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TRANSMISSION DYNAMICS OF CORONAVIRUS AND THE EFFECT OF VACCINATION USING SEIR MODEL

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Abstract. In the present paper, an SEIR mathematical model has been discussed to study the transmission dynamics of the coronavirus and the impact of vaccination in which infected individuals have been classified based on vaccination status. Local stability and global stability analysis have been done for the disease free equilibrium state. It is observed that the disease free equilibrium state is local asymptotically stable when $R_0 < 1$. Sensitivity analysis has been performed and the effects of different classes of infected individuals have been studied. It has been found that the basic reproduction number shows the highest sensitivity towards the nonvaccinated class of infected individuals as compared to other infected classes. Analytical results have been expressed graphically.

2020 *Mathematics Subject Classification:* 34A34, 34D20, 34D23.

Key words: Covid-19, vaccination, disease free equilibrium, stability analysis, sensitivity analysis, basic reproduction number.

1. Introduction. The first case of coronavirus was detected in the Wuhan Province, China in December 2019. It soon converted into a pandemic and spread in other countries in 2020 [22]. It is still alive and threatening the world. General symptoms of coronavirus disease are fever, dry cough, and headache, loss of taste or smell, extreme weakness, shortness of breath and chest pain or pressure. Initially medical practitioners did not know very much about the virus and hence no proper treatment policy was available for the disease. In that case, the only way to save the human being was to enforce a lockdown and those found positive were to be isolated or quarantined. These efforts gave scientists time to study the nature of the virus. Mathematical models are being used for a long time to study infectious diseases. Ross [21] concluded that the transmission of malaria can be controlled by restricting the vector population. Kermack and Mckendrick [13] investigated to analyze the dynamics of disease by involving the incubation period. They showed that the disease could die out if the population density remained below a threshold. Brauer [3] described SIS, SIR, SEIR, and treatment models and provided a unifying structure for complicated models that include demographic effects. Keeling and Rohani [12] explained simple epidemic models and extended their studies to multi-host, spatial, stochastic, and many more. They also enlightened the optimal control strategies such as pulse vaccination, quarantining, and contact tracing. SIR-SEIR models are among the mostly used mathematical compartmental models that analyze the dynamics of infectious diseases. Margenov et al. [17] studied the covid 19 disease spread in Bulgaria using time-depended inverse SEIR model. They conducted their studies for three time zones and calculated model parameters for each zone. Kounchev et al. [14] developed a spline based SEIR model with time-varying transmission and removing rates and analyzed the Bulgarian data. They also build Scenario Building Tool for COVID-19 which can be used in decision making. In [20], the management strategies like lockdown and reopening procedures of various fields have been analyzed. In [22], the epidemic trend of 2019-nCoV/SARS-CoV-2 in Wuhan for different phases has been estimated. Social distancing, isolation of asymptomatic infected, detection of disease and hospitalization can reduce the outbreak size and peak prevalence [2]. In [10], the impact of 2 dose COVID vaccination campaign on healthcare workers and high risk individuals has been evaluated. Lockdown, isolation and quarantine are not permanent solutions in the fight against the virus. Vaccination can be the right weapon against the virus if everyone is vaccinated irrespective of age, gender and occupation. For this purpose, the population considered in the present SEIR model consists of

persons of every age, gender and occupation. The effect of vaccination cannot be observed unless the vaccinated infected person lives in the vicinity of the uninfected person, so the isolation and quarantine classes have not been included in the model. Basic reproduction number R_0 is determined using the method of the next-generation matrix. Basic Reproduction number is defined as the average number of secondary infections produced when one infected individual is introduced into a host population where everyone is susceptible [9]. Sensitivity analysis of variables has been performed by finding normalized sensitivity indices of R_0 to examine the robustness and validity of the results. Normalized sensitivity index of a variable to a parameter is the ratio of the relative change in the variable to the relative change in the parameter [5].

2. Mathematical model. The total population has been divided into four main classes: susceptible, exposed, infected and recovered individuals. The infected population has been further classified into three classes: nonvaccinated individuals, partially vaccinated individuals and fully vaccinated individuals. The total population has been assumed to be variable. Natural immunity gained by the infection protects against re-infection for up to 8 months [25]. Recovered individuals are not supposed to move to susceptible class as the time duration considered for present work is 8 months only.

