ISSN 2515-8260 Volume 07, Issue 03, 2020

Stability and Numerical Investigation of modified SEIR model with Vaccination and Life-long Immunity

Gurpreet Singh Tuteja

Zakir Husain Delhi College J. L. Nehru Marg, New Delhi -11002, India

Email: gstuteja@gmail.com

December 9, 2020

Abstract

In understanding the spread and control of infectious diseases, mathematical modelling has become an important instrument. The epidemic disease COVID-19 caused by SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2) has affected the population of almost all the countries. This disease is highly contagious and spreads through one to one contact (physical closeness)[5]. It spreads through the air in the form of tiny droplets transmitted by the breath, cough, sneezing, or even verbal contact of an infected person [19]. Being highly contagious and mortality rate, the number of confirmed cases and deaths are alarmingly rising. By routinely washing hands, keeping unwashed hands away from the face, avoiding public areas, and maintaining social distance, the various strategies to curb the spread include ensuring adequate hygiene. As a consequence, aggressive measures are required to control the spread of infectious diseases, particularly those for which both vaccines and treatments are available. Besides, combating the occurrence of a disease is always easier than treating it. This paper formulates and solves numerically the modified SEIR model with vital dynamics includes an additional compartment called Vaccination with an assumption that the vaccination will provide lifelong immunity. This assumption is feasible as the immunity can be extended through booster vaccinations in due course. The basic reproduction number is calculated and the stability of the model is discussed using the Lyapunov method. The importance of the various epidemiological parameters related to the Vaccination compartment model is discussed numerically also.

Keywords: SIR, COVID-19, epidemic, basic reproduction number

AMS Classification: 00A71, 34N05

1. Introduction

Mathematical modelling is a valuable method for understanding the mechanism by which infectious diseases propagate into a population. Through such modelling, the potential path of an outbreak and steps to contain an epidemic can also be predicted. In the early 20th

ISSN 2515-8260 Volume 07, Issue 03, 2020

century, the SIR model emerged, and major work was done using a compartment model [13, 18]. This model defines three major compartments as Susceptible, Infectious, and Recovered and hence also called a SIR model. Our model introduces one more compartment: Vaccination. *S(t)* is the number of susceptible individuals that interact-with infectious *t* in time, contracts the disease, and transits to the infectious compartment. *E(t)* is the number of individuals exposed to the disease in time. I(t)is the number of infectious individuals in time who have been infected and are capable of infecting susceptible individuals. *R(t)* is the number of recovered individuals in time who were infected and recovered from the disease and entered the removed compartment. The *V(t)* is the number of individuals vaccinated at any time *t* and acquire life-long immunity (with or without boosters). The individuals who don't show up with any symptoms are kept in compartment *A(t)*. In this model, the vital dynamics are taken into account i.e. the births and deaths are considered. Using first-order non-linear differential equations, this model predicts the nature of Vaccinated compartment *V[t]* with time *t*. Also, it estimates analytically epidemiological parameters related to the Vaccinated compartment and the basic reproductive number [3].

2. Mathematical Model

Consider the SEIR epidemic disease model, where the total initial population is divided into five compartments namely, *S(t)* susceptible, *E(t)* exposed, *I(t)* infected-infectious, V(t) vaccinated, whereas *t* is time variable. We formulate the problem based on the SIR model with vital dynamics and study the effect of Vaccination and epidemiological factors related to it. Let *N* be the total population in the system at time *t*, *S* is susceptible to be exposed, and *E* is the actual number of exposed individuals (a compartment in which the disease is latent; infected but not infectious). The infected-infectious *I(t)* move from the compartment of susceptible *S* to the compartment of exposed *E* depending on the number of contacts infected *I* individuals, multiplied by the probability of infection β (Fig. 1). The $\beta I/N$ is the average number of contacts with infection per unit time of one susceptible person. The exposed (*E*) becomes infectious (I) with a rate$\alpha$and the infectious recover (*R*) with a rate γ. Recovered means an individual who has acquired immunity and may move into the class *S* (susceptible) after a certain time *t*. In COVID-19, there is no possibility of lifelong immunity after recovering from it, despite that the antibodies are developed and during active antibodies[19], it remains in the recovered compartment for a restricted period and then flows back to the susceptible compartment. We assume that vaccination will give life-long immunity either in one dose or with periodic boosters. The population which doesn't receive vaccination after recovering shall flow back in the compartment of susceptible *S* after completing the recovery period γ^{-1}. The reciprocals α^{-1}, average disease incubation period, and μ^{-1} are average natural deaths. Λ and μ describe a model with vital dynamics (endemic model), which has an inflow of births into the class S at a rate Λ and outflow of deceased μS. This model is based on the assumptions proposed by Hethcote[10]; the population size is constant and large enough so that we can consider the population of each compartment as a continuous model. The birth and death rates are equal and the population (fixed) is homogeneously mixed and uniform. The governing differential equations are:

