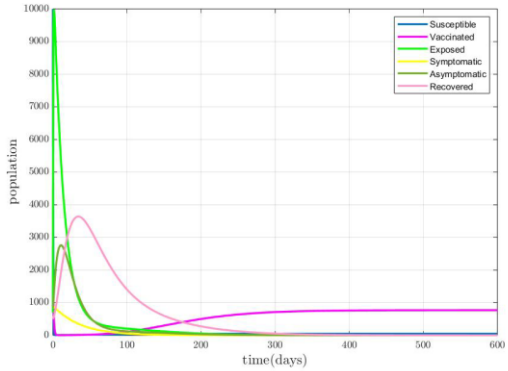

Figure 7. Variation of $SVEII_AR$ with time corresponding to the values of $R_0 > 1$ for different values of initial numbers of each compartment with time $t = 0$ to 600.

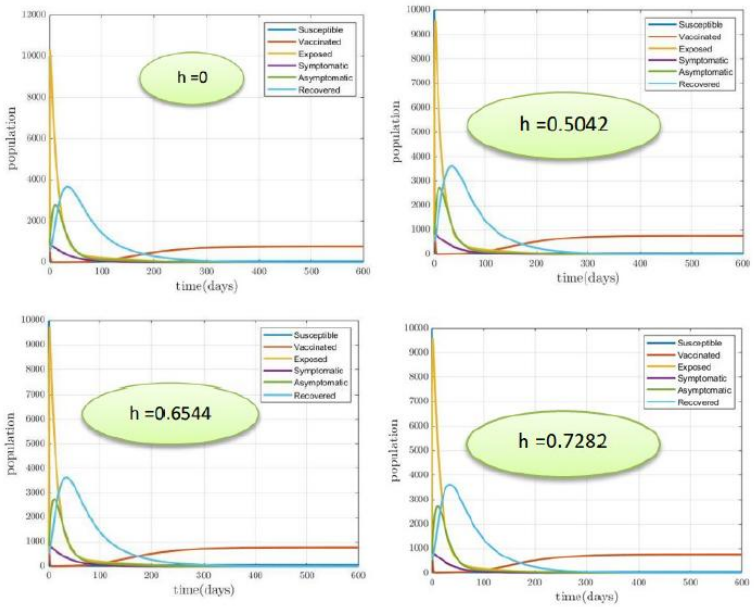

Figure 8. Variation of $SVEII_AR$ with time for different values of h.

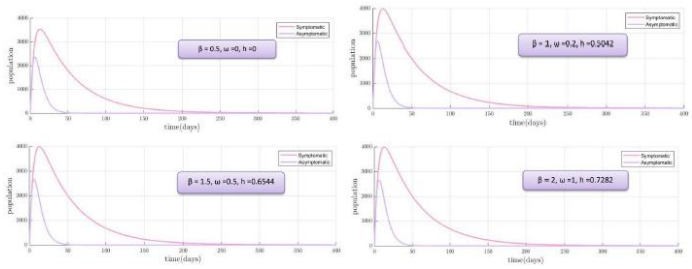

Figure 9. Variation of the Infected population with time for different values of β, ω, and h.

9. Conclusion

The mathematical modelling of COVID-19 has been explored in depth in this paper, with a focus on examining the effects of vaccination and intervention strategies. The kinetics of COVID-19 transmission and the efficiency of various tactics for controlling the virus' propagation have been studied using mathematical modelling approaches. We examined how interventions affected the burden of disease. We mainly focused on the preventive measures that essentially slow down the development of the disease, such as lock-down, media awareness campaigns, adequate hand sanitization, social seclusion, wearing masks, etc.

We discussed the existence and stability of Disease-Free Equilibrium and Endemic Equilibrium. Stability analysis of the equilibrium points shows DFE is locally asymptotically stable whenever the basic reproduction number, $R_0 > 1$, and is globally asymptotically stable whenever $R_0 < 1$. Also, EE is locally asymptotically stable whenever the basic reproduction number, $R_0 > 1$, and is globally asymptotically stable whenever $R_0 > 1$.

Sensitivity analysis for the effect of the parameters involved in the expression of basic reproduction number, R_0 is conducted. It shows that changing these factors causes R_0 to change depending on how they change. It is used to identify the parameters that should be the focus of intervention initiatives because they have a significant impact on R_0. The relative change in a variable when a parameter changes can be measured using sensitivity indices.

The forward sensitivity index of a variable with regard to a specific parameter is used for that. The most sensitive parameter is found to be μ, death rate, which is on the negative side, which means it has an inverse relationship with R_0 since it is not possible to control μ another sensitive parameter which we can control in order to control COVID-19 from the population is β, which have a direct relationship with R_0, we can reduce this by limiting our contact rate, which is why there was a suggestion like quarantine, social distancing, etc. Also if the rate of reduction in risk of infection due to vaccine ω decreases then R_0 also decreases, the higher the number of vaccinated people the lower the Vaccine-induced decrease in infection risk, therefore the Basic Reproduction number can be reduced. Parameters like γ, r, β, ω, η, Λ have positive indices and have direct relationship with R_0. μ, θ, α, ϵ, δ, η, h have negative indices and have inverse relationship with R0. Numerical simulation is also performed using MATLAB.