Table 1. Descriptions of Population classes

S	Susceptible Population
E	Exposed Population
C	Infected population with single dose vaccine before infection (Partially vaccinated individual)
V	Infected population with double dose vaccine before infection (Fully vaccinated individual)
N	Infected population without vaccine before infection (Non-vaccinated individual)
R	Recovered from infection

Λ and μ are the birth rate and natural death rate of the population respectively. β^{-1} is the incubation period of the virus. β_N, β_C and β_v are the transmission rates from non-vaccinated individuals, partially vaccinated individuals and fully vaccinated individuals respectively. The transmission rate is the product of the average number of contacts and the probability of transmission through given contact. μ_N, μ_C and μ_V are disease induced death rates of non-vaccinated

individuals, partially vaccinated individuals and fully vaccinated individuals respectively. γ_N, γ_C and γ_V are recovery rates of non-vaccinated individuals, partially vaccinated individuals and fully vaccinated individuals respectively. q_N, q_C and q_V are the proportions of the non-vaccinated individuals, partially vaccinated individuals and fully vaccinated individuals respectively.

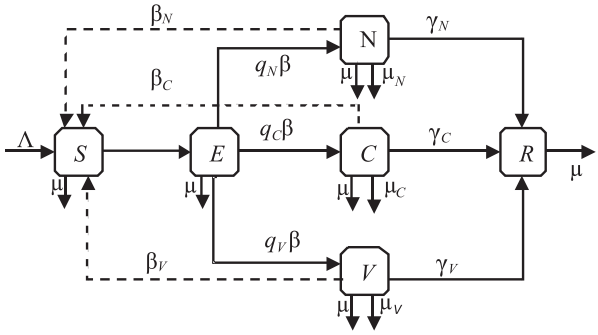

Fig. 1. Transmission diagram of the disease

Mathematical model for the disease transmission is expressed as follows

$$
\begin{aligned}
\frac{dS}{dt} &= \Lambda - \beta_C CS - \beta_V VS - \beta_N NS - \mu S \\
\frac{dE}{dt} &= \beta_C CS + \beta_V VS + \beta_N NS - \mu E - \beta E \\
\frac{dC}{dt} &= q_C \beta E - \mu C - \mu_C C - \gamma_C C \\
\frac{dV}{dt} &= q_V \beta E - \mu V - \mu_V V - \gamma_V V \\
\frac{dN}{dt} &= q_N \beta E - \mu N - \mu_N N - \gamma_N N \\
\frac{dR}{dt} &= \gamma_C C + \gamma_V V + \gamma_N N - \mu R
\end{aligned}
\tag{1}
$$

3. Disease free equilibrium point-DFE. Disease free equilibrium state for (1) is obtained as follows

$$S^0 = \frac{\Lambda}{\mu},\ E^0 = 0,\ C^0 = 0,\ V^0 = 0,\ N^0 = 0,\ R^0 = 0.$$

3.1. Basic reproduction number. Next-generation matrix determined using [8] is

$$FV^{-1} = \begin{bmatrix} \frac{\beta\Lambda}{\mu(\beta+\mu)}\left(\frac{Q_C}{m_C}+\frac{Q_V}{m_V}+\frac{Q_N}{m_N}\right) & \frac{\beta_C\Lambda}{\mu m_C} & \frac{\beta_V\Lambda}{\mu m_V} & \frac{\beta_N\Lambda}{\mu m_N} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix},$$

where,

$$q_C\beta_C = Q_C, q_V\beta_V = Q_V, q_N\beta_N = Q_N$$
$$m_C = \mu + \mu_C + \gamma_C, m_V = \mu + \mu_V + \gamma_V, m_N = \mu + \mu_N + \gamma_N.$$

Spectral radius of the next-generation matrix is called as the basic reproduction number. Here, the eigen values of the charecterstic equation are

$$\lambda = 0, 0, 0, \frac{\beta\Lambda}{\mu(\beta+\mu)}\left(\frac{Q_C}{m_C}+\frac{Q_V}{m_V}+\frac{Q_N}{m_N}\right)$$

Therefore, $R_0 = \frac{\beta\Lambda}{\mu(\beta+\mu)}\left(\frac{Q_C}{m_C}+\frac{Q_V}{m_V}+\frac{Q_N}{m_N}\right)$.