ISSN 2515-8260 Volume 07, Issue 03, 2020

$$\frac{dS}{dt} = \Lambda N - \beta \frac{S(t)I(t)}{N} - \mu\, S(t) - \theta_1 S(t) + \sigma R(t) \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta\, S(t)I(t)}{N} - \alpha E(t) - \mu\, E(t) - \theta_2 E(t) \quad (2)$$

$$\frac{dI}{dt} = \alpha\, E(t)I(t) - \gamma\, I(t) - \mu\, I(t) \quad (3)$$

$$\frac{dR}{dt} = \gamma\, I(t) - \mu\, R(t) - \sigma\, R(t) - \theta_4 R(t) \quad (4)$$

$$\frac{dV}{dt} = \theta_1 S(t) + \theta_2 E(t) + \theta_3\, I(t) + \theta_4 V(t) - \mu\, V(t) \quad (5)$$

Where, $N = S(t) + E(t) + I(t) + R(t) + V(t)$ (6)

with initial conditions:

$$S(0) > 0, E(0) > 0, I \geq 0, R(0) \geq 0, V(0) \geq 0$$

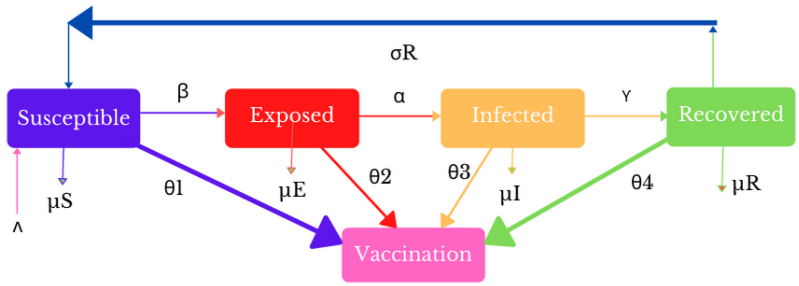


Fig. 1: SEIR Model with Vaccination

The parameters (non-negative constants) are defined as:

Λ: Birth rate per unit time.

μ: Fatality rate per unit time.

β: Probability of disease transmission per contact (dimensionless) times the number of contacts per unit time.

α: Average rate of progression from exposure to infectious (the reciprocal is the incubation period) in per unit time.

γ: Average rate of progression of individuals from Infected I(t) (the reciprocal is the recovery period) having units of (1/T), with time T.

If μ is not zero, the model is termed an endemic SIR model[1] and for σ= 0 studied in [18]. However, the SIR model has no latent stage (no exposed individuals), which is inappropriate as a model for diseases like COVID-19. This model is given in Kermack–McKendrick's theory [1,13]. Practically, numerous mathematical treatments about SEIR models (Susceptible- Exposed – Infected/infectious – Recovered/removed) have been studied, for instance, in Hethcote [10], Keeling and Rohani [12], and Diekmann et al.[7], among others. The basic idea is to compute the number of susceptible, exposed, infected, vaccinated, and recovered individuals based on the number of contacts, disease transmission rate, incubation