This study could give policymakers more information to help them decide whether to retain the strictness of an ongoing intervention plan or to let it up. Our study showed that more intensive action is needed to stop the illness outbreak in a shorter amount of time. Also, our analysis demonstrated that in order to effectively eradicate the condition, the strength of the intervention should not be weakened over time.

In conclusion, we recommend that a combination of strict intervention measures and increased vaccination can be the most effective solution in reducing the number of people infected with the coronavirus.

References

[1] D. Bernoulli, Essai d'une nouvelle analyse de la mortalité causée par la petite vérole, et des avantages de l'inoculation pour la prévenir. Histoire de l'Acad., Roy. Sci.(Paris) avec Mem, (1960), 1-45.

[2] W. O. Kermack and A. G. McKendrick, A contribution to the mathematical theory of epidemics, Proceedings of the royal society of london. Series A, Containing papers of a mathematical and physical character 115(772) (1927), 700-721.

[3] M. Duan, L. Chang and Z. Jin, Turing patterns of an si epidemic model with cross-diffusion on complex networks, Physica A: statistical mechanics and its applications 533, 122023 (2019).

[4] Y. Xie, Z. Wang, J. Lu and Y. Li, Stability analysis and control strategies for a new sis epidemic model in heterogeneous networks, Applied Mathematics and Computation 383, 125381 (2020).

[5] N. Sene, Sir epidemic model with mittag-leffler fractional derivative, Chaos, Solitons and Fractals 137, 109833 (2020).

[6] S. Rezapour, H. Mohammadi and M. E. Samei, Seir epidemic model for covid-19 transmission by caputo derivative of fractional order, Advances in difference equations 2020(1), 1-19 (2020).

[7] A. Senapati, S. Rana, T. Das and J. Chattopadhyay, Impact of intervention on the spread of covid-19 in India: A model based study, Journal of Theoretical Biology 523, 110711 (2021).

[8] A. Mahajan, N. A. Sivadas and R. Solanki, An epidemic model sipherd and its application for prediction of the spread of covid-19 infection in India, Chaos, Solitons and Fractals 140, 110156 (2020).

[9] V. P. Bajiya, S. Bugalia and J. P. Tripathi, Mathematical modeling of covid-19: Impact of non-pharmaceutical interventions in India, Chaos: An Interdisciplinary Journal of Nonlinear Science 30(11), 113143 (2020).

[10] S. Khajanchi and K. Sarkar, Forecasting the daily and cumulative number of cases for the covid-19 pandemic in India, Chaos: An interdisciplinary journal of nonlinear science 30(7), 071101 (2020).

[11] M. Gupta, S. S. Mohanta, A. Rao, G. G. Parameswaran, M. Agarwal, M. Arora, A. Mazumder, A. Lohiya, P. Behera, A. Bansal, et al. Transmission dynamics of the covid-19 epidemic in India and modeling optimal lockdown exit strategies, International Journal of Infectious Diseases 103 (2021), 579-589.

[12] V. Tiwari, N. Deyal and N. S. Bisht, Mathematical modeling based study and prediction of covid-19 epidemic dissemination under the impact of lockdown in India, Frontiers in Physics 8, 586899 (2020).

[13] D. Ray, M. Salvatore, R. Bhattacharyya, L. Wang, J. Du, S. Mohammed, S. Purkayastha, A. Halder, A. Rix, D. Barker, et al. Predictions, role of interventions and effects of a historic national lockdown in India's response to the covid-19 pandemic: data science call to arms, Harvard data science review 2020 (Suppl 1) (2020).

[14] P. Pulla, Covid-19: India imposes lockdown for 21 days and cases rise, BMJ 368 (2020).

[15] V. M. Kumar, S. R. Pandi-Perumal, I. Trakht and S. P. Thyagarajan, Strategy for covid-19 vaccination in India: the country with the second highest population and number of cases, npj Vaccines 6(1) 60 (2021).

[16] F. B. Agusto, Optimal isolation control strategies and cost-effectiveness analysis of a two-strain avian influenza model, Biosystems 113(3) (2013), 155-164.

[17] Y. Bai, L. Yao, T. Wei, F. Tian, D. Y. Jin, L. Chen and M. Wang, Presumed asymptomatic carrier transmission of covid-19, Jama 323(14) (2020), 1406-1407.

[18] B. Tang, X. Wang, Q. Li, N. L. Bragazzi, S. Tang, Y. Xiao and J. Wu, Estimation of the

transmission risk of the 2019-ncov and its implication for public health interventions, Journal of Clinical Medicine 9(2) (2020) https://doi.org/10.3390/jcm9020462

[19] O. Diekmann and J. A. P. Heesterbeek, Mathematical Epidemiology of Infectious Diseases: Model Building, Analysis and Interpretation, vol. 5, John Wiley & Sons, (2000).

[20] P. Driessche and J. Watmough, Further Notes on the Basic Reproduction Number, pp. 159-178. Springer, Berlin, Heidelberg (2008). https://doi.org/10.1007/978-3-540-78911-6 6. https://doi.org/10.1007/978-3-540-78911-6 6

[21] A. Korobeinikov and G. C. Wake, Lyapunov functions and global stability for sir, sirs, and sis epidemiological models. Applied Mathematics Letters 15(8) (2002), 955-960.

[22] M. Y. Li and J. S. Muldowney, Global stability for the seir model in epidemiology, Mathematical biosciences 125(2) (1995), 155-164.

[23] J. P. La Salle, The Stability of Dynamical Systems, SIAM, (1976).