3.2. Local stability of DFE. Local stability of the DFE has been analyzed by using the method given in [2]. Jacobian of the system (1) at DFE is

$$J^0 = \begin{bmatrix} -\mu & 0 & -\beta_C\frac{\Lambda}{\mu} & -\beta_V\frac{\Lambda}{\mu} & -\beta_N\frac{\Lambda}{\mu} & 0 \\ 0 & -(\beta+\mu) & \beta_C\frac{\Lambda}{\mu} & \beta_V\frac{\Lambda}{\mu} & \beta_N\frac{\Lambda}{\mu} & 0 \\ 0 & q_C\beta & -m_C & 0 & 0 & 0 \\ 0 & q_V\beta & 0 & -m_V & 0 & 0 \\ 0 & q_N\beta & 0 & 0 & -m_N & 0 \\ 0 & 0 & \gamma_C & \gamma_V & \gamma_N & -\mu \end{bmatrix}$$

Characteristic equation of the Jacobian is given by

$$(-\mu-\lambda)^2\left\{-1+\frac{\beta\Lambda}{\mu(\beta+\mu+\lambda)}\left(\frac{Q_C}{(m_C+\lambda)}+\frac{Q_V}{(m_V+\lambda)}+\frac{Q_N}{(m_N+\lambda)}\right)\right\} = 0$$

$(-\mu-\lambda)^2P(\lambda) = 0$ where

$$P(\lambda) = \left\{-1+\frac{\beta\Lambda}{\mu(\beta+\mu+\lambda)}\left(\frac{Q_C}{(m_C+\lambda)}+\frac{Q_V}{(m_V+\lambda)}+\frac{Q_N}{(m_N+\lambda)}\right)\right\}$$

$$\lambda = -\mu, -\mu \text{ and}$$

$$\left\{-1 + \frac{\beta\Lambda}{\mu(\beta+\mu+\lambda)}\left(\frac{Q_C}{(m_C+\lambda)} + \frac{Q_V}{(m_V+\lambda)} + \frac{Q_N}{(m_N+\lambda)}\right)\right\} = 0$$

Two roots of the characteristic equation are negative. DFE will be stable if all the roots of $P(\lambda) = 0$ are negative.

At $\lambda = 0$

$$P(0) = \left\{-1 + \frac{\beta\Lambda}{\mu(\beta+\mu)}\left(\frac{Q_C}{m_C} + \frac{Q_V}{m_V} + \frac{Q_N}{m_N}\right)\right\}$$

$$P(0) = -1 + R_0$$

CASE 1

$R_0 > 1$ then $P(0) > 0$

and $P(\infty) < 0$

Therefore there exists at least one positive root of $P(\lambda) = 0$. Hence DFE is unstable when $R_0 > 1$.

CASE 2

$R_0 < 1$ then $P(0) < 0$

Let one of the root of $P(\lambda) = 0$ is $\lambda = x + iy$ where $x \geq 0$

$\Rightarrow P(x+iy) = 0$

$$P(x+iy) = -1 + \frac{\beta\Lambda}{\mu(\beta+\mu+x+iy)}\left(\frac{Q_C}{m_C+x+iy} + \frac{Q_V}{m_V+x+iy} + \frac{Q_N}{m_N+x+iy}\right)$$

$$|P(x+iy)+1| \leq \frac{\beta\Lambda}{\mu|(\beta+\mu+x+iy)|}\left(\frac{Q_C}{|m_C+x+iy|} + \frac{Q_V}{|m_V+x+iy|} + \frac{Q_N}{|m_N+x+iy|}\right).$$

Since $P(x+iy) = 0$

$$|1| \leq \frac{\beta\Lambda}{\mu|(\beta+\mu+x+iy)|}\left(\frac{Q_C}{|m_C+x+iy|} + \frac{Q_V}{|m_V+x+iy|} + \frac{Q_N}{|m_N+x+iy|}\right)$$

$$|1| \leq \frac{\beta\Lambda}{\mu \mid (\beta+\mu+x)}\left(\frac{Q_C}{|m_C+x|} + \frac{Q_V}{|m_V+x|} + \frac{Q_N}{|m_N+x|}\right)$$

$$|1| \leq \frac{\beta\Lambda}{\mu|(\beta+\mu)|}\left(\frac{Q_C}{|m_C|} + \frac{Q_V}{|m_V|} + \frac{Q_N}{|m_N|}\right) \text{ because } x \geq 0$$

$$|1| \leq \frac{\beta\Lambda}{\mu(\beta+\mu)}\left(\frac{Q_C}{m_C} + \frac{Q_V}{m_V} + \frac{Q_N}{m_N}\right)$$

$|1| \leq R_0$

and $R_0 < 1$.

Therefore $|1| < 1$.
This is not possible therefore our assumption x ≥ 0 is not correct.
$\Rightarrow x < 0$, Hence all the roots of $P(\lambda) = 0$ are negative. DFE is stable when $R_0 < 1$.