ISSN 2515-8260 Volume 07, Issue 03, 2020

period, recovery rate, and fatality rate. Variation of the above said epidemiological factors have been studied [4, 6]. Also, the rate of vaccination is θ_1, θ_2, θ_3, θ_4 to the individuals present in Susceptible, Exposed, Infected, and Recovery compartments. The vaccine will be administered to the recovered individuals so that in addition to their natural immunity they can acquire vaccine-induced immunity too. This epidemic disease model predicts a peak of susceptible, exposed, infected, and recovered including vaccinated individuals per day as a function of time. The vaccination and treatment control using the SIR model has been studied in [2]. The μ is defined as the rate of mortality, which includes both natural and due to Covid-19. The mortality within a year has crossed 1.5 million and more than 66 million have been confirmed cases of Covid-19 to date [20]. The equations (1) - (6) are made dimensionless by replacing the variables $S' = S/N$, $E' = E/N$, $I' = I/N$, $V' = V/N$, $R' = R/N$ then omitting dashes, we obtain the dimensionless equations as:

$$\frac{dS}{dt} = \Lambda - \beta\, \mathrm{S(t)I(t)} - \mu\, \mathrm{S(t)} - \theta_1 \mathrm{S(t)} + \sigma \mathrm{R(t)} \qquad (7)$$

$$\frac{dE}{dt} = \beta\, \mathrm{S(t)I(t)} - \alpha \mathrm{E(t)} - \mu\, \mathrm{E(t)} - \theta_2 \mathrm{E(t)} \qquad (8)$$

$$\frac{dI}{dt} = \alpha\, \mathrm{E(t)} - \gamma\, \mathrm{I(t)} - \mu\, \mathrm{I(t)} \qquad (9)$$

$$\frac{dR}{dt} = \gamma\, \mathrm{I(t)} - \mu\, \mathrm{R(t)} - \sigma\, \mathrm{R(t)} - \theta_4 \mathrm{R(t)} \qquad (10)$$

$$\frac{dV}{dt} = \theta_1 \mathrm{S(t)} + \theta_2 \mathrm{E(t)} + \theta_3 \mathrm{I(t)} + \theta_4 \mathrm{V(t)} - \mu\, \mathrm{V(t)} \qquad (11)$$

Where, $$1 = S(\mathrm{t}) + E(\mathrm{t}) + I(\mathrm{t}) + R(\mathrm{t}) + V(\mathrm{t}) \qquad (12)$$

2.1 Conditions of Equilibrium

From Equation (7) to (12), as

$$\frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dV}{dt} = 0$$

Therefore, the feasible region for the system is given by (S*, E*, I*, R*, V*)

$$\mathrm{S}^* = \frac{\Lambda}{\theta_1 + \mu}, \mathrm{E}^* = 0, \mathrm{I}^* = 0, \mathrm{R}^* = 0, \mathrm{V}^* = \frac{\theta_1 \Lambda}{\mu(\theta_1 + \mu)}$$

$$\omega = [(S^*, E^*, I^*, R^*, V^*) \in R^{5+} : S^* + E^* + I^* + R^* + V^* \leq \frac{\Lambda}{\mu}$$

Thus, it sufficient to consider solutions in the region ω. The solutions of the initial value problem starting in ω and defined by (7)-(11) exist and are unique on a maximal interval [8].

ISSN 2515-8260 Volume 07, Issue 03, 2020

Since the solution remains bounded in the positively invariant region ω, the maximal interval defined is [0, 1). So, the initial value problem is both well-posed and is positive.
The above system always has the disease-free equilibrium

$$\left(\frac{\Lambda}{\theta_1+\mu}, 0, 0, 0, \frac{\theta_1\Lambda}{\mu(\theta_1+\mu)}\right)$$

The characteristic equation of the system of equations using the Jacobian matrix method is:

$$\_\frac{(-\lambda-\mu)(\theta1+\lambda+\mu)(-\alpha\beta\Lambda-(-\gamma-\theta3-\lambda-\mu)(\theta1+\mu)(\alpha+\theta2+\lambda+\mu))(-\theta4-\lambda-\mu-\sigma)}{\theta1+\mu}$$

The Characteristic Values are:

$\lambda_1 = -\mu,$

$\lambda_2 = -\theta_1 - \mu,$

$\lambda_3 = -\theta_4 - \mu - \sigma$

$\lambda_{4,5} = \frac{-P \pm Q}{R}$

where, $P = \gamma\theta_1 + \theta_1\theta_2 + \theta_1\theta_3 + \gamma\mu + 2\theta_1\mu + \theta_2\mu + \theta_3\mu + 2\mu^2 + \alpha(\theta_1 + \mu)$

$$Q = \sqrt{(\theta_1+\mu)}\sqrt{(\alpha\text{^}2\,(\theta_1+\mu) + (\gamma-\theta_2+\theta_3)^2\,(\theta_1+\mu) - 2\alpha(-\theta_1\theta_2) + \theta_1\theta_3) - 2\beta\Lambda - \theta_2\mu + \theta_3\mu + \gamma(\theta_1+\mu))}$$

$R = 2(\theta_1 + \mu)$

On simplification, $Q = \left(\alpha(\theta_1 + \mu) + (\theta_1 + \mu)(\gamma - \theta_2 - \theta_3)\right)^2 + 4\beta\gamma\Lambda(\theta_1 + \mu) > 0$

Therefore, $Q > 0$. Hence roots can't be complex. Since $\lambda_1<0$, $\lambda_2<0$, $\lambda_3<0$, $\lambda_5<0$ and we find the condition for $\lambda_6 <0$, as $Q \geq 0$ and for the stability of the system, the real part of all Eigen values must be negative, Hence, $Q < P$. We solve the following equations by substituting the values of Q and P,

$$R_0 = \frac{\alpha\beta\Lambda}{(\theta_1+\mu)(\alpha+\theta_2+\mu)(\gamma+\theta_3+\mu)} < 1\,,$$

is called basic Reproduction number. The endemic equilibrium will exist in the population only if infected individuals I > 0. If $R_0>1$, then ω has another unique positive endemic equilibrium P^*= (S*, E*, I*, R*, V*) On solving, Equation (9) to (15).

We obtain a quadratic equation in I(t) as :

$$I(I\beta + \theta_1 + \mu)(\alpha + \theta_2 + \mu)(\gamma + \theta_3 + \mu) = I\alpha\beta\Lambda$$

And the solutions are obtained by substituting the value of β in terms of R_0

$$\beta = \frac{R_0(\theta_1 + \mu)(\alpha + \theta_2 + \mu)(\gamma + \theta_3 + \mu)}{\alpha\Lambda}$$

:

ISSN 2515-8260 Volume 07, Issue 03, 2020

Either, $I=0$ or

$$I = \frac{(-1 + R_0)\alpha\Lambda}{R_0(\alpha + \theta_2 + \mu)(\gamma + \theta_3 + \mu)}$$

Therefore, for $R_0 > 1$ the system will have endemic equilibrium ($I > 0$).

The disease-free equilibrium DFE $\left(\frac{\Lambda}{\theta_1+\mu}, 0, 0, 0, \frac{\theta_1\Lambda}{\mu(\theta_1+\mu)}\right)$ of (1) - (8) is globally asymptotically stable in ω, if $R_0 \leq 1$ and is unstable if $R_0 > 1$. As V(t) doesn't appear in equations (7)-(10). So, the feasible region for $\eta = ((S, E, I, R) \in R^{4+}: S+E+I+R \leq \Lambda/(\theta_1+\mu)$ is positively invariant for (7) - (10). Consider R_0 as defined above. So, the disease-free equilibrium DFE= $(\Lambda/(\theta_1+\mu),0,0,0)$ exists for all values of parameters. A unique equilibrium exists for (S*,E*,I*,R*).

The other solution from solving equation (7) to (11) :

$$S = \frac{\Lambda}{R_0(\theta_1 + \mu)}$$

$$E = \frac{(-1 + R_0)\Lambda}{R_0(\alpha + \theta_2 + \mu)}$$

$$I = \frac{(-1 + R_0)\alpha\Lambda}{R_0(\alpha + \theta_2 + \mu)(\gamma + \theta_3 + \mu)}$$

$$R = \frac{(-1 + R_0)\alpha\gamma\Lambda}{R_0(\alpha + \theta_2 + \mu)(\gamma + \theta_3 + \mu)(\theta_4 + \mu + \sigma)}$$

Therefore for $R_0 > 1$, the solution is endemic as $I>0$.