3.3. Global Stability of DFE. Following theorem given by [4] has been used to prove the global stability of DFE.

Theorem. *The fixed point $U_0\,(x^*, 0)$ is a globally asymptotic stable equilibrium of system provided $R_0 < 1$ (local asymptotically stable) and those assumptions $(H1)$ and $(H2)$ are satisfied.*

The given system is expressed in the form:

$$\frac{dX}{dt} = F(X, Z)$$
$$\frac{dZ}{dt} = G(X, Z), G(X, 0) = 0$$

where $X \in R^m$ denotes (its components) the number of uninfected individuals and Z $\in R^n$ *denotes (its components) the number of infected individuals including latent, infectious etc. $U_0 = (x^*, 0)$ denotes the disease free equilibrium of this system.*

The condition $(H1)$ and $(H2)$ below must be met to guarantee local asymptotic stability.

$(H1)$ *For* $\dfrac{dX}{dt} = F(X, 0)$, *X^* is globally asymptotically stable (g.a.s.),*

$(H2)$ $G(X, Z) = AZ - \widehat{G}(X, Z), \widehat{G}(X, Z) \geq 0$ *for* $(X, Z) \in \Omega$,

where $A = D_Z G\,(X^*, 0)$ is an M matrix (the off diagonal elements of A are non negative) and Ω is the region where the model makes biological sense.

To apply the above theorem to present model, the model (1) can be expressed in the following form: uninfected class $(S, R) = X$, and infected class $(E, C, V, N) = Z$

$$X = \begin{bmatrix} S \\ R \end{bmatrix} \quad \text{and} \quad Z = \begin{bmatrix} E \\ C \\ V \\ N \end{bmatrix}$$

$$F(X,Z) = \frac{dX}{dt} = \begin{bmatrix} \Lambda - \beta_C CS - \beta_V VS - \beta_N NS - \mu S \\ \gamma_C C + \gamma_V V + \gamma_N N - \mu R \end{bmatrix}$$

$$G(X,Z) = \frac{dY}{dt} = \begin{bmatrix} \beta_C CS + \beta_V VS + \beta_N NS - \mu E - \beta E \\ q_C \beta E - \mu C - \mu_C C - \gamma_C C \\ q_V \beta E - \mu V - \mu_V V - \gamma_V V \\ q_N \beta E - \mu N - \mu_N N - \gamma_N N \end{bmatrix}$$

$$U_0\,(x^*, 0) = (X^*, 0) \quad \text{where} \quad X^* = \left(\frac{\Lambda}{\mu}, 0\right) \quad \text{is DFE of} \quad \frac{dX}{dt}$$

$$G(X,0) = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \end{pmatrix} \quad \text{and} \quad F\,(X^*, 0) = \frac{dX}{dt} = \begin{pmatrix} \Lambda - \mu\dfrac{\Lambda}{\mu} \\ 0 \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$$

Therefore,

$$A = \begin{bmatrix} -\beta - \mu & \beta_C S^0 & \beta_V S^0 & \beta_N S^0 \\ q_C \beta & -m_C & 0 & 0 \\ q_V \beta & 0 & -m_V & 0 \\ q_N \beta & 0 & 0 & -m_N \end{bmatrix}$$

and

$$\hat{G}(X,Z) = \begin{bmatrix} (\beta_C C + \beta_V V + \beta_N N)\left(S^0 - S\right) \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

$\hat{G}(X,Z) \geq 0$, if $(\beta_C C + \beta_V V + \beta_N N)\left(S^0 - S\right) \geq 0$, that is when $\left(S^0 - S\right) \geq 0$, which is always correct. It is clear by observation that A is an M matrix. Also X^* is globally asymptotically stable equilibrium of $\dfrac{dX}{dt} = F(X,0)$. Hence by above theorem DFE is globally asymptotically stable.

3.4. Numerical Simulation for Stability of DFE. Numerical Simulation has been done using MATLAB software to verify analytical results. All the parametric values are taken from Table 2. The incubation period for the coronavirus is 2 to 14 days and the transmission rate from non-vaccinated individuals ranges from 0.1 to 0.3 [20]. Actual data on transmission rates from fully vaccinated individuals is not available and studies only show that double

Table 2. Values of parameters

Parameter	Baseline Values	Source	Parameter	Baseline Values	Source
Λ	17.4/365	[23]	q_V	0.35	Variable
μ	7.3/365	[24]	μ_N	1.17/30	[11]
β	0.14	[20]	μ_C	0.21/30	[11]
β_N	0.2	[20]	μ_V	0.06/30	[11]
β_C	0.1	[6]	γ_N	0.9500	Assumed
β_V	0.04	Assumed	γ_C	0.9700	Assumed
q_N	0.30	Variable	γ_V	0.9800	Assumed
q_C	0.35	Variable			

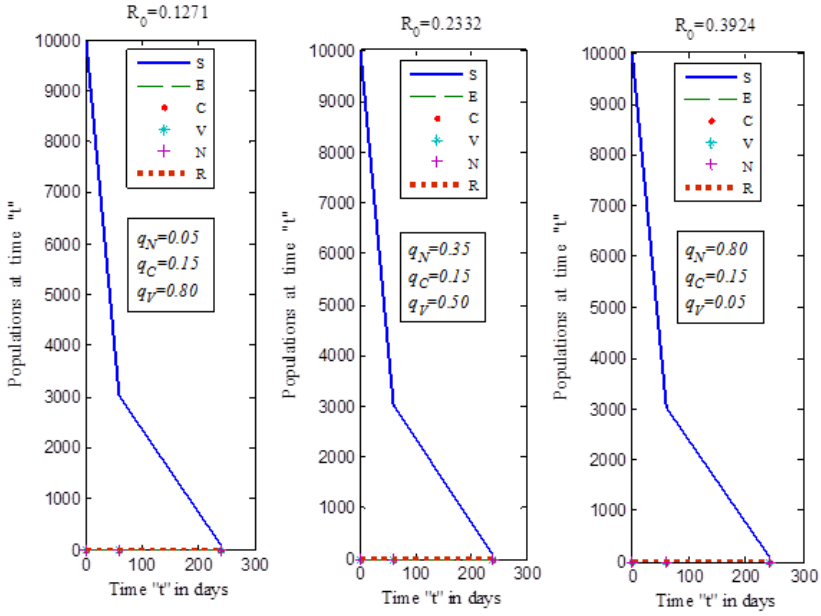

Fig. 2. Illustration for constant q_C

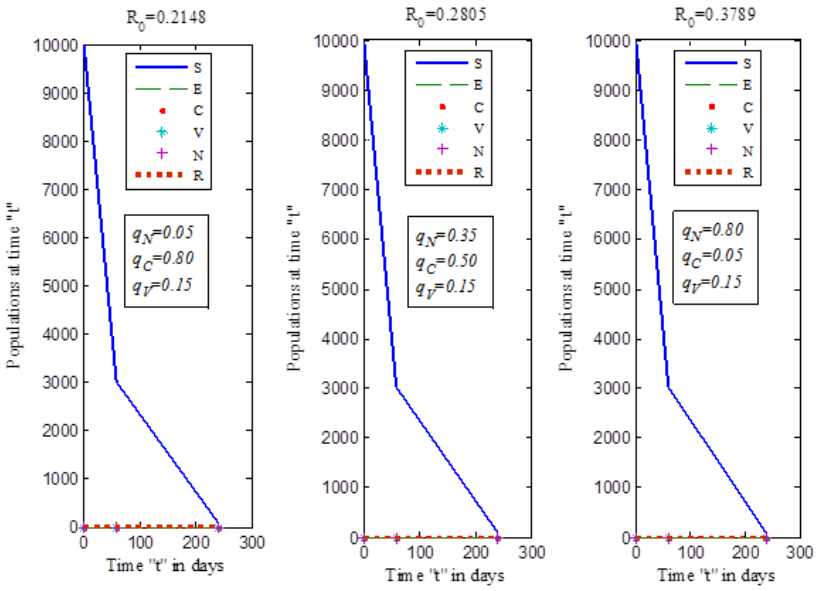

Fig. 3. Illustration for constant q_V

doses of the vaccine reduce disease transmission, so the transmission rate from fully vaccinated individuals is thought to be very low. Recovery rates have been assumed from the data given for the death rate. All parameter values have been taken per day per 1000 people.

Figure 2 represents the time series for all populations for different values of q_N, and q_V keeping q_C constant while Figure 3 represents the times series for all populations for different values of q_N, and q_C keeping q_V constant. R_0 decreases as the populations of partially vaccinated individuals and fully vaccinated individuals increase. R_0 tends to 1 more rapidly with decrease in the population of fully vaccinated individuals as that in partially vaccinated individuals.

Both the figures represent the DFE of the system for different values of q_N, q_C and q_V. Susceptible population decreases with time and all infected populations including exposed population and recovered population remain zero when $R_0 < 1$ that is the system stays disease free if $R_0 < 1$.