Theorem 1: The DFE = $(\Lambda/(\theta_1+\mu), 0, 0, 0)$ of (7) - (10) is globally asymptotically stable in η if $R_0 \leq 1$and is unstable if $R_0 > 1$[16].Consider a Lypunaov function

$$L = \alpha E + (\mu + \alpha + \theta_2) I$$

If $R_0 \leq 1$, using (8) and (9) and $S \leq \Lambda / (\mu+\theta_1)$, we obtain:

$$\dot{L} = \alpha \dot{E} + (\mu + \alpha + \theta_2) \dot{I}$$
$$\leq \Lambda \mu (1-1/R_0) I \alpha \beta \leq 0$$

and $\dot{L}= 0$ if and only if $I = 0$. Therefore, by La Salle's Invariance principle [9], the above system η is globally stable.

Theorem 2: *If $R_0 > 1$, then the region $D - \{(S, E, I, R)/I = 0\}$ is a globally asymptotically stable region for the endemic equilibrium P^*.*

The R related terms can be removed as we have assumed that population size is constant. The proof is available in Global stability in some SEIR epidemic models [14].

3. Numerical Analysis of Modified SEIR Model with Vaccination

Numerical investigation of the SIR model has been done commonly to understand the pattern of the solution [15, 18]. We have used Wolfram Mathematica's NDSolve commands to find the solution to the above non-linear simultaneous differential equations. Most (approximately 80%) of those who experience Covid-19 symptoms recover from the disease and do not need hospital care, while about 15% become critically ill and need oxygen assistance. Around 5% become seriously ill and need intensive care[17]. In more than 30% of cases with COVID-19

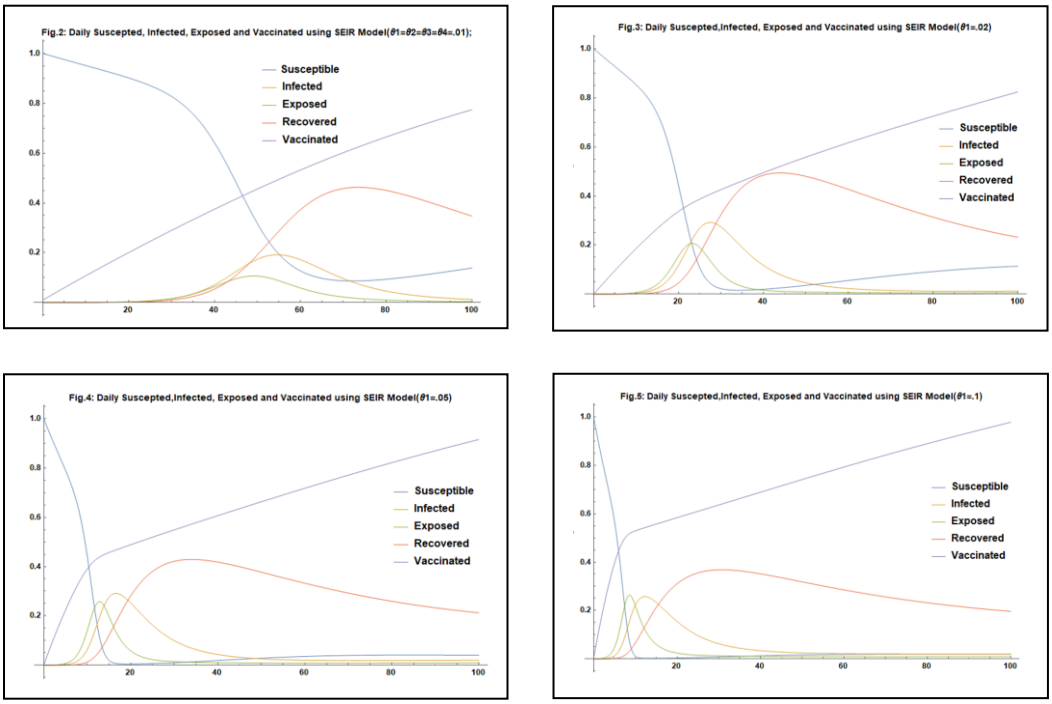
ISSN 2515-8260 Volume 07, Issue 03, 2020

[11], co-morbidity is present. The vaccinations at different stages will play a vital role both in preventing and curing the disease. We will plot the graphs of Susceptible *S[t]*, Exposed *E[t]*, Infected *I[t]*, and Recovered *R[t]* by varying the different parameters related to vaccination.

We begin by plotting a graph of the equations (7) to (12). Different cases are discussed related to the values of θ_i (i=1,4).