4. Sensitivity analysis. "The normalized forward sensitivity index of a variable u that depends differentiably on a parameter p is defined as: $\gamma_P^u = \dfrac{\partial u}{\partial P} \times$

Table 3. Normalized Sensitivity Indices of R_0 to some parameters

Parameter	Normalized Sensitivity Index	Parameter	Normalized Sensitivity Index
β	0.1370	q_N	0.4296
β_N	0.4296	q_C	0.2536
β_C	0.3047	q_V	0.1009
β_V	0.0112		

$\frac{P}{u}$" [5]. Normalized Sensitivity Indices of R_0 with respect to some parameters have been calculated using baseline values given in Table 2 .

Table 3 represents the normalized sensitivity indices of R_0 concerning some parameters. It shows that R_0 is the most sensitive to the non-vaccinated individuals and the least sensitive to the fully vaccinated individuals.

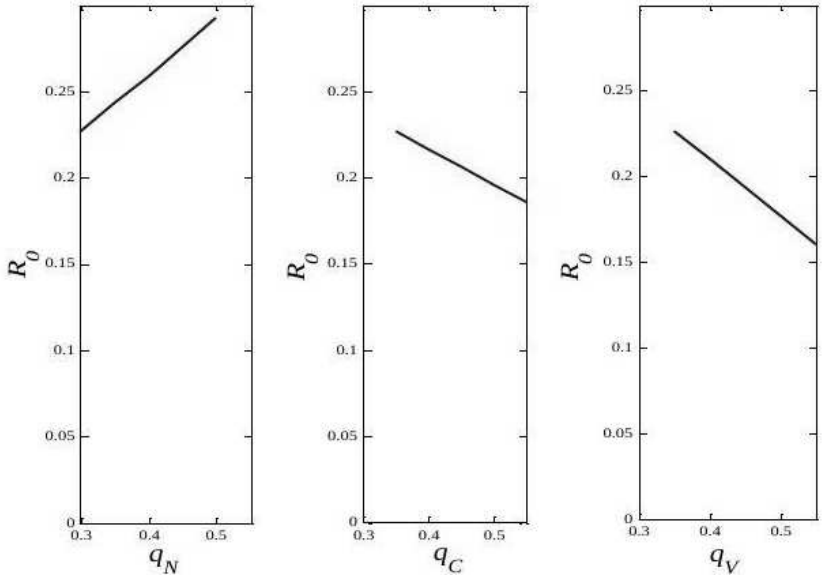

Fig. 4. Illustration of basic reproduction for different q_N, q_C, q_V

Figure 4 represents the change in R_0 according to the change in q_N, q_C and q_V. The inclination is positive in the case of q_N while negative for q_V and q_C. It appears to be steeper for q_V as compared to that for q_C. R_0 increases with an increase in the proportion of non-vaccinated individuals and decreases with an increase in the proportion of partially vaccinated individuals and fully vaccinated individuals rather more rapidly with fully vaccinated individuals.

5. COVID-19 Transmission in India. We can explain our results with the help of data and graphs of COVID spread in India which are available in the 'Our World in Data' [19] repository. India has gone through three waves of corona epidemic. Table 4 shows the peaks of new confirmed cases, new deaths and positivity rate that occurred in the three waves. Figure 5 depicts the time series for new confirmed cases and new deaths. Figure 6 and Figure 7 depict the time series for positivity rate and the percentage of fully vaccinated population from starting till May 2022, respectively.

Table 4. Values at Respective peaks

	First Wave	Second Wave	Third Wave
New comfirmed cases per million	66.89(16/9/2020)	280.77(8/5/2021)	223.9(25/1/2022)
New deaths per million	0.84(19/9/2020)	3.01(23/5/2021)	0.81(4/2/2022)
Positivity rate	12.75(25/7/2020)	22.68(8/5/2021)	16.55(22/1/2022)

Indian government announced a nationwide lockdown on 24 March 2020 that extended up to 31 May 2021. Lockdown was placed when there were only 500 confirmed cases in total. After this, the government started unlocking the country by providing a little relaxation in various phases. During the first wave government was particular about imposition of restriction on mass gathering as no other option was available. From beginning to end, the first wave remained active with restrictions. This could be the reason for minimum new cases at the peak. The first phase of the vaccination started on 16 January 2021 when the first wave was about to an end. However, vaccination had been started in January, yet the share of fully vaccinated people was only 0.67% in March 2021 that increased to 3.10% in May 2021. Among the three waves, second was the deadliest. During the second wave the population that got affected the most was youth. Vaccination for people above 45 was scheduled to start from 1 April 2021 while for those above 18 from 1 May 2021. Surprisingly, a large proportion of the population of these groups became seriously infected before vaccination was introduced. New confirmed cases, deaths and positivity rate attained respective highest peaks. Looking at the severity of the infection state governments enforced lockdowns. Noticeable rise in the share of fully vaccinated population can be seen after august 2021. The share of fully vaccinated people was only 10.61% in August 2021 that enhanced to 43.29% in December 2021. There was no panic in the third wave as requirement of hospitalization, ICU beds, oxygen and ventilators was less. Most of the patients were asymptomatic or having mild symptoms. Hence, no