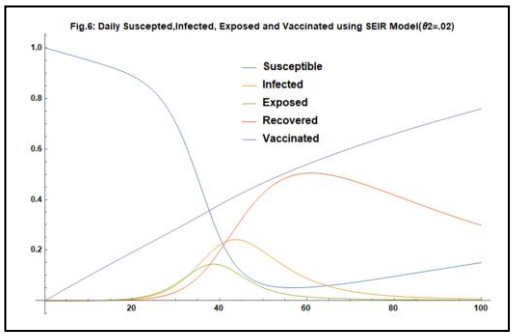
Let us define the parameters θ_1, θ_2, θ_3, and θ_4 as .01 (100 vaccinated days). We assume that in 100 days vaccinations are given to the population of the different compartments and $R_0 = 2.5$, then $\alpha = .3$ (Incubation rate), $\sigma = .011$ (rate of losing immunity), $\gamma = .13$(rate of recovery), μ=.000005(rate of death)(Fig.2).

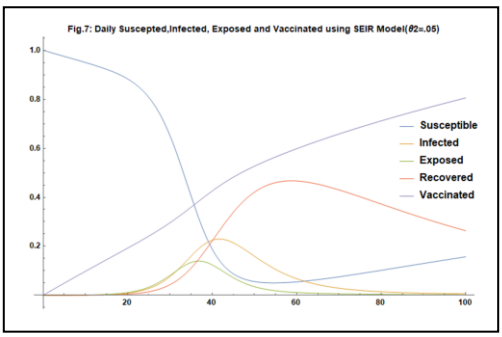
Case I: The corresponding values of θ_1 =.01, .02, .05 and 0.01 are considered in **Fig.2 - 5**. It is observed that the vaccination *V(t)* is rising steadily and there are significant variations in the graphs of *S(t)*. The graph of *S(t)* indicates that when the rate of vaccination for susceptible increases and takes value 0.01, 0.02, 0.05, and 0.1, the susceptible decreases drop down significantly and becomes negligible after 10 days. in case of $\theta_1 = 0.1$ .The graphs of *E(t)* and *I(t)* move towards the left side indicating that the Infected and exposed population will get rid of infection comparatively early with an increase in θ_1.

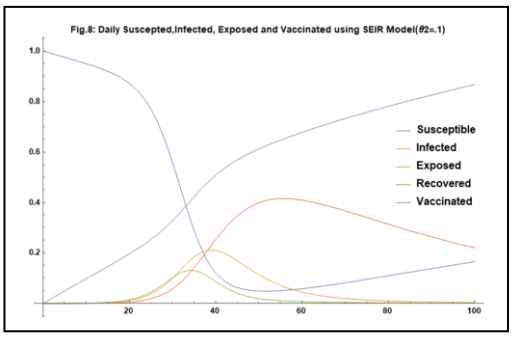


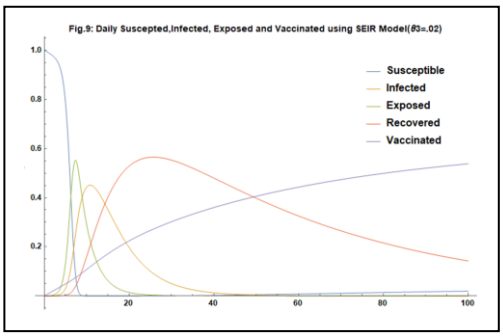
Case II: In **Fig. 6 - 8**, the value for θ_2 = .02, .05 and 0.01 is considered. It is observed that the vaccination *V(t)* rises quickly while become steadily after the Exposed *E(t)* starts decreasing. The graph of *S(t)* indicates that when the rate of vaccination for exposed increases and takes value 0.01, 0.02, 0.05, and 0.1, the susceptible decreases drop down significantly and becomes negligible after 10 days in case of $\theta_1 = 0.1$. The graphs of *E(t)* and *I(t)* move towards the left side indicating that the infected and exposed population will get rid of infection comparatively earlier and also the peak is also flattened which indicates less severity of exposure and infection with the increase in θ_2.