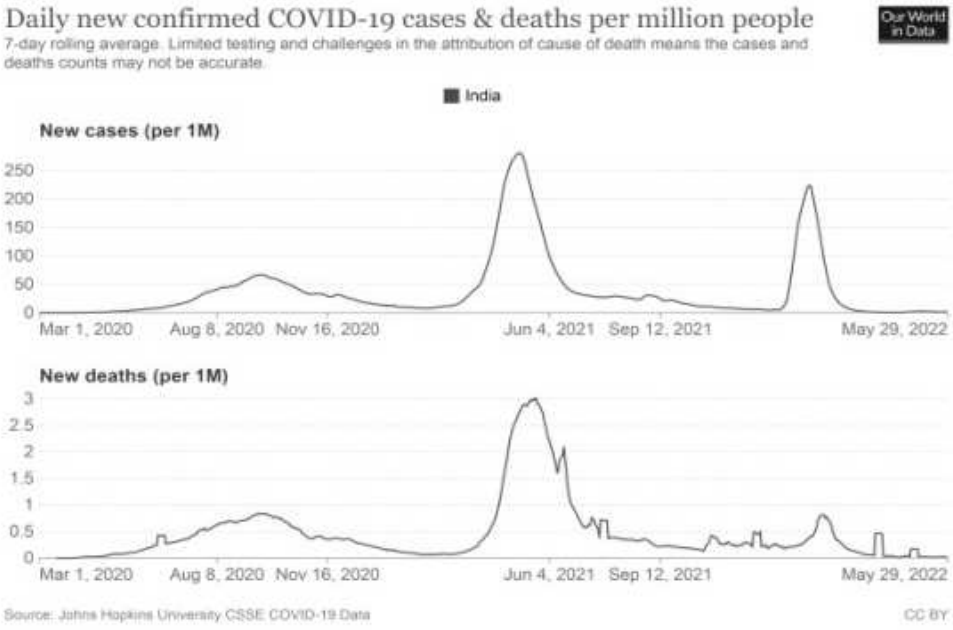

Fig. 5. Time series for daily new confirmed cases and deaths

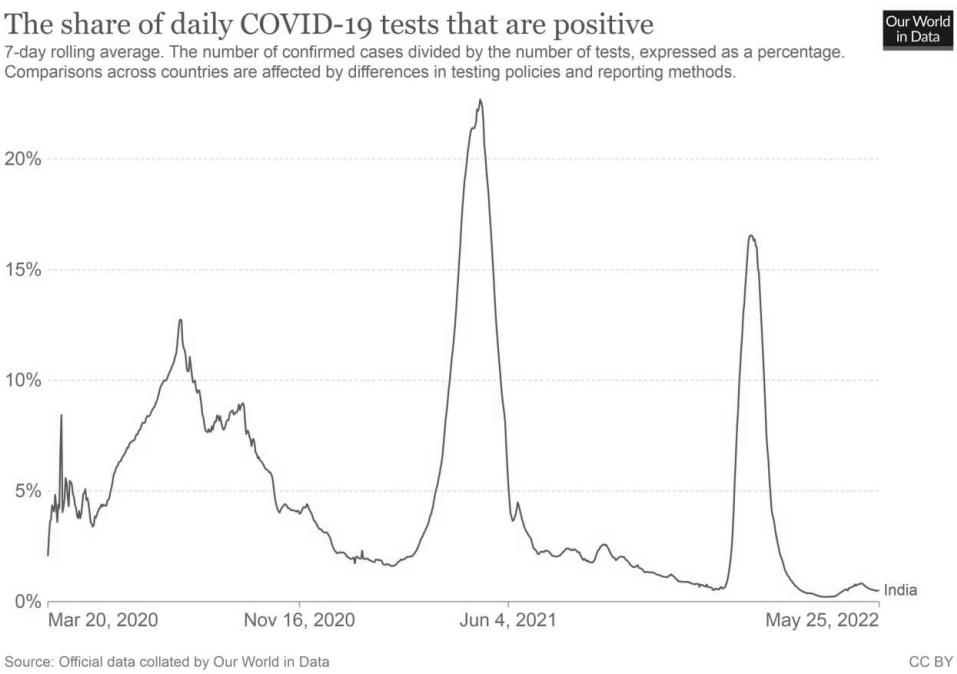

Fig. 6. Time series for positivity rate

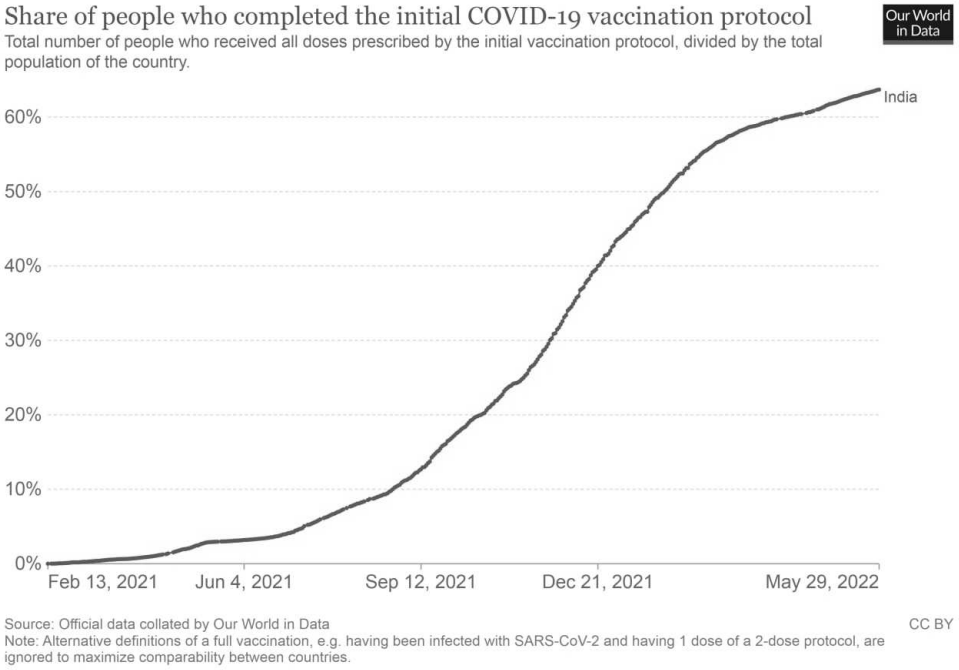

Fig. 7. Time series for share of fully vaccinated population

restrictions were imposed by the government and almost all activities were going on freely.

Omicron was the dominant variant in the third wave while as delta in the second. According to the clinical studies on variants, omicron was found to be less severe than delta [15]. Lower severity was not only because of the characteristic of the variant but vaccination was also a major cause [7, 18]. Hence, disease mortality got reduced in the third wave. In the first and third wave, peak of new death is almost the same, but it is less in the third wave if seen concerning new confirmed cases. In the study for the comparison between variants, Lyngse et al. found that omicron is $2.7 - 3.7$ times more transmissible than Delta [16], yet the third wave had a lower positivity rate. Duration of third wave was also the shortest.

6. Conclusion. The present work discusses an SEIR model to study the spread of the coronavirus disease when there is no strategy such as isolation

and quarantine. To check the exact impact of vaccination, isolation and quarantine classes have not been included. The infected population is divided into non-vaccinated individuals, partially vaccinated individuals and fully vaccinated individuals. The normalized sensitivity index of R_0 is found to be the highest for β_N and q_N, hence the local stability of DFE depends predominantly on the non-vaccinated class. DFE can be maintained by keeping the proportion of non-vaccinated individuals at minimum level. R_0 noticeably changes with the change in the fully vaccinated class compared to the partially vaccinated class. Normalized sensitivity indices of R_0 to q_V and q_C are positive therefore R_0 should increase with an increase in q_V or q_C [1]. But it has been observed that R_0 decreases as q_V or q_C increases. According to the concept of sensitivity, it is not perfect but the result obtained is practically justified. We assume that the reason behind such a result is the low transmission rate from fully vaccinated individuals and partially vaccinated individuals. It can be concluded that the disease can be controlled by reducing the proportion of non-vaccinated individuals. More and more population should be encouraged to get fully vaccinated so that disease can be eradicated.

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