ISSN 2515-8260 Volume 07, Issue 03, 2020

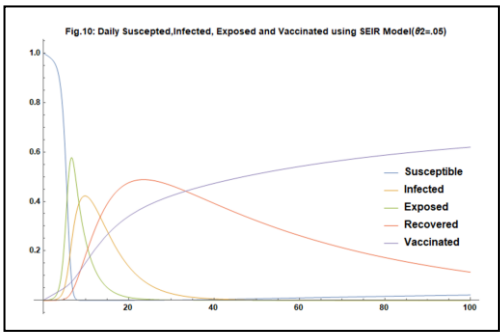


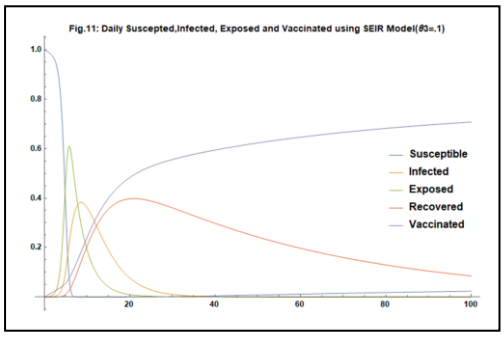






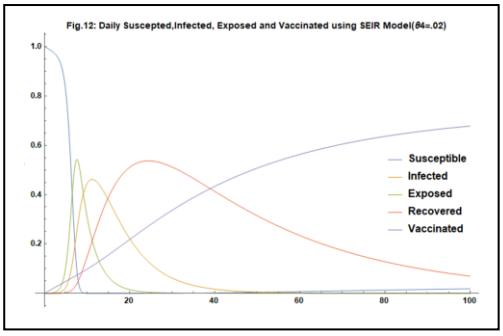
Case III: **Fig. 9 - 11**, the plots of S(t), E(t), I(t) and V(t) and value for θ_3 = .02, .05 and 0.01. It is observed that the vaccination *V(t)* rises steadily and with time it slows down. There is no significant change in the graph of *S(t)* but the peak of exposed *E(t)* and infected *I(t)* is flattened which means that the disease is spreading not more and fast with increasing values of θ_3 =0.01, 0.02, 0.05 and 0.1. The θ_3 is the rate at which infected are being given vaccination. The graphs of *E(t)* and *I(t)* move towards the left side indicating that infected and exposed populations will get rid of infection comparatively earlier and hence recovered population.

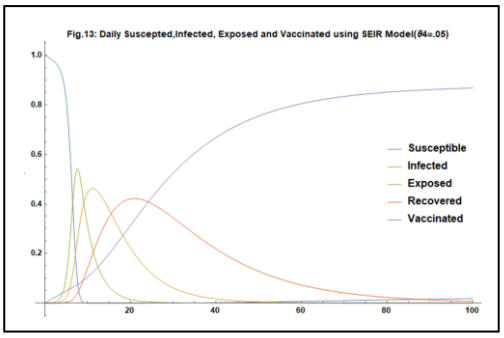


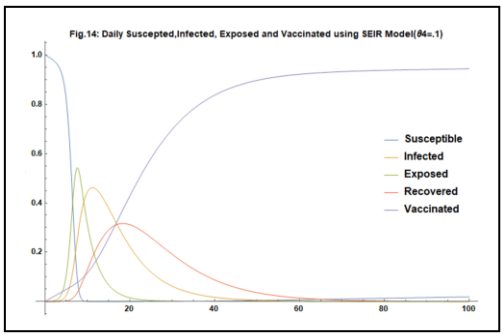


ISSN 2515-8260 Volume 07, Issue 03, 2020

Case IV: **Fig. 12 - 14**, the plots of S(t), E(t), I(t) and V(t) and value for θ_4 = .02, .05 and 0.01. It is observed that as in the above graphs the vaccination *V(t)* rises steadily and with time it slows down. There is no significant change in the graph of *S(t)* and *E(t)* and I(t) but the peak of recovery R(t) is flattened as the values of θ_4=0.01, 0.02, 0.05, and 0.1. The θ_4 is the rate at which recovered are given vaccination. The graphs of *R(t)* move towards the left side indicating that a recovered population will get rid of infection due to the induced immunity of vaccination.







4. Conclusion

The four parameters θ_1, θ_2, θ_3, and θ_4 related to the Vaccination compartment and denote the rate of vaccination for Susceptible, Exposed, Infected, and Recovered compartments. It is found that the increase in the rate of administering vaccination not only flattens the peak of *S(t)*, *E(t)*, *I(t)*, and *R(t)* but also delays the time of peak. The susceptible population is vaccinated selectively to control the spread of the disease quickly and reduce the mortality rate as it has a slow effect if the entire population is considered in one go. Those susceptibles who are constantly at the risk of being exposed, who are already infected or in the recovering stage(losing immunity), wherever mortality rate is higher must be chosen on priority. The recovered population must not be left out for vaccination as it directly becomes part of susceptible after losing its natural immunity in a limited time (Fig 12-14), making vaccinated related immunity mandatory.

REFERENCES

[1] Linda Allen (2017), A primer on stochastic epidemic models: Formulation, numerical simulation, and analysis. Infectious Disease Modeling. infectious disease Modelling Volume 2(2), 128-142.

[2] Francis Benyah (2012) World Journal of Modelling and Simulation, 8(3)194-204.

[3] Ross Beckley, Cametria Weatherspoon, Michael Alexander, Marissa Chan-dler, Anthony Johnson, and Ghan S Bhatt (2013). Modeling epidemics with differential equations(PDF). Tennessee State University Internal Re-port (Retrieved on 9.12.2020).

[4] J. M. Carcione, J. E. Santos, C. Bagaini, and J. Ba (2020), A simulation of a COVID-19 epidemic based on a deterministic SEIR model. arXiv preprintarXiv:2004.03575.

[5] Nanshan Chen, Min Zhou, Xuan Dong, Jieming Qu, et al (2020), Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. Lancet. 395 (10223):507–513.

[6] F. Croccolo, and H.E.Roman (2020), Spreading of infections on random graphs: A percolation-type model for COVID-19. Chaos, Solitons and Fractals, 139, 110077.

[7] O. Diekmann, H Heesterbeek, T Britton (2013), Mathematical Tools for Understanding Infectious Disease Dynamics. Princeton Series in Theoretical and Computational Biology. Princeton, NJ: Princeton University Press.

[8] M. Draief, A. Ganesh, L. Massouili (2008), Thresholds for virus spread on networks, Ann. Appl. Prob. 18 (2) 359–378.

[9] J.K. Hale, Ordinary (1980), Differential Equations, second ed., Krieger, Basel.

[10] H. W. Hethcote (2000), The mathematics of infectious diseases. SIAM re-view, 42(4), 599-653.

[11] C Huang, Y Wang, LiX, et al.(2020), Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet. 395(10223):497–506.

[12] M. J. Keeling, P. Rohani (2008), Modeling Infectious Diseases in Humans and Animals. Princeton, NJ; Oxford: Princeton University Press.

[13] W Kermack, A McKendrick (1991), Contributions to the mathematical theory of epidemics-I. Bulletin of Mathematical Biology. 53 (1–2): 33–5.

[14] Michael Y Li, and Liancheng Wang (2002) "Global stability in some SEIR epidemic models." Mathematical approaches for emerging and reemerging infectious diseases: models, methods, and theory. Springer, New York, NY. 295-311

[15] Z. Liu, P. Magal, O. Seydi, G. Webb (2020), A COVID-19 epidemic model with latency period, Infectious Disease Modelling, 5, 323-337, ISSN 2468-0427, https://doi.org/10.1016/j.idm.2020.03.003.

ISSN 2515-8260 Volume 07, Issue 03, 2020

[16] Bimal Kumar Mishra, Navnit Jha (2010) SEIQRS model for the transmission of malicious objects in the computer network, Applied Mathematical Modelling, 34(3)710-715.

[17] S Murthy, CD Gomersall, RA Fowler (2020), Care for Critically Ill Patients With COVID-19. JAMA.2020;323(15):1499–1500.doi: 10.1001/ jama.2020.3633

[18] Barbara Nussbaumer-Streit, Verena Mayr, Andreea Iulia Dobrescu, Andrea Chapman, Emma Persad, Irma Klerings, Gernot Wagner, et al (2020).Quarantine alone or in combination with other public health measures to control COVID-19: a rapid review. Cochrane Database of Systematic Reviews 9.

[19] https://www.cdc.gov/coronavirus/2019-nCoV/index.html Retreived on 9.12.2020

[20] https://www.worldometers.info/coronavirus/ Retreived on 9.12.2020